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(54) Title: BIOMARKER IDENTIFICATION

(57) Abstract: Disclosed are method and apparatus for identifying biomarkers and in particular for identifying biomarkers for use in making clinical assessments, such as early diagnostic, diagnostic, disease stage, disease severity, disease subtype, response to therapy or prognostic assessments. In one particular example, the techniques are applied to allow assessments of patients suffering from, suspected of suffering from, or with clinical signs of SIRS (Systemic Inflammatory Response Syndrome) being either infection-negative SIRS or infection-positive SIRS.

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BIOMARKER IDENTIFICATION

Related Application

[0001] This application claims priority to Australian Provisional Application No. 2013902243 entitled "Biomarker Identification", filed on 20 June 2013, the subject matter of which is hereby incorporated herein by reference in its entirety.

Field of the Invention

[0002] The present invention relates to a method and apparatus for identifying biomarkers and in particular for identifying biomarkers for use in making clinical assessments, such as early diagnostic, diagnostic, disease stage, disease severity, disease subtype, response to therapy or prognostic assessments. In one particular example, the techniques are applied to allow assessments of patients suffering from, suspected of suffering from, or with clinical signs of SIRS (Systemic Inflammatory Response Syndrome) being either infection-negative SIRS (inSIRS) or infection-positive SIRS (ipSIRS).

Description of the Prior Art

[0003] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgement or admission or any form of suggestion that the prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

[0004] The analysis of gene expression products for diagnostic purposes is known. Such analysis requires identification of one or more genes that can be used to generate a signature for use in distinguishing between different conditions. However, such identification can require the analysis of many gene expression products, which can be mathematically complex, computationally expensive and hence difficult. Much of the biomarker discovery process is devoted to identifying a subset of the data that may have relevant import, from which a signature is derived using a combination of these values to produce a model for diagnostic or prognostic use.

[0005] WO2004044236 describes a method of determining the status of a subject. In particular, this is achieved by obtaining subject data including respective values for each of a number of parameters, the parameter values being indicative of the current biological status of the subject. The subject data are compared to predetermined data that includes values for at least some of the parameters and an indication of the condition. The status of the subject, and in particular, the presence and/or absence of the one or more conditions, can then be determined in accordance with the results of the comparison.

Summary of the Invention

[0006] In one aspect, the present invention provides apparatus for identifying biomarkers, the apparatus including an electronic processing device that:

uses reference data from a plurality of individuals to define a number of groups of individuals, the reference data including measurements of the activity of a plurality of reference biomarkers;

uses a plurality of analysis techniques to identify a number of potential biomarkers from the plurality of reference biomarkers that are potentially useful for distinguishing the groups of individuals, allowing the potential biomarkers to be used in generating signatures for use in clinical assessments.

[0007] Suitably, the electronic processing device, for each analysis technique:

using the analysis technique, identifies a number of reference biomarkers that best distinguish the groups of individuals;

determines if the predictive performance of the identified reference biomarkers exceeds a predetermined threshold; and,

in response to a successful determination, determines the identified reference biomarkers to be potential biomarkers.

[0008] In some embodiments, the number of reference biomarkers is at least one of:

less than 10;
more than 1;
between 2 and 8; and,
5.

[0009] In some embodiments, the predetermined threshold is at least one of:

at least 90%;
at least 85%; and,
at least 80%.

[0010] Suitably, the electronic processing device:

adds potential biomarkers to a potential biomarker collection; and,
removes the potential biomarkers from a reference biomarker collection.

[0011] Suitably, for each of a plurality of analysis techniques the electronic processing device repeatedly identifies reference biomarkers as potential biomarkers until the predictive performance of the identified reference biomarkers falls below the predetermined threshold.

[0012] The electronic processing device may iteratively identify potential biomarkers.

[0013] In some embodiments, the electronic processing device uses a number of iterations including at least one of:

at least 100;

at least 500;
at least 1000;
at least 2000; and,
at least 5000.

[0014] The electronic processing device may repeatedly determine potential biomarkers until a predetermined number of potential biomarkers are identified.

[0015] Suitably, the predetermined number of potential biomarkers includes at least one of:

at least 100;
less than 500;
about 200.

[0016] In some embodiments, the analysis techniques include at least one of:

regression techniques;
correlation analysis; and,
a combination of regression and correlation techniques.

[0017] Suitably, the analysis techniques include:

sparse PLS;
random forest; and,
support vector machines.

[0018] In some embodiments, the electronic processing device:

removes a validation subgroup from the reference data prior to determining the potential biomarkers;

determines the potential biomarkers using the reference data without the validation subgroup; and,

uses the validation subgroup to validate at least one of:

the potential biomarkers; and,
signatures including a number of the potential biomarkers.

[0019] In some embodiments, the processing system determines the number of groups by classifying the individuals using at least one of:

an indication of a presence, absence, degree, or stage, or progression of a condition;

phenotypic traits associated with the individuals;
genetic information associated with the individuals;
biomarkers associated with the individuals.

[0020] Suitably, the processing system determines groups at least in part using input commands from a user.

[0021] The reference data may include time series data indicative of the progression of a condition.

[0022] In some embodiments, the time series data is indicative of whether a condition that is at least one of:

improving;
worsening; and,
static.

[0023] The reference data may include for each of the individuals an indication of at least one of:

an activity of each of the reference biomarkers;
a degree of a condition;
a stage of a condition;
a presence of a condition;
an absence of a condition;
an indication of a condition progression;
phenotypic information;
genetic information; and,
a SOFA score.

[0024] In some embodiments, the electronic processing device identifies a number of potential biomarkers for use as signature biomarkers, the signature biomarkers being used in generating the signatures.

[0025] Suitably, the electronic processing device:

determines a clinical assessment; and,
identifies the signature biomarkers for the clinical assessment.

[0026] Suitably, the electronic processing device:

determines second groups of individuals relevant to the clinical assessment;

using a second analysis technique, identifies a number of the potential biomarkers that best distinguish the second groups of individuals;

determines if the predictive performance of the identified potential biomarkers exceeds a predetermined threshold; and,

in response to a successful determination, determines the identified potential biomarkers to be signature biomarkers.

[0027] In some embodiments, the electronic processing device, in response to an unsuccessful determination:

modifies parameters of the second analysis technique; and,

uses the second analysis technique to identify alternative potential biomarkers.

[0028] In some embodiments, the electronic processing device:

determines if the identified potential biomarkers are to be excluded; and,
in response to a successful determination:

removes the potential biomarkers from a potential biomarker database; and, uses the second analysis technique to identify alternative potential biomarkers for use as signature biomarkers.

[0029] Suitably, the second analysis technique includes at least one of:

ordinal regression and,

support vector machines.

[0030] In some embodiments, the signatures are indicative of:

activities of each of a number of signature biomarkers; and,

at least one of:

a SOFA score; and,

a presence, absence, degree, or stage, or progression of a condition.

[0031] The signatures may be indicative of a presence, absence, degree, or stage or progression of at least one of:

infection-negative SIRS; and,

infection-positive SIRS.

[0032] In some embodiments, activities of at least some of the potential biomarkers are indicative of at least one of:

a presence, absence, degree, or stage, or progression of SIRS;

a healthy diagnosis;

a presence, absence, degree, or stage, or progression of infection positive SIRS; and,

a presence, absence, degree, or stage, or progression of infection negative SIRS.

[0033] Suitably, an activity of biomarkers are indicative of a level or abundance of a molecule selected from one or more of:

A nucleic acid molecule;

A proteinaceous molecule;

An amino acid

A carbohydrate;

A lipid;

A steroid;

An inorganic molecule;

An ion;

A drug;

A chemical;

A metabolite;

A toxin;

A nutrient;

A gas;

A cell;

A pathogenic organism; and,

A non pathogenic organism.

[0034] In another aspect, the present invention provides a method for determining the likelihood of the presence or absence of a condition selected from a healthy condition (e.g., a normal condition or one in which inSIRS and ipSIRS are absent), SIRS generally (i.e., not distinguishing between inSIRS or ipSIRS), inSIRS or ipSIRS, or to assess the likelihood of the presence, absence or risk of development of a stage of ipSIRS (e.g., a stage of ipSIRS with a particular severity), the method comprising: (1) correlating a reference Inflammatory Response Syndrome (IRS) biomarker profile with the presence or absence of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; (2) obtaining an IRS biomarker profile of a sample from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group consisting of: TLR5; CD177; VNN1; UBE2J1; IMP3; RNASE2//LOC643332; CLEC4D; C3AR1; GPR56; ARG1; FCGR1A//FCGR1B//FCGR1C; C11orf82; FAR2; GNLY; GALNT3; OMG; SLC37A3; BMX//HNRPDL; STOM; TDRD9; KREMEN1; FAIM3; CLEC4E; IL18R1; ACER3; ERLIN1; TGFBR1; FKBP5//LOC285847; GPR84; C7orf53; PLB1; DSE; PTGDR; CAMK4; DNAJC13; TNFAIP6; FOXD4L3//FOXD4L6//FOXD4//FOXD4L1//FOXD4L2//FOXD4L4//FOXD4L5; MMP9//LOC100128028; GSR; KLRF1; SH2D1B; ANKRD34B; SGMS2; B3GNT5//MCF2L2; GK3P//GK; PFKFB2; PICALM; METTL7B; HIST1H4C; C9orf72; HIST1H3I; SLC15A2; TLR10; ADM; CD274; CRIP1; LRRN3; HLA-DPB1; VAMP2; SMPDL3A; IFI16; JKAMP; MRPL41; SLC1A3; OLFM4; CASS4; TCN1; WSB2; CLU; ODZ1; KPNA5; PLAC8; CD63; HPSE; C1orf161; DDAH2; KLRK1//KLRC4; ATP13A3; ITK; PMAIP1; LOC284757; GOT2; PDGFC; B3GAT3; HIST1H4E; HPGD; FGFBP2; LRRC70//IPO11; TMEM144//LOC285505; CDS2; BPI; ECHDC3; CCR3; HSPC159; OLAH; PPP2R5A//SNORA16B; TMTC1; EAF2//HCG11//LOC647979; RCBTB2//LOC100131993; SEC24A//SAR1B; SH3PXD2B; HMGB2; KLRD1; CHI3L1; FRMD3; SLC39A9; GIMAP7; ANAPC11; EXOSC4; gene for IL-1beta-regulated neutrophil survival protein as set forth in GenBank Accession No. AF234262; INSIG1; FOLR3//FOLR2; RUNX2; PRR13//PCBP2; HIST1H4L; LGALS1; CCR1; TPST1; HLA-DRA; CD163; FFAR2; PHOSPHO1; PPIF; MTHFS; DNAJC9//FAM149B1//RPL26; LCN2; EIF2AK2; LGALS2; SIAE; AP3B2; ABCA13; gene for transcript set forth in GenBank Accession No. AK098012; EFCAB2; HIST1H2AA; HINT1; HIST1H3J; CDA; SAP30; AGTRAP; SUCNR1; MTRR; PLA2G7; AIG1; PCOLCE2; GAB2; HS2ST1//UBA2; HIST1H3A; C22orf37; HLA-DPA1; VOPP1//LOC100128019; SLC39A8; MKI67; SLC11A1; AREG; ABCA1; DAAM2//LOC100131657; LTF; TREML1; GSTO1; PTGER2; CEACAM8; CLEC4A; PMS2CL//PMS2; RETN; PDE3B; SULF2;

NEK6//LOC100129034; CENPK; TRAF3; GPR65; IRF4; MACF1; AMFR; RPL17//SNORD58B; IRS2; JUP; CD24; GALNT2; HSP90AB1//HSP90AB3P//HSP90AB2P; GLT25D1; OR9A2; HDHD1A; ACTA2; ACPL2; LRRFIP1; KCNMA1; OCR1; ITGA4//CERKL; EIF1AX//SCARNA9L//EIF1AP1; SFRS9; DPH3; ERGIC1; CD300A; NF-E4; MINPP1; TRIM21; ZNF28; NPCDR1; gene for protein FLJ21394 as set forth in GenBank Accession No. BC013935; gene for transcript set forth in GenBank Accession No. AK000992; ICAM1; TAF13; P4HA1//RPL17; C15orf54; KLHL5; HAL; DLEU2//DLEU2L; ANKRD28; LY6G5B//CSNK2B; KIAA1257//ACAD9//LOC100132731; MGST3; KIAA0746; HSPB1//HSPBL2; CCR4; TYMS; RRP12//LOC644215; CCDC125; HIST1H2BM; PDK4; ABCG1; IL1B; THBS1; ITGA2B; LHFP; LAIR1//LAIR2; HIST1H3B; ZRANB1; TIMM10; FSD1L//GARNL1; HIST1H2AJ//HIST1H2AI; PTGS1; gene for transcript set forth in GenBank Accession No. BC008667; UBE2F//C20orf194//SCLY; HIST1H3C; FAM118A; CCRL2; E2F6; MPZL3; SRXN1; CD151; HIST1H3H; FSD1L; RFESD//SPATA9; TPX2; S100B; ZNF587//ZNF417; PYHIN1; KIAA1324; CEACAM6//CEACAM5; APOLD1; FABP2; KDM6B//TMEM88; IGK@//IGKC//IGKV1-5//IGKV3D-11//IGKV3-20//IGKV3D-15//LOC440871//LOC652493//LOC100291464//LOC652694//IGKV3-15//LOC650405//LOC100291682; MYL9; HIST1H2BJ; TAAR1; CLC; CYP4F3//CYP4F2; CEP97; SON; IRF1; SYNE2; MME; LASS4; DEFA4//DEFA8P; C7orf58; DYNLL1; gene for transcript set forth in GenBank Accession No. AY461701; MPO; CPM; TSHZ2; PLIN2; FAM118B; B4GALT3; RASA4//RASA4P//RASA4B//POLR2J4//LOC100132214; CTSL1//CTSLL3; NP; ATF7; SPARC; PLB1; C4orf3; POLE2; TNFRSF17; FBXL13; PLEKHA3; TMEM62//SPCS2//LOC653566; RBP7; PLEKHF2; RGS2; ATP6V0D1//LOC100132855; RPIA; CAMK1D; IL1RL1; CMTM5; AIF1; CFD; MPZL2; LOC100128751; IGJ; CDC26; PPP1R2//PPP1R2P3; IL5RA; ARL17P1//ARL17; ATP5L//ATP5L2; TAS2R31; HIST2H2BF//HIST2H3D; CALM2//C2orf61; SPATA6; IGLV6-57; C1orf128; KRTAP15-1; IFI44; IGL@//IGLV1-44//LOC96610//IGLV2-23//IGLC1//IGLV2-18//IGLV5-45//IGLV3-25//IGLV3-12//IGLV1-36//IGLV3-27//IGLV7-46//IGLV4-3//IGLV3-16//IGLV3-19//IGLV7-43//IGLV3-22//IGLV5-37//IGLV10-54//IGLV8-61//LOC651536; gene for transcript set forth in GenBank Accession No. BC034024; SDHC; NFXL1; GLDC; DCTN5; and KIAA0101//CSNK1G1

[0035] In some embodiments, the method determines the likelihood that SIRS or a healthy condition is present or absent in the subject, and wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the presence or absence of SIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from CD177, CLEC4D, BMX, VNN1, GPR84, ARG1, IL18R1, ERLIN1, IMP3, TLR5, UBE2J1, GPR56, FCGR1A, SLC1A3, SLC37A3, FAIM3, C3AR1, RNASE2, TNFAIP6, GNLY, OMG, FAR2, OLAH, CAMK4, METTL7B, B3GNT5, CLEC4E, MMP9, KREMEN1, GALNT3, PTGDR, TDRD9, GK3P, FKBP5, STOM, SMPDL3A, PFKFB2, ANKRD34B, SGMS2, DNAJC13, LRRN3, SH2D1B, C1orf161, HIST1H4C, IFI16, ACER3, PLB1, C9orf72, HMGB2, KLRK1, C7orf53, GOT2, TCN1, DSE, CCR3, CRIP1, ITK,

KLRF1, TGFBR1, GSR, HIST1H4E, HPGD, FRMD3, ABCA13, C11orf82, PPP2R5A, BPI, CASS4, AP3B2, ODZ1, TMTC1, ADM, FGFBP2, HSPC159, HLA-DRA, HIST1H3I, TMEM144, MRPL41, FOLR3, PICALM, SH3PXD2B, DDAH2, HLA-DPB1, KPNA5, PHOSPHO1, TPST1, EIF2AK2, OR9A2, OLFM4, CD163, CDA, CHI3L1, MTHFS, CLU, ANAPC11, JUP, PMAIP1, GIMAP7, KLRD1, CCR1, CD274, EFCAB2, SUCNR1, KCNMA1, LGALS2, SLC11A1, FOXD4L3, VAMP2, ITGA4, LHFP, PRR13, FFAR2, B3GAT3, EAF2, HPSE, CLC, TLR10, CCR4, HIST1H3A, CENPK, DPH3, HLA-DPA1, ATP13A3, DNAJC9, S100B, HIST1H3J, 110, RPL17, C15orf54, LRRC70, IL5RA, PLA2G7, ECHDC3, HINT1, LCN2, PPIF, SLC15A2, PMS2CL, HIST1H2AA, CEACAM8, HSP90AB1, ABCG1, PDGFC, NPCDR1, PDK4, GAB2, WSB2, FAM118A, JKAMP, TREML1, PYHIN1, IRF4, ABCA1, DAAM2, ACPL2, RCBTB2, SAP30, THBS1, PCOLCE2, GPR65, NF-E4, LTF, LASS4, B4GALT3, RETN, TIMM10, IL1B, CLEC4A, SEC24A, RUNX2, LRRFIP1, CFD, EIF1AX, ZRANB1, SULF2, EXOSC4, CCDC125, LOC284757, ANKRD28, HIST1H2AJ, CD63, PLIN2, SON, HIST1H4L, KRTAP15-1, DLEU2, MYL9, FABP2, CD24, MACF1, GSTO1, RRP12, AIG1, RASA4, FBXL13, PDE3B, CCRL2, C1orf128, E2F6, IL1RL1, CEACAM6, CYP4F3, 199, TAAR1, TSHZ2, PLB1, UBE2F; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and (3) determining a likelihood of the subject having or not having the healthy condition or SIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0036] Suitably, the method determines the likelihood that inSIRS, ipSIRS or a healthy condition is present or absent in the subject, wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS, ipSIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, B3GAT3, CD300A, OCR1, PTGER2, LGALS1, HIST1H4L, AMFR, SIAE, SLC39A8, TGFBR1, GAB2, MRPL41, TYMS, HIST1H3B, MPZL3, KIAA1257, OMG, HIST1H2BM, TDRD9, C22orf37, GALNT3, SYNE2, MGST3, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, HSPB1, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, KREMEN1, IRS2, APOLD1, RBP7, DNAJC13, ERGIC1, FSD1L, TLR5, TMEM62, SDHC, C9orf72, NP, KIAA0746, PMAIP1, DSE, SMPDL3A, DNAJC9, HIST1H3H, CDC26, CRIP1, FAR2, FRMD3, RGS2, METTL7B, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, IRF1, C7orf53, IGK@, RNASE2, FCGR1A, SAP30, PMS2CL, SLC11A1, AREG, PLB1, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, CPM, CCDC125, GPR56, PPP1R2, 110, ACPL2, HIST1H3A, C7orf58, IRF4, ANAPC11, HIST1H3J, KLRD1, GPR84, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, HSP90AB1, HPGD, IFI16, CD177, TAS2R31, CD163, B4GALT3, EIF1AX, CYP4F3, HIST1H2AA, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference

IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS, ipSIRS or a healthy condition the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0037] In some embodiments, the method determines the likelihood that inSIRS or ipSIRS is present or absent in the subject, wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS or ipSIRS, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from C11orf82, PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, FOXD4L3, WSB2, CD63, CD274, B3GAT3, CD300A, OCR1, JKAMP, TLR10, PTGER2, PDGFC, LGALS1, HIST1H4L, AGTRAP, AMFR, SIAE, 200, SLC15A2, SLC39A8, TGFBR1, DDAH2, HPSE, SUCNR1, MTRR, GAB2, P4HA1, HS2ST1, MRPL41, TYMS, RUNX2, GSTO1, LRRC70, HIST1H3B, RCBTB2, MPZL3, KIAA1257, AIG1, NEK6, OMG, HIST1H2BM, TDRD9, GALNT3, ATP13A3, C22orf37, SYNE2, ADM, MGST3, PDE3B, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, KLHL5, EXOSC4, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, TPX2, PCOLCE2, HSPB1, EAF2, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, ACTA2, PTGS1, KREMEN1, IRS2, TAF13, FSD1L, APOLD1, RBP7, DNAJC13, SEC24A, ERGIC1, FSD1L, TLR5, MKI67, TMEM62, CLEC4A, SDHC, C9orf72, NP, CLU, ABCA1, KIAA0746, PMAIP1, DSE, CMTM5, SMPDL3A, DNAJC9, HDHD1A, HIST1H3H, CDC26, ICAM1, LOC100128751, FAR2, CRIP1, MPZL2, FRMD3, CTSL1, METTL7B, RGS2, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, ITGA2B, C7orf53, IRF1, 268, IGK@, RNASE2, FCGR1A, UBE2F, SAP30, LAIR1, PMS2CL, SLC11A1, PLB1, AREG, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, PLA2G7, GALNT2, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, 199, CPM, CCDC125, SULF2, LTF, GPR56, MACF1, PPP1R2, DYNLL1, LCN2, FFAR2, SFRS9, IGJ, FAM118B, 110, ACPL2, HIST1H3A, C7orf58, ANAPC11, HIST1H3J, IRF4, MPO, TREML1, KLRD1, GPR84, CCRL2, CAMK1D, CCR1, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, CD24, HSP90AB1, HPGD, CEACAM8, DEFA4, IL1B, IFI16, CD177, KIAA1324, SRXN1, TAS2R31, CEACAM6, CD163, B4GALT3, ANKRD28, TAAR1, EIF1AX, CYP4F3, 314, HIST1H2AA, LY6G5B, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided); (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS or ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0038] Suitably, the method determines the likelihood that a stage of ipSIRS selected from mild sepsis, severe sepsis and septic shock is present or absent the subject, wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having the stage of ipSIRS, wherein the reference biomarker IRS biomarker profile evaluates at least one IRS biomarker selected from PLEKHA3, PLEKHF2, 232, SFRS9, ZNF587, KPNA5, LOC284757, GPR65, VAMP2, SLC1A3, ITK, ATF7, ZNF28, AIF1, MINPP1, GIMAP7, MKI67, IRF4, TSHZ2, HLA-DPB1,

EFCAB2, POLE2, FAIM3, 110, CAMK4, TRIM21, IFI44, CENPK, ATP5L, GPR56, HLA-DPA1, C4orf3, GSR, GNLY, RFESD, BPI, HIST1H2AA, NF-E4, CALM2, EIF1AX, E2F6, ARL17P1, TLR5, SH3PXD2B, FAM118A, RETN, PMAIP1, DNAJC9, PCOLCE2, TPX2, BMX, LRRFIP1, DLEU2, JKAMP, JUP, ABCG1, SLC39A9, B3GNT5, ACER3, LRRC70, NPCDR1, TYMS, HLA-DRA, TDRD9, FSD1L, FAR2, C7orf53, PPP1R2, SGMS2, EXOSC4, TGFBR1, CD24, TCN1, TAF13, AP3B2, CD63, SLC15A2, IL18R1, ATP6V0D1, SON, HSP90AB1, CEACAM8, SMPDL3A, IMP3, SEC24A, PICALM, 199, CEACAM6, CYP4F3, OLAH, ECHDC3, ODZ1, KIAA0746, KIAA1324, HINT1, VNN1, C22orf37, FSD1L, FOLR3, IL1RL1, OMG, MTHFS, OLFM4, S100B, ITGA4, KLRD1, SLC39A8, KLHL5, KLRK1, MPO, PPIF, GOT2, LRRN3, HIST1H2AJ, CLU, LCN2, 132, CEP97, KLRF1, FBXL13, HIST1H3B, ANKRD34B, RPIA, HPGD, HIST2H2BF, GK3P (where if a gene name is not provided then a SEQ ID NO. is provided). ; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the stage of ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0039] In illustrative examples, an individual IRS biomarker is selected from the group consisting of: (a) a polynucleotide expression product comprising a nucleotide sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1-319, or a complement thereof; (b) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; (c) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with at least a portion of the sequence set forth in SEQ ID NO: 320-619; (d) a polynucleotide expression product comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under medium or high stringency conditions; (e) a polypeptide expression product comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; and (f) a polypeptide expression product comprising an amino acid sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with the sequence set forth in any one of SEQ ID NO: 320-619.

[0040] Evaluation of IRS markers suitably includes determining the levels of individual IRS markers, which correlate with the presence or absence of a condition, as defined above.

[0041] In some embodiments, the method of determining the likelihood of the presence or absence of a condition, as broadly described above, comprises comparing the level of a first IRS biomarker in the sample IRS biomarker profile with the level of a second IRS biomarker in the sample IRS biomarker profile to provide a ratio and determining a likelihood of the presence or absence of the condition based on that ratio. In illustrative examples of this type, the determination is carried out in the absence of comparing the level of the first or second IRS biomarkers in the sample IRS biomarker profile to the level of a corresponding IRS biomarker in the reference IRS biomarker profile. Representative IRS biomarkers that are useful for these embodiments are suitably selected from those listed in Example 6 and Tables 16 – 21.

[0042] In a related aspect, the present invention provides a kit comprising one or more reagents and/or devices for use in performing the method of determining the likelihood of the presence or absence of a condition as broadly described above.

[0043] Another aspect of the present invention provides a method for treating, preventing or inhibiting the development of inSIRS, ipSIRS or a particular stage of ipSIRS in a subject, the method comprising: (1) correlating a reference IRS biomarker profile with the presence or absence of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; (2) obtaining an IRS biomarker profile of a sample from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile, and administering to the subject, on the basis that the subject has an increased likelihood of having inSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of inSIRS, or administering to the subject, on the basis that the subject has an increased likelihood of having ipSIRS or a particular stage of ipSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of ipSIRS or the particular stage of ipSIRS.

[0044] Yet another aspect of the present invention provides a method of monitoring the efficacy of a particular treatment regimen in a subject towards a desired health state (e.g., healthy condition), the method comprising: (1) providing a correlation of a reference IRS biomarker profile with the likelihood of having a healthy condition; (2) obtaining a corresponding IRS biomarker profile of a subject having inSIRS, ipSIRS or a particular stage of ipSIRS after treatment with a treatment regimen, wherein a similarity of the subject's IRS biomarker profile after treatment to the reference IRS biomarker profile indicates the likelihood that the treatment regimen is effective for changing the health status of the subject to the desired health state.

[0045] Still another aspect of the present invention provides a method of correlating a reference IRS biomarker profile with an effective treatment regimen for a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker, the method comprising: (a) determining a sample IRS biomarker profile from a subject with the condition prior to treatment, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and correlating the sample IRS biomarker profile with a treatment regimen that is effective for treating the condition.

[0046] In another aspect, the present invention provides a method of determining whether a treatment regimen is effective for treating a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, the method comprising: (a) correlating a reference biomarker profile prior to treatment with an effective treatment regimen for the condition, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; and (b) obtaining a sample IRS biomarker profile from the subject after treatment, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and wherein the sample IRS biomarker profile after treatment indicates whether the treatment regimen is effective for treating the condition in the subject.

[0047] In a further aspect, the present invention provides a method of correlating an IRS biomarker profile with a positive or negative response to a treatment regimen, the method comprising: (a) obtaining an IRS biomarker profile from a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS following commencement of the treatment regimen, wherein the IRS biomarker profile evaluates at least one IRS biomarker; and (b) correlating the IRS biomarker profile from the subject with a positive or negative response to the treatment regimen.

[0048] Another aspect of the present invention provides a method of determining a positive or negative response to a treatment regimen by a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, the method comprising: (a) correlating a reference IRS biomarker profile with a positive or negative response to the treatment regimen, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and (b) determining a sample IRS biomarker profile from the subject, wherein the subject's sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker and indicates whether the subject is responding to the treatment regimen.

[0049] In some embodiments, the method of determining a positive or negative response to a treatment regimen further comprises: determining a first sample IRS biomarker profile from the subject prior to commencing the treatment regimen, wherein the first sample IRS biomarker profile evaluates at least one IRS biomarker; and comparing the first sample IRS biomarker profile with a second sample IRS biomarker profile from the subject after commencement of the treatment regimen, wherein the second sample IRS biomarker profile evaluates for an individual IRS biomarker in the first sample IRS biomarker profile a corresponding IRS biomarker.

Brief Description of the Drawings

[0050] An example of the present invention will now be described with reference to the accompanying drawings, in which: -

[0051] Figure 1 is a schematic diagram of an example of flow chart of a process for identifying biomarkers for use in a clinical assessment;

[0052] Figure 2 is a schematic diagram of an example of a distributed computer architecture;

[0053] Figure 3 is a schematic diagram of an example of a base station processing system;

[0054] Figure 4 is a schematic diagram of an example of an computer system;

[0055] Figures 5A and 5B are a flowchart of a second example of a process for identifying biomarkers for use in a clinical assessment.

Detailed Description of the Preferred Embodiments

[0056] An example process for performing biomarker identification will now be described with reference to Figure 1. For the purpose of this example, it is assumed that the process is performed at least in part using an electronic processing device, such as a processor of a computer system, as will be described in more detail below.

[0057] Furthermore, for the purpose of explanation, different terms will be used to identify biomarkers at different stages of the process. For example, the term "reference biomarkers" is used to refer to biomarkers whose activity has been quantified for a sample population of reference individuals having different conditions, stages of different conditions, subtypes of different conditions or with different prognoses. The different reference biomarkers measured for the individuals may be referred to as a reference biomarker collection. The term "reference data" refers to data measured for the individuals in the sample population, and may include quantification of the activity of the biomarkers measured for each individual, information regarding any conditions of the individuals, and optionally any other information of interest. The number of reference biomarkers will vary, but is typically more than 1000 biomarkers.

[0058] The term "potential biomarkers" refers to a subset of the reference biomarkers that have been identified as being potentially useful in distinguishing between different groups of individuals, such as individuals suffering from different conditions, or having different stages or prognoses. The number of potential biomarkers will vary, but is typically about 200. The different potential biomarkers may be referred to as a potential biomarker collection.

[0059] The term "remaining reference biomarkers" refers to reference biomarkers remaining in the reference biomarker collection, once potential biomarkers have been removed.

[0060] The term "signature biomarkers" is used to refer to a subset of the potential biomarkers that have been identified as being potentially useful in defining signatures that can be used in performing a clinical assessment, such as to rule in or rule out a specific condition, different stages or severity of conditions, subtypes of different conditions or different prognoses. The number of signature biomarkers will vary, but is typically of the order of 10 or less, with the different signature biomarkers identified being referred to as a signature biomarker collection.

[0061] It will be appreciated that the above described terms and associated definitions are used for the purpose of explanation only and are not intended to be limiting.

[0062] In this example, at step 100, the process involves using reference data from a plurality of individuals to define a number of groups of individuals. The individuals are taken from a reference population, typically including individuals having a range of different conditions, or stages of different conditions, or subtypes of different conditions or with different prognoses.

[0063] The reference data typically includes measurements of a plurality of reference biomarkers, the measurements including information regarding the activity, such as the level or abundance, of any expression product or measurable molecule, as will be described in more detail below. The reference data may also include other additional relevant information such as clinical data regarding one or more conditions suffered by each individual. This can include information regarding a presence, absence, degree, stage, severity or progression of a condition, phenotypic information, such as details of phenotypic traits, genetic or genetically regulated information, amino acid or nucleotide related genomics information, results of other tests including imaging, biochemical and hematological assays, other physiological scores such as a SOFA (Sequential Organ Failure Assessment) score, or the like and this is not intended to be limiting, as will be apparent from the description below.

[0064] At step 110, a plurality of analysis techniques, such as statistical analysis or machine learning techniques, are used to identify a number of potential biomarkers from the plurality of reference biomarkers that are potentially useful for distinguishing the groups of individuals, allowing the potential biomarkers to be used in selecting signature biomarkers for use in generating signatures for use in clinical assessments.

[0065] The analysis techniques are typically applied in an iterative fashion, with each iteration being used to identify a subset of reference biomarkers that might prove suitable for use as potential biomarkers. In one example, as each iteration is performed, the predictive performance of the reference biomarkers in distinguishing the groups is assessed, with reference biomarkers being identified for use as potential biomarkers only in the event that they exceed a predetermined predictive performance threshold, such as at least 90%, at least 85% or more typically, at least 80%. This threshold may be implemented as accuracy in the case of classification or a measure of correlation in the case of continuous outcomes.

[0066] Once reference biomarkers are identified for use as potential biomarkers, they can be removed from the reference biomarker collection, allowing the next iteration to be performed on the remaining reference biomarkers. The number of iterations will depend on the analysis techniques and associated parameters used, and can include at least 100, at least 500, at least 1000, at least 2000 and even at least 5000.

[0067] The process uses a plurality of different analysis techniques, such as classification, regression and/or machine learning techniques, allowing a variety of potential biomarkers to be identified. This is performed as each analysis technique typically operates slightly differently and as a result will often identify different potential biomarkers, so using the plurality of different analysis techniques ensures that as many potentially useful biomarkers as possible are captured for use as potential biomarkers.

[0068] The analysis techniques may be performed until the predictive performance of the remaining reference biomarkers in the reference biomarker collection falls below the predetermined threshold and each technique has been used, or may be repeated until a predetermined number of potential biomarkers, such as at least 100, less than 500 or more typically about 200, are identified.

[0069] Following identification of potential biomarkers, at step 120, a subset of the potential biomarkers can be optionally identified for use as signature biomarkers, to allow signatures for use in specific clinical assessments to be determined. This can be achieved in any suitable manner, but in one example, this involves a further process of identifying specific groups relevant to the clinical assessment, and then performing a further regression or other similar statistical analysis to select those potential biomarkers that can be used as signature biomarkers.

[0070] Accordingly, in one example, the above described process is used to identify a subset of measured reference biomarkers that can act as potential biomarkers, before a more in depth analysis is performed to identify a subset of potential biomarkers for use as signature biomarkers that can be used in specific clinical assessments. As a result, the above process can act as a coarse filter, allowing a relatively large number of potential biomarkers to be identified that can be used in distinguishing the different groups of individuals.

[0071] By way of example, many patients suffer from a condition called Systemic Inflammatory Response Syndrome (SIRS) (M S Rangel-Frausto, D Pittet, M Costigan, T Hwang, C S Davis, and R P Wenzel, "The Natural History of the Systemic Inflammatory Response Syndrome (SIRS). a Prospective Study.," *JAMA : the Journal of the American Medical Association* 273, no. 2 (January 11, 1995): 117–123.). SIRS is an overwhelming whole body reaction that may have an infectious or non-infectious aetiology, whereas sepsis is SIRS that occurs during infection. Both are defined by a number of non-specific host response parameters including changes in heart and respiratory rate, body temperature and white cell counts (Mitchell M Levy et al., "2001 SCCM/ESICM/ACCP/ATS/SIS International Sepsis Definitions Conference," *Critical Care*

Medicine 31, no. 4 (April 2003): 1250–1256, doi:10.1097/01.CCM.0000050454.01978.3B.; K Reinhart, M Bauer, N C Riedemann, and C S Hartog, "New Approaches to Sepsis: Molecular Diagnostics and Biomarkers," *Clinical Microbiology Reviews* 25, no. 4 (October 3, 2012): 609–634, doi:10.1128/CMR.00016-12.) To differentiate these conditions they are referred herein to as SIRS (both conditions), infection-negative SIRS (SIRS without infection, hereafter referred to as "inSIRS") and infection-positive SIRS (sepsis, SIRS with a known or suspected infection, hereafter referred to as "ipSIRS"). The causes of SIRS are multiple and varied and can include, but are not limited to, trauma, burns, pancreatitis, endotoxemia, surgery, adverse drug reactions, and infections (local and systemic). Using two patient populations of healthy individuals and individuals having SIRS, a coarse filter can be used to identify which reference biomarkers can distinguish these two groups of individuals, thereby allowing potential biomarkers to be identified. A coarse filter could also be used to identify which reference biomarkers can separate inSIRS patients from ipSIRS patients, both groups of patients having SIRS in common, but each group of patients differing in whether a clinician has determined the presence of an infection or not.

[0072] Following this, more specific and computationally intensive analyses could be performed to identify a subset of potential biomarkers for use as signature biomarkers to answer more specific clinical questions such as: for patients with ipSIRS which biomarkers can separate out those with severe sepsis or septic shock, or provide a prognosis or indication of likely progression to another stage of disease, or for patients with inSIRS which biomarkers can separate those with pancreatitis from those following surgery.

[0073] Thus, if it is desired to make clinical assessments relating to SIRS, and in particular, inSIRS and ipSIRS, a suite of biomarkers can be quantified for individuals suffering either one of these conditions, as well as healthy individuals and used as reference biomarkers. These data can be used to define first groups of individuals having one of the two conditions or both, as well as of healthy individuals. Potential biomarkers can be ascertained that may be used to distinguish these groups. For example, the first stage could be used to determine biomarkers that differentiate healthy individuals and individuals having SIRS.

[0074] Following this, signature biomarkers for specific clinical assessments within these groups, such as distinguishing inSIRS from ipSIRS (rule in and rule out ipSIRS), can be determined. In this case, second groups are defined that relate to individuals having or not having infection-positive or inSIRS, and then signature biomarkers are determined from the potential biomarkers.

[0075] It can be complex and computationally difficult to select a limited number of clinically useful and manageable biomarkers from a large data set in a single stage. Thus, using a single stage identification process, potentially useful biomarkers can be easily overlooked or omitted, so that the resulting signature biomarkers are not necessarily the best suited for use in a specific clinical assessment. A particular benefit of the described approach is that by separating the process into multiple stages, the chances of overlooking or omitting the discovery of new and clinically useful biomarkers is greatly reduced.

[0076] The multi-stage approach allows coarse filtering to be used first so as to limit the number of measured reference biomarkers to a more manageable number of potential biomarkers, so that more specific, and computationally intensive, techniques can be used to identify signature biomarkers for use in specific clinical assessments. The coarse analysis therefore allows a collection of potential biomarkers to be established that will be relevant to a range of different but related clinical assessments. A more focussed analysis can then be performed to identify specific signature biomarkers, which is less computationally intensive than attempting to do this for a greater number of biomarkers, and also helps ensure the best biomarkers for the clinical assessment are identified by excluding the noise introduced by many uninformative biomarkers which have been removed from consideration.

[0077] The above approach can therefore allow a large number of measured reference biomarkers, typically several thousand, to be used as a basis for the analysis, thereby reducing the likelihood of new and clinically relevant biomarkers being excluded from the resulting potential biomarkers, and ultimately signature biomarkers, hence improving the ability of the signatures to be clinically useful in assessments.

[0078] In one example, the process is performed at least in part using a processing system, such as a suitably programmed computer system. This can be performed on a stand-alone computer, with the microprocessor executing applications software allowing the above-described method to be performed. Alternatively, the process can be performed by one or more processing systems operating as part of a distributed architecture, an example of which will now be described with reference to Figure 2.

[0079] In this example, a base station 201 is coupled via a communications network, such as the Internet 202, and/or a number of local area networks (LANs) 204, to a number of computer systems 203. It will be appreciated that the configuration of the networks 202, 204 are for the purpose of example only, and in practice the base station 201, computer systems 203 can communicate via any appropriate mechanism, such as via wired or wireless connections, including, but not limited to mobile networks, private networks, such as an 802.11 networks, the Internet, LANs, WANs, or the like, as well as via direct or point-to-point connections, such as Bluetooth, or the like.

[0080] In one example, the base station 201 includes a processing system 210 coupled to a database 211. The base station 201 is adapted to be used in analysing reference data, selecting potential biomarkers, and optionally generating signatures for use in clinical assessments. The reference data may be stored in the database 211 and may be received from the computer systems 203, or other remote devices. The base station 201 may also be adapted to assist in performing clinical assessments by comparing individual data relating to a patient or other individual and then comparing this to the signatures to allow a clinical assessment to be made. The computer systems 203 are therefore adapted to communicate with the base station 201, allowing data to be transferred there between and/or to control the operation of the base station 201.

[0081] Whilst the base station 201 is a shown as a single entity, it will be appreciated that the base station 201 can be distributed over a number of geographically separate locations, for example by using processing systems 210 and/or databases 211 that are provided as part of a cloud based environment.

[0082] However, the above-described arrangement is not essential and other suitable configurations could be used. For example, the process for identifying biomarkers, as well as any subsequent clinical assessment of individual data could be performed on a stand-alone computer system.

[0083] An example of a suitable processing system 210 is shown in Figure 3. In this example, the processing system 210 includes at least one microprocessor 300, a memory 301, an input/output device 302, such as a keyboard and/or display, and an external interface 303, interconnected via a bus 304 as shown. In this example the external interface 303 can be utilised for connecting the processing system 210 to peripheral devices, such as the communications networks 202, 204, databases 211, other storage devices, or the like. Although a single external interface 303 is shown, this is for the purpose of example only, and in practice multiple interfaces using various methods (e.g., Ethernet, serial, USB, wireless or the like) may be provided.

[0084] In use, the microprocessor300 executes instructions in the form of applications software stored in the memory 301 to allow the biomarker identification process to be performed, as well as to perform any other required processes, such as communicating with the computer systems 203. The applications software may include one or more software modules, and may be executed in a suitable execution environment, such as an operating system environment, or the like.

[0085] Accordingly, it will be appreciated that the processing system 300 may be formed from any suitable processing system, such as a suitably programmed computer system, PC, web server, network server, or the like. In one particular example, the processing system 100 is a standard processing system such as a 32-bit or 64-bit Intel Architecture based processing system, which executes software applications stored on non-volatile (e.g., hard disk) storage, although this is not essential. However, it will also be understood that the processing system could be any electronic processing device such as a microprocessor, microchip processor, logic gate configuration, firmware optionally associated with implementing logic such as an FPGA (Field Programmable Gate Array), or any other electronic device, system or arrangement.

[0086] As shown in Figure 4, in one example, the computer system 203 includes at least one microprocessor400, a memory 401, an input/output device 402, such as a keyboard and/or display, and an external interface 403, interconnected via a bus 404 as shown. In this example the external interface 403 can be utilised for connecting the computer system 203 to peripheral devices, such as the communications networks 202, 204, databases 211, other storage devices, or the like. Although a single external interface 403 is shown, this is for the purpose of example only, and in practice multiple interfaces using various methods (eg. Ethernet, serial, USB, wireless or the like) may be provided.

[0087] In use, the microprocessor 400 executes instructions in the form of applications software stored in the memory 401 to allow communication with the base station 201, for example to allow data to be supplied thereto and allowing results of any clinical assessment to be displayed to an operator. The computer system 203 may also be used to allow the operation of the base station 201 to be controlled, for example to allow the biomarker identification process to be performed remotely.

[0088] Accordingly, it will be appreciated that the computer systems 203 may be formed from any suitable processing system, such as a suitably programmed PC, Internet terminal, lap-top, hand-held PC, smart phone, PDA, web server, or the like. Thus, in one example, the processing system 100 is a standard processing system such as a 32-bit or 64-bit Intel Architecture based processing system, which executes software applications stored on non-volatile (e.g., hard disk) storage, although this is not essential. However, it will also be understood that the computer systems 203 can be any electronic processing device such as a microprocessor, microchip processor, logic gate configuration, firmware optionally associated with implementing logic such as an FPGA (Field Programmable Gate Array), or any other electronic device, system or arrangement.

[0089] Examples of the biomarker identification process, and subsequent use in a clinical assessment will now be described in further detail. For the purpose of these examples, it is assumed that reference data, including the reference biomarker collection, any potential biomarkers, signature biomarkers or signatures can be stored in the database 211, and that the biomarker identification process is performed using the processing system 210 under control of one of the computer systems 203. Thus, it is assumed that the processing system 210 of the base station 201 hosts applications software for performing the biomarker identification process, with actions performed by the processing system 210 being performed by the processor 300 in accordance with instructions stored as applications software in the memory 301 and/or input commands received from a user via the I/O device 302, or commands received from the computer system 203.

[0090] It will also be assumed that the user interacts with application software executed by the processing system 210 via a GUI, or the like presented on the computer system 203. Actions performed by the computer system 203 are performed by the processor 401 in accordance with instructions stored as applications software in the memory 402 and/or input commands received from a user via the I/O device 403. The base station 201 is typically a server which communicates with the computer system 203 via a LAN, or the like, depending on the particular network infrastructure available.

[0091] However, it will be appreciated that the above-described configuration assumed for the purpose of the following examples is not essential, and numerous other configurations may be used. It will also be appreciated that the partitioning of functionality between the computer system 203, and the base station 201 may vary, depending on the particular implementation.

[0092] A second example of a process for determining biomarkers will now be described with reference to Figures 5A and 5B.

[0093] In this example, at step 500 reference data is acquired for a plurality of individuals with the reference data including at least data regarding a plurality of reference biomarkers, measured for each individual.

[0094] The reference data may be acquired in any appropriate manner but typically this involves obtaining gene expression product data from a plurality of individuals, selected to include individuals diagnosed with one or more conditions of interest, as well as healthy individuals. The terms "expression" or "gene expression" refer to production of RNA message or translation of RNA message into proteins or polypeptides, or both. Detection of either types of gene expression in use of any of the methods described herein is encompassed by the present invention. The conditions are typically medical, veterinary or other health status conditions and may include any illness, disease, stages of disease, disease subtypes, severities of disease, diseases of varying prognoses or the like.

[0095] In order to achieve this, gene expression product data are collected, for example by obtaining a biological sample, such as a peripheral blood sample, and then performing a quantification process, such as a nucleic acid amplification process, including PCR (Polymerase Chain Reaction) or the like, in order to assess the activity, and in particular, level or abundance of a number of reference biomarkers. Quantified values indicative of the relative activity are then stored as part of the reference data.

[0096] Example reference biomarkers will be described in more detail below but it will be appreciated that these could include expression products such as nucleic acid or proteinaceous molecules, as well as other molecules relevant in making a clinical assessment. The number of biomarkers measured for use as reference biomarkers will vary depending upon the preferred implementation, but typically include a large number such as, 1000, 5000, 10000 or above, although this is not intended to be limiting.

[0097] The individuals also typically undergo a clinical assessment allowing any conditions to be clinically identified, and with an indication of any assessment or condition forming part of the reference data. Whilst any conditions can be assessed, in one example the process is utilized specifically to identify conditions such as SIRS,, including inSIRS and ipSIRS or sepsis. It will be appreciated from the following, however, that this can be applied to a range of different conditions, and reference to SIRS or sepsis is not intended to be limiting.

[0098] Additionally, the reference data may include details of one or more phenotypic traits of the individuals and/or their relatives. Phenotypic traits can include information such as the gender, ethnicity, age, or the like. Additionally, in the case of the technology being applied to individuals other than humans, this can also include information such as designation of a species, breed or the like.

[0099] Accordingly, in one example the reference data can include for each of the reference individuals an indication of the activity of a plurality of reference biomarkers, a presence, absence degree, stage, or progression of a condition, phenotypic information such as phenotypic traits, genetic information and a physiological score such as a SOFA score.

[0100] The reference data is typically collected from individuals presenting at a medical centre with clinical signs relating to relevant any conditions of interest, and may involve follow-on consultations in order to confirm clinical assessments, as well as to identify changes in biomarkers, and/or clinical signs, and/or severity of clinical signs, over a period of time. In this latter case, the reference data can include time series data indicative of the progression of a condition, and/or the activity of the reference biomarkers, so that the reference data for an individual can be used to determine if the condition of the individual is improving, worsening or static. It will also be appreciated that the reference biomarkers are preferably substantially similar for the individuals within the sample population, so that comparisons of measured activities between individuals can be made.

[0101] It will be appreciated that once collected, the reference data can be stored in the database 211 allowing this to be subsequently retrieved by the processing system 210 for subsequent analysis. The processing system 210 also typically stores an indication of an identity of each of the reference biomarkers as a reference biomarker collection.

[0102] At step 505, the processing system 210 optionally removes a validation subgroup of individuals from the reference data prior to determining the potential biomarkers. This is performed to allow the processing system 210 to determine the potential biomarkers using the reference data without the validation subgroup so that the validation subgroup can be subsequently used to validate the potential biomarkers or signatures including a number of the potential biomarkers. Thus, data from the validation subgroup is used to validate the efficacy of the potential or signature biomarkers in identifying the presence, absence, degree, stage, severity, prognosis or progression of any one or more of the conditions to ensure the potential or signature biomarkers are effective, as will be described in more detail below.

[0103] In one example, this is achieved by having the processing system 210 flag individuals within the validation subgroup or alternatively store these in either an alternative location within the database 211 or an alternative database to the reference data. The validation subgroup of individuals is typically selected randomly and may optionally be selected to include individuals having different phenotypic traits. When a validation subgroup of individuals is removed, the remaining individuals will simply be referred to as reference data for ease throughout the remaining description.

[0104] At step 510, the individuals remaining within the reference data (ie excluding the validation subgroup) are classified into groups. The groups may be defined in any appropriate manner and may be defined based on any one or more of an indication of a presence, absence, degree, stage, severity, prognosis or progression of a condition, phenotypic traits, other tests or assays, genetic information or measured activity of the reference biomarkers associated with the individuals.

[0105] For example, a first selection of groups may be to identify one or more groups of individuals suffering from SIRS, one or more groups of individuals suffering ipSIRS, one or more groups of individuals suffering inSIRS, and one or more groups of healthy individuals. Further groups may also be defined for individuals suffering from other conditions. Additionally, further subdivision may be performed based on phenotypic traits, so groups could be defined based on gender, ethnicity or the like so that a plurality of groups of individuals suffering from a condition are defined, with each group relating to a different phenotypic trait.

[0106] It will also be appreciated, however, that identification of different groups can be performed in other manners, for example on the basis of particular activities of biomarkers within the biological samples of the reference individuals, and accordingly, reference to conditions is not intended to be limiting and other information may be used as required.

[0107] The manner in which classification into groups is performed may vary depending on the preferred implementation. In one example, this can be performed automatically by the processing system 210, for example, using unsupervised methods such as Principal Components Analysis (PCA), or supervised methods such as k-means or Self Organising Map (SOM). Alternatively, this may be performed manually by an operator by allowing the operator to review reference data presented on a Graphical User Interface (GUI), and define respective groups using appropriate input commands.

[0108] Once the groups have been defined, analysis techniques are utilized in order to identify reference biomarkers that can be utilized to potentially distinguish the groups. The analysis technique typically examines the activity of the reference biomarkers for individuals within and across the groups, to identify reference biomarkers whose activities differ between and hence can distinguish groups. A range of different analysis techniques can be utilized including, for example, regression or correlation analysis techniques. Examples of the techniques used can include established methods for parametized model building such as Partial Least Squares, Random Forest or Support Vector Machines, usually coupled to a feature reduction technique for the selection of the specific subset of the biomarkers to be used in a signature.

[0109] Such techniques are known and described in a number of publications. For example, the use of Partial Least Squares is described in "Partial least squares: a versatile tool for the analysis of high-dimensional genomic data" by Boulesteix, Anne-Laure and Strimmer, Korbinian, from Briefings in Bioinformatics 2007 vol 8. no. 1, pg 32-44. Support Vector machines are described in "LIBSVM: a library for support vector machines" by Chang, C.C. and Lin, C.J. from ACM Transactions on Intelligent Systems and Technology (TIST), 2011 vol 2, no. 3,pg 27. Standard Random Forest in R language is described in "Classification and Regression by random Forest" by Liaw, A. and Wiener, M., in R news 2002, vol2, no. 3, pg 18-22.

[0110] The analysis techniques are implemented by the processing system 210, using applications software, which allows the processing system 210 to perform multiple ones of the analysis techniques in sequence. This is advantageous as the different analysis techniques typically have different biases and can therefore be used to identify different potential biomarkers that can distinguish the groups, thereby reducing the risk of clinically relevant biomarkers being overlooked.

[0111] At step 515 a next analysis technique is selected by the processing system 210, with this being implemented at step 520 to identify the best *N* reference biomarkers for distinguishing the groups, where the variable *N* is a predetermined or algorithmically derived number of biomarkers whose value may vary depending on the analysis technique used and the preferred implementation, but is typically a relatively small number compared to the overall number of biomarkers, such as less than 10, more than 1, between 2 and 8 and 5. This process typically involves a predictive model to assess the ability of activities of particular ones of the reference biomarkers to distinguish between different groups. For example this can examine the manner in which the activity of reference biomarkers differ between groups, and/or are relatively similar within a group. This can be performed iteratively for different combinations of reference biomarkers until a best *N* of the reference biomarkers are identified.

[0112] At step 525, the processing system 210 determines the predictive performance of the identified best *N* reference biomarkers, when used in the model, for in distinguishing the relevant groups. The predictive performance is typically a parameter determined as part of the combination of analysis technique and chosen embodying model, as will be appreciated by persons skilled in the art. For example, receiver operating characteristic (ROC) analysis may be used to determine optimal assay parameters to achieve a specific level of accuracy, specificity, positive predictive value, negative predictive value, and/or false discovery rate.

[0113] Optionally, a cross-validation approach may be used whereby steps 520 and 525 are repeated *M* times to produce a distribution of *M* predictive performance measures, and *N*x*M* selected reference biomarkers. It will be appreciated that there may be none, some, or complete overlap in the sets of selected reference biomarkers for the *M* iterations. The union (unique set) of selected reference biomarkers from all *M* iterations is the set *U*.

[0114] At step 530, the predictive performance is compared to a predetermined threshold, which is typically selected dependent upon the preferred implementation, but may be a relatively low value such as 80%. In the case of cross-validation, in which steps 520 and 525 are repeated *M* times, the predictive performance at step 530 is some property of the *M* predictive performance measurements such as the mean, median or maximum.

[0115] By example, ruling in ipSIRS might have a lower threshold than ruling out ipSIRS since the clinical risk of treating someone with inSIRS with antibiotics might be considered to be less than not treating someone with ipSIRS with antibiotics. Thus, it can be appreciated that the threshold set is influenced by a variety of factors including clinical utility, patient welfare, disease prevalence, and econometrics of test use to name a few examples.

[0116] At step 535, if it is determined that the predictive performance is above the threshold, the identified *N* reference biomarkers are added to a list or collection of potential biomarkers, an indication of which is typically stored in the database 211. In the case of a cross-validation approach, where the set of unique selected biomarkers (*U*) may be larger than the number to be selected as potential biomarkers (*N*), the *N* most frequently selected biomarkers during the *M* iterations are identified as the *N* reference biomarkers and are then removed from the reference biomarker collection before further analysis is performed. The process then returns to step 520 allowing the same analysis technique to be performed and the next *N* reference biomarkers identified.

[0117] It will therefore be appreciated that this is an iterative technique that allows reference biomarkers capable of distinguishing the groups to be progressively identified with the ability of an additional *N* reference biomarkers to act as potential biomarkers being assessed, within each iteration. This process performs a relatively coarse filtering of reference biomarkers allowing groups of reference biomarkers with predictive performance above the threshold to be progressively removed from the reference biomarker collection and added to the potential biomarker collection.

[0118] During this process, if it is determined that the predictive performance of the *N* identified reference biomarkers is below the threshold, then the process moves to step 540 when it is determined by the processing system 210 if all analysis techniques have been used. If not, the process returns to step 515 allowing a next analysis technique to be selected.

[0119] Thus, it will be appreciated that the iterative process is repeated for a number of different analysis techniques allowing biases between the techniques to identify different potential biomarkers. Accordingly, this process progressively identifies reference biomarkers useful as potential biomarkers utilizing a coarse identification process that can be performed relatively rapidly, and optionally in parallel, over a large number of reference biomarkers.

[0120] At this stage, the potential biomarkers may be utilized in an attempt to classify the validation subgroup of individuals. In particular, the different activities of the identified potential biomarkers for individuals within each group are utilized to attempt to classify individuals in the validation subgroup into the groups defined at step 510. In the event that classification of the validation subgroup is successful, potential biomarkers may be retained, whereas if a validation is unsuccessful potential biomarkers may optionally be removed from the potential biomarker collection.

[0121] In one example, the above-described process is performed over several thousand different reference biomarkers allowing a collection of several hundred potential biomarkers to be identified. However, the potential biomarkers may not be ideal for answering specific clinical assessment questions, such as ruling in a condition, ruling out a condition, or determining a stage of progression or likely outcome of a condition or treatment.

[0122] Accordingly, once the potential biomarkers have been identified, more refined processes are used to allow the processing system 210 to identify a number of potential biomarkers for use as signature biomarkers, in turn allowing signatures to be developed for performing specific clinical assessments.

[0123] In this regard, it will be appreciated that typically clinicians will want to perform a specific clinical assessment based on a preliminary diagnosis made using clinical signs, present in a subject presented to them. Accordingly, a clinician could potentially only need to answer the question of whether the subject has ipSIRS, or does not have ipSIRS. As the cost, speed and ability to perform a diagnostic test will typically be heavily dependent on the number of biomarkers assessed as part of the test, it is preferable to be able to identify a minimal number of biomarkers that are able to answer the specific clinical assessment of interest. To address this, the process can use more refined analysis of the potential biomarkers to identify those that are most useful in performing a particular clinical assessment, and hence can be used as signature biomarkers.

[0124] Accordingly, at step 545 a next clinical assessment is determined. This can be achieved in any manner, but usually involves having the user define the clinical assessment using appropriate input commands. As part of this, at step 550, the processing system 210 is used to identify second groups that are relevant to the clinical assessment, for example, by having the user identify criteria, such as the relevant conditions associated with each group, or the stage of progression for the individuals within the groups. This could include, for example, defining groups of individuals having ipSIRS and those not having ipSIRS, or those having mild, major, worsening or improving ipSIRS. Whilst it will be appreciated that the second groups may be the same as the first groups previously defined at step 510, more typically the second groups are more appropriately targeted based on the particular clinical assessment.

[0125] At step 555, the processing system 210 uses a second analysis technique to identify a number of the potential biomarkers that best distinguish the second groups of individuals. In particular, this will attempt to identify potential biomarkers whose level of activity for the individuals within the groups, can be used to distinguish the groups. The nature of the analysis technique will vary depending upon the preferred implementation and can include analysis techniques similar to those outlined above. Alternatively, different analysis techniques can be used such as ordinal classification, which differs from regular classification in that the known order of classes is used without assumptions as to their relative similarity to impose extra constraints in the model leading to more accurate clarification of borderline cases. Such ordinal classification is described in "Support vector ordinal regression" by Chu, W. and Keerthi, S.S., in Neural Computation 2007, vol 19, no. 3, pg 792-815.

[0126] An ordinal SVM for classification consists of the same fundamental elements of any SVM technique that would be familiar to anyone skilled in the art. Namely, the objective is to describe a number of maximally separating hyper-planes in the transformed hyperspace defined by the kernel function. An ordinal classifier differs from a regular SVM classifier in that it imposes an ordinal structure through the use of the cost function. This is implemented by adding to cost functions a component which penalizes incorrect ranks during execution, as described "Support vector ordinal regression" by Chu *et al.* (2007, *supra*).

[0127] Typically, the analysis techniques are implemented to identify a limited overall number of potential biomarkers that can be used as signature biomarkers, and may therefore use more stringent criteria than the analysis techniques used in steps 515 to 530 above. Alternatively, the analysis techniques may not be limited in the number of potential biomarkers identified, and can instead identify more or less potential biomarkers than the predetermined number *N*, above. Additionally, for this reason, only a single analysis technique is typically required at this stage, although this is not essential and multiple second analysis techniques could be used.

[0128] At step 560, the processing system 210 determines if the predictive performance of the identified potential biomarkers exceeds a second predetermined threshold.

[0129] Optionally, a cross-validation approach may be used whereby steps 550 and 560 are repeated *M* times to produce a distribution of *M* predictive performance measures, and *N*x*M* selected reference biomarkers. It will be appreciated that there may be none, some, or complete overlap in the sets of selected reference biomarkers for the *M* iterations. The union (unique set) of selected reference biomarkers from all *M* iterations is the set *U*.

[0130] Optionally, a consensus approach may be used, whereby steps 555 and 560 are repeated multiple times, and the predictive performance measure is some measure of the consensus of the iterations, such as the average value.

[0131] At step 565, if it is determined that the predictive performance is not above the second predetermined threshold, the processing system 210 modifies parameters associated with the analysis technique at step 570 and the process returns to step 555 allowing the same or alternative potential biomarkers to be assessed. This process is repeated until a successful determination occurs when a limited number of potential biomarkers are identified which provide a predictive performance above the threshold, in which case the process moves on to step 575.

[0132] It will be appreciated that as this is attempting to identify a limited number of biomarkers that provide better predictive performance, the second predetermined threshold is typically set to be higher that the first predetermined threshold used at step 530, and as a result of this, the second analysis technique may be computationally more expensive. Despite this, as the process is only being performed on the basis of the potential biomarkers and not the entire set of reference biomarkers, this can typically be performed relatively easily.

[0133] At step 575, the processing system 210 determines if the identified potential biomarkers are to be excluded. This may occur for any one of a number of reasons. For example, a limited number of say five biomarkers may be identified which are capable of providing the required clinical assessment outcome. However, it may not be possible to use some of these biomarkers for legal or technical reasons, in which case the biomarkers may be excluded. In this case, the excluded biomarkers are removed from the potential biomarker database at step 580 and the process returns to step 555 allowing the analysis to be performed.

[0134] It will be appreciated that whilst such excluded biomarkers may be removed from the reference data at an earlier point in the process, the ability to identify excluded biomarkers may be difficult. For example, performing a freedom-to-operate assessment of potential biomarkers can be an expensive process. It is therefore unfeasible to do this to the entire collection of biomarkers within the reference database or even to the entire collection of potential biomarkers. Accordingly, this assessment is only typically made once a potential biomarker has been identified at step 555 to 565 as providing a predictive performance above the threshold.

[0135] In the event that none of the potential biomarkers are excluded, the identified potential biomarkers are used as signature biomarkers, and an indication of the signature biomarkers is typically stored in a signature biomarker collection in the database 211. The measured activities from the reference individuals for the signature biomarkers can then be used to generate signatures for use in performing the clinical assessment at step 585. The signatures will typically define activities or ranges of activities of the signature biomarkers that are indicative of the presence, absence, degree, stage, or progression of a condition. This allows the signatures to be used in performing diagnostic and/or prognostic assessment of subjects.

[0136] For example, an indication of the activity of the signature biomarkers can be obtained from a sample taken from a test subject, and used to derive a signature indicative of the health status of the test subject. This can then be compared to the signatures derived from the reference data to assess the likely heath status of the subject.

[0137] Following this, at step 590 the process moves on to determine whether all clinical assessments have been addressed and if not, returns to step 545 allowing a next clinical assessment to be selected. Otherwise, the process ends at step 595.

[0138] Accordingly, it will be appreciated that the above-described methodology utilizes a staged approach in order to generate potential biomarkers and optionally, further signature biomarkers, for use in performing clinical assessments.

[0139] The process utilizes an initial coarse filtering based on a plurality of analysis techniques in order to identify a limited number of potential biomarkers. The limited number of potential biomarkers, which is typically in the region of less than 500, are selected from a larger database of biomarkers as being those most capable of distinguishing between different conditions, and/or different stages or progressions of a condition.

[0140] Following this, in a further stage, specific clinical assessments are identified with additional analysis techniques being used to select particular biomarkers from the database of potential biomarkers with the particular biomarkers being capable of being use in answering the specific clinical assessments.

[0141] A specific example of the above-described process will now be described with reference to distinguishing between inSIRS and ipSIRS.

[0142] A number of patients clinically identified as having infection negative SIRS and infection positive SIRS had peripheral blood samples taken (N=141). These samples were run on microarray. The microarray data was then normalised and quality control (QC) filtered as per the recommendation of the manufacturer to produce a list of samples with a corresponding clinical diagnosis of SIRS with or without an infection (N=141), and a list of reference biomarkers that passed QC (N=15,989).

[0143] The process of building and testing a model will now be described. In this example, 10% of the samples are randomly selected to act as the testing/validation set and are put aside. The remaining 90% of the samples are the training set, used to identify the potential biomarkers.

[0144] A feature selection algorithm coupled to a machine learning model is then applied to the training set, In this example a Recursive Feature Selection Support Vector Machine, described for example in "Recursive SVM feature selection and sample classification for mass-spectrometry and microarray data", by Xuegong Zhang, Xin Lu, Qian Shi, Xiu-qin Xu, Hon-chiu E Leung, Lyndsay N Harris, James D Iglehart, Alexander Miron, Jun S Liu and Wing H Wong from BMC Bioinformatics 2006, 7:197, was used to build a model with exactly 10 genes as the input.

[0145] Assuming no technical or biological noise and ignoring sample size considerations, these genes best describe the inherent variability between inSIRS and ipSIRS samples when using an SVM model, and therefore provide the best available separation signature.

[0146] For each sample in the testing set, the model is used to predict either inSIRS or ipSIRS. If the prediction matches the clinical record for this sample, it is declared a correct prediction. The performance of the model in this case is measured by accuracy, which can be expressed as the percentage of correct predictions for the testing set.

[0147] Optionally, the building and testing step may be repeated with a different random testing and training set. This could be performed any number of times depending on the preferred implementation, and in one example is performed 100 times. If the accuracy of the model was not significantly better than the last 2 iterations (1 way ANOVA p-value > 0.95), then the selection of biomarkers was terminated.

[0148] If the accuracy remained significantly better than either of the last 2 iterations (as described above), then the 10 genes that were selected in the model (or most frequently appear if repeated runs were used) are then added to the collection of potentially useful biomarkers, and were removed from subsequent iterations.

[0149] The biomarker identification process described above and elsewhere herein has been used to identify 319 biomarker genes (hereafter referred to as "inflammatory response syndrome (IRS) biomarker genes"), which are surrogate markers that are useful for assisting in distinguishing: (1) between SIRS affected subjects (i.e., subject having inSIRS or ipSIRS) and healthy subjects or subjects not affected by SIRS; (2) between subjects with inSIRS and subjects with ipSIRS; and/or (3) between subjects with different stages of ipSIRS (e.g., sepsis, severe sepsis and septic shock). Based on this identification, the present inventors have developed various methods and kits, which take advantage of these biomarkers to determine the likelihood of the presence or absence of a condition selected from a healthy condition (e.g., a normal condition or one in which inSIRS and inSIRS are absent), SIRS generally (i.e., not distinguishing between inSIRS or ipSIRS), inSIRS or ipSIRS, or to assess the likelihood of the presence, absence or risk of development of a stage of ipSIRS (e.g., a stage of ipSIRS with a particular severity, illustrative examples of which include mild sepsis, severe sepsis and septic shock). In advantageous embodiments, the methods and kits involve monitoring the expression of IRS biomarker genes in blood cells (e.g., immune cells such as leukocytes), which may be reflected in changing patterns of RNA levels or protein production that correlate with the presence of active disease or response to disease.

[0150] As used herein, the term SIRS ("systemic inflammatory response syndrome") refers to a clinical response arising from a non-specific insult with two or more of the following measureable clinical characteristics; a body temperature greater than 38° C or less than 36° C, a heart rate greater than 90 beats per minute, a respiratory rate greater than 20 per minute, a white blood cell count (total leukocytes) greater than 12,000 per mm^3 or less than 4,000 per mm^3, or a band neutrophil percentage greater than 10%. From an immunological perspective, it may be seen as representing a systemic response to insult (e.g., major surgery) or systemic inflammation. As used herein, "inSIRS" includes the clinical response noted above but in the absence of a systemic infectious process. By contrast, "ipSIRS" includes the clinical response noted above but in the presence of a presumed or confirmed systemic infectious process. Confirmation of infectious process can be determined using microbiological culture or isolation of the infectious agent. From an immunological perspective, ipSIRS may be seen as a systemic response to microorganisms be it local, peripheral or a systemic infection.

[0151] The terms "surrogate marker" and "biomarker" are used interchangeably herein to refer to a parameter whose measurement (e.g., level, presence or absence) provides information as to the state of a subject. In various exemplary embodiments, a plurality of biomarkers is used to assess a condition (e.g., healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS). Measurements of the biomarkers may be used alone or combined with other data obtained regarding a subject in order to determine the state of the subject biomarker. In some embodiments, the biomarkers are "differentially present" in a sample taken from a subject of one phenotypic status (e.g., having a specified condition) as compared with another phenotypic status (e.g., not having the condition). A biomarker may be determined to be "differentially present" in a variety of ways, for example, between different phenotypic statuses if the presence or absence or mean or median level or concentration of the biomarker in the different groups is calculated to be statistically significant. Common tests for statistical significance include, among others, t-test, ANOVA, Kruskal-Wallis, Wilcoxon, Mann-Whitney and odds ratio.

[0152] In some embodiments, the methods and kits involve: (1) correlating a reference IRS biomarker profile with the presence or absence of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker; (2) obtaining an IRS biomarker profile of a sample (i.e., "a sample IRS biomarker profile") from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0153] As used herein, the term "profile" includes any set of data that represents the distinctive features or characteristics associated with a condition of interest, such as with a particular prediction, diagnosis and/or prognosis of a specified condition as taught herein. The term generally encompasses quantification of one or more biomarkers *inter alia* nucleic acid profiles, such as for example gene expression profiles (sets of gene expression data that represents the mRNA levels of one or more genes associated with a condition of interest), as well as protein, polypeptide or peptide profiles, such as for example protein expression profiles (sets of protein expression data that represents the levels of one or more proteins associated with a condition of interest), and any combinations thereof.

[0154] Biomarker profiles may be created in a number of ways and may be the combination of measurable biomarkers or aspects of biomarkers using methods such as ratios, or other more complex association methods or algorithms (e.g., rule-based methods), as discussed for example in more detail below. A biomarker profile comprises at least two measurements, where the measurements can correspond to the same or different biomarkers. Thus, for example, distinct reference profiles may represent the prediction of a risk (e.g., an abnormally elevated risk) of having a specified condition as compared the prediction of no or normal risk of having that condition. In another example, distinct reference profiles may represent predictions of differing degrees of risk of having a specified condition.

[0155] The terms "subject," "individual" and "patient" are used interchangeably herein to refer to any subject, particularly a vertebrate subject, and even more particularly a mammalian subject. Suitable vertebrate animals that fall within the scope of the invention include, but are not restricted to, any member of the subphylum Chordata including primates, rodents (e.g., mice rats, guinea pigs), lagomorphs (e.g., rabbits, hares), bovines (e.g., cattle), ovines (e.g., sheep), caprines (e.g., goats), porcines (e.g., pigs), equines (e.g., horses), canines (e.g., dogs), felines (e.g., cats), avians (e.g., chickens, turkeys, ducks, geese, companion birds such as canaries, budgerigars etc), marine mammals (e.g., dolphins, whales), reptiles (snakes, frogs, lizards, etc.), and fish. A preferred subject is a primate (e.g., a human, ape, monkey, chimpanzee).

[0156] IRS biomarkers are suitably expression products of IRS biomarker genes, including polynucleotide and polypeptide expression products. The term "gene" as used herein refers to any and all discrete coding regions of the cell's genome, as well as associated non-coding and regulatory regions. The term "gene" is also intended to mean the open reading frame encoding specific polypeptides, introns, and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression. In this regard, the gene may further comprise control signals such as promoters, enhancers, termination and/or polyadenylation signals that are naturally associated with a given gene, or heterologous control signals. The DNA sequences may be cDNA or genomic DNA or a fragment thereof. The gene may be introduced into an appropriate vector for extrachromosomal maintenance or for integration into the host.

[0157] As used herein, polynucleotide expression products of IRS biomarker genes are referred to herein as "IRS biomarker polynucleotides." Polypeptide expression products of the IRS biomarker genes are referred to herein as "IRS biomarker polypeptides."

[0158] Suitably, individual IRS biomarker genes are selected from the group consisting of: TLR5; CD177; VNN1; UBE2J1; IMP3; RNASE2//LOC643332; CLEC4D; C3AR1; GPR56; ARG1; FCGR1A//FCGR1B//FCGR1C; C11orf82; FAR2; GNLY; GALNT3; OMG; SLC37A3; BMX//HNRPDL; STOM; TDRD9; KREMEN1; FAIM3; CLEC4E; IL18R1; ACER3; ERLIN1; TGFBR1; FKBP5//LOC285847; GPR84; C7orf53; PLB1; DSE; PTGDR; CAMK4; DNAJC13; TNFAIP6; FOXD4L3//FOXD4L6//FOXD4//FOXD4L1//FOXD4L2//FOXD4L4//FOXD4L5; MMP9//LOC100128028; GSR; KLRF1; SH2D1B; ANKRD34B; SGMS2; B3GNT5//MCF2L2; GK3P//GK; PFKFB2; PICALM; METTL7B; HIST1H4C; C9orf72; HIST1H3I; SLC15A2; TLR10; ADM; CD274; CRIP1; LRRN3; HLA-DPB1; VAMP2; SMPDL3A; IFI16; JKAMP; MRPL41; SLC1A3; OLFM4; CASS4; TCN1; WSB2; CLU; ODZ1; KPNA5; PLAC8; CD63; HPSE; C1orf161; DDAH2; KLRK1//KLRC4; ATP13A3; ITK; PMAIP1; LOC284757; GOT2; PDGFC; B3GAT3; HIST1H4E; HPGD; FGFBP2; LRRC70//IPO11; TMEM144//LOC285505; CDS2; BPI; ECHDC3; CCR3; HSPC159; OLAH; PPP2R5A//SNORA16B; TMTC1; EAF2//HCG11//LOC647979; RCBTB2//LOC100131993; SEC24A//SAR1B; SH3PXD2B; HMGB2; KLRD1; CHI3L1; FRMD3; SLC39A9; GIMAP7; ANAPC11; EXOSC4; gene for IL-1beta-regulated neutrophil survival protein as set forth in GenBank Accession No. AF234262; INSIG1; FOLR3//FOLR2; RUNX2; PRR13//PCBP2; HIST1H4L; LGALS1; CCR1; TPST1; HLA-DRA; CD163; FFAR2; PHOSPHO1; PPIF; MTHFS;

DNAJC9//FAM149B1//RPL26; LCN2; EIF2AK2; LGALS2; SIAE; AP3B2; ABCA13; gene for transcript set forth in GenBank Accession No. AK098012; EFCAB2; HIST1H2AA; HINT1; HIST1H3J; CDA; SAP30; AGTRAP; SUCNR1; MTRR; PLA2G7; AIG1; PCOLCE2; GAB2; HS2ST1//UBA2; HIST1H3A; C22orf37; HLA-DPA1; VOPP1//LOC100128019; SLC39A8; MKI67; SLC11A1; AREG; ABCA1; DAAM2//LOC100131657; LTF; TREML1; GSTO1; PTGER2; CEACAM8; CLEC4A; PMS2CL//PMS2; RETN; PDE3B; SULF2; NEK6//LOC100129034; CENPK; TRAF3; GPR65; IRF4; MACF1; AMFR; RPL17//SNORD58B; IRS2; JUP; CD24; GALNT2; HSP90AB1//HSP90AB3P//HSP90AB2P; GLT25D1; OR9A2; HDHD1A; ACTA2; ACPL2; LRRFIP1; KCNMA1; OCR1; ITGA4//CERKL; EIF1AX//SCARNA9L//EIF1AP1; SFRS9; DPH3; ERGIC1; CD300A; NF-E4; MINPP1; TRIM21; ZNF28; NPCDR1; gene for protein FLJ21394 as set forth in GenBank Accession No. BC013935; gene for transcript set forth in GenBank Accession No. AK000992; ICAM1; TAF13; P4HA1//RPL17; C15orf54; KLHL5; HAL; DLEU2//DLEU2L; ANKRD28; LY6G5B//CSNK2B; KIAA1257//ACAD9//LOC100132731; MGST3; KIAA0746; HSPB1//HSPBL2; CCR4; TYMS; RRP12//LOC644215; CCDC125; HIST1H2BM; PDK4; ABCG1; IL1B; THBS1; ITGA2B; LHFP; LAIR1//LAIR2; HIST1H3B; ZRANB1; TIMM10; FSD1L//GARNL1; HIST1H2AJ//HIST1H2AI; PTGS1; gene for transcript set forth in GenBank Accession No. BC008667; UBE2F//C20orf194//SCLY; HIST1H3C; FAM118A; CCRL2; E2F6; MPZL3; SRXN1; CD151; HIST1H3H; FSD1L; RFESD//SPATA9; TPX2; S100B; ZNF587//ZNF417; PYHIN1; KIAA1324; CEACAM6//CEACAM5; APOLD1; FABP2; KDM6B//TMEM88; IGK@//IGKC//IGKV1-5//IGKV3D-11//IGKV3-20//IGKV3D-15//LOC440871//LOC652493//LOC100291464//LOC652694//IGKV3-15//LOC650405//LOC100291682; MYL9; HIST1H2BJ; TAAR1; CLC; CYP4F3//CYP4F2; CEP97; SON; IRF1; SYNE2; MME; LASS4; DEFA4//DEFA8P; C7orf58; DYNLL1; gene for transcript set forth in GenBank Accession No. AY461701; MPO; CPM; TSHZ2; PLIN2; FAM118B; B4GALT3; RASA4//RASA4P//RASA4B//POLR2J4//LOC100132214; CTSL1//CTSLL3; NP; ATF7; SPARC; PLB1; C4orf3; POLE2; TNFRSF17; FBXL13; PLEKHA3; TMEM62//SPCS2//LOC653566; RBP7; PLEKHF2; RGS2; ATP6V0D1//LOC100132855; RPIA; CAMK1D; IL1RL1; CMTM5; AIF1; CFD; MPZL2; LOC100128751; IGJ; CDC26; PPP1R2//PPP1R2P3; IL5RA; ARL17P1//ARL17; ATP5L//ATP5L2; TAS2R31; HIST2H2BF//HIST2H3D; CALM2//C2orf61; SPATA6; IGLV6-57; C1orf128; KRTAP15-1; IFI44; IGL@//IGLV1-44//LOC96610//IGLV2-23//IGLC1//IGLV2-18//IGLV5-45//IGLV3-25//IGLV3-12//IGLV1-36//IGLV3-27//IGLV7-46//IGLV4-3//IGLV3-16//IGLV3-19//IGLV7-43//IGLV3-22//IGLV5-37//IGLV10-54//IGLV8-61//LOC651536; gene for transcript set forth in GenBank Accession No. BC034024; SDHC; NFXL1; GLDC; DCTN5; and KIAA0101//CSNK1G1.

[0159] As used herein, the term "likelihood" is used as a measure of whether subjects with a particular IRS biomarker profile actually have a condition (or not) based on a given mathematical model. An increased likelihood for example may be relative or absolute and may be expressed qualitatively or quantitatively. For instance, an increased risk may be expressed as simply determining the subject's level of a given IRS biomarker and placing the test subject in an "increased risk" category, based upon previous population studies. Alternatively, a numerical expression of the test subject's increased risk may be determined based upon IRS biomarker level analysis.

[0160] As used herein, the term "probability" refers strictly to the probability of class membership for a sample as determined by a given mathematical model and is construed to be equivalent likelihood in this context.

[0161] In some embodiments, likelihood is assessed by comparing the level or abundance of individual IRS biomarkers to one or more preselected or threshold levels. Thresholds may be selected that provide an acceptable ability to predict diagnosis, prognostic risk, treatment success, etc. In illustrative examples, receiver operating characteristic (ROC) curves are calculated by plotting the value of a variable versus its relative frequency in two populations in which a first population has a first condition or risk and a second population has a second condition or risk (called arbitrarily, for example, "healthy condition" and "SIRS," "healthy condition" and "inSIRS," "healthy condition" and "ipSIRS," "inSIRS" and "ipSIRS," "mild sepsis" and "severe sepsis," "severe sepsis" and "septic shock," "mild sepsis" and "septic shock," or "low risk" and "high risk").

[0162] For any particular IRS biomarker, a distribution of IRS biomarker levels for subjects with and without a disease will likely overlap. Under such conditions, a test does not absolutely distinguish a first condition and a second condition with 100% accuracy, and the area of overlap indicates where the test cannot distinguish the first condition and the second condition. A threshold is selected, above which (or below which, depending on how an IRS biomarker changes with a specified condition or prognosis) the test is considered to be "positive" and below which the test is considered to be "negative." The area under the ROC curve (AUC) provides the C-statistic, which is a measure of the probability that the perceived measurement will allow correct identification of a condition (*see*, e.g., Hanley *et al.*, Radiology 143: 29-36 (1982).

[0163] Alternatively, or in addition, thresholds may be established by obtaining an earlier biomarker result from the same patient, to which later results may be compared. In these embodiments, the individual in effect acts as their own "control group." In biomarkers that increase with condition severity or prognostic risk, an increase over time in the same patient can indicate a worsening of the condition or a failure of a treatment regimen, while a decrease over time can indicate remission of the condition or success of a treatment regimen.

[0164] In some embodiments, a positive likelihood ratio, negative likelihood ratio, odds ratio, and/or AUC or receiver operating characteristic (ROC) values are used as a measure of a method's ability to predict risk or to diagnose a disease or condition. As used herein, the term "likelihood ratio" is the probability that a given test result would be observed in a subject with a condition of interest divided by the probability that that same result would be observed in a patient without the condition of interest. Thus, a positive likelihood ratio is the probability of a positive result observed in subjects with the specified condition divided by the probability of a positive results in subjects without the specified condition. A negative likelihood ratio is the probability of a negative result in subjects without the specified condition divided by the probability of a negative result in subjects with specified condition. The term "odds ratio," as used herein, refers to the ratio of the odds of an event occurring in one group (e.g., a healthy condition group) to the odds of it occurring in another group (e.g., a SIRS group, an inSIRS group, an ipSIRS group, or a group with particular stage of ipSIRS), or to a data-based estimate of that ratio. The term "area under the curve" or "AUC" refers to the area under the curve of a receiver operating characteristic (ROC) curve, both of which are well known in the art. AUC measures are useful for comparing the accuracy of a classifier across the complete data range. Classifiers with a greater AUC have a greater capacity to classify unknowns correctly between two groups of interest (e.g., a healthy condition IRS biomarker profile and a SIRS, inSIRS, ipSIRS, or ipSIRS stage IRS biomarker profile). ROC curves are useful for plotting the performance of a particular feature (e.g., any of the IRS biomarkers described herein and/or any item of additional biomedical information) in distinguishing or discriminating between two populations (e.g., cases having a condition and controls without the condition). Typically, the feature data across the entire population (e.g., the cases and controls) are sorted in ascending order based on the value of a single feature. Then, for each value for that feature, the true positive and false positive rates for the data are calculated. The sensitivity is determined by counting the number of cases above the value for that feature and then dividing by the total number of cases. The specificity is determined by counting the number of controls below the value for that feature and then dividing by the total number of controls. Although this definition refers to scenarios in which a feature is elevated in cases compared to controls, this definition also applies to scenarios in which a feature is lower in cases compared to the controls (in such a scenario, samples below the value for that feature would be counted). ROC curves can be generated for a single feature as well as for other single outputs, for example, a combination of two or more features can be mathematically combined (e.g., added, subtracted, multiplied, etc.) to produce a single value, and this single value can be plotted in a ROC curve. Additionally, any combination of multiple features, in which the combination derives a single output value, can be plotted in a ROC curve. These combinations of features may comprise a test. The ROC curve is the plot of the sensitivity of a test against the specificity of the test, where sensitivity is traditionally presented on the vertical axis and specificity is traditionally presented on the horizontal axis. Thus, "AUC ROC values" are equal to the probability that a classifier will rank a randomly chosen positive instance higher than a randomly chosen negative one. An AUC ROC value may be thought of as equivalent to the

Mann-Whitney U test, which tests for the median difference between scores obtained in the two groups considered if the groups are of continuous data, or to the Wilcoxon test of ranks.

[0165] In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) IRS biomarker or a panel if IRS biomarkers is selected to discriminate between subjects with a first condition and subjects with a second condition with at least about 50%, 55% 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% accuracy or having a C-statistic of at least about 0.50, 0.55, 0.60, 0.65, 0.70, 0.75, 0.80, 0.85, 0.90, 0.95.

[0166] In the case of a positive likelihood ratio, a value of 1 indicates that a positive result is equally likely among subjects in both the "condition" and "control" groups; a value greater than 1 indicates that a positive result is more likely in the condition group; and a value less than 1 indicates that a positive result is more likely in the control group. In this context, "condition" is meant to refer to a group having one characteristic (e.g., the presence of a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS) and "control" group lacking the same characteristic. In the case of a negative likelihood ratio, a value of 1 indicates that a negative result is equally likely among subjects in both the "condition" and "control" groups; a value greater than 1 indicates that a negative result is more likely in the "condition" group; and a value less than 1 indicates that a negative result is more likely in the "control" group. In the case of an odds ratio, a value of 1 indicates that a positive result is equally likely among subjects in both the condition" and "control" groups; a value greater than 1 indicates that a positive result is more likely in the "condition" group; and a value less than 1 indicates that a positive result is more likely in the "control" group. In the case of an AUC ROC value, this is computed by numerical integration of the ROC curve. The range of this value can be 0.5 to 1.0. A value of 0.5 indicates that a classifier (e.g., a IRS biomarker profile) is no better than a 50% chance to classify unknowns correctly between two groups of interest, while 1.0 indicates the relatively best diagnostic accuracy. In certain embodiments, IRS biomarkers and/or IRS biomarker panels are selected to exhibit a positive or negative likelihood ratio of at least about 1.5 or more or about 0.67 or less, at least about 2 or more or about 0.5 or less, at least about 5 or more or about 0.2 or less, at least about 10 or more or about 0.1 or less, or at least about 20 or more or about 0.05 or less.

[0167] In certain embodiments, IRS biomarkers and/or IRS biomarker panels are selected to exhibit an odds ratio of at least about 2 or more or about 0.5 or less, at least about 3 or more or about 0.33 or less, at least about 4 or more or about 0.25 or less, at least about 5 or more or about 0.2 or less, or at least about 10 or more or about 0.1 or less.

[0168] In certain embodiments, IRS biomarkers and/or IRS biomarker panels are selected to exhibit an AUC ROC value of greater than 0.5, preferably at least 0.6, more preferably 0.7, still more preferably at least 0.8, even more preferably at least 0.9, and most preferably at least 0.95.

[0169] In some cases, multiple thresholds may be determined in so-called "tertile," "quartile," or "quintile" analyses. In these methods, the "diseased" and "control groups" (or "high risk" and "low risk") groups are considered together as a single population, and are divided into 3, 4, or 5 (or more) "bins" having equal numbers of individuals. The boundary between two of these "bins" may be considered "thresholds." A risk (of a particular diagnosis or prognosis for example) can be assigned based on which "bin" a test subject falls into.

[0170] In other embodiments, particular thresholds for the IRS biomarker(s) measured are not relied upon to determine if the biomarker level(s) obtained from a subject are correlated to a particular diagnosis or prognosis. For example, a temporal change in the biomarker(s) can be used to rule in or out one or more particular diagnoses and/or prognoses. Alternatively, IRS biomarker(s) are correlated to a condition, disease, prognosis, etc., by the presence or absence of one or more IRS biomarkers in a particular assay format. In the case of IRS biomarker panels, the present invention may utilize an evaluation of the entire profile of IRS biomarkers to provide a single result value (e.g., a "panel response" value expressed either as a numeric score or as a percentage risk). In such embodiments, an increase, decrease, or other change (e.g., slope over time) in a certain subset of IRS biomarkers may be sufficient to indicate a particular condition or future outcome in one patient, while an increase, decrease, or other change in a different subset of IRS biomarkers may be sufficient to indicate the same or a different condition or outcome in another patient.

[0171] In certain embodiments, a panel of IRS biomarkers is selected to assist in distinguishing a pair of groups (i.e., assist in assessing whether a subject has an increased likelihood of being in one group or the other group of the pair) selected from "healthy condition" and "SIRS," "healthy condition" and "inSIRS," "healthy condition" and "ipSIRS," "inSIRS" and "ipSIRS," "mild sepsis" and "severe sepsis," "severe sepsis" and "septic shock," "mild sepsis" and "septic shock," or "low risk" and "high risk" with at least about 70%, 80%, 85%, 90% or 95% sensitivity, suitably in combination with at least about 70% 80%, 85%, 90% or 95% specificity. In some embodiments, both the sensitivity and specificity are at least about 75%, 80%, 85%, 90% or 95%.

[0172] The phrases "assessing the likelihood" and "determining the likelihood," as used herein, refer to methods by which the skilled artisan can predict the presence or absence of a condition (e.g., a condition selected from healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS) in a patient. The skilled artisan will understand that this phrase includes within its scope an increased probability that a condition is present or absence in a patient; that is, that a condition is more likely to be present or absent in a subject. For example, the probability that an individual identified as having a specified condition actually has the condition may be expressed as a "positive predictive value" or "PPV." Positive predictive value can be calculated as the number of true positives divided by the sum of the true positives and false positives. PPV is determined by the characteristics of the predictive methods of the present invention as well as the prevalence of the condition in the population analysed. The statistical algorithms can be selected such that the positive predictive value in a population having a condition prevalence is in the range of 70% to 99% and can be, for example, at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%.

[0173] In other examples, the probability that an individual identified as not having a specified condition actually does not have that condition may be expressed as a "negative predictive value" or "NPV." Negative predictive value can be calculated as the number of true negatives divided by the sum of the true negatives and false negatives. Negative predictive value is determined by the characteristics of the diagnostic or prognostic method, system, or code as well as the prevalence of the disease in the population analysed. The statistical methods and models can be selected such that the negative predictive value in a population having a condition prevalence is in the range of about 70% to about 99% and can be, for example, at least about 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%.

[0174] In some embodiments, a subject is determined as having a significant likelihood of having or nott having a specified condition. By "significant likelihood" is meant that the subject has a reasonable probability (0.6, 0.7, 0.8, 0.9 or more) of having, or not having, a specified condition.

[0175] The IRS biomarker analysis of the present invention permits the generation of high-density data sets that can be evaluated using informatics approaches. High data density informatics analytical methods are known and software is available to those in the art, e.g., cluster analysis (Pirouette, Informetrix), class prediction (SIMCA-P, Umetrics), principal components analysis of a computationally modeled dataset (SIMCA-P, Umetrics), 2D cluster analysis (GeneLinker Platinum, Improved Outcomes Software), and metabolic pathway analysis (biotech.icmb.utexas.edu). The choice of software packages offers specific tools for questions of interest (Kennedy et al., Solving Data Mining Problems Through Pattern Recognition. Indianapolis: Prentice Hall PTR, 1997; Golub et al., (2999) Science 286:531-7; Eriksson et al., Multi and Megavariate Analysis Principles and Applications: Umetrics, Umea, 2001). In general, any suitable mathematic analyses can be used to evaluate at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, et.) IRS biomarker in an IRS biomarker profile with respect to a condition selected from healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS. For example, methods such as multivariate analysis of variance, multivariate regression, and/or multiple regression can be used to determine relationships between dependent variables (e.g., clinical measures) and independent variables (e.g., levels of IRS biomarkers). Clustering, including both hierarchical and non-hierarchical methods, as well as non-metric Dimensional Scaling can be used to determine associations or relationships among variables and among changes in those variables.

[0176] In addition, principal component analysis is a common way of reducing the dimension of studies, and can be used to interpret the variance-covariance structure of a data set. Principal components may be used in such applications as multiple regression and cluster analysis. Factor analysis is used to describe the covariance by constructing "hidden" variables from the observed variables. Factor analysis may be considered an extension of principal component analysis, where principal component analysis is used as parameter estimation along with the maximum likelihood method. Furthermore, simple hypothesis such as equality of two vectors of means can be tested using Hotelling's T squared statistic.

[0177] In some embodiments, the data sets corresponding to IRS biomarker profiles are used to create a diagnostic or predictive rule or model based on the application of a statistical and machine learning algorithm. Such an algorithm uses relationships between an IRS biomarker profile and a condition selected from healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS observed in control subjects or typically cohorts of control subjects (sometimes referred to as training data), which provides combined control or reference IRS biomarker profiles for comparison with IRS biomarker profiles of a subject. The data are used to infer relationships that are then used to predict the status of a subject, including the presence or absence of one of the conditions referred to above.

[0178] Practitioners skilled in the art of data analysis recognize that many different forms of inferring relationships in the training data may be used without materially changing the present invention. The data presented in the Tables and Examples herein has been used to generate illustrative minimal combinations of IRS biomarkers (models) that differentiate between two conditions selected from healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS using feature selection based on AUC maximisation in combination with support vector machine classification. Tables 1-15 provide illustrative lists of IRS biomarkers ranked according to their p value and Figures 1-331 illustrate the ability of each IRS biomarker to distinguish between at least two of the conditions. Illustrative models comprising at least about 2 IRS biomarkers were able to discriminate between two control groups as defined above with significantly improved positive predictive values compared to conventional methodologies.

[0179] The term "correlating" generally refers to determining a relationship between one type of data with another or with a state. In various embodiments, correlating an IRS biomarker profile with the presence or absence of a condition (e.g., a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS) comprises determining the presence, absence or amount of at least one IRS biomarker in a subject that suffers from that condition; or in persons known to be free of that condition. In specific embodiments, a profile of IRS biomarker levels, absences or presences is correlated to a global probability or a particular outcome, using receiver operating characteristic (ROC) curves.

[0180] Thus, in some embodiments, evaluation of IRS biomarkers includes determining the levels of individual IRS biomarkers, which correlate with the presence or absence of a condition, as defined above. In certain embodiments, the techniques used for detection of IRS biomarkers will include internal or external standards to permit quantitative or semi-quantitative determination of those biomarkers, to thereby enable a valid comparison of the level of the IRS biomarkers in a biological sample with the corresponding IRS biomarkers in a reference sample or samples. Such standards can be determined by the skilled practitioner using standard protocols. In specific examples, absolute values for the level or functional activity of individual expression products are determined.

[0181] In semi-quantitative methods, a threshold or cut-off value is suitably determined, and is optionally a predetermined value. In particular embodiments, the threshold value is predetermined in the sense that it is fixed, for example, based on previous experience with the assay and/or a population of affected and/or unaffected subjects. Alternatively, the predetermined value can also indicate that the method of arriving at the threshold is predetermined or fixed even if the particular value varies among assays or may even be determined for every assay run.

[0182] In some embodiments, the level of an IRS biomarker is normalized against a housekeeping biomarker. The term "housekeeping biomarker" refers to a biomarker or group of biomarkers (e.g., polynucleotides and/or polypeptides), which are typically found at a constant level in the cell type(s) being analysed and across the conditions being assessed. In some embodiments, the housekeeping biomarker is a "housekeeping gene." A "housekeeping gene" refers herein to a gene or group of genes which encode proteins whose activities are essential for the maintenance of cell function and which are typically found at a constant level in the cell type(s) being analysed and across the conditions being assessed.

[0183] Generally, the levels of individual IRS biomarkers in an IRS biomarker profile are derived from a biological sample. The term "biological sample" as used herein refers to a sample that may be extracted, untreated, treated, diluted or concentrated from an animal. The biological sample is suitably a biological fluid such as whole blood, serum, plasma, saliva, urine, sweat, ascitic fluid, peritoneal fluid, synovial fluid, amniotic fluid, cerebrospinal fluid, tissue biopsy, and the like. In certain embodiments, the biological sample contains blood, especially peripheral blood, or a fraction or extract thereof. Typically, the biological sample comprises blood cells such as mature, immature or developing leukocytes, including lymphocytes, polymorphonuclear leukocytes, neutrophils, monocytes, reticulocytes, basophils, coelomocytes, hemocytes, eosinophils, megakaryocytes, macrophages, dendritic cells natural killer cells, or fraction of such cells (e.g., a nucleic acid or protein fraction). In specific embodiments, the biological sample comprises leukocytes including peripheral blood mononuclear cells (PBMC).

[0184] The term "nucleic acid" or "polynucleotide" refers to a polymer, typically a heteropolymer, of nucleotides or the sequence of these nucleotides from the 5' to 3' end of a nucleic acid molecule and includes DNA or RNA molecules, illustrative examples of which include RNA, mRNA, siRNA, miRNA, hpRNA, cRNA, cDNA or DNA. The term encompasses a polymeric form of nucleotides that is linear or branched, single or double stranded, or a hybrid thereof. The term also encompasses RNA/DNA hybrids. Nucleic acid sequences provided herein are presented herein in the 5′ to 3′ direction, from left to right and are represented using the standard code for representing the nucleotide characters as set forth in the U.S. sequence rules, 37 CFR 1.821 - 1.825 and the World Intellectual Property Organization (WIPO) Standard ST.25.

[0185] "Protein," "polypeptide" and "peptide" are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same.

[0186] Suitably, the levels of individual IRS biomarkers in a reference IRS biomarker profile are derived from IRS biomarker samples obtained from one or more control subjects having that condition (e.g., "healthy control subjects," "SIRS control subjects," "inSIRS control subjects," "ipSIRS control subjects," "control subjects with a particular stage of ipSIRS," illustrative examples of which include "mild sepsis control subjects," "severe sepsis control subjects," and "septic shock control subjects," etc.), which are also referred to herein as control groups (e.g., "healthy control group," "SIRS control group," "inSIRS control group," "ipSIRS control group," "ipSIRS stage group," illustrative examples of which include "mild sepsis control group," "severe sepsis control group," and "septic shock control group," etc.) . By "obtained" is meant to come into possession. Biological or reference samples so obtained include, for example, nucleic acid extracts or polypeptide extracts isolated or derived from a particular source. For instance, the extract may be isolated directly from a biological fluid or tissue of a subject.

[0187] As used herein the terms "level" and "amount" are used interchangeably herein to refer to a quantitative amount (e.g., weight or moles), a semi-quantitative amount, a relative amount (e.g., weight % or mole % within class or a ratio), a concentration, and the like. Thus, these terms encompasses absolute or relative amounts or concentrations of IRS biomarkers in a sample, including ratios of levels of IRS biomarkers, and odds ratios of levels or ratios of odds ratios. IRS biomarker levels in cohorts of subjects may be represented as mean levels and standard deviations as shown in the Tables and Figures herein.

[0188] In some embodiments, the level of at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker of the subject's sample IRS biomarker profile is compared to the level of a corresponding IRS biomarker in the reference IRS biomarker profile. By "corresponding IRS biomarker" is meant an IRS biomarker that is structurally and/or functionally similar to a reference IRS biomarker. Representative corresponding IRS biomarkers include expression products of allelic variants (same locus), homologs (different locus), and orthologs (different organism) of reference IRS biomarker genes. Nucleic acid variants of reference IRS biomarker genes and encoded IRS biomarker polynucleotide expression products can contain nucleotide substitutions, deletions, inversions and/or insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product). For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of a reference IRS polypeptide.

[0189] Generally, variants of a particular IRS biomarker gene or polynucleotide will have at least about 40%, 45%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59% 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69% 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs known in the art using default parameters. In some embodiments, the IRS biomarker gene or polynucleotide displays at least about 40%, 45%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59% 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69% 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a nucleotide sequence selected from any one of SEQ ID NO: 1-319.

[0190] Corresponding IRS biomarkers also include amino acid sequence that displays substantial sequence similarity or identity to the amino acid sequence of a reference IRS biomarker polypeptide. In general, an amino acid sequence that corresponds to a reference amino acid sequence will display at least about 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 97, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or even up to 100% sequence similarity or identity to a reference amino acid sequence selected from any one of SEQ ID NO: 320-619.

[0191] In some embodiments, calculations of sequence similarity or sequence identity between sequences are performed as follows:

[0192] To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In some embodiments, the length of a reference sequence aligned for comparison purposes is at least 30%, usually at least 40%, more usually at least 50%, 60%, and even more usually at least 70%, 80%, 90%, 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide at the corresponding position in the second sequence, then the molecules are identical at that position. For amino acid sequence comparison, when a position in the first sequence is occupied by the same or similar amino acid residue (i.e., conservative substitution) at the corresponding position in the second sequence, then the molecules are similar at that position.

[0193] The percent identity between the two sequences is a function of the number of identical amino acid residues shared by the sequences at individual positions, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. By contrast, the percent similarity between the two sequences is a function of the number of identical and similar amino acid residues shared by the sequences at individual positions, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

[0194] The comparison of sequences and determination of percent identity or percent similarity between sequences can be accomplished using a mathematical algorithm. In certain embodiments, the percent identity or similarity between amino acid sequences is determined using the Needleman and Wünsch, (1970, *J. Mol. Biol.* 48: 444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In specific embodiments, the percent identity between nucleotide sequences is determined using the GAP program in the GCG software package (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. An non-limiting set of parameters (and the one that should be used unless otherwise specified) includes a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0195] In some embodiments, the percent identity or similarity between amino acid or nucleotide sequences can be determined using the algorithm of E. Meyers and W. Miller (1989, *Cabios*, 4: 11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

[0196] The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.*, (1990, *J. Mol. Biol*, 215: 403-10). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 53010 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 53010 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997, *Nucleic Acids Res*, 25: 3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

[0197] Corresponding IRS biomarker polynucleotides also include nucleic acid sequences that hybridize to reference IRS biomarker polynucleotides, or to their complements, under stringency conditions described below. As used herein, the term "hybridizes under low stringency, medium stringency, high stringency, or very high stringency conditions" describes conditions for hybridization and washing. "Hybridization" is used herein to denote the pairing of complementary nucleotide sequences to produce a DNA-DNA hybrid or a DNA-RNA hybrid. Complementary base sequences are those sequences that are related by the base-pairing rules. In DNA, A pairs with T and C pairs with G. In RNA, U pairs with A and C pairs with G. In this regard, the terms "match" and "mismatch" as used herein refer to the hybridization potential of paired nucleotides in complementary nucleic acid strands. Matched nucleotides hybridize efficiently, such as the classical A-T and G-C base pair mentioned above. Mismatches are other combinations of nucleotides that do not hybridize efficiently.

[0198] Guidance for performing hybridization reactions can be found in Ausubel *et al.*, (1998, *supra*), Sections 6.3.1-6.3.6. Aqueous and non-aqueous methods are described in that reference and either can be used. Reference herein to low stringency conditions include and encompass from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization at 42° C, and at least about 1 M to at least about 2 M salt for washing at 42° C. Low stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at room temperature. One embodiment of low stringency conditions includes hybridization in 6 × sodium chloride/sodium citrate (SSC) at about 45□□C, followed by two washes in 0.2 × SSC, 0.1% SDS at least at 50° C (the temperature of the washes can be increased to 55° C for low stringency conditions). Medium stringency conditions include and encompass from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization at 42° C, and at least about 0.1 M to at least about 0.2 M salt for washing at 55° C. Medium stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at 60-65° C. One embodiment of medium stringency conditions includes hybridizing in 6 × SSC at about 45□□C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 60° C. High stringency conditions include and encompass from at least about 31% v/v to at least about 50% v/v formamide and from about 0.01 M to about 0.15 M salt for hybridization at 42° C, and about 0.01 M to about 0.02 M salt for washing at 55° C. High stringency conditions also may include 1% BSA, 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 0.2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 1% SDS for washing at a temperature in excess of 65° C. One embodiment of high stringency conditions includes hybridizing in 6 × SSC at about 45□□C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 65° C.

[0199] In certain embodiments, a corresponding IRS biomarker polynucleotide is one that hybridizes to a disclosed nucleotide sequence under very high stringency conditions. One embodiment of very high stringency conditions includes hybridizing 0.5 M sodium phosphate, 7% SDS at 65° C, followed by one or more washes at 0.2 × SSC, 1% SDS at 65° C.

[0200] Other stringency conditions are well known in the art and a skilled addressee will recognize that various factors can be manipulated to optimize the specificity of the hybridization. Optimization of the stringency of the final washes can serve to ensure a high degree of hybridization. For detailed examples, see Ausubel *et al.*, *supra* at pages 2.10.1 to 2.10.16 and Sambrook *et al.* (1989, *supra*) at sections 1.101 to 1.104.

[0201] Thus, in some embodiments, IRS biomarker levels in control groups as broadly defined above and elsewhere herein are used to generate a profile of IRS biomarker levels reflecting difference between levels in two control groups as described above and elsewhere herein. Thus, a particular IRS biomarker may be more abundant or less abundant in one control group as compared to another control group. The data may be represented as an overall signature score or the profile may be represented as a barcode or other graphical representation to facilitate analysis or diagnosis or determination of likelihood. The IRS biomarker levels from a test subject may be represented in the same way and the similarity with the signature score or level of "fit" to a signature barcode or other graphical representation may be determined. In other embodiments, the levels of a particular IRS biomarker are analysed and a downward or an upward trend in IRS biomarker level determined.

[0202] In some embodiments, the individual level of an IRS biomarker in a first control group (e.g., a control group selected from healthy condition control group, SIRS control group, inSIRS control group, ipSIRS control group, or ipSIRS stage control group) is at least 101%, 102%, 103%, 104%, 105%, 106%, 107% 108%, 109%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000% (i.e. an increased or higher level), or no more than about 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.01%, 0.001% or 0.0001% (i.e. a decreased or lower level) of the level of a corresponding IRS biomarker in a second control group (e.g., a control group selected from healthy condition control group, SIRS control group, inSIRS control group, ipSIRS control group, or ipSIRS stage control group, illustrative examples of which include "mild sepsis control group, severe sepsis control group, and septic shock control group, which is different from the first control group).

[0203] An IRS biomarker profile provides a compositional analysis (e.g., concentration or mole percentage (%) of the IRS biomarker) in which two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, twelve or more, fifteen or more, twenty or more, fifty or more, one-hundred or more or a greater number of IRS biomarkers are evaluated.

[0204] The IRS biomarker profile can be quantitative, semi-quantitative and/or qualitative. For example, the IRS biomarker profile can evaluate the presence or absence of an IRS biomarker, can evaluate the presence of an IRS biomarker(s) above or below a particular threshold, and/or can evaluate the relative or absolute amount of an IRS biomarker(s). In particular embodiments, a ratio among two, three, four or more IRS biomarkers is determined (see Example 6 and Tables 16 – 21 for examples of the use of 2-gene ratios in separating various inSIRS and ipSIRS conditions). Changes or perturbations in IRS biomarker ratios can be advantageous in indicating where there are blocks (or releases of such blocks) or other alterations in cellular pathways associated with an IRS condition, response to treatment, development of side effects, and the like.

[0205] IRS biomarkers may be quantified or detected using any suitable technique including nucleic acid- and protein-based assays.

[0206] In illustrative nucleic acid-based assays, nucleic acid is isolated from cells contained in the biological sample according to standard methodologies (Sambrook, *et al.*, 1989, *supra*; and Ausubel *et al.*, 1994, *supra*). The nucleic acid is typically fractionated (e.g., poly A^+ RNA) or whole cell RNA. Where RNA is used as the subject of detection, it may be desired to convert the RNA to a complementary DNA. In some embodiments, the nucleic acid is amplified by a template-dependent nucleic acid amplification technique. A number of template dependent processes are available to amplify the IRS biomarker sequences present in a given template sample. An exemplary nucleic acid amplification technique is the polymerase chain reaction (referred to as PCR), which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, Ausubel *et al.* (*supra*), and in Innis *et al.*, ("PCR Protocols", Academic Press, Inc., San Diego Calif., 1990). Briefly, in PCR, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the biomarker sequence. An excess of deoxynucleotide triphosphates are added to a reaction mixture along with a DNA polymerase, e.g., *Taq* polymerase. If a cognate IRS biomarker sequence is present in a sample, the primers will bind to the biomarker and the polymerase will cause the primers to be extended along the biomarker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the biomarker to form reaction products, excess primers will bind to the biomarker and to the reaction products and the process is repeated. A reverse transcriptase PCR amplification procedure may be performed in order to quantify the amount of mRNA amplified. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989, *supra*. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641. Polymerase chain reaction methodologies are well known in the art.

[0207] In certain advantageous embodiments, the template-dependent amplification involves quantification of transcripts in real-time. For example, RNA or DNA may be quantified using the Real-Time PCR technique (Higuchi, 1992, *et al.*, *Biotechnology* **10**: 413-417). By determining the concentration of the amplified products of the target DNA in PCR reactions that have completed the same number of cycles and are in their linear ranges, it is possible to determine the relative concentrations of the specific target sequence in the original DNA mixture. If the DNA mixtures are cDNAs synthesized from RNAs isolated from different tissues or cells, the relative abundance of the specific mRNA from which the target sequence was derived can be determined for the respective tissues or cells. This direct proportionality between the concentration of the PCR products and the relative mRNA abundance is only true in the linear range of the PCR reaction. The final concentration of the target DNA in the plateau portion of the curve is determined by the availability of reagents in the reaction mix and is independent of the original concentration of target DNA. In specific embodiments, multiplexed, tandem PCR

(MT-PCR) is employed, which uses a two-step process for gene expression profiling from small quantities of RNA or DNA, as described for example in US Pat. Appl. Pub. No. 20070190540. In the first step, RNA is converted into cDNA and amplified using multiplexed gene specific primers. In the second step each individual gene is quantitated by real time PCR.

[0208] In certain embodiments, target nucleic acids are quantified using blotting techniques, which are well known to those of skill in the art. Southern blotting involves the use of DNA as a target, whereas Northern blotting involves the use of RNA as a target. Each provides different types of information, although cDNA blotting is analogous, in many aspects, to blotting or RNA species. Briefly, a probe is used to target a DNA or RNA species that has been immobilized on a suitable matrix, often a filter of nitrocellulose. The different species should be spatially separated to facilitate analysis. This often is accomplished by gel electrophoresis of nucleic acid species followed by "blotting" on to the filter. Subsequently, the blotted target is incubated with a probe (usually labelled) under conditions that promote denaturation and rehybridisation. Because the probe is designed to base pair with the target, the probe will bind a portion of the target sequence under renaturing conditions. Unbound probe is then removed, and detection is accomplished as described above. Following detection/quantification, one may compare the results seen in a given subject with a control reaction or a statistically significant reference group or population of control subjects as defined herein. In this way, it is possible to correlate the amount of a IRS biomarker nucleic acid detected with the progression or severity of the disease.

[0209] Also contemplated are biochip-based technologies such as those described by Hacia *et al.* (1996, *Nature Genetics* 14: 441-447) and Shoemaker *et al.* (1996, Nature Genetics 14: 450-456). Briefly, these techniques involve quantitative methods for analysing large numbers of genes rapidly and accurately. By tagging genes with oligonucleotides or using fixed probe arrays, one can employ biochip technology to segregate target molecules as high-density arrays and screen these molecules on the basis of hybridization. See also Pease *et al.* (1994, *Proc. Natl. Acad. Sci. U.S.A.* 91: 5022-5026); Fodor *et al.* (1991, *Science* 251: 767-773). Briefly, nucleic acid probes to IRS biomarker polynucleotides are made and attached to biochips to be used in screening and diagnostic methods, as outlined herein. The nucleic acid probes attached to the biochip are designed to be substantially complementary to specific expressed IRS biomarker nucleic acids, *i.e.*, the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occur. This complementarity need not be perfect; there may be any number of base pair mismatches, which will interfere with hybridization between the target sequence and the nucleic acid probes of the present invention. However, if the number of mismatches is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. In certain embodiments, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being desirable, are used to build in a redundancy for a particular target. The probes can be overlapping (*i.e.* have some sequence in common), or separate.

[0210] In an illustrative biochip analysis, oligonucleotide probes on the biochip are exposed to or contacted with a nucleic acid sample suspected of containing one or more IRS biomarker polynucleotides under conditions favouring specific hybridization. Sample extracts of DNA or RNA, either single or double-stranded, may be prepared from fluid suspensions of biological materials, or by grinding biological materials, or following a cell lysis step which includes, but is not limited to, lysis effected by treatment with SDS (or other detergents), osmotic shock, guanidinium isothiocyanate and lysozyme. Suitable DNA, which may be used in the method of the invention, includes cDNA. Such DNA may be prepared by any one of a number of commonly used protocols as for example described in Ausubel, *et al.*, 1994, *supra*, and Sambrook, *et al.*, *et al.*, 1989, *supra*.

[0211] Suitable RNA, which may be used in the method of the invention, includes messenger RNA, complementary RNA transcribed from DNA (cRNA) or genomic or subgenomic RNA. Such RNA may be prepared using standard protocols as for example described in the relevant sections of Ausubel, *et al.* 1994, *supra* and Sambrook, *et al.* 1989, *supra*).

[0212] cDNA may be fragmented, for example, by sonication or by treatment with restriction endonucleases. Suitably, cDNA is fragmented such that resultant DNA fragments are of a length greater than the length of the immobilized oligonucleotide probe(s) but small enough to allow rapid access thereto under suitable hybridization conditions. Alternatively, fragments of cDNA may be selected and amplified using a suitable nucleotide amplification technique, as described for example above, involving appropriate random or specific primers.

[0213] Usually the target IRS biomarker polynucleotides are detectably labelled so that their hybridization to individual probes can be determined. The target polynucleotides are typically detectably labelled with a reporter molecule illustrative examples of which include chromogens, catalysts, enzymes, fluorochromes, chemiluminescent molecules, bioluminescent molecules, lanthanide ions (e.g., Eu^{34}), a radioisotope and a direct visual label. In the case of a direct visual label, use may be made of a colloidal metallic or non-metallic particle, a dye particle, an enzyme or a substrate, an organic polymer, a latex particle, a liposome, or other vesicle containing a signal producing substance and the like. Illustrative labels of this type include large colloids, for example, metal colloids such as those from gold, selenium, silver, tin and titanium oxide. In some embodiments in which an enzyme is used as a direct visual label, biotinylated bases are incorporated into a target polynucleotide.

[0214] The hybrid-forming step can be performed under suitable conditions for hybridizing oligonucleotide probes to test nucleic acid including DNA or RNA. In this regard, reference may be made, for example, to NUCLEIC ACID HYBRIDIZATION, A PRACTICAL APPROACH (Homes and Higgins, eds.) (IRL press, Washington D.C., 1985). In general, whether hybridization takes place is influenced by the length of the oligonucleotide probe and the polynucleotide sequence under test, the pH, the temperature, the concentration of mono- and divalent cations, the proportion of G and C nucleotides in the hybrid-forming region, the viscosity of the medium and the possible presence of denaturants. Such variables also influence the time required for hybridization. The preferred conditions will therefore depend upon the particular application. Such empirical conditions, however, can be routinely determined without undue experimentation.

[0215] After the hybrid-forming step, the probes are washed to remove any unbound nucleic acid with a hybridization buffer. This washing step leaves only bound target polynucleotides. The probes are then examined to identify which probes have hybridized to a target polynucleotide.

[0216] The hybridization reactions are then detected to determine which of the probes has hybridized to a corresponding target sequence. Depending on the nature of the reporter molecule associated with a target polynucleotide, a signal may be instrumentally detected by irradiating a fluorescent label with light and detecting fluorescence in a fluorimeter; by providing for an enzyme system to produce a dye which could be detected using a spectrophotometer; or detection of a dye particle or a coloured colloidal metallic or non metallic particle using a reflectometer; in the case of using a radioactive label or chemiluminescent molecule employing a radiation counter or autoradiography. Accordingly, a detection means may be adapted to detect or scan light associated with the label which light may include fluorescent, luminescent, focussed beam or laser light. In such a case, a charge couple device (CCD) or a photocell can be used to scan for emission of light from a probe:target polynucleotide hybrid from each location in the micro-array and record the data directly in a digital computer. In some cases, electronic detection of the signal may not be necessary. For example, with enzymatically generated colour spots associated with nucleic acid array format, visual examination of the array will allow interpretation of the pattern on the array. In the case of a nucleic acid array, the detection means is suitably interfaced with pattern recognition software to convert the pattern of signals from the array into a plain language genetic profile. In certain embodiments, oligonucleotide probes specific for different IRS biomarker polynucleotides are in the form of a nucleic acid array and detection of a signal generated from a reporter molecule on the array is performed using a 'chip reader'. A detection system that can be used by a 'chip reader' is described for example by Pirrung *et al* (U.S. Patent No. 5,143,854). The chip reader will typically also incorporate some signal processing to determine whether the signal at a particular array position or feature is a true positive or maybe a spurious signal. Exemplary chip readers are described for example by Fodor *et al* (U.S. Patent No., 5,925,525). Alternatively, when the array is made using a mixture of individually addressable kinds of labelled microbeads, the reaction may be detected using flow cytometry.

[0217] In other embodiments, IRS biomarker protein levels are assayed using protein-based assays known in the art. For example, when an IRS biomarker protein is an enzyme, the protein can be quantified based upon its catalytic activity or based upon the number of molecules of the protein contained in a sample. Antibody-based techniques may be employed including, for example, immunoassays, such as the enzyme-linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA).

[0218] In specific embodiments, protein-capture arrays that permit simultaneous detection and/or quantification of a large number of proteins are employed. For example, low-density protein arrays on filter membranes, such as the universal protein array system (Ge, 2000 *Nucleic Acids Res.* 28(2):e3) allow imaging of arrayed antigens using standard ELISA techniques and a scanning charge-coupled device (CCD) detector. Immuno-sensor arrays have also been developed that enable the simultaneous detection of clinical analytes. It is now possible using protein arrays, to profile protein expression in bodily fluids, such as in sera of healthy or diseased subjects, as well as in subjects pre- and post-drug treatment.

[0219] Exemplary protein capture arrays include arrays comprising spatially addressed antigen-binding molecules, commonly referred to as antibody arrays, which can facilitate extensive parallel analysis of numerous proteins defining a proteome or subproteome. Antibody arrays have been shown to have the required properties of specificity and acceptable background, and some are available commercially (*e.g.*, BD Biosciences, Clontech, BioRad and Sigma). Various methods for the preparation of antibody arrays have been reported (see, *e.g.*, Lopez *et al.*, 2003 *J.* Chromatogr. B 787:19-27; Cahill, 2000 Trends in Biotechnology 7:47-51; U.S. Pat. App. Pub. 2002/0055186; U.S. Pat. App. Pub. 2003/0003599; PCT publication WO 03/062444; PCT publication WO 03/077851; PCT publication WO 02/59601; PCT publication WO 02/39120; PCT publication WO 01/79849; PCT publication WO 99/39210). The antigen-binding molecules of such arrays may recognise at least a subset of proteins expressed by a cell or population of cells, illustrative examples of which include growth factor receptors, hormone receptors, neurotransmitter receptors, catecholamine receptors, amino acid derivative receptors, cytokine receptors, extracellular matrix receptors, antibodies, lectins, cytokines, serpins, proteases, kinases, phosphatases, ras-like GTPases, hydrolases, steroid hormone receptors, transcription factors, heat-shock transcription factors, DNA-binding proteins, zinc-finger proteins, leucine-zipper proteins, homeodomain proteins, intracellular signal transduction modulators and effectors, apoptosis-related factors, DNA synthesis factors, DNA repair factors, DNA recombination factors and cell-surface antigens.

[0220] Individual spatially distinct protein-capture agents are typically attached to a support surface, which is generally planar or contoured. Common physical supports include glass slides, silicon, microwells, nitrocellulose or PVDF membranes, and magnetic and other microbeads.

[0221] Particles in suspension can also be used as the basis of arrays, providing they are coded for identification; systems include colour coding for microbeads (*e.g.*, available from Luminex, Bio-Rad and Nanomics Biosystems) and semiconductor nanocrystals (*e.g.*, QDots™, available from Quantum Dots), and barcoding for beads (UltraPlex™, available from Smartbeads) and multimetal microrods (Nanobarcodes™ particles, available from Surromed). Beads can also be assembled into planar arrays on semiconductor chips (*e.g.*, available from LEAPS technology and BioArray Solutions). Where particles are used, individual protein-capture agents are typically attached to an individual particle to provide the spatial definition or separation of the array. The particles may then be assayed separately, but in parallel, in a compartmentalized way, for example in the wells of a microtiter plate or in separate test tubes.

[0222] In operation, a protein sample, which is optionally fragmented to form peptide fragments (see, *e.g.*, U.S. Pat. App. Pub. 2002/0055186), is delivered to a protein-capture array under conditions suitable for protein or peptide binding, and the array is washed to remove unbound or non-specifically bound components of the sample from the array. Next, the presence or amount of protein or peptide bound to each feature of the array is detected using a suitable detection system. The amount of protein bound to a feature of the array may be determined relative to the amount of a second protein bound to a second feature of the array. In certain embodiments, the amount of the second protein in the sample is already known or known to be invariant.

[0223] For analysing differential expression of proteins between two cells or cell populations, a protein sample of a first cell or population of cells is delivered to the array under conditions suitable for protein binding. In an analogous manner, a protein sample of a second cell or population of cells to a second array is delivered to a second array that is identical to the first array. Both arrays are then washed to remove unbound or non-specifically bound components of the sample from the arrays. In a final step, the amounts of protein remaining bound to the features of the first array are compared to the amounts of protein remaining bound to the corresponding features of the second array. To determine the differential protein expression pattern of the two cells or populations of cells, the amount of protein bound to individual features of the first array is subtracted from the amount of protein bound to the corresponding features of the second array.

[0224] All the essential materials and reagents required for detecting and quantifying IRS biomarker expression products may be assembled together in a kit, which is encompassed by the present invention. The kits may also optionally include appropriate reagents for detection of labels, positive and negative controls, washing solutions, blotting membranes, microtiter plates dilution buffers and the like. For example, a nucleic acid-based detection kit may include (i) an IRS biomarker polynucleotide (which may be used as a positive control), (ii) a primer or probe that specifically hybridizes to an IRS biomarker polynucleotide. Also included may be enzymes suitable for amplifying nucleic acids including various polymerases (Reverse Transcriptase, *Taq*, Sequenase™, DNA ligase etc. depending on the nucleic acid amplification technique employed), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification. Such kits also generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each primer or probe. Alternatively, a protein-based detection kit may include (i) an IRS biomarker polypeptide (which may be used as a positive control), (ii) an antibody that binds specifically to an IRS biomarker polypeptide. The kit can also feature various devices (e.g., one or more) and reagents (e.g., one or more) for performing one of the assays described herein; and/or printed instructions for using the kit to quantify the expression of an IRS biomarker gene.

[0225] In some embodiments, the methods and kits comprise or enable: comparing the level of at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker in the subject's sample IRS profile to the level of a corresponding IRS biomarker in a reference IRS biomarker profile from at least one control subject or group selected from a healthy control subject or group (hereafter referred to as a "reference healthy IRS biomarker profile"), a SIRS control subject or group (hereafter referred to as a "reference SIRS IRS biomarker profile"), an inSIRS control subject or group (hereafter referred to as a "reference inSIRS IRS biomarker profile"), an ipSIRS control subject or group (hereafter referred to as a "reference ipSIRS IRS biomarker profile") and a control subject or group with a particular stage of ipSIRS (hereafter referred to as a "reference ipSIRS stage IRS biomarker profile"), wherein a similarity between the level of the at least one IRS biomarker in the sample IRS biomarker profile and the level of the corresponding IRS biomarker in the reference healthy IRS biomarker profile identifies that the subject has an IRS biomarker profile that correlates with the presence of a healthy condition, or alternatively the absence of inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein a similarity between the level of the at least one IRS biomarker in the sample IRS biomarker profile and the level of the corresponding IRS biomarker in the SIRS IRS biomarker profile identifies that the subject has an IRS biomarker profile that correlates with the presence of inSIRS or ipSIRS, or alternatively the absence of a healthy condition, wherein a similarity between the level of the at least one IRS biomarker in the sample IRS biomarker profile and the level of the corresponding IRS biomarker in the inSIRS IRS biomarker profile identifies that the subject has an IRS biomarker profile that correlates with the presence of inSIRS, or alternatively the absence of a healthy condition, ipSIRS, or a particular stage of ipSIRS, wherein a similarity between the level of the at least one IRS biomarker in the sample IRS biomarker profile and the level of the corresponding IRS biomarker in the ipSIRS IRS biomarker profile identifies that the subject has an IRS biomarker profile that correlates with the presence of ipSIRS, or alternatively the absence of a healthy condition or inSIRS, and wherein a similarity between the level of the at least one IRS biomarker in the sample IRS biomarker profile and the level of the corresponding IRS biomarker in the ipSIRS stage IRS biomarker profile identifies that the subject has an IRS biomarker profile that correlates with the presence of a particular stage of ipSIRS, or alternatively the absence of a healthy condition or inSIRS.

[0226] A subset of the instantly disclosed IRS biomarkers has been identified as being useful for assisting in distinguishing between healthy subjects and unhealthy subjects that have SIRS (i.e., sick subjects with either inSIRS or ipSIRS). Thus, in some embodiments, the methods and kits involve determining the likelihood that SIRS or a healthy condition (e.g., a normal condition or a condition in which SIRS is absent) is present or absent in a subject. These methods and kits generally comprise or involve: 1) providing a correlation of a reference IRS biomarker profile with the presence or absence of SIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker selected from CD177, CLEC4D, BMX, VNN1, GPR84, ARG1, IL18R1, ERLIN1, IMP3, TLR5, UBE2J1, GPR56, FCGR1A, SLC1A3, SLC37A3, FAIM3, C3AR1, RNASE2, TNFAIP6, GNLY, OMG, FAR2, OLAH, CAMK4, METTL7B, B3GNT5, CLEC4E, MMP9, KREMEN1, GALNT3, PTGDR, TDRD9, GK3P, FKBP5, STOM, SMPDL3A, PFKFB2, ANKRD34B, SGMS2, DNAJC13, LRRN3, SH2D1B, C1orf161, HIST1H4C, IFI16, ACER3, PLB1, C9orf72, HMGB2, KLRK1, C7orf53, GOT2, TCN1, DSE, CCR3, CRIP1, ITK, KLRF1, TGFBR1, GSR, HIST1H4E, HPGD, FRMD3, ABCA13, C11orf82, PPP2R5A, BPI, CASS4, AP3B2, ODZ1, TMTC1, ADM, FGFBP2, HSPC159, HLA-DRA, HIST1H3I, TMEM144, MRPL41, FOLR3, PICALM, SH3PXD2B, DDAH2, HLA-DPB1, KPNA5, PHOSPHO1, TPST1, EIF2AK2, OR9A2, OLFM4, CD163, CDA, CHI3L1, MTHFS, CLU, ANAPC11, JUP, PMAIP1, GIMAP7, KLRD1, CCR1, CD274, EFCAB2, SUCNR1, KCNMA1, LGALS2, SLC11A1, FOXD4L3, VAMP2, ITGA4, LHFP, PRR13, FFAR2, B3GAT3, EAF2, HPSE, CLC, TLR10, CCR4, HIST1H3A, CENPK, DPH3, HLA-DPA1, ATP13A3, DNAJC9, S100B, HIST1H3J, 110, RPL17, C15orf54, LRRC70, IL5RA, PLA2G7, ECHDC3, HINT1, LCN2, PPIF, SLC15A2, PMS2CL, HIST1H2AA, CEACAM8, HSP90AB1, ABCG1, PDGFC, NPCDR1, PDK4, GAB2, WSB2, FAM118A, JKAMP, TREML1, PYHIN1, IRF4, ABCA1, DAAM2, ACPL2, RCBTB2, SAP30, THBS1, PCOLCE2, GPR65, NF-E4, LTF, LASS4, B4GALT3, RETN, TIMM10, IL1B, CLEC4A, SEC24A, RUNX2, LRRFIP1, CFD, EIF1AX, ZRANB1, SULF2, EXOSC4, CCDC125,

LOC284757, ANKRD28, HIST1H2AJ, CD63, PLIN2, SON, HIST1H4L, KRTAP15-1, DLEU2, MYL9, FABP2, CD24, MACF1, GSTO1, RRP12, AIG1, RASA4, FBXL13, PDE3B, CCRL2, C1orf128, E2F6, IL1RL1, CEACAM6, CYP4F3, 199, TAAR1, TSHZ2, PLB1, UBE2F (where if a gene name is not provided then a SEQ ID NO. is provided); (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and (3) determining a likelihood of the subject having or not having the healthy condition or SIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0227] In illustrative examples of this type, a reference healthy condition IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference SIRS IRS biomarker profile, illustrative examples of which include: GNLY, GPR56, KLRF1, HIST1H2AJ, HIST1H4C, KLRK1, CHI3L1, SH2D1B, PTGDR, CAMK4, FAIM3, CRIP1, CLC, HLA-DPB1, FGFBP2, HIST1H3J, IMP3, ITK, HIST1H3I, LRRN3, KLRD1, PHOSPHO1, CCR3, HIST1H4E, MRPL41, HIST1H3A, HLA-DRA, GIMAP7, KPNA5, CENPK, HLA-DPA1, HINT1, HIST1H4L, GOT2, DNAJC9, PLA2G7, CASS4, CFD, ITGA4, HSP90AB1, IL5RA, PMAIP1, LGALS2, SULF2, C1orf128, RPL17, EIF1AX, PYHIN1, S100B, PMS2CL, CCR4, C15orf54, VAMP2, ANAPC11, B3GAT3, E2F6, NPCDR1, FAM118A, PPIF, 199, JUP, B4GALT3, TIMM10, RUNX2, RASA4, SON, ABCG1, TSHZ2, IRF4, PDE3B, RRP12, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).is provided).

[0228] In other illustrative examples, a reference healthy condition IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed relative to a reference SIRS IRS biomarker profile, non-limiting examples of which include: CD177, ARG1, VNN1, CLEC4D, GPR84, IL18R1, OLFM4, FCGR1A, RNASE2, TLR5, TNFAIP6, PFKFB2, C3AR1, TCN1, BMX, FKBP5, TDRD9, OLAH, ERLIN1, LCN2, MMP9, BPI, CEACAM8, CLEC4E, HPGD, CD274, GK3P, KREMEN1, ANKRD34B, SLC37A3, CD163, TMTC1, PLB1, UBE2J1, TPST1, B3GNT5, SMPDL3A, FAR2, ACER3, ODZ1, HMGB2, LTF, SGMS2, EIF2AK2, TMEM144, GALNT3, DNAJC13, IFI16, C11orf82, ABCA13, CD24, METTL7B, FOLR3, C7orf53, SLC1A3, DAAM2, HSPC159, OMG, CCR1, TREML1, STOM, CEACAM6, FOXD4L3, C9orf72, GSR, DSE, THBS1, SH3PXD2B, PDGFC, KCNMA1, PICALM, TLR10, PDK4, ADM, CLU, C1orf161, NF-E4, HPSE, FFAR2, PPP2R5A, CDA, NA, ATP13A3, ABCA1, TGFBR1, OR9A2, EFCAB2, EAF2, AP3B2, SLC15A2, ECHDC3, MTHFS, IL1B, WSB2, SUCNR1, DDAH2, CLEC4A, MACF1, MYL9, IL1RL1, EXOSC4, FBXL13, LOC284757, PRR13, DPH3, SLC11A1, FRMD3, ACPL2, PLB1, RETN, RCBTB2, CD63, CYP4F3, SEC24A, ZRANB1, CCDC125, PCOLCE2, JKAMP, LRRFIP1, GPR65, ANKRD28, LRRC70, AIG1, UBE2F, GAB2, CCRL2, SAP30, DLEU2, HIST1H2AA, GSTO1, PLIN2, LHFP, KRTAP15-1, TAAR1, FABP2 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0229] In still other illustrative examples, a reference healthy condition IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference SIRS IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference SIRS IRS biomarker profile, as broadly described above.

[0230] The term "upregulated," "overexpressed" and the like refer to an upward deviation in the level of expression of an IRS biomarker as compared to a baseline expression level of a corresponding IRS biomarker in a control sample.

[0231] The term "downregulated," "underexpressed" and the like refer to a downward deviation in the level of expression of an IRS biomarker as compared to a baseline expression level of a corresponding IRS biomarker in a control sample.

[0232] Another subset of the instantly disclosed IRS biomarkers has been identified as being useful for assisting in distinguishing between healthy subjects, inSIRS affected subjects and subjects having ipSIRS. Accordingly, in some embodiments, the methods and kits are useful for determining the likelihood that inSIRS, ipSIRS or a healthy condition (e.g., a normal condition or a condition in which SIRS is absent) is present or absent in a subject. These methods and kits generally comprise or involve: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS, ipSIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker selected from PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, B3GAT3, CD300A, OCR1, PTGER2, LGALS1, HIST1H4L, AMFR, SIAE, SLC39A8, TGFBR1, GAB2, MRPL41, TYMS, HIST1H3B, MPZL3, KIAA1257, OMG, HIST1H2BM, TDRD9, C22orf37, GALNT3, SYNE2, MGST3, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, HSPB1, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, KREMEN1, IRS2, APOLD1, RBP7, DNAJC13, ERGIC1, FSD1L, TLR5, TMEM62, SDHC, C9orf72, NP, KIAA0746, PMAIP1, DSE, SMPDL3A, DNAJC9, HIST1H3H, CDC26, CRIP1, FAR2, FRMD3, RGS2, METTL7B, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, IRF1, C7orf53, IGK@, RNASE2, FCGR1A, SAP30, PMS2CL, SLC11A1, AREG, PLB1, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, CPM, CCDC125, GPR56, PPP1R2, 110, ACPL2, HIST1H3A, C7orf58, IRF4, ANAPC11, HIST1H3J, KLRD1, GPR84, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, HSP90AB1, HPGD, IFI16, CD177, TAS2R31, CD163, B4GALT3, EIF1AX, CYP4F3, HIST1H2AA, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS, ipSIRS or a healthy condition the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0233] In illustrative examples of this type, a reference healthy condition IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference inSIRS IRS biomarker profile, representative examples of which include: CD177, CLEC4E, FKBP5, CD163, TPST1, DAAM2, GPR84, FCGR1A, IFI16, RNASE2, TLR5, ECHDC3, OCR1, MME, LOC284757, 110, C3AR1, HAL, PRR13, ACPL2, SLC11A1, CYP4F3, SAP30, OLFM4, ZRANB1, GAB2, CCDC125, KREMEN1, UBE2J1, AREG, FAR2, CPM, PLB1, ERGIC1, RGS2, 132, HPGD, ANKRD34B, TDRD9, DNAJC13, GALNT3, IRS2, HIST1H2AA, RBP7, KDM6B, ACER3, MPZL3, KIAA1257, C7orf53, C9orf72, STOM, METTL7B, SMPDL3A, GSR, SYNE2, OMG, DSE, PICALM, ABCA13, PPP1R2, TGFBR1, AP3B2, FRMD3 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0234] In other illustrative examples, a reference healthy condition IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference inSIRS IRS biomarker profile, illustrative examples of which include: SIAE, FSD1L, GLDC, HSPB1, HIST1H2BJ, CDS2, CASS4, DCTN5, SLC39A9, CDC26, LGALS1, CD151, NP, TYMS, IGLV6-57, TMEM62, CD300A, LASS4, GLT25D1, IRF1, AMFR, IGL@, NFXL1, SLC39A8, APOLD1, TNFRSF17, KIAA0101, C22orf37, VOPP1, KLRD1, TRAF3, RRP12, PTGER2, KIAA0746, MGST3, CHI3L1, TAS2R31, SDHC, IRF4, INSIG1, PPIF, B4GALT3, ANAPC11, PLAC8, HIST1H2BM, KLRF1, B3GAT3, C7orf58, PMS2CL, PTGDR, RPL17, EIF1AX, PMAIP1, HIST1H3B, IGK@, HINT1, HSP90AB1, GPR56, HIST1H3H, HIST1H3A, IMP3, DNAJC9, MRPL41, HIST1H3J, HIST1H3C, HIST1H3I, HIST1H4L, CRIP1, HIST1H4C (where if a gene name is not provided then a SEQ ID NO. is provided).

[0235] In still other illustrative examples, a reference healthy condition IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference inSIRS IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference inSIRS IRS biomarker profile, as broadly described above.

[0236] In other illustrative examples, a reference inSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference ipSIRS IRS biomarker profile, representative examples of which include: OLFM4, PLAC8, HIST1H4L, HIST1H3C, TDRD9, IGK@, HIST1H3B, HIST1H2BM, HPGD, GPR84, TLR5, SMPDL3A, CD177, HIST1H3I, C3AR1, DNAJC9, ABCA13, ANKRD34B, RNASE2, FCGR1A, HIST1H3H, KIAA0746, ACER3, SDHC, CRIP1, IGLV6-57, PLB1, MRPL41, HIST1H4C, SLC39A8, NP, NFXL1, PTGER2, TYMS, LGALS1, C7orf58, CD151, KREMEN1, AMFR, METTL7B, TNFRSF17, HSP90AB1, VOPP1, GLT25D1, GALNT3, OMG, SIAE, FAR2, C7orf53, DNAJC13, HIST1H2BJ, KIAA0101, HSPB1, UBE2J1, HIST1H3J, CDS2, MGST3, PICALM, HINT1, SLC39A9, STOM, TRAF3, INSIG1, AP3B2, B3GAT3, CD300A, TGFBR1, HIST1H3A, PMAIP1, DSE, TMEM62, IGL@, IRF4, GSR, IRF1, EIF1AX, C9orf72, PMS2CL, C22orf37, FRMD3, IMP3, RPL17, FSD1L, APOLD1, B4GALT3, DCTN5, PPIF, CDC26, TAS2R31, RRP12, ANAPC11, GLDC, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided)..

[0237] In yet other illustrative examples, a reference inSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference ipSIRS IRS biomarker profile, non-limiting examples of which include: HIST1H2AA, IFI16, PPP1R2, CCDC125, ZRANB1, SLC11A1, GPR56, 110, KDM6B, GAB2, CYP4F3, RGS2, KIAA1257, CPM, ACPL2, PRR13, ERGIC1, PTGDR, IRS2, MPZL3, AREG, SAP30, RBP7, CASS4, FKBP5, SYNE2, KLRD1, 132, KLRF1, LOC284757, HAL, TPST1, ECHDC3, CD163, CLEC4E, DAAM2, CHI3L1, MME, OCR1 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0238] In still other illustrative examples, a reference inSIRS IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference ipSIRS IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference ipSIRS IRS biomarker profile, as broadly described above.

[0239] In other illustrative examples, a reference ipSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference healthy condition IRS biomarker profile, representative examples of which include: GNLY, GPR56, CHI3L1, KLRF1, KLRK1, PTGDR, SH2D1B, HIST1H2AJ, FAIM3, HLA-DPB1, CAMK4, FGFBP2, KLRD1, CLC, PHOSPHO1, HIST1H4C, ITK, LRRN3, CCR3, CRIP1, IMP3, HIST1H3J, HIST1H4E, HLA-DRA, PLA2G7, GIMAP7, HLA-DPA1, CASS4, HIST1H3I, KPNA5, CENPK, SULF2, KIAA1324, HIST1H3A, CFD, C1orf128, RPIA, MRPL41, GOT2, IL5RA, PYHIN1, ITGA4, HINT1, 200, VAMP2, C15orf54, LGALS2, 199, S100B, HSP90AB1, DNAJC9, PMAIP1, CCR4, RPL17, RUNX2, NPCDR1, JUP, PMS2CL, ANAPC11, PDE3B, RASA4, CAMK1D, LY6G5B, 268, FAM118A, PPIF, B4GALT3, B3GAT3, ABCG1, IRF4, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0240] In yet other illustrative examples, a reference ipSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed relative to a reference healthy condition IRS biomarker profile, illustrative examples of which include: ATP6V0D1, SAP30, GAB2, KRTAP15-1, NEK6, HDHD1A, SLC39A8, HIST1H2AA, FABP2, CDS2, SRXN1, KLHL5, ACPL2, HS2ST1, HIST1H2BJ, PLIN2, ICAM1, HSPB1, PRR13, P4HA1, SLC11A1, ECHDC3, TAF13, LGALS1, TAAR1, TPX2, DLEU2, TRIM21, AGTRAP, PTGS1, LHFP, CEP97, ACTA2, SIAE, GPR65, IL1RL1, MTHFS, FAM118B, MKI67, LRRFIP1, CCRL2, GALNT2, GSTO1, LRRC70, MTRR, ANKRD28, DPH3, 110, AIG1, UBE2F, LAIR1, PCOLCE2, PLB1, CDA, JKAMP, FRMD3, ITGA2B, SEC24A, RETN, THBS1, MYL9, SPARC, RCBTB2, PLAC8, PDK4, PPP2R5A,

SH3PXD2B, DAAM2, NF-E4, DDAH2, MACF1, CD63, CLEC4A, MPO, SUCNR1, EXOSC4, EFCAB2, IL1B, OR9A2, AP3B2, DYNLL1, WSB2, SLC15A2, EAF2, C1orf161, TGFBR1, ABCA1, FFAR2, SLC1A3, ATP13A3, CLU, ADM, IFI16, KCNMA1, C9orf72, GSR, DSE, PICALM, EIF2AK2, HPSE, TLR10, HSPC159, TPST1, ODZ1, STOM, HMGB2, PDGFC, CCR1, OMG, CD163, SGMS2, TREML1, FOXD4L3, C7orf53, CEACAM6, FOLR3, METTL7B, TMEM144, DNAJC13, GALNT3, B3GNT5, CLEC4E, SLC37A3, ABCA13, CD24, C11orf82, FAR2, UBE2J1, GK3P, DEFA4, LTF, ACER3, TMTC1, SMPDL3A, FKBP5, ERLIN1, PLB1, MMP9, KREMEN1, ANKRD34B, OLAH, BMX, PFKFB2, HPGD, BPI, CD274, CEACAM8, TDRD9, LCN2, TNFAIP6, C3AR1, TCN1, IL18R1, CLEC4D, TLR5, RNASE2, FCGR1A, GPR84, OLFM4, VNN1, ARG1, CD177 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0241] In yet other illustrative examples, a reference ipSIRS IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference healthy condition IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed, relative to a reference healthy condition IRS biomarker profile, as broadly described above.

[0242] Yet another subset of the disclosed IRS biomarkers has been identified as being useful for assisting in distinguishing between inSIRS affected subjects and ipSIRS affected subjects. Accordingly, in some embodiments, the methods and kits are useful for determining the likelihood that inSIRS or ipSIRS is present or absent in a subject. These methods and kits generally comprise or involve: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS or ipSIRS, wherein the reference biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker selected from C11orf82, PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, FOXD4L3, WSB2, CD63, CD274, B3GAT3, CD300A, OCR1, JKAMP, TLR10, PTGER2, PDGFC, LGALS1, HIST1H4L, AGTRAP, AMFR, SIAE, 200, SLC15A2, SLC39A8, TGFBR1, DDAH2, HPSE, SUCNR1, MTRR, GAB2, P4HA1, HS2ST1, MRPL41, TYMS, RUNX2, GSTO1, LRRC70, HIST1H3B, RCBTB2, MPZL3, KIAA1257, AIG1, NEK6, OMG, HIST1H2BM, TDRD9, GALNT3, ATP13A3, C22orf37, SYNE2, ADM, MGST3, PDE3B, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, KLHL5, EXOSC4, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, TPX2, PCOLCE2, HSPB1, EAF2, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, ACTA2, PTGS1, KREMEN1, IRS2, TAF13, FSD1L, APOLD1, RBP7, DNAJC13, SEC24A, ERGIC1, FSD1L, TLR5, MKI67, TMEM62, CLEC4A, SDHC, C9orf72, NP, CLU, ABCA1, KIAA0746, PMAIP1, DSE, CMTM5, SMPDL3A, DNAJC9, HDHD1A, HIST1H3H, CDC26, ICAM1, LOC100128751, FAR2, CRIP1, MPZL2, FRMD3, CTSL1, METTL7B, RGS2, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, ITGA2B, C7orf53, IRF1, 268, IGK@, RNASE2, FCGR1A, UBE2F, SAP30, LAIR1, PMS2CL, SLC11A1, PLB1, AREG, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, PLA2G7, GALNT2, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, 199, CPM, CCDC125, SULF2, LTF,

GPR56, MACF1, PPP1R2, DYNLL1, LCN2, FFAR2, SFRS9, IGJ, FAM118B, 110, ACPL2, HIST1H3A, C7orf58, ANAPC11, HIST1H3J, IRF4, MPO, TREML1, KLRD1, GPR84, CCRL2, CAMK1D, CCR1, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, CD24, HSP90AB1, HPGD, CEACAM8, DEFA4, IL1B, IFI16, CD177, KIAA1324, SRXN1, TAS2R31, CEACAM6, CD163, B4GALT3, ANKRD28, TAAR1, EIF1AX, CYP4F3, 314, HIST1H2AA, LY6G5B, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided); (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS or ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0243] In illustrative examples of thus type, a reference inSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference ipSIRS IRS biomarker profile, non-limiting examples of which include: OLFM4, CD274, PLAC8, LCN2, IGJ, HIST1H4L, HIST1H3C, DEFA4, TDRD9, IGK@, HIST1H3B, CEACAM8, C11orf82, HIST1H2BM, LTF, HPGD, FOXD4L3, PDGFC, CD24, GPR84, CEACAM6, TLR5, SMPDL3A, CD177, HIST1H3I, C3AR1, TLR10, DNAJC9, ABCA13, ANKRD34B, RNASE2, FCGR1A, HPSE, HIST1H3H, KIAA0746, ACER3, SDHC, MTRR, WSB2, CRIP1, IGLV6-57, ATP13A3, CD63, TREML1, PLB1, MRPL41, HIST1H4C, SLC39A8, NP, NFXL1, MPO, ITGA2B, LAIR1, PTGER2, EXOSC4, TYMS, LGALS1, C7orf58, SLC15A2, CD151, ADM, KREMEN1, RCBTB2, PTGS1, AMFR, ABCA1, METTL7B, TNFRSF17, DYNLL1, HSP90AB1, CLU, MKI67, VOPP1, UBE2F, P4HA1, GLT25D1, IL1B, SUCNR1, GALNT3, AIG1, CCR1, OMG, MACF1, CLEC4A, SIAE, FAR2, C7orf53, DNAJC13, HIST1H2BJ, JKAMP, KIAA0101, GSTO1, HSPB1, DDAH2, ICAM1, UBE2J1, KLHL5, HIST1H3J, EAF2, CDS2, MGST3, FFAR2, TPX2, PICALM, HINT1, SLC39A9, SEC24A, STOM, TRAF3, INSIG1, AP3B2, PCOLCE2, B3GAT3, TAF13, CD300A, TGFBR1, HIST1H3A, PMAIP1, AGTRAP, FAM118B, DSE, NEK6, CMTM5, GALNT2, TMEM62, HS2ST1, IGL@, ACTA2, LRRC70, IRF4, GSR, IRF1, EIF1AX, C9orf72, PMS2CL, ANKRD28, CTSL1, C22orf37, FRMD3, HDHD1A, CCRL2, IMP3, RPL17, FSD1L, APOLD1, B4GALT3, FSD1L, DCTN5, PPIF, CDC26, TAS2R31, RRP12, SFRS9, TAAR1, ANAPC11, SRXN1, GLDC, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0244] In other illustrative examples, a reference inSIRS IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference ipSIRS IRS biomarker profile, representative examples of which include: HIST1H2AA, LY6G5B, 268, IFI16, PPP1R2, CCDC125, ZRANB1, LOC100128751, SLC11A1, GPR56, RUNX2, 110, KDM6B, GAB2, 199, CYP4F3, RGS2, PDE3B, KIAA1257, CAMK1D, CPM, ACPL2, PRR13, ERGIC1, PTGDR, IRS2, MPZL3, MPZL2, AREG, SAP30, RBP7, CASS4, FKBP5, SYNE2, SULF2, KLRD1, 132, KLRF1, 314, LOC284757, HAL, TPST1, ECHDC3, CD163, KIAA1324, PLA2G7, CLEC4E, DAAM2, 200, CHI3L1, MME, OCR1 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0245] In still other illustrative examples, an inSIRS IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference ipSIRS IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference ipSIRS IRS biomarker profile, as broadly described above .

[0246] Still another subset of the disclosed IRS biomarkers has been identified as being useful for assisting in distinguishing between subjects with different stages of ipSIRS selected from mild sepsis, severe sepsis and septic shock. Accordingly, in some embodiments, the methods and kits are useful for determining the likelihood that a stage of ipSIRS selected from mild sepsis, severe sepsis and septic shock is present or absent in a subject. These methods and kits generally comprise or involve: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having the stage of ipSIRS, wherein the reference biomarker IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker selected from PLEKHA3, PLEKHF2, 232, SFRS9, ZNF587, KPNA5, LOC284757, GPR65, VAMP2, SLC1A3, ITK, ATF7, ZNF28, AIF1, MINPP1, GIMAP7, MKI67, IRF4, TSHZ2, HLA-DPB1, EFCAB2, POLE2, FAIM3, 110, CAMK4, TRIM21, IFI44, CENPK, ATP5L, GPR56, HLA-DPA1, C4orf3, GSR, GNLY, RFESD, BPI, HIST1H2AA, NF-E4, CALM2, EIF1AX, E2F6, ARL17P1, TLR5, SH3PXD2B, FAM118A, RETN, PMAIP1, DNAJC9, PCOLCE2, TPX2, BMX, LRRFIP1, DLEU2, JKAMP, JUP, ABCG1, SLC39A9, B3GNT5, ACER3, LRRC70, NPCDR1, TYMS, HLA-DRA, TDRD9, FSD1L, FAR2, C7orf53, PPP1R2, SGMS2, EXOSC4, TGFBR1, CD24, TCN1, TAF13, AP3B2, CD63, SLC15A2, IL18R1, ATP6V0D1, SON, HSP90AB1, CEACAM8, SMPDL3A, IMP3, SEC24A, PICALM, 199, CEACAM6, CYP4F3, OLAH, ECHDC3, ODZ1, KIAA0746, KIAA1324, HINT1, VNN1, C22orf37, FSD1L, FOLR3, IL1RL1, OMG, MTHFS, OLFM4, S100B, ITGA4, KLRD1, SLC39A8, KLHL5, KLRK1, MPO, PPIF, GOT2, LRRN3, HIST1H2AJ, CLU, LCN2, 132, CEP97, KLRF1, FBXL13, HIST1H3B, ANKRD34B, RPIA, HPGD, HIST2H2BF, GK3P (where if a gene name is not provided then a SEQ ID NO. is provided). ; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the stage of ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

[0247] In illustrative examples of this type, a reference mild sepsis IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference severe sepsis IRS biomarker profile, illustrative examples of which include: OLFM4, CEACAM8, TCN1, BPI, LCN2, CD24, CEACAM6, NF-E4, HIST1H3B, MKI67, OLAH, TYMS, DNAJC9, MPO, LOC284757, ODZ1, HSP90AB1, VNN1, ANKRD34B, FBXL13, TSHZ2, KIAA0746, FOLR3, GSR, IRF4, LRRN3, TPX2, SFRS9, C7orf53, CYP4F3, IL1RL1, TDRD9, IL18R1, BMX, NPCDR1, GOT2, ATF7, CEP97, ITK, SEC24A, KIAA1324, FAM118A, 132, SMPDL3A, CD63, ABCG1, TLR5, CAMK4, CLU, SLC39A9, GK3P, LRRFIP1, AP3B2, SLC15A2, PICALM, HIST1H2AA, SGMS2, OMG, RETN, FAIM3, EXOSC4, SH3PXD2B, FAR2, 199, C4orf3, PCOLCE2 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0248] In other illustrative examples, a reference mild sepsis IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference severe sepsis IRS biomarker profile, non-limiting examples of which include: JUP, SLC1A3, ECHDC3, IMP3, SLC39A8, MTHFS, TGFBR1, FSD1L, HIST2H2BF, HPGD, FSD1L, PPP1R2, B3GNT5, C22orf37, ACER3, GIMAP7, ATP6V0D1, KLHL5, PPIF, KLRK1, HINT1, GPR56, LRRC70, S100B, 110, SON, ZNF587, JKAMP, ITGA4, HLA-DRA, ZNF28, TRIM21, TAF13, HLA-DPA1, ARL17P1, KLRF1, PMAIP1, RPIA, ATP5L, VAMP2, E2F6, KLRD1, EIF1AX, PLEKHA3, GPR65, CENPK, CALM2, GNLY, DLEU2, HLA-DPB1, AIF1, KPNA5, EFCAB2, PLEKHF2, 232, RFESD, MINPP1, HIST1H2AJ, POLE2, IFI44 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0249] In still other illustrative examples, a reference mild sepsis IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference severe sepsis IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference severe sepsis IRS biomarker profile, as broadly described above.

[0250] In other illustrative examples, a reference severe sepsis IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference septic shock IRS biomarker profile, non-limiting examples of which include: HPGD, SLC1A3, B3GNT5, SMPDL3A, ACER3, RETN, IL18R1, FSD1L, SH3PXD2B, SLC39A8, EXOSC4, FSD1L, AP3B2, ECHDC3, GPR65, TDRD9, BMX, PCOLCE2, PLEKHF2, SGMS2, RPIA, GK3P, FAR2, LRRC70, TGFBR1, MTHFS, C4orf3, TLR5, OLAH, TAF13, JKAMP, POLE2, PICALM, RFESD, ANKRD34B, OMG, VNN1, EIF1AX, KLHL5, SON, LRRFIP1, HIST1H2AJ, AIF1, SLC15A2, CALM2, CD63, HIST1H2AA, MINPP1, S100B, DLEU2, PLEKHA3, ODZ1, FOLR3, 232, EFCAB2, SEC24A, E2F6, SLC39A9, ZNF28, KLRF1, ATP6V0D1, IL1RL1, PPIF (where if a gene name is not provided then a SEQ ID NO. is provided).

[0251] In yet other illustrative examples, a reference severe sepsis IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference septic shock IRS biomarker profile, representative examples of which include: LCN2, CENPK, C22orf37, PMAIP1, KPNA5, ATP5L, TCN1, 132, CD24, ITGA4, KLRD1, SFRS9, TRIM21, VAMP2, GSR, LOC284757, PPP1R2, HINT1, 110, IMP3, C7orf53, ATF7, KIAA0746, GNLY, HLA-DRA, IFI44, ZNF587, CEP97, GPR56, OLFM4, CLU, KLRK1, GOT2, JUP, HLA-DPA1, NPCDR1,

TPX2, HIST2H2BF, HLA-DPB1, FAM118A, ABCG1, MKI67, MPO, LRRN3, FBXL13, ARL17P1, CEACAM8, TSHZ2, 199, BPI, HSP90AB1, CYP4F3, TYMS, GIMAP7, DNAJC9, NF-E4, IRF4, HIST1H3B, CAMK4, FAIM3, CEACAM6, ITK, KIAA1324 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0252] In still other illustrative examples, a reference severe sepsis IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference septic shock IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference septic shock IRS biomarker profile, as broadly described above.

[0253] In other illustrative examples, a reference septic shock IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is downregulated or underexpressed relative to a reference mild sepsis IRS biomarker profile, representative examples of which include: IFI44, HLA-DPB1, ARL17P1, HIST1H2AJ, MINPP1, GNLY, GIMAP7, HLA-DPA1, POLE2, 232, KPNA5, GPR56, HLA-DRA, ZNF587, KLRK1, RFESD, VAMP2, CENPK, KIAA1324, KLRD1, EFCAB2, ATP5L, 110, ITK, FAIM3, TRIM21, PMAIP1, HIST2H2BF, HINT1, DLEU2, AIF1, E2F6, ITGA4, KLRF1, CALM2, PLEKHA3, PPP1R2, CAMK4, 199, ZNF28, PLEKHF2, JUP, EIF1AX, PPIF, IMP3, C22orf37, ATP6V0D1, S100B, SON, GPR65, ABCG1, TAF13, FAM118A, RPIA, KLHL5, JKAMP, IRF4, CLU, CYP4F3, LRRC70 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0254] In yet other illustrative examples, a reference septic shock IRS biomarker profile comprises at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker that is upregulated or overexpressed, relative to a reference mild sepsis IRS biomarker profile, illustrative examples of which include: GOT2, NPCDR1, CEP97, LRRN3, DNAJC9, TSHZ2, HSP90AB1, TYMS, HIST1H3B, ATF7, FBXL13, TPX2, TGFBR1, MPO, 132, NF-E4, MTHFS, CEACAM6, C7orf53, FSD1L, FSD1L, SLC39A9, MKI67, KIAA0746, HIST1H2AA, ACER3, ECHDC3, SLC15A2, SLC39A8, SEC24A, SFRS9, LRRFIP1, OMG, GSR, C4orf3, CD63, PICALM, LOC284757, FAR2, PCOLCE2, IL1RL1, B3GNT5, SGMS2, TLR5, EXOSC4, SH3PXD2B, GK3P, AP3B2, FOLR3, BPI, RETN, ODZ1, CEACAM8, BMX, HPGD, VNN1, ANKRD34B, SLC1A3, TDRD9, SMPDL3A, CD24, IL18R1, OLAH, LCN2, TCN1, OLFM4 (where if a gene name is not provided then a SEQ ID NO. is provided).

[0255] In yet other illustrative examples, a reference septic shock IRS biomarker profile comprises: (1) at least one IRS biomarker that is downregulated or underexpressed relative to a reference mild sepsis IRS biomarker profile, as broadly described above and (2) at least one IRS biomarker that is upregulated or overexpressed relative to a reference mild sepsis IRS biomarker profile, as broadly described above.

[0256] In some embodiments, individual IRS biomarkers as broadly described above and elsewhere herein are selected from the group consisting of: (a) a polynucleotide expression product comprising a nucleotide sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1-319, or a complement thereof; (b) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; (c) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with at least a portion of the sequence set forth in SEQ ID NO: 320-619; (d) a polynucleotide expression product comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under medium or high stringency conditions; (e) a polypeptide expression product comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; and (f) a polypeptide expression product comprising an amino acid sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with the sequence set forth in any one of SEQ ID NO: 320-619.

[0257] In some embodiments, the methods and kits comprise or involve: (1) measuring in the biological sample the level of an expression product of at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) IRS biomarker gene and (2) comparing the measured level or functional activity of each expression product to the level or functional activity of a corresponding expression product in a reference sample.

[0258] The present invention also extends to the management of inSIRS, ipSIRS or particular stages of ipSIRS, or prevention of further progression of inSIRS, ipSIRS or particular stages of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock), or assessment of the efficacy of therapies in subjects following positive diagnosis for the presence of inSIRS, ipSIRS or particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock) in a subject. The management of inSIRS or ipSIRS conditions is generally highly intensive and can include identification and amelioration of the underlying cause and aggressive use of therapeutic compounds such as, vasoactive compounds, antibiotics, steroids, antibodies to endotoxin, anti tumour necrosis factor agents, recombinant protein C. In addition, palliative therapies as described for example in Cohen and Glauser (1991, Lancet 338: 736-739) aimed at restoring and protecting organ function can be used such as intravenous fluids and oxygen and tight glycemic control. Therapies for ipSIRS are reviewed in Healy (2002, Ann. Pharmacother. 36(4): 648-54) and Brindley (2005, CJEM. 7(4): 227) and Jenkins (2006, J Hosp Med. 1(5): 285-295).

[0259] Typically, the therapeutic agents will be administered in pharmaceutical (or veterinary) compositions together with a pharmaceutically acceptable carrier and in an effective amount to achieve their intended purpose. The dose of active compounds administered to a subject should be sufficient to achieve a beneficial response in the subject over time such as a reduction in, or relief from, the symptoms of inSIRS, ipSIRS or particular stages of ipSIRS. The quantity of the pharmaceutically active compounds(s) to be administered may depend on the subject to be treated inclusive of the age, sex, weight and general health condition thereof. In this regard, precise amounts of the active compound(s) for administration will depend on the judgment of the practitioner. In determining the effective amount of the active compound(s) to be administered in the treatment or prevention of inSIRS, ipSIRS or particular stages of ipSIRS, the medical practitioner or veterinarian may evaluate severity of any symptom associated with the presence of inSIRS, ipSIRS or particular stages of ipSIRS including, inflammation, blood pressure anomaly, tachycardia, tachypnea fever, chills, vomiting, diarrhoea, skin rash, headaches, confusion, muscle aches, seizures. In any event, those of skill in the art may readily determine suitable dosages of the therapeutic agents and suitable treatment regimens without undue experimentation.

[0260] The therapeutic agents may be administered in concert with adjunctive (palliative) therapies to increase oxygen supply to major organs, increase blood flow to major organs and/or to reduce the inflammatory response. Illustrative examples of such adjunctive therapies include non steroidal-anti inflammatory drugs (NSAIDs), intravenous saline and oxygen.

[0261] Thus, the present invention contemplates the use of the methods and kits described above and elsewhere herein in methods for treating, preventing or inhibiting the development of inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock) in a subject. These methods generally comprise (1) correlating a reference IRS biomarker profile with the presence or absence of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.) IRS biomarker; (2) obtaining an IRS biomarker profile of a sample (i.e., "a sample IRS biomarker profile") from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile, and administering to the subject, on the basis that the subject has an increased likelihood of having inSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of inSIRS, or administering to the subject, on the basis that the subject has an increased likelihood of having ipSIRS or a particular stage of ipSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of ipSIRS or the particular stage of ipSIRS.

[0262] In some embodiments the methods and kits of the present invention are used for monitoring, treatment and management of conditions that can lead to inSIRS or ipSIRS, illustrative examples of which include retained placenta, meningitis, endometriosis, shock, toxic shock (i.e., sequelae to tampon use), gastroenteritis, appendicitis, ulcerative colitis, Crohn's disease, inflammatory bowel disease, acid gut syndrome, liver failure and cirrhosis, failure of colostrum transfer in neonates, ischemia (in any organ), bacteraemia, infections within body cavities such as the peritoneal, pericardial, thecal, and pleural cavities, burns, severe wounds, excessive exercise or stress, haemodialysis, conditions involving intolerable pain (e.g., pancreatitis, kidney stones), surgical operations, and non-healing lesions. In these embodiments, the methods or kits of the present invention are typically used at a frequency that is effective to monitor the early development of inSIRS, ipSIRS or particular stages of ipSIRS, to thereby enable early therapeutic intervention and treatment of that condition. In illustrative examples, the diagnostic methods or kits are used at least at 1, 2, 3, 4,5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 hour intervals or at least 1, 2, 3, 4, 5 or 6 day intervals, or at least weekly, fortnightly or monthly. Accordingly, the present invention encompasses the use of the methods and kits of the present invention for early diagnosis of inSIRS, ipSIRS or particular stages of ipSIRS.

[0263] The term "early diagnosis" as used herein with "early detection" refers to specific screening / monitoring processes that allow detection and evaluation of inSIRS, ipSIRS or particular stages of ipSIRS at an early point in disease development and/or progression. For example, since both inSIRS and ipSIRS patients present with similar clinical signs, early detection of ipSIRS can be achieved through a plurality of evaluations of patients with inSIRS to detect a transition to ipSIRS.

[0264] The present invention can be practiced in the field of predictive medicine for the purposes of diagnosis or monitoring the presence or development of a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS in a subject, and/or monitoring response to therapy efficacy.

[0265] The IRS biomarker profile further enables determination of endpoints in pharmacotranslational studies. For example, clinical trials can take many months or even years to establish the pharmacological parameters for a medicament to be used in treating or preventing inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock). However, these parameters may be associated with an IRS biomarker profile associated with a health state (e.g., a healthy condition). Hence, the clinical trial can be expedited by selecting a treatment regimen (e.g., medicament and pharmaceutical parameters), which results in an IRS biomarker profile associated with the desired health state (e.g., healthy condition). This may be determined for example by (1) providing a correlation of a reference IRS biomarker profile with the likelihood of having the healthy condition; (2) obtaining a corresponding IRS biomarker profile of a subject having inSIRS, ipSIRS or a particular stage of ipSIRS after treatment with a treatment regimen, wherein a similarity of the subject's IRS biomarker profile after treatment to the reference IRS biomarker profile indicates the likelihood that the treatment regimen is effective for changing the health status of the subject to the desired health state (e.g., healthy condition). This aspect of the present invention advantageously provides methods of monitoring the efficacy of a particular treatment regimen in a subject (for example, in the context of a clinical trial) already diagnosed with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS. These methods take advantage of IRS biomarkers that correlate with treatment efficacy, for example, to determine whether the IRS biomarker profile of a subject undergoing treatment partially or completely normalizes during the course of or following therapy or otherwise shows changes associated with responsiveness to the therapy.

[0266] The IRS biomarker profile further enables stratification of patients prior to enrolment in pharmacotranslational studies. For example, a clinical trial can be expedited by selecting *a priori* patients with a particular IRS biomarker profile that would most benefit from a particular treatment regimen (e.g., medicament and pharmaceutical parameters). For instance, patient enrolment into a clinical trial testing the efficacy of a new antibiotic would best include patients with an IRS biomarker profile that indicated that they had ipSIRS rather than inSIRS, and as such the selected patients would most likely benefit from the new therapy. Further, and by example, patient enrolment into a clinical trial testing the efficacy of a new inotrope would best include patients with an IRS biomarker profile that indicated that they had the shock stage of ipSIRS rather than inSIRS or other stage of ipSIRS, and as such the selected patients would most likely benefit from the new therapy.

[0267] As used herein, the term "treatment regimen" refers to prophylactic and/or therapeutic (i.e., after onset of a specified condition) treatments, unless the context specifically indicates otherwise. The term "treatment regimen" encompasses natural substances and pharmaceutical agents (*i.e.*, "drugs") as well as any other treatment regimen including but not limited to dietary treatments, physical therapy or exercise regimens, surgical interventions, and combinations thereof.

[0268] Thus, the invention provides methods of correlating a reference IRS biomarker profile with an effective treatment regimen for a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock), wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker. These methods generally comprise: (a) determining a sample IRS biomarker profile from a subject with the condition prior to treatment (i.e., baseline), wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and correlating the sample IRS biomarker profile with a treatment regimen that is effective for treating that condition.

[0269] The invention further provides methods of determining whether a treatment regimen is effective for treating a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock). These methods generally comprise: (a) correlating a reference biomarker profile prior to treatment (i.e., baseline) with an effective treatment regimen for the condition, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and (b) obtaining a sample IRS biomarker profile from the subject after treatment, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and wherein the sample IRS biomarker profile after treatment indicates whether the treatment regimen is effective for treating the condition in the subject.

[0270] The invention can also be practiced to evaluate whether a subject is responding (i.e., a positive response) or not responding (i.e., a negative response) to a treatment regimen. This aspect of the invention provides methods of correlating an IRS biomarker profile with a positive and/or negative response to a treatment regimen. These methods generally comprise: (a) obtaining an IRS biomarker profile from a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock) following commencement of the treatment regimen, wherein the IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and (b) correlating the IRS biomarker profile from the subject with a positive and/or negative response to the treatment regimen.

[0271] The invention also provides methods of determining a positive and/or negative response to a treatment regimen by a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS (e.g., mild sepsis, severe sepsis and septic shock). These methods generally comprise: (a) correlating a reference IRS biomarker profile with a positive and/or negative response to the treatment regimen, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and (b) determining a sample IRS biomarker profile from the subject, wherein the subject's sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker and indicates whether the subject is responding to the treatment regimen.

[0272] In some embodiments, the methods further comprise determining a first sample IRS biomarker profile from the subject prior to commencing the treatment regimen (i.e., a baseline profile), wherein the first sample IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and comparing the first sample IRS biomarker profile with a second sample IRS biomarker profile from the subject after commencement of the treatment regimen, wherein the second sample IRS biomarker profile evaluates for an individual IRS biomarker in the first sample IRS biomarker profile a corresponding IRS biomarker.

[0273] This aspect of the invention can be practiced to identify responders or non-responders relatively early in the treatment process, i.e., before clinical manifestations of efficacy. In this way, the treatment regimen can optionally be discontinued, a different treatment protocol can be implemented and/or supplemental therapy can be administered. Thus, in some embodiments, a sample IRS biomarker profile is obtained within about 2 hours, 4 hours, 6 hours, 12 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 6 weeks, 8 weeks, 10 weeks, 12 weeks, 4 months, six months or longer of commencing therapy.

[0274] In order that the invention may be readily understood and put into practical effect, particular preferred embodiments will now be described by way of the following non-limiting examples.

EXAMPLES

EXAMPLE 1

MONITORING SEVERITY OF IPSIRS IN PATIENTS IN INTENSIVE CARE

[0275] Patients admitted to intensive care (ICU) often have ipSIRS, or develop ipSIRS during their ICU stay. The ultimate aim of intensive care is to ensure the patient survives and is discharged to a general ward in the minimum time. Patients in intensive care with diagnosed ipSIRS are usually administered a number of therapeutic compounds – many of which have opposing actions on the immune system and many of which could be counterproductive depending on the severity of ipSIRS (mild sepsis, severe sepsis, septic shock). Monitoring intensive care patients on a regular basis with biomarkers of the present invention will allow medical practitioners to determine the stage of ipSIRS and hence choice of therapies and patient management procedures, and ultimately response to therapy. Information provided by these biomarkers disclosed herein ("the IRS biomarkers") will therefore allow medical practitioners to tailor and modify therapies to ensure patients survive and spend less time in intensive care. Less time in intensive care leads to considerable savings in medical expenses including through less occupancy time and appropriate use and timing of medications. Practical examples of the use of the IRS biomarkers in Tables 1 -6 are described.

[0276] Tables 1, 2 and 3 list those top 10 IRS biomarkers (by example) in ascending order of p value (less than 0.05) when comparing the clinical groups of mild sepsis, severe sepsis and septic shock (severe versus mild, shock versus mild and shock versus severe – the appropriate column is filled grey for each group in respective tables). In this and the following examples significance is defined when a p value is less than 0.05. P values were determined by adjusted t-test (Benjamini & Hochberg, 1995) in the case of healthy vs. other and inSIRS vs. ipSIRS, and by Tukey's Honestly Significant Difference for analysis of variance (ANOVA) for the mild/severe/shock comparisons. For the groups severe versus mild, shock versus mild and shock versus severe there were 72, 120 and 47 biomarkers respectively with a p value less than 0.05.

[0277] Tables 4, 5 and 6 list those top 10 biomarkers (by example) in descending order of Area Under Curve (AUC) value when comparing the clinical groups of mild sepsis, severe sepsis and septic shock (severe versus mild, shock versus mild and shock versus severe – the appropriate column is filled grey for each group in respective tables). For the groups severe versus mild, shock versus mild and shock versus severe there were 34, 17 and 2 biomarkers respectively with an AUC greater than 0.8 (a nominal cut-off above which would be considered to be good).

[0278] In each of Tables 1-6 a SEQ ID NO. is provided for each IRS biomarker (IRS biomarker polynucleotides range from SEQ ID NO. 1-319, IRS biomarker polypeptides range from SEQ ID No. 320 – 619), along with a database identification tag (e.g. NM_), a gene name (Gene Name) if there is one, and either; mean expression values for healthy (HC), inSIRS, mild sepsis, severe sepsis and septic shock, and p values for HC vs. all other groups, inSIRS vs. ipSIRS, mild sepsis versus severe sepsis, mild sepsis versus septic shock and septic shock versus severe sepsis, or AUC values for HC vs. Sick, HC vs. inSIRS, HC vs. ipSIRS, inSIRS vs. ipSIRS, Mild Sepsis versus Severe Sepsis, Mild Sepsis versus Septic Shock and Septic Shock versus Severe Sepsis. Such biomarkers have clinical utility in determining ipSIRS severity based on these groups. By example, in Table 1, Severe versus Mild p Value, it can be seen that the gene PLEKHA3 has a significant p value for both Severe versus Mild and Shock versus Mild and therefore has utility in separating mild sepsis from both severe sepsis and septic shock. In Table 2, Severe versus Mild Area Under Curve, it can be seen that the gene PLEKHA3 has an AUC of 0.8748 and therefore has most utility in separating mild sepsis from severe sepsis. It can be seen that the p value for PLEKHA3 for separating septic shock from severe sepsis is not significant (>0.05) and therefore this biomarker has no utility in separating these two groups. From the columns in the table containing mean expression data it can be seen that PLEKHA3 is down-regulated in both severe sepsis (6.689) and septic shock (6.825) compared to mild sepsis (7.281) (also see Figure 1).

[0279] Further and by example in Table 3, Shock vs. Mild p Value, it can be seen that the biomarker VAMP2 has utility in separating mild sepsis from septic shock but also from severe sepsis. VAMP2 does not have utility in separating septic shock from severe sepsis (p = 0.708038) but does have further utility in separating healthy from other groups. From the mean expression columns it can also be seen that the expression level of VAMP2 is downregulated in both severe sepsis (8.454) and septic shock (8.353) compared to mild sepsis (9.016) (see also Figure 2). In Table 4, Shock vs. Mild Area Under Curve, it can be seen that VAMP2 has an AUC of 0.8342.

Further and by example in Table 5, Shock versus Severe p Value, it can be seen that the biomarker ITK has utility in separating Shock versus Severe Sepsis and Mild Sepsis, and healthy from other groups but no utility in separating Severe Sepsis and Mild Sepsis. From the mean expression values for ITK it can be seen that it is comparatively downregulated in Septic Shock compared to both Severe and Mild Sepsis (see also Figure 3). In Table 6, Shock versus Severe Area Under Curve, it can be seen that ITK has an AUC of 0.8054.

Table 1

Severe versus Mild p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval.HC.vs. Other	pval.inSIRS. vs.ipSIRS	pval Severe.vs. Mild	pval Shock.vs .Mild	pval Shock.vs. Severe
285	NM_019091	PLEKHA3	7.058	6.910	7.281	6.689	6.825	1.000000	1.000000	0.000001	0.000011	0.409707
587	NM_019091	PLEKHA3	7.058	6.910	7.281	6.689	6.825	1.000000	1.000000	0.000001	0.000011	0.409707
232	gi|14250459	NA	6.389	5.970	6.875	5.976	6.059	1.000000	0.638753	0.000001	0.000000	0.869569
	gi|14250459	NA	6.389	5.970	6.875	5.976	6.059	1.000000	0.638753	0.000001	0.000000	0.869569
195	NM_004897	MINPP1	8.212	7.697	8.228	7.151	7.317	0.006705	1.000000	0.000005	0.000008	0.707929
504	NM_004897	MINPP1	8.212	7.697	8.228	7.151	7.317	0.006705	1.000000	0.000005	0.000008	0.707929
288	NM_024613	PLEKHF2	7.432	7.660	8.044	7.255	7.671	0.789194	1.000000	0.000012	0.023331	0.029137
590	NM_024613	PLEKHF2	7.432	7.660	8.044	7.255	7.671	0.789194	1.000000	0.000012	0.023331	0.029137
190	NM_176818	SFRS9	9.739	9.666	9.715	10.226	10.128	1.000000	0.000618	0.000018	0.000064	0.627141
499	NM_176818	SFRS9	9.739	9.666	9.715	10.226	10.128	1.000000	0.000618	0.000018	0.000064	0.627141
207	NR_002612	DLEU2	6.549	6.894	7.347	6.699	6.850	0.000171	1.000000	0.000019	0.000152	0.504529
	NR_002612	DLEU2	6.549	6.894	7.347	6.699	6.850	0.000171	1.000000	0.000019	0.000152	0.504529
197	NM_006969	ZNF28	4.936	4.511	5.008	4.554	4.612	0.021118	0.027741	0.000020	0.000018	0.814925
506	NM_006969	ZNF28	4.936	4.511	5.008	4.554	4.612	0.021118	0.027741	0.000020	0.000018	0.814925
71	NM_002269	KPNA5	6.822	5.908	6.451	5.758	5.712	0.000000	1.000000	0.000021	0.000000	0.945115
387	NM_002269	KPNA5	6.822	5.908	6.451	5.758	5.712	0.000000	1.000000	0.000021	0.000000	0.945115
278	NM_001130 059	ATF7	5.212	5.212	5.253	5.605	5.372	1.000000	0.438013	0.000033	0.171523	0.007397
580	NM_001130 059	ATF7	5.212	5.212	5.253	5.605	5.372	1.000000	0.438013	0.000033	0.171523	0.007397
81	NR_046099	LOC284757	6.913	8.028	6.894	7.534	7.376	0.000001	0.000004	0.000039	0.000364	0.493398
	NR_046099	LOC284757	6.913	8.028	6.894	7.534	7.376	0.000001	0.000004	0.000039	0.000364	0.493398

Table 2

Severe versus Mild Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. SIRS AUC	HC vs. ipSIRS AUC	inSIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
195	NM_004897	MINPP1	0.689217443	0.699775533	0.685388685	0.532134532	0.88707483	0.779591837	0.488435374
504	NM_004897	MINPP1	0.689217443	0.699775533	0.685388685	0.532134532	0.88707483	0.779591837	0.488435374
285	NM_019091	PLEKHA3	0.584378734	0.644781145	0.562474562	0.541791542	0.874829932	0.794285714	0.619047619
587	NM_019091	PLEKHA3	0.584378734	0.644781145	0.562474562	0.541791542	0.874829932	0.794285714	0.619047619
282	NM_002692	POLE2	0.675029869	0.693602694	0.668294668	0.501165501	0.854421769	0.707755102	0.563265306
584	NM_002692	POLE2	0.675029869	0.693602694	0.668294668	0.501165501	0.854421769	0.707755102	0.563265306
288	NM_024613	PLEKHF2	0.654868578	0.667227834	0.65038665	0.538794539	0.850340136	0.692244898	0.718367347
590	NM_024613	PLEKHF2	0.654868578	0.667227834	0.65038665	0.538794539	0.850340136	0.692244898	0.718367347
190	NM_176818	SFRS9	0.597520908	0.557800224	0.653846154	0.748917749	0.840816327	0.79755102	0.587755102
499	NM_176818	SFRS9	0.597520908	0.557800224	0.653846154	0.748917749	0.840816327	0.79755102	0.587755102
170	NM_003608	GPR65	0.765681004	0.735690236	0.776556777	0.6003996	0.839455782	0.615510204	0.740136054
480	NM_003608	GPR65	0.765681004	0.735690236	0.776556777	0.6003996	0.839455782	0.615510204	0.740136054
232	gi|14250459	NA	0.571983274	0.7003367	0.525437525	0.661338661	0.838095238	0.83755102	0.559183673
	gi|14250459	NA	0.571983274	0.7003367	0.525437525	0.661338661	0.838095238	0.83755102	0.559183673
197	NM_006969	ZNF28	0.689964158	0.837261504	0.636548637	0.670662671	0.836734694	0.796734694	0.536054422
506	NM_006969	ZNF28	0.689964158	0.837261504	0.636548637	0.670662671	0.836734694	0.796734694	0.536054422
81	NR_046099	LOC284757	0.738948626	0.939393939	0.666259666	0.835497835	0.834013605	0.749387755	0.613605442
	NR_046099	LOC284757	0.738948626	0.939393939	0.666259666	0.835497835	0.834013605	0.749387755	0.613605442
71	NM_002269	KPNA5	0.85483871	0.895061728	0.84025234	0.564768565	0.831292517	0.844897959	0.530612245
387	NM_002269	KPNA5	0.85483871	0.895061728	0.84025234	0.564768565	0.831292517	0.844897959	0.530612245

Table 3

Shock vs. Mild p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval.HC.vs .Other	pval.inSIRS. vs.ipSIRS	pval Severe.vs. Mild	pval Shock.vs. Mild	pval Shock.vs.Sev ere
59	NM_014232	VAMP2	9.213	8.896	9.016	8.454	8.353	0.000000	0.297018	0.000084	0.000000	0.708038
376	NM_014232	VAMP2	9.213	8.896	9.016	8.454	8.353	0.000000	0.297018	0.000084	0.000000	0.708038
71	NM_002269	KPNA5	6.822	5.908	6.451	5.758	5.712	0.000000	1.000000	0.000021	0.000000	0.945115
387	NM_002269	KPNA5	6.822	5.908	6.451	5.758	5.712	0.000000	1.000000	0.000021	0.000000	0.945115
232	gi|14250459	NA	6.389	5.970	6.875	5.976	6.059	1.000000	0.638753	0.000001	0.000000	0.869569
	gi|14250459	NA	6.389	5.970	6.875	5.976	6.059	1.000000	0.638753	0.000001	0.000000	0.869569
246	NM_032828	ZNF587	8.514	8.816	8.783	8.381	8.101	1.000000	0.003242	0.018153	0.000001	0.136854
549	NM_032828	ZNF587	8.514	8.816	8.783	8.381	8.101	1.000000	0.003242	0.018153	0.000001	0.136854
195	NM_004897	MINPP1	8.212	7.697	8.228	7.151	7.317	0.006705	1.000000	0.000005	0.000008	0.707929
504	NM_004897	MINPP1	8.212	7.697	8.228	7.151	7.317	0.006705	1.000000	0.000005	0.000008	0.707929
107	NM_153236	GIMAP7	9.533	8.865	8.974	8.682	8.112	0.000000	1.000000	0.310769	0.000008	0.014285
420	NM_153236	GIMAP7	9.533	8.865	8.974	8.682	8.112	0.000000	1.000000	0.310769	0.000008	0.014285
285	NM_019091	PLEKHA3	7.058	6.910	7.281	6.689	6.825	1.000000	1.000000	0.000001	0.000011	0.409707
587	NM_019091	PLEKHA3	7.058	6.910	7.281	6.689	6.825	1.000000	1.000000	0.000001	0.000011	0.409707
58	NM_002121	HLA-DPB1	11.414	10.665	10.623	9.971	9.578	0.000000	0.067333	0.026428	0.000013	0.253098
375	NM_002121	HLA-DPB1	11.414	10.665	10.623	9.971	9.578	0.000000	0.067333	0.026428	0.000013	0.253098
304	NR_033759	ATP5L	7.242	7.337	7.379	6.824	6.772	1.000000	0.748516	0.000612	0.000014	0.929559
	NR_033759	ATP5L	7.242	7.337	7.379	6.824	6.772	1.000000	0.748516	0.000612	0.000014	0.929559
197	NM_006969	ZNF28	4.936	4.511	5.008	4.554	4.612	0.021118	0.027741	0.000020	0.000018	0.814925
506	NM_006969	ZNF28	4.936	4.511	5.008	4.554	4.612	0.021118	0.027741	0.000020	0.000018	0.814925

Table 4

Shock vs. Mild Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. SIRS AUC	HC vs. ipSIRS AUC	inSIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
71	NM_002269	KPNA5	0.85483871	0.895061728	0.84025234	0.564768565	0.831292517	0.844897959	0.530612245
387	NM_002269	KPNA5	0.85483871	0.895061728	0.84025234	0.564768565	0.831292517	0.844897959	0.530612245
246	NM_032828	ZNF587	0.506571087	0.632435466	0.539072039	0.68964369	0.723809524	0.84244898	0.644897959
549	NM_032828	ZNF587	0.506571087	0.632435466	0.539072039	0.68964369	0.723809524	0.84244898	0.644897959
232	gi|14250459	NA	0.571983274	0.7003367	0.525437525	0.661338661	0.838095238	0.83755102	0.559183673
	gi|14250459	NA	0.571983274	0.7003367	0.525437525	0.661338661	0.838095238	0.83755102	0.559183673
59	NM_014232	VAMP2	0.814366786	0.78338945	0.825600326	0.636363636	0.810884354	0.834285714	0.54829932
376	NM_014232	VAMP2	0.814366786	0.78338945	0.825600326	0.636363636	0.810884354	0.834285714	0.54829932
107	NM_153236	GIMAP7	0.829898447	0.80359147	0.839438339	0.603063603	0.617687075	0.826938776	0.710204082
420	NM_153236	GIMAP7	0.829898447	0.80359147	0.839438339	0.603063603	0.617687075	0.826938776	0.710204082
58	NM_002121	HLA-DPB1	0.857228196	0.814814815	0.872608873	0.682317682	0.693877551	0.809795918	0.628571429
375	NM_002121	HLA-DPB1	0.857228196	0.814814815	0.872608873	0.682317682	0.693877551	0.809795918	0.628571429
110	gi|13182974	NA	0.796893668	0.92704826	0.74969475	0.743589744	0.681632653	0.808163265	0.617687075
423	gi|13182974	NA	0.796893668	0.92704826	0.74969475	0.743589744	0.681632653	0.808163265	0.617687075
64	NM_004172	SLC1A3	0.954599761	0.985409652	0.943426943	0.636030636	0.557823129	0.806530612	0.823129252
381	NM_004172	SLC1A3	0.954599761	0.985409652	0.943426943	0.636030636	0.557823129	0.806530612	0.823129252
190	NM_176818	SFRS9	0.597520908	0.557800224	0.653846154	0.748917749	0.840816327	0.79755102	0.587755102
499	NM_176818	SFRS9	0.597520908	0.557800224	0.653846154	0.748917749	0.840816327	0.79755102	0.587755102
197	NM_006969	ZNF28	0.689964158	0.837261504	0.636548637	0.670662671	0.836734694	0.796734694	0.536054422
506	NM_006969	ZNF28	0.689964158	0.837261504	0.636548637	0.670662671	0.836734694	0.796734694	0.536054422

Table 5

Shock versus Severe p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval.HC.vs.Other	pval.inSIRS.vs.Sepsis	pval Severe.vs.Mild	pval Shock.vs.Mild	pval Shock.vs.Severe
79	NM_005546	ITK	9.271	8.099	8.227	8.536	7.635	0.000000	1.000000	0.276607	0.002832	0.000063
395	NM_005546	ITK	9.271	8.099	8.227	8.536	7.635	0.000000	1.000000	0.276607	0.002832	0.000063
34	NM_001744	CAMK4	8.155	6.723	6.902	7.152	6.470	0.000000	1.000000	0.305982	0.011176	0.000339
352	NM_001744	CAMK4	8.155	6.723	6.902	7.152	6.470	0.000000	1.000000	0.305982	0.011176	0.000339
64	NM_004172	SLC1A3	5.849	6.892	6.472	6.447	7.373	0.000000	1.000000	0.993673	0.000056	0.000352
381	NM_004172	SLC1A3	5.849	6.892	6.472	6.447	7.373	0.000000	1.000000	0.993673	0.000056	0.000352
171	NR_046000	IRF4	8.200	7.491	7.843	8.381	7.762	0.000105	0.000070	0.002770	0.825556	0.000501
	NR_046000	IRF4	8.200	7.491	7.843	8.381	7.762	0.000105	0.000070	0.002770	0.825556	0.000501
271	NM_173485	TSHZ2	7.382	6.972	6.846	7.429	6.929	0.004682	1.000000	0.000051	0.739871	0.000534
574	NM_173485	TSHZ2	7.382	6.972	6.846	7.429	6.929	0.004682	1.000000	0.000051	0.739871	0.000534
22	NM_005449	FAIM3	10.259	9.101	9.036	9.174	8.464	0.000000	1.000000	0.732360	0.001453	0.000582
340	NM_005449	FAIM3	10.259	9.101	9.036	9.174	8.464	0.000000	1.000000	0.732360	0.001453	0.000582
44	NM_032047	B3GNT5	6.871	8.033	8.009	7.744	8.548	0.000000	1.000000	0.438680	0.013149	0.000955
362	NM_032047	B3GNT5	6.871	8.033	8.009	7.744	8.548	0.000000	1.000000	0.438680	0.013149	0.000955
229	NM_207647	FSD1L	4.605	4.402	4.801	4.565	5.099	1.000000	0.000000	0.235142	0.050177	0.001077
534	NM_207647	FSD1L	4.605	4.402	4.801	4.565	5.099	1.000000	0.000000	0.235142	0.050177	0.001077
198	gi|21538810	NPCDR1	5.404	5.022	4.784	5.166	4.817	0.000001	1.000000	0.000589	0.919120	0.001847
507	gi|21538810	NPCDR1	5.404	5.022	4.784	5.166	4.817	0.000001	1.000000	0.000589	0.919120	0.001847
220	NM_207627	ABCG1	8.318	7.923	7.960	8.214	7.791	0.000000	1.000000	0.112606	0.270961	0.003184
526	NM_207627	ABCG1	8.318	7.923	7.960	8.214	7.791	0.000000	1.000000	0.112606	0.270961	0.003184

Table 6

Shock versus Severe Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. SIRS AUC	HC vs. ipSIRS AUC	inSIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
64	NM_004172	SLC1A3	0.954599761	0.985409652	0.943426943	0.636030636	0.557823129	0.806530612	0.823129252
381	NM_004172	SLC1A3	0.954599761	0.985409652	0.943426943	0.636030636	0.557823129	0.806530612	0.823129252
79	NM_005546	ITK	0.888888889	0.873737374	0.894383394	0.520812521	0.646258503	0.735510204	0.805442177
395	NM_005546	ITK	0.888888889	0.873737374	0.894383394	0.520812521	0.646258503	0.735510204	0.805442177
22	NM_005449	FAIM3	0.951612903	0.930415264	0.959299959	0.596070596	0.57414966	0.749387755	0.793197279
340	NM_005449	FAIM3	0.951612903	0.930415264	0.959299959	0.596070596	0.57414966	0.749387755	0.793197279
171	NR_046000	IRF4	0.776433692	0.946127946	0.714896215	0.741258741	0.759183673	0.604897959	0.782312925
	NR_046000	IRF4	0.776433692	0.946127946	0.714896215	0.741258741	0.759183673	0.604897959	0.782312925
34	NM_001744	CAMK4	0.939217443	0.921436588	0.945665446	0.55977356	0.594557823	0.725714286	0.776870748
352	NM_001744	CAMK4	0.939217443	0.921436588	0.945665446	0.55977356	0.594557823	0.725714286	0.776870748
271	NM_173485	TSHZ2	0.705197133	0.733445567	0.694953195	0.543456543	0.828571429	0.528979592	0.776870748
574	NM_173485	TSHZ2	0.705197133	0.733445567	0.694953195	0.543456543	0.828571429	0.528979592	0.776870748
88	NM_181506	LRRC70	0.795997611	0.49382716	0.901098901	0.857808858	0.736054422	0.515102041	0.76462585
402	NM_181506	LRRC70	0.795997611	0.49382716	0.901098901	0.857808858	0.736054422	0.515102041	0.76462585
176	NM_002230	JUP	0.830346476	0.75308642	0.858363858	0.573093573	0.500680272	0.765714286	0.760544218
485	NM_002230	JUP	0.830346476	0.75308642	0.858363858	0.573093573	0.500680272	0.765714286	0.760544218
44	NM_032047	B3GNT5	0.9369773	0.948933782	0.932641433	0.548784549	0.565986395	0.692244898	0.759183673
362	NM_032047	B3GNT5	0.9369773	0.948933782	0.932641433	0.548784549	0.565986395	0.692244898	0.759183673
235	NM_003531	HIST1H3C	0.781212664	0.881593715	0.744810745	0.672327672	0.643537415	0.651428571	0.752380952
539	NM_003531	HIST1H3C	0.781212664	0.881593715	0.744810745	0.672327672	0.643537415	0.651428571	0.752380952

EXAMPLE 2

DIFFERENTIATING INSIRS AND IPSIRS IN POST-SURGICAL AND MEDICAL PATIENTS

[0280] Surgical and medical patients often develop inSIRS post-surgery, post-procedural or as part of a co-morbidity or co-morbidities. Such inpatients have a higher incidence of inSIRS and a higher risk of developing ipSIRS. Medical care in such patients therefore involves monitoring for signs of inSIRS and ipSIRS, differentiating between these two conditions, and determining at the earliest possible time when a patient transitions from inSIRS to ipSIRS. The treatment and management of inSIRS and ipSIRS patients is different, since inSIRS patients can be put on mild anti-inflammatory drugs or anti-pyretics and ipSIRS patients must be started on antibiotics as soon as possible for best outcomes. Monitoring post-surgical and medical patients on a regular basis with biomarkers of the present invention will allow nursing and medical practitioners to differentiate inSIRS and ipSIRS at an early stage and hence make informed decisions on choice of therapies and patient management procedures, and ultimately response to therapy. Information provided by these biomarkers will therefore allow medical practitioners to tailor and modify therapies to ensure patients recover quickly from surgery and do not develop ipSIRS. Less time in hospital and less complications leads to considerable savings in medical expenses including through less occupancy time and appropriate use and timing of medications. Practical examples of the use of the biomarkers in Tables 7 and 8 are described.

[0281] Table 7 lists the top 10 biomarkers (of 216) in order of ascending p value when comparing the two clinical groups of inSIRS and ipSIRS. A SEQ ID NO. is provided for each IRS biomarker (IRS biomarker polynucleotides range from SEQ ID NO. 1-319, IRS biomarker polypeptides range from SEQ ID No. 320 – 619), along with a database identification tag (e.g. NM_), a gene name (Gene Name) if there is one, mean expression values for healthy (HC), inSIRS, mild sepsis, severe sepsis and septic shock, and p values for HC vs. all other groups, inSIRS vs. ipSIRS, mild sepsis versus severe sepsis, mild sepsis versus septic shock and septic shock versus severe sepsis. All biomarkers have clinical utility in distinguishing inSIRS and ipSIRS and for distinguishing inSIRS and ipSIRS as early as possible. Seven (7) of these biomarkers are also useful in distinguishing healthy control from sick although this has no clinical utility for post-surgical or medical patients. Some of these biomarkers also have limited utility in determining ipSIRS severity as indicated by respective p values less than 0.05. By example, in Table 7, inSIRS vs. ipSIRS p Value, it can be seen that the gene C11orf82 has a significant p value for both inSIRS versus ipSIRS and Healthy versus other groups and therefore has utility in separating healthy and inSIRS patients from septic patients. From the columns in the table containing mean expression data it can be seen that C11orf82 is down-regulated in both inSIRS (5.888) and healthy controls (5.776) compared to septic patients of all classes (mild (6.889), severe (7.153) and shock (7.293)) (7.281) (also see Figure 4).

[0282] Table 8 lists the top 10 biomarkers (of 104 with an AUC > 0.8) in order of descending AUC when comparing the two clinical groups of inSIRS and ipSIRS and it can be seen that C11orf82, PLAC8 and INSIG1 have AUCs of 0.9477, 0.9210 and 0.9120, respectively (see also Figures 4, 5 and 6).

Table 7

inSIRS versus ipSIRS p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs. Other	pval inSIRS vs. ipSIRS	pval Severe vs. Mild	pval Shock vs. Mild	pval Shock vs. Severe
12	NM_145018	C11orf82	5.776	5.888	6.889	7.153	7.293	0.000000	0.000000	0.322762	0.032568	0.722429
330	NM_145018	C11orf82	5.776	5.888	6.889	7.153	7.293	0.000000	0.000000	0.322762	0.032568	0.722429
83	NR_036641	PDGFC	6.098	6.117	6.987	7.044	7.466	0.000000	0.000000	0.970637	0.064634	0.196970
	NR_036641	PDGFC	6.098	6.117	6.987	7.044	7.466	0.000000	0.000000	0.970637	0.064634	0.196970
106	NM_018375	SLC39A9	8.038	7.719	8.121	8.368	8.428	1.000000	0.000000	0.034062	0.001276	0.808136
419	NM_018375	SLC39A9	8.038	7.719	8.121	8.368	8.428	1.000000	0.000000	0.034062	0.001276	0.808136
150	NM_030796	VOPP1	9.302	8.771	9.510	9.318	9.517	1.000000	0.000000	0.298375	0.997162	0.269787
461	NM_030796	VOPP1	9.302	8.771	9.510	9.318	9.517	1.000000	0.000000	0.298375	0.997162	0.269787
73	NM_001257400	CD63	9.235	9.126	9.718	9.990	10.159	0.000000	0.000000	0.156468	0.002260	0.485665
389	NM_001257400	CD63	9.235	9.126	9.718	9.990	10.159	0.000000	0.000000	0.156468	0.002260	0.485665
55	NM_014143	CD274	5.508	5.656	7.557	7.211	7.237	0.000000	0.000000	0.536662	0.490374	0.996684
372	NM_014143	CD274	5.508	5.656	7.557	7.211	7.237	0.000000	0.000000	0.536662	0.490374	0.996684
111	NM_198336	INSIG1	8.081	7.370	8.062	7.867	7.913	0.001237	0.000000	0.123875	0.197540	0.883915
424	NM_198336	INSIG1	8.081	7.370	8.062	7.867	7.913	0.001237	0.000000	0.123875	0.197540	0.883915
76	ENST00000443533	DDAH2	8.067	8.170	8.630	8.707	9.015	0.000000	0.000000	0.868573	0.011535	0.108528
392	ENST00000443533	DDAH2	8.067	8.170	8.630	8.707	9.015	0.000000	0.000000	0.868573	0.011535	0.108528
115	NM_003546	HIST1H4L	9.807	7.908	9.466	9.602	9.065	0.000032	0.000000	0.878290	0.231084	0.140998
428	NM_003546	HIST1H4L	9.807	7.908	9.466	9.602	9.065	0.000032	0.000000	0.878290	0.231084	0.140998
226	NM_003537	HIST1H3B	8.783	7.684	8.739	9.501	8.852	1.000000	0.000000	0.042709	0.908040	0.098544
532	NM_003537	HIST1H3B	8.783	7.684	8.739	9.501	8.852	1.000000	0.000000	0.042709	0.908040	0.098544

Table 8

inSIRS versus ipSIRS Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. SIRS AUC	HC vs. ipSIRS AUC	inSIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
12	NM_145018	C11orf82	0.873058542	0.580246914	0.979242979	0.947718948	0.619047619	0.650612245	0.555102041
330	NM_145018	C11orf82	0.873058542	0.580246914	0.979242979	0.947718948	0.619047619	0.650612245	0.555102041
72	NM_001130715	PLAC8	0.635902031	0.828282828	0.804232804	0.921078921	0.506122449	0.653061224	0.642176871
388	NM_001130715	PLAC8	0.635902031	0.828282828	0.804232804	0.921078921	0.506122449	0.653061224	0.642176871
132	gi|21757933	NA	0.533004779	0.867564534	0.588319088	0.912753913	0.708843537	0.631020408	0.540136054
445	gi|21757933	NA	0.533004779	0.867564534	0.588319088	0.912753913	0.708843537	0.631020408	0.540136054
111	NM_198336	INSIG1	0.695191159	0.957351291	0.6001221	0.912087912	0.666666667	0.631836735	0.518367347
424	NM_198336	INSIG1	0.695191159	0.957351291	0.6001221	0.912087912	0.666666667	0.631836735	0.518367347
90	gi|21749325	CDS2	0.669354839	0.730078563	0.814204314	0.907092907	0.586394558	0.56244898	0.504761905
	gi|21749325	CDS2	0.669354839	0.730078563	0.814204314	0.907092907	0.586394558	0.56244898	0.504761905
150	NM_030796	VOPP1	0.53875448	0.937710438	0.605921856	0.906759907	0.63537415	0.544489796	0.66122449
461	NM_030796	VOPP1	0.53875448	0.937710438	0.605921856	0.906759907	0.63537415	0.544489796	0.66122449
106	NM_018375	SLC39A9	0.559587814	0.775533109	0.681115181	0.901098901	0.730612245	0.735510204	0.557823129
419	NM_018375	SLC39A9	0.559587814	0.775533109	0.681115181	0.901098901	0.730612245	0.735510204	0.557823129
37	NM_199135	FOXD4L3	0.815860215	0.49382716	0.928164428	0.900765901	0.597278912	0.608163265	0.48707483
355	NM_199135	FOXD4L3	0.815860215	0.49382716	0.928164428	0.900765901	0.597278912	0.608163265	0.48707483
68	NM_018639	WSB2	0.782108722	0.581369248	0.913919414	0.9004329	0.555102041	0.533877551	0.530612245
384	NM_018639	WSB2	0.782108722	0.581369248	0.913919414	0.9004329	0.555102041	0.533877551	0.530612245
73	NM_001257400	CD63	0.73655914	0.612233446	0.863044363	0.897768898	0.644897959	0.72244898	0.613605442
389	NM_001257400	CD63	0.73655914	0.612233446	0.863044363	0.897768898	0.644897959	0.72244898	0.613605442

EXAMPLE 3

DIFFERENTIATING BOTH INSIRS AND IPSIRS IN EMERGENCY DEPARTMENT PATIENTS AND DETERMINING DEGREE OF ILLNESS

[0283] Patients presenting to emergency departments often have a fever, which is one (of four) of the clinical signs of inSIRS. Such patients need to be assessed to determine if they have either inSIRS or ipSIRS. Further it is important to determine how sick they are to be able to make a judgement call on whether to admit the patient or not. As mentioned above, the treatment and management of pyretic, inSIRS and septic patients are different. By way of example, a patient with a fever without other inSIRS clinical signs and no obvious source of infection may be sent home, or provided with other non-hospital services, without further hospital treatment. However, a patient with a fever may have early ipSIRS and not admitting such a patient may put their life at risk. Because these biomarkers can differentiate inSIRS and ipSIRS and determine how sick a patient is they will allow medical practitioners to triage emergency department patients quickly and effectively. Accurate triage decision-making insures that patients requiring hospital treatment are given it, and those that don't are provided with other appropriate services. Practical examples of the use of the biomarkers in Tables 9 and 10 are described.

[0284] Table 9 lists 30 significant biomarkers when comparing the groups of healthy and sick (sick consisting of those patients with either inSIRS or ipSIRS) and inSIRS versus ipSIRS. A SEQ ID NO. is provided for each IRS biomarker (IRS biomarker polynucleotides range from SEQ ID NO. 1-319, IRS biomarker polypeptides range from SEQ ID No. 320 – 619), along with a database identification tag (e.g. NM_), a gene name (Gene Name) if there is one, mean expression values for healthy (HC), inSIRS, mild sepsis, severe sepsis and septic shock, and p values for HC vs. all other groups, inSIRS vs. ipSIRS, mild sepsis versus severe sepsis, mild sepsis versus septic shock and septic shock versus severe sepsis. Such biomarkers have clinical utility in distinguishing healthy from sick patients and inSIRS from ipSIRS patients. By example, in Table 5, Healthy versus inSIRS versus ipSIRS, it can be seen that the gene FCGR1A has a significant p value for both inSIRS versus ipSIRS and Healthy versus other groups and therefore has utility in separating healthy and inSIRS and ipSIRS patients. From the columns in the table containing mean expression data it can be seen that FCGR1A is up-regulated in inSIRS (9.281) compared to healthy controls (7.871) but more so in ipSIRS patients (9.985 – 10.308). Such a upward gradient in gene expression can be used to determine the degree of illness in patients presenting to an emergency department allowing clinicians to risk stratify and triage with greater certainty (see also Figure 7).

[0285] Table 10 lists 10 significant biomarkers when comparing the groups of healthy and sick (sick consisting of those patients with either inSIRS or ipSIRS) and inSIRS versus ipSIRS. A SEQ ID NO. is provided for each IRS biomarker (IRS biomarker polynucleotides range from SEQ ID NO. 1-319, IRS biomarker polypeptides range from SEQ ID No. 320 – 619), along with a database identification tag (e.g. NM_), a gene name (Gene Name) if there is one, mean expression values for healthy (HC), inSIRS, mild sepsis, severe sepsis and septic shock, and p values for HC vs. all other groups, inSIRS vs. ipSIRS, mild sepsis versus severe sepsis, mild sepsis versus septic shock and septic shock versus severe sepsis. Such biomarkers have clinical utility in distinguishing healthy from sick patients and inSIRS from ipSIRS patients. By example, in Table 10, Healthy versus inSIRS versus ipSIRS, it can be seen that the gene CHI3L1 has a significant p value for both inSIRS versus ipSIRS and Healthy versus other groups and therefore has utility in separating healthy and inSIRS and septic patients. From the columns in the table containing mean expression data it can be seen that CHI3L1 is down-regulated in inSIRS (9.876) compared to healthy controls (10.47) but more so in ipSIRS patients (8.64 – 9.035). Such a downward gradient in gene expression can be used to determine the degree of illness in patients presenting to an emergency department allowing clinicians to risk stratify and triage with greater certainty (see also Figure 8).

Table 9

Healthy versus inSIRS versus ipSIRS p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs. Other	pval inSIRS vs. ipSIRS	pval Severe vs. Mild	pval Shock vs. Mild	pval Shock vs. Severe
79	NR_045213	FCGR1A	7.871	9.281	10.308	9.985	10.273	0.000000	0.001046	0.284201	0.980298	0.366022
395	NR_045213	FCGR1A	7.871	9.281	10.308	9.985	10.273	0.000000	0.001046	0.284201	0.980298	0.366022
34	NM_153046	TDRD9	4.986	5.567	6.483	6.937	7.385	0.000000	0.000000	0.248195	0.001153	0.259068
352	NM_153046	TDRD9	4.986	5.567	6.483	6.937	7.385	0.000000	0.000000	0.248195	0.001153	0.259068
64	NM_020370	GPR84	6.712	8.157	9.030	8.980	9.583	0.000000	0.001894	0.989573	0.184680	0.221197
381	NM_020370	GPR84	6.712	8.157	9.030	8.980	9.583	0.000000	0.001894	0.989573	0.184680	0.221197
171	NM_018367	ACER3	7.317	7.845	8.701	8.417	9.050	0.000000	0.000000	0.362961	0.132905	0.008450
	NM_018367	ACER3	7.317	7.845	8.701	8.417	9.050	0.000000	0.000000	0.362961	0.132905	0.008450
271	NM_000860	HPGD	5.621	6.238	7.085	6.908	7.946	0.000000	0.000025	0.895298	0.035905	0.027021
574	NM_000860	HPGD	5.621	6.238	7.085	6.908	7.946	0.000000	0.000025	0.895298	0.035905	0.027021
22	NM_006418	OLFM4	6.365	7.209	8.023	9.641	9.322	0.000000	0.000069	0.003150	0.006691	0.784808
340	NM_006418	OLFM4	6.365	7.209	8.023	9.641	9.322	0.000000	0.000069	0.003150	0.006691	0.784808
44	NM_004054	C3AR1	8.429	9.449	10.261	10.439	10.593	0.000000	0.000016	0.650271	0.142678	0.725241
362	NM_004054	C3AR1	8.429	9.449	10.261	10.439	10.593	0.000000	0.000016	0.650271	0.142678	0.725241
229	NM_002934	RNASE2	9.164	10.500	11.243	11.670	11.388	0.000000	0.002979	0.095954	0.690976	0.351809
534	NM_002934	RNASE2	9.164	10.500	11.243	11.670	11.388	0.000000	0.002979	0.095954	0.690976	0.351809
198	NM_032045	KREMEN1	8.626	9.409	10.143	10.189	10.055	0.000000	0.000079	0.962640	0.837239	0.731337
507	NM_032045	KREMEN1	8.626	9.409	10.143	10.189	10.055	0.000000	0.000079	0.962640	0.837239	0.731337
220	NM_003268	TLR5	7.747	9.010	9.726	9.979	10.311	0.000000	0.000225	0.275728	0.000244	0.110996
526	NM_003268	TLR5	7.747	9.010	9.726	9.979	10.311	0.000000	0.000225	0.275728	0.000244	0.110996
281	NM_153021	PLB1	8.205	8.887	9.574	9.463	10.019	0.000000	0.000133	0.872838	0.059398	0.037699
583	NM_153021	PLB1	8.205	8.887	9.574	9.463	10.019	0.000000	0.000133	0.872838	0.059398	0.037699
214	NM_004482	GALNT3	5.685	6.251	6.916	6.728	7.075	0.000000	0.000000	0.407446	0.422801	0.051201
520	NM_004482	GALNT3	5.685	6.251	6.916	6.728	7.075	0.000000	0.000000	0.407446	0.422801	0.051201

27	NM_001816	CEACAM8	7.336	7.874	8.503	9.775	9.287	0.000000	0.001298	0.011921	0.098854	0.501991
345	NM_001816	CEACAM8	7.336	7.874	8.503	9.775	9.287	0.000000	0.001298	0.011921	0.098854	0.501991
242	NM_007115	TNFAIP6	7.738	9.246	9.829	9.631	9.738	0.000000	1.000000	0.712067	0.908467	0.905260
545	NM_007115	TNFAIP6	7.738	9.246	9.829	9.631	9.738	0.000000	1.000000	0.712067	0.908467	0.905260
170	NM_016021	UBE2J1	8.792	9.555	10.118	10.044	10.335	0.000000	0.000015	0.817659	0.104460	0.049488
480	NM_016021	UBE2J1	8.792	9.555	10.118	10.044	10.335	0.000000	0.000015	0.817659	0.104460	0.049488
278	NM_015268	DNAJC13	7.507	8.083	8.596	8.693	8.878	0.000000	0.000000	0.833718	0.133216	0.512817
580	NM_015268	DNAJC13	7.507	8.083	8.596	8.693	8.878	0.000000	0.000000	0.833718	0.133216	0.512817

Table 10

Healthy versus inSIRS versus ipSIRS p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs. Other	pval inSIRS vs. ipSIRS	pval Severe vs. Mild	pval Shock vs. Mild	pval Shock vs. Severe
104	NM_001276	CHI3L1	10.470	9.876	8.640	9.035	8.726	0.000000	0.000056	0.485576	0.954853	0.641602
417	NM_001276	CHI3L1	10.470	9.876	8.640	9.035	8.726	0.000000	0.000056	0.485576	0.954853	0.641602
122	NM_001143804	PHOSPHO1	11.398	10.826	10.374	9.837	10.185	0.000000	0.048380	0.088690	0.661703	0.354179
435	NM_001143804	PHOSPHO1	11.398	10.826	10.374	9.837	10.185	0.000000	0.048380	0.088690	0.661703	0.354179
40	NM_016523	KLRF1	6.343	5.438	5.022	4.504	4.543	0.000000	0.007278	0.033428	0.021421	0.979558
358	NM_016523	KLRF1	6.343	5.438	5.022	4.504	4.543	0.000000	0.007278	0.033428	0.021421	0.979558
33	NM_000953	PTGDR	9.310	8.373	8.028	7.790	7.577	0.000000	0.007043	0.500548	0.040553	0.570947
351	NM_000953	PTGDR	9.310	8.373	8.028	7.790	7.577	0.000000	0.007043	0.500548	0.040553	0.570947
103	ENST00000381907	KLRD1	8.651	8.097	7.766	7.201	7.123	0.000000	0.011838	0.056985	0.008125	0.944270
416	ENST00000381907	KLRD1	8.651	8.097	7.766	7.201	7.123	0.000000	0.011838	0.056985	0.008125	0.944270

EXAMPLE 4

DIFFERENTIATING HEALTHY FROM SICK PATIENTS AND DETERMINING DEGREE OF ILLNESS

[0286] Patients presenting to medical clinics often have any one of the four clinical signs of inSIRS (increased heart rate, increased respiratory rate, abnormal white blood cell count, fever or hypothermia). Many different clinical conditions can present with one of the four clinical signs of inSIRS and such patients need to be assessed to determine if they have either inSIRS or ipSIRS and to exclude other differential diagnoses. By way of example, a patient with colic might also present with clinical signs of increased heart rate. Differential diagnoses could be (but not limited to) appendicitis, urolithiasis, cholecystitis, pancreatitis, enterocolitis. In each of these conditions it would be important to determine if there was a systemic inflammatory response (inSIRS) or whether an infection was contributing to the condition. The treatment and management of patients with and without systemic inflammation and/or infection are different. Because these biomarkers can differentiate healthy from sick (inSIRS and ipSIRS), and determine the degree of systemic involvement, the use of them will allow medical practitioners to determine the next medical procedure(s) to perform to satisfactorily resolve the patient issue. Practical examples of the use of the biomarkers in Tables 11, 12, 13 and 14 are described.

[0287] Table 11 lists 20 significant biomarkers (of 150) when comparing the groups of healthy and sick (sick consisting of those patients with either inSIRS or ipSIRS). A SEQ ID NO. is provided for each IRS biomarker (IRS biomarker polynucleotides range from SEQ ID NO. 1-319, IRS biomarker polypeptides range from SEQ ID No. 320 – 619), along with a database identification tag (e.g. NM_), a gene name (Gene Name) if there is one, mean expression values for healthy (HC), inSIRS, mild sepsis, severe sepsis and septic shock, and p values for HC vs. all other groups, inSIRS vs. ipSIRS, mild sepsis versus severe sepsis, mild sepsis versus septic shock and septic shock versus severe sepsis. Such biomarkers have clinical utility in distinguishing healthy from sick patients and determining the level of systemic inflammation and/or infection. For example, in Table 11, Healthy versus Sick, it can be seen that the gene CD177 has a significant p value for healthy control versus other groups and therefore has utility in separating healthy and sick patients. From the columns in the table containing mean expression data it can be seen that CD177 is up-regulated in inSIRS (10.809) compared to healthy controls (8.091) but more so in ipSIRS patients (11.267 – 12.088). Such up-regulated differences in gene expression can be used to determine the degree of systemic inflammation and infection in patients presenting to clinics allowing clinicians to more easily determine the next medical procedure(s) to perform to satisfactorily resolve the patient issue (see also Figure 9).

[0288] Further, and by example, in Table 11, Healthy versus Sick, it can be seen that the gene GNLY has a significant p value for healthy control versus other groups and therefore has utility in separating healthy and sick patients. From the columns in the table containing mean expression data it can be seen that GNLY is down-regulated in inSIRS (9.428) compared to healthy controls (10.653) but more so in septic patients (9.305 – 8.408). GNLY has an AUC of 0.9445 (not shown) for separating healthy and sick patients. Such down-regulated differences in gene expression can be used to determine the degree of systemic inflammation and infection in patients presenting to clinics allowing clinicians to more easily determine the next medical procedure(s) to perform to satisfactorily resolve the patient issue (see also Figure 10).

[0289] Table 12 lists the top 10 biomarkers (of 118 with an AUC of at least 0.8) for separating healthy from sick patients (sick being those patients with either inSIRS or ipSIRS) by decreasing value of Area Under Curve (AUC). It can be seen that the highest AUC is for CD177 for separating healthy from sick (0.9929) (see also Figure 9).

[0290] Table 13 lists the top 10 biomarkers (of 152 with an AUC of at least 0.8) for separating healthy from inSIRS patients by decreasing value of Area Under Curve (AUC). It can be seen that the highest AUC is for BMX for separating healthy from inSIRS (1). That is, this biomarker alone can perfectly separate these two groups (see also Figure 11).

[0291] Table 14 lists the top 10 biomarkers (of 140 with an AUC of at least 0.8) for separating healthy from ipSIRS patients by decreasing value of Area Under Curve (AUC). It can be seen that the highest AUC is for TLR5 for separating healthy from ipSIRS (0.9945) (see also Figure 12).

Table 11

Healthy versus Sick p Value

SEQ ID Number	Database ID	Gene Name	HC Mean	SIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs. Other	pval SIRS vs. ipSIRS	pval Severe vs. Mild	pval Shock vs. Mild	pval Shock vs. Severe
2	NM_020406	CD177	8.091	10.809	11.267	12.088	12.044	0.000000	0.087061	0.048910	0.027926	0.991139
321	NM_020406	CD177	8.091	10.809	11.267	12.088	12.044	0.000000	0.087061	0.048910	0.027926	0.991139
10	NM_001244438	ARG1	5.410	9.054	7.895	8.254	8.919	0.000000	1.000000	0.628534	0.008931	0.209877
329	NM_001244438	ARG1	5.410	9.054	7.895	8.254	8.919	0.000000	1.000000	0.628534	0.008931	0.209877
3	NM_004666	VNN1	7.736	10.013	10.007	10.629	10.876	0.000000	1.000000	0.087388	0.002402	0.671136
322	NM_004666	VNN1	7.736	10.013	10.007	10.629	10.876	0.000000	1.000000	0.087388	0.002402	0.671136
7	NM_080387	CLEC4D	7.187	9.915	9.238	9.152	9.828	0.000000	0.383427	0.945300	0.034026	0.035853
326	NM_080387	CLEC4D	7.187	9.915	9.238	9.152	9.828	0.000000	0.383427	0.945300	0.034026	0.035853
29	NM_020370	GPR84	6.712	8.157	9.030	8.980	9.583	0.000000	0.001894	0.989573	0.184680	0.221197
347	NM_020370	GPR84	6.712	8.157	9.030	8.980	9.583	0.000000	0.001894	0.989573	0.184680	0.221197
24	NM_003855	IL18R1	5.516	8.101	7.098	7.538	8.097	0.000000	1.000000	0.373616	0.001873	0.205385
342	NM_003855	IL18R1	5.516	8.101	7.098	7.538	8.097	0.000000	1.000000	0.373616	0.001873	0.205385
65	NM_006418	OLFM4	6.365	7.209	8.023	9.641	9.322	0.000000	0.000068	0.003150	0.006691	0.784808
382	NM_006418	OLFM4	6.365	7.209	8.023	9.641	9.322	0.000000	0.000068	0.003150	0.006691	0.784808
11	NR_045213	FCGR1A	7.871	9.281	10.308	9.985	10.273	0.000000	0.001046	0.284201	0.980298	0.366022
	NR_045213	FCGR1A	7.871	9.281	10.308	9.985	10.273	0.000000	0.001046	0.284201	0.980298	0.366022
6	NM_002934	RNASE2	9.164	10.500	11.243	11.670	11.388	0.000000	0.002979	0.095954	0.690976	0.351809
325	NM_002934	RNASE2	9.164	10.500	11.243	11.670	11.388	0.000000	0.002979	0.095954	0.690976	0.351809
14	NM_006433	GNLY	10.653	9.428	9.305	8.659	8.408	0.000000	0.020098	0.014566	0.000045	0.511511
332	NM_006433	GNLY	10.653	9.428	9.305	8.659	8.408	0.000000	0.020098	0.014566	0.000045	0.511511

Table 12

Healthy versus Sick Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. inSIRS AUC	HC vs. ipSIRS AUC	SIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
2	NM_020406	CD177	0.992980884	0.991582492	0.993487993	0.718281718	0.668027211	0.675102041	0.540136054
321	NM_020406	CD177	0.992980884	0.991582492	0.993487993	0.718281718	0.668027211	0.675102041	0.540136054
7	NM_080387	CLEC4D	0.981780167	0.998877666	0.975579976	0.64968365	0.52244898	0.671020408	0.691156463
326	NM_080387	CLEC4D	0.981780167	0.998877666	0.975579976	0.64968365	0.52244898	0.671020408	0.691156463
18	NM_203281	BMX	0.979988053	1	0.972730973	0.56043956	0.639455782	0.749387755	0.644897959
336	NM_203281	BMX	0.979988053	1	0.972730973	0.56043956	0.639455782	0.749387755	0.644897959
3	NM_004666	VNN1	0.979241338	0.996632997	0.972934473	0.663003663	0.648979592	0.710204082	0.575510204
322	NM_004666	VNN1	0.979241338	0.996632997	0.972934473	0.663003663	0.648979592	0.710204082	0.575510204
29	NM_020370	GPR84	0.974313023	0.92704826	0.991452991	0.738927739	0.496598639	0.608163265	0.623129252
347	NM_020370	GPR84	0.974313023	0.92704826	0.991452991	0.738927739	0.496598639	0.608163265	0.623129252
10	NM_001244438	ARG1	0.970878136	0.999438833	0.960520961	0.644355644	0.561904762	0.683265306	0.662585034
329	NM_001244438	ARG1	0.970878136	0.999438833	0.960520961	0.644355644	0.561904762	0.683265306	0.662585034
24	NM_003855	IL18R1	0.966845878	0.989337823	0.958689459	0.62970363	0.62585034	0.715102041	0.639455782
342	NM_003855	IL18R1	0.966845878	0.989337823	0.958689459	0.62970363	0.62585034	0.715102041	0.639455782
26	NM_006459	ERLIN1	0.964755078	0.994949495	0.953805454	0.694971695	0.561904762	0.639183673	0.594557823
344	NM_006459	ERLIN1	0.964755078	0.994949495	0.953805454	0.694971695	0.561904762	0.639183673	0.594557823
5	NM_018285	IMP3	0.96385902	0.997755331	0.951566952	0.817515818	0.610884354	0.742040816	0.614965986
324	NM_018285	IMP3	0.96385902	0.997755331	0.951566952	0.817515818	0.610884354	0.742040816	0.614965986
1	NM_003268	TLR5	0.962365591	0.873737374	0.994505495	0.808524809	0.606802721	0.768979592	0.672108844
320	NM_003268	TLR5	0.962365591	0.873737374	0.994505495	0.808524809	0.606802721	0.768979592	0.672108844

Table 13

Healthy versus inSIRS Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. inSIRS AUC	HC vs. ipSIRS AUC	SIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
18	NM_203281	BMX	0.979988053	1	0.972730973	0.56043956	0.639455782	0.749387755	0.644897959
336	NM_203281	BMX	0.979988053	1	0.972730973	0.56043956	0.639455782	0.749387755	0.644897959
10	NM_001244438	ARG1	0.970878136	0.999438833	0.960520961	0.644355644	0.561904762	0.683265306	0.662585034
329	NM_001244438	ARG1	0.970878136	0.999438833	0.960520961	0.644355644	0.561904762	0.683265306	0.662585034
7	NM_080387	CLEC4D	0.981780167	0.998877666	0.975579976	0.64968365	0.52244898	0.671020408	0.691156463
326	NM_080387	CLEC4D	0.981780167	0.998877666	0.975579976	0.64968365	0.52244898	0.671020408	0.691156463
5	NM_018285	IMP3	0.96385902	0.997755331	0.951566952	0.817515818	0.610884354	0.742040816	0.614965986
324	NM_018285	IMP3	0.96385902	0.997755331	0.951566952	0.817515818	0.610884354	0.742040816	0.614965986
3	NM_004666	VNN1	0.979241338	0.996632997	0.972934473	0.663003663	0.648979592	0.710204082	0.575510204
322	NM_004666	VNN1	0.979241338	0.996632997	0.972934473	0.663003663	0.648979592	0.710204082	0.575510204
26	NM_006459	ERLIN1	0.964755078	0.994949495	0.953805454	0.694971695	0.561904762	0.639183673	0.594557823
344	NM_006459	ERLIN1	0.964755078	0.994949495	0.953805454	0.694971695	0.561904762	0.639183673	0.594557823
17	NM_207113	SLC37A3	0.954301075	0.99382716	0.93996744	0.582417582	0.619047619	0.653061224	0.551020408
335	NM_207113	SLC37A3	0.954301075	0.99382716	0.93996744	0.582417582	0.619047619	0.653061224	0.551020408
38	NM_004994	MMP9	0.935782557	0.993265993	0.914936915	0.625374625	0.653061224	0.653877551	0.48707483
356	NM_004994	MMP9	0.935782557	0.993265993	0.914936915	0.625374625	0.653061224	0.653877551	0.48707483
120	NM_004244	CD163	0.842293907	0.993265993	0.787545788	0.716949717	0.481632653	0.663673469	0.648979592
433	NM_004244	CD163	0.842293907	0.993265993	0.787545788	0.716949717	0.481632653	0.663673469	0.648979592
46	NM_006212	PFKFB2	0.922341697	0.992704826	0.896825397	0.678654679	0.51292517	0.679183673	0.68707483
363	NM_006212	PFKFB2	0.922341697	0.992704826	0.896825397	0.678654679	0.51292517	0.679183673	0.68707483

Table 14

Healthy versus ipSIRS Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC vs. Sick AUC	HC vs. inSIRS AUC	HC vs. ipSIRS AUC	SIRS vs. ipSIRS AUC	Mild vs. Severe AUC	Mild vs. Shock AUC	Severe vs. Shock AUC
1	NM_003268	TLR5	0.962365591	0.873737374	0.994505495	0.808524809	0.606802721	0.768979592	0.672108844
320	NM_003268	TLR5	0.962365591	0.873737374	0.994505495	0.808524809	0.606802721	0.768979592	0.672108844
2	NM_020406	CD177	0.992980884	0.991582492	0.993487993	0.718281718	0.668027211	0.675102041	0.540136054
321	NM_020406	CD177	0.992980884	0.991582492	0.993487993	0.718281718	0.668027211	0.675102041	0.540136054
29	NM_020370	GPR84	0.974313023	0.92704826	0.991452991	0.738927739	0.496598639	0.608163265	0.623129252
347	NM_020370	GPR84	0.974313023	0.92704826	0.991452991	0.738927739	0.496598639	0.608163265	0.623129252
20	NM_153046	TDRD9	0.929062127	0.758136925	0.991045991	0.844488844	0.640816327	0.734693878	0.636734694
338	NM_153046	TDRD9	0.929062127	0.758136925	0.991045991	0.844488844	0.640816327	0.734693878	0.636734694
4	NM_016021	UBE2J1	0.959677419	0.888327722	0.985551486	0.826173826	0.468027211	0.644897959	0.682993197
323	NM_016021	UBE2J1	0.959677419	0.888327722	0.985551486	0.826173826	0.468027211	0.644897959	0.682993197
11	NR_045213	FCGR1A	0.954749104	0.87037037	0.985347985	0.77988678	0.612244898	0.492244898	0.621768707
	NR_045213	FCGR1A	0.954749104	0.87037037	0.985347985	0.77988678	0.612244898	0.492244898	0.621768707
6	NM_002934	RNASE2	0.94937276	0.854657688	0.983719984	0.780552781	0.67755102	0.564081633	0.643537415
325	NM_002934	RNASE2	0.94937276	0.854657688	0.983719984	0.780552781	0.67755102	0.564081633	0.643537415
8	NM_004054	C3AR1	0.950119474	0.868125701	0.97985348	0.832833833	0.529251701	0.609795918	0.582312925
327	NM_004054	C3AR1	0.950119474	0.868125701	0.97985348	0.832833833	0.529251701	0.609795918	0.582312925
12	NM_145018	C11orf82	0.873058542	0.580246914	0.979242979	0.947718948	0.619047619	0.650612245	0.555102041
330	NM_145018	C11orf82	0.873058542	0.580246914	0.979242979	0.947718948	0.619047619	0.650612245	0.555102041
13	NM_018099	FAR2	0.942502987	0.843434343	0.978428978	0.794205794	0.561904762	0.746122449	0.693877551
331	NM_018099	FAR2	0.942502987	0.843434343	0.978428978	0.794205794	0.561904762	0.746122449	0.693877551

EXAMPLE 5

DIFFERENTIAL EXPRESSION OF IRS BIOMARKERSMARKERS BETWEEN HEALTHY, INSIRS, MILD SEPSIS, SEVERE SEPSIS AND SEPTIC SHOCK

[0292] Presented below in Figures 13 to 331 are "Box and Whisker" plots for each of the 319 biomarkers where the bottom and top of the box are the first and third quartiles, and the band inside the box is the second quartile (the median) (of gene expression). Biomarkers are presented in order of ascending adjusted p value when comparing "All Classes" (i.e., healthy control, referred to as "Healthy" in Figures 13-331; inSIRS, referred to as "SIRS" in Figures 13-331;; mild sepsis referred to as "Mild" in Figures 13-331;; severe sepsis, referred to as "Severe" in Figures 13-331; and septic shock, referred to as "Shock" in Figures 13-331) – varying from 6.49E-48 to 1.00, and according to the following table (Table 15). Appropriate choice and use of such markers can be used to select patients for inclusion in, or exclusion from, clinical trials. Further, such markers can be used to determine the efficacy of treatment, therapies or management regimens in patients by determining whether a patient has transitioned from one condition to another and by determining the stage or degree of a particular condition. For example, an exemplary clinical trial design testing for the efficacy of an inotrope may include only those patients with shock ipSIRS that are most likely to best respond to such a drug. In addition, and following inclusion of such patients and treatment with the inotrope, such patients could be monitored to determine if, when, how quickly and to what degree they respond to the inotrope by their transition from shock ipSIRS to other degrees of ipSIRS, inSIRS or health. Similarly, a model clinical trial design testing for the efficacy of an antibiotic, or combination of antibiotics, may include only those patients with ipSIRS, and not inSIRS, that are most likely to best respond to such a drug. In addition, and following inclusion of such patients and treatment with the antibiotic(s), such patients could be monitored to determine if, when, how quickly and to what degree they respond to the antibiotic(s) by their transition from ipSIRS to inSIRS or health. Similarly, an exemplary clinical trial design testing for the efficacy of an immune modulating drug (e.g. a steroid) may include only those patients with known stages of ipSIRS, for example those recovering from ipSIRS or those in the early stages of ipSIRS. Following inclusion of such patients and treatment with the immune modulating drug, such patients could be monitored to determine if, when, how quickly and to what degree they respond to the immune modulating drug by their transition from ipSIRS to inSIRS or health. The biomarker response and outcome (e.g. reduced length of hospital stay, reduced mortality) of patients in various stages of ipSIRS (early, late) treated with an immune modulating drug may also indicate when such a drug is best administered for maximum benefit.

Table 15

Healthy versus inSIRS versus ipSIRS versus Mild versus Severe versus Shock p Value and Area Under Curve (AUC)

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
1	NM_003268	TLR5	7.747	9.010	9.726	9.979	10.311	0.000000	0.000225	0.275728	0.000244	0.110996
2	NM_020406	CD177	8.091	10.809	11.267	12.088	12.044	0.000000	0.087061	0.048910	0.027926	0.991139
3	NM_004666	VNN1	7.736	10.013	10.007	10.629	10.876	0.000000	1.000000	0.087388	0.002402	0.671136
4	NM_016021	UBE2J1	8.792	9.555	10.118	10.044	10.335	0.000000	0.000015	0.817659	0.104460	0.049488
5	NM_018285	IMP3	7.951	6.465	7.032	6.934	6.723	0.000000	0.000000	0.645365	0.004479	0.136619
6	NM_002934	RNASE2	9.164	10.500	11.243	11.670	11.388	0.000000	0.002979	0.095954	0.690976	0.351809
7	NM_080387	CLEC4D	7.187	9.915	9.238	9.152	9.828	0.000000	0.383427	0.945300	0.034026	0.035853
8	NM_004054	C3AR1	8.429	9.449	10.261	10.439	10.593	0.000000	0.000016	0.650271	0.142678	0.725241
9	NM_001145772	GPR56	9.741	8.456	8.297	7.926	7.611	0.000000	0.009068	0.118387	0.000147	0.212773
10	NM_001244438	ARG1	5.410	9.054	7.895	8.254	8.919	0.000000	1.000000	0.628534	0.008931	0.209877
11	NR_045213	FCGR1A	7.871	9.281	10.308	9.985	10.273	0.000000	0.001046	0.284201	0.980298	0.366022
12	NM_145018	C11orf82	5.776	5.888	6.889	7.153	7.293	0.000000	0.000000	0.322762	0.032568	0.722429
13	NM_018099	FAR2	8.164	8.881	9.322	9.439	9.813	0.000000	0.000434	0.708180	0.000658	0.034215
14	NM_006433	GNLY	10.653	9.428	9.305	8.659	8.408	0.000000	0.020098	0.014566	0.000045	0.511511
15	NM_004482	GALNT3	5.685	6.251	6.916	6.728	7.075	0.000000	0.000000	0.407446	0.422801	0.051201
16	NM_002544	OMG	4.756	5.187	5.644	5.799	6.063	0.000000	0.000000	0.486295	0.001484	0.125031
17	NM_207113	SLC37A3	8.600	10.048	9.633	9.916	9.990	0.000000	1.000000	0.200617	0.035680	0.892137
18	NM_203281	BMX	4.804	6.547	6.012	6.397	6.839	0.000000	1.000000	0.251812	0.000431	0.163472
19	NM_004099	STOM	9.914	10.377	10.824	10.894	11.148	0.000000	0.000000	0.861884	0.017391	0.144729
20	NM_153046	TDRD9	4.986	5.567	6.483	6.937	7.385	0.000000	0.000000	0.248195	0.001153	0.259068
21	NM_032045	KREMEN1	8.626	9.409	10.143	10.189	10.055	0.000000	0.000079	0.962640	0.837239	0.731337
22	NM_005449	FAIM3	10.259	9.101	9.036	9.174	8.464	0.000000	1.000000	0.732360	0.001453	0.000582
23	NM_014358	CLEC4E	8.446	10.547	9.491	9.618	9.945	0.000000	0.000082	0.796454	0.024690	0.225126
24	NM_003855	IL18R1	5.516	8.101	7.098	7.538	8.097	0.000000	1.000000	0.373616	0.001873	0.205385

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
25	NM_018367	ACER3	7.317	7.845	8.701	8.417	9.050	0.000000	0.000000	0.362961	0.132905	0.008450
26	NM_006459	ERLIN1	7.136	9.162	8.418	8.526	8.855	0.000000	0.431436	0.880592	0.070482	0.316561
27	NM_004612	TGFBR1	9.328	9.614	10.165	9.999	10.368	0.000000	0.000000	0.333550	0.115281	0.005971
28	NM_001145775	FKBP5	9.006	11.106	10.185	10.457	10.750	0.000000	0.035769	0.441852	0.011707	0.389198
29	NM_020370	GPR84	6.712	8.157	9.030	8.980	9.583	0.000000	0.001894	0.989573	0.184680	0.221197
30	NM_182597	C7orf53	6.397	6.878	7.266	7.760	7.532	0.000000	0.000080	0.007994	0.141534	0.338948
31	NM_153021	PLB1	8.205	8.887	9.574	9.463	10.019	0.000000	0.000133	0.872838	0.059398	0.037699
32	NM_013352	DSE	7.272	7.680	8.183	8.109	8.384	0.000000	0.000062	0.830987	0.170622	0.085371
33	NM_000953	PTGDR	9.310	8.373	8.028	7.790	7.577	0.000000	0.007043	0.500548	0.040553	0.570947
34	NM_001744	CAMK4	8.155	6.723	6.902	7.152	6.470	0.000000	1.000000	0.305982	0.011176	0.000339
35	NM_015268	DNAJC13	7.507	8.083	8.596	8.693	8.878	0.000000	0.000000	0.833718	0.133216	0.512817
36	NM_007115	TNFAIP6	7.738	9.246	9.829	9.631	9.738	0.000000	1.000000	0.712067	0.908467	0.905260
37	NM_199135	FOXD4L3	6.441	6.501	7.402	7.610	7.649	0.000000	0.000000	0.417434	0.196375	0.968937
38	NM_004994	MMP9	10.179	12.012	11.383	11.801	11.830	0.000000	1.000000	0.196819	0.086637	0.992129
39	NM_000637	GSR	8.866	9.322	9.492	10.037	9.928	0.000000	0.000039	0.000432	0.001207	0.709854
40	NM_016523	KLRF1	6.343	5.438	5.022	4.504	4.543	0.000000	0.007278	0.033428	0.021421	0.979558
41	NM_053282	SH2D1B	8.067	6.992	6.896	6.451	6.450	0.000000	0.652812	0.064249	0.026676	0.999993
42	NM_001004441	ANKRD34B	4.809	5.415	5.855	6.471	6.738	0.000000	0.000000	0.074815	0.001252	0.606835
43	NM_001136258	SGMS2	6.693	7.708	7.553	7.712	8.128	0.000000	1.000000	0.670176	0.001769	0.073073
44	NM_032047	B3GNT5	6.871	8.033	8.009	7.744	8.548	0.000000	1.000000	0.438680	0.013149	0.000955
45	NR_026575	GK3P	4.227	5.729	5.316	5.552	5.937	0.000000	1.000000	0.493837	0.002433	0.158402
46	NM_006212	PFKFB2	7.955	10.444	9.336	9.326	10.196	0.000000	0.069041	0.999591	0.014557	0.037351
47	NM_007166	PICALM	9.079	9.433	9.822	9.993	10.284	0.000000	0.000000	0.500534	0.001958	0.138243
48	NM_152637	METTL7B	6.693	7.153	7.628	7.927	8.037	0.000000	0.000000	0.315445	0.060594	0.854279
49	NM_003542	HIST1H4C	11.803	9.795	10.815	10.617	10.323	0.000000	0.000004	0.695152	0.055254	0.448113
50	NM_145005	C9orf72	8.262	8.742	9.312	9.073	9.243	0.000000	0.000039	0.180477	0.821921	0.417016
51	NM_003533	HIST1H3I	10.878	9.003	10.144	10.141	9.669	0.000000	0.000000	0.999875	0.029147	0.070614

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
52	NM_021082	SLC15A2	7.246	7.309	7.861	8.034	8.227	0.000000	0.000000	0.350572	0.002949	0.273300
53	NM_030956	TLR10	6.794	6.842	7.713	7.823	7.900	0.000000	0.000000	0.798408	0.423055	0.895083
54	NM_001124	ADM	8.676	8.896	9.739	9.441	9.674	0.000000	0.000001	0.091052	0.855508	0.225820
55	NM_014143	CD274	5.508	5.656	7.557	7.211	7.237	0.000000	0.000000	0.536662	0.490374	0.996684
56	NM_001311	CRIP1	8.880	6.932	7.984	7.844	7.526	0.000000	0.002476	0.799183	0.046887	0.320589
57	NM_001099660	LRRN3	7.163	5.997	5.841	6.367	5.906	0.000000	1.000000	0.002710	0.877917	0.009767
58	NM_002121	HLA-DPB1	11.414	10.665	10.623	9.971	9.578	0.000000	0.067333	0.026428	0.000013	0.253098
59	NM_014232	VAMP2	9.213	8.896	9.016	8.454	8.353	0.000000	0.297018	0.000084	0.000000	0.708038
60	NM_006714	SMPDL3A	6.243	6.701	7.288	7.563	8.227	0.000000	0.000000	0.609142	0.000879	0.060210
61	NM_005531	IFI16	8.973	10.323	9.950	9.942	9.860	0.000000	0.020087	0.998663	0.799026	0.869508
62	NM_016475	JKAMP	8.440	8.442	9.231	8.827	9.150	0.000000	0.000000	0.000984	0.661905	0.010409
63	ENST00000371443	MRPL41	8.037	6.496	7.288	7.313	7.279	0.000000	0.000000	0.986016	0.997776	0.974877
64	NM_004172	SLC1A3	5.849	6.892	6.472	6.447	7.373	0.000000	1.000000	0.993673	0.000056	0.000352
65	NM_006418	OLFM4	6.365	7.209	8.023	9.641	9.322	0.000000	0.000068	0.003150	0.006691	0.784808
66	NM_001164116	CASS4	8.124	7.848	7.410	7.217	7.047	0.000000	0.000000	0.428924	0.022397	0.521806
67	ENST00000533734	TCN1	6.015	6.936	7.241	8.481	8.420	0.000000	0.000290	0.005182	0.001932	0.986095
68	NM_018639	WSB2	8.870	8.808	9.618	9.714	9.657	0.000000	0.000000	0.761189	0.939475	0.910197
69	ENST00000405140	CLU	9.016	9.264	9.889	10.137	9.813	0.000000	0.000063	0.216377	0.819582	0.075588
70	NM_001163278	ODZ1	6.088	7.677	6.668	7.303	7.416	0.000000	0.245652	0.024855	0.001421	0.884318
71	NM_002269	KPNA5	6.822	5.908	6.451	5.758	5.712	0.000000	1.000000	0.000021	0.000000	0.945115
72	NM_001130715	PLAC8	10.873	10.024	11.434	11.500	11.772	1.000000	0.000000	0.950268	0.172935	0.420732
73	NM_001257400	CD63	9.235	9.126	9.718	9.990	10.159	0.000000	0.000000	0.156468	0.002260	0.485665
74	NM_006665	HPSE	8.103	8.173	9.127	9.174	8.937	0.000000	0.000000	0.958822	0.401504	0.346256
75	NM_152367	C1orf161	5.851	6.354	6.479	6.738	6.845	0.000000	0.417891	0.196267	0.015651	0.756446
76	ENST00000443533	DDAH2	8.067	8.170	8.630	8.707	9.015	0.000000	0.000000	0.868573	0.011535	0.108528
77	NM_001199805	KLRK1	8.677	7.641	7.492	7.142	6.815	0.000000	1.000000	0.344640	0.006675	0.394595
78	NM_024524	ATP13A3	7.668	7.763	8.429	8.547	8.804	0.000000	0.000000	0.777976	0.039725	0.310273

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
79	NM_005546	ITK	9.271	8.099	8.227	8.536	7.635	0.000000	1.000000	0.276607	0.002832	0.000063
80	NM_021127	PMAIP1	6.940	5.860	6.770	6.251	6.214	0.000000	0.000000	0.002936	0.000187	0.968287
81	NR_046099	LOC284757	6.913	8.028	6.894	7.534	7.376	0.000001	0.000004	0.000039	0.000364	0.493398
82	NM_002080	GOT2	6.854	5.823	6.017	6.378	6.047	0.000000	0.490985	0.040847	0.969911	0.066504
83	NR_036641	PDGFC	6.098	6.117	6.987	7.044	7.466	0.000000	0.000000	0.970637	0.064634	0.196970
84	NM_012200	B3GAT3	7.939	7.030	7.516	7.658	7.632	0.000000	0.000000	0.387020	0.434149	0.966275
85	NM_003545	HIST1H4E	10.534	9.717	9.907	9.362	9.307	0.000000	1.000000	0.026325	0.003375	0.962707
86	NM_000860	HPGD	5.621	6.238	7.085	6.908	7.946	0.000000	0.000024	0.895298	0.035905	0.027021
87	NM_031950	FGFBP2	8.090	7.266	7.130	6.722	6.520	0.000000	0.976589	0.222869	0.013639	0.687542
88	NM_181506	LRRC70	3.455	3.495	4.144	3.763	4.135	0.000000	0.000000	0.020091	0.996732	0.024012
89	NM_018342	TMEM144	5.697	6.377	6.781	7.043	6.824	0.000000	0.914921	0.404820	0.968067	0.529328
90	gi|21749325	CDS2	10.235	9.988	10.651	10.561	10.570	0.041844	0.000000	0.584395	0.561379	0.994393
91	NM_001725	BPI	7.724	8.603	8.894	10.119	9.589	0.000000	0.026705	0.001145	0.046592	0.253799
92	ENST00000379215	ECHDC3	7.486	8.705	7.801	7.715	8.165	0.000000	0.001975	0.857762	0.030361	0.018763
93	NM_001837	CCR3	7.078	6.226	6.015	6.079	5.783	0.000000	1.000000	0.937302	0.322103	0.253166
94	NM_014181	HSPC159	9.120	9.779	9.933	10.248	10.249	0.000000	1.000000	0.218914	0.132537	0.999989
95	NM_018324	OLAH	4.483	6.220	5.483	6.162	6.492	0.000000	1.000000	0.125688	0.003063	0.604976
96	NM_006243	PPP2R5A	8.141	9.000	8.646	8.931	8.952	0.000000	1.000000	0.109345	0.035683	0.988342
97	NM_001193451	TMTC1	6.316	7.153	7.497	7.783	7.961	0.000000	0.543009	0.580949	0.154696	0.809916
98	NM_001023570	EAF2	8.389	8.607	9.323	9.016	9.301	0.000000	0.000012	0.105531	0.985106	0.141523
99	NM_001268	RCBTB2	8.646	8.621	9.321	9.357	9.340	0.000000	0.000001	0.961397	0.985058	0.991536
100	NM_021982	SEC24A	7.847	7.914	8.266	8.571	8.641	0.000000	0.000000	0.094884	0.010201	0.880791
101	NM_001017995	SH3PXD2B	5.800	6.949	6.262	6.384	6.870	0.000000	1.000000	0.786615	0.000756	0.026622
102	NM_001130688	HMGB2	7.782	9.225	8.769	8.869	8.910	0.000000	1.000000	0.894388	0.745151	0.981575
103	ENST00000381907	KLRD1	8.651	8.097	7.766	7.201	7.123	0.000000	0.011838	0.056985	0.008125	0.944270
104	NM_001276	CHI3L1	10.470	9.876	8.640	9.035	8.726	0.000000	0.000056	0.485576	0.954853	0.641602
105	NM_174938	FRMD3	6.218	6.408	6.959	6.889	6.703	0.000000	0.000000	0.872556	0.096505	0.389383

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
106	NM_018375	SLC39A9	8.038	7.719	8.121	8.368	8.428	1.000000	0.000000	0.034062	0.001276	0.808136
107	NM_153236	GIMAP7	9.533	8.865	8.974	8.682	8.112	0.000000	1.000000	0.310769	0.000008	0.014285
108	NM_016476	ANAPC11	6.716	5.940	6.219	6.214	6.368	0.000000	0.016248	0.998808	0.245788	0.323554
109	NM_019037	EXOSC4	8.216	8.199	8.716	8.845	9.307	0.000000	0.000000	0.796042	0.002754	0.059157
110	gi|13182974	NA	7.793	8.895	8.712	8.321	8.114	0.000000	0.003518	0.039103	0.000094	0.391472
111	NM_198336	INSIG1	8.081	7.370	8.062	7.867	7.913	0.001237	0.000000	0.123875	0.197540	0.883915
112	ENST00000542161	FOLR3	7.767	8.283	8.505	9.059	9.163	0.000000	0.039807	0.074391	0.008772	0.909407
113	NM_001024630	RUNX2	9.359	9.363	8.874	8.973	8.703	0.000000	0.000000	0.683914	0.223731	0.064525
114	NM_018457	PRR13	8.919	9.881	9.380	9.204	9.375	0.000000	0.000085	0.390820	0.998964	0.411767
115	NM_003546	HIST1H4L	9.807	7.908	9.466	9.602	9.065	0.000032	0.000000	0.878290	0.231084	0.140998
116	NM_002305	LGALS1	10.393	10.059	10.730	10.741	10.938	0.246894	0.000000	0.995433	0.137821	0.261564
117	NM_001295	CCR1	9.036	9.458	10.071	10.000	10.253	0.000000	0.009681	0.937695	0.574455	0.448234
118	NM_003596	TPST1	8.526	10.334	9.295	9.600	9.760	0.000000	0.055822	0.518907	0.136190	0.833502
119	NM_019111	HLA-DRA	11.467	10.758	10.870	10.441	10.188	0.000000	1.000000	0.091925	0.000575	0.429491
120	NM_004244	CD163	6.823	8.730	7.652	7.643	8.413	0.000000	0.092636	0.999632	0.037288	0.077812
121	NM_005306	FFAR2	9.559	9.849	10.479	10.309	10.573	0.000000	0.002329	0.564897	0.791331	0.256398
122	NM_001143804	PHOSPHO1	11.398	10.826	10.374	9.837	10.185	0.000000	0.048380	0.088690	0.661703	0.354179
123	NM_005729	PPIF	9.131	8.392	8.994	8.669	8.682	0.000000	0.001262	0.016029	0.006615	0.993122
124	NM_001199760	MTHFS	8.177	9.060	8.644	8.530	8.897	0.000000	0.406481	0.678016	0.086391	0.022355
125	NM_015190	DNAJC9	7.382	5.889	6.594	7.251	6.665	0.000000	0.000027	0.007512	0.921502	0.019348
126	NM_005564	LCN2	7.729	8.168	8.921	10.113	10.092	0.000000	0.000002	0.028722	0.011016	0.998889
127	ENST00000233057	EIF2AK2	7.237	8.670	8.347	8.159	8.071	0.000000	0.263528	0.709245	0.379350	0.929139
128	NM_006498	LGALS2	6.920	6.085	6.594	6.235	6.142	0.000000	0.375827	0.045528	0.001960	0.806041
129	NM_001199922	SIAE	6.721	6.530	7.174	7.284	7.068	0.000300	0.000000	0.666202	0.603123	0.213378
130	NM_004644	AP3B2	5.979	6.181	6.485	6.665	7.116	0.000000	0.000003	0.646507	0.001477	0.071475
131	NM_152701	ABCA13	5.814	6.131	6.688	7.350	7.182	0.000000	0.000000	0.066387	0.130673	0.834277
132	gi|21757933	NA	7.336	7.963	7.065	7.340	7.275	1.000000	0.000000	0.034322	0.071492	0.818353

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
133	NR_026586	EFCAB2	4.462	4.942	5.648	4.939	5.021	0.000000	1.000000	0.000756	0.000575	0.898330
134	NM_170745	HIST1H2AA	6.310	6.872	6.483	6.652	6.820	0.000002	0.020011	0.118625	0.000044	0.124349
135	NR_024610	HINT1	7.948	6.705	7.591	7.235	7.052	0.000000	0.041290	0.142709	0.003549	0.590766
136	NM_003535	HIST1H3J	8.323	6.703	7.484	7.314	7.135	0.000000	0.000274	0.715862	0.160141	0.691744
137	NM_001785	CDA	10.407	11.415	11.045	11.032	11.020	0.000000	0.043371	0.996584	0.982475	0.996794
138	NM_003864	SAP30	9.022	9.883	9.258	9.251	9.295	0.000000	0.001328	0.998061	0.924872	0.921435
139	NM_001040196	AGTRAP	10.055	9.933	10.594	10.356	10.502	0.000787	0.000000	0.083006	0.602023	0.382046
140	NM_033050	SUCNR1	3.660	3.734	4.329	4.517	4.334	0.000000	0.000000	0.487465	0.999396	0.504866
141	NM_002454	MTRR	8.163	7.862	8.523	8.796	8.849	0.122045	0.000000	0.216837	0.057755	0.942570
142	NM_001168357	PLA2G7	6.797	6.685	5.928	5.753	5.816	0.000000	0.011194	0.534519	0.708535	0.921793
143	NM_016108	AIG1	6.298	6.237	6.932	6.735	7.005	0.000001	0.000000	0.470358	0.871019	0.246707
144	NM_013363	PCOLCE2	5.863	5.909	6.292	6.366	6.785	0.000000	0.000000	0.925694	0.013235	0.089534
145	NM_080491	GAB2	9.471	10.280	9.787	9.810	9.689	0.000000	0.000000	0.982341	0.635805	0.599323
146	NM_012262	HS2ST1	7.018	6.874	7.363	7.378	7.465	0.001571	0.000000	0.990909	0.556564	0.723490
147	NM_003529	HIST1H3A	7.822	6.477	7.240	7.007	6.871	0.000000	0.000513	0.477800	0.090217	0.776827
148	gi|21757754	C22orf37	8.047	7.525	8.170	7.898	7.869	0.152851	0.000000	0.021435	0.002302	0.954990
149	ENST00000443117	HLA-DPA1	11.917	11.327	11.426	10.930	10.582	0.000000	1.000000	0.125876	0.000597	0.352649
150	NM_030796	VOPP1	9.302	8.771	9.510	9.318	9.517	1.000000	0.000000	0.298375	0.997162	0.269787
151	NM_001135147	SLC39A8	7.820	7.364	8.061	7.951	8.434	1.000000	0.000000	0.788039	0.031226	0.013434
152	NM_002417	MKI67	5.979	5.822	6.140	6.894	6.463	0.105108	0.000000	0.000163	0.097385	0.045251
153	NM_000578	SLC11A1	10.812	11.719	11.333	11.110	11.214	0.000000	0.000048	0.338648	0.659426	0.788341
154	NM_001657	AREG	6.075	6.806	6.139	6.126	6.310	0.001304	0.023771	0.980680	0.018616	0.030209
155	NM_005502	ABCA1	7.734	7.909	8.601	8.816	8.449	0.000000	0.000000	0.574359	0.692624	0.204976
156	NM_001201427	DAAM2	6.591	8.217	7.135	7.167	7.607	0.000000	0.072069	0.992564	0.124949	0.254325
157	NM_002343	LTF	8.098	8.330	8.923	9.937	9.639	0.000000	0.000019	0.012909	0.052398	0.670808
158	NM_178174	TREML1	8.869	9.169	9.868	10.187	9.876	0.000000	0.000638	0.449927	0.999311	0.468015
159	NM_004832	GSTO1	7.113	7.036	7.593	7.598	7.768	0.000017	0.000000	0.999247	0.345252	0.470840

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
160	NM_000956	PTGER2	8.918	8.348	9.019	8.983	9.315	1.000000	0.000000	0.970366	0.070654	0.081972
161	NM_001816	CEACAM8	7.336	7.874	8.503	9.775	9.287	0.000000	0.001298	0.011921	0.098854	0.501991
162	NM_016184	CLEC4A	8.210	8.289	9.043	8.708	9.051	0.000001	0.000030	0.153416	0.998827	0.141809
163	NR_002217	PMS2CL	7.598	6.664	7.289	7.057	7.040	0.000000	0.000440	0.281314	0.146553	0.993528
164	NM_001193374	RETN	7.747	7.886	8.097	8.248	8.835	0.000000	0.000109	0.767125	0.000526	0.022922
165	NM_000922	PDE3B	8.142	8.242	7.627	7.734	7.730	0.000586	0.000010	0.567468	0.494918	0.999337
166	NM_018837	SULF2	9.831	9.704	9.064	9.248	8.696	0.000000	0.000000	0.721156	0.183689	0.059640
167	NM_001145001	NEK6	9.503	9.287	9.835	9.710	9.943	0.153083	0.000000	0.541334	0.546065	0.125355
168	NM_022145	CENPK	7.073	6.142	6.664	6.040	6.012	0.000000	1.000000	0.003871	0.000401	0.988210
169	NM_145725	TRAF3	8.046	7.482	8.145	8.152	7.882	1.000000	0.000003	0.997488	0.011707	0.028412
170	NM_003608	GPR65	9.085	9.452	9.834	9.216	9.665	0.000000	1.000000	0.000115	0.360571	0.006354
171	NR_046000	IRF4	8.200	7.491	7.843	8.381	7.762	0.000105	0.000070	0.002770	0.825556	0.000501
172	gi|42521648	MACF1	6.473	6.545	7.013	7.187	7.377	0.000009	0.000481	0.609788	0.061186	0.553735
173	NM_001144	AMFR	9.420	8.994	9.671	9.823	9.635	1.000000	0.000000	0.543847	0.954865	0.395265
174	NM_000985	RPL17	6.122	5.182	5.758	5.556	5.513	0.000000	0.000708	0.298432	0.096378	0.944801
175	NM_003749	IRS2	8.965	9.531	8.841	8.998	9.024	1.000000	0.000068	0.322209	0.133169	0.969809
176	NM_002230	JUP	8.165	7.803	7.812	7.804	7.467	0.000000	1.000000	0.997835	0.006010	0.023849
177	NM_013230	CD24	5.563	5.793	6.173	7.205	7.139	0.000000	0.044339	0.008714	0.004161	0.979397
178	NM_004481	GALNT2	8.541	8.534	8.896	8.980	9.333	0.000001	0.000000	0.887956	0.017521	0.130219
179	NM_007355	HSP90AB1	9.881	8.635	9.085	9.720	9.186	0.000000	0.052850	0.015572	0.861439	0.050094
180	NM_024656	GLT25D1	9.757	9.336	9.948	9.861	10.201	1.000000	0.000001	0.826970	0.124352	0.061226
181	NM_001001658	OR9A2	4.207	4.662	4.825	4.991	5.108	0.000000	1.000000	0.671976	0.216358	0.816042
182	NM_001178135	HDHD1A	8.039	7.927	8.296	8.300	8.508	0.156481	0.000026	0.999441	0.101404	0.187976
183	NM_001141945	ACTA2	6.977	6.906	7.430	7.434	7.417	0.000137	0.000000	0.999465	0.993242	0.991119
184	NM_152282	ACPL2	6.821	7.762	7.139	7.253	7.209	0.000000	0.038264	0.736975	0.857652	0.955277
185	NM_001137550	LRRFIP1	6.512	6.814	6.827	7.037	7.241	0.000015	1.000000	0.216163	0.000656	0.232230
186	NM_001161352	KCNMA1	5.664	6.042	6.492	6.317	7.025	0.000000	0.031350	0.804476	0.075606	0.033982

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187	gi|12584148	OCR1	8.817	9.952	8.387	8.844	8.270	1.000000	0.000000	0.273663	0.890199	0.131897
188	NM_000885	ITGA4	8.779	7.932	8.394	7.981	7.906	0.000000	1.000000	0.064191	0.007047	0.909442
189	NM_001412	EIF1AX	7.439	6.463	7.251	6.667	6.907	0.000022	0.033776	0.002586	0.056446	0.338019
190	NM_176818	SFRS9	9.739	9.666	9.715	10.226	10.128	1.000000	0.000618	0.000018	0.000064	0.627141
191	NM_206831	DPH3	6.211	6.602	6.923	6.606	6.842	0.000000	1.000000	0.052319	0.764333	0.189405
192	NM_001031711	ERGIC1	9.539	10.203	9.742	9.565	9.579	0.014810	0.000006	0.364984	0.320097	0.993728
193	NM_007261	CD300A	9.890	9.479	10.058	10.054	10.025	1.000000	0.000000	0.999363	0.929522	0.957280
194	NM_001085386	NF-E4	7.348	8.202	7.715	8.545	7.934	0.000000	1.000000	0.002063	0.535657	0.030775
195	NM_004897	MINPP1	8.212	7.697	8.228	7.151	7.317	0.006705	1.000000	0.000005	0.000008	0.707929
196	NM_003141	TRIM21	8.072	8.151	8.840	8.371	8.271	0.002474	0.019577	0.006536	0.000092	0.782377
197	NM_006969	ZNF28	4.936	4.511	5.008	4.554	4.612	0.021118	0.027741	0.000020	0.000018	0.814925
198	gi|21538810	NPCDR1	5.404	5.022	4.784	5.166	4.817	0.000001	1.000000	0.000589	0.919120	0.001847
199	gi|15530286	NA	9.276	9.224	8.804	8.909	8.390	0.001392	0.000629	0.821276	0.021614	0.011283
200	gi|7021995	NA	7.607	8.002	6.917	7.075	6.999	0.480277	0.000000	0.721694	0.889525	0.926763
201	NM_000201	ICAM1	8.842	8.625	9.470	9.156	9.088	0.069361	0.000002	0.113961	0.015602	0.900519
202	NM_005645	TAF13	5.332	5.173	5.949	5.474	5.798	0.054434	0.000001	0.004467	0.457202	0.072895
203	NM_000917	P4HA1	6.365	6.096	6.773	6.664	6.873	1.000000	0.000000	0.752172	0.731181	0.358637
204	NM_207445	C15orf54	4.953	4.588	4.394	4.290	4.370	0.000000	0.891418	0.669439	0.972296	0.787051
205	NM_002108	HAL	7.142	6.909	7.654	7.331	7.571	0.894890	0.000000	0.049449	0.758572	0.184215
206	NM_015998	KLHL5	9.003	9.971	9.113	9.407	9.083	0.009758	0.000000	0.315312	0.984513	0.248776
207	NR_002612	DLEU2	6.549	6.894	7.347	6.699	6.850	0.000171	1.000000	0.000019	0.000152	0.504529
208	NM_015199	ANKRD28	7.286	7.393	7.898	7.722	7.941	0.000001	0.046283	0.544926	0.951892	0.391621
209	ENST00000375864	LY6G5B	9.037	8.992	8.780	8.654	8.383	0.014059	0.001656	0.642377	0.004351	0.135693
210	ENST00000344062	KIAA1257	6.868	7.365	6.882	6.874	6.689	1.000000	0.000000	0.997049	0.129430	0.242441
211	NM_004528	MGST3	9.104	8.519	9.273	9.098	9.003	1.000000	0.000001	0.377410	0.050613	0.751799
212	NM_015187	KIAA0746	8.174	7.591	8.170	8.747	8.502	1.000000	0.000002	0.015387	0.148674	0.453449
213	NM_001540	HSPB1	9.140	8.923	9.664	9.580	9.371	0.267148	0.000000	0.845749	0.072845	0.359260

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214	NM_005508	CCR4	7.105	6.356	6.598	6.829	6.321	0.000000	1.000000	0.321399	0.120202	0.005850
215	NM_001071	TYMS	6.084	5.695	6.186	6.854	6.291	1.000000	0.000000	0.003309	0.816061	0.015734
216	ENST00000536831	RRP12	8.946	8.381	8.821	8.752	8.721	0.000127	0.000063	0.794423	0.522969	0.952728
217	NM_176816	CCDC125	7.600	8.401	7.883	8.048	7.988	0.000029	0.000070	0.517640	0.700053	0.915690
218	NM_003521	HIST1H2BM	10.104	9.242	10.213	10.837	10.261	1.000000	0.000000	0.055178	0.976895	0.083087
219	NM_002612	PDK4	7.445	8.411	8.080	8.035	8.318	0.000000	1.000000	0.982556	0.521742	0.501879
220	NM_207627	ABCG1	8.318	7.923	7.960	8.214	7.791	0.000000	1.000000	0.112606	0.270961	0.003184
221	NM_000576	IL1B	9.070	9.172	10.021	9.550	9.930	0.000002	0.124840	0.077098	0.874756	0.185371
222	NM_003246	THBS1	8.599	9.860	8.993	9.423	9.387	0.000000	1.000000	0.179953	0.147689	0.987631
223	NM_000419	ITGA2B	8.899	8.768	9.482	9.747	9.378	0.011285	0.000003	0.403390	0.825144	0.174155
224	NM_005780	LHFP	6.216	6.391	6.523	6.665	6.778	0.000000	0.003992	0.475817	0.046096	0.625105
225	NM_002287	LAIR1	9.265	9.118	9.815	9.654	10.179	0.001517	0.000113	0.773401	0.179212	0.071167
226	NM_003537	HIST1H3B	8.783	7.684	8.739	9.501	8.852	1.000000	0.000000	0.042709	0.908040	0.098544
227	gi|29387167	ZRANB1	8.205	9.041	8.641	8.455	8.619	0.000016	0.001723	0.476723	0.985358	0.563742
228	ENST00000525158	TIMM10	7.454	6.704	7.473	7.175	6.921	0.000333	0.000431	0.308861	0.006345	0.426642
229	NM_207647	FSD1L	4.605	4.402	4.801	4.565	5.099	1.000000	0.000000	0.235142	0.050177	0.001077
230	NM_021066	HIST1H2AJ	5.699	4.152	4.990	3.871	4.070	0.000128	1.000000	0.008735	0.013543	0.852098
231	ENST00000362012	PTGS1	8.883	8.605	9.293	9.429	9.247	1.000000	0.000001	0.723148	0.952752	0.562936
232	gi|14250459	NA	6.389	5.970	6.875	5.976	6.059	1.000000	0.638753	0.000001	0.000000	0.869569
233	NM_080678	UBE2F	7.698	7.618	8.235	8.225	8.425	0.009739	0.003879	0.998629	0.495878	0.558822
234	NM_001104595	FAM118A	8.366	7.706	7.946	8.222	7.802	0.000086	0.879292	0.116376	0.451548	0.008324
235	NM_003531	HIST1H3C	9.254	7.630	9.025	9.427	8.749	0.908521	0.000000	0.439119	0.594489	0.101186
236	NM_003965	CCRL2	6.401	6.488	6.982	6.754	7.040	0.000011	0.001007	0.386796	0.919567	0.226387
237	NR_003094	E2F6	4.235	3.673	4.143	3.579	3.647	0.002951	1.000000	0.000262	0.000208	0.874090
238	NM_198275	MPZL3	10.241	10.754	10.209	10.039	10.276	1.000000	0.000000	0.418422	0.832036	0.186944
239	NM_080725	SRXN1	9.497	9.560	9.732	9.815	10.069	0.084230	0.126068	0.777086	0.005812	0.101705
240	NM_004357	CD151	9.083	8.712	9.309	9.522	9.473	1.000000	0.000001	0.408420	0.488688	0.954477

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241	NM_003536	HIST1H3H	9.933	8.623	9.688	9.538	9.310	0.018867	0.000017	0.811822	0.177187	0.617435
242	NM_031919	FSD1L	2.752	2.614	2.977	2.804	3.257	0.713444	0.000000	0.455516	0.068219	0.006227
243	NM_001131065	RFESD	6.745	6.242	6.502	5.562	5.837	0.011176	1.000000	0.000486	0.005152	0.486482
244	NM_012112	TPX2	5.722	5.535	5.917	6.431	6.063	1.000000	0.000000	0.009609	0.587740	0.085624
245	NM_006272	S100B	5.289	4.661	4.917	4.533	4.692	0.000031	1.000000	0.034824	0.206071	0.549376
246	NM_032828	ZNF587	8.514	8.816	8.783	8.381	8.101	1.000000	0.003242	0.018153	0.000001	0.136854
247	NM_152501	PYHIN1	8.390	8.040	7.744	7.890	7.473	0.000001	1.000000	0.732308	0.247163	0.086327
248	NM_020775	KIAA1324	9.383	9.433	8.708	9.010	8.061	0.053345	0.004214	0.630998	0.065841	0.013683
249	NM_002483	CEACAM6	5.249	5.373	5.959	6.957	6.219	0.000014	0.000574	0.023214	0.699643	0.121152
250	NM_001130415	APOLD1	7.318	6.858	7.205	7.363	7.253	0.906687	0.000002	0.263662	0.846643	0.520142
251	NM_000134	FABP2	4.244	4.518	4.396	4.549	4.826	0.000004	1.000000	0.578201	0.004767	0.174039
252	NM_001080424	KDM6B	9.854	10.383	10.147	9.749	9.701	1.000000	0.000332	0.072707	0.013999	0.962410
253	ENST00000390265	IGK@	10.393	9.201	10.307	11.107	10.228	1.000000	0.000007	0.087003	0.967489	0.053514
254	NM_006097	MYL9	9.235	9.445	10.021	9.931	9.763	0.000001	0.017414	0.905037	0.337602	0.704183
255	NM_021058	HIST1H2BJ	5.949	5.710	6.330	6.446	6.237	1.000000	0.000001	0.744162	0.779976	0.389990
256	NM_138327	TAAR1	5.009	5.081	5.282	5.490	5.498	0.000172	0.002470	0.224230	0.119996	0.998003
257	NM_001828	CLC	10.866	9.692	9.618	9.860	9.296	0.000000	1.000000	0.790640	0.575586	0.284504
258	NM_001199208	CYP4F3	9.187	10.093	9.402	9.895	9.361	0.001998	0.007361	0.085034	0.976056	0.056129
259	NM_024548	CEP97	6.566	6.717	6.887	7.228	6.933	0.000121	1.000000	0.035314	0.917808	0.079681
260	NM_138927	SON	8.449	7.921	8.330	7.930	8.146	0.000817	1.000000	0.003077	0.175728	0.168438
261	NM_002198	IRF1	10.490	10.067	10.764	10.511	10.387	1.000000	0.000000	0.154204	0.005202	0.633454
262	NM_182914	SYNE2	7.764	8.208	7.453	7.752	7.322	1.000000	0.000000	0.184100	0.642671	0.032921
263	NM_000902	MME	9.625	10.744	9.401	10.054	8.937	1.000000	0.000000	0.270540	0.411394	0.024808
264	NM_024552	LASS4	8.222	7.808	7.961	8.050	8.099	0.000006	0.005941	0.629532	0.232135	0.868727
265	NM_001925	DEFA4	7.421	7.383	8.289	9.454	8.658	0.001307	0.000125	0.042189	0.642870	0.220174
266	NM_024913	C7orf58	7.727	6.800	7.706	7.617	7.307	0.136406	0.003979	0.899378	0.062794	0.276354
267	ENST00000549649	DYNLL1	7.250	7.328	8.200	7.946	7.948	0.089409	0.021345	0.534724	0.441022	0.999958

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
268	gi|38532374	NA	5.269	5.274	4.828	4.979	4.814	0.188367	0.002418	0.307760	0.984538	0.242328
269	NM_000250	MPO	7.605	7.565	8.053	8.694	8.262	0.003309	0.000013	0.050366	0.644219	0.248933
270	NM_001874	CPM	5.874	6.569	5.926	5.965	6.153	0.263893	0.011698	0.965100	0.195596	0.424691
271	NM_173485	TSHZ2	7.382	6.972	6.846	7.429	6.929	0.004682	1.000000	0.000051	0.739871	0.000534
272	NR_038064	PLIN2	8.210	8.534	8.470	8.589	8.747	0.000009	1.000000	0.661459	0.056585	0.485502
273	NM_024556	FAM118B	7.287	7.256	7.846	7.892	7.670	0.002863	0.002878	0.963051	0.489433	0.425727
274	NM_001199873	B4GALT3	9.539	8.790	9.278	9.265	9.060	0.000004	0.006105	0.996920	0.309691	0.456795
275	NM_006989	RASA4	8.298	8.139	7.796	8.031	7.741	0.000237	0.794307	0.149393	0.868630	0.057952
276	NM_001257971	CTSL1	6.074	5.925	6.577	6.106	6.472	0.556174	0.000261	0.038526	0.798163	0.134791
277	NM_000270	NP	9.487	9.103	9.780	10.001	9.866	1.000000	0.000006	0.557046	0.887942	0.802758
278	NM_001130059	ATF7	5.212	5.212	5.253	5.605	5.372	1.000000	0.438013	0.000033	0.171523	0.007397
279	NM_003118	SPARC	9.083	9.207	9.737	9.964	9.620	0.000424	0.113905	0.627252	0.847118	0.345974
280	NM_153021	PLB1	6.867	7.077	7.318	7.615	7.539	0.001516	1.000000	0.250568	0.355397	0.913465
281	NM_001170330	C4orf3	7.478	7.240	7.324	7.402	7.760	1.000000	0.245460	0.750146	0.000037	0.004098
282	NM_002692	POLE2	7.205	6.613	7.184	6.047	6.359	0.156285	1.000000	0.000226	0.002251	0.494438
283	NM_001192	TNFRSF17	4.474	4.005	4.587	5.008	4.554	1.000000	0.000000	0.122703	0.982429	0.088234
284	NM_145032	FBXL13	6.474	6.987	6.791	7.387	6.914	0.000011	1.000000	0.027018	0.806772	0.098170
285	NM_019091	PLEKHA3	7.058	6.910	7.281	6.689	6.825	1.000000	1.000000	0.000001	0.000011	0.409707
286	NM_024956	TMEM62	7.599	7.189	7.875	7.664	7.625	1.000000	0.002245	0.254101	0.080350	0.953292
287	NM_052960	RBP7	7.270	7.808	7.218	7.267	7.088	1.000000	0.000005	0.953122	0.639431	0.530295
288	NM_024613	PLEKHF2	7.432	7.660	8.044	7.255	7.671	0.789194	1.000000	0.000012	0.023331	0.029137
289	NM_002923	RGS2	11.584	12.239	11.737	11.649	11.703	0.162049	0.000001	0.862749	0.969968	0.947024
290	NM_004691	ATP6V0D1	11.562	11.584	11.951	11.656	11.692	0.064067	1.000000	0.011327	0.010003	0.932084
291	NM_144563	RPIA	9.444	9.221	8.913	8.388	8.784	0.001733	0.264252	0.097918	0.824211	0.261542
292	NM_020397	CAMK1D	9.001	9.118	8.603	8.572	8.527	0.163494	0.002054	0.980872	0.858346	0.960862
293	NM_016232	IL1RL1	5.573	6.273	5.757	6.219	6.253	0.000028	1.000000	0.065034	0.016357	0.984841
294	NM_138460	CMTM5	7.473	7.266	7.853	7.851	7.716	1.000000	0.000000	0.999922	0.538365	0.635314

SEQ ID Number	Database ID	Gene Name	HC Mean	inSIRS Mean	Mild Mean	Severe Mean	Shock Mean	pval HC vs Other	pval inSIRS vs Sepsis	pval Severe vs Mild	pval Shock vs Mild	pval Shock vs Severe
295	NM_004847	AIF1	8.167	8.310	8.735	8.045	8.239	1.000000	1.000000	0.000120	0.001571	0.448676
296	NM_001928	CFD	10.389	9.779	9.631	9.496	9.702	0.000005	1.000000	0.830277	0.934225	0.650508
297	NM_144765	MPZL2	7.015	7.320	6.845	6.660	6.644	1.000000	0.000023	0.471520	0.309485	0.994504
298	gi|27884043	LOC100128751	8.552	8.877	8.333	8.552	8.283	1.000000	0.001039	0.155603	0.877005	0.063053
299	NM_144646	IGJ	8.646	7.900	8.962	10.005	9.230	1.000000	0.000100	0.078833	0.793766	0.239952
300	NM_139286	CDC26	7.968	7.634	8.113	7.886	8.065	1.000000	0.000005	0.095936	0.867921	0.226701
301	NM_006241	PPP1R2	7.446	7.738	7.546	7.286	7.113	1.000000	0.001735	0.115620	0.000618	0.379268
302	NM_000564	IL5RA	6.871	6.298	6.092	6.455	5.954	0.000000	1.000000	0.186587	0.721925	0.044203
303	NM_001113738	ARL17P1	8.846	8.829	8.802	8.293	7.810	1.000000	1.000000	0.160174	0.000219	0.191966
304	NR_033759	ATP5L	7.242	7.337	7.379	6.824	6.772	1.000000	0.748516	0.000612	0.000014	0.929559
305	NM_176885	TAS2R31	6.228	5.589	5.847	6.020	6.056	0.010741	0.032666	0.488873	0.253434	0.969967
306	NM_001024599	HIST2H2BF	8.854	9.615	9.386	9.211	8.840	0.014281	0.064555	0.679691	0.009289	0.184703
307	NM_001743	CALM2	8.475	9.041	9.003	8.357	8.540	1.000000	1.000000	0.000906	0.007024	0.542344
308	NM_019073	SPATA6	6.797	7.301	7.095	6.806	7.221	0.000572	1.000000	0.238268	0.690136	0.055163
309	ENST00000390285	IGLV6-57	5.779	5.379	6.029	6.575	6.026	1.000000	0.000002	0.138073	0.999915	0.135136
310	NM_020362	C1orf128	9.258	9.026	8.605	8.315	8.523	0.000049	0.377958	0.469588	0.921733	0.676477
311	NM_181623	KRTAP15-1	6.250	6.690	6.548	6.617	6.488	0.001154	1.000000	0.779960	0.773039	0.418346
312	NM_006417	IFI44	6.559	6.924	8.107	6.674	6.408	1.000000	1.000000	0.007884	0.000183	0.836520
313	NM_001178126	IGL@	7.052	6.606	7.027	7.343	7.023	1.000000	0.000000	0.162844	0.999656	0.156176
314	gi|21707823	NA	4.903	5.476	4.955	4.639	4.576	1.000000	0.188292	0.144998	0.026471	0.921677
315	NM_003001	SDHC	7.530	6.874	7.879	7.593	7.764	1.000000	0.000026	0.453417	0.841420	0.752519
316	NM_152995	NFXL1	7.326	6.876	7.694	7.644	7.620	1.000000	0.000002	0.977232	0.934372	0.994545
317	NM_000170	GLDC	5.599	5.395	5.679	5.770	5.666	1.000000	0.000010	0.537664	0.982363	0.443725
318	NM_001199743	DCTN5	8.646	8.336	8.737	8.794	8.672	1.000000	0.000532	0.865968	0.779044	0.519467
319	NM_014736	KIAA0101	4.443	3.951	4.537	4.749	4.419	1.000000	0.000000	0.416052	0.694594	0.124264

EXAMPLE 6

RATIOS OF IRS BIOMARKERSMARKERS BETWEEN HEALTHY, INSIRS, MILD SEPSIS, SEVERE SEPSIS AND SEPTIC SHOCK

[0293] Examples of the use of 2-gene ratios as a more informative predictor of clinical condition than either of the two component genes are presented in Tables 16, 17, 18, 19, 20 and 21. These tables show instances of the prediction of Healthy and inSIRS (Table 16), Healthy vs. ipSIRS (Table 17), inSIRS and ipSIRS (Table 18), Mild Sepsis vs.Vs Severe Sepsis (Table 19), Mild Sepsis Vs Septic Shock (Table 20), and Severe Sepsis vs.Vs Septic Shock (Table 21) using 2 genes and their ratios. Columns from left to right are: name of the first component gene (Gene 1 Name), the corresponding Area Under Curve for this gene (Gene 1 AUC), the second component gene (Gene 2 Name), the corresponding AUC for this gene (Gene 2 AUC), the AUC for this ratio (Ratio AUC), the statistical significance using Delong's method (DeLong ER, DeLong DM, Clarke-Pearson DL: Comparing the Areas under Two or More Correlated Receiver Operating Characteristic Curves: A Non parametric Approach. *Biometrics* 1988, **44:**837-845) that the ratio is a better predictor than Gene 1 (Ratio Signif to Gene 1), the statistical significance using Delong's method that the ratio is a better predictor than Gene2 (Ratio Signif to Gene 2). These tables show results for which the ratio AUC is shown to be superior to both of the component genes, and the improvement statistically significant over both genes. Examples of less significant ratios, or cases where the ratio is statistically superior to only one of the component genes are not listed in these tables. Such ratios can also be used in clinical trials in a similar fashion to that described in Example 5.

Table 16

Ratios Healthy Versus inSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
TLR5	0.874	HLA-DPB1	0.815	0.953	0.008	0.004
TLR5	0.874	PLAC8	0.828	0.979	0.003	0.004
TLR5	0.874	CDS2	0.73	0.933	0.003	0.003
TLR5	0.874	SLC39A9	0.776	0.946	0.003	0.002
TLR5	0.874	LGALS1	0.722	0.941	0.015	0
TLR5	0.874	DNAJC9_FAM149B1	0.944	0.994	0.003	0.037
TLR5	0.874	LGALS2	0.922	0.983	0.003	0.019
TLR5	0.874	HINT1	0.9	0.949	0.048	0.036
TLR5	0.874	HS2ST1_UBA2	0.668	0.938	0.006	0
TLR5	0.874	HLA-DPA1	0.796	0.948	0.005	0.003
TLR5	0.874	PTGER2	0.881	0.957	0.007	0.038
TLR5	0.874	TRAF3	0.87	0.966	0.011	0.015
TLR5	0.874	RPL17_SNORD58B	0.917	0.964	0.02	0.029
TLR5	0.874	JUP	0.753	0.938	0.02	0.007
TLR5	0.874	HSP90AB1_HSP90A	0.924	0.991	0.003	0.021
TLR5	0.874	ITGA4_CERKL	0.88	0.957	0.018	0.026
TLR5	0.874	EIF1AX_SCARNA9L	0.871	0.942	0.039	0.032
TLR5	0.874	CD300A	0.841	0.955	0.003	0.02
TLR5	0.874	P4HA1_RPL17	0.664	0.947	0.027	0
TLR5	0.874	MGST3	0.857	0.969	0.002	0.011
TLR5	0.874	KIAA0746	0.776	0.949	0.026	0.001
TLR5	0.874	HSPB1_HSPBL2	0.705	0.915	0.05	0.001
TLR5	0.874	CD151	0.718	0.938	0.047	0
TLR5	0.874	IGK@_IGKC_IGKV	0.855	0.946	0.01	0.02
TLR5	0.874	SON	0.856	0.942	0.02	0.045

TLR5	0.874	IRF1	0.82	0.961	0.003	0.008
TLR5	0.874	C7orf58	0.831	0.996	0.003	0
TLR5	0.874	NP	0.726	0.957	0.021	0
TLR5	0.874	AIF1	0.618	0.941	0.019	0
TLR5	0.874	CDC26	0.799	0.949	0.009	0.003
TLR5	0.874	TAS2R31	0.833	0.946	0.038	0.002
TLR5	0.874	NFXL1	0.728	0.945	0.017	0
TLR5	0.874	DCTN5	0.722	0.929	0.034	0
UBE2J1	0.888	FAIM3	0.93	0.981	0.007	0.023
UBE2J1	0.888	SH2D1B	0.894	0.953	0.034	0.02
UBE2J1	0.888	LRRN3	0.928	0.962	0.029	0.023
UBE2J1	0.888	HLA-DPB1	0.815	0.974	0.015	0
UBE2J1	0.888	PLAC8	0.828	0.997	0.002	0.001
UBE2J1	0.888	GOT2	0.966	0.99	0.004	0.044
UBE2J1	0.888	CDS2	0.73	0.958	0.005	0
UBE2J1	0.888	SLC39A9	0.776	0.981	0.002	0
UBE2J1	0.888	GIMAP7	0.804	0.967	0.034	0
UBE2J1	0.888	INSIG1	0.957	0.997	0.002	0.032
UBE2J1	0.888	LGALS1	0.722	0.946	0.046	0
UBE2J1	0.888	DNAJC9_FAM149B1	0.944	0.992	0.005	0.017
UBE2J1	0.888	LGALS2	0.922	0.979	0.004	0.015
UBE2J1	0.888	HS2ST1_UBA2	0.668	0.956	0.032	0
UBE2J1	0.888	HLA-DPA1	0.796	0.971	0.015	0
UBE2J1	0.888	PTGER2	0.881	0.978	0.007	0.002
UBE2J1	0.888	PMS2CL_PMS2	0.942	0.992	0.003	0.017
UBE2J1	0.888	NEK6_LOC1001290	0.671	0.948	0.047	0
UBE2J1	0.888	TRAF3	0.87	0.981	0.011	0.003
UBE2J1	0.888	IRF4	0.946	0.993	0.002	0.041
UBE2J1	0.888	AMFR	0.867	0.947	0.049	0.025

UBE2J1	0.888	HSP90AB1_HSP90A	0.924	0.996	0.003	0.009
UBE2J1	0.888	ITGA4_CERKL	0.88	0.987	0.005	0.002
UBE2J1	0.888	EIF1AX_SCARNA9L	0.871	0.971	0.023	0.001
UBE2J1	0.888	CD300A	0.841	0.964	0.002	0.005
UBE2J1	0.888	MGST3	0.857	0.98	0.007	0.001
UBE2J1	0.888	KIAA0746	0.776	0.964	0.05	0
UBE2J1	0.888	CCR4	0.871	0.971	0.018	0.004
UBE2J1	0.888	RRP12_LOC644215	0.904	0.976	0.006	0.015
UBE2J1	0.888	TIMM10	0.949	0.992	0.002	0.031
UBE2J1	0.888	FAM118A	0.882	0.976	0.009	0.01
UBE2J1	0.888	IGK@_IGKC_IGKV	0.855	0.962	0.039	0.002
UBE2J1	0.888	SON	0.856	0.967	0.023	0.006
UBE2J1	0.888	IRF1	0.82	0.965	0.004	0.002
UBE2J1	0.888	C7orf58	0.831	0.988	0.007	0
UBE2J1	0.888	B4GALT3	0.917	0.975	0.006	0.041
UBE2J1	0.888	CDC26	0.799	0.956	0.029	0
UBE2J1	0.888	DCTN5	0.722	0.955	0.042	0
RNASE2_LOC64333	0.855	HLA-DPB1	0.815	0.955	0.009	0.004
RNASE2_LOC64333	0.855	PLAC8	0.828	0.969	0.003	0.009
RNASE2_LOC64333	0.855	ITK	0.874	0.94	0.034	0.047
RNASE2_LOC64333	0.855	CDS2	0.73	0.912	0.01	0.008
RNASE2_LOC64333	0.855	CCR3	0.869	0.95	0.008	0.047
RNASE2_LOC64333	0.855	SLC39A9	0.776	0.944	0.003	0.003
RNASE2_LOC64333	0.855	GIMAP7	0.804	0.951	0.009	0.003
RNASE2_LOC64333	0.855	LGALS1	0.722	0.952	0.003	0.001
RNASE2_LOC64333	0.855	HLA-DRA	0.855	0.97	0.005	0.012
RNASE2_LOC64333	0.855	SIAE	0.737	0.921	0.018	0.01
RNASE2_LOC64333	0.855	HIST1H3J	0.898	0.949	0.007	0.021
RNASE2_LOC64333	0.855	MTRR	0.674	0.946	0.018	0

RNASE2_LOC64333	0.855	HIST1H3A	0.908	0.961	0.009	0.015
RNASE2_LOC64333	0.855	HLA-DPA1	0.796	0.951	0.005	0.004
RNASE2_LOC64333	0.855	SLC39A8	0.825	0.954	0.007	0.021
RNASE2_LOC64333	0.855	PTGER2	0.881	0.954	0.005	0.035
RNASE2_LOC64333	0.855	NEK6_LOC1001290	0.671	0.921	0.02	0.001
RNASE2_LOC64333	0.855	TRAF3	0.87	0.97	0.003	0.033
RNASE2_LOC64333	0.855	JUP	0.753	0.931	0.025	0.011
RNASE2_LOC64333	0.855	GALNT2	0.528	0.898	0.017	0
RNASE2_LOC64333	0.855	HSP90AB1_HSP90A	0.924	0.988	0.002	0.036
RNASE2_LOC64333	0.855	GLT25D1	0.77	0.956	0.005	0.004
RNASE2_LOC64333	0.855	ITGA4_CERKL	0.88	0.958	0.007	0.03
RNASE2_LOC64333	0.855	EIF1AX_SCARNA9L	0.871	0.958	0.009	0.011
RNASE2_LOC64333	0.855	ZNF28	0.837	0.921	0.023	0.026
RNASE2_LOC64333	0.855	ICAM1	0.675	0.931	0.013	0
RNASE2_LOC64333	0.855	P4HA1_RPL17	0.664	0.935	0.034	0
RNASE2_LOC64333	0.855	KLHL5	0.657	0.924	0.034	0
RNASE2_LOC64333	0.855	MGST3	0.857	0.97	0.002	0.01
RNASE2_LOC64333	0.855	KIAA0746	0.776	0.945	0.018	0.001
RNASE2_LOC64333	0.855	HSPB1_HSPBL2	0.705	0.913	0.009	0.004
RNASE2_LOC64333	0.855	CCR4	0.871	0.947	0.012	0.047
RNASE2_LOC64333	0.855	HIST1H3B	0.89	0.948	0.013	0.045
RNASE2_LOC64333	0.855	FSD1L_GARNL1	0.779	0.929	0.013	0.008
RNASE2_LOC64333	0.855	CD151	0.718	0.923	0.039	0
RNASE2_LOC64333	0.855	HIST1H3H	0.861	0.919	0.05	0.021
RNASE2_LOC64333	0.855	IGK@_IGKC_IGKV	0.855	0.948	0.013	0.015
RNASE2_LOC64333	0.855	IRF1	0.82	0.926	0.012	0.03
RNASE2_LOC64333	0.855	C7orf58	0.831	0.978	0.006	0.001
RNASE2_LOC64333	0.855	CTSL1_CTSLL3	0.676	0.912	0.042	0
RNASE2_LOC64333	0.855	NP	0.726	0.941	0.017	0

RNASE2_LOC64333	0.855	TMEM62_SPCS2_L	0.78	0.937	0.036	0.002
RNASE2_LOC64333	0.855	TAS2R31	0.833	0.945	0.026	0.002
RNASE2_LOC64333	0.855	DCTN5	0.722	0.925	0.021	0
C3AR1	0.868	GPR56	0.943	0.98	0.009	0.032
C3AR1	0.868	CAMK4	0.921	0.97	0.038	0.034
C3AR1	0.868	SH2D1B	0.894	0.974	0.014	0.003
C3AR1	0.868	HLA-DPB1	0.815	0.935	0.025	0.023
C3AR1	0.868	VAMP2	0.783	0.929	0.029	0.01
C3AR1	0.868	PLAC8	0.828	0.969	0.004	0.018
C3AR1	0.868	ITK	0.874	0.961	0.049	0.008
C3AR1	0.868	SLC39A9	0.776	0.953	0.008	0.004
C3AR1	0.868	GIMAP7	0.804	0.957	0.013	0.002
C3AR1	0.868	LGALS1	0.722	0.928	0.019	0.004
C3AR1	0.868	DNAJC9_FAM149B1	0.944	0.997	0.006	0.026
C3AR1	0.868	SIAE	0.737	0.927	0.042	0.007
C3AR1	0.868	HINT1	0.9	0.965	0.038	0.01
C3AR1	0.868	HLA-DPA1	0.796	0.931	0.025	0.014
C3AR1	0.868	PTGER2	0.881	0.962	0.006	0.044
C3AR1	0.868	PMS2CL_PMS2	0.942	0.992	0.005	0.036
C3AR1	0.868	RPL17_SNORD58B	0.917	0.965	0.033	0.015
C3AR1	0.868	GALNT2	0.528	0.91	0.024	0
C3AR1	0.868	GLT25D1	0.77	0.937	0.01	0.021
C3AR1	0.868	ITGA4_CERKL	0.88	0.967	0.014	0.021
C3AR1	0.868	EIF1AX_SCARNA9L	0.871	0.956	0.035	0.008
C3AR1	0.868	P4HA1_RPL17	0.664	0.942	0.044	0
C3AR1	0.868	KIAA0746	0.776	0.948	0.038	0.001
C3AR1	0.868	FSD1L_GARNL1	0.779	0.928	0.024	0.013
C3AR1	0.868	IGK@_IGKC_IGKV	0.855	0.951	0.035	0.025
C3AR1	0.868	SON	0.856	0.961	0.025	0.012

C3AR1	0.868	C7orf58	0.831	0.958	0.019	0.003
C3AR1	0.868	NP	0.726	0.942	0.016	0.001
C3AR1	0.868	CDC26	0.799	0.934	0.018	0.02
C3AR1	0.868	TAS2R31	0.833	0.947	0.046	0.003
C3AR1	0.868	DCTN5	0.722	0.94	0.017	0.001
GPR56	0.943	TGFBR1	0.734	0.984	0.007	0
GPR56	0.943	DNAJC13	0.819	0.985	0.03	0
GPR56	0.943	ANKRD34B	0.904	0.987	0.037	0.002
GPR56	0.943	SGMS2	0.938	0.996	0.013	0.013
GPR56	0.943	B3GNT5_MCF2L2	0.949	0.987	0.018	0.026
GPR56	0.943	SMPDL3A	0.797	0.981	0.027	0
GPR56	0.943	LOC284757	0.939	0.996	0.013	0.048
GPR56	0.943	PPP2R5A_SNORA16	0.953	0.997	0.009	0.029
GPR56	0.943	FRMD3	0.755	0.98	0.011	0
GPR56	0.943	EIF2AK2	0.964	0.999	0.011	0.034
GPR56	0.943	NA	0.868	0.977	0.043	0.002
GPR56	0.943	HIST1H2AA	0.903	0.978	0.028	0.012
GPR56	0.943	CDA	0.945	0.978	0.03	0.045
GPR56	0.943	SAP30	0.911	0.983	0.029	0.021
GPR56	0.943	ACPL2	0.906	0.99	0.018	0.011
GPR56	0.943	HAL	0.942	0.99	0.018	0.018
GPR56	0.943	KIAA1257_ACAD9/	0.851	0.981	0.031	0.001
GPR56	0.943	CCDC125	0.917	0.995	0.011	0.009
GPR56	0.943	PDK4	0.863	0.987	0.041	0.001
GPR56	0.943	ZRANB1	0.897	0.99	0.023	0.002
GPR56	0.943	MPZL3	0.892	0.975	0.017	0.007
GPR56	0.943	CYP4F3_CYP4F2	0.901	0.995	0.024	0.007
GPR56	0.943	SYNE2	0.748	0.997	0.013	0
GPR56	0.943	MME	0.894	0.986	0.043	0.007

GPR56	0.943	RBP7	0.848	0.974	0.035	0.002
GPR56	0.943	RGS2	0.915	0.979	0.01	0.02
FCGR1A_FCGR1B_	0.87	HLA-DPB1	0.815	0.952	0.002	0.008
FCGR1A_FCGR1B_	0.87	VAMP2	0.783	0.895	0.029	0.038
FCGR1A_FCGR1B_	0.87	CASS4	0.738	0.91	0.024	0.003
FCGR1A_FCGR1B_	0.87	PLAC8	0.828	0.971	0.002	0.009
FCGR1A_FCGR1B_	0.87	ITK	0.874	0.949	0.013	0.041
FCGR1A_FCGR1B_	0.87	CDS2	0.73	0.916	0.004	0.008
FCGR1A_FCGR1B_	0.87	SLC39A9	0.776	0.932	0.002	0.007
FCGR1A_FCGR1B_	0.87	GIMAP7	0.804	0.956	0.004	0.002
FCGR1A_FCGR1B_	0.87	LGALS1	0.722	0.933	0.009	0.001
FCGR1A_FCGR1B_	0.87	FFAR2	0.637	0.934	0.014	0
FCGR1A_FCGR1B_	0.87	LGALS2	0.922	0.986	0.002	0.017
FCGR1A_FCGR1B_	0.87	MTRR	0.674	0.947	0.006	0
FCGR1A_FCGR1B_	0.87	HS2ST1_UBA2	0.668	0.922	0.015	0
FCGR1A_FCGR1B_	0.87	HLA-DPA1	0.796	0.932	0.002	0.018
FCGR1A_FCGR1B_	0.87	SLC39A8	0.825	0.95	0.001	0.041
FCGR1A_FCGR1B_	0.87	NEK6_LOC1001290	0.671	0.907	0.035	0.001
FCGR1A_FCGR1B_	0.87	JUP	0.753	0.936	0.012	0.011
FCGR1A_FCGR1B_	0.87	GALNT2	0.528	0.897	0.026	0
FCGR1A_FCGR1B_	0.87	GLT25D1	0.77	0.933	0.024	0.004
FCGR1A_FCGR1B_	0.87	HDHD1A	0.602	0.914	0.028	0
FCGR1A_FCGR1B_	0.87	EIF1AX_SCARNA9L	0.871	0.965	0.003	0.017
FCGR1A_FCGR1B_	0.87	SFRS9	0.558	0.901	0.039	0
FCGR1A_FCGR1B_	0.87	ZNF28	0.837	0.922	0.029	0.048
FCGR1A_FCGR1B_	0.87	ICAM1	0.675	0.96	0.002	0
FCGR1A_FCGR1B_	0.87	P4HA1_RPL17	0.664	0.942	0.006	0
FCGR1A_FCGR1B_	0.87	KLHL5	0.657	0.933	0.022	0
FCGR1A_FCGR1B_	0.87	MGST3	0.857	0.97	0.002	0.009

FCGR1A_FCGR1B_	0.87	KIAA0746	0.776	0.952	0.012	0.001
FCGR1A_FCGR1B_	0.87	HSPB1_HSPBL2	0.705	0.91	0.018	0.003
FCGR1A_FCGR1B_	0.87	CCR4	0.871	0.964	0.002	0.036
FCGR1A_FCGR1B_	0.87	IL1B	0.576	0.977	0.012	0
FCGR1A_FCGR1B_	0.87	FSD1L_GARNL1	0.779	0.908	0.044	0.01
FCGR1A_FCGR1B_	0.87	NA	0.7	0.95	0.02	0
FCGR1A_FCGR1B_	0.87	IGK@_IGKC_IGKV	0.855	0.941	0.01	0.028
FCGR1A_FCGR1B_	0.87	IRF1	0.82	0.95	0.001	0.021
FCGR1A_FCGR1B_	0.87	C7orf58	0.831	0.983	0.003	0.001
FCGR1A_FCGR1B_	0.87	NP	0.726	0.932	0.033	0.001
FCGR1A_FCGR1B_	0.87	PLEKHA3	0.645	0.919	0.025	0
FCGR1A_FCGR1B_	0.87	CDC26	0.799	0.919	0.02	0.024
FCGR1A_FCGR1B_	0.87	TAS2R31	0.833	0.961	0.003	0.003
FCGR1A_FCGR1B_	0.87	IGLV6-57	0.761	0.914	0.044	0.002
FCGR1A_FCGR1B_	0.87	NFXL1	0.728	0.929	0.019	0
FCGR1A_FCGR1B_	0.87	DCTN5	0.722	0.932	0.005	0.001
C11orf82	0.58	C7orf58	0.831	0.911	0	0.023
FAR2	0.843	PTGDR	0.896	0.953	0.014	0.035
FAR2	0.843	SH2D1B	0.894	0.961	0.007	0.006
FAR2	0.843	VAMP2	0.783	0.936	0.005	0.006
FAR2	0.843	SLC39A9	0.776	0.921	0.013	0.004
FAR2	0.843	NEK6_LOC1001290	0.671	0.893	0.046	0.001
FAR2	0.843	GLT25D1	0.77	0.912	0.016	0.027
FAR2	0.843	ITGA4_CERKL	0.88	0.955	0.011	0.013
FAR2	0.843	EIF1AX_SCARNA9L	0.871	0.939	0.028	0.01
FAR2	0.843	CD300A	0.841	0.946	0.001	0.02
FAR2	0.843	ZNF28	0.837	0.934	0.021	0.006
FAR2	0.843	ABCG1	0.85	0.952	0.001	0.037
FAR2	0.843	HIST1H3B	0.89	0.946	0.016	0.037

FAR2	0.843	FSD1L_GARNL1	0.779	0.921	0.006	0.007
FAR2	0.843	APOLD1	0.871	0.956	0.003	0.021
FAR2	0.843	IGK@_IGKC_IGKV	0.855	0.926	0.031	0.024
FAR2	0.843	SON	0.856	0.948	0.009	0.024
FAR2	0.843	IRF1	0.82	0.921	0.006	0.044
FAR2	0.843	TNFRSF17	0.875	0.935	0.021	0.048
FAR2	0.843	CDC26	0.799	0.935	0.003	0.008
GNLY	0.914	GALNT3	0.837	0.97	0.036	0.001
GNLY	0.914	STOM	0.825	0.952	0.02	0.003
GNLY	0.914	TGFBR1	0.734	0.958	0.01	0
GNLY	0.914	DNAJC13	0.819	0.961	0.03	0.001
GNLY	0.914	ANKRD34B	0.904	0.964	0.019	0.035
GNLY	0.914	SGMS2	0.938	0.989	0.006	0.028
GNLY	0.914	C9orf72	0.796	0.959	0.028	0.001
GNLY	0.914	SMPDL3A	0.797	0.977	0.007	0.001
GNLY	0.914	PPP2R5A_SNORA16	0.953	0.993	0.005	0.044
GNLY	0.914	FRMD3	0.755	0.955	0.018	0
GNLY	0.914	NA	0.927	0.99	0.01	0.012
GNLY	0.914	EIF2AK2	0.964	0.997	0.005	0.048
GNLY	0.914	NA	0.868	0.967	0.027	0.003
GNLY	0.914	ACPL2	0.906	0.978	0.014	0.029
GNLY	0.914	OCR1	0.896	0.977	0.046	0.009
GNLY	0.914	CCDC125	0.917	0.988	0.004	0.017
GNLY	0.914	ZRANB1	0.897	0.989	0.008	0.004
GNLY	0.914	CYP4F3_CYP4F2	0.901	0.981	0.045	0.007
GNLY	0.914	SYNE2	0.748	0.973	0.019	0
GNLY	0.914	RBP7	0.848	0.976	0.013	0.002
GALNT3	0.837	FAIM3	0.93	0.983	0	0.032
GALNT3	0.837	PTGDR	0.896	0.964	0.002	0.024

GALNT3	0.837	CAMK4	0.921	0.98	0.001	0.033
GALNT3	0.837	SH2D1B	0.894	0.976	0.001	0.003
GALNT3	0.837	TLR10	0.521	0.942	0.031	0
GALNT3	0.837	CRIP1	0.943	0.957	0.004	0.05
GALNT3	0.837	LRRN3	0.928	0.974	0.001	0.017
GALNT3	0.837	HLA-DPB1	0.815	0.934	0.005	0.007
GALNT3	0.837	CASS4	0.738	0.92	0.008	0.001
GALNT3	0.837	KPNA5	0.895	0.98	0.001	0.005
GALNT3	0.837	PLAC8	0.828	0.985	0.001	0.001
GALNT3	0.837	KLRK1_KLRC4	0.865	0.948	0.018	0.006
GALNT3	0.837	ITK	0.874	0.969	0.003	0.006
GALNT3	0.837	FGFBP2	0.814	0.937	0.015	0.001
GALNT3	0.837	CDS2	0.73	0.925	0	0.004
GALNT3	0.837	CCR3	0.869	0.937	0.014	0.003
GALNT3	0.837	CHI3L1	0.722	0.911	0.03	0.001
GALNT3	0.837	SLC39A9	0.776	0.958	0	0
GALNT3	0.837	GIMAP7	0.804	0.982	0	0
GALNT3	0.837	LGALS1	0.722	0.901	0.009	0.003
GALNT3	0.837	DNAJC9_FAM149B1	0.944	0.989	0	0.024
GALNT3	0.837	LGALS2	0.922	0.972	0	0.046
GALNT3	0.837	SIAE	0.737	0.927	0.002	0.003
GALNT3	0.837	HINT1	0.9	0.965	0.002	0.017
GALNT3	0.837	MTRR	0.674	0.954	0.003	0
GALNT3	0.837	AIG1	0.56	0.921	0.023	0
GALNT3	0.837	HS2ST1_UBA2	0.668	0.973	0	0
GALNT3	0.837	HLA-DPA1	0.796	0.939	0.003	0.002
GALNT3	0.837	PTGER2	0.881	0.969	0	0.016
GALNT3	0.837	PMS2CL_PMS2	0.942	0.994	0	0.028
GALNT3	0.837	NEK6_LOC1001290	0.671	0.899	0.039	0

GALNT3	0.837	CENPK	0.834	0.942	0.023	0.001
GALNT3	0.837	TRAF3	0.87	0.971	0.002	0.004
GALNT3	0.837	RPL17_SNORD58B	0.917	0.978	0.001	0.01
GALNT3	0.837	HSP90AB1_HSP90A	0.924	0.988	0	0.009
GALNT3	0.837	GLT25D1	0.77	0.905	0.02	0.009
GALNT3	0.837	ITGA4_CERKL	0.88	0.993	0	0.004
GALNT3	0.837	EIF1AX_SCARNA9L	0.871	0.976	0.001	0.002
GALNT3	0.837	CD300A	0.841	0.946	0	0.03
GALNT3	0.837	ZNF28	0.837	0.946	0.003	0.005
GALNT3	0.837	P4HA1_RPL17	0.664	0.956	0.006	0
GALNT3	0.837	KLHL5	0.657	0.971	0.001	0
GALNT3	0.837	MGST3	0.857	0.964	0.001	0.002
GALNT3	0.837	KIAA0746	0.776	0.949	0.012	0
GALNT3	0.837	CCR4	0.871	0.99	0	0.002
GALNT3	0.837	FSD1L_GARNL1	0.779	0.916	0.009	0.003
GALNT3	0.837	FAM118A	0.882	0.965	0	0.042
GALNT3	0.837	CD151	0.718	0.901	0.048	0.001
GALNT3	0.837	HIST1H3H	0.861	0.914	0.047	0.029
GALNT3	0.837	PYHIN1	0.686	0.926	0.044	0
GALNT3	0.837	IGK@_IGKC_IGKV	0.855	0.964	0.002	0.002
GALNT3	0.837	IRF1	0.82	0.953	0	0.01
GALNT3	0.837	C7orf58	0.831	0.987	0.001	0
GALNT3	0.837	B4GALT3	0.917	0.99	0	0.035
GALNT3	0.837	NP	0.726	0.976	0	0
GALNT3	0.837	C4orf3	0.723	0.891	0.032	0.002
GALNT3	0.837	TNFRSF17	0.875	0.944	0.005	0.024
GALNT3	0.837	CDC26	0.799	0.938	0.001	0.005
GALNT3	0.837	TAS2R31	0.833	0.96	0.003	0.001
GALNT3	0.837	NFXL1	0.728	0.942	0.014	0

GALNT3	0.837	DCTN5	0.722	0.925	0.014	0
OMG	0.851	SH2D1B	0.894	0.951	0.005	0.03
OMG	0.851	LRRN3	0.928	0.955	0.015	0.047
OMG	0.851	CDS2	0.73	0.895	0.044	0.004
OMG	0.851	HIST1H4L	0.961	0.996	0	0.042
OMG	0.851	LGALS1	0.722	0.91	0.013	0.001
OMG	0.851	LGALS2	0.922	0.972	0.001	0.036
OMG	0.851	HIST1H3J	0.898	0.961	0.005	0.006
OMG	0.851	HS2ST1_UBA2	0.668	0.897	0.047	0.001
OMG	0.851	HIST1H3A	0.908	0.971	0.006	0.004
OMG	0.851	RPL17_SNORD58B	0.917	0.971	0.002	0.035
OMG	0.851	GLT25D1	0.77	0.913	0.032	0.014
OMG	0.851	ITGA4_CERKL	0.88	0.946	0.005	0.031
OMG	0.851	EIF1AX_SCARNA9L	0.871	0.94	0.022	0.017
OMG	0.851	ZNF28	0.837	0.957	0.005	0.002
OMG	0.851	MGST3	0.857	0.921	0.011	0.039
OMG	0.851	HIST1H3B	0.89	0.969	0.004	0.01
OMG	0.851	FSD1L_GARNL1	0.779	0.924	0.018	0.004
OMG	0.851	HIST1H3H	0.861	0.958	0.014	0.001
OMG	0.851	APOLD1	0.871	0.964	0.001	0.016
OMG	0.851	IRF1	0.82	0.909	0.026	0.047
OMG	0.851	CDC26	0.799	0.947	0.003	0.003
STOM	0.825	CAMK4	0.921	0.94	0.014	0.046
STOM	0.825	SH2D1B	0.894	0.938	0.016	0.004
STOM	0.825	KPNA5	0.895	0.929	0.028	0.013
STOM	0.825	PLAC8	0.828	0.912	0.048	0.014
STOM	0.825	HIST1H4E	0.915	0.975	0	0.04
STOM	0.825	CCR3	0.869	0.906	0.037	0.017
STOM	0.825	HIST1H4L	0.961	0.992	0	0.018

STOM	0.825	HINT1	0.9	0.934	0.015	0.043
STOM	0.825	HIST1H3J	0.898	0.962	0.004	0.002
STOM	0.825	HIST1H3A	0.908	0.962	0.003	0.004
STOM	0.825	PTGER2	0.881	0.939	0.002	0.032
STOM	0.825	AMFR	0.867	0.966	0	0.013
STOM	0.825	RPL17_SNORD58B	0.917	0.957	0.007	0.03
STOM	0.825	EIF1AX_SCARNA9L	0.871	0.92	0.03	0.011
STOM	0.825	CD300A	0.841	0.909	0.009	0.039
STOM	0.825	ZNF28	0.837	0.923	0.026	0.005
STOM	0.825	MGST3	0.857	0.939	0.003	0.012
STOM	0.825	TYMS	0.863	0.961	0.001	0.005
STOM	0.825	HIST1H2BM	0.891	0.969	0.001	0.01
STOM	0.825	HIST1H3B	0.89	0.96	0.003	0.004
STOM	0.825	FAM118A	0.882	0.963	0.002	0.008
STOM	0.825	HIST1H3H	0.861	0.944	0.017	0
STOM	0.825	APOLD1	0.871	0.949	0.001	0.015
STOM	0.825	IGK@_IGKC_IGKV	0.855	0.912	0.044	0.008
STOM	0.825	SON	0.856	0.921	0.045	0.011
STOM	0.825	IRF1	0.82	0.911	0.016	0.025
STOM	0.825	B4GALT3	0.917	0.986	0	0.021
STOM	0.825	TNFRSF17	0.875	0.918	0.03	0.032
STOM	0.825	CDC26	0.799	0.919	0.004	0.007
TDRD9	0.758	PLAC8	0.828	0.937	0.001	0.046
TDRD9	0.758	GIMAP7	0.804	0.891	0.015	0.05
TDRD9	0.758	LGALS1	0.722	0.898	0.003	0.018
TDRD9	0.758	HS2ST1_UBA2	0.668	0.836	0.022	0.03
TDRD9	0.758	NEK6_LOC1001290	0.671	0.821	0.041	0.049
TDRD9	0.758	GLT25D1	0.77	0.932	0.002	0.002
TDRD9	0.758	P4HA1_RPL17	0.664	0.845	0.045	0.003

TDRD9	0.758	C15orf54	0.72	0.859	0.037	0.002
TDRD9	0.758	KIAA0746	0.776	0.9	0.006	0.014
TDRD9	0.758	LAIR1_LAIR2	0.607	0.87	0.018	0
TDRD9	0.758	E2F6	0.787	0.882	0.039	0.003
TDRD9	0.758	CD151	0.718	0.9	0.014	0.001
TDRD9	0.758	FSD1L	0.674	0.847	0.04	0.003
TDRD9	0.758	C7orf58	0.831	0.957	0.002	0.002
TDRD9	0.758	CTSL1_CTSLL3	0.676	0.863	0.04	0.007
TDRD9	0.758	NP	0.726	0.863	0.048	0.03
TDRD9	0.758	IGLV6-57	0.761	0.864	0.016	0.033
KREMEN1	0.848	PLAC8	0.828	0.947	0.004	0.029
KREMEN1	0.848	CDS2	0.73	0.902	0.006	0.012
KREMEN1	0.848	SLC39A9	0.776	0.894	0.021	0.017
KREMEN1	0.848	LGALS2	0.922	0.987	0.002	0.012
KREMEN1	0.848	HIST1H3J	0.898	0.939	0.028	0.04
KREMEN1	0.848	CD300A	0.841	0.939	0.002	0.04
KREMEN1	0.848	MGST3	0.857	0.945	0.008	0.027
KREMEN1	0.848	IGK@_IGKC_IGKV	0.855	0.928	0.035	0.01
KREMEN1	0.848	IRF1	0.82	0.951	0.003	0.007
KREMEN1	0.848	C7orf58	0.831	0.96	0.014	0.001
KREMEN1	0.848	TNFRSF17	0.875	0.947	0.009	0.014
KREMEN1	0.848	CDC26	0.799	0.913	0.004	0.033
FAIM3	0.93	DNAJC13	0.819	0.989	0.04	0
FAIM3	0.93	GSR	0.799	0.973	0.045	0
FAIM3	0.93	SGMS2	0.938	0.99	0.036	0.012
FAIM3	0.93	METTL7B	0.898	0.954	0.05	0.023
FAIM3	0.93	C9orf72	0.796	0.976	0.038	0
FAIM3	0.93	SMPDL3A	0.797	0.992	0.019	0
FAIM3	0.93	NA	0.927	0.997	0.03	0.013

FAIM3	0.93	EIF2AK2	0.964	0.998	0.027	0.038
FAIM3	0.93	NA	0.868	0.992	0.02	0.001
FAIM3	0.93	CCDC125	0.917	1	0.025	0.006
FAIM3	0.93	MPZL3	0.892	0.966	0.017	0.018
FAIM3	0.93	SYNE2	0.748	0.994	0.038	0
FAIM3	0.93	RBP7	0.848	0.969	0.045	0.003
FAIM3	0.93	RGS2	0.915	0.975	0.02	0.03
FAIM3	0.93	PPP1R2_PPP1R2P3	0.702	0.993	0.041	0
ACER3	0.746	HLA-DPB1	0.815	0.934	0	0.009
ACER3	0.746	PLAC8	0.828	0.968	0	0.007
ACER3	0.746	SLC39A9	0.776	0.918	0	0.003
ACER3	0.746	GIMAP7	0.804	0.921	0.002	0.005
ACER3	0.746	LGALS1	0.722	0.923	0	0.002
ACER3	0.746	HLA-DRA	0.855	0.942	0.002	0.008
ACER3	0.746	SIAE	0.737	0.888	0.003	0.027
ACER3	0.746	AGTRAP	0.611	0.809	0.024	0.005
ACER3	0.746	MTRR	0.674	0.91	0.005	0
ACER3	0.746	AIG1	0.56	0.856	0.016	0
ACER3	0.746	HS2ST1_UBA2	0.668	0.838	0.016	0.018
ACER3	0.746	HIST1H3A	0.908	0.946	0	0.032
ACER3	0.746	HLA-DPA1	0.796	0.93	0	0.009
ACER3	0.746	SLC39A8	0.825	0.934	0.001	0.018
ACER3	0.746	PTGER2	0.881	0.959	0	0.015
ACER3	0.746	NEK6_LOC1001290	0.671	0.858	0.007	0.01
ACER3	0.746	TRAF3	0.87	0.953	0	0.048
ACER3	0.746	RPL17_SNORD58B	0.917	0.955	0	0.045
ACER3	0.746	JUP	0.753	0.888	0.009	0.035
ACER3	0.746	GALNT2	0.528	0.817	0.025	0.001
ACER3	0.746	HSP90AB1_HSP90A	0.924	0.984	0	0.029

ACER3	0.746	GLT25D1	0.77	0.952	0	0.003
ACER3	0.746	HDHD1A	0.602	0.855	0.024	0
ACER3	0.746	ITGA4_CERKL	0.88	0.956	0	0.022
ACER3	0.746	EIF1AX_SCARNA9L	0.871	0.944	0.001	0.015
ACER3	0.746	ICAM1	0.675	0.865	0.011	0.004
ACER3	0.746	P4HA1_RPL17	0.664	0.919	0.005	0
ACER3	0.746	C15orf54	0.72	0.844	0.041	0.002
ACER3	0.746	KLHL5	0.657	0.865	0.022	0.001
ACER3	0.746	MGST3	0.857	0.97	0	0.005
ACER3	0.746	KIAA0746	0.776	0.923	0.002	0.002
ACER3	0.746	HSPB1_HSPBL2	0.705	0.866	0.002	0.017
ACER3	0.746	FSD1L_GARNL1	0.779	0.902	0.001	0.015
ACER3	0.746	NA	0.7	0.886	0.042	0
ACER3	0.746	E2F6	0.787	0.863	0.05	0.002
ACER3	0.746	CD151	0.718	0.878	0.012	0.002
ACER3	0.746	SON	0.856	0.946	0	0.027
ACER3	0.746	C7orf58	0.831	0.97	0	0.001
ACER3	0.746	NP	0.726	0.915	0.003	0.001
ACER3	0.746	C4orf3	0.723	0.842	0.024	0.039
ACER3	0.746	TMEM62_SPCS2_L	0.78	0.903	0.024	0.001
ACER3	0.746	TAS2R31	0.833	0.925	0.002	0.002
ACER3	0.746	IGLV6-57	0.761	0.846	0.019	0.048
ACER3	0.746	SDHC	0.736	0.877	0.045	0
ACER3	0.746	NFXL1	0.728	0.865	0.021	0.002
ACER3	0.746	DCTN5	0.722	0.893	0.005	0.001
ACER3	0.746	KIAA0101_CSNK1G	0.736	0.851	0.027	0.002
TGFBR1	0.734	PTGDR	0.896	0.956	0.001	0.005
TGFBR1	0.734	SH2D1B	0.894	0.952	0	0.001
TGFBR1	0.734	LRRN3	0.928	0.95	0	0.043

TGFBR1	0.734	HLA-DPB1	0.815	0.888	0.005	0.024
TGFBR1	0.734	VAMP2	0.783	0.891	0.002	0.013
TGFBR1	0.734	CASS4	0.738	0.861	0.022	0.001
TGFBR1	0.734	KPNA5	0.895	0.935	0.002	0.016
TGFBR1	0.734	PLAC8	0.828	0.928	0.002	0.002
TGFBR1	0.734	KLRK1_KLRC4	0.865	0.908	0.015	0.023
TGFBR1	0.734	ITK	0.874	0.925	0.002	0.006
TGFBR1	0.734	FGFBP2	0.814	0.878	0.034	0.001
TGFBR1	0.734	CDS2	0.73	0.902	0.001	0.001
TGFBR1	0.734	SLC39A9	0.776	0.949	0	0
TGFBR1	0.734	GIMAP7	0.804	0.91	0.004	0
TGFBR1	0.734	ANAPC11	0.943	0.974	0	0.037
TGFBR1	0.734	INSIG1	0.957	0.992	0	0.048
TGFBR1	0.734	HIST1H4L	0.961	0.98	0	0.042
TGFBR1	0.734	LGALS1	0.722	0.848	0.022	0.008
TGFBR1	0.734	DNAJC9_FAM149B1	0.944	0.985	0	0.013
TGFBR1	0.734	SIAE	0.737	0.868	0.033	0.008
TGFBR1	0.734	HINT1	0.9	0.935	0.001	0.019
TGFBR1	0.734	HLA-DPA1	0.796	0.886	0.003	0.021
TGFBR1	0.734	VOPP1_LOC100128	0.938	0.985	0	0.029
TGFBR1	0.734	SLC39A8	0.825	0.899	0.014	0.008
TGFBR1	0.734	PTGER2	0.881	0.97	0	0.005
TGFBR1	0.734	PMS2CL_PMS2	0.942	0.984	0	0.02
TGFBR1	0.734	NEK6_LOC1001290	0.671	0.868	0.005	0.001
TGFBR1	0.734	CENPK	0.834	0.879	0.035	0.009
TGFBR1	0.734	TRAF3	0.87	0.922	0.002	0.035
TGFBR1	0.734	AMFR	0.867	0.959	0	0.011
TGFBR1	0.734	RPL17_SNORD58B	0.917	0.953	0	0.008
TGFBR1	0.734	HSP90AB1_HSP90A	0.924	0.971	0	0.011

TGFBR1	0.734	GLT25D1	0.77	0.873	0.006	0.026
TGFBR1	0.734	ITGA4_CERKL	0.88	0.966	0	0.003
TGFBR1	0.734	EIF1AX_SCARNA9L	0.871	0.937	0.001	0.002
TGFBR1	0.734	CD300A	0.841	0.935	0	0.013
TGFBR1	0.734	ZNF28	0.837	0.918	0.002	0.002
TGFBR1	0.734	MGST3	0.857	0.94	0	0.007
TGFBR1	0.734	CCR4	0.871	0.914	0.006	0.007
TGFBR1	0.734	FSD1L_GARNL1	0.779	0.918	0.001	0.001
TGFBR1	0.734	FAM118A	0.882	0.958	0	0.009
TGFBR1	0.734	S100B	0.841	0.89	0.022	0.011
TGFBR1	0.734	IGK@_IGKC_IGKV	0.855	0.906	0.003	0.009
TGFBR1	0.734	SON	0.856	0.953	0	0.003
TGFBR1	0.734	IRF1	0.82	0.941	0	0.005
TGFBR1	0.734	C7orf58	0.831	0.894	0.01	0.005
TGFBR1	0.734	B4GALT3	0.917	0.97	0	0.05
TGFBR1	0.734	NP	0.726	0.884	0.021	0
TGFBR1	0.734	TNFRSF17	0.875	0.924	0	0.022
TGFBR1	0.734	TMEM62_SPCS2_L	0.78	0.909	0.004	0
TGFBR1	0.734	CDC26	0.799	0.926	0	0.004
TGFBR1	0.734	TAS2R31	0.833	0.907	0.007	0
TGFBR1	0.734	DCTN5	0.722	0.851	0.046	0.002
GPR84	0.927	PLAC8	0.828	0.971	0.038	0.01
GPR84	0.927	HIST1H4E	0.915	0.989	0.045	0.033
GPR84	0.927	SLC39A8	0.825	0.971	0.039	0.012
GPR84	0.927	TRAF3	0.87	0.975	0.032	0.035
GPR84	0.927	RRP12_LOC644215	0.904	0.987	0.044	0.021
GPR84	0.927	IRF1	0.82	0.982	0.038	0.001
GPR84	0.927	CTSL1_CTSLL3	0.676	0.966	0.05	0
C7orf53	0.786	SH2D1B	0.894	0.943	0.002	0.009

C7orf53	0.786	HLA-DPB1	0.815	0.901	0.005	0.046
C7orf53	0.786	CASS4	0.738	0.898	0.004	0.006
C7orf53	0.786	PLAC8	0.828	0.93	0.002	0.022
C7orf53	0.786	CDS2	0.73	0.883	0	0.038
C7orf53	0.786	CHI3L1	0.722	0.902	0.006	0.002
C7orf53	0.786	SLC39A9	0.776	0.896	0.002	0.02
C7orf53	0.786	GIMAP7	0.804	0.905	0.015	0.004
C7orf53	0.786	LGALS1	0.722	0.852	0.015	0.034
C7orf53	0.786	SIAE	0.737	0.864	0.019	0.05
C7orf53	0.786	HS2ST1_UBA2	0.668	0.882	0.008	0.003
C7orf53	0.786	HLA-DPA1	0.796	0.895	0.006	0.038
C7orf53	0.786	NEK6_LOC1001290	0.671	0.863	0.029	0.004
C7orf53	0.786	GLT25D1	0.77	0.877	0.014	0.045
C7orf53	0.786	ITGA4_CERKL	0.88	0.94	0.001	0.043
C7orf53	0.786	ICAM1	0.675	0.855	0.04	0.004
C7orf53	0.786	KIAA0746	0.776	0.892	0.04	0.001
C7orf53	0.786	CCR4	0.871	0.932	0.002	0.031
C7orf53	0.786	FSD1L_GARNL1	0.779	0.868	0.025	0.05
C7orf53	0.786	E2F6	0.787	0.893	0.042	0.001
C7orf53	0.786	S100B	0.841	0.905	0.034	0.018
C7orf53	0.786	IGK@_IGKC_IGKV	0.855	0.92	0.003	0.034
C7orf53	0.786	C7orf58	0.831	0.971	0.001	0
C7orf53	0.786	NP	0.726	0.909	0.003	0.002
C7orf53	0.786	TAS2R31	0.833	0.904	0.009	0.017
PLB1	0.783	HLA-DPB1	0.815	0.938	0.002	0.006
PLB1	0.783	PLAC8	0.828	0.975	0	0.004
PLB1	0.783	CDS2	0.73	0.864	0.011	0.049
PLB1	0.783	CCR3	0.869	0.921	0.012	0.03
PLB1	0.783	SLC39A9	0.776	0.909	0.002	0.009

PLB1	0.783	GIMAP7	0.804	0.906	0.017	0.016
PLB1	0.783	LGALS1	0.722	0.906	0.003	0.004
PLB1	0.783	HLA-DRA	0.855	0.936	0.019	0.007
PLB1	0.783	SIAE	0.737	0.87	0.038	0.03
PLB1	0.783	MTRR	0.674	0.896	0.041	0
PLB1	0.783	HLA-DPA1	0.796	0.923	0.002	0.014
PLB1	0.783	PTGER2	0.881	0.951	0.001	0.027
PLB1	0.783	NEK6_LOC1001290	0.671	0.877	0.01	0.004
PLB1	0.783	TRAF3	0.87	0.954	0.002	0.024
PLB1	0.783	JUP	0.753	0.895	0.049	0.025
PLB1	0.783	GALNT2	0.528	0.849	0.004	0
PLB1	0.783	HSP90AB1_HSP90A	0.924	0.992	0	0.014
PLB1	0.783	GLT25D1	0.77	0.936	0.001	0.005
PLB1	0.783	EIF1AX_SCARNA9L	0.871	0.938	0.005	0.021
PLB1	0.783	MGST3	0.857	0.956	0	0.014
PLB1	0.783	KIAA0746	0.776	0.923	0.008	0.002
PLB1	0.783	HSPB1_HSPBL2	0.705	0.868	0.029	0.01
PLB1	0.783	CCR4	0.871	0.936	0.006	0.023
PLB1	0.783	FSD1L_GARNL1	0.779	0.877	0.015	0.044
PLB1	0.783	CD151	0.718	0.875	0.047	0.001
PLB1	0.783	IGK@_IGKC_IGKV	0.855	0.923	0.002	0.039
PLB1	0.783	C7orf58	0.831	0.963	0.002	0.001
PLB1	0.783	NP	0.726	0.901	0.016	0.001
PLB1	0.783	CDC26	0.799	0.894	0.004	0.035
PLB1	0.783	TAS2R31	0.833	0.919	0.014	0.003
PLB1	0.783	IGLV6-57	0.761	0.87	0.016	0.018
PLB1	0.783	NFXL1	0.728	0.879	0.048	0.001
PLB1	0.783	DCTN5	0.722	0.896	0.011	0.001
DSE	0.747	HLA-DPB1	0.815	0.915	0.001	0.023

DSE	0.747	KPNA5	0.895	0.933	0.002	0.049
DSE	0.747	PLAC8	0.828	0.978	0	0.003
DSE	0.747	ITK	0.874	0.934	0.001	0.011
DSE	0.747	FGFBP2	0.814	0.873	0.027	0.035
DSE	0.747	SLC39A9	0.776	0.899	0	0.019
DSE	0.747	GIMAP7	0.804	0.942	0.001	0.001
DSE	0.747	LGALS1	0.722	0.891	0	0.013
DSE	0.747	HLA-DRA	0.855	0.932	0.001	0.006
DSE	0.747	HINT1	0.9	0.944	0.001	0.039
DSE	0.747	MTRR	0.674	0.885	0.018	0
DSE	0.747	HS2ST1_UBA2	0.668	0.847	0.021	0.009
DSE	0.747	HLA-DPA1	0.796	0.919	0	0.013
DSE	0.747	SLC39A8	0.825	0.933	0.002	0.007
DSE	0.747	NEK6_LOC1001290	0.671	0.815	0.049	0.028
DSE	0.747	CENPK	0.834	0.886	0.029	0.01
DSE	0.747	TRAF3	0.87	0.966	0	0.017
DSE	0.747	RPL17_SNORD58B	0.917	0.95	0.001	0.038
DSE	0.747	JUP	0.753	0.877	0.017	0.045
DSE	0.747	HSP90AB1_HSP90A	0.924	0.994	0	0.015
DSE	0.747	GLT25D1	0.77	0.877	0.004	0.036
DSE	0.747	ITGA4_CERKL	0.88	0.944	0	0.032
DSE	0.747	EIF1AX_SCARNA9L	0.871	0.943	0	0.021
DSE	0.747	ICAM1	0.675	0.872	0.004	0.003
DSE	0.747	P4HA1_RPL17	0.664	0.861	0.05	0
DSE	0.747	KLHL5	0.657	0.896	0.014	0
DSE	0.747	MGST3	0.857	0.975	0	0.004
DSE	0.747	KIAA0746	0.776	0.928	0.002	0.001
DSE	0.747	HSPB1_HSPBL2	0.705	0.842	0.014	0.033
DSE	0.747	CCR4	0.871	0.941	0.001	0.019

DSE	0.747	LAIR1_LAIR2	0.607	0.874	0.016	0
DSE	0.747	CD151	0.718	0.852	0.048	0.005
DSE	0.747	IGK@_IGKC_IGKV	0.855	0.928	0	0.024
DSE	0.747	C7orf58	0.831	0.957	0	0.001
DSE	0.747	NP	0.726	0.893	0.016	0.001
DSE	0.747	TAS2R31	0.833	0.915	0.004	0.004
DSE	0.747	IGLV6-57	0.761	0.856	0.012	0.021
DSE	0.747	DCTN5	0.722	0.884	0.006	0.002
PTGDR	0.896	DNAJC13	0.819	0.955	0.011	0.004
PTGDR	0.896	GSR	0.799	0.942	0.035	0.002
PTGDR	0.896	PICALM	0.723	0.954	0.038	0
PTGDR	0.896	C9orf72	0.796	0.952	0.018	0.002
PTGDR	0.896	SMPDL3A	0.797	0.953	0.012	0.007
PTGDR	0.896	NA	0.868	0.952	0.023	0.025
PTGDR	0.896	DAAM2_LOC100131	0.903	0.96	0.034	0.044
PTGDR	0.896	IRS2	0.817	0.937	0.05	0.024
PTGDR	0.896	ACPL2	0.906	0.983	0.006	0.027
PTGDR	0.896	OCR1	0.896	0.987	0.013	0.01
PTGDR	0.896	NF-E4	0.861	0.961	0.044	0.006
PTGDR	0.896	KIAA1257_ACAD9/	0.851	0.95	0.019	0.017
PTGDR	0.896	PDK4	0.863	0.966	0.028	0.005
PTGDR	0.896	ZRANB1	0.897	0.978	0.007	0.011
PTGDR	0.896	CYP4F3_CYP4F2	0.901	0.98	0.008	0.025
PTGDR	0.896	SYNE2	0.748	0.985	0.003	0
PTGDR	0.896	MME	0.894	0.979	0.01	0.017
PTGDR	0.896	RBP7	0.848	0.969	0.005	0.006
PTGDR	0.896	PPP1R2_PPP1R2P3	0.702	0.944	0.044	0
PTGDR	0.896	CALM2_C2orf61	0.749	0.962	0.026	0
CAMK4	0.921	TNFAIP6	0.911	0.989	0.05	0.021

CAMK4	0.921	ANKRD34B	0.904	0.969	0.033	0.044
CAMK4	0.921	C9orf72	0.796	0.96	0.026	0.002
CAMK4	0.921	SMPDL3A	0.797	0.985	0.038	0.001
CAMK4	0.921	NA	0.927	0.989	0.035	0.036
CAMK4	0.921	NA	0.868	0.97	0.033	0.011
CAMK4	0.921	GPR65	0.736	0.96	0.025	0
CAMK4	0.921	OCR1	0.896	0.987	0.036	0.021
CAMK4	0.921	CCDC125	0.917	0.991	0.032	0.015
CAMK4	0.921	ZRANB1	0.897	0.983	0.033	0.012
CAMK4	0.921	CYP4F3_CYP4F2	0.901	0.98	0.032	0.05
CAMK4	0.921	SYNE2	0.748	0.979	0.043	0
CAMK4	0.921	RBP7	0.848	0.959	0.045	0.016
CAMK4	0.921	PPP1R2_PPP1R2P3	0.702	0.987	0.032	0
DNAJC13	0.819	SH2D1B	0.894	0.978	0.001	0.002
DNAJC13	0.819	LRRN3	0.928	0.966	0.001	0.027
DNAJC13	0.819	HLA-DPB1	0.815	0.945	0.003	0.001
DNAJC13	0.819	VAMP2	0.783	0.9	0.012	0.019
DNAJC13	0.819	CASS4	0.738	0.902	0.015	0.002
DNAJC13	0.819	KPNA5	0.895	0.965	0.002	0.007
DNAJC13	0.819	PLAC8	0.828	0.977	0.001	0.001
DNAJC13	0.819	KLRK1_KLRC4	0.865	0.938	0.022	0.009
DNAJC13	0.819	ITK	0.874	0.962	0.003	0.008
DNAJC13	0.819	FGFBP2	0.814	0.918	0.038	0
DNAJC13	0.819	CDS2	0.73	0.909	0.001	0.005
DNAJC13	0.819	CCR3	0.869	0.935	0.007	0.029
DNAJC13	0.819	SEC24A_SAR1B	0.478	0.905	0.036	0
DNAJC13	0.819	SLC39A9	0.776	0.988	0	0
DNAJC13	0.819	GIMAP7	0.804	0.968	0.001	0
DNAJC13	0.819	LGALS1	0.722	0.885	0.032	0.006

DNAJC13	0.819	HLA-DRA	0.855	0.948	0.005	0.018
DNAJC13	0.819	DNAJC9_FAM149B1	0.944	0.987	0	0.016
DNAJC13	0.819	SIAE	0.737	0.92	0.016	0.003
DNAJC13	0.819	HINT1	0.9	0.947	0.007	0.013
DNAJC13	0.819	MTRR	0.674	0.957	0.004	0
DNAJC13	0.819	HS2ST1_UBA2	0.668	0.905	0.019	0
DNAJC13	0.819	HLA-DPA1	0.796	0.951	0.001	0.001
DNAJC13	0.819	SLC39A8	0.825	0.918	0.027	0.017
DNAJC13	0.819	PTGER2	0.881	0.977	0	0.003
DNAJC13	0.819	PMS2CL_PMS2	0.942	0.998	0	0.016
DNAJC13	0.819	NEK6_LOC1001290	0.671	0.903	0.008	0
DNAJC13	0.819	TRAF3	0.87	0.95	0.003	0.018
DNAJC13	0.819	RPL17_SNORD58B	0.917	0.965	0.003	0.007
DNAJC13	0.819	HSP90AB1_HSP90A	0.924	0.979	0	0.02
DNAJC13	0.819	GLT25D1	0.77	0.922	0.003	0.011
DNAJC13	0.819	ITGA4_CERKL	0.88	0.994	0	0.003
DNAJC13	0.819	EIF1AX_SCARNA9L	0.871	0.958	0.005	0.001
DNAJC13	0.819	ZNF28	0.837	0.933	0.008	0.004
DNAJC13	0.819	P4HA1_RPL17	0.664	0.952	0.007	0
DNAJC13	0.819	KLHL5	0.657	0.934	0.007	0
DNAJC13	0.819	MGST3	0.857	0.957	0	0.006
DNAJC13	0.819	KIAA0746	0.776	0.974	0.002	0
DNAJC13	0.819	CCR4	0.871	0.964	0.001	0.008
DNAJC13	0.819	FSD1L_GARNL1	0.779	0.93	0.003	0.003
DNAJC13	0.819	FAM118A	0.882	0.965	0.001	0.023
DNAJC13	0.819	IGK@_IGKC_IGKV	0.855	0.966	0.001	0.002
DNAJC13	0.819	SON	0.856	0.953	0.008	0.004
DNAJC13	0.819	IRF1	0.82	0.94	0	0.022
DNAJC13	0.819	C7orf58	0.831	0.965	0.002	0.001

DNAJC13	0.819	B4GALT3	0.917	0.98	0	0.044
DNAJC13	0.819	NP	0.726	0.939	0.01	0
DNAJC13	0.819	TNFRSF17	0.875	0.943	0.003	0.029
DNAJC13	0.819	TMEM62_SPCS2_L	0.78	0.946	0.024	0
DNAJC13	0.819	CDC26	0.799	0.926	0.001	0.009
DNAJC13	0.819	TAS2R31	0.833	0.942	0.011	0
DNAJC13	0.819	DCTN5	0.722	0.937	0.004	0
TNFAIP6	0.911	SH2D1B	0.894	0.988	0.026	0.002
TNFAIP6	0.911	LRRN3	0.928	0.992	0.019	0.019
TNFAIP6	0.911	HLA-DPB1	0.815	0.952	0.014	0.011
TNFAIP6	0.911	CASS4	0.738	0.953	0.019	0
TNFAIP6	0.911	KPNA5	0.895	0.982	0.044	0.008
TNFAIP6	0.911	PLAC8	0.828	0.969	0.012	0.01
TNFAIP6	0.911	ITK	0.874	0.978	0.025	0.013
TNFAIP6	0.911	SLC39A9	0.776	0.946	0.013	0.002
TNFAIP6	0.911	GIMAP7	0.804	0.978	0.034	0
TNFAIP6	0.911	LGALS2	0.922	0.985	0.006	0.031
TNFAIP6	0.911	HLA-DPA1	0.796	0.944	0.016	0.008
TNFAIP6	0.911	SLC39A8	0.825	0.969	0.007	0.012
TNFAIP6	0.911	TRAF3	0.87	0.965	0.01	0.042
TNFAIP6	0.911	JUP	0.753	0.943	0.047	0.008
TNFAIP6	0.911	HSP90AB1_HSP90A	0.924	0.991	0.012	0.026
TNFAIP6	0.911	EIF1AX_SCARNA9L	0.871	0.962	0.014	0.021
TNFAIP6	0.911	CD300A	0.841	0.952	0.006	0.024
TNFAIP6	0.911	ICAM1	0.675	0.946	0.01	0
TNFAIP6	0.911	MGST3	0.857	0.963	0.011	0.018
TNFAIP6	0.911	KIAA0746	0.776	0.966	0.033	0
TNFAIP6	0.911	IGK@_IGKC_IGKV	0.855	0.983	0.027	0.002
TNFAIP6	0.911	IRF1	0.82	0.963	0.003	0.009

TNFAIP6	0.911	C7orf58	0.831	0.981	0.044	0
TNFAIP6	0.911	TNFRSF17	0.875	0.975	0.022	0.009
TNFAIP6	0.911	CDC26	0.799	0.94	0.036	0.007
GSR	0.799	SH2D1B	0.894	0.938	0.005	0.014
GSR	0.799	HLA-DPB1	0.815	0.93	0.004	0.003
GSR	0.799	VAMP2	0.783	0.907	0.001	0.013
GSR	0.799	CASS4	0.738	0.897	0.015	0.001
GSR	0.799	KPNA5	0.895	0.928	0.007	0.037
GSR	0.799	PLAC8	0.828	0.962	0	0.002
GSR	0.799	KLRK1_KLRC4	0.865	0.907	0.027	0.041
GSR	0.799	ITK	0.874	0.937	0.008	0.012
GSR	0.799	CDS2	0.73	0.89	0.004	0.004
GSR	0.799	SLC39A9	0.776	0.988	0	0
GSR	0.799	GIMAP7	0.804	0.935	0.004	0.001
GSR	0.799	HLA-DRA	0.855	0.952	0.004	0.003
GSR	0.799	DNAJC9_FAM149B1	0.944	0.984	0	0.018
GSR	0.799	HLA-DPA1	0.796	0.925	0.002	0.003
GSR	0.799	PTGER2	0.881	0.952	0	0.025
GSR	0.799	PMS2CL_PMS2	0.942	0.985	0	0.033
GSR	0.799	NEK6_LOC1001290	0.671	0.88	0.037	0
GSR	0.799	TRAF3	0.87	0.966	0	0.007
GSR	0.799	RPL17_SNORD58B	0.917	0.942	0.005	0.047
GSR	0.799	HSP90AB1_HSP90A	0.924	0.994	0	0.006
GSR	0.799	GLT25D1	0.77	0.89	0.035	0.016
GSR	0.799	ITGA4_CERKL	0.88	0.955	0	0.013
GSR	0.799	EIF1AX_SCARNA9L	0.871	0.925	0.006	0.015
GSR	0.799	CD300A	0.841	0.927	0	0.032
GSR	0.799	ZNF28	0.837	0.893	0.024	0.032
GSR	0.799	MGST3	0.857	0.957	0.001	0.002

GSR	0.799	KIAA0746	0.776	0.915	0.031	0
GSR	0.799	CCR4	0.871	0.921	0.011	0.026
GSR	0.799	FSD1L_GARNL1	0.779	0.908	0.005	0.004
GSR	0.799	FAM118A	0.882	0.978	0	0.006
GSR	0.799	IGK@_IGKC_IGKV	0.855	0.94	0.005	0.003
GSR	0.799	SON	0.856	0.941	0.006	0.009
GSR	0.799	IRF1	0.82	0.947	0	0.005
GSR	0.799	C7orf58	0.831	0.914	0.031	0.002
GSR	0.799	TNFRSF17	0.875	0.951	0.002	0.005
GSR	0.799	CDC26	0.799	0.892	0.007	0.022
GSR	0.799	TAS2R31	0.833	0.905	0.031	0.002
GSR	0.799	DCTN5	0.722	0.92	0.008	0
KLRF1	0.8	PICALM	0.723	0.865	0.002	0.041
KLRF1	0.8	EAF2_HCG11_LOC	0.613	0.847	0.03	0.001
KLRF1	0.8	PDE3B	0.567	0.831	0.017	0.003
KLRF1	0.8	LRRFIP1	0.678	0.847	0.04	0.012
KLRF1	0.8	DPH3	0.749	0.885	0	0.039
KLRF1	0.8	NA	0.682	0.888	0.005	0.002
KLRF1	0.8	DLEU2_DLEU2L	0.711	0.898	0.001	0.005
KLRF1	0.8	ZNF587_ZNF417	0.632	0.848	0.014	0.003
KLRF1	0.8	CEP97	0.554	0.859	0.033	0
KLRF1	0.8	SYNE2	0.748	0.908	0	0.022
KLRF1	0.8	PLEKHF2	0.667	0.866	0.004	0.009
KLRF1	0.8	IL1RL1	0.738	0.879	0.026	0.013
KLRF1	0.8	MPZL2	0.699	0.838	0.033	0.042
KLRF1	0.8	PPP1R2_PPP1R2P3	0.702	0.861	0.003	0.028
KLRF1	0.8	ATP5L_ATP5L2	0.547	0.859	0.023	0
KLRF1	0.8	CALM2_C2orf61	0.749	0.885	0.001	0.043
SH2D1B	0.894	ANKRD34B	0.904	0.964	0.004	0.046

SH2D1B	0.894	SGMS2	0.938	0.989	0.003	0.027
SH2D1B	0.894	GK3P_GK	0.961	0.99	0.005	0.031
SH2D1B	0.894	PICALM	0.723	0.951	0.016	0
SH2D1B	0.894	C9orf72	0.796	0.955	0.003	0.002
SH2D1B	0.894	SMPDL3A	0.797	0.965	0.003	0.002
SH2D1B	0.894	TCN1	0.855	0.964	0.019	0.002
SH2D1B	0.894	HPGD	0.823	0.947	0.013	0.009
SH2D1B	0.894	FRMD3	0.755	0.944	0.006	0.001
SH2D1B	0.894	NA	0.927	0.998	0.002	0.013
SH2D1B	0.894	RUNX2	0.507	0.926	0.021	0
SH2D1B	0.894	TPST1	0.92	0.974	0.026	0.036
SH2D1B	0.894	EIF2AK2	0.964	1	0.002	0.032
SH2D1B	0.894	NA	0.868	0.962	0.002	0.019
SH2D1B	0.894	AREG	0.849	0.951	0.05	0.003
SH2D1B	0.894	DAAM2_LOC100131	0.903	0.967	0.014	0.021
SH2D1B	0.894	GPR65	0.736	0.947	0.009	0
SH2D1B	0.894	IRS2	0.817	0.938	0.044	0.011
SH2D1B	0.894	ACPL2	0.906	0.979	0.002	0.036
SH2D1B	0.894	OCR1	0.896	0.994	0.002	0.012
SH2D1B	0.894	DPH3	0.749	0.95	0.021	0
SH2D1B	0.894	NF-E4	0.861	0.974	0.003	0.008
SH2D1B	0.894	KIAA1257_ACAD9/	0.851	0.965	0.003	0.005
SH2D1B	0.894	CCDC125	0.917	0.99	0.002	0.017
SH2D1B	0.894	PDK4	0.863	0.971	0.005	0.004
SH2D1B	0.894	THBS1	0.849	0.953	0.022	0.005
SH2D1B	0.894	ZRANB1	0.897	0.973	0.002	0.017
SH2D1B	0.894	ZNF587_ZNF417	0.632	0.942	0.021	0
SH2D1B	0.894	CYP4F3_CYP4F2	0.901	0.978	0.001	0.045
SH2D1B	0.894	SYNE2	0.748	0.981	0.002	0

SH2D1B	0.894	MME	0.894	0.994	0.002	0.009
SH2D1B	0.894	PLIN2	0.706	0.942	0.014	0
SH2D1B	0.894	FBXL13	0.795	0.971	0.006	0
SH2D1B	0.894	RBP7	0.848	0.963	0.002	0.01
SH2D1B	0.894	PPP1R2_PPP1R2P3	0.702	0.949	0.02	0
SH2D1B	0.894	HIST2H2BF_HIST2	0.855	0.938	0.032	0.041
SH2D1B	0.894	CALM2_C2orf61	0.749	0.966	0.016	0
SH2D1B	0.894	SPATA6	0.812	0.954	0.013	0.005
ANKRD34B	0.904	HLA-DPB1	0.815	0.953	0.047	0.001
ANKRD34B	0.904	PLAC8	0.828	0.962	0.034	0.003
ANKRD34B	0.904	HIST1H4E	0.915	0.971	0.007	0.05
ANKRD34B	0.904	CCR3	0.869	0.976	0.014	0.005
ANKRD34B	0.904	ANAPC11	0.943	0.984	0.004	0.027
ANKRD34B	0.904	HLA-DRA	0.855	0.965	0.013	0.015
ANKRD34B	0.904	DNAJC9_FAM149B1	0.944	0.985	0.006	0.03
ANKRD34B	0.904	LGALS2	0.922	0.977	0.004	0.018
ANKRD34B	0.904	SIAE	0.737	0.951	0.039	0
ANKRD34B	0.904	HIST1H3A	0.908	0.964	0.019	0.017
ANKRD34B	0.904	C22orf37	0.924	0.985	0.002	0.026
ANKRD34B	0.904	HLA-DPA1	0.796	0.957	0.041	0
ANKRD34B	0.904	PTGER2	0.881	0.971	0.01	0.005
ANKRD34B	0.904	PMS2CL_PMS2	0.942	0.988	0.002	0.032
ANKRD34B	0.904	NEK6_LOC1001290	0.671	0.949	0.038	0
ANKRD34B	0.904	IRF4	0.946	0.99	0.002	0.048
ANKRD34B	0.904	AMFR	0.867	0.965	0.003	0.021
ANKRD34B	0.904	HSP90AB1_HSP90A	0.924	0.971	0.018	0.021
ANKRD34B	0.904	GLT25D1	0.77	0.951	0.037	0.001
ANKRD34B	0.904	ITGA4_CERKL	0.88	0.98	0.01	0.004
ANKRD34B	0.904	CD300A	0.841	0.965	0.008	0.002

ANKRD34B	0.904	MGST3	0.857	0.955	0.025	0.002
ANKRD34B	0.904	CCR4	0.871	0.97	0.038	0.003
ANKRD34B	0.904	TYMS	0.863	0.969	0.007	0.006
ANKRD34B	0.904	RRP12_LOC644215	0.904	0.973	0.003	0.021
ANKRD34B	0.904	HIST1H2BM	0.891	0.971	0.015	0.009
ANKRD34B	0.904	ABCG1	0.85	0.964	0.007	0.007
ANKRD34B	0.904	HIST1H3B	0.89	0.973	0.015	0.008
ANKRD34B	0.904	FAM118A	0.882	0.969	0.011	0.016
ANKRD34B	0.904	APOLD1	0.871	0.973	0.006	0.006
ANKRD34B	0.904	IRF1	0.82	0.955	0.022	0.003
ANKRD34B	0.904	B4GALT3	0.917	0.981	0.003	0.043
ANKRD34B	0.904	CDC26	0.799	0.956	0.015	0
SGMS2	0.938	LRRN3	0.928	0.981	0.031	0.014
SGMS2	0.938	VAMP2	0.783	0.981	0.022	0
SGMS2	0.938	PLAC8	0.828	0.985	0.026	0.001
SGMS2	0.938	GOT2	0.966	0.994	0.019	0.042
SGMS2	0.938	SLC39A9	0.776	0.99	0.012	0
SGMS2	0.938	ANAPC11	0.943	0.984	0.025	0.02
SGMS2	0.938	INSIG1	0.957	0.995	0.009	0.046
SGMS2	0.938	HIST1H4L	0.961	0.988	0.038	0.047
SGMS2	0.938	HLA-DRA	0.855	0.99	0.011	0.004
SGMS2	0.938	DNAJC9_FAM149B1	0.944	0.992	0.022	0.021
SGMS2	0.938	LGALS2	0.922	0.98	0.02	0.015
SGMS2	0.938	C22orf37	0.924	0.973	0.038	0.03
SGMS2	0.938	HLA-DPA1	0.796	0.983	0.035	0
SGMS2	0.938	VOPP1_LOC100128	0.938	0.979	0.015	0.05
SGMS2	0.938	PTGER2	0.881	0.988	0.018	0.003
SGMS2	0.938	PMS2CL_PMS2	0.942	0.998	0.009	0.017
SGMS2	0.938	IRF4	0.946	0.994	0.01	0.035

SGMS2	0.938	GALNT2	0.528	0.971	0.034	0
SGMS2	0.938	HSP90AB1_HSP90A	0.924	0.998	0.01	0.009
SGMS2	0.938	GLT25D1	0.77	0.985	0.018	0
SGMS2	0.938	ITGA4_CERKL	0.88	0.991	0.019	0.002
SGMS2	0.938	MGST3	0.857	0.98	0.035	0.001
SGMS2	0.938	RRP12_LOC644215	0.904	0.979	0.027	0.016
SGMS2	0.938	ABCG1	0.85	0.981	0.026	0.003
SGMS2	0.938	TIMM10	0.949	0.987	0.021	0.029
SGMS2	0.938	FSD1L_GARNL1	0.779	0.986	0.018	0
SGMS2	0.938	IGK@_IGKC_IGKV	0.855	0.987	0.029	0.001
SGMS2	0.938	IRF1	0.82	0.974	0.046	0
SGMS2	0.938	B4GALT3	0.917	0.989	0.03	0.01
SGMS2	0.938	TNFRSF17	0.875	0.99	0.024	0.001
SGMS2	0.938	DCTN5	0.722	0.985	0.017	0
B3GNT5_MCF2L2	0.949	MRPL41	0.976	0.999	0.012	0.05
B3GNT5_MCF2L2	0.949	PLAC8	0.828	0.992	0.022	0.001
B3GNT5_MCF2L2	0.949	GOT2	0.966	0.989	0.033	0.044
B3GNT5_MCF2L2	0.949	HIST1H4E	0.915	0.998	0.01	0.015
B3GNT5_MCF2L2	0.949	CDS2	0.73	0.979	0.021	0
B3GNT5_MCF2L2	0.949	SLC39A9	0.776	0.982	0.041	0
B3GNT5_MCF2L2	0.949	ANAPC11	0.943	0.994	0.017	0.011
B3GNT5_MCF2L2	0.949	INSIG1	0.957	0.999	0.011	0.028
B3GNT5_MCF2L2	0.949	HIST1H4L	0.961	0.992	0.028	0.032
B3GNT5_MCF2L2	0.949	LGALS1	0.722	0.983	0.039	0
B3GNT5_MCF2L2	0.949	PPIF	0.934	0.998	0.01	0.05
B3GNT5_MCF2L2	0.949	DNAJC9_FAM149B1	0.944	0.997	0.013	0.027
B3GNT5_MCF2L2	0.949	LGALS2	0.922	0.995	0.02	0.004
B3GNT5_MCF2L2	0.949	HS2ST1_UBA2	0.668	0.979	0.049	0
B3GNT5_MCF2L2	0.949	C22orf37	0.924	0.993	0.019	0.011

B3GNT5_MCF2L2	0.949	VOPP1_LOC100128	0.938	0.991	0.011	0.026
B3GNT5_MCF2L2	0.949	SLC39A8	0.825	0.985	0.044	0.002
B3GNT5_MCF2L2	0.949	PTGER2	0.881	0.986	0.02	0.002
B3GNT5_MCF2L2	0.949	PMS2CL_PMS2	0.942	0.998	0.011	0.016
B3GNT5_MCF2L2	0.949	HSP90AB1_HSP90A	0.924	0.996	0.013	0.013
B3GNT5_MCF2L2	0.949	CD300A	0.841	0.987	0.019	0.001
B3GNT5_MCF2L2	0.949	ICAM1	0.675	0.981	0.043	0
B3GNT5_MCF2L2	0.949	MGST3	0.857	0.997	0.013	0.001
B3GNT5_MCF2L2	0.949	RRP12_LOC644215	0.904	0.984	0.024	0.014
B3GNT5_MCF2L2	0.949	TIMM10	0.949	0.995	0.011	0.027
B3GNT5_MCF2L2	0.949	FAM118A	0.882	0.987	0.024	0.009
B3GNT5_MCF2L2	0.949	APOLD1	0.871	0.984	0.034	0.002
B3GNT5_MCF2L2	0.949	IRF1	0.82	0.997	0.012	0
B3GNT5_MCF2L2	0.949	LASS4	0.924	0.982	0.019	0.038
B3GNT5_MCF2L2	0.949	B4GALT3	0.917	0.987	0.018	0.026
B3GNT5_MCF2L2	0.949	CDC26	0.799	0.984	0.02	0
GK3P_GK	0.961	HIST1H4E	0.915	0.984	0.028	0.047
GK3P_GK	0.961	DNAJC9_FAM149B1	0.944	0.997	0.03	0.03
GK3P_GK	0.961	LGALS2	0.922	0.99	0.032	0.013
GK3P_GK	0.961	HIST1H3A	0.908	0.989	0.033	0.006
GK3P_GK	0.961	C22orf37	0.924	0.982	0.03	0.046
GK3P_GK	0.961	PMS2CL_PMS2	0.942	0.993	0.025	0.036
GK3P_GK	0.961	AMFR	0.867	0.977	0.03	0.017
GK3P_GK	0.961	HSP90AB1_HSP90A	0.924	0.99	0.034	0.025
GK3P_GK	0.961	CD300A	0.841	0.982	0.031	0.001
GK3P_GK	0.961	MGST3	0.857	0.98	0.048	0.003
GK3P_GK	0.961	TYMS	0.863	0.976	0.043	0.004
GK3P_GK	0.961	RRP12_LOC644215	0.904	0.993	0.033	0.011
GK3P_GK	0.961	HIST1H3B	0.89	0.983	0.038	0.009

GK3P_GK	0.961	FAM118A	0.882	0.984	0.038	0.017
GK3P_GK	0.961	IRF1	0.82	0.985	0.023	0.001
PICALM	0.723	MRPL41	0.976	1	0	0.048
PICALM	0.723	CASS4	0.738	0.863	0.002	0.012
PICALM	0.723	PLAC8	0.828	0.907	0.001	0.015
PICALM	0.723	KLRK1_KLRC4	0.865	0.914	0.002	0.038
PICALM	0.723	ITK	0.874	0.917	0.001	0.022
PICALM	0.723	FGFBP2	0.814	0.89	0.006	0.004
PICALM	0.723	CDS2	0.73	0.857	0.001	0.037
PICALM	0.723	CHI3L1	0.722	0.861	0.013	0.005
PICALM	0.723	SLC39A9	0.776	0.917	0	0.002
PICALM	0.723	GIMAP7	0.804	0.906	0.001	0.004
PICALM	0.723	PHOSPHO1	0.721	0.821	0.039	0.025
PICALM	0.723	DNAJC9_FAM149B1	0.944	0.983	0	0.028
PICALM	0.723	HS2ST1_UBA2	0.668	0.851	0.016	0.003
PICALM	0.723	SLC39A8	0.825	0.886	0.01	0.026
PICALM	0.723	PTGER2	0.881	0.955	0	0.041
PICALM	0.723	NEK6_LOC1001290	0.671	0.814	0.043	0.019
PICALM	0.723	CENPK	0.834	0.898	0.007	0.009
PICALM	0.723	RPL17_SNORD58B	0.917	0.968	0	0.009
PICALM	0.723	EIF1AX_SCARNA9L	0.871	0.929	0	0.029
PICALM	0.723	CD300A	0.841	0.931	0	0.028
PICALM	0.723	ZNF28	0.837	0.915	0	0.026
PICALM	0.723	MGST3	0.857	0.937	0	0.012
PICALM	0.723	KIAA0746	0.776	0.85	0.04	0.006
PICALM	0.723	FSD1L_GARNL1	0.779	0.865	0.002	0.047
PICALM	0.723	E2F6	0.787	0.851	0.041	0.004
PICALM	0.723	S100B	0.841	0.893	0.012	0.007
PICALM	0.723	IRF1	0.82	0.923	0	0.032

PICALM	0.723	C7orf58	0.831	0.915	0.002	0.002
PICALM	0.723	NP	0.726	0.871	0.011	0.001
PICALM	0.723	C4orf3	0.723	0.827	0.036	0.025
PICALM	0.723	PLEKHA3	0.645	0.829	0.038	0.001
PICALM	0.723	TMEM62_SPCS2_L	0.78	0.868	0.017	0.002
PICALM	0.723	CDC26	0.799	0.938	0	0.007
PICALM	0.723	TAS2R31	0.833	0.916	0.001	0.002
PICALM	0.723	IGLV6-57	0.761	0.831	0.027	0.041
PICALM	0.723	NFXL1	0.728	0.858	0.031	0
PICALM	0.723	DCTN5	0.722	0.852	0.014	0.008
PICALM	0.723	KIAA0101_CSNK1G	0.736	0.841	0.037	0.003
METTL7B	0.898	HIST1H4E	0.915	0.973	0.02	0.01
METTL7B	0.898	HIST1H4L	0.961	0.99	0.006	0.017
METTL7B	0.898	PPIF	0.934	0.966	0.029	0.047
METTL7B	0.898	LGALS2	0.922	0.992	0.003	0.007
METTL7B	0.898	C22orf37	0.924	0.98	0.005	0.023
METTL7B	0.898	HSP90AB1_HSP90A	0.924	0.97	0.009	0.046
METTL7B	0.898	MGST3	0.857	0.957	0.028	0.005
METTL7B	0.898	TYMS	0.863	0.971	0.015	0.001
METTL7B	0.898	RRP12_LOC644215	0.904	0.965	0.016	0.031
METTL7B	0.898	TIMM10	0.949	0.983	0.004	0.048
METTL7B	0.898	FAM118A	0.882	0.956	0.036	0.025
METTL7B	0.898	LASS4	0.924	0.973	0.004	0.036
METTL7B	0.898	B4GALT3	0.917	0.979	0.008	0.02
C9orf72	0.796	LRRN3	0.928	0.965	0.001	0.012
C9orf72	0.796	HLA-DPB1	0.815	0.934	0.002	0.002
C9orf72	0.796	MRPL41	0.976	0.999	0	0.049
C9orf72	0.796	CASS4	0.738	0.915	0.004	0
C9orf72	0.796	KPNA5	0.895	0.951	0.005	0.003

C9orf72	0.796	PLAC8	0.828	0.969	0.001	0
C9orf72	0.796	KLRK1_KLRC4	0.865	0.92	0.032	0.009
C9orf72	0.796	ITK	0.874	0.943	0.007	0.003
C9orf72	0.796	CDS2	0.73	0.937	0	0.001
C9orf72	0.796	SLC39A9	0.776	0.969	0	0
C9orf72	0.796	GIMAP7	0.804	0.961	0.002	0
C9orf72	0.796	INSIG1	0.957	0.996	0	0.026
C9orf72	0.796	HIST1H4L	0.961	0.986	0	0.025
C9orf72	0.796	LGALS1	0.722	0.891	0.01	0.003
C9orf72	0.796	HLA-DRA	0.855	0.936	0.008	0.004
C9orf72	0.796	DNAJC9_FAM149B1	0.944	0.988	0	0.025
C9orf72	0.796	LGALS2	0.922	0.969	0	0.032
C9orf72	0.796	HINT1	0.9	0.955	0.002	0.013
C9orf72	0.796	MTRR	0.674	0.911	0.05	0
C9orf72	0.796	HS2ST1_UBA2	0.668	0.914	0.006	0
C9orf72	0.796	HLA-DPA1	0.796	0.942	0.001	0.001
C9orf72	0.796	SLC39A8	0.825	0.923	0.03	0.002
C9orf72	0.796	PTGER2	0.881	0.967	0	0.017
C9orf72	0.796	PMS2CL_PMS2	0.942	0.988	0	0.014
C9orf72	0.796	NEK6_LOC1001290	0.671	0.887	0.016	0
C9orf72	0.796	TRAF3	0.87	0.967	0	0.008
C9orf72	0.796	RPL17_SNORD58B	0.917	0.962	0.001	0.015
C9orf72	0.796	HSP90AB1_HSP90A	0.924	0.977	0	0.011
C9orf72	0.796	GLT25D1	0.77	0.894	0.013	0.01
C9orf72	0.796	ITGA4_CERKL	0.88	0.984	0	0.003
C9orf72	0.796	EIF1AX_SCARNA9L	0.871	0.954	0.002	0.002
C9orf72	0.796	CD300A	0.841	0.934	0	0.038
C9orf72	0.796	ZNF28	0.837	0.922	0.007	0.01
C9orf72	0.796	P4HA1_RPL17	0.664	0.924	0.02	0

C9orf72	0.796	KLHL5	0.657	0.916	0.04	0
C9orf72	0.796	MGST3	0.857	0.979	0	0
C9orf72	0.796	KIAA0746	0.776	0.915	0.04	0
C9orf72	0.796	CCR4	0.871	0.951	0.004	0.001
C9orf72	0.796	FSD1L_GARNL1	0.779	0.9	0.011	0.003
C9orf72	0.796	FAM118A	0.882	0.957	0	0.042
C9orf72	0.796	IGK@_IGKC_IGKV	0.855	0.935	0.006	0.003
C9orf72	0.796	SON	0.856	0.938	0.002	0.021
C9orf72	0.796	IRF1	0.82	0.941	0	0.012
C9orf72	0.796	C7orf58	0.831	0.96	0.002	0
C9orf72	0.796	NP	0.726	0.925	0.012	0
C9orf72	0.796	TNFRSF17	0.875	0.931	0.003	0.029
C9orf72	0.796	CDC26	0.799	0.921	0	0.008
C9orf72	0.796	TAS2R31	0.833	0.923	0.012	0.001
C9orf72	0.796	DCTN5	0.722	0.927	0.008	0
SLC15A2	0.534	C7orf58	0.831	0.932	0	0.004
TLR10	0.521	C7orf58	0.831	0.9	0	0.029
LRRN3	0.928	SMPDL3A	0.797	0.971	0.044	0.001
LRRN3	0.928	NA	0.927	0.989	0.007	0.035
LRRN3	0.928	NA	0.868	0.976	0.008	0.005
LRRN3	0.928	GPR65	0.736	0.961	0.022	0
LRRN3	0.928	ACPL2	0.906	0.972	0.043	0.031
LRRN3	0.928	OCR1	0.896	0.981	0.013	0.028
LRRN3	0.928	CCDC125	0.917	0.982	0.014	0.028
LRRN3	0.928	ZRANB1	0.897	0.98	0.009	0.011
LRRN3	0.928	CYP4F3_CYP4F2	0.901	0.98	0.006	0.047
LRRN3	0.928	MME	0.894	0.98	0.031	0.015
LRRN3	0.928	PLIN2	0.706	0.956	0.038	0
HLA-DPB1	0.815	SMPDL3A	0.797	0.941	0.002	0.004

HLA-DPB1	0.815	TCN1	0.855	0.915	0.02	0.02
HLA-DPB1	0.815	HPGD	0.823	0.947	0.002	0.011
HLA-DPB1	0.815	FRMD3	0.755	0.881	0.021	0.017
HLA-DPB1	0.815	NA	0.927	0.97	0.001	0.041
HLA-DPB1	0.815	NA	0.868	0.957	0	0.014
HLA-DPB1	0.815	OR9A2	0.823	0.894	0.038	0.027
HLA-DPB1	0.815	PDK4	0.863	0.974	0.001	0.001
HLA-DPB1	0.815	SYNE2	0.748	0.898	0.037	0.001
HLA-DPB1	0.815	PLIN2	0.706	0.908	0.018	0.001
HLA-DPB1	0.815	HIST2H2BF_HIST2	0.855	0.913	0.027	0.048
VAMP2	0.783	TCN1	0.855	0.921	0.017	0.004
VAMP2	0.783	LOC284757	0.939	0.978	0	0.02
VAMP2	0.783	HPGD	0.823	0.905	0.02	0.029
VAMP2	0.783	HSPC159	0.809	0.883	0.039	0.018
VAMP2	0.783	FRMD3	0.755	0.903	0.006	0.002
VAMP2	0.783	NA	0.927	0.951	0.001	0.045
VAMP2	0.783	TPST1	0.92	0.955	0.003	0.037
VAMP2	0.783	EIF2AK2	0.964	0.994	0	0.049
VAMP2	0.783	NA	0.868	0.92	0.003	0.021
VAMP2	0.783	CDA	0.945	0.98	0	0.039
VAMP2	0.783	SAP30	0.911	0.961	0	0.029
VAMP2	0.783	AREG	0.849	0.903	0.01	0.037
VAMP2	0.783	DAAM2_LOC100131	0.903	0.956	0.001	0.021
VAMP2	0.783	IRS2	0.817	0.932	0.002	0.006
VAMP2	0.783	ACPL2	0.906	0.981	0	0.013
VAMP2	0.783	OCR1	0.896	0.935	0.006	0.023
VAMP2	0.783	ERGIC1	0.886	0.965	0.001	0.013
VAMP2	0.783	NF-E4	0.861	0.928	0.014	0.002
VAMP2	0.783	HAL	0.942	0.984	0	0.021

VAMP2	0.783	KIAA1257_ACAD9/	0.851	0.93	0.007	0.002
VAMP2	0.783	CCDC125	0.917	0.98	0	0.009
VAMP2	0.783	PDK4	0.863	0.903	0.017	0.03
VAMP2	0.783	THBS1	0.849	0.923	0.009	0.007
VAMP2	0.783	ZRANB1	0.897	0.949	0	0.023
VAMP2	0.783	MPZL3	0.892	0.939	0	0.042
VAMP2	0.783	CYP4F3_CYP4F2	0.901	0.955	0.003	0.014
VAMP2	0.783	SYNE2	0.748	0.896	0.037	0
VAMP2	0.783	MME	0.894	0.945	0.004	0.006
VAMP2	0.783	CPM	0.854	0.901	0.029	0.036
VAMP2	0.783	RBP7	0.848	0.946	0.001	0.005
VAMP2	0.783	HIST2H2BF_HIST2	0.855	0.902	0.047	0.004
VAMP2	0.783	SPATA6	0.812	0.901	0.027	0.018
SMPDL3A	0.797	CASS4	0.738	0.884	0.042	0.001
SMPDL3A	0.797	KPNA5	0.895	0.966	0.004	0.007
SMPDL3A	0.797	PLAC8	0.828	0.985	0	0.002
SMPDL3A	0.797	KLRK1_KLRC4	0.865	0.937	0.03	0.003
SMPDL3A	0.797	ITK	0.874	0.968	0.003	0.006
SMPDL3A	0.797	FGFBP2	0.814	0.925	0.034	0
SMPDL3A	0.797	CCR3	0.869	0.92	0.011	0.023
SMPDL3A	0.797	SLC39A9	0.776	0.935	0.002	0.001
SMPDL3A	0.797	GIMAP7	0.804	0.99	0	0
SMPDL3A	0.797	LGALS1	0.722	0.921	0.002	0.001
SMPDL3A	0.797	HLA-DRA	0.855	0.924	0.017	0.009
SMPDL3A	0.797	DNAJC9_FAM149B1	0.944	0.991	0	0.03
SMPDL3A	0.797	LGALS2	0.922	0.973	0	0.042
SMPDL3A	0.797	HINT1	0.9	0.975	0.002	0.009
SMPDL3A	0.797	MTRR	0.674	0.948	0.006	0
SMPDL3A	0.797	HS2ST1_UBA2	0.668	0.897	0.046	0

SMPDL3A	0.797	HIST1H3A	0.908	0.941	0.004	0.047
SMPDL3A	0.797	HLA-DPA1	0.796	0.929	0.004	0.003
SMPDL3A	0.797	SLC39A8	0.825	0.985	0	0.003
SMPDL3A	0.797	PTGER2	0.881	0.964	0.001	0.012
SMPDL3A	0.797	PMS2CL_PMS2	0.942	0.994	0	0.017
SMPDL3A	0.797	TRAF3	0.87	0.976	0.001	0.011
SMPDL3A	0.797	RPL17_SNORD58B	0.917	0.962	0.004	0.008
SMPDL3A	0.797	HSP90AB1_HSP90A	0.924	0.996	0	0.012
SMPDL3A	0.797	GLT25D1	0.77	0.893	0.03	0.009
SMPDL3A	0.797	ITGA4_CERKL	0.88	0.978	0.001	0.005
SMPDL3A	0.797	EIF1AX_SCARNA9L	0.871	0.949	0.004	0.007
SMPDL3A	0.797	ZNF28	0.837	0.909	0.023	0.018
SMPDL3A	0.797	ICAM1	0.675	0.877	0.007	0.004
SMPDL3A	0.797	KLHL5	0.657	0.923	0.027	0
SMPDL3A	0.797	MGST3	0.857	0.982	0	0.001
SMPDL3A	0.797	KIAA0746	0.776	0.968	0.002	0
SMPDL3A	0.797	HSPB1_HSPBL2	0.705	0.881	0.006	0.007
SMPDL3A	0.797	CCR4	0.871	0.974	0.001	0.007
SMPDL3A	0.797	FAM118A	0.882	0.969	0.001	0.019
SMPDL3A	0.797	CD151	0.718	0.893	0.039	0
SMPDL3A	0.797	HIST1H3H	0.861	0.897	0.044	0.046
SMPDL3A	0.797	IGK@_IGKC_IGKV	0.855	0.954	0.006	0.002
SMPDL3A	0.797	SON	0.856	0.93	0.01	0.022
SMPDL3A	0.797	IRF1	0.82	0.93	0.001	0.012
SMPDL3A	0.797	C7orf58	0.831	0.933	0.01	0.008
SMPDL3A	0.797	NP	0.726	0.921	0.032	0
SMPDL3A	0.797	TNFRSF17	0.875	0.932	0.009	0.043
SMPDL3A	0.797	CDC26	0.799	0.901	0.006	0.021
SMPDL3A	0.797	TAS2R31	0.833	0.94	0.01	0

SMPDL3A	0.797	DCTN5	0.722	0.911	0.019	0
JKAMP	0.493	RPL17_SNORD58B	0.917	0.947	0	0.024
MRPL41	0.976	PPP2R5A_SNORA16	0.953	0.999	0.05	0.02
MRPL41	0.976	MTHFS	0.933	0.999	0.048	0.019
MRPL41	0.976	EIF2AK2	0.964	0.999	0.049	0.035
MRPL41	0.976	ACPL2	0.906	0.999	0.049	0.007
MRPL41	0.976	CCDC125	0.917	0.996	0.05	0.008
MRPL41	0.976	RBP7	0.848	1	0.048	0
OLFM4	0.715	LTF	0.593	0.776	0.025	0.003
OLFM4	0.715	DEFA4_DEFA8P	0.481	0.81	0.048	0
OLFM4	0.715	MPO	0.508	0.775	0.008	0
CASS4	0.738	LOC284757	0.939	0.971	0	0.033
CASS4	0.738	HSPC159	0.809	0.879	0.022	0.01
CASS4	0.738	NA	0.927	0.987	0	0.005
CASS4	0.738	PRR13_PCBP2	0.947	0.987	0	0.041
CASS4	0.738	NA	0.868	0.93	0	0.048
CASS4	0.738	GPR65	0.736	0.858	0.016	0.008
CASS4	0.738	OR9A2	0.823	0.877	0.005	0.043
CASS4	0.738	OCR1	0.896	0.951	0	0.006
CASS4	0.738	NF-E4	0.861	0.942	0.001	0.001
CASS4	0.738	KIAA1257_ACAD9/	0.851	0.983	0	0
CASS4	0.738	CCDC125	0.917	0.974	0	0.025
CASS4	0.738	PDK4	0.863	0.909	0.002	0.04
CASS4	0.738	THBS1	0.849	0.92	0.001	0.007
CASS4	0.738	ZRANB1	0.897	0.977	0	0.002
CASS4	0.738	ZNF587_ZNF417	0.632	0.883	0.018	0
CASS4	0.738	CYP4F3_CYP4F2	0.901	0.958	0	0.026
CASS4	0.738	SYNE2	0.748	0.889	0.01	0
CASS4	0.738	MME	0.894	0.951	0	0.013

CASS4	0.738	FBXL13	0.795	0.89	0.012	0.003
CASS4	0.738	HIST2H2BF_HIST2	0.855	0.924	0.001	0.014
CASS4	0.738	SPATA6	0.812	0.891	0.003	0.045
TCN1	0.855	KPNA5	0.895	0.965	0.003	0.033
TCN1	0.855	KLRK1_KLRC4	0.865	0.949	0.028	0.011
TCN1	0.855	ITK	0.874	0.952	0.008	0.034
TCN1	0.855	FGFBP2	0.814	0.932	0.032	0.004
TCN1	0.855	CCR3	0.869	0.963	0.001	0.025
TCN1	0.855	SLC39A9	0.776	0.906	0.002	0.02
TCN1	0.855	GIMAP7	0.804	0.923	0.004	0.015
TCN1	0.855	LGALS1	0.722	0.889	0.024	0.007
TCN1	0.855	PHOSPHO1	0.721	0.948	0.002	0.001
TCN1	0.855	DNAJC9_FAM149B1	0.944	0.994	0	0.042
TCN1	0.855	HINT1	0.9	0.969	0.002	0.04
TCN1	0.855	HIST1H3J	0.898	0.973	0.003	0.007
TCN1	0.855	HIST1H3A	0.908	0.972	0.001	0.03
TCN1	0.855	HLA-DPA1	0.796	0.893	0.025	0.037
TCN1	0.855	SLC39A8	0.825	0.938	0.001	0.049
TCN1	0.855	MKI67	0.621	0.914	0.013	0
TCN1	0.855	NEK6_LOC1001290	0.671	0.887	0.033	0.001
TCN1	0.855	CENPK	0.834	0.946	0.031	0.002
TCN1	0.855	RPL17_SNORD58B	0.917	0.973	0.001	0.045
TCN1	0.855	EIF1AX_SCARNA9L	0.871	0.961	0.002	0.015
TCN1	0.855	ZNF28	0.837	0.948	0.002	0.014
TCN1	0.855	KIAA0746	0.776	0.912	0.03	0.007
TCN1	0.855	CCR4	0.871	0.945	0.005	0.049
TCN1	0.855	HIST1H3B	0.89	0.977	0.001	0.015
TCN1	0.855	FSD1L_GARNL1	0.779	0.929	0.001	0.01
TCN1	0.855	HIST1H3C	0.863	0.956	0.015	0.001

TCN1	0.855	HIST1H3H	0.861	0.955	0.006	0.005
TCN1	0.855	TPX2	0.635	0.901	0.022	0
TCN1	0.855	IGK@_IGKC_IGKV	0.855	0.925	0.036	0.024
TCN1	0.855	CLC	0.782	0.958	0.006	0.002
TCN1	0.855	SON	0.856	0.953	0.001	0.041
TCN1	0.855	C7orf58	0.831	0.906	0.049	0.026
TCN1	0.855	MPO	0.508	0.912	0.024	0
TCN1	0.855	NP	0.726	0.921	0.004	0.002
TCN1	0.855	C4orf3	0.723	0.889	0.045	0.008
TCN1	0.855	CDC26	0.799	0.922	0.003	0.022
TCN1	0.855	TAS2R31	0.833	0.951	0.007	0.003
TCN1	0.855	IGLV6-57	0.761	0.909	0.046	0.003
CLU	0.664	ITGA2B	0.58	0.806	0.039	0.001
CLU	0.664	PTGS1	0.675	0.89	0	0.002
CLU	0.664	E2F6	0.787	0.842	0.01	0.042
CLU	0.664	KIAA0101_CSNK1G	0.736	0.82	0.008	0.024
KPNA5	0.895	HPGD	0.823	0.95	0.024	0.016
KPNA5	0.895	NA	0.927	0.99	0.008	0.023
KPNA5	0.895	NA	0.868	0.944	0.023	0.044
KPNA5	0.895	GPR65	0.736	0.962	0.003	0
KPNA5	0.895	OCR1	0.896	0.979	0.009	0.032
KPNA5	0.895	DPH3	0.749	0.948	0.014	0
KPNA5	0.895	NF-E4	0.861	0.957	0.042	0.014
KPNA5	0.895	NA	0.682	0.956	0.041	0
KPNA5	0.895	KIAA1257_ACAD9/	0.851	0.945	0.026	0.02
KPNA5	0.895	CCDC125	0.917	0.98	0.005	0.042
KPNA5	0.895	PDK4	0.863	0.961	0.02	0.007
KPNA5	0.895	ZRANB1	0.897	0.984	0.007	0.008
KPNA5	0.895	SYNE2	0.748	0.97	0.006	0

KPNA5	0.895	MME	0.894	0.983	0.014	0.011
KPNA5	0.895	RBP7	0.848	0.955	0.007	0.024
KPNA5	0.895	PPP1R2_PPP1R2P3	0.702	0.957	0.016	0
PLAC8	0.828	HPGD	0.823	0.946	0.007	0.008
PLAC8	0.828	HSPC159	0.809	0.917	0.048	0.003
PLAC8	0.828	TMTC1	0.809	0.942	0.027	0.001
PLAC8	0.828	SH3PXD2B	0.9	0.948	0.03	0.032
PLAC8	0.828	FRMD3	0.755	0.891	0.04	0.016
PLAC8	0.828	NA	0.927	0.989	0.002	0.012
PLAC8	0.828	MTHFS	0.933	0.995	0.001	0.031
PLAC8	0.828	EIF2AK2	0.964	0.997	0.001	0.035
PLAC8	0.828	NA	0.868	0.952	0.007	0.012
PLAC8	0.828	GPR65	0.736	0.953	0.002	0
PLAC8	0.828	OR9A2	0.823	0.916	0.01	0.018
PLAC8	0.828	PDK4	0.863	0.983	0.003	0.001
PLAC8	0.828	PLIN2	0.706	0.926	0.014	0
PLAC8	0.828	PPP1R2_PPP1R2P3	0.702	0.916	0.025	0
CD63	0.612	PDK4	0.863	0.903	0	0.03
HPSE	0.462	C7orf58	0.831	0.928	0	0.017
C1orf161	0.842	CDS2	0.73	0.903	0.037	0.006
C1orf161	0.842	HIST1H3A	0.908	0.961	0.022	0.007
C1orf161	0.842	CD300A	0.841	0.942	0.01	0.016
C1orf161	0.842	HIST1H2BM	0.891	0.956	0.013	0.041
C1orf161	0.842	HIST1H3B	0.89	0.956	0.02	0.017
C1orf161	0.842	APOLD1	0.871	0.966	0.008	0.008
C1orf161	0.842	CDC26	0.799	0.908	0.04	0.037
DDAH2	0.681	LGALS1	0.722	0.82	0.049	0.025
DDAH2	0.681	C22orf37	0.924	0.957	0	0.048
DDAH2	0.681	GLT25D1	0.77	0.878	0.008	0.007

DDAH2	0.681	CD300A	0.841	0.902	0	0.043
DDAH2	0.681	MGST3	0.857	0.926	0	0.029
DDAH2	0.681	S100B	0.841	0.864	0.019	0.032
DDAH2	0.681	IRF1	0.82	0.903	0.001	0.006
KLRK1_KLRC4	0.865	AREG	0.849	0.951	0.018	0.014
KLRK1_KLRC4	0.865	GPR65	0.736	0.932	0.006	0.003
KLRK1_KLRC4	0.865	OCR1	0.896	0.971	0.01	0.036
KLRK1_KLRC4	0.865	DPH3	0.749	0.929	0.02	0.001
KLRK1_KLRC4	0.865	NF-E4	0.861	0.945	0.023	0.038
KLRK1_KLRC4	0.865	PDK4	0.863	0.942	0.01	0.048
KLRK1_KLRC4	0.865	ZRANB1	0.897	0.968	0.003	0.043
KLRK1_KLRC4	0.865	SYNE2	0.748	0.962	0.002	0.001
KLRK1_KLRC4	0.865	MME	0.894	0.973	0.005	0.042
KLRK1_KLRC4	0.865	PPP1R2_PPP1R2P3	0.702	0.931	0.02	0
KLRK1_KLRC4	0.865	CALM2_C2orf61	0.749	0.935	0.018	0.002
ATP13A3	0.545	MTRR	0.674	0.814	0	0.032
ATP13A3	0.545	KIAA0746	0.776	0.896	0	0.007
ATP13A3	0.545	C7orf58	0.831	0.906	0	0.04
ITK	0.874	HPGD	0.823	0.936	0.018	0.04
ITK	0.874	FRMD3	0.755	0.913	0.045	0.009
ITK	0.874	NA	0.927	0.987	0.005	0.036
ITK	0.874	NA	0.868	0.966	0.002	0.02
ITK	0.874	GPR65	0.736	0.948	0.004	0.001
ITK	0.874	LRRFIP1	0.678	0.944	0.021	0
ITK	0.874	OCR1	0.896	0.977	0.008	0.025
ITK	0.874	KIAA1257_ACAD9/	0.851	0.933	0.04	0.043
ITK	0.874	CCDC125	0.917	0.99	0.004	0.018
ITK	0.874	PDK4	0.863	0.955	0.011	0.019
ITK	0.874	ZRANB1	0.897	0.978	0.005	0.016

ITK	0.874	ZNF587_ZNF417	0.632	0.941	0.03	0
ITK	0.874	CYP4F3_CYP4F2	0.901	0.976	0.005	0.05
ITK	0.874	SYNE2	0.748	0.973	0.005	0
ITK	0.874	MME	0.894	0.974	0.014	0.017
ITK	0.874	PLIN2	0.706	0.936	0.01	0.001
ITK	0.874	RBP7	0.848	0.935	0.013	0.046
ITK	0.874	PPP1R2_PPP1R2P3	0.702	0.975	0.005	0
LOC284757	0.939	SLC39A9	0.776	0.975	0.026	0
LOC284757	0.939	HLA-DRA	0.855	0.979	0.04	0.011
LOC284757	0.939	DNAJC9_FAM149B1	0.944	0.988	0.047	0.035
LOC284757	0.939	PMS2CL_PMS2	0.942	0.988	0.033	0.044
LOC284757	0.939	TRAF3	0.87	0.975	0.027	0.022
LOC284757	0.939	MGST3	0.857	0.967	0.05	0.009
LOC284757	0.939	ABCG1	0.85	0.986	0.018	0.005
GOT2	0.966	PRR13_PCBP2	0.947	0.988	0.044	0.049
GOT2	0.966	HAL	0.942	0.988	0.033	0.025
GOT2	0.966	MPZL3	0.892	0.979	0.04	0.01
B3GAT3	0.973	PPP2R5A_SNORA16	0.953	1	0.046	0.019
B3GAT3	0.973	MTHFS	0.933	0.999	0.046	0.018
B3GAT3	0.973	CDA	0.945	1	0.046	0.022
HIST1H4E	0.915	PPP2R5A_SNORA16	0.953	0.993	0.022	0.018
HIST1H4E	0.915	PRR13_PCBP2	0.947	0.986	0.023	0.025
HIST1H4E	0.915	MTHFS	0.933	0.995	0.018	0.016
HIST1H4E	0.915	CDA	0.945	0.994	0.014	0.021
HIST1H4E	0.915	SAP30	0.911	0.971	0.037	0.039
HIST1H4E	0.915	HAL	0.942	0.978	0.035	0.034
HIST1H4E	0.915	MPZL3	0.892	0.986	0.012	0.005
HIST1H4E	0.915	RBP7	0.848	0.981	0.046	0
HIST1H4E	0.915	RGS2	0.915	0.987	0.013	0.011

HPGD	0.823	CDS2	0.73	0.888	0.039	0.006
HPGD	0.823	CCR3	0.869	0.941	0.024	0.004
HPGD	0.823	SLC39A9	0.776	0.915	0.015	0.004
HPGD	0.823	GIMAP7	0.804	0.918	0.049	0.002
HPGD	0.823	LGALS2	0.922	0.973	0.001	0.036
HPGD	0.823	SIAE	0.737	0.92	0.034	0.003
HPGD	0.823	HINT1	0.9	0.947	0.015	0.041
HPGD	0.823	HIST1H3J	0.898	0.936	0.009	0.037
HPGD	0.823	HIST1H3A	0.908	0.95	0.007	0.018
HPGD	0.823	HLA-DPA1	0.796	0.955	0.005	0
HPGD	0.823	PTGER2	0.881	0.973	0.001	0.02
HPGD	0.823	PMS2CL_PMS2	0.942	0.987	0.001	0.019
HPGD	0.823	TRAF3	0.87	0.935	0.012	0.048
HPGD	0.823	RPL17_SNORD58B	0.917	0.965	0.005	0.034
HPGD	0.823	GLT25D1	0.77	0.928	0.011	0.008
HPGD	0.823	ITGA4_CERKL	0.88	0.987	0.002	0.002
HPGD	0.823	EIF1AX_SCARNA9L	0.871	0.944	0.014	0.002
HPGD	0.823	ZNF28	0.837	0.924	0.029	0.01
HPGD	0.823	MGST3	0.857	0.933	0.007	0.032
HPGD	0.823	CCR4	0.871	0.944	0.026	0.004
HPGD	0.823	FSD1L_GARNL1	0.779	0.909	0.028	0.003
HPGD	0.823	HIST1H3H	0.861	0.923	0.031	0.004
HPGD	0.823	S100B	0.841	0.923	0.018	0.006
HPGD	0.823	IGK@_IGKC_IGKV	0.855	0.932	0.03	0.01
HPGD	0.823	SON	0.856	0.925	0.019	0.018
HPGD	0.823	C7orf58	0.831	0.95	0.012	0.003
HPGD	0.823	CDC26	0.799	0.915	0.03	0.004
HPGD	0.823	TAS2R31	0.833	0.922	0.043	0.002
FGFBP2	0.814	TMTC1	0.809	0.894	0.035	0.035

FGFBP2	0.814	AREG	0.849	0.92	0.005	0.037
FGFBP2	0.814	GPR65	0.736	0.884	0.008	0.015
FGFBP2	0.814	DPH3	0.749	0.897	0.007	0.005
FGFBP2	0.814	NF-E4	0.861	0.939	0.002	0.031
FGFBP2	0.814	SYNE2	0.748	0.947	0	0
FGFBP2	0.814	MME	0.894	0.965	0	0.05
FGFBP2	0.814	FBXL13	0.795	0.914	0.013	0.008
FGFBP2	0.814	PPP1R2_PPP1R2P3	0.702	0.886	0.049	0.002
FGFBP2	0.814	CALM2_C2orf61	0.749	0.898	0.005	0.012
TMEM144_LOC2855	0.747	MTRR	0.674	0.879	0.002	0.006
TMEM144_LOC2855	0.747	HDHD1A	0.602	0.816	0.006	0.017
TMEM144_LOC2855	0.747	NPCDR1	0.726	0.862	0.013	0.016
TMEM144_LOC2855	0.747	ICAM1	0.675	0.842	0.01	0.03
TMEM144_LOC2855	0.747	TAF13	0.617	0.846	0.025	0.002
TMEM144_LOC2855	0.747	P4HA1_RPL17	0.664	0.877	0.003	0.003
TMEM144_LOC2855	0.747	C15orf54	0.72	0.837	0.015	0.028
TMEM144_LOC2855	0.747	KLHL5	0.657	0.858	0.007	0.011
TMEM144_LOC2855	0.747	KIAA0746	0.776	0.91	0	0.024
TMEM144_LOC2855	0.747	NA	0.7	0.885	0.011	0.001
TMEM144_LOC2855	0.747	E2F6	0.787	0.871	0.018	0.02
TMEM144_LOC2855	0.747	CD151	0.718	0.859	0.007	0.038
TMEM144_LOC2855	0.747	FSD1L	0.674	0.838	0.036	0.008
TMEM144_LOC2855	0.747	C7orf58	0.831	0.996	0	0
TMEM144_LOC2855	0.747	NP	0.726	0.874	0.001	0.043
TMEM144_LOC2855	0.747	IGJ	0.698	0.827	0.037	0.018
TMEM144_LOC2855	0.747	SDHC	0.736	0.888	0.014	0.002
TMEM144_LOC2855	0.747	NFXL1	0.728	0.869	0.003	0.018
CDS2	0.73	HSPC159	0.809	0.878	0.036	0.007
CDS2	0.73	FRMD3	0.755	0.866	0.006	0.012

CDS2	0.73	NA	0.927	0.959	0	0.041
CDS2	0.73	MTHFS	0.933	0.979	0	0.01
CDS2	0.73	OR9A2	0.823	0.873	0.015	0.028
CDS2	0.73	KIAA1257_ACAD9/	0.851	0.907	0.001	0.037
CDS2	0.73	PDK4	0.863	0.918	0.003	0.005
CDS2	0.73	ZRANB1	0.897	0.942	0	0.024
CDS2	0.73	SYNE2	0.748	0.848	0.045	0.003
CDS2	0.73	FBXL13	0.795	0.854	0.041	0.027
CDS2	0.73	HIST2H2BF_HIST2	0.855	0.928	0.003	0.003
CDS2	0.73	SPATA6	0.812	0.882	0.015	0.037
BPI	0.817	LGALS1	0.722	0.86	0.029	0.029
BPI	0.817	PHOSPHO1	0.721	0.885	0.022	0.013
BPI	0.817	HIST1H3J	0.898	0.955	0.001	0.031
BPI	0.817	NEK6_LOC1001290	0.671	0.852	0.037	0.01
BPI	0.817	ICAM1	0.675	0.861	0.04	0.005
BPI	0.817	PTGS1	0.675	0.861	0.047	0.004
BPI	0.817	HIST1H3C	0.863	0.933	0.007	0.018
BPI	0.817	CLC	0.782	0.896	0.015	0.049
BPI	0.817	MPO	0.508	0.914	0.001	0
BPI	0.817	NP	0.726	0.857	0.042	0.037
BPI	0.817	TAS2R31	0.833	0.906	0.015	0.05
BPI	0.817	KIAA0101_CSNK1G	0.736	0.886	0.045	0.003
CCR3	0.869	TMTC1	0.809	0.949	0.036	0.001
CCR3	0.869	FRMD3	0.755	0.909	0.025	0.008
CCR3	0.869	NA	0.868	0.944	0.005	0.047
CCR3	0.869	SAP30	0.911	0.955	0.017	0.021
CCR3	0.869	AREG	0.849	0.965	0.021	0.002
CCR3	0.869	DAAM2_LOC100131	0.903	0.961	0.016	0.037
CCR3	0.869	IRS2	0.817	0.939	0.019	0.013

CCR3	0.869	OR9A2	0.823	0.932	0.01	0.014
CCR3	0.869	ACPL2	0.906	0.963	0.014	0.035
CCR3	0.869	NF-E4	0.861	0.933	0.018	0.047
CCR3	0.869	KIAA1257_ACAD9/	0.851	0.942	0.02	0.012
CCR3	0.869	CCDC125	0.917	0.973	0.003	0.048
CCR3	0.869	PDK4	0.863	0.945	0.025	0.011
CCR3	0.869	RBP7	0.848	0.935	0.007	0.048
HSPC159	0.809	SLC39A9	0.776	0.887	0.003	0.045
HSPC159	0.809	GIMAP7	0.804	0.884	0.037	0.031
HSPC159	0.809	PHOSPHO1	0.721	0.896	0.047	0.002
HSPC159	0.809	SIAE	0.737	0.91	0.002	0.013
HSPC159	0.809	ITGA4_CERKL	0.88	0.961	0.001	0.013
HSPC159	0.809	EIF1AX_SCARNA9L	0.871	0.925	0.027	0.007
HSPC159	0.809	ZNF28	0.837	0.926	0.009	0.015
HSPC159	0.809	FSD1L_GARNL1	0.779	0.888	0.014	0.042
HSPC159	0.809	PTGS1	0.675	0.925	0.008	0
HSPC159	0.809	HIST1H3C	0.863	0.92	0.05	0.004
HSPC159	0.809	HIST1H3H	0.861	0.933	0.018	0.005
HSPC159	0.809	C7orf58	0.831	0.937	0.016	0.004
HSPC159	0.809	NP	0.726	0.893	0.011	0.004
PPP2R5A_SNORA16	0.953	SLC39A9	0.776	0.996	0.024	0
PPP2R5A_SNORA16	0.953	ANAPC11	0.943	0.996	0.033	0.009
PPP2R5A_SNORA16	0.953	INSIG1	0.957	0.999	0.018	0.028
PPP2R5A_SNORA16	0.953	HIST1H4L	0.961	0.996	0.034	0.028
PPP2R5A_SNORA16	0.953	C22orf37	0.924	0.993	0.026	0.011
PPP2R5A_SNORA16	0.953	VOPP1_LOC100128	0.938	0.992	0.026	0.016
PPP2R5A_SNORA16	0.953	PTGER2	0.881	0.99	0.046	0.002
PPP2R5A_SNORA16	0.953	PMS2CL_PMS2	0.942	1	0.019	0.015
PPP2R5A_SNORA16	0.953	IRF4	0.946	0.997	0.023	0.028

PPP2R5A_SNORA16	0.953	AMFR	0.867	0.987	0.05	0.004
PPP2R5A_SNORA16	0.953	HSP90AB1_HSP90A	0.924	0.996	0.027	0.01
PPP2R5A_SNORA16	0.953	ITGA4_CERKL	0.88	1	0.019	0.002
PPP2R5A_SNORA16	0.953	RRP12_LOC644215	0.904	0.99	0.047	0.006
PPP2R5A_SNORA16	0.953	TIMM10	0.949	0.989	0.03	0.031
PPP2R5A_SNORA16	0.953	FAM118A	0.882	0.99	0.048	0.005
PPP2R5A_SNORA16	0.953	IRF1	0.82	0.996	0.027	0
PPP2R5A_SNORA16	0.953	B4GALT3	0.917	0.999	0.019	0.013
PPP2R5A_SNORA16	0.953	CDC26	0.799	0.989	0.027	0
TMTC1	0.809	GIMAP7	0.804	0.911	0.007	0.011
TMTC1	0.809	LGALS1	0.722	0.896	0.002	0.009
TMTC1	0.809	DNAJC9_FAM149B1	0.944	0.983	0	0.042
TMTC1	0.809	HINT1	0.9	0.949	0.003	0.049
TMTC1	0.809	HLA-DPA1	0.796	0.898	0.006	0.035
TMTC1	0.809	NEK6_LOC1001290	0.671	0.855	0.033	0.007
TMTC1	0.809	GLT25D1	0.77	0.922	0	0.03
TMTC1	0.809	ITGA4_CERKL	0.88	0.946	0.001	0.048
TMTC1	0.809	ZNF28	0.837	0.916	0.005	0.034
TMTC1	0.809	KIAA0746	0.776	0.903	0.022	0.005
TMTC1	0.809	HIST1H3C	0.863	0.922	0.008	0.014
TMTC1	0.809	CD151	0.718	0.885	0.01	0.005
TMTC1	0.809	HIST1H3H	0.861	0.928	0.003	0.013
TMTC1	0.809	C7orf58	0.831	0.916	0.009	0.015
TMTC1	0.809	CTSL1_CTSLL3	0.676	0.879	0.047	0.003
TMTC1	0.809	NP	0.726	0.874	0.041	0.011
TMTC1	0.809	TMEM62_SPCS2_L	0.78	0.911	0.004	0.022
TMTC1	0.809	CDC26	0.799	0.897	0.005	0.048
TMTC1	0.809	TAS2R31	0.833	0.906	0.019	0.013
EAF2_HCG11_LOC	0.613	DNAJC9_FAM149B1	0.944	0.979	0	0.046

EAF2_HCG11_LOC	0.613	MTRR	0.674	0.861	0	0.002
EAF2_HCG11_LOC	0.613	P4HA1_RPL17	0.664	0.857	0	0
EAF2_HCG11_LOC	0.613	KLHL5	0.657	0.8	0.003	0.022
EAF2_HCG11_LOC	0.613	KIAA0746	0.776	0.899	0	0.006
EAF2_HCG11_LOC	0.613	NA	0.7	0.792	0.019	0.015
EAF2_HCG11_LOC	0.613	C7orf58	0.831	0.935	0	0.002
EAF2_HCG11_LOC	0.613	TMEM62_SPCS2_L	0.78	0.866	0	0.026
EAF2_HCG11_LOC	0.613	SDHC	0.736	0.801	0.006	0.033
RCBTB2_LOC10013	0.506	PDK4	0.863	0.933	0	0.038
RCBTB2_LOC10013	0.506	C7orf58	0.831	0.9	0	0.006
SEC24A_SAR1B	0.478	GIMAP7	0.804	0.889	0	0.043
SEC24A_SAR1B	0.478	MTRR	0.674	0.791	0	0.015
SEC24A_SAR1B	0.478	PMS2CL_PMS2	0.942	0.997	0	0.018
SEC24A_SAR1B	0.478	P4HA1_RPL17	0.664	0.763	0.001	0.028
SEC24A_SAR1B	0.478	KIAA0746	0.776	0.861	0	0.024
SEC24A_SAR1B	0.478	E2F6	0.787	0.823	0	0.038
SEC24A_SAR1B	0.478	SDHC	0.736	0.823	0	0.002
SH3PXD2B	0.9	LGALS2	0.922	0.976	0.019	0.048
SH3PXD2B	0.9	GALNT2	0.528	0.93	0.025	0
SH3PXD2B	0.9	GLT25D1	0.77	0.961	0.017	0.006
KLRD1	0.731	CCR1	0.693	0.808	0.047	0.012
KLRD1	0.731	PDE3B	0.567	0.799	0.035	0.007
KLRD1	0.731	NA	0.682	0.84	0.018	0.006
KLRD1	0.731	DLEU2_DLEU2L	0.711	0.86	0.001	0.017
KLRD1	0.731	ZNF587_ZNF417	0.632	0.828	0.009	0.005
KLRD1	0.731	SYNE2	0.748	0.904	0	0.019
KLRD1	0.731	PLEKHF2	0.667	0.808	0.041	0.041
KLRD1	0.731	LOC100128751	0.686	0.814	0.03	0.05
CHI3L1	0.722	OCR1	0.896	0.966	0	0.045

CHI3L1	0.722	DPH3	0.749	0.833	0.032	0.041
CHI3L1	0.722	NF-E4	0.861	0.97	0	0.006
CHI3L1	0.722	DLEU2_DLEU2L	0.711	0.82	0.032	0.022
CHI3L1	0.722	THBS1	0.849	0.916	0.001	0.038
CHI3L1	0.722	ZNF587_ZNF417	0.632	0.816	0.03	0.002
CHI3L1	0.722	SYNE2	0.748	0.888	0.003	0.004
CHI3L1	0.722	FBXL13	0.795	0.9	0.002	0.025
CHI3L1	0.722	HIST2H2BF_HIST2	0.855	0.932	0	0.047
FRMD3	0.755	SLC39A9	0.776	0.884	0.007	0.009
FRMD3	0.755	LGALS1	0.722	0.83	0.05	0.014
FRMD3	0.755	HINT1	0.9	0.926	0.003	0.048
FRMD3	0.755	HIST1H3J	0.898	0.93	0.002	0.027
FRMD3	0.755	HLA-DPA1	0.796	0.883	0.009	0.012
FRMD3	0.755	AMFR	0.867	0.96	0	0.006
FRMD3	0.755	RPL17_SNORD58B	0.917	0.952	0.001	0.022
FRMD3	0.755	ITGA4_CERKL	0.88	0.951	0	0.01
FRMD3	0.755	EIF1AX_SCARNA9L	0.871	0.907	0.003	0.026
FRMD3	0.755	ZNF28	0.837	0.913	0.005	0.007
FRMD3	0.755	HIST1H3B	0.89	0.934	0.002	0.019
FRMD3	0.755	FSD1L_GARNL1	0.779	0.877	0.028	0.005
FRMD3	0.755	HIST1H3C	0.863	0.891	0.027	0.011
FRMD3	0.755	HIST1H3H	0.861	0.897	0.017	0.01
FRMD3	0.755	S100B	0.841	0.877	0.019	0.041
FRMD3	0.755	IGK@_IGKC_IGKV	0.855	0.909	0.006	0.028
FRMD3	0.755	SON	0.856	0.926	0.001	0.015
FRMD3	0.755	TNFRSF17	0.875	0.922	0.003	0.041
FRMD3	0.755	CDC26	0.799	0.904	0.001	0.012
SLC39A9	0.776	NA	0.927	0.973	0	0.023
SLC39A9	0.776	EIF2AK2	0.964	0.997	0	0.037

SLC39A9	0.776	NA	0.868	0.944	0.001	0.008
SLC39A9	0.776	GPR65	0.736	0.898	0.011	0
SLC39A9	0.776	OR9A2	0.823	0.883	0.02	0.027
SLC39A9	0.776	ACPL2	0.906	0.97	0	0.039
SLC39A9	0.776	ERGIC1	0.886	0.949	0	0.029
SLC39A9	0.776	NF-E4	0.861	0.919	0.008	0.007
SLC39A9	0.776	HAL	0.942	0.982	0	0.05
SLC39A9	0.776	KIAA1257_ACAD9/	0.851	0.951	0	0.001
SLC39A9	0.776	CCDC125	0.917	0.984	0	0.006
SLC39A9	0.776	PDK4	0.863	0.971	0	0
SLC39A9	0.776	THBS1	0.849	0.905	0.008	0.019
SLC39A9	0.776	ZRANB1	0.897	0.965	0	0.003
SLC39A9	0.776	MPZL3	0.892	0.956	0	0.046
SLC39A9	0.776	ZNF587_ZNF417	0.632	0.906	0.019	0
SLC39A9	0.776	CYP4F3_CYP4F2	0.901	0.956	0.001	0.022
SLC39A9	0.776	SYNE2	0.748	0.921	0.011	0
SLC39A9	0.776	MME	0.894	0.931	0.005	0.017
SLC39A9	0.776	CPM	0.854	0.915	0.005	0.025
SLC39A9	0.776	FBXL13	0.795	0.888	0.048	0.001
SLC39A9	0.776	HIST2H2BF_HIST2	0.855	0.928	0.006	0.007
SLC39A9	0.776	SPATA6	0.812	0.921	0.006	0.003
GIMAP7	0.804	NA	0.927	0.996	0	0.016
GIMAP7	0.804	NA	0.868	0.973	0	0.006
GIMAP7	0.804	GPR65	0.736	0.947	0	0
GIMAP7	0.804	OR9A2	0.823	0.896	0.012	0.023
GIMAP7	0.804	LRRFIP1	0.678	0.914	0.012	0
GIMAP7	0.804	CCDC125	0.917	0.991	0	0.015
GIMAP7	0.804	PDK4	0.863	0.968	0	0.003
GIMAP7	0.804	ZRANB1	0.897	0.968	0	0.015

GIMAP7	0.804	CYP4F3_CYP4F2	0.901	0.955	0.003	0.04
GIMAP7	0.804	SYNE2	0.748	0.939	0.001	0
GIMAP7	0.804	MME	0.894	0.956	0.003	0.017
GIMAP7	0.804	PLIN2	0.706	0.899	0.021	0.001
GIMAP7	0.804	FBXL13	0.795	0.898	0.046	0.007
GIMAP7	0.804	PPP1R2_PPP1R2P3	0.702	0.945	0.001	0
ANAPC11	0.943	NA	0.927	0.992	0.026	0.007
ANAPC11	0.943	SAP30	0.911	0.979	0.046	0.026
ANAPC11	0.943	ERGIC1	0.886	0.98	0.048	0.011
ANAPC11	0.943	HAL	0.942	0.984	0.024	0.033
ANAPC11	0.943	CCDC125	0.917	0.981	0.041	0.013
ANAPC11	0.943	MPZL3	0.892	0.974	0.024	0.008
ANAPC11	0.943	RGS2	0.915	0.975	0.023	0.023
NA	0.927	DNAJC9_FAM149B1	0.944	0.988	0.016	0.04
NA	0.927	LGALS2	0.922	0.979	0.032	0.015
NA	0.927	MTRR	0.674	0.974	0.021	0
NA	0.927	HLA-DPA1	0.796	0.979	0.012	0
NA	0.927	PTGER2	0.881	0.97	0.017	0.021
NA	0.927	PMS2CL_PMS2	0.942	0.997	0.01	0.021
NA	0.927	TRAF3	0.87	0.989	0.013	0.006
NA	0.927	AMFR	0.867	0.963	0.029	0.026
NA	0.927	RPL17_SNORD58B	0.917	0.988	0.039	0.007
NA	0.927	HSP90AB1_HSP90A	0.924	0.996	0.014	0.013
NA	0.927	ITGA4_CERKL	0.88	0.99	0.006	0.007
NA	0.927	CD300A	0.841	0.954	0.04	0.007
NA	0.927	P4HA1_RPL17	0.664	0.97	0.048	0
NA	0.927	KLHL5	0.657	0.981	0.042	0
NA	0.927	MGST3	0.857	0.975	0.028	0.002
NA	0.927	KIAA0746	0.776	0.993	0.019	0

NA	0.927	CCR4	0.871	0.989	0.028	0.003
NA	0.927	ABCG1	0.85	0.965	0.039	0.003
NA	0.927	FAM118A	0.882	0.974	0.022	0.02
NA	0.927	IGK@_IGKC_IGKV	0.855	0.992	0.025	0.001
NA	0.927	IRF1	0.82	0.965	0.016	0.003
NA	0.927	C7orf58	0.831	0.989	0.037	0
NA	0.927	B4GALT3	0.917	0.984	0.008	0.039
NA	0.927	TNFRSF17	0.875	0.984	0.043	0.001
NA	0.927	DCTN5	0.722	0.975	0.015	0
INSIG1	0.957	PRR13_PCBP2	0.947	0.993	0.04	0.015
INSIG1	0.957	MTHFS	0.933	0.999	0.024	0.019
INSIG1	0.957	EIF2AK2	0.964	0.999	0.028	0.033
INSIG1	0.957	CDA	0.945	0.996	0.042	0.015
INSIG1	0.957	GAB2	0.969	0.996	0.033	0.045
INSIG1	0.957	HAL	0.942	0.994	0.037	0.011
INSIG1	0.957	MPZL3	0.892	0.993	0.027	0.003
INSIG1	0.957	RGS2	0.915	0.997	0.023	0.003
FOLR3_FOLR2	0.78	HIST1H3J	0.898	0.943	0.001	0.05
FOLR3_FOLR2	0.78	HIST1H3A	0.908	0.962	0.001	0.015
FOLR3_FOLR2	0.78	GLT25D1	0.77	0.926	0.002	0.012
FOLR3_FOLR2	0.78	HIST1H3B	0.89	0.943	0.001	0.05
FOLR3_FOLR2	0.78	HIST1H3C	0.863	0.915	0.013	0.02
FOLR3_FOLR2	0.78	HIST1H3H	0.861	0.92	0.006	0.023
PRR13_PCBP2	0.947	LGALS2	0.922	0.989	0.035	0.003
PRR13_PCBP2	0.947	C22orf37	0.924	0.985	0.024	0.021
PRR13_PCBP2	0.947	VOPP1_LOC100128	0.938	0.981	0.028	0.017
PRR13_PCBP2	0.947	PMS2CL_PMS2	0.942	0.992	0.019	0.019
PRR13_PCBP2	0.947	IRF4	0.946	0.994	0.015	0.032
PRR13_PCBP2	0.947	HSP90AB1_HSP90A	0.924	0.988	0.05	0.007

PRR13_PCBP2	0.947	CD300A	0.841	0.985	0.038	0
PRR13_PCBP2	0.947	RRP12_LOC644215	0.904	0.989	0.025	0.008
PRR13_PCBP2	0.947	TIMM10	0.949	0.993	0.017	0.022
PRR13_PCBP2	0.947	IRF1	0.82	0.985	0.042	0
PRR13_PCBP2	0.947	LASS4	0.924	0.979	0.018	0.041
PRR13_PCBP2	0.947	B4GALT3	0.917	0.991	0.024	0.014
PRR13_PCBP2	0.947	CDC26	0.799	0.982	0.035	0
PRR13_PCBP2	0.947	IGL@_IGLV1-44_	0.953	0.992	0.018	0.033
HIST1H4L	0.961	SAP30	0.911	0.988	0.018	0.036
HIST1H4L	0.961	IRS2	0.817	0.985	0.023	0.002
HIST1H4L	0.961	ERGIC1	0.886	0.98	0.048	0.026
HIST1H4L	0.961	MPZL3	0.892	0.979	0.027	0.012
HIST1H4L	0.961	MYL9	0.641	0.992	0.038	0
HIST1H4L	0.961	RBP7	0.848	0.992	0.038	0
HIST1H4L	0.961	RGS2	0.915	0.985	0.017	0.022
LGALS1	0.722	RETN	0.694	0.851	0.014	0.011
LGALS1	0.722	GPR65	0.736	0.853	0.015	0.011
LGALS1	0.722	OR9A2	0.823	0.888	0.004	0.028
LGALS1	0.722	KCNMA1	0.707	0.825	0.037	0.007
LGALS1	0.722	PDK4	0.863	0.948	0	0.003
LGALS1	0.722	LHFP	0.731	0.814	0.032	0.039
LGALS1	0.722	FABP2	0.744	0.832	0.05	0.023
LGALS1	0.722	RBP7	0.848	0.902	0.002	0.039
CCR1	0.693	MTRR	0.674	0.854	0.005	0.012
CCR1	0.693	P4HA1_RPL17	0.664	0.824	0.017	0.012
CCR1	0.693	KLHL5	0.657	0.808	0.019	0.044
CCR1	0.693	LAIR1_LAIR2	0.607	0.802	0.043	0.014
CCR1	0.693	PYHIN1	0.686	0.805	0.021	0.022
CCR1	0.693	C7orf58	0.831	0.939	0	0.004

CCR1	0.693	SDHC	0.736	0.834	0.04	0.008
CCR1	0.693	NFXL1	0.728	0.827	0.013	0.039
TPST1	0.92	PHOSPHO1	0.721	0.985	0.047	0
TPST1	0.92	HIST1H3J	0.898	0.979	0.046	0.008
TPST1	0.92	HIST1H3A	0.908	0.979	0.039	0.018
TPST1	0.92	TYMS	0.863	0.957	0.037	0.042
TPST1	0.92	ABCG1	0.85	0.966	0.043	0.018
TPST1	0.92	HIST1H3B	0.89	0.981	0.037	0.013
TPST1	0.92	TNFRSF17	0.875	0.964	0.036	0.035
HLA-DRA	0.855	NA	0.868	0.946	0.009	0.04
HLA-DRA	0.855	GPR65	0.736	0.911	0.022	0.001
HLA-DRA	0.855	ACPL2	0.906	0.96	0.031	0.01
HLA-DRA	0.855	KIAA1257_ACAD9/	0.851	0.937	0.042	0.011
HLA-DRA	0.855	PDK4	0.863	0.985	0.005	0.001
HLA-DRA	0.855	PLIN2	0.706	0.965	0.024	0
FFAR2	0.637	LAIR1_LAIR2	0.607	0.759	0.021	0.029
FFAR2	0.637	C7orf58	0.831	0.905	0	0.045
PHOSPHO1	0.721	ABCA13	0.743	0.895	0.003	0.005
PHOSPHO1	0.721	DAAM2_LOC100131	0.903	0.986	0	0.016
PHOSPHO1	0.721	IRS2	0.817	0.96	0	0.015
PHOSPHO1	0.721	DPH3	0.749	0.886	0.004	0.003
PHOSPHO1	0.721	NF-E4	0.861	0.926	0.001	0.049
PHOSPHO1	0.721	DLEU2_DLEU2L	0.711	0.819	0.044	0.02
PHOSPHO1	0.721	THBS1	0.849	0.952	0	0.003
PHOSPHO1	0.721	MYL9	0.641	0.832	0.023	0.008
PHOSPHO1	0.721	FBXL13	0.795	0.898	0.005	0.019
PHOSPHO1	0.721	RBP7	0.848	0.942	0	0.018
PHOSPHO1	0.721	CALM2_C2orf61	0.749	0.895	0.004	0.001
PPIF	0.934	MTHFS	0.933	0.997	0.048	0.021

MTHFS	0.933	DNAJC9_FAM149B1	0.944	0.992	0.032	0.023
MTHFS	0.933	LGALS2	0.922	0.994	0.031	0.003
MTHFS	0.933	C22orf37	0.924	0.979	0.033	0.042
MTHFS	0.933	PTGER2	0.881	0.979	0.043	0.004
MTHFS	0.933	PMS2CL_PMS2	0.942	0.994	0.028	0.012
MTHFS	0.933	HSP90AB1_HSP90A	0.924	0.996	0.026	0.01
MTHFS	0.933	CD300A	0.841	0.97	0.029	0.002
MTHFS	0.933	MGST3	0.857	0.996	0.021	0.001
MTHFS	0.933	RRP12_LOC644215	0.904	0.989	0.022	0.011
MTHFS	0.933	TIMM10	0.949	0.993	0.022	0.027
MTHFS	0.933	FAM118A	0.882	0.982	0.049	0.009
MTHFS	0.933	IRF1	0.82	0.988	0.031	0
MTHFS	0.933	B4GALT3	0.917	0.984	0.03	0.029
MTHFS	0.933	ATP6V0D1_LOC100	0.567	0.969	0.01	0
MTHFS	0.933	CDC26	0.799	0.972	0.031	0
DNAJC9_FAM149B1	0.944	EIF2AK2	0.964	0.997	0.023	0.044
DNAJC9_FAM149B1	0.944	NA	0.868	0.98	0.035	0.002
DNAJC9_FAM149B1	0.944	HIST1H2AA	0.903	0.974	0.035	0.018
DNAJC9_FAM149B1	0.944	GPR65	0.736	0.975	0.048	0
DNAJC9_FAM149B1	0.944	ACPL2	0.906	0.988	0.024	0.022
DNAJC9_FAM149B1	0.944	LRRFIP1	0.678	0.983	0.041	0
DNAJC9_FAM149B1	0.944	TRIM21	0.538	0.974	0.049	0
DNAJC9_FAM149B1	0.944	HAL	0.942	0.989	0.021	0.037
DNAJC9_FAM149B1	0.944	CCDC125	0.917	0.991	0.016	0.016
DNAJC9_FAM149B1	0.944	PDK4	0.863	0.996	0.02	0.001
DNAJC9_FAM149B1	0.944	ZRANB1	0.897	0.988	0.018	0.006
DNAJC9_FAM149B1	0.944	MPZL3	0.892	0.974	0.03	0.024
DNAJC9_FAM149B1	0.944	CYP4F3_CYP4F2	0.901	0.991	0.027	0.017
DNAJC9_FAM149B1	0.944	SYNE2	0.748	0.986	0.023	0

DNAJC9_FAM149B1	0.944	RBP7	0.848	0.984	0.036	0.001
DNAJC9_FAM149B1	0.944	RGS2	0.915	0.98	0.019	0.025
DNAJC9_FAM149B1	0.944	PPP1R2_PPP1R2P3	0.702	0.981	0.047	0
DNAJC9_FAM149B1	0.944	HIST2H2BF_HIST2	0.855	0.992	0.03	0.002
LCN2	0.653	HIST1H2AJ_HIST1	0.77	0.82	0.033	0.005
LCN2	0.653	HIST1H3C	0.863	0.924	0	0.048
LCN2	0.653	MPO	0.508	0.74	0.012	0.001
EIF2AK2	0.964	LGALS2	0.922	0.99	0.048	0.006
EIF2AK2	0.964	VOPP1_LOC100128	0.938	0.993	0.03	0.019
EIF2AK2	0.964	PTGER2	0.881	0.997	0.037	0.002
EIF2AK2	0.964	PMS2CL_PMS2	0.942	1	0.032	0.015
EIF2AK2	0.964	TRAF3	0.87	0.995	0.048	0.004
EIF2AK2	0.964	IRF4	0.946	1	0.032	0.023
EIF2AK2	0.964	HSP90AB1_HSP90A	0.924	0.999	0.031	0.01
EIF2AK2	0.964	ITGA4_CERKL	0.88	0.998	0.037	0.002
EIF2AK2	0.964	CD300A	0.841	0.997	0.035	0
EIF2AK2	0.964	TRIM21	0.538	0.993	0.042	0
EIF2AK2	0.964	KIAA0746	0.776	0.996	0.044	0
EIF2AK2	0.964	TIMM10	0.949	0.997	0.034	0.019
EIF2AK2	0.964	IGK@_IGKC_IGKV	0.855	0.994	0.043	0.001
EIF2AK2	0.964	IRF1	0.82	0.999	0.032	0
EIF2AK2	0.964	B4GALT3	0.917	1	0.032	0.012
EIF2AK2	0.964	DCTN5	0.722	0.99	0.035	0
LGALS2	0.922	HIST1H2AA	0.903	0.977	0.013	0.009
LGALS2	0.922	ACPL2	0.906	0.961	0.045	0.041
LGALS2	0.922	ERGIC1	0.886	0.961	0.021	0.037
LGALS2	0.922	CCDC125	0.917	0.974	0.009	0.027
LGALS2	0.922	ZRANB1	0.897	0.971	0.016	0.007
LGALS2	0.922	MPZL3	0.892	0.974	0.003	0.02

LGALS2	0.922	KDM6B_TMEM88	0.869	0.971	0.019	0.019
LGALS2	0.922	RBP7	0.848	0.958	0.048	0.001
LGALS2	0.922	RGS2	0.915	0.978	0.004	0.03
SIAE	0.737	GPR65	0.736	0.844	0.048	0.032
SIAE	0.737	PDK4	0.863	0.924	0.005	0.024
AP3B2	0.756	HIST1H3J	0.898	0.926	0.005	0.01
AP3B2	0.756	HIST1H3A	0.908	0.944	0.002	0.002
AP3B2	0.756	GLT25D1	0.77	0.875	0.036	0.027
AP3B2	0.756	HIST1H2BM	0.891	0.928	0.004	0.018
AP3B2	0.756	HIST1H3B	0.89	0.924	0.006	0.006
AP3B2	0.756	HIST1H3C	0.863	0.895	0.03	0.006
AP3B2	0.756	HIST1H3H	0.861	0.903	0.021	0.005
AP3B2	0.756	APOLD1	0.871	0.924	0.003	0.012
AP3B2	0.756	C7orf58	0.831	0.886	0.028	0.05
AP3B2	0.756	CDC26	0.799	0.859	0.04	0.05
ABCA13	0.743	HIST1H3J	0.898	0.962	0	0.002
ABCA13	0.743	AGTRAP	0.611	0.811	0.049	0.003
ABCA13	0.743	HIST1H3A	0.908	0.97	0	0.006
ABCA13	0.743	CENPK	0.834	0.879	0.029	0.036
ABCA13	0.743	HIST1H3B	0.89	0.978	0	0.004
ABCA13	0.743	HIST1H3C	0.863	0.933	0.003	0.002
ABCA13	0.743	HIST1H3H	0.861	0.934	0.001	0.004
ABCA13	0.743	TPX2	0.635	0.833	0.035	0.002
ABCA13	0.743	MPO	0.508	0.853	0.028	0
ABCA13	0.743	KIAA0101_CSNK1G	0.736	0.875	0.018	0.001
NA	0.868	HINT1	0.9	0.956	0.025	0.013
NA	0.868	HLA-DPA1	0.796	0.951	0.009	0.001
NA	0.868	PMS2CL_PMS2	0.942	0.984	0.001	0.039
NA	0.868	SULF2	0.591	0.931	0.033	0

NA	0.868	TRAF3	0.87	0.993	0.001	0.004
NA	0.868	IRF4	0.946	0.996	0.001	0.035
NA	0.868	RPL17_SNORD58B	0.917	0.947	0.047	0.02
NA	0.868	HSP90AB1_HSP90A	0.924	0.996	0.001	0.01
NA	0.868	ITGA4_CERKL	0.88	0.981	0.002	0.002
NA	0.868	CD300A	0.841	0.928	0.011	0.023
NA	0.868	MGST3	0.857	0.941	0.014	0.023
NA	0.868	KIAA0746	0.776	0.969	0.011	0
NA	0.868	CCR4	0.871	0.965	0.015	0.001
NA	0.868	ABCG1	0.85	0.947	0.005	0.018
NA	0.868	FAM118A	0.882	0.947	0.025	0.025
NA	0.868	IGK@_IGKC_IGKV	0.855	0.957	0.03	0.001
NA	0.868	IRF1	0.82	0.932	0.013	0.008
NA	0.868	TNFRSF17	0.875	0.958	0.024	0.002
NA	0.868	DCTN5	0.722	0.947	0.041	0
EFCAB2	0.773	AIG1	0.56	0.829	0.029	0.001
EFCAB2	0.773	HS2ST1_UBA2	0.668	0.829	0.012	0.048
EFCAB2	0.773	NEK6_LOC1001290	0.671	0.832	0.021	0.04
EFCAB2	0.773	MINPP1	0.7	0.857	0.038	0.005
EFCAB2	0.773	C15orf54	0.72	0.875	0.004	0.007
EFCAB2	0.773	PTGS1	0.675	0.855	0.011	0.012
EFCAB2	0.773	E2F6	0.787	0.882	0.021	0.012
EFCAB2	0.773	CD151	0.718	0.843	0.036	0.031
EFCAB2	0.773	TPX2	0.635	0.823	0.037	0.009
EFCAB2	0.773	HIST1H2BJ	0.703	0.854	0.042	0.022
EFCAB2	0.773	C7orf58	0.831	0.937	0.003	0.004
EFCAB2	0.773	NP	0.726	0.862	0.008	0.043
EFCAB2	0.773	SDHC	0.736	0.899	0.014	0.001
EFCAB2	0.773	NFXL1	0.728	0.865	0.048	0.006

EFCAB2	0.773	KIAA0101_CSNK1G	0.736	0.872	0.009	0.01
HIST1H2AA	0.903	C22orf37	0.924	0.978	0.006	0.015
HIST1H2AA	0.903	IRF4	0.946	0.98	0.01	0.047
HIST1H2AA	0.903	HSP90AB1_HSP90A	0.924	0.964	0.032	0.043
HIST1H2AA	0.903	TYMS	0.863	0.959	0.041	0.002
HIST1H2AA	0.903	RRP12_LOC644215	0.904	0.959	0.029	0.03
HINT1	0.9	GPR65	0.736	0.95	0.035	0
HINT1	0.9	OCR1	0.896	0.978	0.008	0.042
HINT1	0.9	KIAA1257_ACAD9/	0.851	0.932	0.049	0.04
HINT1	0.9	PDK4	0.863	0.978	0.014	0.002
HINT1	0.9	ZRANB1	0.897	0.963	0.014	0.035
HINT1	0.9	CYP4F3_CYP4F2	0.901	0.978	0.008	0.046
HINT1	0.9	SYNE2	0.748	0.962	0.006	0
HINT1	0.9	MME	0.894	0.971	0.018	0.034
HINT1	0.9	PLIN2	0.706	0.938	0.049	0
HINT1	0.9	RBP7	0.848	0.963	0.005	0.013
HINT1	0.9	PPP1R2_PPP1R2P3	0.702	0.953	0.033	0
HIST1H3J	0.898	PCOLCE2	0.567	0.925	0.008	0
HIST1H3J	0.898	AREG	0.849	0.961	0.003	0.007
HIST1H3J	0.898	DAAM2_LOC100131	0.903	0.977	0.003	0.023
HIST1H3J	0.898	IRS2	0.817	0.955	0.005	0.009
HIST1H3J	0.898	OR9A2	0.823	0.943	0.03	0.004
HIST1H3J	0.898	KCNMA1	0.707	0.93	0.032	0
HIST1H3J	0.898	DPH3	0.749	0.951	0.045	0
HIST1H3J	0.898	NF-E4	0.861	0.957	0.027	0.01
HIST1H3J	0.898	THBS1	0.849	0.956	0.026	0.003
HIST1H3J	0.898	LHFP	0.731	0.928	0.044	0.001
HIST1H3J	0.898	ZRANB1	0.897	0.964	0.023	0.018
HIST1H3J	0.898	FABP2	0.744	0.928	0.026	0.001

HIST1H3J	0.898	MYL9	0.641	0.952	0.01	0
HIST1H3J	0.898	RBP7	0.848	0.973	0.002	0.004
HIST1H3J	0.898	HIST2H2BF_HIST2	0.855	0.939	0.048	0.028
HIST1H3J	0.898	CALM2_C2orf61	0.749	0.953	0.041	0
CDA	0.945	C22orf37	0.924	0.986	0.05	0.015
CDA	0.945	VOPP1_LOC100128	0.938	0.985	0.014	0.025
CDA	0.945	PMS2CL_PMS2	0.942	0.998	0.022	0.017
CDA	0.945	HSP90AB1_HSP90A	0.924	0.997	0.02	0.011
CDA	0.945	MGST3	0.857	0.989	0.031	0.001
CDA	0.945	RRP12_LOC644215	0.904	0.996	0.022	0.006
CDA	0.945	TIMM10	0.949	0.986	0.031	0.033
CDA	0.945	IRF1	0.82	0.994	0.033	0
CDA	0.945	LASS4	0.924	0.993	0.018	0.019
CDA	0.945	B4GALT3	0.917	0.992	0.031	0.012
CDA	0.945	CDC26	0.799	0.981	0.04	0
SAP30	0.911	C22orf37	0.924	0.976	0.017	0.035
SAP30	0.911	TYMS	0.863	0.972	0.047	0.001
SAP30	0.911	ABCG1	0.85	0.978	0.014	0.005
SAP30	0.911	TIMM10	0.949	0.98	0.036	0.034
SAP30	0.911	B4GALT3	0.917	0.976	0.036	0.02
AGTRAP	0.611	HIST1H3A	0.908	0.93	0	0.03
AGTRAP	0.611	RBP7	0.848	0.926	0	0.007
MTRR	0.674	LRRFIP1	0.678	0.848	0.002	0.004
MTRR	0.674	DLEU2_DLEU2L	0.711	0.813	0.005	0.045
MTRR	0.674	PDK4	0.863	0.953	0	0.017
MTRR	0.674	ZNF587_ZNF417	0.632	0.807	0.009	0.007
MTRR	0.674	PLEKHF2	0.667	0.807	0.018	0.021
MTRR	0.674	IL1RL1	0.738	0.842	0.006	0.026
MTRR	0.674	AIF1	0.618	0.788	0.027	0.024

MTRR	0.674	PPP1R2_PPP1R2P3	0.702	0.836	0.003	0.032
PCOLCE2	0.567	HIST1H3A	0.908	0.936	0	0.025
PCOLCE2	0.567	HIST1H2BM	0.891	0.924	0	0.023
PCOLCE2	0.567	HIST1H3B	0.89	0.916	0	0.012
PCOLCE2	0.567	HIST1H3C	0.863	0.894	0	0.011
PCOLCE2	0.567	HIST1H3H	0.861	0.898	0	0.011
PCOLCE2	0.567	CMTM5	0.671	0.738	0.05	0.033
HS2ST1_UBA2	0.668	KCNMA1	0.707	0.808	0.019	0.039
HS2ST1_UBA2	0.668	DLEU2_DLEU2L	0.711	0.806	0.04	0.017
HS2ST1_UBA2	0.668	PDK4	0.863	0.914	0	0.049
HS2ST1_UBA2	0.668	SYNE2	0.748	0.848	0.005	0.033
HS2ST1_UBA2	0.668	FBXL13	0.795	0.857	0.005	0.033
HIST1H3A	0.908	AREG	0.849	0.967	0.005	0.005
HIST1H3A	0.908	DAAM2_LOC100131	0.903	0.98	0.004	0.027
HIST1H3A	0.908	IRS2	0.817	0.961	0.003	0.007
HIST1H3A	0.908	ACPL2	0.906	0.967	0.014	0.043
HIST1H3A	0.908	DPH3	0.749	0.958	0.039	0
HIST1H3A	0.908	NF-E4	0.861	0.959	0.019	0.01
HIST1H3A	0.908	DLEU2_DLEU2L	0.711	0.965	0.032	0
HIST1H3A	0.908	PDK4	0.863	0.949	0.035	0.02
HIST1H3A	0.908	THBS1	0.849	0.966	0.036	0.001
HIST1H3A	0.908	LHFP	0.731	0.94	0.028	0
HIST1H3A	0.908	ZRANB1	0.897	0.961	0.028	0.024
HIST1H3A	0.908	FABP2	0.744	0.943	0.041	0
HIST1H3A	0.908	MYL9	0.641	0.946	0.046	0
HIST1H3A	0.908	RBP7	0.848	0.966	0.006	0.007
HIST1H3A	0.908	HIST2H2BF_HIST2	0.855	0.955	0.048	0.009
C22orf37	0.924	ERGIC1	0.886	0.978	0.047	0.008
C22orf37	0.924	HAL	0.942	0.988	0.024	0.01

C22orf37	0.924	CCDC125	0.917	0.984	0.033	0.006
C22orf37	0.924	MPZL3	0.892	0.973	0.007	0.014
C22orf37	0.924	RGS2	0.915	0.975	0.028	0.011
HLA-DPA1	0.796	GPR65	0.736	0.9	0.031	0
HLA-DPA1	0.796	OR9A2	0.823	0.889	0.028	0.029
HLA-DPA1	0.796	KIAA1257_ACAD9/	0.851	0.914	0.002	0.035
HLA-DPA1	0.796	PDK4	0.863	0.966	0.001	0.001
HLA-DPA1	0.796	THBS1	0.849	0.895	0.022	0.047
HLA-DPA1	0.796	PLIN2	0.706	0.892	0.04	0.001
HLA-DPA1	0.796	HIST2H2BF_HIST2	0.855	0.912	0.019	0.029
VOPP1_LOC100128	0.938	HAL	0.942	0.98	0.033	0.012
VOPP1_LOC100128	0.938	MPZL3	0.892	0.981	0.021	0.005
VOPP1_LOC100128	0.938	RGS2	0.915	0.985	0.019	0.006
SLC39A8	0.825	GPR65	0.736	0.917	0.007	0.005
SLC39A8	0.825	PDK4	0.863	0.935	0.01	0.036
SLC39A8	0.825	SPATA6	0.812	0.894	0.013	0.035
MKI67	0.621	HIST1H3C	0.863	0.897	0	0.021
AREG	0.849	GLT25D1	0.77	0.918	0.024	0.011
AREG	0.849	CD300A	0.841	0.905	0.039	0.025
AREG	0.849	ZNF28	0.837	0.915	0.041	0.023
AREG	0.849	HIST1H2BM	0.891	0.947	0.009	0.045
AREG	0.849	HIST1H3B	0.89	0.949	0.017	0.006
AREG	0.849	HIST1H3C	0.863	0.942	0.032	0.001
AREG	0.849	HIST1H3H	0.861	0.951	0.017	0.001
AREG	0.849	APOLD1	0.871	0.937	0.016	0.033
AREG	0.849	CLC	0.782	0.937	0.026	0.002
AREG	0.849	CDC26	0.799	0.912	0.036	0.011
DAAM2_LOC100131	0.903	GLT25D1	0.77	0.965	0.033	0.002
DAAM2_LOC100131	0.903	CD300A	0.841	0.958	0.032	0.003

DAAM2_LOC100131	0.903	TYMS	0.863	0.965	0.012	0.014
DAAM2_LOC100131	0.903	RRP12_LOC644215	0.904	0.969	0.022	0.048
DAAM2_LOC100131	0.903	HIST1H2BM	0.891	0.971	0.021	0.026
DAAM2_LOC100131	0.903	ABCG1	0.85	0.977	0.022	0.006
DAAM2_LOC100131	0.903	HIST1H3B	0.89	0.986	0.018	0.004
DAAM2_LOC100131	0.903	APOLD1	0.871	0.971	0.019	0.008
DAAM2_LOC100131	0.903	SON	0.856	0.955	0.036	0.022
DAAM2_LOC100131	0.903	IRF1	0.82	0.946	0.014	0.008
DAAM2_LOC100131	0.903	TNFRSF17	0.875	0.968	0.019	0.012
DAAM2_LOC100131	0.903	CDC26	0.799	0.965	0.023	0.001
DAAM2_LOC100131	0.903	GLDC	0.714	0.966	0.042	0
TREML1	0.634	CENPK	0.834	0.88	0	0.049
TREML1	0.634	MINPP1	0.7	0.795	0.017	0.044
TREML1	0.634	ITGA2B	0.58	0.827	0	0.002
TREML1	0.634	HIST1H2AJ_HIST1	0.77	0.803	0.039	0.01
TREML1	0.634	PTGS1	0.675	0.909	0	0.001
TREML1	0.634	HIST1H3C	0.863	0.916	0	0.017
TREML1	0.634	E2F6	0.787	0.856	0.001	0.033
TREML1	0.634	HIST1H3H	0.861	0.936	0	0.015
TREML1	0.634	HIST1H2BJ	0.703	0.838	0.001	0.03
TREML1	0.634	RPIA	0.601	0.761	0.049	0.022
TREML1	0.634	CMTM5	0.671	0.828	0	0.045
TREML1	0.634	SDHC	0.736	0.814	0.005	0.044
TREML1	0.634	KIAA0101_CSNK1G	0.736	0.836	0.001	0.02
PTGER2	0.881	GPR65	0.736	0.96	0.032	0
PTGER2	0.881	ACPL2	0.906	0.969	0.012	0.032
PTGER2	0.881	HAL	0.942	0.976	0.006	0.039
PTGER2	0.881	CCDC125	0.917	0.968	0.011	0.021
PTGER2	0.881	PDK4	0.863	0.976	0.011	0.001

PTGER2	0.881	ZRANB1	0.897	0.973	0.012	0.003
PTGER2	0.881	MPZL3	0.892	0.962	0.002	0.05
PTGER2	0.881	RBP7	0.848	0.942	0.05	0.006
PTGER2	0.881	RGS2	0.915	0.974	0.003	0.021
CEACAM8	0.647	HIST1H2AJ_HIST1	0.77	0.823	0.019	0.006
CEACAM8	0.647	DEFA4_DEFA8P	0.481	0.824	0.004	0
CEACAM8	0.647	MPO	0.508	0.732	0	0
PMS2CL_PMS2	0.942	ACPL2	0.906	0.999	0.017	0.007
PMS2CL_PMS2	0.942	ERGIC1	0.886	0.98	0.043	0.012
PMS2CL_PMS2	0.942	HAL	0.942	0.992	0.015	0.019
PMS2CL_PMS2	0.942	CCDC125	0.917	0.996	0.016	0.008
PMS2CL_PMS2	0.942	PDK4	0.863	0.991	0.041	0.001
PMS2CL_PMS2	0.942	ZRANB1	0.897	0.995	0.022	0.002
PMS2CL_PMS2	0.942	MPZL3	0.892	0.983	0.015	0.007
PMS2CL_PMS2	0.942	SYNE2	0.748	0.983	0.037	0
PMS2CL_PMS2	0.942	RBP7	0.848	0.984	0.047	0.001
PMS2CL_PMS2	0.942	RGS2	0.915	0.99	0.016	0.007
RETN	0.694	GLT25D1	0.77	0.842	0.031	0.044
PDE3B	0.567	TAS2R31	0.833	0.891	0	0.03
SULF2	0.591	ZNF587_ZNF417	0.632	0.759	0.017	0.005
NEK6_LOC1001290	0.671	OR9A2	0.823	0.878	0.001	0.045
NEK6_LOC1001290	0.671	KCNMA1	0.707	0.815	0.013	0.013
NEK6_LOC1001290	0.671	PDK4	0.863	0.924	0	0.004
NEK6_LOC1001290	0.671	FABP2	0.744	0.823	0.033	0.023
CENPK	0.834	GPR65	0.736	0.895	0.006	0.015
CENPK	0.834	DPH3	0.749	0.907	0.008	0.006
CENPK	0.834	NA	0.682	0.925	0.013	0
CENPK	0.834	DLEU2_DLEU2L	0.711	0.92	0.022	0
CENPK	0.834	LHFP	0.731	0.86	0.048	0.036

CENPK	0.834	MYL9	0.641	0.869	0.027	0.002
CENPK	0.834	SYNE2	0.748	0.926	0.001	0.005
CENPK	0.834	FBXL13	0.795	0.912	0.019	0.015
CENPK	0.834	CALM2_C2orf61	0.749	0.914	0.011	0.004
TRAF3	0.87	GPR65	0.736	0.966	0.012	0
TRAF3	0.87	CCDC125	0.917	0.983	0.004	0.023
TRAF3	0.87	PDK4	0.863	0.967	0.017	0.003
TRAF3	0.87	ZRANB1	0.897	0.97	0.005	0.02
GPR65	0.736	HSP90AB1_HSP90A	0.924	0.975	0	0.021
GPR65	0.736	GLT25D1	0.77	0.866	0.01	0.016
GPR65	0.736	ITGA4_CERKL	0.88	0.969	0	0.015
GPR65	0.736	EIF1AX_SCARNA9L	0.871	0.935	0	0.008
GPR65	0.736	ZNF28	0.837	0.916	0	0.019
GPR65	0.736	MGST3	0.857	0.934	0	0.022
GPR65	0.736	KIAA0746	0.776	0.891	0.012	0.001
GPR65	0.736	HSPB1_HSPBL2	0.705	0.823	0.047	0.048
GPR65	0.736	CCR4	0.871	0.936	0.001	0.008
GPR65	0.736	FSD1L_GARNL1	0.779	0.854	0.014	0.036
GPR65	0.736	CD151	0.718	0.843	0.044	0.004
GPR65	0.736	IGK@_IGKC_IGKV	0.855	0.906	0.002	0.042
GPR65	0.736	C7orf58	0.831	0.914	0.006	0.001
GPR65	0.736	NP	0.726	0.895	0.008	0.001
GPR65	0.736	TMEM62_SPCS2_L	0.78	0.872	0.026	0.005
GPR65	0.736	TAS2R31	0.833	0.902	0.005	0.005
GPR65	0.736	IGLV6-57	0.761	0.839	0.044	0.014
GPR65	0.736	DCTN5	0.722	0.858	0.016	0.003
IRF4	0.946	HAL	0.942	0.989	0.036	0.016
IRF4	0.946	CCDC125	0.917	0.995	0.02	0.008
IRF4	0.946	RGS2	0.915	0.99	0.045	0.003

AMFR	0.867	ACPL2	0.906	0.979	0.014	0.011
AMFR	0.867	ZRANB1	0.897	0.971	0.022	0.002
RPL17_SNORD58B	0.917	ACPL2	0.906	0.981	0.013	0.029
RPL17_SNORD58B	0.917	OCR1	0.896	0.979	0.021	0.026
RPL17_SNORD58B	0.917	NF-E4	0.861	0.977	0.034	0.003
RPL17_SNORD58B	0.917	KIAA1257_ACAD9/	0.851	0.958	0.029	0.01
RPL17_SNORD58B	0.917	PDK4	0.863	0.978	0.022	0.003
RPL17_SNORD58B	0.917	ZRANB1	0.897	0.969	0.041	0.024
RPL17_SNORD58B	0.917	CYP4F3_CYP4F2	0.901	0.979	0.012	0.031
RPL17_SNORD58B	0.917	SYNE2	0.748	0.967	0.01	0
RPL17_SNORD58B	0.917	MME	0.894	0.969	0.027	0.038
RPL17_SNORD58B	0.917	FBXL13	0.795	0.966	0.044	0
RPL17_SNORD58B	0.917	RBP7	0.848	0.971	0.007	0.007
RPL17_SNORD58B	0.917	CALM2_C2orf61	0.749	0.998	0.013	0
IRS2	0.817	GLT25D1	0.77	0.925	0.02	0.007
IRS2	0.817	ZNF28	0.837	0.915	0.046	0.007
IRS2	0.817	TYMS	0.863	0.933	0.007	0.04
IRS2	0.817	HIST1H2BM	0.891	0.947	0.008	0.039
IRS2	0.817	ABCG1	0.85	0.962	0.001	0.017
IRS2	0.817	HIST1H3B	0.89	0.958	0.01	0.002
IRS2	0.817	HIST1H3H	0.861	0.937	0.039	0.001
IRS2	0.817	APOLD1	0.871	0.949	0.012	0.004
IRS2	0.817	B4GALT3	0.917	0.963	0.005	0.025
IRS2	0.817	CDC26	0.799	0.919	0.033	0.002
GALNT2	0.528	PDK4	0.863	0.911	0	0.002
HSP90AB1_HSP90A	0.924	ACPL2	0.906	0.979	0.019	0.019
HSP90AB1_HSP90A	0.924	CCDC125	0.917	0.994	0.008	0.009
HSP90AB1_HSP90A	0.924	PDK4	0.863	0.993	0.016	0.001
HSP90AB1_HSP90A	0.924	ZRANB1	0.897	0.985	0.009	0.004

HSP90AB1_HSP90A	0.924	MPZL3	0.892	0.979	0.009	0.015
HSP90AB1_HSP90A	0.924	PLIN2	0.706	0.987	0.007	0
HSP90AB1_HSP90A	0.924	RGS2	0.915	0.973	0.006	0.046
GLT25D1	0.77	OR9A2	0.823	0.909	0.011	0.016
GLT25D1	0.77	KCNMA1	0.707	0.867	0.04	0.002
GLT25D1	0.77	PDK4	0.863	0.96	0.004	0
GLT25D1	0.77	THBS1	0.849	0.918	0.026	0.002
GLT25D1	0.77	LHFP	0.731	0.839	0.044	0.021
GLT25D1	0.77	CPM	0.854	0.92	0.022	0.014
GLT25D1	0.77	ATP6V0D1_LOC100	0.567	0.851	0.006	0
GLT25D1	0.77	HIST2H2BF_HIST2	0.855	0.925	0.009	0.018
GLT25D1	0.77	SPATA6	0.812	0.916	0.025	0.004
OR9A2	0.823	EIF1AX_SCARNA9L	0.871	0.933	0.006	0.039
OR9A2	0.823	ZNF28	0.837	0.904	0.025	0.016
OR9A2	0.823	HIST1H3C	0.863	0.918	0.041	0.018
OR9A2	0.823	HIST1H3H	0.861	0.923	0.018	0.007
OR9A2	0.823	S100B	0.841	0.919	0.019	0.033
OR9A2	0.823	IGK@_IGKC_IGKV	0.855	0.914	0.009	0.046
OR9A2	0.823	C7orf58	0.831	0.942	0.011	0.001
OR9A2	0.823	C4orf3	0.723	0.9	0.033	0.002
OR9A2	0.823	CDC26	0.799	0.901	0.004	0.025
OR9A2	0.823	TAS2R31	0.833	0.919	0.011	0.01
OR9A2	0.823	GLDC	0.714	0.882	0.045	0
ACPL2	0.906	CD300A	0.841	0.964	0.028	0.001
ACPL2	0.906	MGST3	0.857	0.964	0.045	0.003
ACPL2	0.906	TYMS	0.863	0.965	0.013	0.01
ACPL2	0.906	RRP12_LOC644215	0.904	0.976	0.01	0.035
ACPL2	0.906	HIST1H2BM	0.891	0.975	0.012	0.023
ACPL2	0.906	ABCG1	0.85	0.979	0.007	0.005

ACPL2	0.906	HIST1H3B	0.89	0.985	0.011	0.006
ACPL2	0.906	FSD1L_GARNL1	0.779	0.956	0.012	0.001
ACPL2	0.906	APOLD1	0.871	0.966	0.036	0.007
ACPL2	0.906	SON	0.856	0.973	0.044	0.003
ACPL2	0.906	IRF1	0.82	0.979	0.014	0.001
ACPL2	0.906	B4GALT3	0.917	0.988	0.009	0.035
ACPL2	0.906	TNFRSF17	0.875	0.978	0.021	0.004
ACPL2	0.906	CDC26	0.799	0.983	0.01	0
LRRFIP1	0.678	ITGA4_CERKL	0.88	0.955	0	0.033
LRRFIP1	0.678	SFRS9	0.558	0.746	0.047	0.033
LRRFIP1	0.678	NPCDR1	0.726	0.817	0.025	0.023
LRRFIP1	0.678	P4HA1_RPL17	0.664	0.857	0.005	0
LRRFIP1	0.678	KLHL5	0.657	0.799	0.019	0.032
LRRFIP1	0.678	KIAA0746	0.776	0.9	0	0.004
LRRFIP1	0.678	E2F6	0.787	0.85	0.004	0.028
LRRFIP1	0.678	PYHIN1	0.686	0.803	0.039	0.016
LRRFIP1	0.678	C7orf58	0.831	0.925	0	0.002
LRRFIP1	0.678	TMEM62_SPCS2_L	0.78	0.884	0	0.048
LRRFIP1	0.678	TAS2R31	0.833	0.9	0	0.046
LRRFIP1	0.678	SDHC	0.736	0.822	0.022	0.023
LRRFIP1	0.678	NFXL1	0.728	0.834	0.004	0.029
KCNMA1	0.707	KIAA0746	0.776	0.843	0.006	0.033
KCNMA1	0.707	HIST1H3C	0.863	0.897	0.002	0.032
KCNMA1	0.707	E2F6	0.787	0.839	0.027	0.023
KCNMA1	0.707	CD151	0.718	0.832	0.027	0.006
KCNMA1	0.707	HIST1H3H	0.861	0.912	0.001	0.013
KCNMA1	0.707	C7orf58	0.831	0.909	0	0.023
KCNMA1	0.707	NP	0.726	0.809	0.03	0.049
KCNMA1	0.707	C4orf3	0.723	0.832	0.011	0.018

KCNMA1	0.707	IGLV6-57	0.761	0.868	0.003	0.005
KCNMA1	0.707	NFXL1	0.728	0.805	0.038	0.029
KCNMA1	0.707	GLDC	0.714	0.825	0.024	0.007
KCNMA1	0.707	DCTN5	0.722	0.792	0.042	0.047
OCR1	0.896	ITGA4_CERKL	0.88	0.964	0.006	0.044
OCR1	0.896	CCR4	0.871	0.978	0.029	0.004
OCR1	0.896	ABCG1	0.85	0.949	0.021	0.012
OCR1	0.896	IGK@_IGKC_IGKV	0.855	0.957	0.049	0.005
OCR1	0.896	TNFRSF17	0.875	0.967	0.023	0.01
OCR1	0.896	CDC26	0.799	0.932	0.042	0.009
ITGA4_CERKL	0.88	KIAA1257_ACAD9/	0.851	0.944	0.029	0.007
ITGA4_CERKL	0.88	CCDC125	0.917	0.995	0.002	0.007
ITGA4_CERKL	0.88	PDK4	0.863	0.985	0.006	0.001
ITGA4_CERKL	0.88	ZRANB1	0.897	0.983	0.005	0.002
ITGA4_CERKL	0.88	ZNF587_ZNF417	0.632	0.957	0.025	0
ITGA4_CERKL	0.88	CYP4F3_CYP4F2	0.901	0.965	0.05	0.014
ITGA4_CERKL	0.88	SYNE2	0.748	0.986	0.005	0
ITGA4_CERKL	0.88	MME	0.894	0.965	0.038	0.006
ITGA4_CERKL	0.88	PLIN2	0.706	0.953	0.024	0
ITGA4_CERKL	0.88	RBP7	0.848	0.94	0.036	0.012
ITGA4_CERKL	0.88	SPATA6	0.812	0.942	0.038	0.006
EIF1AX_SCARNA9L	0.871	DPH3	0.749	0.928	0.019	0.001
EIF1AX_SCARNA9L	0.871	KIAA1257_ACAD9/	0.851	0.935	0.004	0.034
EIF1AX_SCARNA9L	0.871	PDK4	0.863	0.943	0.006	0.026
EIF1AX_SCARNA9L	0.871	THBS1	0.849	0.923	0.022	0.032
EIF1AX_SCARNA9L	0.871	MYL9	0.641	0.908	0.036	0
EIF1AX_SCARNA9L	0.871	SYNE2	0.748	0.934	0.006	0.001
EIF1AX_SCARNA9L	0.871	MME	0.894	0.96	0.009	0.028
EIF1AX_SCARNA9L	0.871	RBP7	0.848	0.951	0.008	0.013

EIF1AX_SCARNA9L	0.871	PLEKHF2	0.667	0.93	0.044	0
EIF1AX_SCARNA9L	0.871	CALM2_C2orf61	0.749	0.935	0.019	0
EIF1AX_SCARNA9L	0.871	SPATA6	0.812	0.926	0.013	0.019
DPH3	0.749	ZNF28	0.837	0.932	0	0.026
DPH3	0.749	CCR4	0.871	0.913	0.001	0.048
DPH3	0.749	HIST1H3B	0.89	0.957	0	0.034
DPH3	0.749	HIST1H3C	0.863	0.921	0.002	0.014
DPH3	0.749	HIST1H3H	0.861	0.947	0	0.01
DPH3	0.749	S100B	0.841	0.9	0.011	0.03
DPH3	0.749	NP	0.726	0.84	0.023	0.042
DPH3	0.749	TAS2R31	0.833	0.909	0.001	0.015
DPH3	0.749	KIAA0101_CSNK1G	0.736	0.869	0.02	0.001
ERGIC1	0.886	CD300A	0.841	0.969	0.018	0.001
ERGIC1	0.886	TYMS	0.863	0.954	0.028	0.009
ERGIC1	0.886	RRP12_LOC644215	0.904	0.981	0.013	0.012
ERGIC1	0.886	ABCG1	0.85	0.974	0.016	0.005
ERGIC1	0.886	IRF1	0.82	0.967	0.011	0.001
ERGIC1	0.886	B4GALT3	0.917	0.976	0.015	0.044
ERGIC1	0.886	CDC26	0.799	0.969	0.04	0
CD300A	0.841	HAL	0.942	0.992	0	0.019
CD300A	0.841	KIAA1257_ACAD9/	0.851	0.941	0.019	0.002
CD300A	0.841	CCDC125	0.917	0.969	0.001	0.018
CD300A	0.841	PDK4	0.863	0.941	0.028	0.001
CD300A	0.841	ZRANB1	0.897	0.945	0.01	0.01
CD300A	0.841	MPZL3	0.892	0.972	0	0.018
CD300A	0.841	KDM6B_TMEM88	0.869	0.967	0.004	0.014
CD300A	0.841	CYP4F3_CYP4F2	0.901	0.948	0.011	0.046
CD300A	0.841	MME	0.894	0.944	0.015	0.023
CD300A	0.841	RBP7	0.848	0.928	0.026	0.005

CD300A	0.841	HIST2H2BF_HIST2	0.855	0.962	0.015	0.001
NF-E4	0.861	ZNF28	0.837	0.949	0.01	0.006
NF-E4	0.861	CCR4	0.871	0.938	0.031	0.04
NF-E4	0.861	ABCG1	0.85	0.953	0.004	0.013
NF-E4	0.861	HIST1H3B	0.89	0.957	0.004	0.042
NF-E4	0.861	HIST1H3H	0.861	0.938	0.037	0.004
NF-E4	0.861	IRF1	0.82	0.929	0.001	0.044
NF-E4	0.861	C7orf58	0.831	0.931	0.047	0.005
NF-E4	0.861	TNFRSF17	0.875	0.941	0.019	0.04
NF-E4	0.861	CDC26	0.799	0.938	0.001	0.012
NF-E4	0.861	TAS2R31	0.833	0.939	0.039	0.002
NF-E4	0.861	DCTN5	0.722	0.91	0.039	0.001
MINPP1	0.7	DLEU2_DLEU2L	0.711	0.829	0.002	0.047
ZNF28	0.837	DLEU2_DLEU2L	0.711	0.935	0.02	0
ZNF28	0.837	KIAA1257_ACAD9/	0.851	0.923	0.011	0.045
ZNF28	0.837	PDK4	0.863	0.939	0.009	0.012
ZNF28	0.837	THBS1	0.849	0.918	0.027	0.016
ZNF28	0.837	LHFP	0.731	0.887	0.029	0.004
ZNF28	0.837	ZRANB1	0.897	0.951	0.004	0.037
ZNF28	0.837	SYNE2	0.748	0.91	0.043	0.001
ZNF28	0.837	MME	0.894	0.956	0.004	0.036
ZNF28	0.837	CPM	0.854	0.916	0.027	0.047
ZNF28	0.837	RBP7	0.848	0.957	0.001	0.008
ZNF28	0.837	CALM2_C2orf61	0.749	0.934	0.017	0
ZNF28	0.837	SPATA6	0.812	0.922	0.007	0.02
NPCDR1	0.726	ZNF587_ZNF417	0.632	0.82	0.004	0.007
NA	0.682	PYHIN1	0.686	0.805	0.025	0.036
NA	0.682	SDHC	0.736	0.821	0.027	0.015
NA	0.682	KIAA0101_CSNK1G	0.736	0.833	0.005	0.032

ICAM1	0.675	ATP6V0D1_LOC100	0.567	0.788	0.003	0.01
P4HA1_RPL17	0.664	DLEU2_DLEU2L	0.711	0.822	0.002	0.039
P4HA1_RPL17	0.664	PDK4	0.863	0.953	0	0.014
P4HA1_RPL17	0.664	ZNF587_ZNF417	0.632	0.816	0.002	0.005
P4HA1_RPL17	0.664	PLEKHF2	0.667	0.816	0.003	0.021
P4HA1_RPL17	0.664	IL1RL1	0.738	0.834	0.004	0.03
C15orf54	0.72	DLEU2_DLEU2L	0.711	0.819	0.015	0.034
KLHL5	0.657	ZNF587_ZNF417	0.632	0.787	0.006	0.016
HAL	0.942	ABCG1	0.85	0.99	0.018	0.002
HAL	0.942	TIMM10	0.949	0.986	0.03	0.028
HAL	0.942	IRF1	0.82	0.986	0.016	0
HAL	0.942	LASS4	0.924	0.982	0.01	0.045
HAL	0.942	B4GALT3	0.917	0.989	0.019	0.02
HAL	0.942	CDC26	0.799	0.99	0.02	0
DLEU2_DLEU2L	0.711	KIAA0746	0.776	0.85	0.007	0.046
DLEU2_DLEU2L	0.711	FSD1L_GARNL1	0.779	0.879	0	0.043
DLEU2_DLEU2L	0.711	NA	0.7	0.865	0.023	0
DLEU2_DLEU2L	0.711	HIST1H3C	0.863	0.918	0.001	0.035
DLEU2_DLEU2L	0.711	E2F6	0.787	0.856	0.01	0.014
DLEU2_DLEU2L	0.711	HIST1H3H	0.861	0.934	0	0.023
DLEU2_DLEU2L	0.711	C7orf58	0.831	0.9	0.001	0.017
DLEU2_DLEU2L	0.711	NP	0.726	0.851	0.004	0.024
DLEU2_DLEU2L	0.711	PLEKHA3	0.645	0.868	0.002	0
DLEU2_DLEU2L	0.711	TMEM62_SPCS2_L	0.78	0.865	0.006	0.049
DLEU2_DLEU2L	0.711	SDHC	0.736	0.869	0.015	0
DLEU2_DLEU2L	0.711	NFXL1	0.728	0.825	0.019	0.021
DLEU2_DLEU2L	0.711	KIAA0101_CSNK1G	0.736	0.863	0.003	0.005
KIAA1257_ACAD9/	0.851	ABCG1	0.85	0.963	0.001	0.01
KIAA1257_ACAD9/	0.851	HIST1H3B	0.89	0.943	0.017	0.048

KIAA1257_ACAD9/	0.851	IGK@_IGKC_IGKV	0.855	0.924	0.045	0.014
KIAA1257_ACAD9/	0.851	SON	0.856	0.936	0.045	0.014
KIAA1257_ACAD9/	0.851	IRF1	0.82	0.941	0.001	0.016
KIAA1257_ACAD9/	0.851	TNFRSF17	0.875	0.944	0.015	0.013
KIAA1257_ACAD9/	0.851	CDC26	0.799	0.941	0.003	0.004
MGST3	0.857	CCDC125	0.917	0.963	0.003	0.048
MGST3	0.857	PDK4	0.863	0.974	0.006	0.001
MGST3	0.857	ZRANB1	0.897	0.952	0.007	0.021
MGST3	0.857	KDM6B_TMEM88	0.869	0.953	0.01	0.027
MGST3	0.857	CYP4F3_CYP4F2	0.901	0.951	0.032	0.027
MGST3	0.857	RBP7	0.848	0.956	0.005	0.004
KIAA0746	0.776	PDK4	0.863	0.963	0	0.007
KIAA0746	0.776	ZNF587_ZNF417	0.632	0.893	0.001	0
KIAA0746	0.776	SYNE2	0.748	0.911	0.002	0.004
KIAA0746	0.776	PLIN2	0.706	0.892	0.001	0.008
KIAA0746	0.776	PLEKHF2	0.667	0.871	0.014	0.001
KIAA0746	0.776	IL1RL1	0.738	0.88	0.034	0.003
KIAA0746	0.776	MPZL2	0.699	0.867	0.023	0.004
KIAA0746	0.776	LOC100128751	0.686	0.864	0.02	0.006
KIAA0746	0.776	PPP1R2_PPP1R2P3	0.702	0.903	0.002	0.001
HSPB1_HSPBL2	0.705	PDK4	0.863	0.905	0.001	0.03
CCR4	0.871	PDK4	0.863	0.966	0.012	0.004
CCR4	0.871	ZRANB1	0.897	0.97	0.003	0.027
CCR4	0.871	ZNF587_ZNF417	0.632	0.931	0.033	0
CCR4	0.871	SYNE2	0.748	0.948	0.013	0
CCR4	0.871	MME	0.894	0.967	0.009	0.037
CCR4	0.871	RBP7	0.848	0.929	0.018	0.047
CCR4	0.871	PPP1R2_PPP1R2P3	0.702	0.939	0.035	0
TYMS	0.863	ZRANB1	0.897	0.961	0.005	0.01

TYMS	0.863	CYP4F3_CYP4F2	0.901	0.947	0.049	0.031
TYMS	0.863	MME	0.894	0.954	0.026	0.02
TYMS	0.863	CPM	0.854	0.934	0.049	0.013
TYMS	0.863	RBP7	0.848	0.973	0.007	0
RRP12_LOC644215	0.904	CCDC125	0.917	0.967	0.019	0.028
RRP12_LOC644215	0.904	MPZL3	0.892	0.983	0.005	0.009
RRP12_LOC644215	0.904	KDM6B_TMEM88	0.869	0.976	0.017	0.015
RRP12_LOC644215	0.904	RGS2	0.915	0.971	0.011	0.044
CCDC125	0.917	ABCG1	0.85	0.987	0.009	0.001
CCDC125	0.917	FAM118A	0.882	0.974	0.03	0.008
CCDC125	0.917	IRF1	0.82	0.987	0.007	0
CCDC125	0.917	B4GALT3	0.917	0.99	0.008	0.016
CCDC125	0.917	TNFRSF17	0.875	0.981	0.032	0.002
CCDC125	0.917	CDC26	0.799	0.959	0.034	0
CCDC125	0.917	DCTN5	0.722	0.969	0.039	0
HIST1H2BM	0.891	ZRANB1	0.897	0.976	0.014	0.006
HIST1H2BM	0.891	MME	0.894	0.963	0.03	0.027
HIST1H2BM	0.891	RBP7	0.848	0.966	0.03	0.001
PDK4	0.863	LAIR1_LAIR2	0.607	0.932	0.033	0
PDK4	0.863	HIST1H3B	0.89	0.946	0.015	0.039
PDK4	0.863	FSD1L_GARNL1	0.779	0.941	0.002	0.003
PDK4	0.863	CD151	0.718	0.932	0.036	0
PDK4	0.863	IGK@_IGKC_IGKV	0.855	0.955	0.009	0.006
PDK4	0.863	SON	0.856	0.948	0.008	0.018
PDK4	0.863	IRF1	0.82	0.941	0.001	0.018
PDK4	0.863	C7orf58	0.831	0.97	0.009	0
PDK4	0.863	CTSL1_CTSLL3	0.676	0.929	0.038	0
PDK4	0.863	NP	0.726	0.947	0.014	0
PDK4	0.863	TNFRSF17	0.875	0.938	0.018	0.049

PDK4	0.863	TMEM62_SPCS2_L	0.78	0.966	0.015	0
PDK4	0.863	CDC26	0.799	0.942	0.004	0.002
PDK4	0.863	TAS2R31	0.833	0.952	0.016	0.001
PDK4	0.863	NFXL1	0.728	0.946	0.039	0
PDK4	0.863	DCTN5	0.722	0.955	0.004	0
ABCG1	0.85	ZRANB1	0.897	0.944	0.018	0.019
ABCG1	0.85	CYP4F3_CYP4F2	0.901	0.965	0.008	0.026
ABCG1	0.85	MME	0.894	0.969	0.006	0.013
ABCG1	0.85	RBP7	0.848	0.963	0.009	0.001
THBS1	0.849	HIST1H3B	0.89	0.96	0.002	0.028
THBS1	0.849	FSD1L_GARNL1	0.779	0.909	0.008	0.015
THBS1	0.849	PTGS1	0.675	0.93	0.012	0
THBS1	0.849	HIST1H3C	0.863	0.936	0.023	0.011
THBS1	0.849	HIST1H3H	0.861	0.941	0.011	0.012
THBS1	0.849	IGK@_IGKC_IGKV	0.855	0.928	0.021	0.028
THBS1	0.849	SON	0.856	0.926	0.031	0.042
THBS1	0.849	C4orf3	0.723	0.911	0.027	0.001
THBS1	0.849	CDC26	0.799	0.919	0.005	0.015
THBS1	0.849	DCTN5	0.722	0.894	0.03	0.002
ITGA2B	0.58	MYL9	0.641	0.819	0	0.023
LHFP	0.731	HIST1H3B	0.89	0.929	0	0.02
LHFP	0.731	HIST1H3C	0.863	0.903	0.005	0.009
LHFP	0.731	HIST1H3H	0.861	0.907	0.003	0.012
LHFP	0.731	APOLD1	0.871	0.937	0	0.009
LHFP	0.731	IGLV6-57	0.761	0.864	0.036	0
LAIR1_LAIR2	0.607	PLIN2	0.706	0.827	0.002	0.037
HIST1H3B	0.89	ZRANB1	0.897	0.959	0.024	0.037
HIST1H3B	0.89	MYL9	0.641	0.948	0.029	0
HIST1H3B	0.89	CPM	0.854	0.946	0.026	0.018

HIST1H3B	0.89	RBP7	0.848	0.97	0.003	0.004
HIST1H3B	0.89	CALM2_C2orf61	0.749	0.959	0.022	0
HIST1H3B	0.89	SPATA6	0.812	0.939	0.043	0.011
ZRANB1	0.897	FAM118A	0.882	0.975	0.012	0.007
ZRANB1	0.897	IRF1	0.82	0.954	0.011	0.004
ZRANB1	0.897	B4GALT3	0.917	0.982	0.002	0.046
ZRANB1	0.897	NP	0.726	0.955	0.036	0
ZRANB1	0.897	TNFRSF17	0.875	0.959	0.028	0.006
ZRANB1	0.897	CDC26	0.799	0.95	0.016	0.001
TIMM10	0.949	MPZL3	0.892	0.983	0.03	0.006
TIMM10	0.949	RBP7	0.848	0.985	0.045	0.001
TIMM10	0.949	RGS2	0.915	0.981	0.04	0.008
FSD1L_GARNL1	0.779	CPM	0.854	0.909	0.014	0.033
FSD1L_GARNL1	0.779	HIST2H2BF_HIST2	0.855	0.917	0.005	0.041
FSD1L_GARNL1	0.779	SPATA6	0.812	0.913	0.013	0.004
HIST1H2AJ_HIST1	0.77	NA	0.627	0.824	0.021	0.005
PTGS1	0.675	MYL9	0.641	0.933	0	0
PTGS1	0.675	SPARC	0.574	0.854	0.018	0
NA	0.7	ZNF587_ZNF417	0.632	0.771	0.017	0.046
NA	0.7	PLEKHF2	0.667	0.873	0	0.005
HIST1H3C	0.863	MYL9	0.641	0.918	0.005	0
HIST1H3C	0.863	CALM2_C2orf61	0.749	0.922	0.015	0.004
E2F6	0.787	ZNF587_ZNF417	0.632	0.838	0.024	0.002
E2F6	0.787	IL1RL1	0.738	0.859	0.016	0.019
E2F6	0.787	MPZL2	0.699	0.844	0.021	0.015
E2F6	0.787	CALM2_C2orf61	0.749	0.896	0	0.013
MPZL3	0.892	LASS4	0.924	0.987	0.004	0.015
MPZL3	0.892	B4GALT3	0.917	0.96	0.044	0.019
SRXN1	0.513	HIST1H3H	0.861	0.918	0	0.013

SRXN1	0.513	POLE2	0.694	0.743	0.013	0.035
CD151	0.718	ATP6V0D1_LOC100	0.567	0.77	0.048	0.024
HIST1H3H	0.861	MYL9	0.641	0.944	0.002	0
HIST1H3H	0.861	RBP7	0.848	0.948	0.001	0.029
HIST1H3H	0.861	CALM2_C2orf61	0.749	0.93	0.015	0.001
HIST1H3H	0.861	SPATA6	0.812	0.923	0.002	0.045
FSD1L	0.674	IL1RL1	0.738	0.82	0.016	0.041
S100B	0.841	SYNE2	0.748	0.898	0.035	0.014
S100B	0.841	LOC100128751	0.686	0.898	0.04	0
S100B	0.841	CALM2_C2orf61	0.749	0.895	0.026	0.017
ZNF587_ZNF417	0.632	PYHIN1	0.686	0.804	0.015	0.009
ZNF587_ZNF417	0.632	IGK@_IGKC_IGKV	0.855	0.915	0	0.027
ZNF587_ZNF417	0.632	TSHZ2	0.733	0.819	0.007	0.021
ZNF587_ZNF417	0.632	TMEM62_SPCS2_L	0.78	0.873	0	0.018
ZNF587_ZNF417	0.632	NFXL1	0.728	0.841	0.001	0.005
ZNF587_ZNF417	0.632	DCTN5	0.722	0.875	0	0.006
PYHIN1	0.686	SYNE2	0.748	0.956	0	0
PYHIN1	0.686	PPP1R2_PPP1R2P3	0.702	0.847	0.001	0.03
APOLD1	0.871	RBP7	0.848	0.948	0.033	0.001
FABP2	0.744	TAS2R31	0.833	0.88	0.01	0.05
FABP2	0.744	IGLV6-57	0.761	0.866	0.018	0.004
KDM6B_TMEM88	0.869	IRF1	0.82	0.956	0.03	0.001
IGK@_IGKC_IGKV	0.855	SYNE2	0.748	0.923	0.036	0
IGK@_IGKC_IGKV	0.855	MME	0.894	0.944	0.018	0.046
IGK@_IGKC_IGKV	0.855	PLIN2	0.706	0.911	0.039	0.001
IGK@_IGKC_IGKV	0.855	LOC100128751	0.686	0.916	0.044	0
IGK@_IGKC_IGKV	0.855	HIST2H2BF_HIST2	0.855	0.934	0.029	0.017
MYL9	0.641	HIST1H2BJ	0.703	0.815	0.02	0.005
MYL9	0.641	CMTM5	0.671	0.872	0.001	0.001

MYL9	0.641	SDHC	0.736	0.793	0.039	0.031
MYL9	0.641	KIAA0101_CSNK1G	0.736	0.82	0.01	0.008
CLC	0.782	PLIN2	0.706	0.901	0.003	0.013
CLC	0.782	IL1RL1	0.738	0.93	0.015	0
CYP4F3_CYP4F2	0.901	IRF1	0.82	0.96	0.019	0.009
CYP4F3_CYP4F2	0.901	CDC26	0.799	0.952	0.026	0.004
SON	0.856	SYNE2	0.748	0.938	0.009	0.001
SON	0.856	RBP7	0.848	0.966	0.007	0.006
IRF1	0.82	MME	0.894	0.947	0.017	0.008
IRF1	0.82	RBP7	0.848	0.944	0.007	0.002
IRF1	0.82	RGS2	0.915	0.975	0	0.03
IRF1	0.82	HIST2H2BF_HIST2	0.855	0.951	0.019	0.001
SYNE2	0.748	C7orf58	0.831	0.912	0.003	0.017
SYNE2	0.748	NP	0.726	0.883	0.008	0.004
SYNE2	0.748	TMEM62_SPCS2_L	0.78	0.919	0.002	0
SYNE2	0.748	TAS2R31	0.833	0.938	0.001	0
SYNE2	0.748	NFXL1	0.728	0.881	0.009	0.001
SYNE2	0.748	DCTN5	0.722	0.893	0.002	0.004
MME	0.894	TNFRSF17	0.875	0.96	0.007	0.029
MME	0.894	CDC26	0.799	0.939	0.014	0.007
C7orf58	0.831	FBXL13	0.795	0.897	0.045	0.019
C7orf58	0.831	PLEKHF2	0.667	0.895	0.046	0
C7orf58	0.831	IL1RL1	0.738	0.898	0.042	0.003
C7orf58	0.831	AIF1	0.618	0.918	0.004	0
C7orf58	0.831	PPP1R2_PPP1R2P3	0.702	0.898	0.016	0.002
C7orf58	0.831	HIST2H2BF_HIST2	0.855	0.961	0	0.022
C7orf58	0.831	SPATA6	0.812	0.92	0.001	0.049
CPM	0.854	CDC26	0.799	0.931	0.01	0.01
TSHZ2	0.733	LOC100128751	0.686	0.824	0.036	0.042

TSHZ2	0.733	PPP1R2_PPP1R2P3	0.702	0.83	0.045	0.044
PLIN2	0.706	NP	0.726	0.836	0.009	0.04
PLIN2	0.706	TMEM62_SPCS2_L	0.78	0.918	0.003	0.003
PLIN2	0.706	DCTN5	0.722	0.861	0.005	0.011
B4GALT3	0.917	RBP7	0.848	0.981	0.045	0.001
B4GALT3	0.917	RGS2	0.915	0.987	0.009	0.012
NP	0.726	FBXL13	0.795	0.857	0.009	0.05
TNFRSF17	0.875	RBP7	0.848	0.934	0.013	0.048
FBXL13	0.795	TAS2R31	0.833	0.92	0.003	0.019
FBXL13	0.795	DCTN5	0.722	0.859	0.032	0.018
PLEKHA3	0.645	PLEKHF2	0.667	0.781	0.045	0.029
TMEM62_SPCS2_L	0.78	PLEKHF2	0.667	0.859	0.042	0.002
TMEM62_SPCS2_L	0.78	PPP1R2_PPP1R2P3	0.702	0.877	0.015	0.002
TMEM62_SPCS2_L	0.78	CALM2_C2orf61	0.749	0.889	0.02	0.014
RBP7	0.848	CDC26	0.799	0.964	0.001	0.001
RBP7	0.848	TAS2R31	0.833	0.936	0.046	0.001
PLEKHF2	0.667	SDHC	0.736	0.842	0.021	0.001
PLEKHF2	0.667	NFXL1	0.728	0.814	0.012	0.027
RGS2	0.915	CDC26	0.799	0.975	0.019	0
IL1RL1	0.738	IL5RA	0.782	0.975	0	0.002
IL1RL1	0.738	TAS2R31	0.833	0.928	0	0.019
IL1RL1	0.738	KIAA0101_CSNK1G	0.736	0.829	0.029	0.03
AIF1	0.618	SDHC	0.736	0.801	0.023	0.017
MPZL2	0.699	NFXL1	0.728	0.814	0.034	0.029
MPZL2	0.699	DCTN5	0.722	0.845	0.002	0.028
CDC26	0.799	HIST2H2BF_HIST2	0.855	0.94	0.012	0.001
CDC26	0.799	SPATA6	0.812	0.923	0.012	0.004
PPP1R2_PPP1R2P3	0.702	NFXL1	0.728	0.835	0.03	0.009
TAS2R31	0.833	HIST2H2BF_HIST2	0.855	0.926	0.012	0.019

TAS2R31	0.833	CALM2_C2orf61	0.749	0.896	0.037	0.003
CALM2_C2orf61	0.749	IGLV6-57	0.761	0.852	0.01	0.034
CALM2_C2orf61	0.749	SDHC	0.736	0.879	0.05	0
CALM2_C2orf61	0.749	KIAA0101_CSNK1G	0.736	0.903	0.003	0

Table 17

Ratios Healthy Versus ipSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
VNN1	0.933	GNLY	0.917	0.986	0.042	0.019
VNN1	0.933	PTGDR	0.919	0.991	0.043	0.013
VNN1	0.933	SH2D1B	0.867	0.986	0.046	0.005
VNN1	0.933	HIST1H4C	0.859	0.976	0.041	0.008
VNN1	0.933	VAMP2	0.673	0.963	0.029	0
VNN1	0.933	MRPL41	0.811	0.985	0.039	0
VNN1	0.933	CASS4	0.877	0.981	0.037	0.006
VNN1	0.933	ITK	0.899	0.991	0.034	0.004
VNN1	0.933	B3GAT3	0.783	0.975	0.05	0
VNN1	0.933	HIST1H4E	0.83	0.978	0.027	0.002
VNN1	0.933	CHI3L1	0.909	0.985	0.043	0.047
VNN1	0.933	RUNX2	0.848	0.982	0.023	0.004
VNN1	0.933	DNAJC9_FAM149B1	0.811	0.99	0.048	0
VNN1	0.933	PDE3B	0.85	0.978	0.031	0.005
VNN1	0.933	IRF4	0.781	0.97	0.031	0.001
VNN1	0.933	LY6G5B_CSNK2B	0.661	0.979	0.029	0
VNN1	0.933	KIAA0746	0.544	0.985	0.044	0
VNN1	0.933	CCR4	0.784	0.972	0.05	0
VNN1	0.933	MME	0.507	0.98	0.05	0

VNN1	0.933	TSHZ2	0.801	0.973	0.035	0.001
VNN1	0.933	RASA4_RASA4P_R	0.779	0.969	0.045	0
VNN1	0.933	RGS2	0.605	0.975	0.034	0
IMP3	0.942	OMG	0.96	0.997	0.019	0.031
IMP3	0.942	SLC37A3	0.885	0.99	0.05	0.007
IMP3	0.942	IL18R1	0.933	0.993	0.026	0.013
IMP3	0.942	ERLIN1	0.937	0.989	0.04	0.023
IMP3	0.942	C7orf53	0.921	0.99	0.024	0.008
IMP3	0.942	DSE	0.936	0.994	0.02	0.038
IMP3	0.942	DNAJC13	0.948	0.998	0.021	0.038
IMP3	0.942	GSR	0.831	0.981	0.045	0
IMP3	0.942	B3GNT5_MCF2L2	0.956	0.997	0.018	0.026
IMP3	0.942	PICALM	0.879	0.992	0.021	0.003
IMP3	0.942	METTL7B	0.943	0.99	0.022	0.035
IMP3	0.942	IFI16	0.912	0.984	0.033	0.011
IMP3	0.942	JKAMP	0.93	1	0.021	0.008
IMP3	0.942	WSB2	0.911	0.995	0.024	0.003
IMP3	0.942	CLU	0.894	0.979	0.041	0.006
IMP3	0.942	CD63	0.757	0.999	0.022	0
IMP3	0.942	HPSE	0.939	0.997	0.023	0.007
IMP3	0.942	DDAH2	0.886	0.984	0.016	0.017
IMP3	0.942	ATP13A3	0.841	0.985	0.039	0.004
IMP3	0.942	LRRC70_IPO11	0.923	0.995	0.023	0.009
IMP3	0.942	CDS2	0.869	0.982	0.022	0.007
IMP3	0.942	OLAH	0.885	0.981	0.036	0.008
IMP3	0.942	EAF2_HCG11_LOC	0.917	0.986	0.032	0.029
IMP3	0.942	EXOSC4	0.731	0.977	0.031	0
IMP3	0.942	FOLR3_FOLR2	0.848	0.992	0.046	0
IMP3	0.942	LGALS1	0.736	0.99	0.028	0

IMP3	0.942	SIAE	0.814	0.984	0.03	0
IMP3	0.942	EFCAB2	0.96	0.989	0.04	0.03
IMP3	0.942	AGTRAP	0.856	0.989	0.025	0.001
IMP3	0.942	SUCNR1	0.922	0.996	0.029	0.005
IMP3	0.942	AIG1	0.842	0.986	0.042	0.001
IMP3	0.942	HS2ST1_UBA2	0.758	0.977	0.035	0
IMP3	0.942	VOPP1_LOC100128	0.618	0.98	0.037	0
IMP3	0.942	CLEC4A	0.87	0.985	0.044	0.002
IMP3	0.942	TRIM21	0.874	0.989	0.026	0.004
IMP3	0.942	MGST3	0.602	0.988	0.038	0
IMP3	0.942	ATP6V0D1_LOC100	0.856	0.978	0.016	0.008
IMP3	0.942	CALM2_C2orf61	0.733	0.99	0.026	0
CLEC4D	0.976	CASS4	0.877	0.996	0.048	0.001
GPR56	0.933	FAR2	0.963	0.998	0.007	0.042
GPR56	0.933	CLEC4E	0.883	0.982	0.03	0.003
GPR56	0.933	IL18R1	0.933	0.98	0.048	0.014
GPR56	0.933	ERLIN1	0.937	0.996	0.007	0.031
GPR56	0.933	C7orf53	0.921	0.984	0.018	0.012
GPR56	0.933	DSE	0.936	0.972	0.043	0.037
GPR56	0.933	DNAJC13	0.948	0.981	0.034	0.033
GPR56	0.933	FOXD4L3_FOXD4L6	0.892	0.981	0.041	0.004
GPR56	0.933	GSR	0.831	0.977	0.021	0.001
GPR56	0.933	PICALM	0.879	0.968	0.03	0.012
GPR56	0.933	IFI16	0.912	0.983	0.011	0.012
GPR56	0.933	JKAMP	0.93	0.984	0.004	0.043
GPR56	0.933	WSB2	0.911	0.978	0.007	0.019
GPR56	0.933	CLU	0.894	0.975	0.02	0.006
GPR56	0.933	HPSE	0.939	0.986	0.007	0.023
GPR56	0.933	LRRC70_IPO11	0.923	0.975	0.035	0.025

GPR56	0.933	CDS2	0.869	0.97	0.011	0.016
GPR56	0.933	OLAH	0.885	0.976	0.023	0.01
GPR56	0.933	RCBTB2_LOC10013	0.905	0.972	0.038	0.016
GPR56	0.933	SIAE	0.814	0.968	0.049	0
GPR56	0.933	AP3B2	0.887	0.961	0.044	0.028
GPR56	0.933	SUCNR1	0.922	0.976	0.022	0.023
GPR56	0.933	ACTA2	0.783	0.977	0.042	0
GPR56	0.933	KCNMA1	0.897	0.975	0.02	0.03
GPR56	0.933	TRIM21	0.874	0.986	0.011	0.006
GPR56	0.933	ICAM1	0.821	0.971	0.028	0.002
GPR56	0.933	ATP6V0D1_LOC100	0.856	0.968	0.005	0.019
ARG1	0.922	HIST1H4C	0.859	0.968	0.043	0.021
ARG1	0.922	VAMP2	0.673	0.944	0.049	0
ARG1	0.922	MRPL41	0.811	0.978	0.046	0.001
ARG1	0.922	HIST1H4E	0.83	0.963	0.04	0.01
ARG1	0.922	RUNX2	0.848	0.961	0.04	0.026
ARG1	0.922	HIST1H3A	0.715	0.967	0.043	0
ARG1	0.922	IRF4	0.781	0.952	0.05	0.006
ARG1	0.922	IRS2	0.648	0.954	0.048	0
FAR2	0.963	CAMK4	0.953	0.998	0.041	0.04
FAR2	0.963	CASS4	0.877	0.998	0.037	0
FAR2	0.963	RUNX2	0.848	0.996	0.043	0
FAR2	0.963	PDE3B	0.85	0.997	0.041	0
GNLY	0.917	SLC37A3	0.885	0.983	0.02	0.01
GNLY	0.917	CLEC4E	0.883	0.977	0.03	0.003
GNLY	0.917	IL18R1	0.933	0.981	0.018	0.027
GNLY	0.917	ERLIN1	0.937	0.978	0.041	0.01
GNLY	0.917	C7orf53	0.921	0.983	0.01	0.009
GNLY	0.917	DSE	0.936	0.983	0.019	0.017

GNLY	0.917	DNAJC13	0.948	0.986	0.02	0.015
GNLY	0.917	FOXD4L3_FOXD4L6	0.892	0.977	0.042	0.004
GNLY	0.917	B3GNT5_MCF2L2	0.956	0.992	0.004	0.029
GNLY	0.917	PICALM	0.879	0.974	0.015	0.007
GNLY	0.917	TLR10	0.905	0.974	0.023	0.007
GNLY	0.917	IFI16	0.912	0.984	0.008	0.005
GNLY	0.917	JKAMP	0.93	0.993	0.004	0.013
GNLY	0.917	WSB2	0.911	0.987	0.004	0.007
GNLY	0.917	CLU	0.894	0.975	0.01	0.007
GNLY	0.917	HPSE	0.939	0.993	0.006	0.008
GNLY	0.917	LRRC70_IPO11	0.923	0.988	0.007	0.01
GNLY	0.917	CDS2	0.869	0.959	0.009	0.029
GNLY	0.917	OLAH	0.885	0.974	0.008	0.01
GNLY	0.917	EAF2_HCG11_LOC	0.917	0.975	0.046	0.02
GNLY	0.917	RCBTB2_LOC10013	0.905	0.967	0.024	0.016
GNLY	0.917	FOLR3_FOLR2	0.848	0.98	0.014	0.001
GNLY	0.917	SIAE	0.814	0.972	0.023	0
GNLY	0.917	AP3B2	0.887	0.947	0.046	0.048
GNLY	0.917	ABCA13	0.868	0.976	0.032	0.001
GNLY	0.917	CDA	0.804	0.97	0.04	0
GNLY	0.917	SAP30	0.728	0.952	0.011	0
GNLY	0.917	AGTRAP	0.856	0.969	0.004	0.005
GNLY	0.917	SUCNR1	0.922	0.987	0.012	0.008
GNLY	0.917	KCNMA1	0.897	0.964	0.015	0.044
GNLY	0.917	TRIM21	0.874	0.972	0.026	0.007
GNLY	0.917	DLEU2_DLEU2L	0.874	0.966	0.036	0.002
GNLY	0.917	ANKRD28	0.8	0.977	0.039	0
GNLY	0.917	ATP6V0D1_LOC100	0.856	0.953	0.021	0.029
OMG	0.96	PTGDR	0.919	0.998	0.026	0.01

OMG	0.96	CAMK4	0.953	0.997	0.034	0.042
OMG	0.96	LRRN3	0.947	0.998	0.023	0.033
OMG	0.96	PDE3B	0.85	0.997	0.028	0.001
SLC37A3	0.885	PTGDR	0.919	0.979	0.022	0.021
SLC37A3	0.885	VAMP2	0.673	0.941	0.018	0
SLC37A3	0.885	MRPL41	0.811	0.958	0.046	0.001
SLC37A3	0.885	CASS4	0.877	0.972	0.01	0.013
SLC37A3	0.885	ITK	0.899	0.985	0.011	0.004
SLC37A3	0.885	GOT2	0.905	0.975	0.01	0.034
SLC37A3	0.885	B3GAT3	0.783	0.961	0.021	0
SLC37A3	0.885	HIST1H4E	0.83	0.968	0.014	0.002
SLC37A3	0.885	ANAPC11	0.818	0.954	0.035	0.002
SLC37A3	0.885	RUNX2	0.848	0.969	0.01	0.007
SLC37A3	0.885	PMS2CL_PMS2	0.685	0.948	0.043	0
SLC37A3	0.885	PDE3B	0.85	0.975	0.008	0.007
SLC37A3	0.885	SFRS9	0.527	0.942	0.027	0
SLC37A3	0.885	NPCDR1	0.86	0.954	0.035	0.006
SLC37A3	0.885	LY6G5B_CSNK2B	0.661	0.965	0.014	0
SLC37A3	0.885	CCR4	0.784	0.945	0.043	0.001
SLC37A3	0.885	LASS4	0.794	0.951	0.021	0.009
SLC37A3	0.885	TSHZ2	0.801	0.955	0.023	0.002
SLC37A3	0.885	CAMK1D	0.702	0.949	0.03	0
BMX_HNRPDL	0.947	GOT2	0.905	0.988	0.05	0.018
BMX_HNRPDL	0.947	ABCG1	0.789	0.965	0.045	0.003
FAIM3	0.938	C7orf53	0.921	0.98	0.044	0.047
FAIM3	0.938	SLC15A2	0.824	0.992	0.046	0
FAIM3	0.938	IFI16	0.912	0.977	0.037	0.05
FAIM3	0.938	WSB2	0.911	0.985	0.045	0.02
FAIM3	0.938	HPSE	0.939	0.989	0.042	0.04

FAIM3	0.938	HS2ST1_UBA2	0.758	0.969	0.025	0.001
FAIM3	0.938	KLHL5	0.826	0.972	0.043	0.002
CLEC4E	0.883	PTGDR	0.919	0.963	0.022	0.032
CLEC4E	0.883	KLRF1	0.872	0.959	0.048	0
CLEC4E	0.883	CASS4	0.877	0.976	0.001	0.008
CLEC4E	0.883	ITK	0.899	0.98	0.005	0.003
CLEC4E	0.883	GOT2	0.905	0.96	0.018	0.038
CLEC4E	0.883	HIST1H4E	0.83	0.942	0.022	0.007
CLEC4E	0.883	CCR3	0.905	0.953	0.02	0.04
CLEC4E	0.883	CHI3L1	0.909	0.987	0.006	0.019
CLEC4E	0.883	GIMAP7	0.755	0.946	0.033	0
CLEC4E	0.883	RUNX2	0.848	0.969	0.003	0.005
CLEC4E	0.883	PHOSPHO1	0.85	0.947	0.009	0.025
CLEC4E	0.883	PDE3B	0.85	0.979	0.002	0.004
CLEC4E	0.883	SULF2	0.819	0.948	0.041	0.003
CLEC4E	0.883	IRS2	0.648	0.946	0.009	0
CLEC4E	0.883	NPCDR1	0.86	0.946	0.031	0.004
CLEC4E	0.883	CCR4	0.784	0.949	0.028	0
CLEC4E	0.883	ABCG1	0.789	0.937	0.026	0.008
CLEC4E	0.883	LASS4	0.794	0.919	0.036	0.031
CLEC4E	0.883	TSHZ2	0.801	0.965	0.005	0.001
CLEC4E	0.883	CAMK1D	0.702	0.947	0.023	0
IL18R1	0.933	LRRN3	0.947	0.997	0.01	0.036
IL18R1	0.933	VAMP2	0.673	0.962	0.036	0
IL18R1	0.933	CASS4	0.877	0.979	0.008	0.003
IL18R1	0.933	ITK	0.899	0.995	0.013	0.002
IL18R1	0.933	B3GAT3	0.783	0.984	0.017	0
IL18R1	0.933	HIST1H4E	0.83	0.967	0.042	0.002
IL18R1	0.933	GIMAP7	0.755	0.974	0.017	0

IL18R1	0.933	RUNX2	0.848	0.972	0.037	0.002
IL18R1	0.933	PMS2CL_PMS2	0.685	0.979	0.027	0
IL18R1	0.933	PDE3B	0.85	0.988	0.007	0.002
IL18R1	0.933	IRS2	0.648	0.958	0.034	0
IL18R1	0.933	KIAA1257_ACAD9/	0.496	0.976	0.016	0
IL18R1	0.933	CCR4	0.784	0.976	0.013	0
IL18R1	0.933	RRP12_LOC644215	0.632	0.957	0.047	0
IL18R1	0.933	ABCG1	0.789	0.965	0.016	0.003
IL18R1	0.933	TSHZ2	0.801	0.975	0.026	0
ERLIN1	0.937	LRRN3	0.947	0.995	0.017	0.049
ERLIN1	0.937	CASS4	0.877	0.992	0.028	0.001
ERLIN1	0.937	ITK	0.899	0.991	0.028	0.003
ERLIN1	0.937	B3GAT3	0.783	0.979	0.036	0
ERLIN1	0.937	RUNX2	0.848	0.963	0.044	0.008
ERLIN1	0.937	PDE3B	0.85	0.987	0.016	0.002
ERLIN1	0.937	LASS4	0.794	0.957	0.05	0.005
ERLIN1	0.937	TSHZ2	0.801	0.98	0.012	0
FKBP5_LOC285847	0.841	KLRF1	0.872	0.935	0.022	0.005
FKBP5_LOC285847	0.841	SH2D1B	0.867	0.928	0.041	0.029
FKBP5_LOC285847	0.841	VAMP2	0.673	0.894	0.028	0.001
FKBP5_LOC285847	0.841	KLRK1_KLRC4	0.857	0.914	0.045	0.042
FKBP5_LOC285847	0.841	ITK	0.899	0.967	0.002	0.021
FKBP5_LOC285847	0.841	B3GAT3	0.783	0.908	0.024	0.012
FKBP5_LOC285847	0.841	GIMAP7	0.755	0.911	0.016	0.003
FKBP5_LOC285847	0.841	NA	0.696	0.902	0.039	0.001
FKBP5_LOC285847	0.841	PLA2G7	0.834	0.923	0.046	0.011
FKBP5_LOC285847	0.841	PMS2CL_PMS2	0.685	0.902	0.029	0
FKBP5_LOC285847	0.841	PDE3B	0.85	0.957	0.001	0.017
FKBP5_LOC285847	0.841	SULF2	0.819	0.913	0.043	0.036

FKBP5_LOC285847	0.841	IRS2	0.648	0.903	0.012	0.001
FKBP5_LOC285847	0.841	NPCDR1	0.86	0.941	0.003	0.012
FKBP5_LOC285847	0.841	LY6G5B_CSNK2B	0.661	0.915	0.013	0
FKBP5_LOC285847	0.841	CCR4	0.784	0.909	0.016	0.008
FKBP5_LOC285847	0.841	ABCG1	0.789	0.915	0.003	0.042
FKBP5_LOC285847	0.841	FAM118A	0.759	0.901	0.021	0.01
FKBP5_LOC285847	0.841	PYHIN1	0.807	0.922	0.033	0.006
FKBP5_LOC285847	0.841	NA	0.746	0.915	0.048	0
FKBP5_LOC285847	0.841	TSHZ2	0.801	0.944	0.002	0.004
FKBP5_LOC285847	0.841	RASA4_RASA4P_R	0.779	0.894	0.049	0.008
FKBP5_LOC285847	0.841	CAMK1D	0.702	0.921	0.007	0
FKBP5_LOC285847	0.841	CFD	0.767	0.911	0.048	0.003
C7orf53	0.921	PTGDR	0.919	0.979	0.04	0.006
C7orf53	0.921	CAMK4	0.953	0.997	0.006	0.045
C7orf53	0.921	LRRN3	0.947	0.992	0.005	0.045
C7orf53	0.921	CASS4	0.877	0.999	0.004	0
C7orf53	0.921	ITK	0.899	0.987	0.014	0.002
C7orf53	0.921	GOT2	0.905	0.976	0.039	0.008
C7orf53	0.921	HIST1H4E	0.83	0.967	0.04	0.001
C7orf53	0.921	CCR3	0.905	0.967	0.042	0.006
C7orf53	0.921	CHI3L1	0.909	0.978	0.023	0.026
C7orf53	0.921	RUNX2	0.848	0.994	0.007	0
C7orf53	0.921	PDE3B	0.85	0.996	0.005	0.001
C7orf53	0.921	NPCDR1	0.86	0.969	0.037	0.001
C7orf53	0.921	LY6G5B_CSNK2B	0.661	0.973	0.044	0
C7orf53	0.921	KIAA1257_ACAD9/	0.496	0.98	0.022	0
C7orf53	0.921	CCR4	0.784	0.976	0.033	0
C7orf53	0.921	ABCG1	0.789	0.965	0.028	0.001
C7orf53	0.921	TSHZ2	0.801	0.974	0.035	0

C7orf53	0.921	CAMK1D	0.702	0.978	0.033	0
PLB1	0.938	RUNX2	0.848	0.989	0.034	0.002
PLB1	0.938	PDE3B	0.85	0.975	0.046	0.005
DSE	0.936	CAMK4	0.953	0.999	0.031	0.04
DSE	0.936	LRRN3	0.947	0.993	0.045	0.033
DSE	0.936	CASS4	0.877	0.974	0.013	0.008
DSE	0.936	RUNX2	0.848	0.974	0.019	0.004
DSE	0.936	PDE3B	0.85	0.974	0.019	0.006
DSE	0.936	LY6G5B_CSNK2B	0.661	0.972	0.039	0
PTGDR	0.919	FOXD4L3_FOXD4L6	0.892	0.991	0.019	0.006
PTGDR	0.919	SGMS2	0.859	0.971	0.038	0.005
PTGDR	0.919	PICALM	0.879	0.983	0.006	0.008
PTGDR	0.919	TLR10	0.905	0.972	0.021	0.022
PTGDR	0.919	JKAMP	0.93	0.986	0.004	0.047
PTGDR	0.919	WSB2	0.911	0.983	0.004	0.02
PTGDR	0.919	CLU	0.894	0.961	0.012	0.03
PTGDR	0.919	HPSE	0.939	0.987	0.014	0.026
PTGDR	0.919	PDGFC	0.837	0.969	0.018	0.013
PTGDR	0.919	HPGD	0.871	0.96	0.041	0.047
PTGDR	0.919	CDS2	0.869	0.954	0.022	0.049
PTGDR	0.919	HSPC159	0.823	0.97	0.016	0.001
PTGDR	0.919	PPP2R5A_SNORA16	0.775	0.958	0.032	0
PTGDR	0.919	EAF2_HCG11_LOC	0.917	0.974	0.039	0.046
PTGDR	0.919	RCBTB2_LOC10013	0.905	0.981	0.022	0.011
PTGDR	0.919	HMGB2	0.849	0.972	0.016	0.01
PTGDR	0.919	SIAE	0.814	0.956	0.031	0.002
PTGDR	0.919	ABCA13	0.868	0.96	0.034	0.009
PTGDR	0.919	AGTRAP	0.856	0.949	0.021	0.015
PTGDR	0.919	SUCNR1	0.922	0.979	0.007	0.034

PTGDR	0.919	TREML1	0.793	0.958	0.043	0.002
PTGDR	0.919	NEK6_LOC1001290	0.765	0.943	0.029	0.002
PTGDR	0.919	ANKRD28	0.8	0.968	0.009	0.001
CAMK4	0.953	DNAJC13	0.948	1	0.04	0.036
CAMK4	0.953	TNFAIP6	0.971	0.997	0.042	0.041
CAMK4	0.953	B3GNT5_MCF2L2	0.956	0.997	0.043	0.019
CAMK4	0.953	PICALM	0.879	0.999	0.043	0.001
CAMK4	0.953	C9orf72	0.958	0.999	0.044	0.039
CAMK4	0.953	SLC15A2	0.824	0.987	0.025	0
CAMK4	0.953	TLR10	0.905	1	0.04	0.003
CAMK4	0.953	IFI16	0.912	0.992	0.039	0.005
CAMK4	0.953	JKAMP	0.93	0.998	0.038	0.009
CAMK4	0.953	WSB2	0.911	0.986	0.021	0.01
CAMK4	0.953	HPSE	0.939	0.992	0.026	0.018
CAMK4	0.953	DDAH2	0.886	0.974	0.045	0.034
CAMK4	0.953	LRRC70_IPO11	0.923	0.994	0.048	0.011
CAMK4	0.953	TMEM144_LOC2855	0.92	0.999	0.042	0.016
CAMK4	0.953	EAF2_HCG11_LOC	0.917	0.998	0.043	0.018
CAMK4	0.953	RCBTB2_LOC10013	0.905	0.994	0.037	0.005
CAMK4	0.953	SLC39A9	0.551	0.975	0.037	0
CAMK4	0.953	LGALS1	0.736	0.977	0.022	0
CAMK4	0.953	SIAE	0.814	0.979	0.044	0
CAMK4	0.953	EFCAB2	0.96	0.999	0.044	0.023
CAMK4	0.953	AGTRAP	0.856	0.973	0.049	0.003
CAMK4	0.953	SUCNR1	0.922	0.993	0.04	0.009
CAMK4	0.953	MTRR	0.703	0.99	0.028	0
CAMK4	0.953	AIG1	0.842	0.993	0.042	0.001
CAMK4	0.953	HS2ST1_UBA2	0.758	0.995	0.047	0
CAMK4	0.953	NEK6_LOC1001290	0.765	0.972	0.027	0

CAMK4	0.953	GPR65	0.886	0.992	0.03	0.007
CAMK4	0.953	LRRFIP1	0.673	0.995	0.039	0
CAMK4	0.953	SFRS9	0.527	0.981	0.025	0
CAMK4	0.953	TAF13	0.854	0.995	0.044	0.001
CAMK4	0.953	KLHL5	0.826	0.997	0.035	0
CAMK4	0.953	ANKRD28	0.8	0.998	0.043	0
CAMK4	0.953	MGST3	0.602	0.986	0.038	0
CAMK4	0.953	CEP97	0.695	0.987	0.031	0
CAMK4	0.953	FAM118B	0.737	0.992	0.031	0
CAMK4	0.953	TMEM62_SPCS2_L	0.645	0.984	0.05	0
CAMK4	0.953	AIF1	0.816	0.993	0.05	0
DNAJC13	0.948	CASS4	0.877	0.982	0.028	0.003
DNAJC13	0.948	ITK	0.899	1	0.036	0.002
DNAJC13	0.948	GOT2	0.905	0.998	0.038	0.007
DNAJC13	0.948	HIST1H4E	0.83	0.981	0.041	0.001
DNAJC13	0.948	SLC39A9	0.551	0.978	0.02	0
DNAJC13	0.948	GIMAP7	0.755	0.997	0.042	0
DNAJC13	0.948	RUNX2	0.848	0.975	0.04	0.003
DNAJC13	0.948	LY6G5B_CSNK2B	0.661	0.979	0.03	0
DNAJC13	0.948	TSHZ2	0.801	0.99	0.043	0
TNFAIP6	0.971	LRRN3	0.947	0.998	0.035	0.03
TNFAIP6	0.971	HLA-DPB1	0.765	0.995	0.039	0
TNFAIP6	0.971	CASS4	0.877	0.998	0.031	0
TNFAIP6	0.971	GIMAP7	0.755	0.992	0.05	0
TNFAIP6	0.971	RUNX2	0.848	0.993	0.038	0.001
TNFAIP6	0.971	HLA-DPA1	0.65	0.995	0.036	0
TNFAIP6	0.971	PDE3B	0.85	0.997	0.035	0.001
FOXD4L3_FOXD4L6	0.892	SH2D1B	0.867	0.973	0.034	0.002
FOXD4L3_FOXD4L6	0.892	KLRK1_KLRC4	0.857	0.97	0.029	0.003

FOXD4L3_FOXD4L6	0.892	ITK	0.899	0.97	0.005	0.031
FOXD4L3_FOXD4L6	0.892	HIST1H4E	0.83	0.937	0.027	0.02
FOXD4L3_FOXD4L6	0.892	CCR3	0.905	0.97	0.005	0.034
FOXD4L3_FOXD4L6	0.892	CHI3L1	0.909	0.987	0.005	0.039
FOXD4L3_FOXD4L6	0.892	GIMAP7	0.755	0.951	0.011	0
FOXD4L3_FOXD4L6	0.892	ANAPC11	0.818	0.948	0.015	0.007
FOXD4L3_FOXD4L6	0.892	RUNX2	0.848	0.966	0.003	0.015
FOXD4L3_FOXD4L6	0.892	HLA-DRA	0.768	0.929	0.023	0.002
FOXD4L3_FOXD4L6	0.892	PDE3B	0.85	0.977	0.003	0.006
FOXD4L3_FOXD4L6	0.892	ITGA4_CERKL	0.694	0.946	0.041	0
FOXD4L3_FOXD4L6	0.892	NPCDR1	0.86	0.948	0.021	0.017
FOXD4L3_FOXD4L6	0.892	CCR4	0.784	0.939	0.037	0.001
FOXD4L3_FOXD4L6	0.892	ABCG1	0.789	0.946	0.021	0.007
FOXD4L3_FOXD4L6	0.892	PYHIN1	0.807	0.952	0.038	0.002
FOXD4L3_FOXD4L6	0.892	TSHZ2	0.801	0.952	0.013	0.002
FOXD4L3_FOXD4L6	0.892	RASA4_RASA4P_R	0.779	0.943	0.018	0.001
FOXD4L3_FOXD4L6	0.892	CAMK1D	0.702	0.937	0.045	0
MMP9_LOC1001280	0.887	CASS4	0.877	0.962	0.034	0.03
MMP9_LOC1001280	0.887	ITK	0.899	0.959	0.041	0.031
MMP9_LOC1001280	0.887	HIST1H4E	0.83	0.956	0.008	0.014
MMP9_LOC1001280	0.887	PHOSPHO1	0.85	0.957	0.049	0.025
MMP9_LOC1001280	0.887	RRP12_LOC644215	0.632	0.928	0.049	0
MMP9_LOC1001280	0.887	LASS4	0.794	0.935	0.022	0.027
GSR	0.831	KLRF1	0.872	0.927	0.031	0.005
GSR	0.831	SH2D1B	0.867	0.935	0.016	0.031
GSR	0.831	MRPL41	0.811	0.926	0.031	0.002
GSR	0.831	CASS4	0.877	0.981	0	0.002
GSR	0.831	KLRK1_KLRC4	0.857	0.943	0.01	0.009
GSR	0.831	ITK	0.899	0.985	0.001	0.002

GSR	0.831	GOT2	0.905	0.988	0	0.008
GSR	0.831	B3GAT3	0.783	0.925	0.012	0.002
GSR	0.831	CCR3	0.905	0.95	0.005	0.037
GSR	0.831	SLC39A9	0.551	0.916	0.025	0
GSR	0.831	GIMAP7	0.755	0.921	0.012	0.001
GSR	0.831	ANAPC11	0.818	0.908	0.028	0.026
GSR	0.831	RUNX2	0.848	0.95	0	0.022
GSR	0.831	HLA-DRA	0.768	0.893	0.046	0.013
GSR	0.831	PDE3B	0.85	0.949	0.009	0.003
GSR	0.831	SULF2	0.819	0.957	0.007	0.001
GSR	0.831	IRF4	0.781	0.933	0.01	0.002
GSR	0.831	HSP90AB1_HSP90A	0.799	0.933	0.023	0.002
GSR	0.831	NPCDR1	0.86	0.939	0.01	0.003
GSR	0.831	LY6G5B_CSNK2B	0.661	0.952	0.004	0
GSR	0.831	CCR4	0.784	0.91	0.044	0.003
GSR	0.831	FAM118A	0.759	0.94	0.01	0
GSR	0.831	PYHIN1	0.807	0.949	0.006	0.001
GSR	0.831	TSHZ2	0.801	0.962	0	0.001
GSR	0.831	RASA4_RASA4P_R	0.779	0.917	0.034	0.001
GSR	0.831	CAMK1D	0.702	0.941	0.005	0
KLRF1	0.872	ANKRD34B	0.846	0.95	0.004	0.013
KLRF1	0.872	SGMS2	0.859	0.957	0.001	0.032
KLRF1	0.872	GK3P_GK	0.877	0.952	0.006	0.012
KLRF1	0.872	SLC15A2	0.824	0.933	0.001	0.013
KLRF1	0.872	OLFM4	0.806	0.935	0.034	0.003
KLRF1	0.872	TCN1	0.816	0.953	0.002	0.004
KLRF1	0.872	ATP13A3	0.841	0.951	0.001	0.035
KLRF1	0.872	TMEM144_LOC2855	0.92	0.976	0.001	0.045
KLRF1	0.872	BPI	0.83	0.932	0.004	0.015

KLRF1	0.872	HSPC159	0.823	0.944	0.002	0.015
KLRF1	0.872	PPP2R5A_SNORA16	0.775	0.937	0.001	0.003
KLRF1	0.872	TMTC1	0.826	0.946	0.004	0.01
KLRF1	0.872	SEC24A_SAR1B	0.761	0.917	0.006	0.004
KLRF1	0.872	HMGB2	0.849	0.951	0.001	0.031
KLRF1	0.872	NA	0.866	0.958	0.001	0.02
KLRF1	0.872	LGALS1	0.736	0.901	0.018	0.011
KLRF1	0.872	CD163	0.735	0.927	0.009	0.002
KLRF1	0.872	MTHFS	0.757	0.916	0.015	0.003
KLRF1	0.872	LCN2	0.752	0.921	0.026	0.001
KLRF1	0.872	EIF2AK2	0.857	0.948	0.008	0.013
KLRF1	0.872	SIAE	0.814	0.92	0.006	0.026
KLRF1	0.872	CDA	0.804	0.912	0.018	0.029
KLRF1	0.872	SAP30	0.728	0.903	0.005	0.011
KLRF1	0.872	MTRR	0.703	0.912	0.048	0
KLRF1	0.872	AIG1	0.842	0.928	0.001	0.048
KLRF1	0.872	HS2ST1_UBA2	0.758	0.904	0.043	0.01
KLRF1	0.872	TREML1	0.793	0.932	0.006	0.01
KLRF1	0.872	GSTO1	0.793	0.928	0.001	0.015
KLRF1	0.872	MACF1	0.742	0.919	0.037	0
KLRF1	0.872	AMFR	0.69	0.903	0.017	0.003
KLRF1	0.872	OR9A2	0.813	0.926	0.005	0.01
KLRF1	0.872	HDHD1A	0.63	0.915	0.006	0
KLRF1	0.872	ACTA2	0.783	0.922	0.01	0.013
KLRF1	0.872	DPH3	0.86	0.943	0.003	0.022
KLRF1	0.872	ZNF28	0.558	0.911	0.033	0
KLRF1	0.872	TAF13	0.854	0.95	0.004	0.02
KLRF1	0.872	P4HA1_RPL17	0.715	0.931	0.01	0
KLRF1	0.872	KLHL5	0.826	0.932	0.005	0.019

KLRF1	0.872	DLEU2_DLEU2L	0.874	0.958	0.001	0.022
KLRF1	0.872	ANKRD28	0.8	0.942	0.001	0.006
KLRF1	0.872	HSPB1_HSPBL2	0.778	0.911	0.01	0.014
KLRF1	0.872	CCDC125	0.632	0.912	0.041	0
KLRF1	0.872	LHFP	0.759	0.903	0.015	0.005
KLRF1	0.872	ZRANB1	0.724	0.941	0.001	0
KLRF1	0.872	FSD1L_GARNL1	0.66	0.906	0.034	0
KLRF1	0.872	UBE2F_C20orf194	0.762	0.924	0.007	0.002
KLRF1	0.872	MYL9	0.771	0.921	0.013	0.009
KLRF1	0.872	CYP4F3_CYP4F2	0.593	0.925	0.005	0
KLRF1	0.872	CEP97	0.695	0.923	0.01	0
KLRF1	0.872	DYNLL1	0.776	0.947	0.003	0
KLRF1	0.872	PLIN2	0.671	0.915	0.003	0
KLRF1	0.872	FAM118B	0.737	0.941	0.001	0.001
KLRF1	0.872	NP	0.633	0.901	0.038	0
KLRF1	0.872	SPARC	0.703	0.932	0.008	0
KLRF1	0.872	PLEKHA3	0.658	0.921	0.006	0
KLRF1	0.872	TMEM62_SPCS2_L	0.645	0.929	0.003	0
KLRF1	0.872	PLEKHF2	0.822	0.941	0.004	0.011
KLRF1	0.872	CMTM5	0.694	0.906	0.035	0.001
KLRF1	0.872	AIF1	0.816	0.933	0.001	0.022
KLRF1	0.872	HIST2H2BF_HIST2	0.754	0.916	0.031	0.002
KLRF1	0.872	CALM2_C2orf61	0.733	0.934	0.003	0
KLRF1	0.872	SPATA6	0.642	0.917	0.01	0
KLRF1	0.872	DCTN5	0.557	0.903	0.05	0
SH2D1B	0.867	ANKRD34B	0.846	0.938	0.018	0.033
SH2D1B	0.867	SGMS2	0.859	0.974	0.003	0.008
SH2D1B	0.867	GK3P_GK	0.877	0.947	0.025	0.018
SH2D1B	0.867	SLC15A2	0.824	0.966	0.002	0.002

SH2D1B	0.867	TCN1	0.816	0.959	0.028	0.001
SH2D1B	0.867	PLAC8	0.767	0.922	0.027	0.008
SH2D1B	0.867	ATP13A3	0.841	0.96	0.005	0.02
SH2D1B	0.867	HSPC159	0.823	0.938	0.008	0.023
SH2D1B	0.867	PPP2R5A_SNORA16	0.775	0.939	0.008	0.003
SH2D1B	0.867	SEC24A_SAR1B	0.761	0.921	0.018	0.006
SH2D1B	0.867	HMGB2	0.849	0.962	0.016	0.012
SH2D1B	0.867	SLC39A9	0.551	0.908	0.042	0
SH2D1B	0.867	NA	0.866	0.948	0.006	0.03
SH2D1B	0.867	LGALS1	0.736	0.914	0.021	0.007
SH2D1B	0.867	EIF2AK2	0.857	0.948	0.005	0.028
SH2D1B	0.867	ABCA13	0.868	0.959	0.017	0.01
SH2D1B	0.867	CDA	0.804	0.928	0.023	0.015
SH2D1B	0.867	SAP30	0.728	0.903	0.009	0.013
SH2D1B	0.867	SUCNR1	0.922	0.985	0.003	0.022
SH2D1B	0.867	MTRR	0.703	0.928	0.002	0.001
SH2D1B	0.867	AIG1	0.842	0.961	0.006	0.008
SH2D1B	0.867	HS2ST1_UBA2	0.758	0.91	0.03	0.015
SH2D1B	0.867	GSTO1	0.793	0.944	0.006	0.008
SH2D1B	0.867	MACF1	0.742	0.93	0.022	0.001
SH2D1B	0.867	AMFR	0.69	0.897	0.046	0.006
SH2D1B	0.867	HDHD1A	0.63	0.93	0.016	0
SH2D1B	0.867	DPH3	0.86	0.948	0.011	0.026
SH2D1B	0.867	TAF13	0.854	0.972	0.001	0.01
SH2D1B	0.867	P4HA1_RPL17	0.715	0.941	0.011	0
SH2D1B	0.867	KLHL5	0.826	0.946	0.003	0.022
SH2D1B	0.867	DLEU2_DLEU2L	0.874	0.954	0.003	0.041
SH2D1B	0.867	ANKRD28	0.8	0.948	0.004	0.005
SH2D1B	0.867	MGST3	0.602	0.932	0.019	0

SH2D1B	0.867	HSPB1_HSPBL2	0.778	0.917	0.008	0.014
SH2D1B	0.867	ZRANB1	0.724	0.913	0.019	0.002
SH2D1B	0.867	UBE2F_C20orf194	0.762	0.943	0.01	0.001
SH2D1B	0.867	CCRL2	0.786	0.935	0.033	0.004
SH2D1B	0.867	MYL9	0.771	0.917	0.021	0.013
SH2D1B	0.867	CEP97	0.695	0.943	0.025	0
SH2D1B	0.867	DYNLL1	0.776	0.956	0.013	0
SH2D1B	0.867	PLIN2	0.671	0.934	0.012	0
SH2D1B	0.867	FAM118B	0.737	0.951	0.003	0.001
SH2D1B	0.867	CTSL1_CTSLL3	0.715	0.939	0.041	0
SH2D1B	0.867	PLEKHA3	0.658	0.919	0.027	0
SH2D1B	0.867	TMEM62_SPCS2_L	0.645	0.929	0.006	0
SH2D1B	0.867	PLEKHF2	0.822	0.957	0.004	0.006
SH2D1B	0.867	AIF1	0.816	0.941	0.008	0.021
SH2D1B	0.867	HIST2H2BF_HIST2	0.754	0.918	0.022	0.004
SH2D1B	0.867	CALM2_C2orf61	0.733	0.957	0.005	0
SH2D1B	0.867	DCTN5	0.557	0.916	0.019	0
ANKRD34B	0.846	HIST1H4C	0.859	0.944	0.006	0.026
ANKRD34B	0.846	HIST1H3I	0.787	0.921	0.022	0.003
ANKRD34B	0.846	MRPL41	0.811	0.952	0.01	0
ANKRD34B	0.846	KLRK1_KLRC4	0.857	0.952	0.005	0.017
ANKRD34B	0.846	B3GAT3	0.783	0.911	0.006	0.015
ANKRD34B	0.846	HIST1H4E	0.83	0.934	0.002	0.028
ANKRD34B	0.846	FGFBP2	0.812	0.938	0.019	0.003
ANKRD34B	0.846	KLRD1	0.784	0.932	0.021	0.002
ANKRD34B	0.846	GIMAP7	0.755	0.908	0.027	0.006
ANKRD34B	0.846	ANAPC11	0.818	0.924	0.008	0.028
ANKRD34B	0.846	DNAJC9_FAM149B1	0.811	0.952	0.013	0.001
ANKRD34B	0.846	PLA2G7	0.834	0.938	0.024	0.006

ANKRD34B	0.846	SULF2	0.819	0.923	0.015	0.014
ANKRD34B	0.846	IRF4	0.781	0.914	0.006	0.023
ANKRD34B	0.846	HSP90AB1_HSP90A	0.799	0.921	0.043	0.015
ANKRD34B	0.846	NPCDR1	0.86	0.921	0.008	0.034
ANKRD34B	0.846	CCR4	0.784	0.917	0.02	0.005
ANKRD34B	0.846	PYHIN1	0.807	0.931	0.006	0.015
ANKRD34B	0.846	TSHZ2	0.801	0.938	0.002	0.006
SGMS2	0.859	CRIP1	0.83	0.95	0.041	0.001
SGMS2	0.859	MRPL41	0.811	0.957	0.018	0
SGMS2	0.859	CASS4	0.877	0.962	0.001	0.027
SGMS2	0.859	KLRK1_KLRC4	0.857	0.951	0.022	0.009
SGMS2	0.859	ITK	0.899	0.984	0.001	0.01
SGMS2	0.859	GOT2	0.905	0.976	0.002	0.036
SGMS2	0.859	B3GAT3	0.783	0.936	0.018	0.003
SGMS2	0.859	HIST1H4E	0.83	0.938	0.004	0.021
SGMS2	0.859	CHI3L1	0.909	0.99	0.002	0.028
SGMS2	0.859	SLC39A9	0.551	0.91	0.043	0
SGMS2	0.859	GIMAP7	0.755	0.959	0.004	0
SGMS2	0.859	ANAPC11	0.818	0.943	0.033	0.002
SGMS2	0.859	RUNX2	0.848	0.965	0.003	0.007
SGMS2	0.859	DNAJC9_FAM149B1	0.811	0.959	0.046	0
SGMS2	0.859	PLA2G7	0.834	0.955	0.026	0.001
SGMS2	0.859	PDE3B	0.85	0.976	0.003	0.003
SGMS2	0.859	SULF2	0.819	0.978	0.003	0.001
SGMS2	0.859	IRF4	0.781	0.923	0.047	0.01
SGMS2	0.859	HSP90AB1_HSP90A	0.799	0.929	0.045	0.014
SGMS2	0.859	NPCDR1	0.86	0.942	0.014	0.013
SGMS2	0.859	LY6G5B_CSNK2B	0.661	0.933	0.005	0
SGMS2	0.859	CCR4	0.784	0.969	0.003	0

SGMS2	0.859	FAM118A	0.759	0.931	0.002	0.005
SGMS2	0.859	PYHIN1	0.807	0.948	0.017	0.003
SGMS2	0.859	CLC	0.81	0.943	0.048	0.003
SGMS2	0.859	TSHZ2	0.801	0.971	0.002	0.001
SGMS2	0.859	RASA4_RASA4P_R	0.779	0.928	0.031	0.002
SGMS2	0.859	CAMK1D	0.702	0.938	0.013	0
SGMS2	0.859	IL5RA	0.832	0.939	0.05	0.004
B3GNT5_MCF2L2	0.956	LRRN3	0.947	0.999	0.018	0.028
B3GNT5_MCF2L2	0.956	VAMP2	0.673	0.985	0.016	0
B3GNT5_MCF2L2	0.956	CASS4	0.877	0.998	0.014	0
B3GNT5_MCF2L2	0.956	RUNX2	0.848	0.986	0.023	0.001
B3GNT5_MCF2L2	0.956	PDE3B	0.85	0.998	0.015	0.001
GK3P_GK	0.877	CRIP1	0.83	0.932	0.037	0.015
GK3P_GK	0.877	VAMP2	0.673	0.911	0.015	0.001
GK3P_GK	0.877	MRPL41	0.811	0.951	0.006	0.001
GK3P_GK	0.877	CASS4	0.877	0.953	0.002	0.047
GK3P_GK	0.877	B3GAT3	0.783	0.935	0.003	0.005
GK3P_GK	0.877	HIST1H4E	0.83	0.928	0.006	0.035
GK3P_GK	0.877	CCR3	0.905	0.959	0.002	0.043
GK3P_GK	0.877	CHI3L1	0.909	0.96	0.012	0.048
GK3P_GK	0.877	GIMAP7	0.755	0.924	0.009	0.001
GK3P_GK	0.877	ANAPC11	0.818	0.93	0.013	0.008
GK3P_GK	0.877	HLA-DRA	0.768	0.907	0.047	0.007
GK3P_GK	0.877	DNAJC9_FAM149B1	0.811	0.943	0.034	0.003
GK3P_GK	0.877	NA	0.696	0.931	0.013	0
GK3P_GK	0.877	PLA2G7	0.834	0.944	0.02	0.004
GK3P_GK	0.877	PMS2CL_PMS2	0.685	0.915	0.02	0
GK3P_GK	0.877	PDE3B	0.85	0.949	0.001	0.041
GK3P_GK	0.877	SULF2	0.819	0.922	0.038	0.031

GK3P_GK	0.877	HSP90AB1_HSP90A	0.799	0.925	0.038	0.011
GK3P_GK	0.877	NPCDR1	0.86	0.942	0.009	0.017
GK3P_GK	0.877	LY6G5B_CSNK2B	0.661	0.931	0.013	0
GK3P_GK	0.877	CCR4	0.784	0.938	0.002	0.003
GK3P_GK	0.877	ABCG1	0.789	0.91	0.033	0.041
GK3P_GK	0.877	FAM118A	0.759	0.913	0.041	0.004
GK3P_GK	0.877	CLC	0.81	0.933	0.019	0.014
GK3P_GK	0.877	TSHZ2	0.801	0.94	0.004	0.005
GK3P_GK	0.877	RASA4_RASA4P_R	0.779	0.921	0.021	0.003
GK3P_GK	0.877	CAMK1D	0.702	0.927	0.009	0
GK3P_GK	0.877	CFD	0.767	0.951	0.003	0.001
GK3P_GK	0.877	IL5RA	0.832	0.935	0.017	0.016
PFKFB2	0.874	MRPL41	0.811	0.954	0.025	0.002
PFKFB2	0.874	ITK	0.899	0.962	0.015	0.047
PFKFB2	0.874	B3GAT3	0.783	0.954	0.019	0.001
PFKFB2	0.874	HIST1H4E	0.83	0.937	0.023	0.025
PFKFB2	0.874	DNAJC9_FAM149B1	0.811	0.961	0.04	0.001
PFKFB2	0.874	PMS2CL_PMS2	0.685	0.935	0.035	0
PFKFB2	0.874	PDE3B	0.85	0.948	0.013	0.045
PFKFB2	0.874	IRF4	0.781	0.929	0.024	0.014
PFKFB2	0.874	IRS2	0.648	0.925	0.039	0
PFKFB2	0.874	HSP90AB1_HSP90A	0.799	0.954	0.044	0.003
PFKFB2	0.874	ABCG1	0.789	0.927	0.017	0.033
PFKFB2	0.874	FAM118A	0.759	0.935	0.032	0.001
PFKFB2	0.874	TSHZ2	0.801	0.946	0.019	0.005
PFKFB2	0.874	CAMK1D	0.702	0.93	0.05	0
PICALM	0.879	LRRN3	0.947	0.993	0.002	0.033
PICALM	0.879	VAMP2	0.673	0.952	0.015	0
PICALM	0.879	CASS4	0.877	0.989	0.002	0.001

PICALM	0.879	ITK	0.899	0.983	0.004	0.002
PICALM	0.879	GOT2	0.905	0.976	0.013	0.005
PICALM	0.879	B3GAT3	0.783	0.953	0.047	0
PICALM	0.879	HIST1H4E	0.83	0.962	0.019	0
PICALM	0.879	CCR3	0.905	0.967	0.01	0.009
PICALM	0.879	CHI3L1	0.909	0.975	0.006	0.039
PICALM	0.879	GIMAP7	0.755	0.958	0.018	0
PICALM	0.879	ANAPC11	0.818	0.96	0.033	0
PICALM	0.879	RUNX2	0.848	0.989	0.002	0.001
PICALM	0.879	PDE3B	0.85	0.989	0.002	0.001
PICALM	0.879	LY6G5B_CSNK2B	0.661	0.948	0.039	0
PICALM	0.879	CCR4	0.784	0.972	0.014	0
PICALM	0.879	TSHZ2	0.801	0.947	0.048	0
METTL7B	0.943	GOT2	0.905	0.983	0.047	0.014
METTL7B	0.943	HIST1H4E	0.83	0.978	0.043	0.001
HIST1H4C	0.859	JKAMP	0.93	0.982	0.001	0.036
HIST1H4C	0.859	CD63	0.757	0.953	0.005	0.001
HIST1H4C	0.859	ATP13A3	0.841	0.928	0.044	0.045
HIST1H4C	0.859	HSPC159	0.823	0.937	0.036	0.006
HIST1H4C	0.859	PPP2R5A_SNORA16	0.775	0.925	0.038	0.002
HIST1H4C	0.859	TMTC1	0.826	0.923	0.032	0.018
HIST1H4C	0.859	HMGB2	0.849	0.95	0.029	0.007
HIST1H4C	0.859	EXOSC4	0.731	0.935	0.009	0.001
HIST1H4C	0.859	FOLR3_FOLR2	0.848	0.959	0.012	0.001
HIST1H4C	0.859	LGALS1	0.736	0.929	0.034	0.001
HIST1H4C	0.859	SIAE	0.814	0.942	0.003	0.008
HIST1H4C	0.859	ABCA13	0.868	0.985	0.003	0
HIST1H4C	0.859	CDA	0.804	0.927	0.037	0.007
HIST1H4C	0.859	SAP30	0.728	0.895	0.029	0.008

HIST1H4C	0.859	AGTRAP	0.856	0.955	0.001	0.039
HIST1H4C	0.859	SUCNR1	0.922	0.996	0.001	0.006
HIST1H4C	0.859	AIG1	0.842	0.945	0.025	0.004
HIST1H4C	0.859	PCOLCE2	0.709	0.937	0.009	0
HIST1H4C	0.859	VOPP1_LOC100128	0.618	0.907	0.037	0
HIST1H4C	0.859	SLC39A8	0.698	0.933	0.02	0
HIST1H4C	0.859	SLC11A1	0.785	0.917	0.025	0.017
HIST1H4C	0.859	TREML1	0.793	0.952	0.012	0.002
HIST1H4C	0.859	GSTO1	0.793	0.926	0.046	0.005
HIST1H4C	0.859	CLEC4A	0.87	0.933	0.027	0.043
HIST1H4C	0.859	NEK6_LOC1001290	0.765	0.906	0.024	0.011
HIST1H4C	0.859	AMFR	0.69	0.908	0.046	0.002
HIST1H4C	0.859	DPH3	0.86	0.966	0.001	0.006
HIST1H4C	0.859	TAF13	0.854	0.952	0.048	0.003
HIST1H4C	0.859	DLEU2_DLEU2L	0.874	0.955	0.003	0.016
HIST1H4C	0.859	ANKRD28	0.8	0.932	0.036	0.005
HIST1H4C	0.859	HSPB1_HSPBL2	0.778	0.915	0.046	0.006
HIST1H4C	0.859	LHFP	0.759	0.907	0.027	0.005
HIST1H4C	0.859	UBE2F_C20orf194	0.762	0.952	0.014	0
HIST1H4C	0.859	MYL9	0.771	0.95	0.003	0.002
HIST1H4C	0.859	CMTM5	0.694	0.947	0.007	0
HIST1H4C	0.859	CALM2_C2orf61	0.733	0.94	0.031	0
C9orf72	0.958	LRRN3	0.947	0.998	0.05	0.026
C9orf72	0.958	CASS4	0.877	0.998	0.043	0
C9orf72	0.958	GIMAP7	0.755	0.989	0.041	0
C9orf72	0.958	RUNX2	0.848	0.995	0.044	0.001
C9orf72	0.958	PDE3B	0.85	0.999	0.04	0.001
HIST1H3I	0.787	TCN1	0.816	0.899	0.044	0.006
HIST1H3I	0.787	CD63	0.757	0.901	0.002	0.015

HIST1H3I	0.787	BPI	0.83	0.913	0.025	0.002
HIST1H3I	0.787	PPP2R5A_SNORA16	0.775	0.878	0.015	0.043
HIST1H3I	0.787	SEC24A_SAR1B	0.761	0.866	0.033	0.039
HIST1H3I	0.787	HMGB2	0.849	0.917	0.01	0.047
HIST1H3I	0.787	EXOSC4	0.731	0.888	0.007	0.017
HIST1H3I	0.787	FOLR3_FOLR2	0.848	0.924	0.003	0.018
HIST1H3I	0.787	LGALS1	0.736	0.87	0.017	0.033
HIST1H3I	0.787	ABCA13	0.868	0.952	0.001	0.007
HIST1H3I	0.787	SUCNR1	0.922	0.981	0	0.025
HIST1H3I	0.787	PCOLCE2	0.709	0.886	0.003	0.005
HIST1H3I	0.787	VOPP1_LOC100128	0.618	0.844	0.02	0.003
HIST1H3I	0.787	SLC39A8	0.698	0.875	0.005	0.009
HIST1H3I	0.787	TREML1	0.793	0.892	0.035	0.025
HIST1H3I	0.787	RETN	0.663	0.858	0.043	0.002
HIST1H3I	0.787	DPH3	0.86	0.936	0	0.044
HIST1H3I	0.787	TAF13	0.854	0.932	0.003	0.026
HIST1H3I	0.787	HSPB1_HSPBL2	0.778	0.884	0.005	0.044
HIST1H3I	0.787	LHFP	0.759	0.866	0.005	0.047
HIST1H3I	0.787	UBE2F_C20orf194	0.762	0.903	0.014	0.003
HIST1H3I	0.787	MYL9	0.771	0.912	0.003	0.011
HIST1H3I	0.787	CTSL1_CTSLL3	0.715	0.874	0.045	0.003
HIST1H3I	0.787	PLEKHA3	0.658	0.857	0.039	0.002
HIST1H3I	0.787	CMTM5	0.694	0.877	0.045	0.002
SLC15A2	0.824	LRRN3	0.947	0.979	0	0.023
SLC15A2	0.824	HLA-DPB1	0.765	0.917	0.011	0
SLC15A2	0.824	VAMP2	0.673	0.905	0.01	0
SLC15A2	0.824	MRPL41	0.811	0.926	0.015	0.002
SLC15A2	0.824	CASS4	0.877	0.959	0	0.017
SLC15A2	0.824	KLRK1_KLRC4	0.857	0.95	0.004	0.004

SLC15A2	0.824	ITK	0.899	0.998	0	0.002
SLC15A2	0.824	GOT2	0.905	0.979	0	0.018
SLC15A2	0.824	B3GAT3	0.783	0.931	0.004	0.002
SLC15A2	0.824	FGFBP2	0.812	0.907	0.044	0.006
SLC15A2	0.824	CCR3	0.905	0.957	0.001	0.021
SLC15A2	0.824	SLC39A9	0.551	0.902	0.022	0
SLC15A2	0.824	GIMAP7	0.755	0.946	0.001	0
SLC15A2	0.824	ANAPC11	0.818	0.914	0.007	0.018
SLC15A2	0.824	RUNX2	0.848	0.946	0.001	0.01
SLC15A2	0.824	HLA-DRA	0.768	0.926	0.006	0.001
SLC15A2	0.824	DNAJC9_FAM149B1	0.811	0.947	0.014	0
SLC15A2	0.824	NA	0.696	0.924	0.008	0
SLC15A2	0.824	PLA2G7	0.834	0.934	0.018	0.001
SLC15A2	0.824	PDE3B	0.85	0.941	0.006	0.007
SLC15A2	0.824	SULF2	0.819	0.92	0.012	0.008
SLC15A2	0.824	IRF4	0.781	0.966	0.001	0
SLC15A2	0.824	HSP90AB1_HSP90A	0.799	0.942	0.006	0.002
SLC15A2	0.824	ITGA4_CERKL	0.694	0.933	0.012	0
SLC15A2	0.824	NPCDR1	0.86	0.956	0.002	0.001
SLC15A2	0.824	LY6G5B_CSNK2B	0.661	0.948	0.001	0
SLC15A2	0.824	CCR4	0.784	0.949	0.002	0
SLC15A2	0.824	ABCG1	0.789	0.913	0.008	0.015
SLC15A2	0.824	FAM118A	0.759	0.923	0.008	0
SLC15A2	0.824	PYHIN1	0.807	0.965	0.002	0
SLC15A2	0.824	CLC	0.81	0.929	0.014	0.005
SLC15A2	0.824	SYNE2	0.678	0.945	0.006	0
SLC15A2	0.824	NA	0.746	0.92	0.022	0
SLC15A2	0.824	TSHZ2	0.801	0.953	0.001	0.001
SLC15A2	0.824	RASA4_RASA4P_R	0.779	0.93	0.003	0.001

SLC15A2	0.824	CAMK1D	0.702	0.919	0.013	0
SLC15A2	0.824	LOC100128751	0.651	0.903	0.038	0
SLC15A2	0.824	IL5RA	0.832	0.922	0.031	0.002
TLR10	0.905	VAMP2	0.673	0.952	0.011	0
TLR10	0.905	CASS4	0.877	0.983	0.004	0.002
TLR10	0.905	ITK	0.899	0.983	0.006	0.004
TLR10	0.905	GOT2	0.905	0.971	0.022	0.017
TLR10	0.905	HIST1H4E	0.83	0.958	0.018	0.003
TLR10	0.905	CCR3	0.905	0.965	0.025	0.01
TLR10	0.905	CHI3L1	0.909	0.968	0.033	0.035
TLR10	0.905	GIMAP7	0.755	0.964	0.018	0
TLR10	0.905	ANAPC11	0.818	0.966	0.034	0
TLR10	0.905	RUNX2	0.848	0.972	0.005	0.005
TLR10	0.905	PDE3B	0.85	0.984	0.002	0.002
TLR10	0.905	NPCDR1	0.86	0.96	0.034	0.002
TLR10	0.905	LY6G5B_CSNK2B	0.661	0.969	0.011	0
TLR10	0.905	CCR4	0.784	0.979	0.003	0
TLR10	0.905	TSHZ2	0.801	0.962	0.017	0
TLR10	0.905	RASA4_RASA4P_R	0.779	0.949	0.042	0
TLR10	0.905	CAMK1D	0.702	0.969	0.015	0
ADM	0.963	PPIF	0.614	0.989	0.035	0
CD274	0.966	CCR4	0.784	0.984	0.049	0
CRIP1	0.83	CD63	0.757	0.917	0.003	0.012
CRIP1	0.83	PPP2R5A_SNORA16	0.775	0.899	0.015	0.023
CRIP1	0.83	SEC24A_SAR1B	0.761	0.892	0.007	0.027
CRIP1	0.83	SH3PXD2B	0.734	0.885	0.019	0.005
CRIP1	0.83	HMGB2	0.849	0.957	0.002	0.023
CRIP1	0.83	EXOSC4	0.731	0.888	0.018	0.017
CRIP1	0.83	LGALS1	0.736	0.908	0.003	0.016

CRIP1	0.83	MTHFS	0.757	0.893	0.013	0.029
CRIP1	0.83	ABCA13	0.868	0.952	0.008	0.006
CRIP1	0.83	SAP30	0.728	0.868	0.01	0.035
CRIP1	0.83	SUCNR1	0.922	0.986	0	0.02
CRIP1	0.83	AIG1	0.842	0.94	0.005	0.016
CRIP1	0.83	PCOLCE2	0.709	0.871	0.035	0.011
CRIP1	0.83	SLC11A1	0.785	0.904	0.006	0.048
CRIP1	0.83	TREML1	0.793	0.901	0.049	0.043
CRIP1	0.83	GSTO1	0.793	0.919	0.011	0.017
CRIP1	0.83	NEK6_LOC1001290	0.765	0.899	0.009	0.027
CRIP1	0.83	AMFR	0.69	0.878	0.02	0.017
CRIP1	0.83	OR9A2	0.813	0.915	0.01	0.026
CRIP1	0.83	TAF13	0.854	0.921	0.032	0.045
CRIP1	0.83	ANKRD28	0.8	0.911	0.003	0.04
CRIP1	0.83	MGST3	0.602	0.894	0.046	0
CRIP1	0.83	LHFP	0.759	0.86	0.038	0.045
CRIP1	0.83	UBE2F_C20orf194	0.762	0.916	0.013	0.004
CRIP1	0.83	MYL9	0.771	0.905	0.007	0.024
CRIP1	0.83	CEP97	0.695	0.895	0.033	0.001
CRIP1	0.83	DYNLL1	0.776	0.949	0.006	0
CRIP1	0.83	FAM118B	0.737	0.903	0.02	0.005
CRIP1	0.83	CDC26	0.619	0.88	0.049	0
CRIP1	0.83	CALM2_C2orf61	0.733	0.931	0.002	0.001
LRRN3	0.947	IFI16	0.912	0.989	0.016	0.01
LRRN3	0.947	JKAMP	0.93	0.996	0.025	0.013
LRRN3	0.947	SLC1A3	0.896	0.975	0.047	0.014
LRRN3	0.947	WSB2	0.911	0.975	0.026	0.029
LRRN3	0.947	HPSE	0.939	0.988	0.013	0.035
LRRN3	0.947	DDAH2	0.886	0.976	0.02	0.041

LRRN3	0.947	LRRC70_IPO11	0.923	0.994	0.042	0.013
LRRN3	0.947	TMEM144_LOC2855	0.92	0.997	0.035	0.018
LRRN3	0.947	PPP2R5A_SNORA16	0.775	0.988	0.047	0
LRRN3	0.947	EAF2_HCG11_LOC	0.917	0.996	0.02	0.024
LRRN3	0.947	RCBTB2_LOC10013	0.905	0.988	0.018	0.015
LRRN3	0.947	SEC24A_SAR1B	0.761	0.979	0.021	0
LRRN3	0.947	EXOSC4	0.731	0.974	0.046	0
LRRN3	0.947	NA	0.866	0.994	0.039	0.001
LRRN3	0.947	LGALS1	0.736	0.969	0.041	0
LRRN3	0.947	CCR1	0.897	0.976	0.042	0.011
LRRN3	0.947	FFAR2	0.868	0.976	0.036	0.003
LRRN3	0.947	EIF2AK2	0.857	0.99	0.025	0.001
LRRN3	0.947	SIAE	0.814	0.976	0.03	0.001
LRRN3	0.947	EFCAB2	0.96	0.999	0.03	0.022
LRRN3	0.947	AGTRAP	0.856	0.974	0.019	0.005
LRRN3	0.947	SUCNR1	0.922	0.993	0.017	0.012
LRRN3	0.947	MTRR	0.703	0.978	0.04	0
LRRN3	0.947	AIG1	0.842	0.986	0.024	0.001
LRRN3	0.947	GSTO1	0.793	0.978	0.023	0.001
LRRN3	0.947	CLEC4A	0.87	0.988	0.023	0.004
LRRN3	0.947	GPR65	0.886	0.984	0.021	0.013
LRRN3	0.947	MACF1	0.742	0.983	0.048	0
LRRN3	0.947	HDHD1A	0.63	0.985	0.043	0
LRRN3	0.947	TRIM21	0.874	0.977	0.027	0.009
LRRN3	0.947	TAF13	0.854	0.989	0.034	0.002
LRRN3	0.947	P4HA1_RPL17	0.715	0.984	0.03	0
LRRN3	0.947	KLHL5	0.826	0.985	0.029	0.001
LRRN3	0.947	MGST3	0.602	0.977	0.03	0
LRRN3	0.947	FAM118B	0.737	0.982	0.036	0

LRRN3	0.947	TMEM62_SPCS2_L	0.645	0.978	0.033	0
LRRN3	0.947	AIF1	0.816	0.987	0.022	0.001
HLA-DPB1	0.765	IFI16	0.912	0.975	0	0.025
HLA-DPB1	0.765	PLAC8	0.767	0.864	0.05	0.043
HLA-DPB1	0.765	PPP2R5A_SNORA16	0.775	0.868	0.019	0.029
HLA-DPB1	0.765	SEC24A_SAR1B	0.761	0.895	0	0.017
HLA-DPB1	0.765	NA	0.866	0.931	0.001	0.036
HLA-DPB1	0.765	FFAR2	0.868	0.936	0	0.026
HLA-DPB1	0.765	EIF2AK2	0.857	0.947	0.001	0.007
HLA-DPB1	0.765	AIG1	0.842	0.912	0.002	0.047
HLA-DPB1	0.765	GAB2	0.729	0.849	0.016	0.035
HLA-DPB1	0.765	GSTO1	0.793	0.899	0.001	0.041
HLA-DPB1	0.765	CLEC4A	0.87	0.946	0	0.034
HLA-DPB1	0.765	TRAF3	0.594	0.856	0.037	0
HLA-DPB1	0.765	MACF1	0.742	0.859	0.029	0.007
HLA-DPB1	0.765	TRIM21	0.874	0.978	0	0.011
HLA-DPB1	0.765	ICAM1	0.821	0.943	0	0.01
HLA-DPB1	0.765	TAF13	0.854	0.907	0.004	0.032
HLA-DPB1	0.765	P4HA1_RPL17	0.715	0.884	0.024	0
HLA-DPB1	0.765	KLHL5	0.826	0.922	0	0.018
HLA-DPB1	0.765	HSPB1_HSPBL2	0.778	0.888	0.005	0.023
HLA-DPB1	0.765	LAIR1_LAIR2	0.749	0.855	0.025	0.04
HLA-DPB1	0.765	UBE2F_C20orf194	0.762	0.862	0.021	0.02
HLA-DPB1	0.765	CCRL2	0.786	0.916	0.006	0.004
HLA-DPB1	0.765	IRF1	0.651	0.876	0.008	0.001
HLA-DPB1	0.765	DYNLL1	0.776	0.89	0.008	0.003
HLA-DPB1	0.765	FAM118B	0.737	0.872	0.048	0.003
HLA-DPB1	0.765	CTSL1_CTSLL3	0.715	0.886	0.006	0.002
HLA-DPB1	0.765	TMEM62_SPCS2_L	0.645	0.861	0.035	0

HLA-DPB1	0.765	PLEKHF2	0.822	0.905	0.005	0.028
HLA-DPB1	0.765	AIF1	0.816	0.915	0.001	0.027
HLA-DPB1	0.765	CALM2_C2orf61	0.733	0.862	0.024	0.004
VAMP2	0.673	JKAMP	0.93	0.977	0	0.023
VAMP2	0.673	OLFM4	0.806	0.837	0.04	0.027
VAMP2	0.673	TCN1	0.816	0.875	0.004	0.021
VAMP2	0.673	WSB2	0.911	0.978	0	0.016
VAMP2	0.673	PLAC8	0.767	0.857	0.001	0.019
VAMP2	0.673	CD63	0.757	0.915	0	0.003
VAMP2	0.673	PDGFC	0.837	0.913	0.001	0.037
VAMP2	0.673	HPGD	0.871	0.921	0.001	0.046
VAMP2	0.673	LRRC70_IPO11	0.923	0.954	0	0.039
VAMP2	0.673	BPI	0.83	0.876	0.002	0.032
VAMP2	0.673	PPP2R5A_SNORA16	0.775	0.854	0.004	0.022
VAMP2	0.673	TMTC1	0.826	0.859	0.01	0.038
VAMP2	0.673	SEC24A_SAR1B	0.761	0.865	0	0.022
VAMP2	0.673	HMGB2	0.849	0.921	0.001	0.005
VAMP2	0.673	EXOSC4	0.731	0.851	0.003	0.009
VAMP2	0.673	FOLR3_FOLR2	0.848	0.929	0	0.002
VAMP2	0.673	PRR13_PCBP2	0.77	0.861	0.004	0.02
VAMP2	0.673	LGALS1	0.736	0.833	0.006	0.047
VAMP2	0.673	FFAR2	0.868	0.926	0	0.011
VAMP2	0.673	MTHFS	0.757	0.885	0.001	0.002
VAMP2	0.673	SIAE	0.814	0.919	0	0.026
VAMP2	0.673	ABCA13	0.868	0.916	0	0.036
VAMP2	0.673	CDA	0.804	0.907	0	0.007
VAMP2	0.673	MTRR	0.703	0.807	0.022	0.007
VAMP2	0.673	AIG1	0.842	0.924	0	0.012
VAMP2	0.673	PCOLCE2	0.709	0.803	0.008	0.022

VAMP2	0.673	GAB2	0.729	0.823	0.021	0.042
VAMP2	0.673	HS2ST1_UBA2	0.758	0.892	0	0.007
VAMP2	0.673	VOPP1_LOC100128	0.618	0.806	0.033	0.004
VAMP2	0.673	SLC11A1	0.785	0.892	0.001	0.019
VAMP2	0.673	ABCA1	0.866	0.922	0	0.018
VAMP2	0.673	GSTO1	0.793	0.891	0	0.019
VAMP2	0.673	CLEC4A	0.87	0.932	0	0.003
VAMP2	0.673	NEK6_LOC1001290	0.765	0.892	0	0.011
VAMP2	0.673	MACF1	0.742	0.837	0.02	0.002
VAMP2	0.673	GALNT2	0.651	0.802	0.01	0.026
VAMP2	0.673	OR9A2	0.813	0.871	0.004	0.032
VAMP2	0.673	DPH3	0.86	0.92	0	0.017
VAMP2	0.673	TRIM21	0.874	0.944	0	0.042
VAMP2	0.673	ICAM1	0.821	0.916	0	0.024
VAMP2	0.673	TAF13	0.854	0.914	0	0.005
VAMP2	0.673	P4HA1_RPL17	0.715	0.819	0.033	0.001
VAMP2	0.673	KLHL5	0.826	0.91	0	0.004
VAMP2	0.673	ANKRD28	0.8	0.906	0	0.02
VAMP2	0.673	LAIR1_LAIR2	0.749	0.878	0.002	0.002
VAMP2	0.673	UBE2F_C20orf194	0.762	0.863	0.007	0.002
VAMP2	0.673	KDM6B_TMEM88	0.711	0.852	0.003	0.014
VAMP2	0.673	DYNLL1	0.776	0.829	0.024	0.028
VAMP2	0.673	FAM118B	0.737	0.828	0.02	0.031
VAMP2	0.673	PLEKHF2	0.822	0.897	0.001	0.008
VAMP2	0.673	AIF1	0.816	0.888	0.001	0.016
VAMP2	0.673	CALM2_C2orf61	0.733	0.838	0.019	0.002
IFI16	0.912	CASS4	0.877	0.989	0.005	0.001
IFI16	0.912	ITK	0.899	0.99	0.006	0.002
IFI16	0.912	GOT2	0.905	0.974	0.049	0.003

IFI16	0.912	CCR3	0.905	0.97	0.037	0.005
IFI16	0.912	CHI3L1	0.909	0.974	0.034	0.017
IFI16	0.912	GIMAP7	0.755	0.979	0.005	0
IFI16	0.912	RUNX2	0.848	0.963	0.017	0.002
IFI16	0.912	HLA-DRA	0.768	0.976	0.012	0
IFI16	0.912	NPCDR1	0.86	0.97	0.038	0
IFI16	0.912	TSHZ2	0.801	0.962	0.046	0
JKAMP	0.93	MRPL41	0.811	0.981	0.041	0
JKAMP	0.93	CASS4	0.877	0.988	0.016	0.001
JKAMP	0.93	ITK	0.899	0.987	0.026	0.002
JKAMP	0.93	GOT2	0.905	0.986	0.021	0.007
JKAMP	0.93	B3GAT3	0.783	0.985	0.008	0
JKAMP	0.93	HIST1H4E	0.83	0.999	0.009	0
JKAMP	0.93	ANAPC11	0.818	0.979	0.022	0
JKAMP	0.93	RUNX2	0.848	0.979	0.023	0.001
JKAMP	0.93	PDE3B	0.85	0.999	0.009	0
MRPL41	0.811	TCN1	0.816	0.933	0.014	0.002
MRPL41	0.811	CD63	0.757	0.958	0	0.001
MRPL41	0.811	BPI	0.83	0.924	0.024	0.003
MRPL41	0.811	HSPC159	0.823	0.922	0.001	0.035
MRPL41	0.811	PPP2R5A_SNORA16	0.775	0.927	0.001	0.004
MRPL41	0.811	TMTC1	0.826	0.9	0.042	0.014
MRPL41	0.811	SEC24A_SAR1B	0.761	0.926	0	0.004
MRPL41	0.811	SH3PXD2B	0.734	0.866	0.026	0.016
MRPL41	0.811	HMGB2	0.849	0.984	0	0.003
MRPL41	0.811	EXOSC4	0.731	0.916	0.001	0.004
MRPL41	0.811	INSIG1	0.509	0.872	0.012	0
MRPL41	0.811	FOLR3_FOLR2	0.848	0.962	0	0.003
MRPL41	0.811	PRR13_PCBP2	0.77	0.889	0.017	0.024

MRPL41	0.811	LGALS1	0.736	0.916	0	0.007
MRPL41	0.811	MTHFS	0.757	0.923	0.001	0.006
MRPL41	0.811	EIF2AK2	0.857	0.935	0.002	0.04
MRPL41	0.811	SIAE	0.814	0.935	0	0.024
MRPL41	0.811	ABCA13	0.868	0.962	0.001	0.001
MRPL41	0.811	CDA	0.804	0.938	0	0.011
MRPL41	0.811	SAP30	0.728	0.853	0.023	0.045
MRPL41	0.811	SUCNR1	0.922	0.986	0	0.012
MRPL41	0.811	AIG1	0.842	0.97	0	0.002
MRPL41	0.811	HS2ST1_UBA2	0.758	0.908	0	0.015
MRPL41	0.811	C22orf37	0.582	0.88	0.018	0
MRPL41	0.811	VOPP1_LOC100128	0.618	0.892	0.003	0
MRPL41	0.811	SLC39A8	0.698	0.898	0.007	0.002
MRPL41	0.811	SLC11A1	0.785	0.915	0	0.033
MRPL41	0.811	TREML1	0.793	0.918	0.006	0.013
MRPL41	0.811	GSTO1	0.793	0.949	0.001	0.003
MRPL41	0.811	CLEC4A	0.87	0.952	0.001	0.028
MRPL41	0.811	NEK6_LOC1001290	0.765	0.906	0.001	0.021
MRPL41	0.811	MACF1	0.742	0.907	0.016	0.001
MRPL41	0.811	AMFR	0.69	0.887	0.002	0.01
MRPL41	0.811	OR9A2	0.813	0.908	0.01	0.016
MRPL41	0.811	HDHD1A	0.63	0.901	0.01	0
MRPL41	0.811	ACPL2	0.651	0.898	0.026	0
MRPL41	0.811	DPH3	0.86	0.958	0	0.014
MRPL41	0.811	TAF13	0.854	0.958	0.003	0.001
MRPL41	0.811	P4HA1_RPL17	0.715	0.897	0.046	0
MRPL41	0.811	KLHL5	0.826	0.92	0.002	0.038
MRPL41	0.811	ANKRD28	0.8	0.938	0	0.01
MRPL41	0.811	MGST3	0.602	0.916	0.005	0

MRPL41	0.811	HSPB1_HSPBL2	0.778	0.884	0.008	0.04
MRPL41	0.811	LHFP	0.759	0.86	0.019	0.045
MRPL41	0.811	LAIR1_LAIR2	0.749	0.904	0.014	0.004
MRPL41	0.811	PTGS1	0.68	0.889	0.012	0.001
MRPL41	0.811	UBE2F_C20orf194	0.762	0.958	0	0
MRPL41	0.811	SRXN1	0.612	0.89	0.028	0
MRPL41	0.811	KDM6B_TMEM88	0.711	0.86	0.032	0.019
MRPL41	0.811	MYL9	0.771	0.916	0.001	0.011
MRPL41	0.811	HIST1H2BJ	0.697	0.905	0.031	0
MRPL41	0.811	CEP97	0.695	0.933	0.002	0
MRPL41	0.811	DYNLL1	0.776	0.95	0.002	0
MRPL41	0.811	FAM118B	0.737	0.914	0.004	0.002
MRPL41	0.811	CTSL1_CTSLL3	0.715	0.919	0.016	0
MRPL41	0.811	NP	0.633	0.888	0.015	0
MRPL41	0.811	PLEKHA3	0.658	0.906	0.005	0
MRPL41	0.811	TMEM62_SPCS2_L	0.645	0.895	0.019	0
MRPL41	0.811	PLEKHF2	0.822	0.934	0.004	0.006
MRPL41	0.811	CMTM5	0.694	0.889	0.019	0.001
MRPL41	0.811	AIF1	0.816	0.931	0.001	0.018
MRPL41	0.811	CDC26	0.619	0.904	0.004	0
MRPL41	0.811	CALM2_C2orf61	0.733	0.959	0	0
OLFM4	0.806	KLRD1	0.784	0.901	0.005	0.024
OLFM4	0.806	HIST1H3J	0.722	0.883	0.029	0.002
OLFM4	0.806	HIST1H3A	0.715	0.887	0.006	0.005
OLFM4	0.806	PMS2CL_PMS2	0.685	0.852	0.028	0.012
OLFM4	0.806	NA	0.763	0.877	0.009	0.035
OLFM4	0.806	B4GALT3	0.659	0.859	0.008	0.012
OLFM4	0.806	CFD	0.767	0.889	0.012	0.027
OLFM4	0.806	IGL@_IGLV1-44_	0.657	0.846	0.043	0.027

CASS4	0.877	WSB2	0.911	0.984	0.001	0.005
CASS4	0.877	CLU	0.894	0.97	0.001	0.007
CASS4	0.877	HPSE	0.939	0.997	0	0.009
CASS4	0.877	C1orf161	0.888	0.963	0.016	0.009
CASS4	0.877	HPGD	0.871	0.968	0.018	0.01
CASS4	0.877	LRRC70_IPO11	0.923	0.974	0.002	0.021
CASS4	0.877	TMEM144_LOC2855	0.92	0.966	0.023	0.017
CASS4	0.877	CDS2	0.869	0.977	0.001	0.006
CASS4	0.877	OLAH	0.885	0.97	0.006	0.005
CASS4	0.877	PPP2R5A_SNORA16	0.775	0.96	0.016	0
CASS4	0.877	EAF2_HCG11_LOC	0.917	0.97	0.011	0.013
CASS4	0.877	RCBTB2_LOC10013	0.905	0.989	0.001	0.004
CASS4	0.877	SEC24A_SAR1B	0.761	0.95	0.018	0
CASS4	0.877	HMGB2	0.849	0.963	0.02	0.003
CASS4	0.877	NA	0.866	0.977	0.008	0.001
CASS4	0.877	PRR13_PCBP2	0.77	0.967	0.012	0
CASS4	0.877	CCR1	0.897	0.977	0.001	0.011
CASS4	0.877	FFAR2	0.868	0.978	0.003	0.001
CASS4	0.877	MTHFS	0.757	0.979	0.003	0
CASS4	0.877	EIF2AK2	0.857	0.95	0.04	0.004
CASS4	0.877	SIAE	0.814	0.952	0.006	0.001
CASS4	0.877	ABCA13	0.868	0.967	0.013	0.001
CASS4	0.877	CDA	0.804	0.961	0.017	0
CASS4	0.877	AGTRAP	0.856	0.937	0.024	0.012
CASS4	0.877	SUCNR1	0.922	0.969	0.004	0.021
CASS4	0.877	AIG1	0.842	0.961	0.014	0.001
CASS4	0.877	GAB2	0.729	0.981	0.002	0
CASS4	0.877	HS2ST1_UBA2	0.758	0.943	0.027	0
CASS4	0.877	SLC11A1	0.785	0.969	0.003	0.001

CASS4	0.877	ABCA1	0.866	0.963	0.023	0.002
CASS4	0.877	CLEC4A	0.87	0.963	0.028	0.003
CASS4	0.877	NEK6_LOC1001290	0.765	0.965	0.002	0
CASS4	0.877	GPR65	0.886	0.952	0.044	0.007
CASS4	0.877	ACTA2	0.783	0.943	0.041	0.001
CASS4	0.877	KCNMA1	0.897	0.959	0.006	0.042
CASS4	0.877	DPH3	0.86	0.967	0.013	0.001
CASS4	0.877	TRIM21	0.874	0.993	0.001	0.003
CASS4	0.877	ICAM1	0.821	0.959	0.004	0.002
CASS4	0.877	KLHL5	0.826	0.955	0.042	0
CASS4	0.877	DLEU2_DLEU2L	0.874	0.969	0.005	0.001
CASS4	0.877	ANKRD28	0.8	0.97	0.007	0
CASS4	0.877	IL1B	0.871	0.98	0.002	0.005
CASS4	0.877	KDM6B_TMEM88	0.711	0.959	0.004	0
CASS4	0.877	ATP6V0D1_LOC100	0.856	0.957	0.001	0.025
CASS4	0.877	AIF1	0.816	0.956	0.043	0.001
TCN1	0.816	KPNA5	0.705	0.881	0.043	0.002
TCN1	0.816	KLRK1_KLRC4	0.857	0.943	0.003	0.025
TCN1	0.816	B3GAT3	0.783	0.896	0.004	0.042
TCN1	0.816	FGFBP2	0.812	0.937	0.006	0.004
TCN1	0.816	KLRD1	0.784	0.918	0.02	0.003
TCN1	0.816	CHI3L1	0.909	0.985	0	0.024
TCN1	0.816	GIMAP7	0.755	0.88	0.027	0.022
TCN1	0.816	DNAJC9_FAM149B1	0.811	0.94	0.004	0.006
TCN1	0.816	PLA2G7	0.834	0.914	0.011	0.043
TCN1	0.816	HSP90AB1_HSP90A	0.799	0.91	0.011	0.043
TCN1	0.816	NA	0.763	0.903	0.014	0.003
TCN1	0.816	C15orf54	0.821	0.914	0.017	0.014
TCN1	0.816	CCR4	0.784	0.915	0.01	0.007

TCN1	0.816	FAM118A	0.759	0.893	0.017	0.016
TCN1	0.816	PYHIN1	0.807	0.914	0.007	0.032
TCN1	0.816	CLC	0.81	0.939	0.002	0.017
TCN1	0.816	B4GALT3	0.659	0.88	0.017	0.002
TCN1	0.816	RASA4_RASA4P_R	0.779	0.901	0.003	0.015
TCN1	0.816	CAMK1D	0.702	0.865	0.02	0.012
TCN1	0.816	IL5RA	0.832	0.917	0.004	0.047
TCN1	0.816	C1orf128	0.751	0.896	0.047	0.004
TCN1	0.816	IGL@_IGLV1-44_	0.657	0.871	0.04	0.007
WSB2	0.911	ITK	0.899	0.987	0.007	0.002
WSB2	0.911	GOT2	0.905	0.993	0.005	0.008
WSB2	0.911	B3GAT3	0.783	0.979	0.022	0
WSB2	0.911	HIST1H4E	0.83	0.968	0.039	0
WSB2	0.911	CCR3	0.905	0.968	0.045	0.003
WSB2	0.911	CHI3L1	0.909	0.981	0.019	0.024
WSB2	0.911	RUNX2	0.848	0.977	0.017	0
WSB2	0.911	HLA-DRA	0.768	0.968	0.049	0
CLU	0.894	ITK	0.899	0.956	0.042	0.004
CLU	0.894	GOT2	0.905	0.968	0.03	0.004
CLU	0.894	HIST1H4E	0.83	0.961	0.016	0.001
CLU	0.894	CCR3	0.905	0.966	0.022	0.005
CLU	0.894	CHI3L1	0.909	0.985	0.006	0.019
CLU	0.894	RUNX2	0.848	0.97	0.005	0.003
CLU	0.894	PHOSPHO1	0.85	0.984	0.004	0.002
CLU	0.894	SULF2	0.819	0.966	0.016	0.001
CLU	0.894	LASS4	0.794	0.959	0.002	0.004
CLU	0.894	TSHZ2	0.801	0.954	0.045	0
KPNA5	0.705	PPP2R5A_SNORA16	0.775	0.888	0	0.036
KPNA5	0.705	NA	0.866	0.934	0	0.033

KPNA5	0.705	MTRR	0.703	0.814	0.013	0.049
KPNA5	0.705	HDHD1A	0.63	0.816	0.009	0.006
KPNA5	0.705	LRRFIP1	0.673	0.802	0.043	0.009
KPNA5	0.705	DPH3	0.86	0.935	0	0.045
KPNA5	0.705	TAF13	0.854	0.943	0	0.021
KPNA5	0.705	P4HA1_RPL17	0.715	0.866	0.002	0.003
KPNA5	0.705	DLEU2_DLEU2L	0.874	0.956	0	0.017
KPNA5	0.705	MGST3	0.602	0.805	0.006	0.01
KPNA5	0.705	FSD1L_GARNL1	0.66	0.829	0.019	0.006
KPNA5	0.705	NA	0.705	0.867	0.01	0
KPNA5	0.705	UBE2F_C20orf194	0.762	0.879	0	0.023
KPNA5	0.705	CEP97	0.695	0.841	0.005	0.017
KPNA5	0.705	DYNLL1	0.776	0.896	0.001	0.001
KPNA5	0.705	FAM118B	0.737	0.842	0.004	0.047
KPNA5	0.705	PLEKHA3	0.658	0.873	0	0.001
KPNA5	0.705	TMEM62_SPCS2_L	0.645	0.843	0	0.007
KPNA5	0.705	PLEKHF2	0.822	0.961	0	0.002
KPNA5	0.705	CMTM5	0.694	0.797	0.036	0.044
KPNA5	0.705	CDC26	0.619	0.786	0.025	0.018
KPNA5	0.705	CALM2_C2orf61	0.733	0.913	0	0
PLAC8	0.767	ITK	0.899	0.971	0	0.005
PLAC8	0.767	B3GAT3	0.783	0.901	0.003	0.036
PLAC8	0.767	GIMAP7	0.755	0.877	0.021	0.008
PLAC8	0.767	HLA-DRA	0.768	0.891	0.015	0.021
PLAC8	0.767	PLA2G7	0.834	0.9	0.024	0.01
PLAC8	0.767	C15orf54	0.821	0.887	0.007	0.034
PLAC8	0.767	LY6G5B_CSNK2B	0.661	0.851	0.037	0.001
PLAC8	0.767	CLC	0.81	0.89	0.026	0.02
CD63	0.757	GOT2	0.905	0.962	0	0.041

CD63	0.757	B3GAT3	0.783	0.961	0	0
CD63	0.757	HIST1H4E	0.83	0.957	0.001	0.001
CD63	0.757	FGFBP2	0.812	0.879	0.045	0.006
CD63	0.757	ANAPC11	0.818	0.925	0.003	0.004
CD63	0.757	RUNX2	0.848	0.921	0.002	0.029
CD63	0.757	PDE3B	0.85	0.917	0.008	0.016
CD63	0.757	JUP	0.804	0.885	0.013	0.039
CD63	0.757	NPCDR1	0.86	0.905	0.004	0.043
CD63	0.757	C15orf54	0.821	0.879	0.048	0.009
CD63	0.757	CCR4	0.784	0.879	0.022	0.009
CD63	0.757	LASS4	0.794	0.92	0.003	0.016
CD63	0.757	TSHZ2	0.801	0.883	0.025	0.015
CD63	0.757	RASA4_RASA4P_R	0.779	0.861	0.027	0.016
HPSE	0.939	ITK	0.899	0.997	0.008	0.002
HPSE	0.939	GOT2	0.905	0.996	0.011	0.006
HPSE	0.939	HIST1H4E	0.83	0.979	0.029	0
HPSE	0.939	CHI3L1	0.909	0.998	0.009	0.016
HPSE	0.939	GIMAP7	0.755	0.994	0.01	0
HPSE	0.939	RUNX2	0.848	0.984	0.025	0
HPSE	0.939	LY6G5B_CSNK2B	0.661	0.985	0.028	0
HPSE	0.939	CCR4	0.784	0.992	0.015	0
HPSE	0.939	PYHIN1	0.807	0.989	0.029	0
C1orf161	0.888	CCR3	0.905	0.954	0.038	0.038
C1orf161	0.888	RUNX2	0.848	0.967	0.02	0.005
C1orf161	0.888	PHOSPHO1	0.85	0.954	0.035	0.017
C1orf161	0.888	PDE3B	0.85	0.959	0.019	0.011
C1orf161	0.888	ABCG1	0.789	0.95	0.008	0.008
KLRK1_KLRC4	0.857	ATP13A3	0.841	0.965	0.001	0.022
KLRK1_KLRC4	0.857	HSPC159	0.823	0.94	0.008	0.007

KLRK1_KLRC4	0.857	PPP2R5A_SNORA16	0.775	0.947	0.002	0.003
KLRK1_KLRC4	0.857	TMTC1	0.826	0.934	0.012	0.013
KLRK1_KLRC4	0.857	HMGB2	0.849	0.951	0.007	0.024
KLRK1_KLRC4	0.857	NA	0.866	0.95	0.003	0.034
KLRK1_KLRC4	0.857	FOLR3_FOLR2	0.848	0.942	0.017	0.009
KLRK1_KLRC4	0.857	LGALS1	0.736	0.905	0.02	0.009
KLRK1_KLRC4	0.857	MTHFS	0.757	0.907	0.021	0.007
KLRK1_KLRC4	0.857	EIF2AK2	0.857	0.946	0.018	0.009
KLRK1_KLRC4	0.857	SIAE	0.814	0.932	0.004	0.017
KLRK1_KLRC4	0.857	CDA	0.804	0.917	0.033	0.015
KLRK1_KLRC4	0.857	SAP30	0.728	0.89	0.009	0.011
KLRK1_KLRC4	0.857	AIG1	0.842	0.93	0.021	0.04
KLRK1_KLRC4	0.857	HS2ST1_UBA2	0.758	0.902	0.017	0.017
KLRK1_KLRC4	0.857	SLC11A1	0.785	0.896	0.022	0.039
KLRK1_KLRC4	0.857	TREML1	0.793	0.919	0.038	0.011
KLRK1_KLRC4	0.857	GSTO1	0.793	0.934	0.004	0.017
KLRK1_KLRC4	0.857	NEK6_LOC1001290	0.765	0.886	0.025	0.039
KLRK1_KLRC4	0.857	DPH3	0.86	0.942	0.002	0.034
KLRK1_KLRC4	0.857	TAF13	0.854	0.953	0.015	0.016
KLRK1_KLRC4	0.857	KLHL5	0.826	0.921	0.015	0.043
KLRK1_KLRC4	0.857	DLEU2_DLEU2L	0.874	0.954	0.003	0.023
KLRK1_KLRC4	0.857	ANKRD28	0.8	0.945	0.005	0.006
KLRK1_KLRC4	0.857	HSPB1_HSPBL2	0.778	0.918	0.012	0.006
KLRK1_KLRC4	0.857	LHFP	0.759	0.903	0.012	0.007
KLRK1_KLRC4	0.857	ZRANB1	0.724	0.923	0.014	0
KLRK1_KLRC4	0.857	UBE2F_C20orf194	0.762	0.916	0.013	0.002
KLRK1_KLRC4	0.857	MYL9	0.771	0.912	0.023	0.011
KLRK1_KLRC4	0.857	CEP97	0.695	0.929	0.031	0
KLRK1_KLRC4	0.857	DYNLL1	0.776	0.95	0.017	0

KLRK1_KLRC4	0.857	FAM118B	0.737	0.933	0.024	0
KLRK1_KLRC4	0.857	PLEKHA3	0.658	0.913	0.014	0
KLRK1_KLRC4	0.857	TMEM62_SPCS2_L	0.645	0.94	0.007	0
KLRK1_KLRC4	0.857	PLEKHF2	0.822	0.939	0.005	0.015
KLRK1_KLRC4	0.857	CALM2_C2orf61	0.733	0.914	0.01	0.001
ATP13A3	0.841	ITK	0.899	0.978	0.004	0.044
ATP13A3	0.841	B3GAT3	0.783	0.94	0.018	0.002
ATP13A3	0.841	HIST1H4E	0.83	0.937	0.009	0.03
ATP13A3	0.841	GIMAP7	0.755	0.92	0.026	0.009
ATP13A3	0.841	ANAPC11	0.818	0.941	0.012	0.01
ATP13A3	0.841	RUNX2	0.848	0.945	0.007	0.032
ATP13A3	0.841	PDE3B	0.85	0.961	0.01	0.017
ATP13A3	0.841	NPCDR1	0.86	0.937	0.024	0.026
ATP13A3	0.841	CCR4	0.784	0.947	0.01	0.002
ATP13A3	0.841	ABCG1	0.789	0.909	0.017	0.039
ATP13A3	0.841	PYHIN1	0.807	0.941	0.021	0.006
ATP13A3	0.841	TSHZ2	0.801	0.94	0.004	0.016
ATP13A3	0.841	RASA4_RASA4P_R	0.779	0.903	0.039	0.02
ITK	0.899	PDGFC	0.837	0.961	0.01	0.011
ITK	0.899	HPGD	0.871	0.955	0.033	0.034
ITK	0.899	TMEM144_LOC2855	0.92	0.983	0.005	0.039
ITK	0.899	PPP2R5A_SNORA16	0.775	0.977	0.006	0
ITK	0.899	EAF2_HCG11_LOC	0.917	0.992	0.004	0.021
ITK	0.899	RCBTB2_LOC10013	0.905	0.973	0.011	0.024
ITK	0.899	SEC24A_SAR1B	0.761	0.977	0.005	0
ITK	0.899	HMGB2	0.849	0.976	0.008	0.004
ITK	0.899	SLC39A9	0.551	0.969	0.006	0
ITK	0.899	NA	0.866	0.978	0.009	0.002
ITK	0.899	FFAR2	0.868	0.957	0.021	0.004

ITK	0.899	MTHFS	0.757	0.962	0.009	0
ITK	0.899	EIF2AK2	0.857	0.98	0.009	0.001
ITK	0.899	SIAE	0.814	0.961	0.006	0.001
ITK	0.899	ABCA13	0.868	0.953	0.046	0.004
ITK	0.899	CDA	0.804	0.96	0.015	0.001
ITK	0.899	SUCNR1	0.922	0.976	0.004	0.03
ITK	0.899	MTRR	0.703	0.993	0.002	0
ITK	0.899	AIG1	0.842	0.976	0.004	0.001
ITK	0.899	HS2ST1_UBA2	0.758	0.948	0.01	0.001
ITK	0.899	GSTO1	0.793	0.966	0.019	0
ITK	0.899	CLEC4A	0.87	0.978	0.008	0.003
ITK	0.899	TRAF3	0.594	0.966	0.007	0
ITK	0.899	GPR65	0.886	0.974	0.004	0.02
ITK	0.899	MACF1	0.742	0.978	0.023	0
ITK	0.899	GALNT2	0.651	0.932	0.045	0
ITK	0.899	HDHD1A	0.63	0.961	0.016	0
ITK	0.899	ACTA2	0.783	0.953	0.015	0.001
ITK	0.899	LRRFIP1	0.673	0.981	0.009	0
ITK	0.899	SFRS9	0.527	0.959	0.021	0
ITK	0.899	DPH3	0.86	0.961	0.021	0.003
ITK	0.899	TRIM21	0.874	0.985	0.002	0.005
ITK	0.899	ICAM1	0.821	0.944	0.015	0.007
ITK	0.899	TAF13	0.854	0.974	0.01	0.002
ITK	0.899	P4HA1_RPL17	0.715	0.984	0.007	0
ITK	0.899	KLHL5	0.826	0.984	0.003	0
ITK	0.899	DLEU2_DLEU2L	0.874	0.959	0.033	0.003
ITK	0.899	ANKRD28	0.8	0.975	0.011	0
ITK	0.899	CCDC125	0.632	0.968	0.018	0
ITK	0.899	LAIR1_LAIR2	0.749	0.979	0.006	0

ITK	0.899	CEP97	0.695	0.967	0.015	0
ITK	0.899	DYNLL1	0.776	0.97	0.035	0
ITK	0.899	PLIN2	0.671	0.971	0.009	0
ITK	0.899	FAM118B	0.737	0.989	0.003	0
ITK	0.899	NP	0.633	0.956	0.041	0
ITK	0.899	TMEM62_SPCS2_L	0.645	0.977	0.011	0
ITK	0.899	PLEKHF2	0.822	0.958	0.042	0.001
ITK	0.899	AIF1	0.816	0.961	0.022	0.001
ITK	0.899	DCTN5	0.557	0.988	0.004	0
PMAIP1	0.622	NA	0.705	0.808	0.009	0.026
GOT2	0.905	LRRC70_IPO11	0.923	0.972	0.024	0.042
GOT2	0.905	PPP2R5A_SNORA16	0.775	0.96	0.048	0
GOT2	0.905	EAF2_HCG11_LOC	0.917	0.978	0.018	0.04
GOT2	0.905	RCBTB2_LOC10013	0.905	0.968	0.007	0.037
GOT2	0.905	SEC24A_SAR1B	0.761	0.965	0.014	0
GOT2	0.905	FOLR3_FOLR2	0.848	0.964	0.046	0.002
GOT2	0.905	CCR1	0.897	0.963	0.024	0.024
GOT2	0.905	FFAR2	0.868	0.961	0.02	0.007
GOT2	0.905	EIF2AK2	0.857	0.975	0.021	0.003
GOT2	0.905	SIAE	0.814	0.967	0.013	0.001
GOT2	0.905	AGTRAP	0.856	0.949	0.04	0.023
GOT2	0.905	SUCNR1	0.922	0.992	0.011	0.008
GOT2	0.905	AIG1	0.842	0.979	0.028	0.001
GOT2	0.905	GSTO1	0.793	0.985	0.012	0
GOT2	0.905	CLEC4A	0.87	0.978	0.009	0.006
GOT2	0.905	ACTA2	0.783	0.948	0.032	0.002
GOT2	0.905	TRIM21	0.874	0.989	0.005	0.005
GOT2	0.905	ICAM1	0.821	0.956	0.018	0.007
GOT2	0.905	TAF13	0.854	0.972	0.049	0.001

GOT2	0.905	KLHL5	0.826	0.961	0.024	0.002
GOT2	0.905	DLEU2_DLEU2L	0.874	0.948	0.037	0.018
GOT2	0.905	ANKRD28	0.8	0.967	0.038	0.001
GOT2	0.905	LAIR1_LAIR2	0.749	0.968	0.041	0
GOT2	0.905	AIF1	0.816	0.958	0.02	0.004
GOT2	0.905	CALM2_C2orf61	0.733	0.961	0.047	0
PDGFC	0.837	B3GAT3	0.783	0.958	0.01	0
PDGFC	0.837	HIST1H4E	0.83	0.948	0.02	0.002
PDGFC	0.837	RUNX2	0.848	0.966	0.004	0.008
PDGFC	0.837	PMS2CL_PMS2	0.685	0.924	0.027	0
PDGFC	0.837	PDE3B	0.85	0.945	0.01	0.034
PDGFC	0.837	NPCDR1	0.86	0.925	0.035	0.041
PDGFC	0.837	CCR4	0.784	0.935	0.028	0.001
PDGFC	0.837	FAM118A	0.759	0.907	0.05	0.009
PDGFC	0.837	TSHZ2	0.801	0.929	0.026	0.009
B3GAT3	0.783	HPGD	0.871	0.945	0	0.047
B3GAT3	0.783	LRRC70_IPO11	0.923	0.96	0	0.04
B3GAT3	0.783	BPI	0.83	0.901	0.031	0.004
B3GAT3	0.783	PPP2R5A_SNORA16	0.775	0.9	0.011	0.006
B3GAT3	0.783	SEC24A_SAR1B	0.761	0.944	0.001	0
B3GAT3	0.783	HMGB2	0.849	0.967	0	0.004
B3GAT3	0.783	EXOSC4	0.731	0.93	0	0.001
B3GAT3	0.783	FOLR3_FOLR2	0.848	0.957	0	0.003
B3GAT3	0.783	PRR13_PCBP2	0.77	0.889	0.029	0.006
B3GAT3	0.783	LGALS1	0.736	0.912	0.002	0.003
B3GAT3	0.783	FFAR2	0.868	0.95	0	0.008
B3GAT3	0.783	MTHFS	0.757	0.926	0.001	0.001
B3GAT3	0.783	EIF2AK2	0.857	0.914	0.013	0.013
B3GAT3	0.783	SIAE	0.814	0.947	0	0.006

B3GAT3	0.783	ABCA13	0.868	0.934	0.002	0.02
B3GAT3	0.783	CDA	0.804	0.942	0	0.003
B3GAT3	0.783	AGTRAP	0.856	0.952	0	0.025
B3GAT3	0.783	AIG1	0.842	0.963	0	0.001
B3GAT3	0.783	PCOLCE2	0.709	0.872	0.033	0.001
B3GAT3	0.783	HS2ST1_UBA2	0.758	0.92	0.001	0.003
B3GAT3	0.783	VOPP1_LOC100128	0.618	0.865	0.028	0
B3GAT3	0.783	SLC11A1	0.785	0.894	0.003	0.049
B3GAT3	0.783	GSTO1	0.793	0.934	0.002	0.001
B3GAT3	0.783	CLEC4A	0.87	0.952	0.001	0.006
B3GAT3	0.783	NEK6_LOC1001290	0.765	0.906	0.002	0.01
B3GAT3	0.783	GALNT2	0.651	0.889	0.012	0
B3GAT3	0.783	GLT25D1	0.607	0.876	0.035	0
B3GAT3	0.783	OR9A2	0.813	0.882	0.029	0.03
B3GAT3	0.783	ACTA2	0.783	0.897	0.024	0.008
B3GAT3	0.783	DPH3	0.86	0.944	0.001	0.014
B3GAT3	0.783	TRIM21	0.874	0.968	0	0.012
B3GAT3	0.783	ICAM1	0.821	0.94	0	0.012
B3GAT3	0.783	TAF13	0.854	0.944	0.005	0.001
B3GAT3	0.783	KLHL5	0.826	0.923	0.003	0.009
B3GAT3	0.783	ANKRD28	0.8	0.93	0.002	0.004
B3GAT3	0.783	IL1B	0.871	0.929	0.003	0.041
B3GAT3	0.783	LAIR1_LAIR2	0.749	0.906	0.014	0.001
B3GAT3	0.783	UBE2F_C20orf194	0.762	0.924	0.011	0
B3GAT3	0.783	CCRL2	0.786	0.881	0.048	0.02
B3GAT3	0.783	KDM6B_TMEM88	0.711	0.857	0.04	0.014
B3GAT3	0.783	MYL9	0.771	0.87	0.014	0.035
B3GAT3	0.783	IRF1	0.651	0.872	0.04	0
B3GAT3	0.783	FAM118B	0.737	0.888	0.046	0.001

B3GAT3	0.783	CTSL1_CTSLL3	0.715	0.916	0.011	0
B3GAT3	0.783	PLEKHA3	0.658	0.869	0.043	0
B3GAT3	0.783	PLEKHF2	0.822	0.917	0.007	0.009
B3GAT3	0.783	AIF1	0.816	0.939	0.001	0.002
B3GAT3	0.783	CALM2_C2orf61	0.733	0.913	0.008	0
HIST1H4E	0.83	HPGD	0.871	0.948	0.003	0.042
HIST1H4E	0.83	LRRC70_IPO11	0.923	0.975	0	0.042
HIST1H4E	0.83	ECHDC3	0.629	0.892	0.042	0
HIST1H4E	0.83	HSPC159	0.823	0.936	0.031	0.001
HIST1H4E	0.83	OLAH	0.885	0.968	0	0.025
HIST1H4E	0.83	PPP2R5A_SNORA16	0.775	0.953	0.005	0
HIST1H4E	0.83	HMGB2	0.849	0.959	0.008	0.003
HIST1H4E	0.83	EXOSC4	0.731	0.957	0	0
HIST1H4E	0.83	NA	0.866	0.926	0.024	0.011
HIST1H4E	0.83	FOLR3_FOLR2	0.848	0.967	0.002	0.001
HIST1H4E	0.83	LGALS1	0.736	0.946	0.002	0
HIST1H4E	0.83	MTHFS	0.757	0.921	0.006	0.001
HIST1H4E	0.83	SIAE	0.814	0.979	0	0
HIST1H4E	0.83	ABCA13	0.868	0.971	0.003	0.001
HIST1H4E	0.83	EFCAB2	0.96	0.987	0	0.04
HIST1H4E	0.83	CDA	0.804	0.955	0.002	0.001
HIST1H4E	0.83	SAP30	0.728	0.902	0.008	0.003
HIST1H4E	0.83	AGTRAP	0.856	0.98	0	0.004
HIST1H4E	0.83	SUCNR1	0.922	0.988	0.001	0.004
HIST1H4E	0.83	AIG1	0.842	0.951	0.01	0.001
HIST1H4E	0.83	PCOLCE2	0.709	0.914	0.018	0
HIST1H4E	0.83	HS2ST1_UBA2	0.758	0.92	0.005	0.002
HIST1H4E	0.83	C22orf37	0.582	0.916	0.011	0
HIST1H4E	0.83	VOPP1_LOC100128	0.618	0.906	0.023	0

HIST1H4E	0.83	SLC39A8	0.698	0.934	0.021	0
HIST1H4E	0.83	SLC11A1	0.785	0.945	0.001	0.004
HIST1H4E	0.83	GSTO1	0.793	0.925	0.023	0.003
HIST1H4E	0.83	CLEC4A	0.87	0.935	0.008	0.03
HIST1H4E	0.83	NEK6_LOC1001290	0.765	0.919	0.001	0.005
HIST1H4E	0.83	AMFR	0.69	0.9	0.034	0.001
HIST1H4E	0.83	OR9A2	0.813	0.914	0.044	0.003
HIST1H4E	0.83	DPH3	0.86	0.965	0.001	0.002
HIST1H4E	0.83	TRIM21	0.874	0.926	0.02	0.044
HIST1H4E	0.83	ICAM1	0.821	0.914	0.014	0.02
HIST1H4E	0.83	TAF13	0.854	0.957	0.018	0.001
HIST1H4E	0.83	KLHL5	0.826	0.916	0.037	0.014
HIST1H4E	0.83	DLEU2_DLEU2L	0.874	0.956	0.002	0.006
HIST1H4E	0.83	ANKRD28	0.8	0.945	0.005	0.002
HIST1H4E	0.83	HSPB1_HSPBL2	0.778	0.921	0.019	0.002
HIST1H4E	0.83	LHFP	0.759	0.897	0.01	0.005
HIST1H4E	0.83	UBE2F_C20orf194	0.762	0.936	0.038	0
HIST1H4E	0.83	MYL9	0.771	0.948	0.003	0.001
HIST1H4E	0.83	PLEKHA3	0.658	0.916	0.036	0
HIST1H4E	0.83	PLEKHF2	0.822	0.941	0.035	0
HIST1H4E	0.83	CMTM5	0.694	0.924	0.041	0
HIST1H4E	0.83	AIF1	0.816	0.915	0.036	0.013
HIST1H4E	0.83	CDC26	0.619	0.908	0.041	0
HIST1H4E	0.83	CALM2_C2orf61	0.733	0.938	0.021	0
HPGD	0.871	RUNX2	0.848	0.95	0.009	0.029
HPGD	0.871	PDE3B	0.85	0.957	0.005	0.04
HPGD	0.871	NPCDR1	0.86	0.94	0.048	0.014
HPGD	0.871	C15orf54	0.821	0.941	0.027	0.005
HPGD	0.871	ABCG1	0.789	0.936	0.02	0.021

HPGD	0.871	LASS4	0.794	0.935	0.033	0.017
HPGD	0.871	TSHZ2	0.801	0.935	0.035	0.01
FGFBP2	0.812	BPI	0.83	0.913	0.018	0.017
FGFBP2	0.812	HSPC159	0.823	0.915	0.003	0.047
FGFBP2	0.812	PPP2R5A_SNORA16	0.775	0.9	0.001	0.03
FGFBP2	0.812	TMTC1	0.826	0.917	0.004	0.038
FGFBP2	0.812	EXOSC4	0.731	0.865	0.032	0.018
FGFBP2	0.812	PCOLCE2	0.709	0.86	0.022	0.009
FGFBP2	0.812	TREML1	0.793	0.914	0.005	0.023
FGFBP2	0.812	AMFR	0.69	0.867	0.006	0.021
FGFBP2	0.812	ANKRD28	0.8	0.913	0.002	0.037
FGFBP2	0.812	HSPB1_HSPBL2	0.778	0.876	0.014	0.049
FGFBP2	0.812	LHFP	0.759	0.871	0.005	0.042
FGFBP2	0.812	ZRANB1	0.724	0.877	0.025	0.007
FGFBP2	0.812	PTGS1	0.68	0.871	0.031	0.002
FGFBP2	0.812	UBE2F_C20orf194	0.762	0.895	0.005	0.01
FGFBP2	0.812	MYL9	0.771	0.905	0.004	0.019
FGFBP2	0.812	HIST1H2BJ	0.697	0.887	0.035	0.002
FGFBP2	0.812	CEP97	0.695	0.882	0.031	0.002
FGFBP2	0.812	DYNLL1	0.776	0.901	0.031	0.002
FGFBP2	0.812	FAM118B	0.737	0.885	0.039	0.007
FGFBP2	0.812	SPARC	0.703	0.889	0.026	0.001
FGFBP2	0.812	PLEKHA3	0.658	0.866	0.034	0.002
FGFBP2	0.812	CMTM5	0.694	0.868	0.047	0.004
FGFBP2	0.812	CALM2_C2orf61	0.733	0.865	0.028	0.019
LRRC70_IPO11	0.923	RUNX2	0.848	0.965	0.022	0.005
LRRC70_IPO11	0.923	PHOSPHO1	0.85	0.965	0.018	0.009
LRRC70_IPO11	0.923	PDE3B	0.85	0.987	0.021	0.001
LRRC70_IPO11	0.923	ABCG1	0.789	0.979	0.015	0.001

TMEM144_LOC2855	0.92	CCR3	0.905	0.986	0.036	0.005
TMEM144_LOC2855	0.92	GIMAP7	0.755	0.99	0.02	0
TMEM144_LOC2855	0.92	RUNX2	0.848	0.963	0.035	0.009
TMEM144_LOC2855	0.92	HLA-DRA	0.768	0.975	0.047	0
TMEM144_LOC2855	0.92	PLA2G7	0.834	0.985	0.047	0.001
TMEM144_LOC2855	0.92	PMS2CL_PMS2	0.685	0.952	0.043	0
TMEM144_LOC2855	0.92	PDE3B	0.85	0.968	0.021	0.011
TMEM144_LOC2855	0.92	CCR4	0.784	0.99	0.014	0
TMEM144_LOC2855	0.92	ABCG1	0.789	0.962	0.021	0.001
TMEM144_LOC2855	0.92	FAM118A	0.759	0.949	0.033	0.001
TMEM144_LOC2855	0.92	TSHZ2	0.801	0.967	0.029	0.001
TMEM144_LOC2855	0.92	CFD	0.767	0.963	0.042	0
CDS2	0.869	CHI3L1	0.909	0.965	0.042	0.01
CDS2	0.869	RUNX2	0.848	0.979	0.005	0.001
BPI	0.83	DNAJC9_FAM149B1	0.811	0.914	0.014	0.022
BPI	0.83	IRS2	0.648	0.879	0.047	0.002
BPI	0.83	NA	0.763	0.897	0.023	0.004
BPI	0.83	CCR4	0.784	0.894	0.029	0.024
BPI	0.83	RRP12_LOC644215	0.632	0.869	0.038	0.001
BPI	0.83	CLC	0.81	0.926	0.006	0.021
BPI	0.83	B4GALT3	0.659	0.898	0.004	0.001
BPI	0.83	RASA4_RASA4P_R	0.779	0.897	0.012	0.017
ECHDC3	0.629	PHOSPHO1	0.85	0.941	0	0.033
ECHDC3	0.629	HIST1H3J	0.722	0.784	0.034	0.012
ECHDC3	0.629	HIST1H3A	0.715	0.796	0.022	0.011
ECHDC3	0.629	IRS2	0.648	0.871	0	0.005
ECHDC3	0.629	S100B	0.72	0.799	0.018	0.005
ECHDC3	0.629	C4orf3	0.629	0.744	0.031	0.049
ECHDC3	0.629	TAS2R31	0.685	0.751	0.028	0.046

CCR3	0.905	RCBTB2_LOC10013	0.905	0.974	0.005	0.02
CCR3	0.905	SEC24A_SAR1B	0.761	0.943	0.024	0
CCR3	0.905	NA	0.866	0.968	0.015	0.004
CCR3	0.905	CCR1	0.897	0.978	0.005	0.015
CCR3	0.905	FFAR2	0.868	0.975	0.005	0.003
CCR3	0.905	EIF2AK2	0.857	0.967	0.022	0.002
CCR3	0.905	SIAE	0.814	0.946	0.029	0.002
CCR3	0.905	AGTRAP	0.856	0.948	0.015	0.021
CCR3	0.905	SUCNR1	0.922	0.978	0.004	0.033
CCR3	0.905	AIG1	0.842	0.954	0.028	0.004
CCR3	0.905	GAB2	0.729	0.948	0.045	0
CCR3	0.905	ABCA1	0.866	0.976	0.012	0.009
CCR3	0.905	GSTO1	0.793	0.956	0.014	0.002
CCR3	0.905	CLEC4A	0.87	0.988	0.003	0.004
CCR3	0.905	GPR65	0.886	0.982	0.004	0.012
CCR3	0.905	KCNMA1	0.897	0.963	0.029	0.019
CCR3	0.905	DPH3	0.86	0.956	0.026	0.003
CCR3	0.905	TRIM21	0.874	0.979	0.004	0.009
CCR3	0.905	ICAM1	0.821	0.976	0.002	0.002
CCR3	0.905	TAF13	0.854	0.967	0.02	0.004
CCR3	0.905	KLHL5	0.826	0.958	0.016	0.001
CCR3	0.905	DLEU2_DLEU2L	0.874	0.974	0.01	0.002
CCR3	0.905	ANKRD28	0.8	0.953	0.02	0.002
CCR3	0.905	IL1B	0.871	0.979	0.003	0.013
CCR3	0.905	UBE2F_C20orf194	0.762	0.949	0.039	0
CCR3	0.905	PLEKHF2	0.822	0.967	0.027	0.001
CCR3	0.905	AIF1	0.816	0.966	0.005	0.002
CCR3	0.905	CALM2_C2orf61	0.733	0.948	0.047	0
HSPC159	0.823	KLRD1	0.784	0.91	0.043	0.001

HSPC159	0.823	CHI3L1	0.909	0.989	0.001	0.027
HSPC159	0.823	ANAPC11	0.818	0.928	0.005	0.012
HSPC159	0.823	RUNX2	0.848	0.963	0	0.016
HSPC159	0.823	PHOSPHO1	0.85	0.943	0.003	0.032
HSPC159	0.823	PDE3B	0.85	0.966	0.001	0.008
HSPC159	0.823	SULF2	0.819	0.929	0.005	0.032
HSPC159	0.823	C15orf54	0.821	0.923	0.041	0.001
HSPC159	0.823	CCR4	0.784	0.925	0.008	0.002
HSPC159	0.823	FAM118A	0.759	0.89	0.019	0.02
HSPC159	0.823	PYHIN1	0.807	0.911	0.011	0.02
HSPC159	0.823	CLC	0.81	0.914	0.039	0.014
HSPC159	0.823	TSHZ2	0.801	0.929	0.001	0.014
HSPC159	0.823	CAMK1D	0.702	0.884	0.037	0.003
OLAH	0.885	CHI3L1	0.909	0.968	0.047	0.018
OLAH	0.885	RUNX2	0.848	0.968	0.012	0.003
OLAH	0.885	PHOSPHO1	0.85	0.96	0.01	0.011
OLAH	0.885	PDE3B	0.85	0.977	0.009	0.002
OLAH	0.885	IRS2	0.648	0.98	0.003	0
OLAH	0.885	ABCG1	0.789	0.96	0.006	0.003
OLAH	0.885	LASS4	0.794	0.967	0.002	0.003
PPP2R5A_SNORA16	0.775	KLRD1	0.784	0.899	0.033	0
PPP2R5A_SNORA16	0.775	GIMAP7	0.755	0.913	0.003	0.001
PPP2R5A_SNORA16	0.775	ANAPC11	0.818	0.915	0.003	0.014
PPP2R5A_SNORA16	0.775	RUNX2	0.848	0.945	0	0.02
PPP2R5A_SNORA16	0.775	HLA-DRA	0.768	0.87	0.014	0.032
PPP2R5A_SNORA16	0.775	DNAJC9_FAM149B1	0.811	0.92	0.027	0.001
PPP2R5A_SNORA16	0.775	PLA2G7	0.834	0.898	0.023	0.015
PPP2R5A_SNORA16	0.775	PMS2CL_PMS2	0.685	0.887	0.014	0
PPP2R5A_SNORA16	0.775	PDE3B	0.85	0.966	0	0.003

PPP2R5A_SNORA16	0.775	SULF2	0.819	0.908	0.004	0.034
PPP2R5A_SNORA16	0.775	IRF4	0.781	0.897	0.012	0.012
PPP2R5A_SNORA16	0.775	HSP90AB1_HSP90A	0.799	0.904	0.003	0.015
PPP2R5A_SNORA16	0.775	ITGA4_CERKL	0.694	0.885	0.03	0.001
PPP2R5A_SNORA16	0.775	NPCDR1	0.86	0.929	0.001	0.016
PPP2R5A_SNORA16	0.775	NA	0.763	0.883	0.028	0.003
PPP2R5A_SNORA16	0.775	C15orf54	0.821	0.888	0.031	0.005
PPP2R5A_SNORA16	0.775	LY6G5B_CSNK2B	0.661	0.887	0.008	0
PPP2R5A_SNORA16	0.775	CCR4	0.784	0.938	0.001	0.001
PPP2R5A_SNORA16	0.775	FAM118A	0.759	0.875	0.015	0.018
PPP2R5A_SNORA16	0.775	PYHIN1	0.807	0.933	0.004	0.001
PPP2R5A_SNORA16	0.775	CLC	0.81	0.905	0.013	0.016
PPP2R5A_SNORA16	0.775	SYNE2	0.678	0.884	0.035	0
PPP2R5A_SNORA16	0.775	TSHZ2	0.801	0.925	0	0.008
PPP2R5A_SNORA16	0.775	RASA4_RASA4P_R	0.779	0.885	0.007	0.01
PPP2R5A_SNORA16	0.775	CAMK1D	0.702	0.887	0.01	0.001
PPP2R5A_SNORA16	0.775	IL5RA	0.832	0.893	0.019	0.034
TMTC1	0.826	ANAPC11	0.818	0.905	0.011	0.047
TMTC1	0.826	PHOSPHO1	0.85	0.937	0.006	0.046
TMTC1	0.826	C15orf54	0.821	0.925	0.006	0.013
TMTC1	0.826	CCR4	0.784	0.893	0.023	0.021
TMTC1	0.826	CFD	0.767	0.901	0.027	0.008
EAF2_HCG11_LOC	0.917	GIMAP7	0.755	0.975	0.04	0
EAF2_HCG11_LOC	0.917	RUNX2	0.848	0.952	0.043	0.012
EAF2_HCG11_LOC	0.917	PDE3B	0.85	0.97	0.05	0.004
EAF2_HCG11_LOC	0.917	ITGA4_CERKL	0.694	0.989	0.035	0
EAF2_HCG11_LOC	0.917	TSHZ2	0.801	0.974	0.028	0
RCBTB2_LOC10013	0.905	CHI3L1	0.909	0.966	0.048	0.029
RCBTB2_LOC10013	0.905	GIMAP7	0.755	0.97	0.008	0

RCBTB2_LOC10013	0.905	RUNX2	0.848	0.98	0.007	0.002
RCBTB2_LOC10013	0.905	CCR4	0.784	0.962	0.05	0
SEC24A_SAR1B	0.761	GIMAP7	0.755	0.915	0.001	0.001
SEC24A_SAR1B	0.761	ANAPC11	0.818	0.895	0.004	0.043
SEC24A_SAR1B	0.761	HLA-DRA	0.768	0.897	0.003	0.005
SEC24A_SAR1B	0.761	DNAJC9_FAM149B1	0.811	0.912	0.022	0.001
SEC24A_SAR1B	0.761	PLA2G7	0.834	0.903	0.014	0.006
SEC24A_SAR1B	0.761	PDE3B	0.85	0.935	0.002	0.017
SEC24A_SAR1B	0.761	SULF2	0.819	0.893	0.007	0.026
SEC24A_SAR1B	0.761	IRF4	0.781	0.88	0.022	0.024
SEC24A_SAR1B	0.761	HSP90AB1_HSP90A	0.799	0.927	0.004	0.001
SEC24A_SAR1B	0.761	ITGA4_CERKL	0.694	0.881	0.024	0.001
SEC24A_SAR1B	0.761	NPCDR1	0.86	0.922	0.001	0.012
SEC24A_SAR1B	0.761	NA	0.763	0.875	0.031	0.001
SEC24A_SAR1B	0.761	C15orf54	0.821	0.886	0.023	0.011
SEC24A_SAR1B	0.761	LY6G5B_CSNK2B	0.661	0.874	0.024	0
SEC24A_SAR1B	0.761	CCR4	0.784	0.903	0.004	0.004
SEC24A_SAR1B	0.761	FAM118A	0.759	0.872	0.039	0.004
SEC24A_SAR1B	0.761	PYHIN1	0.807	0.912	0.006	0.004
SEC24A_SAR1B	0.761	CLC	0.81	0.901	0.013	0.008
SEC24A_SAR1B	0.761	SON	0.604	0.87	0.037	0
SEC24A_SAR1B	0.761	TSHZ2	0.801	0.909	0.002	0.01
SEC24A_SAR1B	0.761	RASA4_RASA4P_R	0.779	0.893	0.005	0.003
SEC24A_SAR1B	0.761	IL5RA	0.832	0.889	0.02	0.016
SH3PXD2B	0.734	NA	0.696	0.817	0.032	0.02
SH3PXD2B	0.734	NA	0.746	0.825	0.047	0.017
SH3PXD2B	0.734	CFD	0.767	0.857	0.029	0.035
HMGB2	0.849	GIMAP7	0.755	0.934	0.011	0.001
HMGB2	0.849	ANAPC11	0.818	0.963	0.008	0.001

HMGB2	0.849	RUNX2	0.848	0.969	0.004	0.004
HMGB2	0.849	DNAJC9_FAM149B1	0.811	0.974	0.011	0
HMGB2	0.849	PMS2CL_PMS2	0.685	0.93	0.008	0
HMGB2	0.849	PDE3B	0.85	0.973	0.003	0.007
HMGB2	0.849	IRF4	0.781	0.932	0.005	0.012
HMGB2	0.849	NPCDR1	0.86	0.933	0.017	0.035
HMGB2	0.849	C15orf54	0.821	0.93	0.039	0.003
HMGB2	0.849	LY6G5B_CSNK2B	0.661	0.935	0.004	0
HMGB2	0.849	CCR4	0.784	0.958	0.007	0
HMGB2	0.849	FAM118A	0.759	0.91	0.038	0.007
HMGB2	0.849	PYHIN1	0.807	0.937	0.033	0.003
HMGB2	0.849	LASS4	0.794	0.915	0.049	0.038
HMGB2	0.849	TSHZ2	0.801	0.957	0.004	0.002
HMGB2	0.849	CAMK1D	0.702	0.924	0.03	0
KLRD1	0.784	AMFR	0.69	0.841	0.013	0.038
KLRD1	0.784	HDHD1A	0.63	0.837	0.048	0.004
KLRD1	0.784	ZRANB1	0.724	0.872	0.004	0.016
KLRD1	0.784	UBE2F_C20orf194	0.762	0.882	0.002	0.017
KLRD1	0.784	HIST1H2BJ	0.697	0.858	0.035	0.005
KLRD1	0.784	CEP97	0.695	0.871	0.019	0.003
KLRD1	0.784	DYNLL1	0.776	0.897	0.016	0.002
KLRD1	0.784	FAM118B	0.737	0.868	0.024	0.024
KLRD1	0.784	SPARC	0.703	0.868	0.024	0.004
KLRD1	0.784	PLEKHA3	0.658	0.839	0.049	0.008
KLRD1	0.784	TMEM62_SPCS2_L	0.645	0.863	0.014	0.002
KLRD1	0.784	CMTM5	0.694	0.843	0.045	0.012
KLRD1	0.784	HIST2H2BF_HIST2	0.754	0.854	0.031	0.048
KLRD1	0.784	CALM2_C2orf61	0.733	0.86	0.008	0.018
CHI3L1	0.909	PRR13_PCBP2	0.77	0.962	0.045	0

CHI3L1	0.909	FFAR2	0.868	0.949	0.045	0.013
CHI3L1	0.909	SIAE	0.814	0.981	0.037	0
CHI3L1	0.909	ABCA13	0.868	0.98	0.028	0.004
CHI3L1	0.909	SAP30	0.728	0.944	0.016	0.001
CHI3L1	0.909	AGTRAP	0.856	0.957	0.023	0.02
CHI3L1	0.909	SUCNR1	0.922	0.996	0.02	0.006
CHI3L1	0.909	AIG1	0.842	0.969	0.046	0.003
CHI3L1	0.909	ACTA2	0.783	0.97	0.016	0.001
CHI3L1	0.909	TRIM21	0.874	0.984	0.018	0.01
CHI3L1	0.909	ICAM1	0.821	0.937	0.039	0.026
CHI3L1	0.909	ZRANB1	0.724	0.967	0.042	0
CHI3L1	0.909	UBE2F_C20orf194	0.762	0.968	0.033	0
CHI3L1	0.909	MYL9	0.771	0.97	0.045	0
CHI3L1	0.909	CYP4F3_CYP4F2	0.593	0.979	0.046	0
CHI3L1	0.909	FAM118B	0.737	0.98	0.047	0
CHI3L1	0.909	NP	0.633	0.965	0.047	0
CHI3L1	0.909	ATP6V0D1_LOC100	0.856	0.958	0.011	0.049
SLC39A9	0.551	DNAJC9_FAM149B1	0.811	0.882	0	0.001
SLC39A9	0.551	P4HA1_RPL17	0.715	0.792	0.001	0.028
SLC39A9	0.551	FAM118B	0.737	0.833	0	0.019
GIMAP7	0.755	NA	0.866	0.933	0.001	0.013
GIMAP7	0.755	CCR1	0.897	0.963	0	0.005
GIMAP7	0.755	MTHFS	0.757	0.87	0.005	0.021
GIMAP7	0.755	EIF2AK2	0.857	0.955	0	0.002
GIMAP7	0.755	SIAE	0.814	0.897	0.001	0.039
GIMAP7	0.755	MTRR	0.703	0.923	0	0
GIMAP7	0.755	AIG1	0.842	0.939	0	0.009
GIMAP7	0.755	GAB2	0.729	0.858	0.025	0.014
GIMAP7	0.755	HS2ST1_UBA2	0.758	0.865	0.009	0.026

GIMAP7	0.755	TREML1	0.793	0.863	0.045	0.033
GIMAP7	0.755	GSTO1	0.793	0.902	0.001	0.03
GIMAP7	0.755	CLEC4A	0.87	0.957	0	0.012
GIMAP7	0.755	GPR65	0.886	0.972	0	0.018
GIMAP7	0.755	MACF1	0.742	0.877	0.03	0.001
GIMAP7	0.755	HDHD1A	0.63	0.859	0.012	0
GIMAP7	0.755	LRRFIP1	0.673	0.887	0.025	0
GIMAP7	0.755	TRIM21	0.874	0.944	0	0.023
GIMAP7	0.755	TAF13	0.854	0.925	0	0.039
GIMAP7	0.755	P4HA1_RPL17	0.715	0.923	0.003	0
GIMAP7	0.755	KLHL5	0.826	0.954	0	0.002
GIMAP7	0.755	ANKRD28	0.8	0.924	0.001	0.004
GIMAP7	0.755	MGST3	0.602	0.84	0.03	0
GIMAP7	0.755	LAIR1_LAIR2	0.749	0.857	0.034	0.032
GIMAP7	0.755	ZRANB1	0.724	0.87	0.019	0.003
GIMAP7	0.755	UBE2F_C20orf194	0.762	0.852	0.044	0.012
GIMAP7	0.755	CCRL2	0.786	0.868	0.029	0.034
GIMAP7	0.755	ZNF587_ZNF417	0.648	0.865	0.049	0
GIMAP7	0.755	CEP97	0.695	0.891	0.013	0
GIMAP7	0.755	DYNLL1	0.776	0.915	0.004	0
GIMAP7	0.755	PLIN2	0.671	0.887	0.003	0.001
GIMAP7	0.755	FAM118B	0.737	0.966	0	0
GIMAP7	0.755	CTSL1_CTSLL3	0.715	0.862	0.024	0.005
GIMAP7	0.755	TMEM62_SPCS2_L	0.645	0.886	0.011	0
GIMAP7	0.755	PLEKHF2	0.822	0.914	0.002	0.014
GIMAP7	0.755	AIF1	0.816	0.953	0	0.002
GIMAP7	0.755	HIST2H2BF_HIST2	0.754	0.875	0.036	0.001
GIMAP7	0.755	CALM2_C2orf61	0.733	0.898	0.003	0.001
ANAPC11	0.818	NA	0.866	0.924	0.014	0.024

ANAPC11	0.818	FOLR3_FOLR2	0.848	0.93	0.008	0.007
ANAPC11	0.818	LGALS1	0.736	0.915	0.005	0.003
ANAPC11	0.818	MTHFS	0.757	0.911	0.004	0.003
ANAPC11	0.818	SIAE	0.814	0.917	0.004	0.016
ANAPC11	0.818	ABCA13	0.868	0.94	0.005	0.006
ANAPC11	0.818	CDA	0.804	0.912	0.006	0.016
ANAPC11	0.818	SAP30	0.728	0.86	0.046	0.025
ANAPC11	0.818	AIG1	0.842	0.937	0.006	0.006
ANAPC11	0.818	HS2ST1_UBA2	0.758	0.879	0.035	0.022
ANAPC11	0.818	VOPP1_LOC100128	0.618	0.88	0.034	0
ANAPC11	0.818	SLC11A1	0.785	0.903	0.008	0.031
ANAPC11	0.818	GSTO1	0.793	0.91	0.022	0.008
ANAPC11	0.818	CLEC4A	0.87	0.939	0.003	0.024
ANAPC11	0.818	NEK6_LOC1001290	0.765	0.895	0.005	0.017
ANAPC11	0.818	OR9A2	0.813	0.918	0.009	0.005
ANAPC11	0.818	DPH3	0.86	0.949	0.001	0.009
ANAPC11	0.818	TAF13	0.854	0.94	0.017	0.004
ANAPC11	0.818	KLHL5	0.826	0.903	0.028	0.034
ANAPC11	0.818	DLEU2_DLEU2L	0.874	0.95	0.001	0.014
ANAPC11	0.818	ANKRD28	0.8	0.928	0.005	0.006
ANAPC11	0.818	LHFP	0.759	0.866	0.048	0.02
ANAPC11	0.818	MYL9	0.771	0.895	0.036	0.009
ANAPC11	0.818	FAM118B	0.737	0.907	0.034	0.001
ANAPC11	0.818	AIF1	0.816	0.917	0.007	0.022
ANAPC11	0.818	CALM2_C2orf61	0.733	0.915	0.015	0
EXOSC4	0.731	DNAJC9_FAM149B1	0.811	0.864	0.043	0.032
EXOSC4	0.731	JUP	0.804	0.905	0.002	0.025
EXOSC4	0.731	C15orf54	0.821	0.878	0.013	0.017
EXOSC4	0.731	CFD	0.767	0.869	0.021	0.02

NA	0.866	RUNX2	0.848	0.943	0.001	0.047
NA	0.866	HLA-DRA	0.768	0.925	0.022	0.002
NA	0.866	NA	0.696	0.939	0.032	0
NA	0.866	PLA2G7	0.834	0.952	0.016	0.003
NA	0.866	PMS2CL_PMS2	0.685	0.92	0.049	0
NA	0.866	PDE3B	0.85	0.972	0.001	0.006
NA	0.866	SULF2	0.819	0.933	0.017	0.02
NA	0.866	ITGA4_CERKL	0.694	0.931	0.035	0
NA	0.866	NPCDR1	0.86	0.957	0.006	0.005
NA	0.866	NA	0.763	0.927	0.035	0.001
NA	0.866	LY6G5B_CSNK2B	0.661	0.934	0.017	0
NA	0.866	CCR4	0.784	0.949	0.009	0.001
NA	0.866	ABCG1	0.789	0.915	0.038	0.015
NA	0.866	FAM118A	0.759	0.921	0.026	0.002
NA	0.866	PYHIN1	0.807	0.949	0.024	0.001
NA	0.866	SYNE2	0.678	0.945	0.011	0
NA	0.866	TSHZ2	0.801	0.942	0.005	0.003
NA	0.866	RASA4_RASA4P_R	0.779	0.93	0.024	0.001
NA	0.866	CAMK1D	0.702	0.933	0.009	0
INSIG1	0.509	TAF13	0.854	0.904	0	0.029
INSIG1	0.509	CALM2_C2orf61	0.733	0.8	0	0.049
FOLR3_FOLR2	0.848	RUNX2	0.848	0.933	0.005	0.039
FOLR3_FOLR2	0.848	PHOSPHO1	0.85	0.944	0.003	0.024
FOLR3_FOLR2	0.848	PPIF	0.614	0.908	0.016	0
FOLR3_FOLR2	0.848	PDE3B	0.85	0.926	0.035	0.04
FOLR3_FOLR2	0.848	RRP12_LOC644215	0.632	0.905	0.038	0
FOLR3_FOLR2	0.848	LASS4	0.794	0.946	0	0.013
RUNX2	0.848	CCR1	0.897	0.94	0.019	0.025
RUNX2	0.848	FFAR2	0.868	0.935	0.014	0.014

RUNX2	0.848	MTHFS	0.757	0.943	0.022	0
RUNX2	0.848	SIAE	0.814	0.965	0.003	0
RUNX2	0.848	ABCA13	0.868	0.951	0.018	0.003
RUNX2	0.848	CDA	0.804	0.953	0.013	0
RUNX2	0.848	SAP30	0.728	0.95	0.008	0
RUNX2	0.848	AGTRAP	0.856	0.938	0.005	0.022
RUNX2	0.848	SUCNR1	0.922	0.97	0.003	0.009
RUNX2	0.848	AIG1	0.842	0.948	0.009	0.005
RUNX2	0.848	HS2ST1_UBA2	0.758	0.953	0.004	0
RUNX2	0.848	SLC11A1	0.785	0.959	0.013	0.001
RUNX2	0.848	CLEC4A	0.87	0.944	0.028	0.002
RUNX2	0.848	NEK6_LOC1001290	0.765	0.943	0.006	0.001
RUNX2	0.848	GPR65	0.886	0.933	0.027	0.018
RUNX2	0.848	DPH3	0.86	0.949	0.017	0.001
RUNX2	0.848	TRIM21	0.874	0.941	0.016	0.029
RUNX2	0.848	TAF13	0.854	0.943	0.029	0.002
RUNX2	0.848	KLHL5	0.826	0.941	0.024	0.001
RUNX2	0.848	DLEU2_DLEU2L	0.874	0.944	0.012	0.006
RUNX2	0.848	ANKRD28	0.8	0.979	0.002	0
RUNX2	0.848	MYL9	0.771	0.939	0.048	0
RUNX2	0.848	FAM118B	0.737	0.939	0.037	0
PRR13_PCBP2	0.77	PLA2G7	0.834	0.888	0.039	0.029
PRR13_PCBP2	0.77	C15orf54	0.821	0.879	0.041	0.04
PRR13_PCBP2	0.77	LY6G5B_CSNK2B	0.661	0.871	0.046	0
PRR13_PCBP2	0.77	CCR4	0.784	0.884	0.017	0.02
PRR13_PCBP2	0.77	RASA4_RASA4P_R	0.779	0.886	0.012	0.008
LGALS1	0.736	CCR4	0.784	0.865	0.036	0.005
LGALS1	0.736	CLC	0.81	0.884	0.03	0.026
LGALS1	0.736	LASS4	0.794	0.891	0.002	0.049

LGALS1	0.736	TSHZ2	0.801	0.872	0.022	0.027
CCR1	0.897	HLA-DRA	0.768	0.965	0.017	0
CCR1	0.897	NPCDR1	0.86	0.971	0.019	0.001
CCR1	0.897	CCR4	0.784	0.961	0.012	0
HLA-DRA	0.768	FFAR2	0.868	0.949	0.001	0.002
HLA-DRA	0.768	EIF2AK2	0.857	0.942	0.003	0.006
HLA-DRA	0.768	AIG1	0.842	0.91	0.008	0.032
HLA-DRA	0.768	GSTO1	0.793	0.893	0.016	0.018
HLA-DRA	0.768	CLEC4A	0.87	0.967	0	0.011
HLA-DRA	0.768	GPR65	0.886	0.959	0	0.034
HLA-DRA	0.768	ACTA2	0.783	0.878	0.043	0.017
HLA-DRA	0.768	TRIM21	0.874	0.985	0	0.002
HLA-DRA	0.768	ICAM1	0.821	0.933	0.002	0.005
HLA-DRA	0.768	P4HA1_RPL17	0.715	0.883	0.032	0
HLA-DRA	0.768	KLHL5	0.826	0.952	0	0.002
HLA-DRA	0.768	HSPB1_HSPBL2	0.778	0.867	0.021	0.048
HLA-DRA	0.768	IL1B	0.871	0.945	0.001	0.023
HLA-DRA	0.768	CCRL2	0.786	0.892	0.029	0.007
HLA-DRA	0.768	PLIN2	0.671	0.874	0.045	0
HLA-DRA	0.768	CTSL1_CTSLL3	0.715	0.887	0.018	0.001
HLA-DRA	0.768	TMEM62_SPCS2_L	0.645	0.874	0.017	0
HLA-DRA	0.768	PLEKHF2	0.822	0.916	0.002	0.007
HLA-DRA	0.768	AIF1	0.816	0.952	0	0.004
CD163	0.735	NA	0.696	0.834	0.014	0.044
CD163	0.735	PLA2G7	0.834	0.918	0.004	0.018
CD163	0.735	PMS2CL_PMS2	0.685	0.818	0.03	0.034
CD163	0.735	SULF2	0.819	0.933	0	0.034
CD163	0.735	NA	0.718	0.857	0.017	0.022
CD163	0.735	LY6G5B_CSNK2B	0.661	0.835	0.007	0.023

CD163	0.735	NA	0.746	0.881	0.002	0.007
CD163	0.735	CAMK1D	0.702	0.866	0.004	0.013
CD163	0.735	CFD	0.767	0.874	0.01	0.031
FFAR2	0.868	NPCDR1	0.86	0.958	0.013	0.001
FFAR2	0.868	CCR4	0.784	0.934	0.034	0
FFAR2	0.868	ABCG1	0.789	0.937	0.017	0.006
PHOSPHO1	0.85	SIAE	0.814	0.949	0.003	0.006
PHOSPHO1	0.85	ABCA13	0.868	0.981	0.003	0.001
PHOSPHO1	0.85	CDA	0.804	0.919	0.021	0.023
PHOSPHO1	0.85	SAP30	0.728	0.933	0.004	0.001
PHOSPHO1	0.85	SUCNR1	0.922	0.99	0.001	0.009
PHOSPHO1	0.85	NEK6_LOC1001290	0.765	0.904	0.017	0.02
PHOSPHO1	0.85	AMFR	0.69	0.93	0.015	0
PHOSPHO1	0.85	DPH3	0.86	0.951	0.004	0.01
PHOSPHO1	0.85	ICAM1	0.821	0.919	0.011	0.033
PHOSPHO1	0.85	TAF13	0.854	0.931	0.019	0.01
PHOSPHO1	0.85	DLEU2_DLEU2L	0.874	0.947	0.007	0.019
PHOSPHO1	0.85	ANKRD28	0.8	0.932	0.044	0.005
PHOSPHO1	0.85	HSPB1_HSPBL2	0.778	0.933	0.013	0.003
PHOSPHO1	0.85	LHFP	0.759	0.92	0.036	0.001
PHOSPHO1	0.85	ZRANB1	0.724	0.94	0.029	0
PHOSPHO1	0.85	PTGS1	0.68	0.965	0.007	0
PHOSPHO1	0.85	UBE2F_C20orf194	0.762	0.949	0.015	0
PHOSPHO1	0.85	MYL9	0.771	0.98	0.005	0
PHOSPHO1	0.85	CMTM5	0.694	0.969	0.012	0
PHOSPHO1	0.85	AIF1	0.816	0.922	0.03	0.008
PPIF	0.614	C22orf37	0.582	0.774	0.027	0.004
PPIF	0.614	OR9A2	0.813	0.881	0	0.02
PPIF	0.614	ICAM1	0.821	0.898	0	0.042

PPIF	0.614	IL1B	0.871	0.935	0	0.035
PPIF	0.614	MYL9	0.771	0.83	0.003	0.04
PPIF	0.614	CALM2_C2orf61	0.733	0.801	0.011	0.039
MTHFS	0.757	DNAJC9_FAM149B1	0.811	0.904	0.024	0.002
MTHFS	0.757	PLA2G7	0.834	0.891	0.014	0.03
MTHFS	0.757	PMS2CL_PMS2	0.685	0.863	0.035	0.001
MTHFS	0.757	PDE3B	0.85	0.985	0	0.002
MTHFS	0.757	C15orf54	0.821	0.884	0.019	0.014
MTHFS	0.757	CCR4	0.784	0.911	0.003	0.001
MTHFS	0.757	FAM118A	0.759	0.863	0.021	0.023
MTHFS	0.757	PYHIN1	0.807	0.887	0.016	0.011
MTHFS	0.757	CLC	0.81	0.89	0.025	0.018
MTHFS	0.757	SYNE2	0.678	0.861	0.042	0
MTHFS	0.757	TSHZ2	0.801	0.899	0.003	0.013
MTHFS	0.757	RASA4_RASA4P_R	0.779	0.859	0.014	0.036
MTHFS	0.757	CAMK1D	0.702	0.889	0.008	0
MTHFS	0.757	CFD	0.767	0.878	0.025	0.008
MTHFS	0.757	IL5RA	0.832	0.883	0.02	0.024
DNAJC9_FAM149B1	0.811	ABCA13	0.868	0.932	0.005	0.049
DNAJC9_FAM149B1	0.811	MTRR	0.703	0.916	0	0.004
DNAJC9_FAM149B1	0.811	AIG1	0.842	0.953	0	0.021
DNAJC9_FAM149B1	0.811	HS2ST1_UBA2	0.758	0.887	0.005	0.05
DNAJC9_FAM149B1	0.811	GSTO1	0.793	0.912	0.004	0.048
DNAJC9_FAM149B1	0.811	MACF1	0.742	0.927	0.002	0.003
DNAJC9_FAM149B1	0.811	AMFR	0.69	0.853	0.022	0.045
DNAJC9_FAM149B1	0.811	GALNT2	0.651	0.86	0.039	0.01
DNAJC9_FAM149B1	0.811	OR9A2	0.813	0.897	0.018	0.037
DNAJC9_FAM149B1	0.811	HDHD1A	0.63	0.884	0.011	0.002
DNAJC9_FAM149B1	0.811	LRRFIP1	0.673	0.919	0.007	0

DNAJC9_FAM149B1	0.811	P4HA1_RPL17	0.715	0.933	0.001	0.001
DNAJC9_FAM149B1	0.811	MGST3	0.602	0.877	0.02	0
DNAJC9_FAM149B1	0.811	CCDC125	0.632	0.886	0.019	0
DNAJC9_FAM149B1	0.811	PDK4	0.71	0.922	0.008	0.002
DNAJC9_FAM149B1	0.811	LAIR1_LAIR2	0.749	0.887	0.007	0.05
DNAJC9_FAM149B1	0.811	FSD1L_GARNL1	0.66	0.889	0.004	0.003
DNAJC9_FAM149B1	0.811	UBE2F_C20orf194	0.762	0.88	0.026	0.037
DNAJC9_FAM149B1	0.811	CEP97	0.695	0.906	0.006	0.002
DNAJC9_FAM149B1	0.811	DYNLL1	0.776	0.959	0.001	0
DNAJC9_FAM149B1	0.811	PLIN2	0.671	0.872	0.022	0.007
DNAJC9_FAM149B1	0.811	FAM118B	0.737	0.927	0.001	0.006
DNAJC9_FAM149B1	0.811	CTSL1_CTSLL3	0.715	0.897	0.039	0.002
DNAJC9_FAM149B1	0.811	NP	0.633	0.876	0.013	0.001
DNAJC9_FAM149B1	0.811	TMEM62_SPCS2_L	0.645	0.895	0.004	0.001
DNAJC9_FAM149B1	0.811	CALM2_C2orf61	0.733	0.907	0.002	0.007
LCN2	0.752	HIST1H3J	0.722	0.874	0.016	0.002
LCN2	0.752	HIST1H3A	0.715	0.876	0.005	0.005
LCN2	0.752	RRP12_LOC644215	0.632	0.794	0.03	0.047
LCN2	0.752	B4GALT3	0.659	0.855	0.001	0.014
LCN2	0.752	C4orf3	0.629	0.818	0.023	0.012
LCN2	0.752	RPIA	0.713	0.843	0.039	0.027
LCN2	0.752	C1orf128	0.751	0.864	0.013	0.049
EIF2AK2	0.857	PLA2G7	0.834	0.957	0.011	0.002
EIF2AK2	0.857	PMS2CL_PMS2	0.685	0.922	0.037	0
EIF2AK2	0.857	PDE3B	0.85	0.956	0.008	0.008
EIF2AK2	0.857	SULF2	0.819	0.944	0.022	0.002
EIF2AK2	0.857	HSP90AB1_HSP90A	0.799	0.964	0.007	0.001
EIF2AK2	0.857	ITGA4_CERKL	0.694	0.953	0.002	0
EIF2AK2	0.857	NPCDR1	0.86	0.959	0.002	0.006

EIF2AK2	0.857	NA	0.763	0.954	0.008	0
EIF2AK2	0.857	CCR4	0.784	0.961	0.002	0
EIF2AK2	0.857	FAM118A	0.759	0.907	0.036	0.005
EIF2AK2	0.857	PYHIN1	0.807	0.939	0.015	0.004
EIF2AK2	0.857	SYNE2	0.678	0.932	0.015	0
EIF2AK2	0.857	NA	0.746	0.95	0.007	0
EIF2AK2	0.857	TSHZ2	0.801	0.951	0.003	0.002
EIF2AK2	0.857	RASA4_RASA4P_R	0.779	0.925	0.021	0.001
EIF2AK2	0.857	MPZL2	0.612	0.914	0.044	0
EIF2AK2	0.857	IL5RA	0.832	0.943	0.035	0.002
SIAE	0.814	PDE3B	0.85	0.95	0.011	0.002
SIAE	0.814	SULF2	0.819	0.926	0.005	0.011
SIAE	0.814	NPCDR1	0.86	0.916	0.011	0.033
SIAE	0.814	CCR4	0.784	0.919	0.019	0
SIAE	0.814	FAM118A	0.759	0.918	0.013	0.001
SIAE	0.814	PYHIN1	0.807	0.911	0.036	0.004
SIAE	0.814	LASS4	0.794	0.945	0.001	0.007
SIAE	0.814	TSHZ2	0.801	0.931	0.004	0.002
SIAE	0.814	RASA4_RASA4P_R	0.779	0.906	0.029	0.001
ABCA13	0.868	PDE3B	0.85	0.947	0.005	0.016
ABCA13	0.868	NPCDR1	0.86	0.924	0.035	0.033
ABCA13	0.868	CCR4	0.784	0.925	0.03	0.002
ABCA13	0.868	CLC	0.81	0.939	0.02	0.009
ABCA13	0.868	LASS4	0.794	0.953	0.001	0.009
ABCA13	0.868	B4GALT3	0.659	0.945	0.017	0
ABCA13	0.868	IL5RA	0.832	0.925	0.042	0.014
NA	0.696	MTRR	0.703	0.826	0.032	0.006
NA	0.696	MACF1	0.742	0.866	0.004	0.003
NA	0.696	GALNT2	0.651	0.805	0.03	0.012

NA	0.696	P4HA1_RPL17	0.715	0.825	0.024	0.008
NA	0.696	ZRANB1	0.724	0.81	0.023	0.043
NA	0.696	CCRL2	0.786	0.892	0	0.012
NA	0.696	IRF1	0.651	0.776	0.049	0.05
NA	0.696	DYNLL1	0.776	0.839	0.008	0.028
NA	0.696	FAM118B	0.737	0.826	0.015	0.045
EFCAB2	0.96	PMS2CL_PMS2	0.685	0.988	0.047	0
EFCAB2	0.96	PDE3B	0.85	0.988	0.022	0.001
EFCAB2	0.96	CFD	0.767	0.988	0.05	0
HINT1	0.658	DYNLL1	0.776	0.894	0	0.004
HINT1	0.658	CALM2_C2orf61	0.733	0.856	0	0.041
HIST1H3J	0.722	C22orf37	0.582	0.758	0.037	0.032
HIST1H3J	0.722	AREG	0.598	0.76	0.033	0.046
HIST1H3J	0.722	DAAM2_LOC100131	0.664	0.799	0.021	0.016
HIST1H3J	0.722	CEACAM8	0.748	0.844	0.015	0.029
HIST1H3J	0.722	MINPP1	0.497	0.816	0.018	0
HIST1H3J	0.722	HIST1H2BM	0.504	0.794	0.04	0.001
HIST1H3J	0.722	ITGA2B	0.699	0.83	0.002	0.039
HIST1H3J	0.722	NA	0.705	0.82	0.007	0.045
HIST1H3J	0.722	HIST1H2BJ	0.697	0.865	0	0.015
HIST1H3J	0.722	CMTM5	0.694	0.863	0	0.021
HIST1H3J	0.722	IFI44	0.762	0.842	0.014	0.046
HIST1H3J	0.722	KIAA0101_CSNK1G	0.581	0.858	0.015	0
CDA	0.804	PDE3B	0.85	0.929	0.009	0.023
CDA	0.804	JUP	0.804	0.896	0.014	0.04
CDA	0.804	NPCDR1	0.86	0.914	0.009	0.049
CDA	0.804	LY6G5B_CSNK2B	0.661	0.892	0.038	0
CDA	0.804	CCR4	0.784	0.925	0.006	0.001
CDA	0.804	PYHIN1	0.807	0.901	0.03	0.01

CDA	0.804	CLC	0.81	0.92	0.023	0.008
CDA	0.804	LASS4	0.794	0.902	0.018	0.042
CDA	0.804	TSHZ2	0.801	0.894	0.023	0.016
CDA	0.804	RASA4_RASA4P_R	0.779	0.895	0.026	0.004
CDA	0.804	IL5RA	0.832	0.903	0.027	0.016
SAP30	0.728	PLA2G7	0.834	0.859	0.043	0.031
SAP30	0.728	PDE3B	0.85	0.942	0	0.002
SAP30	0.728	SULF2	0.819	0.864	0.034	0.033
SAP30	0.728	C15orf54	0.821	0.857	0.038	0.03
SAP30	0.728	IL5RA	0.832	0.862	0.049	0.02
AGTRAP	0.856	LASS4	0.794	0.944	0.028	0.001
SUCNR1	0.922	PDE3B	0.85	0.976	0.038	0.001
SUCNR1	0.922	B4GALT3	0.659	0.977	0.018	0
MTRR	0.703	PLA2G7	0.834	0.897	0.004	0.007
MTRR	0.703	ITGA4_CERKL	0.694	0.839	0.012	0.012
MTRR	0.703	NPCDR1	0.86	0.92	0	0.039
MTRR	0.703	NA	0.763	0.868	0.005	0.002
MTRR	0.703	LY6G5B_CSNK2B	0.661	0.839	0.006	0.006
MTRR	0.703	CCR4	0.784	0.89	0	0.016
MTRR	0.703	PYHIN1	0.807	0.904	0.001	0.027
MTRR	0.703	CLC	0.81	0.881	0.003	0.034
MTRR	0.703	NA	0.746	0.832	0.029	0.02
MTRR	0.703	TSHZ2	0.801	0.904	0	0.039
MTRR	0.703	CAMK1D	0.702	0.821	0.025	0.018
PLA2G7	0.834	CLEC4A	0.87	0.956	0.001	0.036
PLA2G7	0.834	TRAF3	0.594	0.888	0.013	0
PLA2G7	0.834	OR9A2	0.813	0.928	0.005	0.017
PLA2G7	0.834	ACTA2	0.783	0.901	0.023	0.031
PLA2G7	0.834	TAF13	0.854	0.947	0.002	0.028

PLA2G7	0.834	P4HA1_RPL17	0.715	0.923	0.005	0
PLA2G7	0.834	KLHL5	0.826	0.932	0.001	0.033
PLA2G7	0.834	LHFP	0.759	0.863	0.043	0.039
PLA2G7	0.834	CCRL2	0.786	0.907	0.038	0.014
PLA2G7	0.834	DYNLL1	0.776	0.92	0.023	0.001
PLA2G7	0.834	PLIN2	0.671	0.89	0.01	0.004
PLA2G7	0.834	FAM118B	0.737	0.929	0.005	0.002
PLA2G7	0.834	CTSL1_CTSLL3	0.715	0.901	0.035	0.002
PLA2G7	0.834	TMEM62_SPCS2_L	0.645	0.894	0.039	0
PLA2G7	0.834	PLEKHF2	0.822	0.929	0.003	0.026
PLA2G7	0.834	AIF1	0.816	0.939	0.002	0.022
PLA2G7	0.834	PPP1R2_PPP1R2P3	0.569	0.893	0.048	0
PLA2G7	0.834	HIST2H2BF_HIST2	0.754	0.905	0.036	0.004
PLA2G7	0.834	CALM2_C2orf61	0.733	0.918	0.006	0.001
AIG1	0.842	PMS2CL_PMS2	0.685	0.937	0.031	0
AIG1	0.842	PDE3B	0.85	0.955	0.014	0.006
AIG1	0.842	IRF4	0.781	0.923	0.017	0.005
AIG1	0.842	HSP90AB1_HSP90A	0.799	0.94	0.023	0.003
AIG1	0.842	ITGA4_CERKL	0.694	0.92	0.04	0
AIG1	0.842	NPCDR1	0.86	0.941	0.009	0.012
AIG1	0.842	LY6G5B_CSNK2B	0.661	0.913	0.034	0
AIG1	0.842	CCR4	0.784	0.946	0.007	0
AIG1	0.842	CLC	0.81	0.929	0.038	0.01
AIG1	0.842	TSHZ2	0.801	0.924	0.024	0.005
AIG1	0.842	RASA4_RASA4P_R	0.779	0.921	0.019	0.002
AIG1	0.842	IL5RA	0.832	0.921	0.039	0.008
PCOLCE2	0.709	NA	0.763	0.817	0.046	0.017
PCOLCE2	0.709	CFD	0.767	0.84	0.019	0.044
GAB2	0.729	SULF2	0.819	0.932	0	0.011

GAB2	0.729	HSP90AB1_HSP90A	0.799	0.878	0.015	0.03
GAB2	0.729	NA	0.718	0.872	0.033	0
GAB2	0.729	LY6G5B_CSNK2B	0.661	0.866	0.026	0
GAB2	0.729	CCR4	0.784	0.883	0.006	0.018
GAB2	0.729	CLC	0.81	0.859	0.03	0.047
GAB2	0.729	NA	0.746	0.872	0.03	0
GAB2	0.729	RASA4_RASA4P_R	0.779	0.887	0.003	0.003
GAB2	0.729	CAMK1D	0.702	0.876	0.014	0.002
HS2ST1_UBA2	0.758	PDE3B	0.85	0.963	0	0.008
HS2ST1_UBA2	0.758	NPCDR1	0.86	0.908	0.003	0.041
HS2ST1_UBA2	0.758	C15orf54	0.821	0.882	0.037	0.006
HS2ST1_UBA2	0.758	CCR4	0.784	0.892	0.013	0.002
HS2ST1_UBA2	0.758	ABCG1	0.789	0.89	0.011	0.049
HS2ST1_UBA2	0.758	TSHZ2	0.801	0.907	0.005	0.007
HS2ST1_UBA2	0.758	RASA4_RASA4P_R	0.779	0.869	0.024	0.012
HS2ST1_UBA2	0.758	IL5RA	0.832	0.885	0.021	0.017
HIST1H3A	0.715	C22orf37	0.582	0.77	0.015	0.024
HIST1H3A	0.715	DAAM2_LOC100131	0.664	0.801	0.032	0.018
HIST1H3A	0.715	CEACAM8	0.748	0.841	0.029	0.019
HIST1H3A	0.715	HIST1H2BM	0.504	0.79	0.046	0.001
HIST1H3A	0.715	ITGA2B	0.699	0.82	0.012	0.05
HIST1H3A	0.715	HIST1H2BJ	0.697	0.854	0.001	0.027
HIST1H3A	0.715	CMTM5	0.694	0.856	0	0.03
HIST1H3A	0.715	SDHC	0.627	0.821	0.041	0.003
C22orf37	0.582	PMS2CL_PMS2	0.685	0.775	0.011	0.027
HLA-DPA1	0.65	TRAF3	0.594	0.767	0.036	0.015
HLA-DPA1	0.65	P4HA1_RPL17	0.715	0.823	0.006	0.015
HLA-DPA1	0.65	PDK4	0.71	0.808	0.027	0.016
HLA-DPA1	0.65	CCRL2	0.786	0.888	0	0.031

HLA-DPA1	0.65	IRF1	0.651	0.779	0.021	0.043
HLA-DPA1	0.65	FAM118B	0.737	0.832	0.005	0.028
HLA-DPA1	0.65	TMEM62_SPCS2_L	0.645	0.772	0.026	0.032
VOPP1_LOC100128	0.618	PMS2CL_PMS2	0.685	0.766	0.037	0.05
SLC11A1	0.785	PDE3B	0.85	0.937	0.005	0.016
SLC11A1	0.785	CCR4	0.784	0.896	0.028	0.003
SLC11A1	0.785	RRP12_LOC644215	0.632	0.867	0.036	0.001
SLC11A1	0.785	ABCG1	0.789	0.913	0.014	0.023
SLC11A1	0.785	LASS4	0.794	0.915	0.005	0.033
ABCA1	0.866	CCR4	0.784	0.916	0.029	0.015
ABCA1	0.866	ABCG1	0.789	0.966	0.005	0.007
ABCA1	0.866	TSHZ2	0.801	0.921	0.034	0.032
ABCA1	0.866	CAMK1D	0.702	0.914	0.035	0.001
DAAM2_LOC100131	0.664	IRS2	0.648	0.825	0	0.05
LTF	0.732	B4GALT3	0.659	0.814	0.014	0.037
TREML1	0.793	IRS2	0.648	0.861	0.036	0.011
TREML1	0.793	C15orf54	0.821	0.929	0.006	0.004
TREML1	0.793	CCR4	0.784	0.901	0.004	0.025
TREML1	0.793	CLC	0.81	0.897	0.046	0.028
TREML1	0.793	B4GALT3	0.659	0.871	0.028	0.005
TREML1	0.793	CFD	0.767	0.886	0.046	0.022
TREML1	0.793	IL5RA	0.832	0.907	0.017	0.048
GSTO1	0.793	HSP90AB1_HSP90A	0.799	0.896	0.028	0.021
GSTO1	0.793	NPCDR1	0.86	0.93	0.002	0.029
GSTO1	0.793	NA	0.763	0.911	0.044	0
GSTO1	0.793	C15orf54	0.821	0.904	0.048	0.001
GSTO1	0.793	CCR4	0.784	0.933	0.006	0
GSTO1	0.793	ABCG1	0.789	0.893	0.011	0.033
GSTO1	0.793	PYHIN1	0.807	0.908	0.035	0.003

GSTO1	0.793	CLC	0.81	0.937	0.013	0.003
GSTO1	0.793	TSHZ2	0.801	0.923	0.005	0.006
GSTO1	0.793	RASA4_RASA4P_R	0.779	0.89	0.013	0.016
GSTO1	0.793	IL5RA	0.832	0.923	0.026	0.005
CEACAM8	0.748	B4GALT3	0.659	0.84	0	0.03
CLEC4A	0.87	PDE3B	0.85	0.952	0.015	0.018
CLEC4A	0.87	ITGA4_CERKL	0.694	0.952	0.031	0
CLEC4A	0.87	NPCDR1	0.86	0.938	0.048	0.006
CLEC4A	0.87	LY6G5B_CSNK2B	0.661	0.933	0.024	0
CLEC4A	0.87	CCR4	0.784	0.952	0.017	0
CLEC4A	0.87	ABCG1	0.789	0.955	0.007	0.001
CLEC4A	0.87	TSHZ2	0.801	0.954	0.009	0.001
CLEC4A	0.87	CAMK1D	0.702	0.938	0.028	0
PMS2CL_PMS2	0.685	MACF1	0.742	0.852	0.007	0.007
PMS2CL_PMS2	0.685	LRRFIP1	0.673	0.821	0.024	0.003
PMS2CL_PMS2	0.685	DPH3	0.86	0.928	0	0.033
PMS2CL_PMS2	0.685	TAF13	0.854	0.913	0	0.036
PMS2CL_PMS2	0.685	P4HA1_RPL17	0.715	0.848	0.011	0.002
PMS2CL_PMS2	0.685	ZRANB1	0.724	0.823	0.009	0.035
PMS2CL_PMS2	0.685	NA	0.705	0.833	0.032	0.002
PMS2CL_PMS2	0.685	UBE2F_C20orf194	0.762	0.899	0	0.006
PMS2CL_PMS2	0.685	CEP97	0.695	0.832	0.011	0.016
PMS2CL_PMS2	0.685	DYNLL1	0.776	0.87	0.003	0.006
PMS2CL_PMS2	0.685	FAM118B	0.737	0.841	0.005	0.043
PMS2CL_PMS2	0.685	PLEKHA3	0.658	0.861	0.001	0.001
PMS2CL_PMS2	0.685	TMEM62_SPCS2_L	0.645	0.79	0.04	0.023
PMS2CL_PMS2	0.685	PLEKHF2	0.822	0.912	0	0.012
PMS2CL_PMS2	0.685	AIF1	0.816	0.916	0	0.02
PMS2CL_PMS2	0.685	CALM2_C2orf61	0.733	0.897	0	0.001

PDE3B	0.85	NEK6_LOC1001290	0.765	0.906	0.026	0.016
PDE3B	0.85	OR9A2	0.813	0.943	0.042	0
PDE3B	0.85	DPH3	0.86	0.962	0.012	0.001
PDE3B	0.85	TRIM21	0.874	0.962	0.001	0.036
PDE3B	0.85	ICAM1	0.821	0.915	0.014	0.023
PDE3B	0.85	TAF13	0.854	0.959	0.017	0.004
PDE3B	0.85	KLHL5	0.826	0.944	0.019	0.01
PDE3B	0.85	DLEU2_DLEU2L	0.874	0.986	0.001	0.001
PDE3B	0.85	ANKRD28	0.8	0.995	0.001	0
PDE3B	0.85	UBE2F_C20orf194	0.762	0.929	0.045	0
PDE3B	0.85	CEP97	0.695	0.929	0.04	0
PDE3B	0.85	FAM118B	0.737	0.941	0.016	0.001
PDE3B	0.85	PLEKHF2	0.822	0.961	0.021	0
PDE3B	0.85	AIF1	0.816	0.934	0.042	0.008
PDE3B	0.85	CALM2_C2orf61	0.733	0.978	0.002	0
SULF2	0.819	ACTA2	0.783	0.926	0.013	0.005
SULF2	0.819	ICAM1	0.821	0.929	0.002	0.038
SULF2	0.819	ANKRD28	0.8	0.904	0.024	0.036
SULF2	0.819	HSPB1_HSPBL2	0.778	0.895	0.038	0.017
SULF2	0.819	ZRANB1	0.724	0.908	0.031	0.001
SULF2	0.819	PLIN2	0.671	0.906	0.008	0.001
SULF2	0.819	FAM118B	0.737	0.928	0.008	0.001
SULF2	0.819	CALM2_C2orf61	0.733	0.89	0.043	0.003
NEK6_LOC1001290	0.765	CCR4	0.784	0.872	0.045	0.008
NEK6_LOC1001290	0.765	ABCG1	0.789	0.89	0.037	0.024
NEK6_LOC1001290	0.765	LASS4	0.794	0.887	0.028	0.014
CENPK	0.688	NA	0.705	0.811	0.011	0.039
CENPK	0.688	DYNLL1	0.776	0.864	0.001	0.05
TRAF3	0.594	ITGA4_CERKL	0.694	0.807	0.002	0.039

TRAF3	0.594	NPCDR1	0.86	0.901	0	0.048
TRAF3	0.594	NA	0.718	0.788	0.016	0.04
TRAF3	0.594	SYNE2	0.678	0.775	0.01	0.034
TRAF3	0.594	NA	0.746	0.827	0.003	0.004
TRAF3	0.594	CAMK1D	0.702	0.82	0.001	0.013
GPR65	0.886	ITGA4_CERKL	0.694	0.969	0.047	0
MACF1	0.742	HSP90AB1_HSP90A	0.799	0.913	0	0.016
MACF1	0.742	ITGA4_CERKL	0.694	0.85	0.012	0.008
MACF1	0.742	NPCDR1	0.86	0.925	0	0.025
MACF1	0.742	NA	0.718	0.834	0.025	0.031
MACF1	0.742	NA	0.763	0.86	0.006	0.019
MACF1	0.742	LY6G5B_CSNK2B	0.661	0.874	0.001	0.002
MACF1	0.742	CCR4	0.784	0.904	0	0.015
MACF1	0.742	RRP12_LOC644215	0.632	0.803	0.04	0.007
MACF1	0.742	PYHIN1	0.807	0.902	0.001	0.042
MACF1	0.742	SON	0.604	0.806	0.043	0.005
MACF1	0.742	SYNE2	0.678	0.881	0.001	0.001
MACF1	0.742	NA	0.746	0.884	0.002	0.003
MACF1	0.742	TSHZ2	0.801	0.918	0	0.024
MACF1	0.742	CAMK1D	0.702	0.881	0.001	0.003
MACF1	0.742	LOC100128751	0.651	0.822	0.021	0.016
AMFR	0.69	CCR4	0.784	0.873	0.008	0.008
AMFR	0.69	B4GALT3	0.659	0.869	0.012	0
RPL17_SNORD58B	0.694	HDHD1A	0.63	0.786	0.011	0.031
RPL17_SNORD58B	0.694	MGST3	0.602	0.772	0.02	0.033
RPL17_SNORD58B	0.694	FSD1L_GARNL1	0.66	0.812	0.006	0.028
RPL17_SNORD58B	0.694	NA	0.705	0.842	0.006	0.008
RPL17_SNORD58B	0.694	UBE2F_C20orf194	0.762	0.866	0	0.048
RPL17_SNORD58B	0.694	CEP97	0.695	0.838	0.001	0.025

RPL17_SNORD58B	0.694	DYNLL1	0.776	0.925	0	0
RPL17_SNORD58B	0.694	PLEKHA3	0.658	0.834	0	0.021
RPL17_SNORD58B	0.694	TMEM62_SPCS2_L	0.645	0.797	0.003	0.048
RPL17_SNORD58B	0.694	CALM2_C2orf61	0.733	0.909	0	0.001
IRS2	0.648	ITGA2B	0.699	0.831	0.038	0.001
IRS2	0.648	LHFP	0.759	0.879	0	0.032
IRS2	0.648	PTGS1	0.68	0.817	0.04	0.008
IRS2	0.648	MYL9	0.771	0.879	0.002	0.024
IRS2	0.648	CMTM5	0.694	0.814	0.047	0.005
GALNT2	0.651	HSP90AB1_HSP90A	0.799	0.861	0.005	0.024
GALNT2	0.651	NPCDR1	0.86	0.904	0	0.047
GALNT2	0.651	PYHIN1	0.807	0.852	0.005	0.045
GALNT2	0.651	NA	0.746	0.805	0.029	0.011
GALNT2	0.651	RASA4_RASA4P_R	0.779	0.85	0.001	0.049
HSP90AB1_HSP90A	0.799	ACTA2	0.783	0.931	0.001	0.012
HSP90AB1_HSP90A	0.799	TRIM21	0.874	0.977	0	0.014
HSP90AB1_HSP90A	0.799	P4HA1_RPL17	0.715	0.898	0.035	0
HSP90AB1_HSP90A	0.799	HSPB1_HSPBL2	0.778	0.903	0.005	0.029
HSP90AB1_HSP90A	0.799	LAIR1_LAIR2	0.749	0.883	0.037	0.008
HSP90AB1_HSP90A	0.799	UBE2F_C20orf194	0.762	0.91	0.033	0.001
HSP90AB1_HSP90A	0.799	CCRL2	0.786	0.904	0.044	0.008
HSP90AB1_HSP90A	0.799	DYNLL1	0.776	0.922	0.025	0
HSP90AB1_HSP90A	0.799	PLIN2	0.671	0.895	0.027	0.001
HSP90AB1_HSP90A	0.799	FAM118B	0.737	0.91	0.017	0.001
HSP90AB1_HSP90A	0.799	NP	0.633	0.911	0.031	0
HSP90AB1_HSP90A	0.799	TMEM62_SPCS2_L	0.645	0.886	0.01	0
OR9A2	0.813	C15orf54	0.821	0.895	0.034	0.033
OR9A2	0.813	CCR4	0.784	0.908	0.004	0.007
OR9A2	0.813	FAM118A	0.759	0.871	0.031	0.028

OR9A2	0.813	TSHZ2	0.801	0.914	0.003	0.016
OR9A2	0.813	RASA4_RASA4P_R	0.779	0.885	0.015	0.018
OR9A2	0.813	CAMK1D	0.702	0.899	0.011	0.001
OR9A2	0.813	CFD	0.767	0.924	0.016	0.001
OR9A2	0.813	IL5RA	0.832	0.914	0.018	0.03
HDHD1A	0.63	ITGA4_CERKL	0.694	0.799	0.01	0.029
HDHD1A	0.63	NA	0.763	0.825	0.004	0.047
HDHD1A	0.63	CCR4	0.784	0.879	0	0.018
HDHD1A	0.63	S100B	0.72	0.795	0.033	0.02
HDHD1A	0.63	SYNE2	0.678	0.797	0.013	0.015
ACTA2	0.783	C15orf54	0.821	0.889	0.029	0.022
ACTA2	0.783	CCR4	0.784	0.882	0.011	0.027
ACTA2	0.783	PYHIN1	0.807	0.892	0.032	0.03
ACTA2	0.783	RASA4_RASA4P_R	0.779	0.892	0.023	0.004
ACTA2	0.783	IL5RA	0.832	0.896	0.021	0.021
ACPL2	0.651	TAS2R31	0.685	0.778	0.039	0.05
LRRFIP1	0.673	SFRS9	0.527	0.794	0.004	0.002
LRRFIP1	0.673	NPCDR1	0.86	0.916	0	0.047
LRRFIP1	0.673	LY6G5B_CSNK2B	0.661	0.877	0	0.004
LRRFIP1	0.673	CCR4	0.784	0.906	0	0.012
LRRFIP1	0.673	S100B	0.72	0.804	0.05	0.022
LRRFIP1	0.673	SON	0.604	0.754	0.031	0.04
LRRFIP1	0.673	SYNE2	0.678	0.846	0.001	0.005
LRRFIP1	0.673	NA	0.746	0.861	0.001	0.008
LRRFIP1	0.673	TSHZ2	0.801	0.93	0	0.01
LRRFIP1	0.673	CAMK1D	0.702	0.903	0	0.002
OCR1	0.647	NF-E4	0.628	0.823	0.015	0.001
OCR1	0.647	PDK4	0.71	0.819	0.011	0.041
OCR1	0.647	CYP4F3_CYP4F2	0.593	0.754	0.044	0.046

OCR1	0.647	DYNLL1	0.776	0.859	0	0.041
OCR1	0.647	SPARC	0.703	0.839	0.001	0.026
OCR1	0.647	FBXL13	0.614	0.807	0.03	0.002
ITGA4_CERKL	0.694	TRIM21	0.874	0.953	0	0.014
ITGA4_CERKL	0.694	TAF13	0.854	0.922	0	0.035
ITGA4_CERKL	0.694	P4HA1_RPL17	0.715	0.889	0.003	0
ITGA4_CERKL	0.694	KLHL5	0.826	0.923	0	0.043
ITGA4_CERKL	0.694	DLEU2_DLEU2L	0.874	0.943	0	0.036
ITGA4_CERKL	0.694	MGST3	0.602	0.798	0.027	0.005
ITGA4_CERKL	0.694	CCRL2	0.786	0.867	0.003	0.027
ITGA4_CERKL	0.694	ZNF587_ZNF417	0.648	0.816	0.036	0.004
ITGA4_CERKL	0.694	CEP97	0.695	0.832	0.029	0.005
ITGA4_CERKL	0.694	DYNLL1	0.776	0.884	0.002	0.002
ITGA4_CERKL	0.694	PLIN2	0.671	0.821	0.026	0.013
ITGA4_CERKL	0.694	FAM118B	0.737	0.895	0.003	0.001
ITGA4_CERKL	0.694	CTSL1_CTSLL3	0.715	0.845	0.009	0.014
ITGA4_CERKL	0.694	PLEKHA3	0.658	0.822	0.022	0.005
ITGA4_CERKL	0.694	TMEM62_SPCS2_L	0.645	0.887	0	0
ITGA4_CERKL	0.694	PLEKHF2	0.822	0.935	0	0.004
ITGA4_CERKL	0.694	HIST2H2BF_HIST2	0.754	0.842	0.013	0.033
ITGA4_CERKL	0.694	CALM2_C2orf61	0.733	0.863	0.002	0.007
DPH3	0.86	NA	0.763	0.938	0.038	0
DPH3	0.86	CCR4	0.784	0.944	0.019	0
DPH3	0.86	CLC	0.81	0.944	0.029	0.003
DPH3	0.86	LASS4	0.794	0.917	0.021	0.02
DPH3	0.86	TSHZ2	0.801	0.92	0.037	0.005
DPH3	0.86	C4orf3	0.629	0.927	0.048	0
DPH3	0.86	CAMK1D	0.702	0.917	0.043	0
DPH3	0.86	IL5RA	0.832	0.94	0.05	0.002

ERGIC1	0.628	LY6G5B_CSNK2B	0.661	0.784	0.024	0.019
ERGIC1	0.628	CCR4	0.784	0.859	0	0.039
ERGIC1	0.628	CAMK1D	0.702	0.838	0.002	0.012
CD300A	0.623	CAMK1D	0.702	0.792	0.016	0.045
NF-E4	0.628	KIAA1324	0.666	0.778	0.015	0.045
TRIM21	0.874	NPCDR1	0.86	0.956	0.032	0.001
TRIM21	0.874	LY6G5B_CSNK2B	0.661	0.952	0.037	0
TRIM21	0.874	CCR4	0.784	0.957	0.019	0
NPCDR1	0.86	ICAM1	0.821	0.937	0.003	0.017
NPCDR1	0.86	TAF13	0.854	0.935	0.021	0.014
NPCDR1	0.86	KLHL5	0.826	0.943	0.004	0.008
NPCDR1	0.86	ANKRD28	0.8	0.917	0.033	0.006
NPCDR1	0.86	HSPB1_HSPBL2	0.778	0.91	0.029	0.009
NPCDR1	0.86	IL1B	0.871	0.951	0.004	0.017
NPCDR1	0.86	CCRL2	0.786	0.935	0.016	0.001
NPCDR1	0.86	PLEKHF2	0.822	0.919	0.046	0.012
NPCDR1	0.86	AIF1	0.816	0.932	0.008	0.01
NA	0.718	P4HA1_RPL17	0.715	0.849	0.005	0.007
NA	0.763	P4HA1_RPL17	0.715	0.879	0.004	0.002
NA	0.763	DLEU2_DLEU2L	0.874	0.942	0	0.035
NA	0.763	ZRANB1	0.724	0.834	0.05	0.029
NA	0.763	UBE2F_C20orf194	0.762	0.878	0.001	0.02
NA	0.763	CEP97	0.695	0.874	0.005	0.003
NA	0.763	DYNLL1	0.776	0.898	0.01	0.001
NA	0.763	PLIN2	0.671	0.845	0.009	0.009
NA	0.763	FAM118B	0.737	0.873	0.003	0.014
NA	0.763	CTSL1_CTSLL3	0.715	0.862	0.002	0.018
NA	0.763	HIST2H2BF_HIST2	0.754	0.854	0.03	0.023
NA	0.763	CALM2_C2orf61	0.733	0.869	0.004	0.011

ICAM1	0.821	CCR4	0.784	0.9	0.045	0.004
ICAM1	0.821	ABCG1	0.789	0.916	0.012	0.018
ICAM1	0.821	RASA4_RASA4P_R	0.779	0.914	0.045	0.001
TAF13	0.854	CCR4	0.784	0.935	0.009	0.002
TAF13	0.854	ABCG1	0.789	0.922	0.019	0.005
TAF13	0.854	PYHIN1	0.807	0.929	0.038	0.009
TAF13	0.854	CLC	0.81	0.946	0.027	0.003
TAF13	0.854	LASS4	0.794	0.913	0.011	0.017
TAF13	0.854	TSHZ2	0.801	0.924	0.01	0.016
TAF13	0.854	RASA4_RASA4P_R	0.779	0.91	0.034	0.007
P4HA1_RPL17	0.715	LY6G5B_CSNK2B	0.661	0.857	0.001	0.004
P4HA1_RPL17	0.715	CCR4	0.784	0.893	0	0.032
P4HA1_RPL17	0.715	PYHIN1	0.807	0.917	0	0.015
P4HA1_RPL17	0.715	CLC	0.81	0.905	0	0.022
P4HA1_RPL17	0.715	SON	0.604	0.847	0.002	0.001
P4HA1_RPL17	0.715	SYNE2	0.678	0.875	0	0.002
P4HA1_RPL17	0.715	NA	0.746	0.87	0.002	0.005
P4HA1_RPL17	0.715	TSHZ2	0.801	0.911	0	0.035
P4HA1_RPL17	0.715	CAMK1D	0.702	0.884	0	0.002
P4HA1_RPL17	0.715	LOC100128751	0.651	0.817	0.02	0.01
P4HA1_RPL17	0.715	IL5RA	0.832	0.894	0.001	0.047
P4HA1_RPL17	0.715	TAS2R31	0.685	0.833	0.035	0.001
P4HA1_RPL17	0.715	C1orf128	0.751	0.813	0.028	0.022
C15orf54	0.821	ANKRD28	0.8	0.929	0	0.013
C15orf54	0.821	ITGA2B	0.699	0.881	0.05	0.002
C15orf54	0.821	LHFP	0.759	0.894	0.001	0.024
C15orf54	0.821	ZRANB1	0.724	0.898	0.022	0.001
C15orf54	0.821	PTGS1	0.68	0.886	0.014	0.002
C15orf54	0.821	UBE2F_C20orf194	0.762	0.912	0.003	0.004

C15orf54	0.821	MYL9	0.771	0.915	0.003	0.008
C15orf54	0.821	HIST1H2BJ	0.697	0.91	0.018	0.001
C15orf54	0.821	CTSL1_CTSLL3	0.715	0.875	0.049	0.004
C15orf54	0.821	SPARC	0.703	0.905	0.01	0.001
C15orf54	0.821	PLEKHA3	0.658	0.897	0.012	0
C15orf54	0.821	CMTM5	0.694	0.888	0.031	0.001
C15orf54	0.821	HIST2H2BF_HIST2	0.754	0.884	0.03	0.013
C15orf54	0.821	CALM2_C2orf61	0.733	0.905	0.008	0.002
KLHL5	0.826	LY6G5B_CSNK2B	0.661	0.931	0.002	0
KLHL5	0.826	CCR4	0.784	0.958	0.002	0
KLHL5	0.826	ABCG1	0.789	0.932	0.002	0.003
KLHL5	0.826	TSHZ2	0.801	0.928	0.01	0.004
KLHL5	0.826	RASA4_RASA4P_R	0.779	0.905	0.02	0.008
KLHL5	0.826	CAMK1D	0.702	0.902	0.044	0
KLHL5	0.826	IL5RA	0.832	0.919	0.048	0.004
DLEU2_DLEU2L	0.874	CCR4	0.784	0.947	0.009	0
DLEU2_DLEU2L	0.874	ABCG1	0.789	0.939	0.042	0.001
DLEU2_DLEU2L	0.874	IL5RA	0.832	0.936	0.049	0.005
ANKRD28	0.8	LY6G5B_CSNK2B	0.661	0.904	0.006	0
ANKRD28	0.8	CCR4	0.784	0.946	0.005	0
ANKRD28	0.8	ABCG1	0.789	0.897	0.024	0.015
ANKRD28	0.8	FAM118A	0.759	0.906	0.006	0.005
ANKRD28	0.8	PYHIN1	0.807	0.926	0.01	0.003
ANKRD28	0.8	SYNE2	0.678	0.891	0.045	0
ANKRD28	0.8	TSHZ2	0.801	0.933	0.001	0.007
ANKRD28	0.8	RASA4_RASA4P_R	0.779	0.9	0.023	0.004
ANKRD28	0.8	CAMK1D	0.702	0.907	0.017	0
LY6G5B_CSNK2B	0.661	LAIR1_LAIR2	0.749	0.886	0	0.008
LY6G5B_CSNK2B	0.661	ZRANB1	0.724	0.811	0.01	0.032

LY6G5B_CSNK2B	0.661	UBE2F_C20orf194	0.762	0.84	0.003	0.029
LY6G5B_CSNK2B	0.661	FSD1L	0.7	0.783	0.043	0.035
LY6G5B_CSNK2B	0.661	ZNF587_ZNF417	0.648	0.833	0.013	0
LY6G5B_CSNK2B	0.661	KDM6B_TMEM88	0.711	0.839	0	0.047
LY6G5B_CSNK2B	0.661	CEP97	0.695	0.85	0.005	0.001
LY6G5B_CSNK2B	0.661	IRF1	0.651	0.774	0.024	0.044
LY6G5B_CSNK2B	0.661	DYNLL1	0.776	0.856	0.005	0.006
LY6G5B_CSNK2B	0.661	PLIN2	0.671	0.801	0.023	0.018
LY6G5B_CSNK2B	0.661	FAM118B	0.737	0.885	0.001	0.001
LY6G5B_CSNK2B	0.661	PLEKHA3	0.658	0.773	0.04	0.021
LY6G5B_CSNK2B	0.661	AIF1	0.816	0.902	0	0.019
LY6G5B_CSNK2B	0.661	HIST2H2BF_HIST2	0.754	0.826	0.007	0.05
LY6G5B_CSNK2B	0.661	CALM2_C2orf61	0.733	0.826	0.008	0.017
MGST3	0.602	CCR4	0.784	0.868	0	0.024
HSPB1_HSPBL2	0.778	CCR4	0.784	0.874	0.047	0.009
HSPB1_HSPBL2	0.778	PYHIN1	0.807	0.884	0.033	0.021
HSPB1_HSPBL2	0.778	RASA4_RASA4P_R	0.779	0.883	0.023	0.005
HSPB1_HSPBL2	0.778	IL5RA	0.832	0.89	0.048	0.019
CCR4	0.784	LHFP	0.759	0.85	0.013	0.032
CCR4	0.784	LAIR1_LAIR2	0.749	0.885	0.03	0.008
CCR4	0.784	ZRANB1	0.724	0.878	0.022	0.001
CCR4	0.784	UBE2F_C20orf194	0.762	0.923	0.002	0.001
CCR4	0.784	ZNF587_ZNF417	0.648	0.882	0.05	0
CCR4	0.784	MYL9	0.771	0.903	0.006	0.003
CCR4	0.784	CEP97	0.695	0.93	0.003	0
CCR4	0.784	DYNLL1	0.776	0.91	0.013	0
CCR4	0.784	PLIN2	0.671	0.872	0.021	0.001
CCR4	0.784	FAM118B	0.737	0.94	0.001	0
CCR4	0.784	NP	0.633	0.874	0.018	0

CCR4	0.784	PLEKHA3	0.658	0.869	0.046	0
CCR4	0.784	TMEM62_SPCS2_L	0.645	0.872	0.038	0
CCR4	0.784	PLEKHF2	0.822	0.923	0.005	0.002
CCR4	0.784	AIF1	0.816	0.946	0	0.006
CCR4	0.784	HIST2H2BF_HIST2	0.754	0.887	0.049	0.001
CCR4	0.784	CALM2_C2orf61	0.733	0.923	0.002	0
CCDC125	0.632	SYNE2	0.678	0.804	0.002	0.036
ABCG1	0.789	PLEKHF2	0.822	0.908	0.012	0.008
ABCG1	0.789	AIF1	0.816	0.905	0.003	0.05
ITGA2B	0.699	B4GALT3	0.659	0.801	0.019	0.05
LHFP	0.759	LASS4	0.794	0.91	0.001	0.016
LHFP	0.759	TSHZ2	0.801	0.861	0.021	0.049
LAIR1_LAIR2	0.749	PYHIN1	0.807	0.888	0.024	0.028
LAIR1_LAIR2	0.749	TSHZ2	0.801	0.896	0.002	0.045
ZRANB1	0.724	FAM118A	0.759	0.867	0.002	0.033
ZRANB1	0.724	PYHIN1	0.807	0.884	0.003	0.031
ZRANB1	0.724	CLC	0.81	0.88	0.006	0.021
ZRANB1	0.724	NA	0.746	0.855	0.012	0.004
ZRANB1	0.724	TSHZ2	0.801	0.899	0	0.047
ZRANB1	0.724	CAMK1D	0.702	0.855	0.004	0.006
ZRANB1	0.724	IL5RA	0.832	0.886	0.003	0.047
ZRANB1	0.724	C1orf128	0.751	0.866	0.015	0.006
TIMM10	0.554	IFI44	0.762	0.82	0.004	0.024
FSD1L_GARNL1	0.66	TAS2R31	0.685	0.811	0.026	0.002
HIST1H2AJ_HIST1	0.631	POLE2	0.539	0.689	0.007	0.007
PTGS1	0.68	CLC	0.81	0.852	0.011	0.05
PTGS1	0.68	B4GALT3	0.659	0.825	0.008	0.01
PTGS1	0.68	CFD	0.767	0.843	0.012	0.047
PTGS1	0.68	C1orf128	0.751	0.849	0.01	0.047

UBE2F_C20orf194	0.762	FAM118A	0.759	0.87	0.012	0.018
UBE2F_C20orf194	0.762	PYHIN1	0.807	0.895	0.005	0.008
UBE2F_C20orf194	0.762	CLC	0.81	0.906	0.007	0.019
UBE2F_C20orf194	0.762	B4GALT3	0.659	0.922	0	0
UBE2F_C20orf194	0.762	RASA4_RASA4P_R	0.779	0.878	0.001	0.038
UBE2F_C20orf194	0.762	C4orf3	0.629	0.851	0.025	0
UBE2F_C20orf194	0.762	RPIA	0.713	0.884	0.035	0
UBE2F_C20orf194	0.762	IL5RA	0.832	0.906	0.003	0.025
UBE2F_C20orf194	0.762	C1orf128	0.751	0.92	0.007	0
FAM118A	0.759	DYNLL1	0.776	0.878	0.043	0.001
FAM118A	0.759	FAM118B	0.737	0.88	0.027	0.002
FAM118A	0.759	CALM2_C2orf61	0.733	0.862	0.036	0.004
CCRL2	0.786	CLC	0.81	0.908	0.016	0.029
CCRL2	0.786	NA	0.746	0.887	0.014	0.003
CCRL2	0.786	TSHZ2	0.801	0.905	0.003	0.024
CCRL2	0.786	IL5RA	0.832	0.912	0.007	0.029
SRXN1	0.612	RPIA	0.713	0.799	0.017	0.025
SRXN1	0.612	C1orf128	0.751	0.848	0.002	0.022
ZNF587_ZNF417	0.648	SYNE2	0.678	0.849	0.001	0.008
ZNF587_ZNF417	0.648	CAMK1D	0.702	0.857	0	0.018
PYHIN1	0.807	MYL9	0.771	0.876	0.046	0.03
PYHIN1	0.807	CEP97	0.695	0.91	0.018	0
PYHIN1	0.807	DYNLL1	0.776	0.91	0.047	0
PYHIN1	0.807	PLIN2	0.671	0.879	0.04	0.002
PYHIN1	0.807	FAM118B	0.737	0.927	0.004	0.001
PYHIN1	0.807	TMEM62_SPCS2_L	0.645	0.904	0.009	0
PYHIN1	0.807	DCTN5	0.557	0.879	0.046	0
KIAA1324	0.666	CYP4F3_CYP4F2	0.593	0.765	0.039	0.033
KDM6B_TMEM88	0.711	RASA4_RASA4P_R	0.779	0.852	0.012	0.022

KDM6B_TMEM88	0.711	CAMK1D	0.702	0.835	0.041	0.004
MYL9	0.771	CLC	0.81	0.886	0.048	0.013
MYL9	0.771	LASS4	0.794	0.926	0	0.048
MYL9	0.771	B4GALT3	0.659	0.881	0.022	0
MYL9	0.771	CFD	0.767	0.882	0.04	0.006
MYL9	0.771	IL5RA	0.832	0.903	0.012	0.025
MYL9	0.771	C1orf128	0.751	0.879	0.037	0.014
TAAR1	0.657	TAS2R31	0.685	0.763	0.016	0.049
CLC	0.81	CEP97	0.695	0.908	0.016	0.001
CLC	0.81	DYNLL1	0.776	0.914	0.033	0.001
CLC	0.81	PLIN2	0.671	0.893	0.02	0.002
CLC	0.81	FAM118B	0.737	0.914	0.008	0.002
CLC	0.81	CTSL1_CTSLL3	0.715	0.903	0.034	0.001
CLC	0.81	PLEKHF2	0.822	0.923	0.014	0.021
CLC	0.81	CALM2_C2orf61	0.733	0.908	0.018	0.002
CEP97	0.695	SYNE2	0.678	0.845	0.011	0.002
CEP97	0.695	B4GALT3	0.659	0.814	0.01	0.019
CEP97	0.695	CAMK1D	0.702	0.825	0.014	0.032
CEP97	0.695	IL5RA	0.832	0.902	0	0.025
SON	0.604	DYNLL1	0.776	0.837	0.002	0.027
SON	0.604	FAM118B	0.737	0.835	0.001	0.027
SON	0.604	TMEM62_SPCS2_L	0.645	0.768	0.02	0.019
SON	0.604	CALM2_C2orf61	0.733	0.816	0.002	0.036
IRF1	0.651	NA	0.746	0.818	0.015	0.01
IRF1	0.651	CAMK1D	0.702	0.797	0.024	0.027
IRF1	0.651	IL5RA	0.832	0.884	0	0.041
IRF1	0.651	C1orf128	0.751	0.803	0.042	0.038
SYNE2	0.678	DYNLL1	0.776	0.882	0.001	0.005
SYNE2	0.678	FAM118B	0.737	0.887	0	0.004

SYNE2	0.678	NP	0.633	0.778	0.027	0.035
SYNE2	0.678	TMEM62_SPCS2_L	0.645	0.814	0.007	0.011
SYNE2	0.678	CALM2_C2orf61	0.733	0.843	0.001	0.025
SYNE2	0.678	DCTN5	0.557	0.78	0.026	0.003
DYNLL1	0.776	NA	0.746	0.862	0.014	0.012
DYNLL1	0.776	B4GALT3	0.659	0.857	0.007	0.006
DYNLL1	0.776	CAMK1D	0.702	0.883	0.001	0.004
DYNLL1	0.776	IL5RA	0.832	0.91	0.002	0.038
DYNLL1	0.776	C1orf128	0.751	0.885	0.013	0.006
NA	0.746	PLIN2	0.671	0.821	0.024	0.025
NA	0.746	FAM118B	0.737	0.85	0.009	0.023
NA	0.746	HIST2H2BF_HIST2	0.754	0.875	0.002	0.018
TSHZ2	0.801	PLIN2	0.671	0.919	0.009	0
TSHZ2	0.801	FAM118B	0.737	0.935	0.002	0
TSHZ2	0.801	PLEKHF2	0.822	0.902	0.04	0.009
TSHZ2	0.801	AIF1	0.816	0.92	0.007	0.013
PLIN2	0.671	CAMK1D	0.702	0.805	0.02	0.034
FAM118B	0.737	RASA4_RASA4P_R	0.779	0.874	0.002	0.042
FAM118B	0.737	CAMK1D	0.702	0.881	0.002	0.002
FAM118B	0.737	CFD	0.767	0.855	0.045	0.01
FAM118B	0.737	IL5RA	0.832	0.895	0.003	0.038
B4GALT3	0.659	NP	0.633	0.84	0.007	0.001
B4GALT3	0.659	PLEKHA3	0.658	0.761	0.036	0.049
B4GALT3	0.659	TMEM62_SPCS2_L	0.645	0.752	0.044	0.044
B4GALT3	0.659	CMTM5	0.694	0.816	0.019	0.015
B4GALT3	0.659	CALM2_C2orf61	0.733	0.84	0.001	0.024
RASA4_RASA4P_R	0.779	PLEKHF2	0.822	0.877	0.037	0.045
RASA4_RASA4P_R	0.779	AIF1	0.816	0.898	0.01	0.013
NP	0.633	C1orf128	0.751	0.849	0.003	0.014

PLEKHF2	0.822	IL5RA	0.832	0.915	0.027	0.017
CAMK1D	0.702	AIF1	0.816	0.906	0	0.049
CAMK1D	0.702	HIST2H2BF_HIST2	0.754	0.839	0.011	0.049
CAMK1D	0.702	CALM2_C2orf61	0.733	0.856	0.006	0.006
CAMK1D	0.702	SPATA6	0.642	0.832	0.035	0.001
AIF1	0.816	IL5RA	0.832	0.926	0.034	0.005
CFD	0.767	HIST2H2BF_HIST2	0.754	0.861	0.036	0.025
CFD	0.767	CALM2_C2orf61	0.733	0.879	0.01	0.007
MPZL2	0.612	IFI44	0.762	0.809	0.016	0.009
IL5RA	0.832	HIST2H2BF_HIST2	0.754	0.905	0.021	0.008
IL5RA	0.832	CALM2_C2orf61	0.733	0.901	0.033	0.002
CALM2_C2orf61	0.733	C1orf128	0.751	0.855	0.025	0.007

Table 18

Ratios inSIRS Versus ipSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
TLR5	0.725	CLEC4D	0.732	0.868	0.016	0.015
TLR5	0.725	SLC37A3	0.668	0.907	0.001	0
TLR5	0.725	BMX_HNRPDL	0.716	0.877	0.027	0.001
TLR5	0.725	FKBP5_LOC285847	0.79	0.901	0.003	0.026
TLR5	0.725	MMP9_LOC1001280	0.729	0.861	0.01	0.02
TLR5	0.725	PFKFB2	0.777	0.888	0.011	0.007
TLR5	0.725	ODZ1	0.777	0.891	0.015	0.002
TLR5	0.725	SH3PXD2B	0.751	0.873	0.032	0.009
TLR5	0.725	PRR13_PCBP2	0.758	0.898	0	0.048
TLR5	0.725	CD163	0.808	0.887	0.022	0.019
TLR5	0.725	MTHFS	0.733	0.909	0	0.013

TLR5	0.725	PLA2G7	0.738	0.868	0.019	0.005
TLR5	0.725	KDM6B_TMEM88	0.672	0.842	0	0.049
TLR5	0.725	HIST2H2BF_HIST2	0.62	0.82	0.035	0.007
CD177	0.611	ARG1	0.715	0.816	0.01	0.014
VNN1	0.523	ARG1	0.715	0.842	0	0.012
UBE2J1	0.814	SLC37A3	0.668	0.943	0.011	0
UBE2J1	0.814	CLEC4E	0.849	0.918	0.031	0.022
UBE2J1	0.814	PPP2R5A_SNORA16	0.716	0.935	0.015	0
UBE2J1	0.814	PRR13_PCBP2	0.758	0.918	0.029	0.003
UBE2J1	0.814	MTHFS	0.733	0.96	0.005	0
UBE2J1	0.814	CDA	0.694	0.902	0.043	0.001
UBE2J1	0.814	HAL	0.846	0.916	0.021	0.045
UBE2J1	0.814	CCDC125	0.79	0.906	0.043	0.011
UBE2J1	0.814	RGS2	0.789	0.935	0.006	0.005
IMP3	0.908	RUNX2	0.868	0.98	0.018	0.016
IMP3	0.908	SYNE2	0.886	0.99	0.049	0.003
RNASE2_LOC64333	0.718	CLEC4D	0.732	0.836	0.045	0.016
RNASE2_LOC64333	0.718	SLC37A3	0.668	0.858	0.007	0.004
RNASE2_LOC64333	0.718	MMP9_LOC1001280	0.729	0.857	0.006	0.037
RNASE2_LOC64333	0.718	PFKFB2	0.777	0.855	0.031	0.026
RNASE2_LOC64333	0.718	CD163	0.808	0.881	0.017	0.004
RNASE2_LOC64333	0.718	MTHFS	0.733	0.862	0.006	0.027
RNASE2_LOC64333	0.718	PLA2G7	0.738	0.874	0.022	0.003
CLEC4D	0.732	C3AR1	0.777	0.875	0.008	0.038
CLEC4D	0.732	FAR2	0.706	0.842	0.035	0.019
CLEC4D	0.732	OMG	0.769	0.901	0.004	0.009
CLEC4D	0.732	TDRD9	0.752	0.904	0.014	0
CLEC4D	0.732	ACER3	0.842	0.926	0	0.048
CLEC4D	0.732	GPR84	0.71	0.874	0.043	0

CLEC4D	0.732	PLB1	0.722	0.904	0.005	0.001
CLEC4D	0.732	DSE	0.784	0.907	0.001	0.026
CLEC4D	0.732	GSR	0.605	0.822	0.019	0.008
CLEC4D	0.732	SMPDL3A	0.736	0.911	0.003	0.001
CLEC4D	0.732	ATP13A3	0.796	0.894	0.007	0.042
CLEC4D	0.732	PDGFC	0.822	0.943	0.001	0.009
CLEC4D	0.732	SEC24A_SAR1B	0.739	0.86	0.004	0.046
CLEC4D	0.732	EXOSC4	0.742	0.957	0	0.001
CLEC4D	0.732	CCR1	0.72	0.848	0.017	0.039
CLEC4D	0.732	AP3B2	0.697	0.843	0.046	0.015
CLEC4D	0.732	PCOLCE2	0.667	0.889	0.003	0.002
CLEC4D	0.732	GALNT2	0.673	0.892	0.001	0.002
CLEC4D	0.732	HDHD1A	0.7	0.823	0.026	0.039
CLEC4D	0.732	KIAA0746	0.713	0.854	0.038	0.007
CLEC4D	0.732	PLEKHF2	0.737	0.868	0.005	0.039
CLEC4D	0.732	IGLV6-57	0.757	0.849	0.025	0.034
C3AR1	0.777	SLC37A3	0.668	0.863	0.037	0.001
C3AR1	0.777	ERLIN1	0.756	0.868	0.048	0.033
C3AR1	0.777	FKBP5_LOC285847	0.79	0.898	0.009	0.046
C3AR1	0.777	MMP9_LOC1001280	0.729	0.884	0.011	0.02
C3AR1	0.777	PFKFB2	0.777	0.887	0.035	0.026
C3AR1	0.777	CDA	0.694	0.86	0.022	0.02
C3AR1	0.777	SLC11A1	0.705	0.842	0.044	0.04
C3AR1	0.777	ACPL2	0.756	0.868	0.035	0.024
C3AR1	0.777	CPM	0.812	0.89	0.036	0.046
ARG1	0.715	TDRD9	0.752	0.906	0	0.008
ARG1	0.715	GPR84	0.71	0.828	0.018	0.044
ARG1	0.715	HPGD	0.655	0.864	0.008	0.003
ARG1	0.715	HSPC159	0.577	0.792	0.04	0.012

ARG1	0.715	FOLR3_FOLR2	0.585	0.795	0.026	0.02
ARG1	0.715	LCN2	0.639	0.851	0.008	0.003
ARG1	0.715	ABCA13	0.699	0.868	0.001	0.026
ARG1	0.715	MKI67	0.674	0.835	0.009	0.043
ARG1	0.715	LTF	0.642	0.809	0.036	0.022
ARG1	0.715	RETN	0.473	0.792	0.033	0
ARG1	0.715	ANKRD28	0.71	0.858	0.002	0.04
ARG1	0.715	LHFP	0.561	0.783	0.026	0.017
ARG1	0.715	TAAR1	0.589	0.81	0.029	0.005
ARG1	0.715	DEFA4_DEFA8P	0.663	0.829	0.022	0.013
ARG1	0.715	SPARC	0.661	0.802	0.044	0.033
ARG1	0.715	IGJ	0.683	0.833	0.028	0.011
FCGR1A_FCGR1B_	0.797	IFI16	0.721	0.902	0.006	0.008
FCGR1A_FCGR1B_	0.797	PRR13_PCBP2	0.758	0.895	0.005	0.025
FCGR1A_FCGR1B_	0.797	MTHFS	0.733	0.914	0.003	0.006
FCGR1A_FCGR1B_	0.797	KDM6B_TMEM88	0.672	0.869	0.022	0.007
C11orf82	0.927	MMP9_LOC1001280	0.729	0.976	0.025	0
C11orf82	0.927	PPP2R5A_SNORA16	0.716	0.974	0.049	0
C11orf82	0.927	PRR13_PCBP2	0.758	0.974	0.016	0
C11orf82	0.927	HIST1H2AA	0.825	0.973	0.033	0.002
C11orf82	0.927	CDA	0.694	0.965	0.022	0
C11orf82	0.927	SYNE2	0.886	0.971	0.043	0.023
FAR2	0.706	BMX_HNRPDL	0.716	0.85	0.037	0.003
FAR2	0.706	CLEC4E	0.849	0.954	0	0.013
FAR2	0.706	ERLIN1	0.756	0.897	0.006	0.001
FAR2	0.706	FKBP5_LOC285847	0.79	0.907	0.001	0.022
FAR2	0.706	PFKFB2	0.777	0.904	0.004	0.003
FAR2	0.706	ECHDC3	0.823	0.941	0.001	0.004
FAR2	0.706	PPP2R5A_SNORA16	0.716	0.869	0.002	0.023

FAR2	0.706	HMGB2	0.673	0.868	0.009	0.003
FAR2	0.706	TPST1	0.754	0.874	0.024	0.001
FAR2	0.706	CD163	0.808	0.873	0.036	0.023
FAR2	0.706	SAP30	0.789	0.913	0	0.044
FAR2	0.706	DAAM2_LOC100131	0.778	0.89	0.024	0.001
FAR2	0.706	ACPL2	0.756	0.892	0.004	0.006
FAR2	0.706	CCDC125	0.79	0.913	0	0.049
FAR2	0.706	THBS1	0.698	0.851	0.039	0.001
FAR2	0.706	CPM	0.812	0.908	0.003	0.022
FAR2	0.706	CAMK1D	0.735	0.882	0.002	0.016
GALNT3	0.859	CLEC4E	0.849	0.944	0.026	0.018
GALNT3	0.859	IFI16	0.721	0.923	0.041	0.002
GALNT3	0.859	ECHDC3	0.823	0.929	0.043	0.01
GALNT3	0.859	PPP2R5A_SNORA16	0.716	0.962	0.003	0
GALNT3	0.859	PRR13_PCBP2	0.758	0.93	0.02	0.007
GALNT3	0.859	MTHFS	0.733	0.946	0.022	0.001
GALNT3	0.859	SAP30	0.789	0.917	0.019	0.022
GALNT3	0.859	AREG	0.814	0.916	0.028	0.032
GALNT3	0.859	ERGIC1	0.758	0.92	0.022	0.003
GALNT3	0.859	NA	0.884	0.959	0.012	0.028
GALNT3	0.859	HAL	0.846	0.933	0.011	0.037
GALNT3	0.859	KIAA1257_ACAD9/	0.823	0.926	0.022	0.02
GALNT3	0.859	CCDC125	0.79	0.938	0.016	0.01
GALNT3	0.859	RGS2	0.789	0.945	0.002	0.018
OMG	0.769	SLC37A3	0.668	0.902	0.01	0
OMG	0.769	CLEC4E	0.849	0.947	0	0.036
OMG	0.769	FKBP5_LOC285847	0.79	0.915	0.007	0.013
OMG	0.769	MMP9_LOC1001280	0.729	0.888	0.014	0.004
OMG	0.769	PFKFB2	0.777	0.906	0.016	0.003

OMG	0.769	IFI16	0.721	0.845	0.033	0.047
OMG	0.769	ODZ1	0.777	0.906	0.036	0.001
OMG	0.769	ECHDC3	0.823	0.934	0.001	0.024
OMG	0.769	PPP2R5A_SNORA16	0.716	0.916	0.001	0.005
OMG	0.769	HMGB2	0.673	0.917	0.011	0
OMG	0.769	PRR13_PCBP2	0.758	0.89	0.002	0.041
OMG	0.769	TPST1	0.754	0.926	0.019	0
OMG	0.769	MTHFS	0.733	0.893	0.012	0.012
OMG	0.769	CDA	0.694	0.873	0.011	0.012
OMG	0.769	SLC11A1	0.705	0.898	0.003	0.008
OMG	0.769	DAAM2_LOC100131	0.778	0.899	0.035	0.004
OMG	0.769	ACPL2	0.756	0.935	0.003	0.002
OMG	0.769	ERGIC1	0.758	0.903	0.003	0.03
OMG	0.769	HAL	0.846	0.947	0	0.039
OMG	0.769	CCDC125	0.79	0.913	0.001	0.039
OMG	0.769	ZRANB1	0.718	0.85	0.028	0.038
OMG	0.769	CYP4F3_CYP4F2	0.755	0.868	0.035	0.029
OMG	0.769	MME	0.847	0.94	0.001	0.027
OMG	0.769	CPM	0.812	0.908	0.009	0.031
OMG	0.769	RBP7	0.803	0.939	0.001	0.014
OMG	0.769	RGS2	0.789	0.94	0	0.023
OMG	0.769	CAMK1D	0.735	0.864	0.007	0.048
SLC37A3	0.668	TDRD9	0.752	0.894	0.007	0
SLC37A3	0.668	ACER3	0.842	0.934	0	0.02
SLC37A3	0.668	C7orf53	0.711	0.847	0.006	0.012
SLC37A3	0.668	PLB1	0.722	0.922	0	0
SLC37A3	0.668	DSE	0.784	0.924	0	0.005
SLC37A3	0.668	GSR	0.605	0.773	0.042	0.026
SLC37A3	0.668	SMPDL3A	0.736	0.861	0.004	0.019

SLC37A3	0.668	ATP13A3	0.796	0.919	0.001	0.004
SLC37A3	0.668	PDGFC	0.822	0.941	0	0.014
SLC37A3	0.668	EXOSC4	0.742	0.924	0	0.003
SLC37A3	0.668	CCR1	0.72	0.826	0.015	0.027
SLC37A3	0.668	ABCA13	0.699	0.8	0.046	0.03
SLC37A3	0.668	PCOLCE2	0.667	0.832	0.001	0.026
SLC37A3	0.668	MKI67	0.674	0.79	0.028	0.026
SLC37A3	0.668	MACF1	0.699	0.817	0.025	0.019
SLC37A3	0.668	GALNT2	0.673	0.866	0	0.008
SLC37A3	0.668	HDHD1A	0.7	0.829	0.004	0.024
SLC37A3	0.668	KIAA0746	0.713	0.847	0.007	0.008
SLC37A3	0.668	LAIR1_LAIR2	0.777	0.874	0.001	0.03
SLC37A3	0.668	CD151	0.767	0.892	0	0.018
SLC37A3	0.668	IGK@_IGKC_IGKV	0.774	0.848	0.017	0.04
SLC37A3	0.668	MYL9	0.695	0.816	0.019	0.028
SLC37A3	0.668	HIST1H2BJ	0.797	0.874	0.001	0.047
SLC37A3	0.668	IGLV6-57	0.757	0.851	0.007	0.025
SLC37A3	0.668	SDHC	0.85	0.907	0.001	0.042
BMX_HNRPDL	0.716	TDRD9	0.752	0.938	0.002	0
BMX_HNRPDL	0.716	GPR84	0.71	0.904	0.006	0
BMX_HNRPDL	0.716	PLB1	0.722	0.884	0	0.021
BMX_HNRPDL	0.716	GSR	0.605	0.805	0.012	0.035
BMX_HNRPDL	0.716	SMPDL3A	0.736	0.9	0.001	0.008
BMX_HNRPDL	0.716	PDGFC	0.822	0.936	0	0.033
BMX_HNRPDL	0.716	EXOSC4	0.742	0.918	0	0.015
BMX_HNRPDL	0.716	DNAJC9_FAM149B1	0.742	0.835	0.033	0.036
BMX_HNRPDL	0.716	ABCA13	0.699	0.839	0.014	0.026
BMX_HNRPDL	0.716	PCOLCE2	0.667	0.857	0.002	0.024
BMX_HNRPDL	0.716	MKI67	0.674	0.839	0.007	0.032

BMX_HNRPDL	0.716	RETN	0.473	0.828	0.019	0
BMX_HNRPDL	0.716	MACF1	0.699	0.836	0.018	0.033
BMX_HNRPDL	0.716	GALNT2	0.673	0.864	0	0.024
BMX_HNRPDL	0.716	KIAA0746	0.713	0.857	0.012	0.018
BMX_HNRPDL	0.716	LHFP	0.561	0.798	0.02	0.009
BMX_HNRPDL	0.716	IGK@_IGKC_IGKV	0.774	0.87	0.007	0.026
BMX_HNRPDL	0.716	TAAR1	0.589	0.806	0.047	0.006
BMX_HNRPDL	0.716	IGLV6-57	0.757	0.867	0.004	0.043
STOM	0.792	CLEC4E	0.849	0.922	0.033	0.005
STOM	0.792	LOC284757	0.921	0.958	0.003	0.03
STOM	0.792	PPP2R5A_SNORA16	0.716	0.908	0.044	0
STOM	0.792	PRR13_PCBP2	0.758	0.926	0.016	0.001
STOM	0.792	GAB2	0.842	0.919	0.012	0.02
STOM	0.792	AREG	0.814	0.92	0.01	0.008
STOM	0.792	IRS2	0.851	0.906	0.045	0.044
STOM	0.792	CCDC125	0.79	0.912	0.038	0.005
STOM	0.792	MME	0.847	0.887	0.047	0.04
TDRD9	0.752	IL18R1	0.748	0.895	0.01	0.008
TDRD9	0.752	MMP9_LOC1001280	0.729	0.906	0	0.026
TDRD9	0.752	GK3P_GK	0.654	0.874	0.015	0.001
TDRD9	0.752	PFKFB2	0.777	0.942	0	0.007
TDRD9	0.752	ODZ1	0.777	0.914	0.002	0.007
TDRD9	0.752	SH3PXD2B	0.751	0.894	0.004	0.017
TDRD9	0.752	HMGB2	0.673	0.835	0.03	0.025
TDRD9	0.752	TPST1	0.754	0.86	0.026	0.032
TDRD9	0.752	THBS1	0.698	0.837	0.041	0.029
KREMEN1	0.835	PRR13_PCBP2	0.758	0.926	0.013	0.012
KREMEN1	0.835	SLC11A1	0.705	0.9	0.018	0.011
KREMEN1	0.835	KDM6B_TMEM88	0.672	0.919	0.017	0.002

CLEC4E	0.849	DNAJC13	0.772	0.921	0.03	0.005
CLEC4E	0.849	FOXD4L3_FOXD4L6	0.861	0.951	0.012	0.015
CLEC4E	0.849	SLC15A2	0.817	0.913	0.043	0.039
CLEC4E	0.849	VAMP2	0.595	0.911	0.012	0
CLEC4E	0.849	CLU	0.784	0.921	0.017	0.009
CLEC4E	0.849	CD63	0.813	0.956	0.001	0.011
CLEC4E	0.849	DDAH2	0.809	0.942	0.003	0.029
CLEC4E	0.849	PDGFC	0.822	0.958	0.005	0.006
CLEC4E	0.849	LRRC70_IPO11	0.886	0.952	0.012	0.033
CLEC4E	0.849	EXOSC4	0.742	0.934	0.012	0.002
CLEC4E	0.849	HIST1H3J	0.829	0.955	0.006	0.009
CLEC4E	0.849	SUCNR1	0.861	0.942	0.024	0.008
CLEC4E	0.849	AIG1	0.873	0.962	0.001	0.039
CLEC4E	0.849	PCOLCE2	0.667	0.901	0.037	0.001
CLEC4E	0.849	HS2ST1_UBA2	0.837	0.942	0.005	0.032
CLEC4E	0.849	HIST1H3A	0.822	0.947	0.009	0.008
CLEC4E	0.849	GSTO1	0.83	0.939	0.005	0.026
CLEC4E	0.849	ACTA2	0.818	0.946	0.006	0.015
CLEC4E	0.849	DPH3	0.706	0.932	0.038	0
CLEC4E	0.849	TYMS	0.838	0.944	0.004	0.026
CLEC4E	0.849	ITGA2B	0.752	0.924	0.038	0.001
CLEC4E	0.849	HIST1H3B	0.829	0.936	0.038	0.01
CLEC4E	0.849	PTGS1	0.794	0.94	0.01	0.003
CLEC4E	0.849	HIST1H3C	0.854	0.951	0.023	0.004
CLEC4E	0.849	CD151	0.767	0.921	0.046	0.003
CLEC4E	0.849	HIST1H3H	0.836	0.932	0.035	0.02
CLEC4E	0.849	FSD1L	0.834	0.937	0.015	0.01
CLEC4E	0.849	TPX2	0.745	0.928	0.021	0.002
CLEC4E	0.849	APOLD1	0.777	0.911	0.03	0.014

CLEC4E	0.849	HIST1H2BJ	0.797	0.941	0.031	0.004
CLEC4E	0.849	SON	0.794	0.921	0.024	0.02
CLEC4E	0.849	LASS4	0.669	0.902	0.035	0.002
CLEC4E	0.849	B4GALT3	0.785	0.917	0.029	0.015
CLEC4E	0.849	TNFRSF17	0.827	0.932	0.028	0.008
CLEC4E	0.849	CMTM5	0.814	0.957	0.008	0.002
CLEC4E	0.849	IGL@_IGLV1-44_	0.77	0.922	0.022	0.005
CLEC4E	0.849	GLDC	0.775	0.939	0.002	0.005
CLEC4E	0.849	KIAA0101_CSNK1G	0.87	0.948	0.014	0.025
IL18R1	0.748	HPGD	0.655	0.874	0.027	0.001
IL18R1	0.748	FOLR3_FOLR2	0.585	0.81	0.024	0.014
IL18R1	0.748	PCOLCE2	0.667	0.842	0.014	0.04
IL18R1	0.748	LHFP	0.561	0.8	0.045	0.01
IL18R1	0.748	TAAR1	0.589	0.834	0.024	0.004
ACER3	0.842	PRR13_PCBP2	0.758	0.911	0.034	0.009
ACER3	0.842	MTHFS	0.733	0.939	0.009	0.001
ACER3	0.842	AREG	0.814	0.906	0.023	0.04
ACER3	0.842	KDM6B_TMEM88	0.672	0.9	0.039	0.001
ERLIN1	0.756	GSR	0.605	0.819	0.043	0.013
ERLIN1	0.756	SMPDL3A	0.736	0.859	0.036	0.01
ERLIN1	0.756	EXOSC4	0.742	0.876	0.004	0.039
ERLIN1	0.756	EFCAB2	0.784	0.87	0.049	0.016
ERLIN1	0.756	PCOLCE2	0.667	0.855	0.017	0.005
ERLIN1	0.756	GALNT2	0.673	0.86	0.008	0.012
ERLIN1	0.756	HDHD1A	0.7	0.841	0.022	0.035
ERLIN1	0.756	DPH3	0.706	0.845	0.035	0.03
ERLIN1	0.756	ANKRD28	0.71	0.851	0.03	0.017
TGFBR1	0.874	LOC284757	0.921	0.977	0.025	0.02
TGFBR1	0.874	RUNX2	0.868	0.952	0.024	0.029

TGFBR1	0.874	MPZL3	0.889	0.969	0.016	0.011
TGFBR1	0.874	SYNE2	0.886	0.974	0.029	0.005
TGFBR1	0.874	RGS2	0.789	0.965	0.028	0
FKBP5_LOC285847	0.79	C7orf53	0.711	0.882	0.041	0.004
FKBP5_LOC285847	0.79	PLB1	0.722	0.908	0.015	0.002
FKBP5_LOC285847	0.79	DNAJC13	0.772	0.913	0.004	0.017
FKBP5_LOC285847	0.79	GSR	0.605	0.866	0.034	0.002
FKBP5_LOC285847	0.79	METTL7B	0.749	0.874	0.042	0.018
FKBP5_LOC285847	0.79	VAMP2	0.595	0.853	0.048	0.002
FKBP5_LOC285847	0.79	CD63	0.813	0.935	0	0.05
FKBP5_LOC285847	0.79	PDGFC	0.822	0.948	0.001	0.013
FKBP5_LOC285847	0.79	SEC24A_SAR1B	0.739	0.87	0.032	0.031
FKBP5_LOC285847	0.79	EXOSC4	0.742	0.906	0.005	0.009
FKBP5_LOC285847	0.79	PCOLCE2	0.667	0.888	0.007	0.002
FKBP5_LOC285847	0.79	GALNT2	0.673	0.887	0.014	0.004
FKBP5_LOC285847	0.79	DPH3	0.706	0.882	0.033	0.006
FKBP5_LOC285847	0.79	ANKRD28	0.71	0.882	0.045	0.003
FKBP5_LOC285847	0.79	ITGA2B	0.752	0.878	0.039	0.017
FKBP5_LOC285847	0.79	CD151	0.767	0.881	0.029	0.043
FKBP5_LOC285847	0.79	FSD1L	0.834	0.919	0.005	0.043
FKBP5_LOC285847	0.79	HIST1H2BJ	0.797	0.897	0.029	0.034
FKBP5_LOC285847	0.79	FAM118B	0.74	0.875	0.04	0.02
FKBP5_LOC285847	0.79	PLEKHF2	0.737	0.868	0.041	0.038
GPR84	0.71	GK3P_GK	0.654	0.831	0.037	0.004
GPR84	0.71	SH3PXD2B	0.751	0.858	0.009	0.029
C7orf53	0.711	PFKFB2	0.777	0.857	0.032	0.015
C7orf53	0.711	ODZ1	0.777	0.871	0.023	0.006
C7orf53	0.711	PPP2R5A_SNORA16	0.716	0.869	0.002	0.029
C7orf53	0.711	CHI3L1	0.798	0.861	0.02	0.049

C7orf53	0.711	TPST1	0.754	0.869	0.034	0.001
C7orf53	0.711	MTHFS	0.733	0.856	0.007	0.036
C7orf53	0.711	HAL	0.846	0.945	0	0.047
C7orf53	0.711	CPM	0.812	0.905	0.001	0.031
C7orf53	0.711	PPP1R2_PPP1R2P3	0.637	0.791	0.038	0.043
PLB1	0.722	MMP9_LOC1001280	0.729	0.88	0.004	0.012
PLB1	0.722	PFKFB2	0.777	0.927	0.001	0.001
PLB1	0.722	ODZ1	0.777	0.902	0.015	0
PLB1	0.722	SH3PXD2B	0.751	0.877	0.018	0.005
PLB1	0.722	CD163	0.808	0.894	0.011	0.032
PLB1	0.722	MTHFS	0.733	0.906	0	0.014
PLB1	0.722	SLC11A1	0.705	0.864	0	0.045
DSE	0.784	MMP9_LOC1001280	0.729	0.881	0.043	0.005
DSE	0.784	PPP2R5A_SNORA16	0.716	0.894	0.021	0.002
DSE	0.784	PRR13_PCBP2	0.758	0.878	0.017	0.038
DSE	0.784	MTHFS	0.733	0.934	0.003	0.001
DSE	0.784	CDA	0.694	0.879	0.026	0.006
DSE	0.784	SLC11A1	0.705	0.875	0.025	0.004
DSE	0.784	CCDC125	0.79	0.894	0.012	0.044
DSE	0.784	KDM6B_TMEM88	0.672	0.86	0.047	0.004
DSE	0.784	RGS2	0.789	0.915	0.001	0.037
PTGDR	0.616	DNAJC9_FAM149B1	0.742	0.835	0.002	0.049
DNAJC13	0.772	PFKFB2	0.777	0.903	0.031	0.002
DNAJC13	0.772	IFI16	0.721	0.892	0.018	0.006
DNAJC13	0.772	PPP2R5A_SNORA16	0.716	0.913	0.005	0.002
DNAJC13	0.772	PRR13_PCBP2	0.758	0.891	0.01	0.014
DNAJC13	0.772	SLC11A1	0.705	0.869	0.033	0.003
DNAJC13	0.772	ERGIC1	0.758	0.894	0.014	0.003
DNAJC13	0.772	CCDC125	0.79	0.932	0.002	0.007

DNAJC13	0.772	CPM	0.812	0.907	0.021	0.007
DNAJC13	0.772	MPZL2	0.775	0.879	0.032	0.011
TNFAIP6	0.676	EIF2AK2	0.646	0.824	0.025	0.006
TNFAIP6	0.676	HIST2H2BF_HIST2	0.62	0.773	0.046	0.041
FOXD4L3_FOXD4L6	0.861	PPP2R5A_SNORA16	0.716	0.93	0.022	0.001
FOXD4L3_FOXD4L6	0.861	MTHFS	0.733	0.919	0.049	0.003
FOXD4L3_FOXD4L6	0.861	SAP30	0.789	0.926	0.008	0.017
FOXD4L3_FOXD4L6	0.861	AREG	0.814	0.914	0.041	0.034
FOXD4L3_FOXD4L6	0.861	HAL	0.846	0.945	0.006	0.044
FOXD4L3_FOXD4L6	0.861	CCDC125	0.79	0.921	0.032	0.021
FOXD4L3_FOXD4L6	0.861	ZRANB1	0.718	0.91	0.049	0.003
FOXD4L3_FOXD4L6	0.861	RGS2	0.789	0.926	0.003	0.035
FOXD4L3_FOXD4L6	0.861	CAMK1D	0.735	0.923	0.02	0.003
MMP9_LOC1001280	0.729	METTL7B	0.749	0.875	0.016	0.011
MMP9_LOC1001280	0.729	SLC15A2	0.817	0.914	0.001	0.042
MMP9_LOC1001280	0.729	SMPDL3A	0.736	0.89	0.012	0.003
MMP9_LOC1001280	0.729	CD63	0.813	0.949	0	0.016
MMP9_LOC1001280	0.729	DDAH2	0.809	0.933	0	0.025
MMP9_LOC1001280	0.729	ATP13A3	0.796	0.898	0.01	0.017
MMP9_LOC1001280	0.729	PDGFC	0.822	0.94	0	0.017
MMP9_LOC1001280	0.729	SEC24A_SAR1B	0.739	0.882	0.006	0.013
MMP9_LOC1001280	0.729	EXOSC4	0.742	0.911	0.002	0.003
MMP9_LOC1001280	0.729	AP3B2	0.697	0.843	0.046	0.011
MMP9_LOC1001280	0.729	SUCNR1	0.861	0.918	0.003	0.021
MMP9_LOC1001280	0.729	AIG1	0.873	0.955	0	0.039
MMP9_LOC1001280	0.729	PCOLCE2	0.667	0.886	0.001	0.004
MMP9_LOC1001280	0.729	GALNT2	0.673	0.906	0	0.002
MMP9_LOC1001280	0.729	ITGA2B	0.752	0.863	0.029	0.015
MMP9_LOC1001280	0.729	LHFP	0.561	0.832	0.046	0

MMP9_LOC1001280	0.729	LAIR1_LAIR2	0.777	0.887	0.011	0.016
MMP9_LOC1001280	0.729	HIST1H3B	0.829	0.912	0.002	0.047
MMP9_LOC1001280	0.729	PTGS1	0.794	0.881	0.005	0.049
MMP9_LOC1001280	0.729	CD151	0.767	0.899	0.002	0.011
MMP9_LOC1001280	0.729	FSD1L	0.834	0.914	0.003	0.03
MMP9_LOC1001280	0.729	TPX2	0.745	0.855	0.019	0.027
MMP9_LOC1001280	0.729	IGK@_IGKC_IGKV	0.774	0.873	0.036	0.004
MMP9_LOC1001280	0.729	HIST1H2BJ	0.797	0.874	0.013	0.047
MMP9_LOC1001280	0.729	TNFRSF17	0.827	0.921	0.002	0.01
MMP9_LOC1001280	0.729	IGLV6-57	0.757	0.881	0.019	0.002
MMP9_LOC1001280	0.729	IGL@_IGLV1-44_	0.77	0.883	0.006	0.021
GSR	0.605	PFKFB2	0.777	0.861	0.003	0.005
GSR	0.605	ODZ1	0.777	0.819	0.021	0.027
GSR	0.605	CD163	0.808	0.849	0.01	0.015
GSR	0.605	THBS1	0.698	0.771	0.046	0.033
KLRF1	0.635	IGJ	0.683	0.81	0.01	0.015
GK3P_GK	0.654	C1orf161	0.577	0.754	0.031	0.042
GK3P_GK	0.654	HPGD	0.655	0.797	0.039	0.01
GK3P_GK	0.654	TAAR1	0.589	0.763	0.028	0.026
PFKFB2	0.777	METTL7B	0.749	0.875	0.009	0.03
PFKFB2	0.777	VAMP2	0.595	0.833	0.019	0.009
PFKFB2	0.777	SMPDL3A	0.736	0.894	0.018	0.004
PFKFB2	0.777	PDGFC	0.822	0.958	0.001	0.01
PFKFB2	0.777	LRRC70_IPO11	0.886	0.965	0	0.048
PFKFB2	0.777	SEC24A_SAR1B	0.739	0.881	0.003	0.031
PFKFB2	0.777	EXOSC4	0.742	0.94	0.001	0.003
PFKFB2	0.777	FOLR3_FOLR2	0.585	0.855	0.034	0.001
PFKFB2	0.777	AP3B2	0.697	0.859	0.037	0.019
PFKFB2	0.777	ABCA13	0.699	0.867	0.043	0.009

PFKFB2	0.777	EFCAB2	0.784	0.887	0.041	0.012
PFKFB2	0.777	PCOLCE2	0.667	0.913	0.002	0.001
PFKFB2	0.777	MKI67	0.674	0.861	0.03	0.005
PFKFB2	0.777	RETN	0.473	0.868	0.026	0
PFKFB2	0.777	IRF4	0.74	0.844	0.012	0.034
PFKFB2	0.777	MACF1	0.699	0.879	0.015	0.007
PFKFB2	0.777	GALNT2	0.673	0.911	0.002	0.002
PFKFB2	0.777	HDHD1A	0.7	0.855	0.025	0.016
PFKFB2	0.777	DPH3	0.706	0.874	0.013	0.015
PFKFB2	0.777	KIAA0746	0.713	0.876	0.024	0.005
PFKFB2	0.777	LHFP	0.561	0.848	0.034	0
PFKFB2	0.777	LAIR1_LAIR2	0.777	0.9	0.005	0.044
PFKFB2	0.777	FSD1L	0.834	0.932	0.003	0.019
PFKFB2	0.777	TPX2	0.745	0.873	0.009	0.046
PFKFB2	0.777	IGK@_IGKC_IGKV	0.774	0.871	0.015	0.047
PFKFB2	0.777	LASS4	0.669	0.835	0.015	0.027
PFKFB2	0.777	IGLV6-57	0.757	0.881	0.015	0.015
PICALM	0.758	ECHDC3	0.823	0.894	0.037	0.005
PICALM	0.758	PPP2R5A_SNORA16	0.716	0.882	0.041	0.001
PICALM	0.758	PRR13_PCBP2	0.758	0.862	0.046	0.03
PICALM	0.758	SLC11A1	0.705	0.861	0.038	0.01
PICALM	0.758	PDE3B	0.861	0.95	0.001	0.017
PICALM	0.758	ERGIC1	0.758	0.87	0.026	0.021
PICALM	0.758	NA	0.884	0.943	0.002	0.035
PICALM	0.758	HAL	0.846	0.958	0.001	0.004
PICALM	0.758	KIAA1257_ACAD9/	0.823	0.906	0.005	0.038
PICALM	0.758	SYNE2	0.886	0.958	0.001	0.033
PICALM	0.758	MME	0.847	0.93	0.013	0.003
PICALM	0.758	RBP7	0.803	0.913	0.023	0.006

PICALM	0.758	RGS2	0.789	0.973	0	0.001
PICALM	0.758	CAMK1D	0.735	0.859	0.039	0.027
METTL7B	0.749	PPP2R5A_SNORA16	0.716	0.86	0.006	0.018
METTL7B	0.749	MTHFS	0.733	0.861	0.023	0.016
METTL7B	0.749	CDA	0.694	0.861	0.007	0.015
METTL7B	0.749	SLC11A1	0.705	0.848	0.026	0.011
METTL7B	0.749	ERGIC1	0.758	0.853	0.017	0.038
METTL7B	0.749	CAMK1D	0.735	0.835	0.007	0.036
HIST1H4C	0.881	RUNX2	0.868	0.969	0.004	0.027
HIST1H4C	0.881	AREG	0.814	0.936	0.038	0.01
HIST1H4C	0.881	PDE3B	0.861	0.973	0.012	0.006
HIST1H4C	0.881	OCR1	0.934	0.979	0.014	0.049
HIST1H4C	0.881	NA	0.884	0.984	0.008	0.003
HIST1H4C	0.881	HAL	0.846	0.945	0.042	0.016
HIST1H4C	0.881	CCDC125	0.79	0.945	0.044	0.004
HIST1H4C	0.881	SYNE2	0.886	0.971	0.011	0.013
HIST1H4C	0.881	RGS2	0.789	0.944	0.021	0.008
C9orf72	0.843	NA	0.884	0.951	0.009	0.042
C9orf72	0.843	HAL	0.846	0.946	0.024	0.007
C9orf72	0.843	KIAA1257_ACAD9/	0.823	0.939	0.02	0.006
C9orf72	0.843	RGS2	0.789	0.97	0.005	0.001
HIST1H3I	0.895	PPP2R5A_SNORA16	0.716	0.951	0.05	0
HIST1H3I	0.895	RUNX2	0.868	0.955	0.023	0.039
HIST1H3I	0.895	OCR1	0.934	0.984	0.015	0.042
HIST1H3I	0.895	NA	0.884	0.995	0.008	0.003
HIST1H3I	0.895	SYNE2	0.886	0.977	0.014	0.014
SLC15A2	0.817	PPP2R5A_SNORA16	0.716	0.906	0.033	0.001
SLC15A2	0.817	PRR13_PCBP2	0.758	0.894	0.043	0.013
SLC15A2	0.817	AREG	0.814	0.897	0.041	0.029

SLC15A2	0.817	CCDC125	0.79	0.93	0.015	0.009
SLC15A2	0.817	SYNE2	0.886	0.959	0.002	0.03
SLC15A2	0.817	RGS2	0.789	0.895	0.013	0.035
SLC15A2	0.817	LOC100128751	0.809	0.934	0.017	0.01
TLR10	0.884	CASS4	0.732	0.936	0.035	0.001
TLR10	0.884	PPP2R5A_SNORA16	0.716	0.951	0.039	0
TLR10	0.884	HIST1H2AA	0.825	0.932	0.031	0.032
TLR10	0.884	PDE3B	0.861	0.965	0.008	0.03
TLR10	0.884	ERGIC1	0.758	0.945	0.033	0.002
TLR10	0.884	NA	0.884	0.96	0.008	0.05
TLR10	0.884	HAL	0.846	0.974	0.013	0.006
TLR10	0.884	KIAA1257_ACAD9/	0.823	0.958	0.018	0.009
TLR10	0.884	ZRANB1	0.718	0.94	0.036	0
TLR10	0.884	SYNE2	0.886	0.962	0.013	0.047
TLR10	0.884	MME	0.847	0.963	0.039	0.004
TLR10	0.884	RBP7	0.803	0.958	0.048	0.002
TLR10	0.884	RGS2	0.789	0.971	0.003	0.004
TLR10	0.884	CAMK1D	0.735	0.936	0.039	0.001
ADM	0.888	LOC284757	0.921	0.968	0.031	0.032
ADM	0.888	PRR13_PCBP2	0.758	0.963	0.037	0
ADM	0.888	MTHFS	0.733	0.978	0.016	0
ADM	0.888	GAB2	0.842	0.959	0.013	0.012
ADM	0.888	AREG	0.814	0.959	0.032	0.003
ADM	0.888	MPZL3	0.889	0.975	0.006	0.022
ADM	0.888	KDM6B_TMEM88	0.672	0.953	0.045	0
CD274	0.926	IFI16	0.721	0.961	0.022	0
CD274	0.926	NA	0.884	0.968	0.018	0.031
CRIP1	0.833	CASS4	0.732	0.881	0.035	0.023
CRIP1	0.833	PPP2R5A_SNORA16	0.716	0.888	0.027	0.018

CRIP1	0.833	ZRANB1	0.718	0.888	0.037	0.014
CRIP1	0.833	RASA4_RASA4P_R	0.713	0.881	0.033	0.027
CRIP1	0.833	CAMK1D	0.735	0.928	0.006	0.005
VAMP2	0.595	TPST1	0.754	0.804	0.022	0.044
VAMP2	0.595	SAP30	0.789	0.871	0	0.023
VAMP2	0.595	ACPL2	0.756	0.822	0.01	0.03
VAMP2	0.595	CCDC125	0.79	0.863	0.001	0.036
SMPDL3A	0.736	SLC1A3	0.777	0.88	0.007	0.04
SMPDL3A	0.736	PPP2R5A_SNORA16	0.716	0.868	0.002	0.024
SMPDL3A	0.736	MTHFS	0.733	0.882	0.003	0.024
SMPDL3A	0.736	CDA	0.694	0.87	0.001	0.025
SMPDL3A	0.736	SLC11A1	0.705	0.835	0.009	0.027
SMPDL3A	0.736	ACPL2	0.756	0.844	0.02	0.048
IFI16	0.721	SEC24A_SAR1B	0.739	0.862	0.007	0.035
IFI16	0.721	CCR1	0.72	0.874	0.026	0.003
IFI16	0.721	FFAR2	0.744	0.895	0.006	0.004
IFI16	0.721	TRIM21	0.857	0.95	0	0.045
IFI16	0.721	UBE2F_C20orf194	0.758	0.857	0.042	0.017
IFI16	0.721	DYNLL1	0.787	0.864	0.024	0.038
IFI16	0.721	CTSL1_CTSLL3	0.819	0.899	0.009	0.029
MRPL41	0.845	CASS4	0.732	0.906	0.034	0.003
MRPL41	0.845	PPP2R5A_SNORA16	0.716	0.932	0.016	0.001
MRPL41	0.845	AREG	0.814	0.896	0.043	0.048
MRPL41	0.845	SFRS9	0.523	0.895	0.013	0
MRPL41	0.845	HAL	0.846	0.934	0.012	0.029
MRPL41	0.845	KIAA1257_ACAD9/	0.823	0.923	0.021	0.036
MRPL41	0.845	CCDC125	0.79	0.936	0.003	0.017
MRPL41	0.845	SYNE2	0.886	0.98	0.002	0.012
MRPL41	0.845	MME	0.847	0.946	0.027	0.006

MRPL41	0.845	RBP7	0.803	0.974	0.005	0.001
MRPL41	0.845	RGS2	0.789	0.923	0.007	0.039
MRPL41	0.845	CAMK1D	0.735	0.919	0.014	0.004
SLC1A3	0.777	PDGFC	0.822	0.926	0.007	0.004
SLC1A3	0.777	EXOSC4	0.742	0.894	0.002	0.029
SLC1A3	0.777	PCOLCE2	0.667	0.923	0.005	0
SLC1A3	0.777	GALNT2	0.673	0.898	0.002	0.003
CASS4	0.732	CLU	0.784	0.863	0.012	0.041
CASS4	0.732	KPNA5	0.793	0.862	0.037	0.031
CASS4	0.732	FFAR2	0.744	0.846	0.015	0.017
CASS4	0.732	LGALS2	0.77	0.881	0.008	0.005
CASS4	0.732	EFCAB2	0.784	0.865	0.022	0.012
CASS4	0.732	HINT1	0.819	0.882	0.015	0.015
CASS4	0.732	HIST1H3A	0.822	0.891	0.005	0.031
CASS4	0.732	PMS2CL_PMS2	0.857	0.932	0	0.045
CASS4	0.732	NEK6_LOC1001290	0.844	0.928	0	0.047
CASS4	0.732	RPL17_SNORD58B	0.842	0.908	0.004	0.028
CASS4	0.732	DLEU2_DLEU2L	0.758	0.876	0.007	0.011
CASS4	0.732	IL1B	0.769	0.867	0.015	0.009
CASS4	0.732	ITGA2B	0.752	0.844	0.05	0.016
CASS4	0.732	PTGS1	0.794	0.887	0.004	0.014
CASS4	0.732	HIST1H3C	0.854	0.897	0.009	0.047
CASS4	0.732	E2F6	0.798	0.882	0.019	0.018
CASS4	0.732	CD151	0.767	0.85	0.038	0.043
CASS4	0.732	HIST1H3H	0.836	0.895	0.009	0.019
CASS4	0.732	TPX2	0.745	0.852	0.024	0.033
CASS4	0.732	APOLD1	0.777	0.9	0.003	0.012
CASS4	0.732	HIST1H2BJ	0.797	0.876	0.024	0.011
CASS4	0.732	C7orf58	0.787	0.879	0.012	0.006

CASS4	0.732	DYNLL1	0.787	0.888	0.008	0.006
CASS4	0.732	B4GALT3	0.785	0.89	0.006	0.018
CASS4	0.732	NP	0.787	0.883	0.008	0.015
CASS4	0.732	CMTM5	0.814	0.882	0.008	0.042
CASS4	0.732	AIF1	0.745	0.87	0.012	0.011
CASS4	0.732	NFXL1	0.808	0.907	0.002	0.013
CLU	0.784	PPP2R5A_SNORA16	0.716	0.903	0.015	0.002
CLU	0.784	PRR13_PCBP2	0.758	0.905	0.014	0.003
CLU	0.784	SULF2	0.775	0.91	0.012	0.007
CLU	0.784	OCR1	0.934	0.966	0.001	0.043
CLU	0.784	ERGIC1	0.758	0.882	0.033	0.017
CLU	0.784	HAL	0.846	0.946	0.001	0.01
CLU	0.784	KIAA1257_ACAD9/	0.823	0.92	0.004	0.021
CLU	0.784	CCDC125	0.79	0.919	0.008	0.007
CLU	0.784	ZRANB1	0.718	0.913	0.006	0.001
CLU	0.784	MME	0.847	0.922	0.009	0.025
CLU	0.784	CPM	0.812	0.912	0.034	0.002
CLU	0.784	RBP7	0.803	0.91	0.017	0.007
CLU	0.784	RGS2	0.789	0.903	0.006	0.033
CLU	0.784	CAMK1D	0.735	0.863	0.048	0.012
CLU	0.784	MPZL2	0.775	0.899	0.02	0.006
CLU	0.784	LOC100128751	0.809	0.895	0.014	0.045
ODZ1	0.777	ANAPC11	0.705	0.837	0.05	0.045
ODZ1	0.777	DNAJC9_FAM149B1	0.742	0.868	0.035	0.027
ODZ1	0.777	TREML1	0.704	0.868	0.038	0.01
ODZ1	0.777	MACF1	0.699	0.861	0.035	0.011
ODZ1	0.777	GALNT2	0.673	0.837	0.011	0.048
ODZ1	0.777	ANKRD28	0.71	0.87	0.02	0.007
ODZ1	0.777	KIAA0746	0.713	0.861	0.012	0.023

ODZ1	0.777	ITGA2B	0.752	0.892	0.002	0.031
ODZ1	0.777	MYL9	0.695	0.872	0.007	0.015
ODZ1	0.777	PLB1	0.609	0.841	0.036	0.003
KPNA5	0.793	PPP2R5A_SNORA16	0.716	0.853	0.047	0.044
KPNA5	0.793	ZRANB1	0.718	0.882	0.016	0.011
KPNA5	0.793	PYHIN1	0.647	0.919	0.026	0
KPNA5	0.793	PPP1R2_PPP1R2P3	0.637	0.871	0.02	0.003
CD63	0.813	LOC284757	0.921	0.984	0.001	0.015
CD63	0.813	PPP2R5A_SNORA16	0.716	0.924	0.028	0
CD63	0.813	RUNX2	0.868	0.953	0.003	0.019
CD63	0.813	MTHFS	0.733	0.936	0.034	0
CD63	0.813	HIST1H2AA	0.825	0.917	0.016	0.013
CD63	0.813	CDA	0.694	0.936	0.02	0
CD63	0.813	SAP30	0.789	0.919	0.032	0.002
CD63	0.813	GAB2	0.842	0.942	0.003	0.033
CD63	0.813	SLC11A1	0.705	0.965	0.003	0
CD63	0.813	AREG	0.814	0.952	0.002	0.003
CD63	0.813	PDE3B	0.861	0.945	0.018	0.009
CD63	0.813	IRS2	0.851	0.962	0.007	0.002
CD63	0.813	ERGIC1	0.758	0.947	0.013	0
CD63	0.813	NA	0.884	0.924	0.019	0.039
CD63	0.813	HAL	0.846	0.945	0.012	0.006
CD63	0.813	KIAA1257_ACAD9/	0.823	0.927	0.032	0.005
CD63	0.813	CCDC125	0.79	0.93	0.026	0.004
CD63	0.813	SYNE2	0.886	0.94	0.01	0.036
CD63	0.813	RGS2	0.789	0.929	0.014	0.004
HPSE	0.894	PPP2R5A_SNORA16	0.716	0.966	0.026	0
HPSE	0.894	RUNX2	0.868	0.95	0.04	0.02
HPSE	0.894	GAB2	0.842	0.965	0.022	0.003

HPSE	0.894	OCR1	0.934	0.977	0.02	0.038
HPSE	0.894	NA	0.884	0.975	0.016	0.007
HPSE	0.894	MPZL3	0.889	0.963	0.011	0.037
HPSE	0.894	SYNE2	0.886	0.969	0.02	0.01
HPSE	0.894	RGS2	0.789	0.96	0.018	0.001
C1orf161	0.577	OLAH	0.706	0.778	0.05	0.004
C1orf161	0.577	CD163	0.808	0.875	0.001	0.03
DDAH2	0.809	PRR13_PCBP2	0.758	0.935	0.018	0
DDAH2	0.809	CDA	0.694	0.95	0.011	0
DDAH2	0.809	GAB2	0.842	0.933	0.008	0.022
DDAH2	0.809	SLC11A1	0.705	0.932	0.026	0
DDAH2	0.809	AREG	0.814	0.936	0.006	0.005
DDAH2	0.809	IRS2	0.851	0.921	0.046	0.019
DDAH2	0.809	RGS2	0.789	0.907	0.044	0.007
ATP13A3	0.796	PPP2R5A_SNORA16	0.716	0.921	0.001	0.004
ATP13A3	0.796	MTHFS	0.733	0.915	0.002	0.01
ATP13A3	0.796	CDA	0.694	0.88	0.014	0.015
ATP13A3	0.796	CCDC125	0.79	0.915	0.004	0.039
PMAIP1	0.945	RUNX2	0.868	0.974	0.029	0.018
LOC284757	0.921	PDGFC	0.822	0.98	0.036	0.002
LOC284757	0.921	B3GAT3	0.857	0.977	0.013	0.013
LOC284757	0.921	RCBTB2_LOC10013	0.882	0.966	0.01	0.046
LOC284757	0.921	SLC39A9	0.837	0.968	0.008	0.014
LOC284757	0.921	LGALS1	0.855	0.965	0.03	0.016
LOC284757	0.921	AIG1	0.873	0.975	0.034	0.012
LOC284757	0.921	PCOLCE2	0.667	0.964	0.039	0
LOC284757	0.921	SLC39A8	0.867	0.984	0.032	0.01
LOC284757	0.921	GSTO1	0.83	0.971	0.041	0.004
LOC284757	0.921	PTGER2	0.842	0.979	0.026	0.007

LOC284757	0.921	PMS2CL_PMS2	0.857	0.957	0.024	0.016
LOC284757	0.921	NEK6_LOC1001290	0.844	0.976	0.01	0.009
LOC284757	0.921	GLT25D1	0.808	0.977	0.016	0.001
LOC284757	0.921	ICAM1	0.895	0.975	0.019	0.032
LOC284757	0.921	P4HA1_RPL17	0.88	0.961	0.037	0.04
LOC284757	0.921	RRP12_LOC644215	0.84	0.973	0.019	0.007
LOC284757	0.921	LAIR1_LAIR2	0.777	0.966	0.034	0.001
LOC284757	0.921	FSD1L_GARNL1	0.844	0.981	0.023	0.008
LOC284757	0.921	FSD1L	0.834	0.977	0.033	0.001
LOC284757	0.921	MPO	0.684	0.954	0.043	0
LOC284757	0.921	ATP6V0D1_LOC100	0.828	0.955	0.027	0.025
PDGFC	0.822	ECHDC3	0.823	0.926	0.031	0.011
PDGFC	0.822	PPP2R5A_SNORA16	0.716	0.939	0.006	0.001
PDGFC	0.822	HMGB2	0.673	0.942	0.033	0
PDGFC	0.822	RUNX2	0.868	0.962	0.001	0.049
PDGFC	0.822	PRR13_PCBP2	0.758	0.906	0.028	0.007
PDGFC	0.822	CD163	0.808	0.938	0.019	0.008
PDGFC	0.822	MTHFS	0.733	0.914	0.029	0.002
PDGFC	0.822	CDA	0.694	0.927	0.015	0.001
PDGFC	0.822	SAP30	0.789	0.92	0.008	0.013
PDGFC	0.822	SLC11A1	0.705	0.93	0.017	0
PDGFC	0.822	AREG	0.814	0.922	0.01	0.014
PDGFC	0.822	IRS2	0.851	0.948	0.01	0.018
PDGFC	0.822	ACPL2	0.756	0.943	0.023	0
PDGFC	0.822	ERGIC1	0.758	0.933	0.017	0.001
PDGFC	0.822	HAL	0.846	0.943	0.01	0.022
PDGFC	0.822	KIAA1257_ACAD9/	0.823	0.929	0.025	0.015
PDGFC	0.822	CCDC125	0.79	0.952	0.005	0.006
PDGFC	0.822	MME	0.847	0.94	0.036	0.003

PDGFC	0.822	CPM	0.812	0.915	0.047	0.011
PDGFC	0.822	RBP7	0.803	0.937	0.017	0.007
PDGFC	0.822	RGS2	0.789	0.944	0.005	0.007
B3GAT3	0.857	RUNX2	0.868	0.945	0.022	0.022
B3GAT3	0.857	PDE3B	0.861	0.957	0.014	0.009
B3GAT3	0.857	NA	0.884	0.962	0.025	0.004
B3GAT3	0.857	HAL	0.846	0.934	0.048	0.009
B3GAT3	0.857	KIAA1257_ACAD9/	0.823	0.932	0.045	0.018
B3GAT3	0.857	CCDC125	0.79	0.946	0.034	0.004
B3GAT3	0.857	SYNE2	0.886	0.953	0.016	0.041
HPGD	0.655	OLAH	0.706	0.834	0.01	0.03
HPGD	0.655	IL1RL1	0.655	0.812	0.008	0.026
LRRC70_IPO11	0.886	ECHDC3	0.823	0.958	0.032	0.004
LRRC70_IPO11	0.886	MTHFS	0.733	0.938	0.04	0.001
LRRC70_IPO11	0.886	HIST1H2AA	0.825	0.943	0.014	0.021
LRRC70_IPO11	0.886	SAP30	0.789	0.939	0.017	0.009
LRRC70_IPO11	0.886	SLC11A1	0.705	0.942	0.012	0.001
LRRC70_IPO11	0.886	AREG	0.814	0.96	0.01	0.004
LRRC70_IPO11	0.886	IRS2	0.851	0.946	0.021	0.033
LRRC70_IPO11	0.886	ACPL2	0.756	0.955	0.035	0
LRRC70_IPO11	0.886	ERGIC1	0.758	0.938	0.017	0.004
LRRC70_IPO11	0.886	NA	0.884	0.95	0.032	0.042
LRRC70_IPO11	0.886	KIAA1257_ACAD9/	0.823	0.946	0.018	0.012
LRRC70_IPO11	0.886	RGS2	0.789	0.937	0.008	0.009
TMEM144_LOC2855	0.653	PLA2G7	0.738	0.857	0.003	0.023
TMEM144_LOC2855	0.653	PDK4	0.598	0.782	0.05	0.009
CDS2	0.944	RUNX2	0.868	0.987	0.05	0.004
CDS2	0.944	MPZL3	0.889	0.995	0.023	0.005
ECHDC3	0.823	EXOSC4	0.742	0.889	0.048	0.017

ECHDC3	0.823	HIST1H3J	0.829	0.933	0.003	0.039
ECHDC3	0.823	HIST1H3A	0.822	0.929	0.005	0.028
ECHDC3	0.823	DPH3	0.706	0.922	0.008	0.001
ECHDC3	0.823	DLEU2_DLEU2L	0.758	0.902	0.029	0.015
ECHDC3	0.823	ANKRD28	0.71	0.914	0.05	0
ECHDC3	0.823	HIST1H3B	0.829	0.926	0.018	0.037
ECHDC3	0.823	PTGS1	0.794	0.915	0.022	0.015
ECHDC3	0.823	HIST1H3C	0.854	0.948	0.007	0.015
ECHDC3	0.823	HIST1H3H	0.836	0.926	0.022	0.024
ECHDC3	0.823	TPX2	0.745	0.884	0.031	0.041
ECHDC3	0.823	APOLD1	0.777	0.901	0.01	0.036
ECHDC3	0.823	HIST1H2BJ	0.797	0.941	0.019	0.002
ECHDC3	0.823	FAM118B	0.74	0.89	0.033	0.011
ECHDC3	0.823	CMTM5	0.814	0.939	0.008	0.012
ECHDC3	0.823	SDHC	0.85	0.928	0.01	0.036
ECHDC3	0.823	GLDC	0.775	0.902	0.003	0.048
OLAH	0.706	TAAR1	0.589	0.777	0.02	0.03
PPP2R5A_SNORA16	0.716	EAF2_HCG11_LOC	0.869	0.955	0	0.042
PPP2R5A_SNORA16	0.716	SEC24A_SAR1B	0.739	0.906	0.003	0.003
PPP2R5A_SNORA16	0.716	EXOSC4	0.742	0.905	0.002	0.003
PPP2R5A_SNORA16	0.716	HIST1H4L	0.929	0.978	0	0.046
PPP2R5A_SNORA16	0.716	CCR1	0.72	0.823	0.047	0.022
PPP2R5A_SNORA16	0.716	SIAE	0.894	0.975	0	0.024
PPP2R5A_SNORA16	0.716	HINT1	0.819	0.876	0.018	0.032
PPP2R5A_SNORA16	0.716	HIST1H3J	0.829	0.906	0.004	0.014
PPP2R5A_SNORA16	0.716	SUCNR1	0.861	0.939	0.001	0.007
PPP2R5A_SNORA16	0.716	MTRR	0.832	0.913	0.002	0.036
PPP2R5A_SNORA16	0.716	AIG1	0.873	0.975	0	0.003
PPP2R5A_SNORA16	0.716	PCOLCE2	0.667	0.835	0.011	0.012

PPP2R5A_SNORA16	0.716	HS2ST1_UBA2	0.837	0.954	0	0.013
PPP2R5A_SNORA16	0.716	HIST1H3A	0.822	0.914	0.002	0.011
PPP2R5A_SNORA16	0.716	GSTO1	0.83	0.937	0	0.014
PPP2R5A_SNORA16	0.716	IRF4	0.74	0.841	0.021	0.05
PPP2R5A_SNORA16	0.716	GALNT2	0.673	0.839	0.017	0.014
PPP2R5A_SNORA16	0.716	HDHD1A	0.7	0.887	0.006	0.002
PPP2R5A_SNORA16	0.716	EIF1AX_SCARNA9L	0.814	0.895	0.008	0.01
PPP2R5A_SNORA16	0.716	DPH3	0.706	0.888	0.012	0
PPP2R5A_SNORA16	0.716	TAF13	0.908	0.971	0	0.021
PPP2R5A_SNORA16	0.716	HIST1H2BM	0.862	0.939	0	0.029
PPP2R5A_SNORA16	0.716	IL1B	0.769	0.839	0.031	0.032
PPP2R5A_SNORA16	0.716	ITGA2B	0.752	0.874	0.019	0.005
PPP2R5A_SNORA16	0.716	HIST1H3B	0.829	0.893	0.01	0.035
PPP2R5A_SNORA16	0.716	FSD1L_GARNL1	0.844	0.943	0	0.038
PPP2R5A_SNORA16	0.716	PTGS1	0.794	0.901	0.002	0.016
PPP2R5A_SNORA16	0.716	UBE2F_C20orf194	0.758	0.886	0.018	0.002
PPP2R5A_SNORA16	0.716	HIST1H3C	0.854	0.924	0.004	0.007
PPP2R5A_SNORA16	0.716	CD151	0.767	0.919	0.001	0.004
PPP2R5A_SNORA16	0.716	HIST1H3H	0.836	0.909	0.005	0.013
PPP2R5A_SNORA16	0.716	FSD1L	0.834	0.913	0.002	0.013
PPP2R5A_SNORA16	0.716	TPX2	0.745	0.901	0.004	0.003
PPP2R5A_SNORA16	0.716	MYL9	0.695	0.866	0.027	0.001
PPP2R5A_SNORA16	0.716	HIST1H2BJ	0.797	0.913	0.008	0.001
PPP2R5A_SNORA16	0.716	C7orf58	0.787	0.861	0.03	0.019
PPP2R5A_SNORA16	0.716	DYNLL1	0.787	0.896	0.012	0.006
PPP2R5A_SNORA16	0.716	FAM118B	0.74	0.867	0.023	0.009
PPP2R5A_SNORA16	0.716	B4GALT3	0.785	0.913	0.001	0.025
PPP2R5A_SNORA16	0.716	NP	0.787	0.919	0.002	0.005
PPP2R5A_SNORA16	0.716	TNFRSF17	0.827	0.901	0.003	0.023

PPP2R5A_SNORA16	0.716	PLEKHF2	0.737	0.897	0.004	0.005
PPP2R5A_SNORA16	0.716	CMTM5	0.814	0.924	0.001	0.013
PPP2R5A_SNORA16	0.716	AIF1	0.745	0.853	0.017	0.019
PPP2R5A_SNORA16	0.716	IGLV6-57	0.757	0.874	0.017	0.005
PPP2R5A_SNORA16	0.716	IGL@_IGLV1-44_	0.77	0.873	0.003	0.05
PPP2R5A_SNORA16	0.716	SDHC	0.85	0.925	0.006	0.011
PPP2R5A_SNORA16	0.716	KIAA0101_CSNK1G	0.87	0.926	0.003	0.03
EAF2_HCG11_LOC	0.869	NA	0.884	0.956	0.036	0.027
EAF2_HCG11_LOC	0.869	CCDC125	0.79	0.946	0.041	0.005
RCBTB2_LOC10013	0.882	RUNX2	0.868	0.951	0.014	0.047
RCBTB2_LOC10013	0.882	GAB2	0.842	0.952	0.029	0.007
RCBTB2_LOC10013	0.882	SYNE2	0.886	0.961	0.026	0.015
SEC24A_SAR1B	0.739	PRR13_PCBP2	0.758	0.869	0.012	0.033
SEC24A_SAR1B	0.739	MTHFS	0.733	0.873	0.024	0.007
SEC24A_SAR1B	0.739	CDA	0.694	0.861	0.016	0.014
SEC24A_SAR1B	0.739	SLC11A1	0.705	0.823	0.042	0.026
SEC24A_SAR1B	0.739	ERGIC1	0.758	0.84	0.042	0.044
SEC24A_SAR1B	0.739	CCDC125	0.79	0.912	0.003	0.014
SEC24A_SAR1B	0.739	MPZL2	0.775	0.872	0.027	0.014
SH3PXD2B	0.751	PCOLCE2	0.667	0.846	0.009	0.026
SH3PXD2B	0.751	MACF1	0.699	0.861	0.005	0.027
SH3PXD2B	0.751	GALNT2	0.673	0.868	0	0.03
SH3PXD2B	0.751	KIAA0746	0.713	0.846	0.013	0.05
HMGB2	0.673	DNAJC9_FAM149B1	0.742	0.823	0.027	0.05
HMGB2	0.673	ABCA13	0.699	0.861	0.004	0.006
HMGB2	0.673	MKI67	0.674	0.819	0.013	0.036
HMGB2	0.673	TREML1	0.704	0.829	0.018	0.024
HMGB2	0.673	DPH3	0.706	0.856	0.002	0.036
HMGB2	0.673	ANKRD28	0.71	0.845	0.006	0.022

HMGB2	0.673	LHFP	0.561	0.76	0.034	0.016
HMGB2	0.673	HIST1H3C	0.854	0.929	0	0.025
HMGB2	0.673	MYL9	0.695	0.825	0.005	0.048
HMGB2	0.673	HIST1H2BJ	0.797	0.914	0	0.018
HMGB2	0.673	TAAR1	0.589	0.794	0.045	0.002
KLRD1	0.594	IGJ	0.683	0.776	0.028	0.018
CHI3L1	0.798	LGALS2	0.77	0.9	0.002	0.028
CHI3L1	0.798	SUCNR1	0.861	0.946	0.001	0.042
CHI3L1	0.798	MKI67	0.674	0.881	0.017	0.005
CHI3L1	0.798	MINPP1	0.718	0.896	0.02	0.005
CHI3L1	0.798	ITGA2B	0.752	0.885	0.013	0.025
CHI3L1	0.798	UBE2F_C20orf194	0.758	0.887	0.006	0.046
CHI3L1	0.798	CD151	0.767	0.889	0.007	0.04
CHI3L1	0.798	TPX2	0.745	0.889	0.01	0.026
CHI3L1	0.798	MYL9	0.695	0.874	0.02	0.008
CHI3L1	0.798	HIST1H2BJ	0.797	0.932	0.002	0.017
CHI3L1	0.798	C7orf58	0.787	0.906	0.005	0.022
CHI3L1	0.798	DYNLL1	0.787	0.898	0.008	0.023
CHI3L1	0.798	TNFRSF17	0.827	0.926	0.004	0.039
CHI3L1	0.798	IGLV6-57	0.757	0.919	0.006	0.005
FRMD3	0.884	RUNX2	0.868	0.977	0.011	0.01
FRMD3	0.884	GAB2	0.842	0.958	0.033	0.006
FRMD3	0.884	OCR1	0.934	0.967	0.041	0.035
FRMD3	0.884	MPZL3	0.889	0.955	0.018	0.043
SLC39A9	0.837	RUNX2	0.868	0.972	0.006	0.003
SLC39A9	0.837	GAB2	0.842	0.933	0.024	0.008
SLC39A9	0.837	PDE3B	0.861	0.956	0.033	0.003
SLC39A9	0.837	NA	0.884	0.954	0.024	0.004
SLC39A9	0.837	CCDC125	0.79	0.953	0.032	0.001

SLC39A9	0.837	MPZL3	0.889	0.961	0.004	0.031
SLC39A9	0.837	SYNE2	0.886	0.975	0.008	0.003
SLC39A9	0.837	RGS2	0.789	0.939	0.036	0.001
EXOSC4	0.742	PRR13_PCBP2	0.758	0.893	0.003	0.012
EXOSC4	0.742	CD163	0.808	0.887	0.04	0.01
EXOSC4	0.742	MTHFS	0.733	0.95	0	0
EXOSC4	0.742	CDA	0.694	0.939	0	0
EXOSC4	0.742	SLC11A1	0.705	0.875	0.011	0.006
EXOSC4	0.742	AREG	0.814	0.907	0.001	0.041
EXOSC4	0.742	ACPL2	0.756	0.871	0.048	0.006
EXOSC4	0.742	ERGIC1	0.758	0.876	0.018	0.008
EXOSC4	0.742	CCDC125	0.79	0.898	0.005	0.031
NA	0.601	MACF1	0.699	0.804	0.005	0.035
NA	0.601	C7orf58	0.787	0.85	0.002	0.043
RUNX2	0.868	HIST1H4L	0.929	0.978	0.019	0.017
RUNX2	0.868	LGALS1	0.855	0.962	0.015	0.006
RUNX2	0.868	SIAE	0.894	0.968	0.024	0.008
RUNX2	0.868	AIG1	0.873	0.952	0.028	0.015
RUNX2	0.868	PTGER2	0.842	0.967	0.02	0.003
RUNX2	0.868	PMS2CL_PMS2	0.857	0.956	0.046	0.003
RUNX2	0.868	NEK6_LOC1001290	0.844	0.962	0.008	0.006
RUNX2	0.868	AMFR	0.874	0.983	0.011	0.005
RUNX2	0.868	CD300A	0.888	0.957	0.019	0.03
RUNX2	0.868	ZNF28	0.891	0.977	0.017	0.007
RUNX2	0.868	TAF13	0.908	0.96	0.045	0.022
RUNX2	0.868	KLHL5	0.913	0.954	0.044	0.047
RUNX2	0.868	MGST3	0.897	0.962	0.022	0.028
RUNX2	0.868	HSPB1_HSPBL2	0.886	0.953	0.035	0.022
RUNX2	0.868	TYMS	0.838	0.941	0.047	0.009

RUNX2	0.868	HIST1H2BM	0.862	0.952	0.038	0.008
RUNX2	0.868	CDC26	0.868	0.978	0.012	0.003
PRR13_PCBP2	0.758	FFAR2	0.744	0.888	0.028	0.002
PRR13_PCBP2	0.758	AIG1	0.873	0.953	0	0.034
PRR13_PCBP2	0.758	PCOLCE2	0.667	0.868	0.019	0.001
PRR13_PCBP2	0.758	HS2ST1_UBA2	0.837	0.924	0.002	0.031
PRR13_PCBP2	0.758	GSTO1	0.83	0.924	0.001	0.022
PRR13_PCBP2	0.758	GALNT2	0.673	0.861	0.043	0.002
PRR13_PCBP2	0.758	GLT25D1	0.808	0.898	0.006	0.037
PRR13_PCBP2	0.758	ACTA2	0.818	0.944	0.001	0.006
PRR13_PCBP2	0.758	LAIR1_LAIR2	0.777	0.859	0.048	0.031
PRR13_PCBP2	0.758	PTGS1	0.794	0.885	0.011	0.017
PRR13_PCBP2	0.758	UBE2F_C20orf194	0.758	0.888	0.033	0.004
PRR13_PCBP2	0.758	CD151	0.767	0.894	0.016	0.008
PRR13_PCBP2	0.758	FSD1L	0.834	0.904	0.006	0.029
PRR13_PCBP2	0.758	TPX2	0.745	0.868	0.034	0.007
PRR13_PCBP2	0.758	APOLD1	0.777	0.886	0.009	0.027
PRR13_PCBP2	0.758	HIST1H2BJ	0.797	0.901	0.012	0.015
PRR13_PCBP2	0.758	LASS4	0.669	0.823	0.047	0.009
PRR13_PCBP2	0.758	CTSL1_CTSLL3	0.819	0.874	0.041	0.038
PRR13_PCBP2	0.758	NP	0.787	0.878	0.031	0.026
PRR13_PCBP2	0.758	SDHC	0.85	0.915	0.014	0.024
PRR13_PCBP2	0.758	NFXL1	0.808	0.888	0.026	0.04
HIST1H4L	0.929	PDE3B	0.861	0.98	0.023	0.013
HIST1H4L	0.929	OCR1	0.934	0.993	0.028	0.042
HIST1H4L	0.929	NA	0.884	0.992	0.022	0.005
HIST1H4L	0.929	HAL	0.846	0.977	0.046	0.007
HIST1H4L	0.929	CCDC125	0.79	0.972	0.04	0.002
HIST1H4L	0.929	SYNE2	0.886	0.991	0.021	0.008

HIST1H4L	0.929	MME	0.847	0.985	0.045	0.002
LGALS1	0.855	NA	0.884	0.946	0.044	0.007
LGALS1	0.855	MPZL3	0.889	0.977	0.002	0.024
LGALS1	0.855	SYNE2	0.886	0.959	0.026	0.006
LGALS1	0.855	RGS2	0.789	0.969	0.008	0.001
CCR1	0.72	MTHFS	0.733	0.858	0.004	0.049
CCR1	0.72	CDA	0.694	0.822	0.013	0.044
CCR1	0.72	PLA2G7	0.738	0.874	0.027	0.001
CCR1	0.72	KDM6B_TMEM88	0.672	0.829	0.013	0.024
TPST1	0.754	ABCA13	0.699	0.866	0.01	0.015
TPST1	0.754	MKI67	0.674	0.843	0.014	0.02
TPST1	0.754	TREML1	0.704	0.867	0.013	0.014
TPST1	0.754	HDHD1A	0.7	0.844	0.011	0.047
TPST1	0.754	DPH3	0.706	0.871	0.003	0.031
TPST1	0.754	ANKRD28	0.71	0.878	0.006	0.017
TPST1	0.754	ITGA2B	0.752	0.884	0.001	0.041
TPST1	0.754	MYL9	0.695	0.878	0.002	0.015
TPST1	0.754	HIST1H2BJ	0.797	0.919	0.001	0.035
TPST1	0.754	SPARC	0.661	0.848	0.029	0.007
CD163	0.808	GALNT2	0.673	0.883	0.008	0.01
CD163	0.808	HDHD1A	0.7	0.87	0.017	0.018
CD163	0.808	FAM118B	0.74	0.883	0.003	0.048
FFAR2	0.744	MTHFS	0.733	0.891	0.005	0.01
FFAR2	0.744	CDA	0.694	0.829	0.034	0.026
FFAR2	0.744	KDM6B_TMEM88	0.672	0.852	0.009	0.017
PHOSPHO1	0.63	HIST1H3H	0.836	0.927	0	0.021
PHOSPHO1	0.63	POLE2	0.704	0.838	0.01	0.006
PPIF	0.879	GAB2	0.842	0.937	0.031	0.036
PPIF	0.879	KIAA1257_ACAD9/	0.823	0.943	0.048	0.009

PPIF	0.879	MPZL3	0.889	0.965	0.006	0.05
MTHFS	0.733	MTRR	0.832	0.922	0.002	0.033
MTHFS	0.733	AIG1	0.873	0.958	0	0.03
MTHFS	0.733	PCOLCE2	0.667	0.873	0.005	0.002
MTHFS	0.733	HS2ST1_UBA2	0.837	0.939	0	0.032
MTHFS	0.733	GALNT2	0.673	0.901	0.001	0.001
MTHFS	0.733	GLT25D1	0.808	0.904	0.002	0.041
MTHFS	0.733	HDHD1A	0.7	0.855	0.022	0.006
MTHFS	0.733	DPH3	0.706	0.855	0.047	0.01
MTHFS	0.733	DLEU2_DLEU2L	0.758	0.848	0.029	0.049
MTHFS	0.733	IL1B	0.769	0.874	0.044	0.007
MTHFS	0.733	LAIR1_LAIR2	0.777	0.88	0.013	0.018
MTHFS	0.733	NA	0.87	0.933	0.001	0.022
MTHFS	0.733	FSD1L	0.834	0.906	0.003	0.026
MTHFS	0.733	DYNLL1	0.787	0.886	0.011	0.01
MTHFS	0.733	FAM118B	0.74	0.861	0.014	0.026
MTHFS	0.733	PLEKHF2	0.737	0.86	0.04	0.027
MTHFS	0.733	AIF1	0.745	0.865	0.029	0.028
MTHFS	0.733	SDHC	0.85	0.927	0.006	0.01
DNAJC9_FAM149B1	0.742	PYHIN1	0.647	0.851	0.008	0.01
DNAJC9_FAM149B1	0.742	PPP1R2_PPP1R2P3	0.637	0.811	0.026	0.033
LGALS2	0.77	SULF2	0.775	0.911	0.001	0.029
LGALS2	0.77	RASA4_RASA4P_R	0.713	0.872	0.034	0.005
LGALS2	0.77	RBP7	0.803	0.902	0.005	0.024
LGALS2	0.77	CAMK1D	0.735	0.873	0.011	0.009
LGALS2	0.77	MPZL2	0.775	0.877	0.025	0.034
SIAE	0.894	GAB2	0.842	0.945	0.04	0.027
SIAE	0.894	IRS2	0.851	0.958	0.032	0.012
SIAE	0.894	OCR1	0.934	0.975	0.036	0.026

SIAE	0.894	NA	0.884	0.967	0.033	0.008
SIAE	0.894	HAL	0.846	0.958	0.037	0.006
SIAE	0.894	CCDC125	0.79	0.969	0.026	0.001
SIAE	0.894	SYNE2	0.886	0.965	0.031	0.013
SIAE	0.894	RGS2	0.789	0.953	0.03	0.002
ABCA13	0.699	CDA	0.694	0.857	0.002	0.04
ABCA13	0.699	DAAM2_LOC100131	0.778	0.866	0.029	0.002
ABCA13	0.699	ACPL2	0.756	0.873	0.006	0.017
ABCA13	0.699	THBS1	0.698	0.832	0.032	0.01
EFCAB2	0.784	KDM6B_TMEM88	0.672	0.845	0.016	0.03
EFCAB2	0.784	CAMK1D	0.735	0.863	0.011	0.04
EFCAB2	0.784	HIST2H2BF_HIST2	0.62	0.856	0.048	0.003
HIST1H2AA	0.825	AIG1	0.873	0.93	0.013	0.049
HIST1H2AA	0.825	PCOLCE2	0.667	0.905	0.033	0.001
HIST1H2AA	0.825	TYMS	0.838	0.912	0.026	0.044
HIST1H2AA	0.825	HIST1H2BM	0.862	0.925	0.019	0.028
HIST1H2AA	0.825	NA	0.87	0.926	0.037	0.037
HIST1H2AA	0.825	TNFRSF17	0.827	0.928	0.038	0.004
HINT1	0.819	NA	0.884	0.966	0.001	0.038
HINT1	0.819	LY6G5B_CSNK2B	0.63	0.879	0.01	0.002
HINT1	0.819	CCDC125	0.79	0.915	0.002	0.043
HINT1	0.819	ZRANB1	0.718	0.891	0.031	0.005
HINT1	0.819	PYHIN1	0.647	0.913	0.015	0
HINT1	0.819	CYP4F3_CYP4F2	0.755	0.897	0.044	0.009
HINT1	0.819	MME	0.847	0.93	0.008	0.05
HINT1	0.819	RASA4_RASA4P_R	0.713	0.879	0.039	0.014
HINT1	0.819	RBP7	0.803	0.919	0.005	0.042
HINT1	0.819	CAMK1D	0.735	0.887	0.004	0.029
HINT1	0.819	PPP1R2_PPP1R2P3	0.637	0.889	0.024	0.001

HIST1H3J	0.829	CDA	0.694	0.888	0.038	0.004
HIST1H3J	0.829	SAP30	0.789	0.932	0.003	0.015
HIST1H3J	0.829	AREG	0.814	0.917	0.009	0.047
HIST1H3J	0.829	NA	0.884	0.963	0.005	0.013
HIST1H3J	0.829	CCDC125	0.79	0.942	0.001	0.015
HIST1H3J	0.829	ZRANB1	0.718	0.922	0.033	0
HIST1H3J	0.829	CYP4F3_CYP4F2	0.755	0.925	0.034	0.002
HIST1H3J	0.829	MME	0.847	0.949	0.012	0.013
HIST1H3J	0.829	RBP7	0.803	0.952	0.006	0.004
CDA	0.694	SUCNR1	0.861	0.912	0.001	0.047
CDA	0.694	AIG1	0.873	0.961	0	0.014
CDA	0.694	PCOLCE2	0.667	0.857	0.004	0.006
CDA	0.694	HIST1H3A	0.822	0.908	0.001	0.018
CDA	0.694	GALNT2	0.673	0.832	0.015	0.021
CDA	0.694	HDHD1A	0.7	0.819	0.044	0.024
CDA	0.694	DPH3	0.706	0.85	0.027	0.004
CDA	0.694	ITGA2B	0.752	0.827	0.036	0.048
CDA	0.694	HIST1H3B	0.829	0.893	0.005	0.038
CDA	0.694	UBE2F_C20orf194	0.758	0.874	0.016	0.005
CDA	0.694	HIST1H3C	0.854	0.9	0.004	0.027
CDA	0.694	CD151	0.767	0.875	0.003	0.034
CDA	0.694	FSD1L	0.834	0.894	0.002	0.043
CDA	0.694	TPX2	0.745	0.862	0.011	0.011
CDA	0.694	IGK@_IGKC_IGKV	0.774	0.848	0.045	0.016
CDA	0.694	HIST1H2BJ	0.797	0.889	0.007	0.015
CDA	0.694	DYNLL1	0.787	0.858	0.017	0.039
CDA	0.694	PLEKHF2	0.737	0.851	0.02	0.042
CDA	0.694	AIF1	0.745	0.837	0.018	0.036
CDA	0.694	IGLV6-57	0.757	0.843	0.035	0.012

CDA	0.694	SDHC	0.85	0.926	0.003	0.005
SAP30	0.789	SUCNR1	0.861	0.923	0.012	0.02
SAP30	0.789	HS2ST1_UBA2	0.837	0.913	0.021	0.039
SAP30	0.789	HIST1H3A	0.822	0.923	0.013	0.004
SAP30	0.789	ACTA2	0.818	0.913	0.014	0.019
SAP30	0.789	EIF1AX_SCARNA9L	0.814	0.891	0.048	0.008
SAP30	0.789	TYMS	0.838	0.932	0.002	0.028
SAP30	0.789	HIST1H3B	0.829	0.906	0.043	0.011
SAP30	0.789	FSD1L_GARNL1	0.844	0.939	0.004	0.014
SAP30	0.789	PTGS1	0.794	0.911	0.023	0.004
SAP30	0.789	HIST1H3C	0.854	0.937	0.019	0.001
SAP30	0.789	HIST1H3H	0.836	0.931	0.02	0.003
SAP30	0.789	FSD1L	0.834	0.919	0.016	0.013
SAP30	0.789	TPX2	0.745	0.881	0.046	0.013
SAP30	0.789	APOLD1	0.777	0.89	0.038	0.016
SAP30	0.789	HIST1H2BJ	0.797	0.914	0.038	0.003
SAP30	0.789	LASS4	0.669	0.878	0.012	0.003
SAP30	0.789	B4GALT3	0.785	0.89	0.033	0.024
SAP30	0.789	TNFRSF17	0.827	0.902	0.018	0.014
SAP30	0.789	PLEKHA3	0.777	0.876	0.049	0.037
SAP30	0.789	CMTM5	0.814	0.935	0.012	0.002
SAP30	0.789	IGL@_IGLV1-44_	0.77	0.883	0.021	0.019
SAP30	0.789	GLDC	0.775	0.921	0.003	0.007
SAP30	0.789	KIAA0101_CSNK1G	0.87	0.929	0.009	0.03
AGTRAP	0.928	MPZL3	0.889	0.991	0.034	0.003
SUCNR1	0.861	SLC11A1	0.705	0.905	0.031	0.003
SUCNR1	0.861	AREG	0.814	0.935	0.01	0.019
SUCNR1	0.861	PDE3B	0.861	0.948	0.011	0.037
SUCNR1	0.861	ERGIC1	0.758	0.913	0.027	0.007

SUCNR1	0.861	NA	0.884	0.965	0.004	0.028
SUCNR1	0.861	HAL	0.846	0.94	0.004	0.044
SUCNR1	0.861	KIAA1257_ACAD9/	0.823	0.939	0.007	0.028
SUCNR1	0.861	CCDC125	0.79	0.953	0.004	0.006
SUCNR1	0.861	ZRANB1	0.718	0.939	0.008	0.001
SUCNR1	0.861	CYP4F3_CYP4F2	0.755	0.95	0.005	0.001
SUCNR1	0.861	MME	0.847	0.965	0.005	0.007
SUCNR1	0.861	RBP7	0.803	0.954	0.014	0.003
SUCNR1	0.861	RGS2	0.789	0.925	0.006	0.036
MTRR	0.832	AREG	0.814	0.896	0.047	0.034
MTRR	0.832	NA	0.884	0.954	0.007	0.019
MTRR	0.832	CCDC125	0.79	0.929	0.012	0.01
MTRR	0.832	RGS2	0.789	0.907	0.024	0.033
PLA2G7	0.738	MACF1	0.699	0.826	0.043	0.021
PLA2G7	0.738	HSP90AB1_HSP90A	0.65	0.84	0.027	0.008
PLA2G7	0.738	ITGA4_CERKL	0.721	0.854	0.008	0.035
PLA2G7	0.738	IL1B	0.769	0.888	0.002	0.042
PLA2G7	0.738	C7orf58	0.787	0.937	0	0.004
PLA2G7	0.738	DYNLL1	0.787	0.901	0.001	0.037
AIG1	0.873	GAB2	0.842	0.949	0.019	0.011
AIG1	0.873	AREG	0.814	0.956	0.015	0.003
AIG1	0.873	NA	0.884	0.964	0.013	0.011
AIG1	0.873	KIAA1257_ACAD9/	0.823	0.952	0.041	0.002
AIG1	0.873	CCDC125	0.79	0.965	0.016	0.002
AIG1	0.873	SYNE2	0.886	0.954	0.017	0.039
AIG1	0.873	RGS2	0.789	0.946	0.018	0.003
PCOLCE2	0.667	SLC11A1	0.705	0.845	0.016	0.003
PCOLCE2	0.667	AREG	0.814	0.907	0	0.016
PCOLCE2	0.667	DAAM2_LOC100131	0.778	0.848	0.023	0.017

PCOLCE2	0.667	ACPL2	0.756	0.848	0.02	0.002
PCOLCE2	0.667	ERGIC1	0.758	0.831	0.019	0.031
PCOLCE2	0.667	CYP4F3_CYP4F2	0.755	0.823	0.04	0.048
GAB2	0.842	GSTO1	0.83	0.915	0.05	0.017
GAB2	0.842	PMS2CL_PMS2	0.857	0.926	0.043	0.027
GAB2	0.842	NEK6_LOC1001290	0.844	0.927	0.035	0.015
GAB2	0.842	ACTA2	0.818	0.965	0.012	0.001
GAB2	0.842	CD300A	0.888	0.974	0.004	0.01
GAB2	0.842	TRIM21	0.857	0.972	0.006	0.008
GAB2	0.842	ICAM1	0.895	0.964	0.008	0.02
GAB2	0.842	P4HA1_RPL17	0.88	0.945	0.01	0.044
GAB2	0.842	RRP12_LOC644215	0.84	0.958	0.009	0.004
GAB2	0.842	TIMM10	0.868	0.933	0.049	0.017
GAB2	0.842	IRF1	0.894	0.979	0.001	0.015
GAB2	0.842	ATP6V0D1_LOC100	0.828	0.954	0.002	0.023
GAB2	0.842	CDC26	0.868	0.941	0.012	0.021
HS2ST1_UBA2	0.837	PDE3B	0.861	0.943	0.012	0.032
HS2ST1_UBA2	0.837	NA	0.884	0.943	0.024	0.026
HS2ST1_UBA2	0.837	HAL	0.846	0.949	0.013	0.01
HS2ST1_UBA2	0.837	KIAA1257_ACAD9/	0.823	0.926	0.037	0.012
HS2ST1_UBA2	0.837	SYNE2	0.886	0.953	0.009	0.024
HS2ST1_UBA2	0.837	RGS2	0.789	0.967	0.003	0.001
HIST1H3A	0.822	SLC11A1	0.705	0.897	0.028	0.007
HIST1H3A	0.822	AREG	0.814	0.927	0.003	0.031
HIST1H3A	0.822	ERGIC1	0.758	0.917	0.01	0.008
HIST1H3A	0.822	NA	0.884	0.96	0.002	0.016
HIST1H3A	0.822	KIAA1257_ACAD9/	0.823	0.937	0.002	0.027
HIST1H3A	0.822	CCDC125	0.79	0.945	0.002	0.01
HIST1H3A	0.822	CYP4F3_CYP4F2	0.755	0.91	0.028	0.004

HIST1H3A	0.822	MME	0.847	0.945	0.006	0.018
HIST1H3A	0.822	RBP7	0.803	0.939	0.019	0.002
HIST1H3A	0.822	CAMK1D	0.735	0.887	0.023	0.015
SLC39A8	0.867	NA	0.884	0.951	0.019	0.045
SLC39A8	0.867	CCDC125	0.79	0.946	0.019	0.006
SLC39A8	0.867	RGS2	0.789	0.922	0.021	0.034
MKI67	0.674	CCDC125	0.79	0.925	0	0.034
MKI67	0.674	CYP4F3_CYP4F2	0.755	0.855	0.009	0.028
MKI67	0.674	RBP7	0.803	0.898	0.001	0.027
SLC11A1	0.705	GALNT2	0.673	0.831	0.009	0.022
SLC11A1	0.705	GLT25D1	0.808	0.902	0.001	0.038
SLC11A1	0.705	DPH3	0.706	0.85	0.028	0.002
SLC11A1	0.705	DLEU2_DLEU2L	0.758	0.845	0.044	0.024
SLC11A1	0.705	ITGA2B	0.752	0.84	0.05	0.012
SLC11A1	0.705	HIST1H3B	0.829	0.889	0.011	0.049
SLC11A1	0.705	PTGS1	0.794	0.875	0.007	0.033
SLC11A1	0.705	CD151	0.767	0.874	0.007	0.019
SLC11A1	0.705	APOLD1	0.777	0.874	0.009	0.039
SLC11A1	0.705	HIST1H2BJ	0.797	0.88	0.017	0.019
SLC11A1	0.705	LASS4	0.669	0.822	0.032	0.019
SLC11A1	0.705	PLEKHF2	0.737	0.851	0.025	0.013
SLC11A1	0.705	CMTM5	0.814	0.892	0.007	0.025
SLC11A1	0.705	AIF1	0.745	0.841	0.027	0.026
SLC11A1	0.705	KIAA0101_CSNK1G	0.87	0.906	0.005	0.048
AREG	0.814	GSTO1	0.83	0.918	0.018	0.011
AREG	0.814	PTGER2	0.842	0.923	0.007	0.029
AREG	0.814	RPL17_SNORD58B	0.842	0.909	0.02	0.045
AREG	0.814	GLT25D1	0.808	0.92	0.011	0.012
AREG	0.814	ACTA2	0.818	0.905	0.049	0.021

AREG	0.814	EIF1AX_SCARNA9L	0.814	0.905	0.049	0.007
AREG	0.814	TAF13	0.908	0.958	0.005	0.036
AREG	0.814	TYMS	0.838	0.92	0.022	0.019
AREG	0.814	HIST1H2BM	0.862	0.939	0.009	0.019
AREG	0.814	LAIR1_LAIR2	0.777	0.901	0.036	0.017
AREG	0.814	HIST1H3B	0.829	0.926	0.048	0.004
AREG	0.814	FSD1L_GARNL1	0.844	0.942	0.006	0.011
AREG	0.814	NA	0.87	0.932	0.02	0.029
AREG	0.814	HIST1H3C	0.854	0.923	0.038	0.011
AREG	0.814	FSD1L	0.834	0.933	0.022	0.004
AREG	0.814	TNFRSF17	0.827	0.914	0.015	0.02
AREG	0.814	PLEKHA3	0.777	0.904	0.03	0.005
AREG	0.814	CDC26	0.868	0.944	0.005	0.035
AREG	0.814	GLDC	0.775	0.919	0.018	0.004
AREG	0.814	KIAA0101_CSNK1G	0.87	0.927	0.031	0.03
DAAM2_LOC100131	0.778	DPH3	0.706	0.858	0.007	0.037
DAAM2_LOC100131	0.778	ANKRD28	0.71	0.859	0.014	0.032
DAAM2_LOC100131	0.778	MYL9	0.695	0.842	0.041	0.03
LTF	0.642	THBS1	0.698	0.823	0.002	0.031
TREML1	0.704	NF-E4	0.674	0.864	0.023	0.002
TREML1	0.704	THBS1	0.698	0.858	0.008	0.008
TREML1	0.704	MME	0.847	0.94	0	0.031
GSTO1	0.83	PDE3B	0.861	0.929	0.025	0.05
GSTO1	0.83	NA	0.884	0.972	0.004	0.008
GSTO1	0.83	KIAA1257_ACAD9/	0.823	0.923	0.026	0.012
GSTO1	0.83	CCDC125	0.79	0.948	0.012	0.003
GSTO1	0.83	CYP4F3_CYP4F2	0.755	0.912	0.049	0.004
GSTO1	0.83	SYNE2	0.886	0.953	0.008	0.028
GSTO1	0.83	RGS2	0.789	0.926	0.01	0.013

PTGER2	0.842	PDE3B	0.861	0.953	0.018	0.009
PTGER2	0.842	IRS2	0.851	0.932	0.035	0.019
PTGER2	0.842	NA	0.884	0.957	0.021	0.008
PTGER2	0.842	HAL	0.846	0.934	0.048	0.005
PTGER2	0.842	CCDC125	0.79	0.937	0.042	0.005
PTGER2	0.842	SYNE2	0.886	0.971	0.004	0.02
PTGER2	0.842	RGS2	0.789	0.952	0.015	0.001
PMS2CL_PMS2	0.857	PDE3B	0.861	0.961	0.009	0.015
PMS2CL_PMS2	0.857	NA	0.884	0.977	0.005	0.01
PMS2CL_PMS2	0.857	HAL	0.846	0.938	0.02	0.029
PMS2CL_PMS2	0.857	KIAA1257_ACAD9/	0.823	0.942	0.018	0.011
PMS2CL_PMS2	0.857	CCDC125	0.79	0.96	0.012	0.002
PMS2CL_PMS2	0.857	SYNE2	0.886	0.993	0.002	0.006
PMS2CL_PMS2	0.857	RBP7	0.803	0.952	0.022	0.002
PMS2CL_PMS2	0.857	RGS2	0.789	0.93	0.017	0.011
PMS2CL_PMS2	0.857	CAMK1D	0.735	0.92	0.02	0.002
PDE3B	0.861	NEK6_LOC1001290	0.844	0.95	0.004	0.035
PDE3B	0.861	AMFR	0.874	0.961	0.01	0.039
PDE3B	0.861	RPL17_SNORD58B	0.842	0.961	0.05	0.001
PDE3B	0.861	GLT25D1	0.808	0.916	0.034	0.031
PDE3B	0.861	EIF1AX_SCARNA9L	0.814	0.956	0.039	0
PDE3B	0.861	ZNF28	0.891	0.973	0.003	0.05
PDE3B	0.861	TYMS	0.838	0.939	0.034	0.038
PDE3B	0.861	HIST1H2BM	0.862	0.945	0.032	0.034
PDE3B	0.861	FSD1L_GARNL1	0.844	0.959	0.009	0.019
PDE3B	0.861	PTGS1	0.794	0.943	0.038	0.001
PDE3B	0.861	FSD1L	0.834	0.948	0.015	0.005
PDE3B	0.861	APOLD1	0.777	0.95	0.023	0.001
PDE3B	0.861	SON	0.794	0.946	0.012	0.007

PDE3B	0.861	PLEKHA3	0.777	0.946	0.018	0.001
PDE3B	0.861	CDC26	0.868	0.958	0.006	0.039
PDE3B	0.861	GLDC	0.775	0.922	0.028	0.008
PDE3B	0.861	KIAA0101_CSNK1G	0.87	0.953	0.05	0.008
SULF2	0.775	IRF4	0.74	0.868	0.015	0.046
SULF2	0.775	RPL17_SNORD58B	0.842	0.904	0.017	0.034
SULF2	0.775	ACTA2	0.818	0.924	0.003	0.033
SULF2	0.775	PTGS1	0.794	0.909	0.009	0.015
SULF2	0.775	E2F6	0.798	0.906	0.018	0.01
SULF2	0.775	CD151	0.767	0.896	0.02	0.01
SULF2	0.775	TPX2	0.745	0.874	0.017	0.026
SULF2	0.775	C7orf58	0.787	0.9	0.028	0.002
SULF2	0.775	DYNLL1	0.787	0.893	0.03	0.013
SULF2	0.775	NP	0.787	0.895	0.015	0.024
SULF2	0.775	NFXL1	0.808	0.889	0.044	0.044
SULF2	0.775	DCTN5	0.773	0.892	0.01	0.042
NEK6_LOC1001290	0.844	NA	0.884	0.931	0.045	0.038
NEK6_LOC1001290	0.844	SYNE2	0.886	0.946	0.027	0.026
NEK6_LOC1001290	0.844	RGS2	0.789	0.936	0.038	0.001
CENPK	0.739	PYHIN1	0.647	0.854	0.026	0.007
CENPK	0.739	PPP1R2_PPP1R2P3	0.637	0.812	0.032	0.043
TRAF3	0.889	SYNE2	0.886	0.962	0.032	0.017
IRF4	0.74	NA	0.884	0.935	0.002	0.034
IRF4	0.74	CCDC125	0.79	0.89	0.003	0.044
IRF4	0.74	CYP4F3_CYP4F2	0.755	0.874	0.04	0.004
IRF4	0.74	SYNE2	0.886	0.954	0	0.017
IRF4	0.74	MME	0.847	0.906	0.008	0.022
IRF4	0.74	RBP7	0.803	0.873	0.032	0.04
MACF1	0.699	ACPL2	0.756	0.858	0.008	0.041

MACF1	0.699	CAMK1D	0.735	0.854	0.003	0.05
MACF1	0.699	PPP1R2_PPP1R2P3	0.637	0.797	0.026	0.034
AMFR	0.874	IRS2	0.851	0.952	0.031	0.011
AMFR	0.874	OCR1	0.934	0.977	0.033	0.021
AMFR	0.874	NA	0.884	0.965	0.042	0.005
AMFR	0.874	HAL	0.846	0.971	0.028	0.003
AMFR	0.874	ZRANB1	0.718	0.965	0.044	0
AMFR	0.874	SYNE2	0.886	0.973	0.023	0.01
AMFR	0.874	RGS2	0.789	0.954	0.019	0.004
RPL17_SNORD58B	0.842	NA	0.884	0.98	0.004	0.006
RPL17_SNORD58B	0.842	LY6G5B_CSNK2B	0.63	0.892	0.044	0
RPL17_SNORD58B	0.842	KIAA1257_ACAD9/	0.823	0.922	0.011	0.049
RPL17_SNORD58B	0.842	CCDC125	0.79	0.939	0.005	0.015
RPL17_SNORD58B	0.842	ZRANB1	0.718	0.921	0.039	0.001
RPL17_SNORD58B	0.842	MME	0.847	0.947	0.011	0.017
RPL17_SNORD58B	0.842	RBP7	0.803	0.944	0.005	0.011
RPL17_SNORD58B	0.842	CAMK1D	0.735	0.894	0.023	0.014
IRS2	0.851	GLT25D1	0.808	0.926	0.023	0.016
IRS2	0.851	RRP12_LOC644215	0.84	0.938	0.008	0.038
IRS2	0.851	PTGS1	0.794	0.953	0.021	0.001
IRS2	0.851	CMTM5	0.814	0.949	0.031	0.002
IRS2	0.851	GLDC	0.775	0.946	0.016	0.001
GALNT2	0.673	ACPL2	0.756	0.832	0.033	0.019
GALNT2	0.673	ERGIC1	0.758	0.845	0.011	0.018
GLT25D1	0.808	ERGIC1	0.758	0.905	0.046	0.001
GLT25D1	0.808	HAL	0.846	0.916	0.024	0.019
GLT25D1	0.808	RGS2	0.789	0.887	0.038	0.016
GLT25D1	0.808	CAMK1D	0.735	0.925	0.023	0
HDHD1A	0.7	ACPL2	0.756	0.855	0.01	0.018

HDHD1A	0.7	LY6G5B_CSNK2B	0.63	0.811	0.028	0.009
HDHD1A	0.7	CCDC125	0.79	0.927	0	0.021
HDHD1A	0.7	ZRANB1	0.718	0.84	0.018	0.02
HDHD1A	0.7	CYP4F3_CYP4F2	0.755	0.844	0.028	0.018
HDHD1A	0.7	SYNE2	0.886	0.952	0	0.047
HDHD1A	0.7	CPM	0.812	0.906	0.002	0.009
HDHD1A	0.7	CAMK1D	0.735	0.871	0.001	0.021
ACTA2	0.818	ERGIC1	0.758	0.906	0.03	0.008
ACTA2	0.818	HAL	0.846	0.944	0.006	0.028
ACTA2	0.818	KIAA1257_ACAD9/	0.823	0.932	0.006	0.018
ACTA2	0.818	CCDC125	0.79	0.914	0.03	0.012
ACTA2	0.818	ZRANB1	0.718	0.93	0.021	0
ACTA2	0.818	MPZL2	0.775	0.919	0.034	0.004
ACPL2	0.756	DPH3	0.706	0.882	0.009	0.008
ACPL2	0.756	ANKRD28	0.71	0.906	0.005	0.001
ACPL2	0.756	ITGA2B	0.752	0.878	0.009	0.016
ACPL2	0.756	HIST1H3C	0.854	0.935	0.002	0.016
ACPL2	0.756	MYL9	0.695	0.861	0.022	0.006
ACPL2	0.756	HIST1H2BJ	0.797	0.92	0.004	0.01
ACPL2	0.756	MPO	0.684	0.832	0.025	0.043
ACPL2	0.756	FAM118B	0.74	0.869	0.008	0.033
ACPL2	0.756	SDHC	0.85	0.93	0.002	0.038
OCR1	0.934	ZNF28	0.891	0.976	0.038	0.043
OCR1	0.934	HSPB1_HSPBL2	0.886	0.977	0.018	0.033
OCR1	0.934	PTGS1	0.794	0.974	0.023	0.001
OCR1	0.934	MYL9	0.695	0.977	0.028	0
OCR1	0.934	CMTM5	0.814	0.979	0.024	0.002
OCR1	0.934	CDC26	0.868	0.965	0.044	0.033
EIF1AX_SCARNA9L	0.814	LY6G5B_CSNK2B	0.63	0.88	0.024	0.001

EIF1AX_SCARNA9L	0.814	CCDC125	0.79	0.929	0.001	0.028
EIF1AX_SCARNA9L	0.814	ZRANB1	0.718	0.901	0.009	0.004
EIF1AX_SCARNA9L	0.814	MME	0.847	0.94	0.008	0.012
EIF1AX_SCARNA9L	0.814	CPM	0.812	0.9	0.029	0.048
EIF1AX_SCARNA9L	0.814	RASA4_RASA4P_R	0.713	0.881	0.041	0.008
EIF1AX_SCARNA9L	0.814	RBP7	0.803	0.937	0.005	0.013
EIF1AX_SCARNA9L	0.814	CAMK1D	0.735	0.898	0.003	0.013
DPH3	0.706	ERGIC1	0.758	0.883	0	0.035
DPH3	0.706	HAL	0.846	0.938	0	0.05
DPH3	0.706	RBP7	0.803	0.905	0.001	0.048
ERGIC1	0.758	HIST1H3B	0.829	0.89	0.031	0.035
ERGIC1	0.758	PTGS1	0.794	0.91	0.008	0.004
ERGIC1	0.758	HIST1H3C	0.854	0.901	0.03	0.013
ERGIC1	0.758	CD151	0.767	0.885	0.018	0.014
ERGIC1	0.758	HIST1H3H	0.836	0.898	0.032	0.019
ERGIC1	0.758	FSD1L	0.834	0.901	0.005	0.042
ERGIC1	0.758	TPX2	0.745	0.861	0.037	0.023
ERGIC1	0.758	APOLD1	0.777	0.917	0.004	0.004
ERGIC1	0.758	HIST1H2BJ	0.797	0.901	0.032	0.003
ERGIC1	0.758	LASS4	0.669	0.85	0.017	0.012
ERGIC1	0.758	PLEKHF2	0.737	0.867	0.043	0.011
ERGIC1	0.758	CMTM5	0.814	0.927	0.005	0.006
ERGIC1	0.758	AIF1	0.745	0.87	0.028	0.007
ERGIC1	0.758	CDC26	0.868	0.955	0	0.05
ERGIC1	0.758	SDHC	0.85	0.919	0.006	0.015
ERGIC1	0.758	GLDC	0.775	0.893	0.004	0.023
CD300A	0.888	MPZL3	0.889	0.974	0.014	0.01
NF-E4	0.674	MYL9	0.695	0.868	0	0.023
NF-E4	0.674	HIST1H2BJ	0.797	0.926	0	0.027

NF-E4	0.674	SPARC	0.661	0.834	0.007	0.02
MINPP1	0.718	ZRANB1	0.718	0.895	0	0.009
MINPP1	0.718	RPIA	0.655	0.887	0.011	0
MINPP1	0.718	C1orf128	0.662	0.86	0.033	0.001
TRIM21	0.857	NA	0.884	0.945	0.029	0.048
TRIM21	0.857	SYNE2	0.886	0.956	0.024	0.033
ZNF28	0.891	NA	0.884	0.977	0.019	0.008
ZNF28	0.891	SYNE2	0.886	0.982	0.012	0.008
ZNF28	0.891	RGS2	0.789	0.953	0.044	0.004
NA	0.884	TAF13	0.908	0.984	0.005	0.026
NA	0.884	P4HA1_RPL17	0.88	0.969	0.018	0.018
NA	0.884	TYMS	0.838	0.953	0.018	0.012
NA	0.884	RRP12_LOC644215	0.84	0.939	0.019	0.048
NA	0.884	HIST1H2BM	0.862	0.977	0.006	0.007
NA	0.884	HIST1H3B	0.829	0.961	0.034	0.003
NA	0.884	TIMM10	0.868	0.958	0.01	0.034
NA	0.884	FSD1L_GARNL1	0.844	0.951	0.02	0.024
NA	0.884	PTGS1	0.794	0.949	0.033	0.002
NA	0.884	NA	0.87	0.963	0.025	0.004
NA	0.884	HIST1H3C	0.854	0.971	0.023	0.003
NA	0.884	HIST1H3H	0.836	0.972	0.018	0.002
NA	0.884	FSD1L	0.834	0.956	0.032	0.003
NA	0.884	TPX2	0.745	0.955	0.015	0.001
NA	0.884	APOLD1	0.777	0.943	0.013	0.004
NA	0.884	MPO	0.684	0.94	0.04	0
NA	0.884	B4GALT3	0.785	0.948	0.03	0.002
NA	0.884	CTSL1_CTSLL3	0.819	0.945	0.033	0.009
NA	0.884	TNFRSF17	0.827	0.962	0.029	0.002
NA	0.884	PLEKHA3	0.777	0.951	0.033	0.001

NA	0.884	CMTM5	0.814	0.944	0.032	0.009
NA	0.884	IGL@_IGLV1-44_	0.77	0.939	0.028	0.002
NA	0.884	DCTN5	0.773	0.939	0.034	0.003
NA	0.884	KIAA0101_CSNK1G	0.87	0.985	0.006	0.008
TAF13	0.908	CCDC125	0.79	0.965	0.031	0.003
TAF13	0.908	SYNE2	0.886	0.965	0.036	0.043
TAF13	0.908	RGS2	0.789	0.953	0.048	0.008
P4HA1_RPL17	0.88	CCDC125	0.79	0.961	0.032	0.002
P4HA1_RPL17	0.88	SYNE2	0.886	0.984	0.005	0.016
C15orf54	0.672	POLE2	0.704	0.824	0.039	0.01
KLHL5	0.913	SYNE2	0.886	0.976	0.03	0.016
KLHL5	0.913	RGS2	0.789	0.963	0.011	0.005
HAL	0.846	TYMS	0.838	0.932	0.02	0.031
HAL	0.846	RRP12_LOC644215	0.84	0.936	0.011	0.031
HAL	0.846	TIMM10	0.868	0.931	0.034	0.041
HAL	0.846	FSD1L_GARNL1	0.844	0.937	0.015	0.046
HAL	0.846	PTGS1	0.794	0.955	0.016	0.001
HAL	0.846	CD151	0.767	0.926	0.047	0.002
HAL	0.846	FSD1L	0.834	0.919	0.041	0.019
HAL	0.846	APOLD1	0.777	0.962	0.006	0.001
HAL	0.846	SON	0.794	0.918	0.043	0.011
HAL	0.846	LASS4	0.669	0.925	0.015	0
HAL	0.846	B4GALT3	0.785	0.945	0.015	0.002
HAL	0.846	PLEKHA3	0.777	0.912	0.045	0.01
HAL	0.846	CMTM5	0.814	0.97	0.013	0.001
HAL	0.846	AIF1	0.745	0.936	0.018	0.001
HAL	0.846	CDC26	0.868	0.957	0.004	0.036
HAL	0.846	GLDC	0.775	0.946	0.01	0.002
HAL	0.846	DCTN5	0.773	0.905	0.023	0.012

DLEU2_DLEU2L	0.758	KIAA1257_ACAD9/	0.823	0.918	0.002	0.033
DLEU2_DLEU2L	0.758	MME	0.847	0.916	0.004	0.045
DLEU2_DLEU2L	0.758	CAMK1D	0.735	0.87	0.008	0.022
ANKRD28	0.71	LY6G5B_CSNK2B	0.63	0.791	0.024	0.048
ANKRD28	0.71	THBS1	0.698	0.836	0.039	0.005
ANKRD28	0.71	ZRANB1	0.718	0.874	0.001	0.016
ANKRD28	0.71	CPM	0.812	0.9	0.002	0.032
ANKRD28	0.71	CAMK1D	0.735	0.867	0.001	0.036
LY6G5B_CSNK2B	0.63	KIAA0746	0.713	0.792	0.048	0.015
KIAA1257_ACAD9/	0.823	TYMS	0.838	0.929	0.012	0.039
KIAA1257_ACAD9/	0.823	RRP12_LOC644215	0.84	0.939	0.004	0.038
KIAA1257_ACAD9/	0.823	TIMM10	0.868	0.937	0.019	0.023
KIAA1257_ACAD9/	0.823	PTGS1	0.794	0.935	0.016	0.002
KIAA1257_ACAD9/	0.823	NA	0.87	0.928	0.018	0.036
KIAA1257_ACAD9/	0.823	CD151	0.767	0.909	0.05	0.004
KIAA1257_ACAD9/	0.823	HIST1H3H	0.836	0.933	0.045	0.002
KIAA1257_ACAD9/	0.823	FSD1L	0.834	0.911	0.036	0.035
KIAA1257_ACAD9/	0.823	APOLD1	0.777	0.941	0.007	0.003
KIAA1257_ACAD9/	0.823	B4GALT3	0.785	0.938	0.009	0.007
KIAA1257_ACAD9/	0.823	CMTM5	0.814	0.952	0.008	0.002
KIAA1257_ACAD9/	0.823	SDHC	0.85	0.926	0.039	0.011
KIAA1257_ACAD9/	0.823	GLDC	0.775	0.904	0.033	0.014
KIAA1257_ACAD9/	0.823	KIAA0101_CSNK1G	0.87	0.939	0.044	0.015
MGST3	0.897	MPZL3	0.889	0.983	0.005	0.022
MGST3	0.897	RGS2	0.789	0.948	0.036	0.005
HSPB1_HSPBL2	0.886	MPZL3	0.889	0.976	0.005	0.024
TYMS	0.838	CCDC125	0.79	0.956	0.007	0.003
TYMS	0.838	SYNE2	0.886	0.965	0.004	0.025
CCDC125	0.79	HIST1H2BM	0.862	0.965	0.002	0.009

CCDC125	0.79	HIST1H3B	0.829	0.921	0.03	0.014
CCDC125	0.79	FSD1L_GARNL1	0.844	0.964	0.001	0.013
CCDC125	0.79	PTGS1	0.794	0.915	0.009	0.016
CCDC125	0.79	UBE2F_C20orf194	0.758	0.91	0.048	0.001
CCDC125	0.79	HIST1H3C	0.854	0.943	0.021	0.001
CCDC125	0.79	CD151	0.767	0.889	0.05	0.016
CCDC125	0.79	HIST1H3H	0.836	0.931	0.02	0.007
CCDC125	0.79	FSD1L	0.834	0.935	0.009	0.005
CCDC125	0.79	TPX2	0.745	0.969	0.003	0
CCDC125	0.79	APOLD1	0.777	0.886	0.014	0.039
CCDC125	0.79	HIST1H2BJ	0.797	0.932	0.032	0
CCDC125	0.79	SON	0.794	0.913	0.017	0.02
CCDC125	0.79	LASS4	0.669	0.846	0.032	0.015
CCDC125	0.79	DYNLL1	0.787	0.917	0.041	0.001
CCDC125	0.79	FAM118B	0.74	0.921	0.033	0
CCDC125	0.79	B4GALT3	0.785	0.923	0.014	0.005
CCDC125	0.79	CTSL1_CTSLL3	0.819	0.897	0.048	0.049
CCDC125	0.79	NP	0.787	0.927	0.012	0.003
CCDC125	0.79	TNFRSF17	0.827	0.927	0.009	0.012
CCDC125	0.79	PLEKHA3	0.777	0.901	0.022	0.014
CCDC125	0.79	TMEM62_SPCS2_L	0.849	0.94	0.012	0.018
CCDC125	0.79	CMTM5	0.814	0.922	0.013	0.017
CCDC125	0.79	IGL@_IGLV1-44_	0.77	0.899	0.021	0.02
CCDC125	0.79	SDHC	0.85	0.932	0.031	0.007
CCDC125	0.79	GLDC	0.775	0.899	0.01	0.026
CCDC125	0.79	DCTN5	0.773	0.91	0.008	0.02
CCDC125	0.79	KIAA0101_CSNK1G	0.87	0.956	0.01	0.005
HIST1H2BM	0.862	SYNE2	0.886	0.982	0.006	0.011
HIST1H2BM	0.862	MME	0.847	0.947	0.047	0.004

HIST1H2BM	0.862	RGS2	0.789	0.932	0.028	0.011
IL1B	0.769	KDM6B_TMEM88	0.672	0.842	0.014	0.031
THBS1	0.698	ITGA2B	0.752	0.919	0	0.007
THBS1	0.698	MYL9	0.695	0.858	0.001	0.021
THBS1	0.698	SPARC	0.661	0.835	0.016	0.007
ITGA2B	0.752	ZRANB1	0.718	0.906	0	0.006
ITGA2B	0.752	CYP4F3_CYP4F2	0.755	0.894	0.011	0.008
ITGA2B	0.752	MME	0.847	0.941	0.001	0.014
ITGA2B	0.752	RBP7	0.803	0.913	0.003	0.015
ITGA2B	0.752	MPZL2	0.775	0.885	0.007	0.019
LAIR1_LAIR2	0.777	MPZL2	0.775	0.883	0.044	0.01
HIST1H3B	0.829	CYP4F3_CYP4F2	0.755	0.909	0.038	0.008
ZRANB1	0.718	PTGS1	0.794	0.945	0	0.002
ZRANB1	0.718	UBE2F_C20orf194	0.758	0.87	0.009	0.016
ZRANB1	0.718	HIST1H3C	0.854	0.914	0.003	0.038
ZRANB1	0.718	E2F6	0.798	0.899	0.01	0.011
ZRANB1	0.718	CD151	0.767	0.881	0.005	0.014
ZRANB1	0.718	HIST1H3H	0.836	0.946	0	0.006
ZRANB1	0.718	TPX2	0.745	0.861	0.004	0.049
ZRANB1	0.718	MYL9	0.695	0.866	0.031	0.001
ZRANB1	0.718	HIST1H2BJ	0.797	0.929	0.002	0.001
ZRANB1	0.718	C7orf58	0.787	0.886	0.01	0.003
ZRANB1	0.718	DYNLL1	0.787	0.887	0.013	0.009
ZRANB1	0.718	FAM118B	0.74	0.833	0.041	0.024
ZRANB1	0.718	B4GALT3	0.785	0.926	0	0.018
ZRANB1	0.718	NP	0.787	0.913	0.001	0.014
ZRANB1	0.718	TNFRSF17	0.827	0.891	0.003	0.031
ZRANB1	0.718	CMTM5	0.814	0.946	0	0.005
ZRANB1	0.718	IGLV6-57	0.757	0.846	0.026	0.047

TIMM10	0.868	SYNE2	0.886	0.971	0.017	0.007
FSD1L_GARNL1	0.844	SYNE2	0.886	0.965	0.007	0.02
FSD1L_GARNL1	0.844	RGS2	0.789	0.94	0.036	0.002
PTGS1	0.794	CYP4F3_CYP4F2	0.755	0.902	0.049	0.001
PTGS1	0.794	MME	0.847	0.951	0.005	0.004
PTGS1	0.794	CPM	0.812	0.906	0.031	0.006
PTGS1	0.794	RBP7	0.803	0.952	0.003	0.001
PTGS1	0.794	RGS2	0.789	0.91	0.004	0.027
PTGS1	0.794	CAMK1D	0.735	0.874	0.041	0.014
PTGS1	0.794	MPZL2	0.775	0.901	0.036	0.002
UBE2F_C20orf194	0.758	CYP4F3_CYP4F2	0.755	0.861	0.05	0.026
UBE2F_C20orf194	0.758	RBP7	0.803	0.906	0.008	0.012
HIST1H3C	0.854	RBP7	0.803	0.949	0.007	0.008
HIST1H3C	0.854	CAMK1D	0.735	0.9	0.021	0.016
FAM118A	0.717	SYNE2	0.886	0.961	0	0.018
FAM118A	0.717	RBP7	0.803	0.894	0.009	0.035
E2F6	0.798	RASA4_RASA4P_R	0.713	0.894	0.008	0.013
E2F6	0.798	RBP7	0.803	0.93	0.002	0.023
E2F6	0.798	CAMK1D	0.735	0.883	0.01	0.023
MPZL3	0.889	IRF1	0.894	0.971	0.011	0.026
MPZL3	0.889	ATP6V0D1_LOC100	0.828	0.965	0.027	0.004
MPZL3	0.889	CDC26	0.868	0.972	0.015	0.004
CD151	0.767	KDM6B_TMEM88	0.672	0.856	0.024	0.008
CD151	0.767	CYP4F3_CYP4F2	0.755	0.894	0.015	0.005
CD151	0.767	RBP7	0.803	0.919	0.009	0.004
CD151	0.767	RGS2	0.789	0.909	0.002	0.042
CD151	0.767	MPZL2	0.775	0.87	0.026	0.02
HIST1H3H	0.836	CYP4F3_CYP4F2	0.755	0.948	0.01	0
HIST1H3H	0.836	MME	0.847	0.973	0.004	0.003

HIST1H3H	0.836	RBP7	0.803	0.958	0.006	0.002
HIST1H3H	0.836	RGS2	0.789	0.923	0.001	0.046
FSD1L	0.834	RGS2	0.789	0.9	0.022	0.02
FSD1L	0.834	CAMK1D	0.735	0.912	0.028	0.001
TPX2	0.745	CYP4F3_CYP4F2	0.755	0.893	0.02	0.003
TPX2	0.745	SYNE2	0.886	0.965	0	0.017
TPX2	0.745	MME	0.847	0.913	0.009	0.022
TPX2	0.745	RBP7	0.803	0.908	0.02	0.006
TPX2	0.745	MPZL2	0.775	0.85	0.04	0.034
PYHIN1	0.647	IGK@_IGKC_IGKV	0.774	0.855	0.006	0.032
APOLD1	0.777	SYNE2	0.886	0.945	0.001	0.048
APOLD1	0.777	MME	0.847	0.917	0.013	0.011
APOLD1	0.777	RGS2	0.789	0.918	0.004	0.01
APOLD1	0.777	CAMK1D	0.735	0.887	0.031	0.003
KDM6B_TMEM88	0.672	AIF1	0.745	0.833	0.017	0.039
MYL9	0.695	CYP4F3_CYP4F2	0.755	0.886	0.004	0.009
MYL9	0.695	MME	0.847	0.949	0	0.007
MYL9	0.695	RBP7	0.803	0.948	0	0.004
HIST1H2BJ	0.797	CYP4F3_CYP4F2	0.755	0.929	0.003	0.004
HIST1H2BJ	0.797	MME	0.847	0.96	0.001	0.012
HIST1H2BJ	0.797	RBP7	0.803	0.957	0.001	0.005
CYP4F3_CYP4F2	0.755	LASS4	0.669	0.837	0.007	0.043
CYP4F3_CYP4F2	0.755	DYNLL1	0.787	0.89	0.007	0.021
CYP4F3_CYP4F2	0.755	MPO	0.684	0.861	0.039	0.005
CYP4F3_CYP4F2	0.755	FAM118B	0.74	0.85	0.039	0.041
CYP4F3_CYP4F2	0.755	TNFRSF17	0.827	0.927	0.002	0.013
CYP4F3_CYP4F2	0.755	CMTM5	0.814	0.927	0.001	0.035
CYP4F3_CYP4F2	0.755	IGLV6-57	0.757	0.933	0.001	0.002
CYP4F3_CYP4F2	0.755	IGL@_IGLV1-44_	0.77	0.903	0.001	0.024

SON	0.794	SYNE2	0.886	0.962	0	0.047
SON	0.794	LOC100128751	0.809	0.926	0.005	0.008
SYNE2	0.886	B4GALT3	0.785	0.96	0.018	0.002
SYNE2	0.886	NP	0.787	0.965	0.013	0.001
SYNE2	0.886	PLEKHA3	0.777	0.955	0.042	0.001
SYNE2	0.886	CDC26	0.868	0.967	0.008	0.013
SYNE2	0.886	KIAA0101_CSNK1G	0.87	0.971	0.036	0.003
MME	0.847	LASS4	0.669	0.906	0.003	0.003
MME	0.847	DYNLL1	0.787	0.919	0.043	0.006
MME	0.847	B4GALT3	0.785	0.926	0.009	0.014
MME	0.847	NP	0.787	0.912	0.03	0.021
MME	0.847	SPARC	0.661	0.929	0.043	0
MME	0.847	TNFRSF17	0.827	0.953	0.006	0.003
MME	0.847	PLEKHA3	0.777	0.919	0.02	0.017
MME	0.847	CMTM5	0.814	0.968	0.002	0.005
MME	0.847	IGLV6-57	0.757	0.92	0.047	0.002
MME	0.847	IGL@_IGLV1-44_	0.77	0.919	0.006	0.013
MME	0.847	GLDC	0.775	0.9	0.008	0.033
MME	0.847	KIAA0101_CSNK1G	0.87	0.947	0.016	0.026
LASS4	0.669	RBP7	0.803	0.883	0.009	0.004
C7orf58	0.787	CAMK1D	0.735	0.881	0.004	0.022
DYNLL1	0.787	RBP7	0.803	0.921	0.003	0.02
DYNLL1	0.787	CAMK1D	0.735	0.887	0.005	0.021
DYNLL1	0.787	PPP1R2_PPP1R2P3	0.637	0.869	0.018	0.004
CPM	0.812	FAM118B	0.74	0.919	0.011	0.002
CPM	0.812	AIF1	0.745	0.897	0.04	0.009
FAM118B	0.74	CAMK1D	0.735	0.874	0.002	0.027
B4GALT3	0.785	RBP7	0.803	0.921	0.024	0.001
NP	0.787	RBP7	0.803	0.912	0.026	0.003

NP	0.787	MPZL2	0.775	0.879	0.039	0.013
POLE2	0.704	RPIA	0.655	0.854	0.001	0.017
POLE2	0.704	C1orf128	0.662	0.864	0.003	0.008
TNFRSF17	0.827	RGS2	0.789	0.913	0.007	0.039
PLEKHA3	0.777	RBP7	0.803	0.906	0.026	0.015
PLEKHA3	0.777	RGS2	0.789	0.913	0.005	0.02
PLEKHA3	0.777	CAMK1D	0.735	0.866	0.039	0.02
RBP7	0.803	CMTM5	0.814	0.976	0.001	0.001
RBP7	0.803	IGLV6-57	0.757	0.899	0.03	0.01
RBP7	0.803	IGL@_IGLV1-44_	0.77	0.894	0.013	0.035
RBP7	0.803	SDHC	0.85	0.919	0.038	0.036
RBP7	0.803	GLDC	0.775	0.89	0.005	0.046
RBP7	0.803	KIAA0101_CSNK1G	0.87	0.958	0.004	0.01
RGS2	0.789	CMTM5	0.814	0.941	0.017	0.001
RGS2	0.789	CDC26	0.868	0.956	0.001	0.016
RGS2	0.789	IGL@_IGLV1-44_	0.77	0.888	0.033	0.013
RGS2	0.789	KIAA0101_CSNK1G	0.87	0.932	0.032	0.008
CAMK1D	0.735	AIF1	0.745	0.876	0.011	0.009
CAMK1D	0.735	NFXL1	0.808	0.893	0.009	0.029
CAMK1D	0.735	DCTN5	0.773	0.885	0.004	0.022
CAMK1D	0.735	KIAA0101_CSNK1G	0.87	0.919	0.007	0.029
LOC100128751	0.809	DCTN5	0.773	0.899	0.033	0.031
IFI44	0.712	NA	0.623	0.83	0.007	0.01

Table 19

Ratios Mild ipSIRS Versus Severe ipSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
CD177	0.668	ACER3	0.649	0.815	0.046	0.049
CD177	0.668	NEK6_LOC1001290	0.471	0.748	0.043	0.008
CD177	0.668	GLT25D1	0.454	0.777	0.018	0.001
VNN1	0.649	UBE2J1	0.468	0.713	0.021	0.001
UBE2J1	0.468	SEC24A_SAR1B	0.679	0.795	0	0.04
IMP3	0.611	DNAJC9_FAM149B1	0.759	0.837	0.03	0.028
CLEC4D	0.522	FKBP5_LOC285847	0.423	0.654	0.035	0.027
GPR56	0.686	NA	0.629	0.797	0.045	0.016
C11orf82	0.619	DPH3	0.648	0.799	0.016	0.046
GNLY	0.691	GOT2	0.702	0.86	0.015	0.035
GNLY	0.691	HSPC159	0.612	0.789	0.018	0.047
TGFBR1	0.6	SEC24A_SAR1B	0.679	0.803	0.031	0.035
TGFBR1	0.6	MTRR	0.66	0.786	0.049	0.03
TGFBR1	0.6	KIAA0746	0.727	0.812	0.035	0.013
FKBP5_LOC285847	0.423	B3GNT5_MCF2L2	0.566	0.735	0.006	0.018
FKBP5_LOC285847	0.423	GLT25D1	0.454	0.698	0.042	0.03
C7orf53	0.75	DLEU2_DLEU2L	0.785	0.913	0.007	0.027
CAMK4	0.595	KPNA5	0.831	0.967	0	0.033
CAMK4	0.595	ITGA4_CERKL	0.659	0.842	0.002	0.034
GSR	0.795	VAMP2	0.811	0.92	0.004	0.042
GSR	0.795	JKAMP	0.752	0.94	0.005	0.004
GSR	0.795	SON	0.722	0.909	0.046	0.003
GSR	0.795	ATP6V0D1_LOC100	0.754	0.903	0.004	0.027
GSR	0.795	AIF1	0.826	0.918	0.034	0.03
KLRF1	0.702	MME	0.68	0.848	0.046	0.035

PICALM	0.595	DLEU2_DLEU2L	0.785	0.899	0.001	0.022
HIST1H4C	0.571	HIST1H3B	0.712	0.81	0.034	0.041
C9orf72	0.603	PPP2R5A_SNORA16	0.649	0.81	0.01	0.025
SLC15A2	0.629	EAF2_HCG11_LOC	0.682	0.844	0.012	0.025
ADM	0.649	CD63	0.645	0.818	0.022	0.025
LRRN3	0.724	EIF1AX_SCARNA9L	0.767	0.89	0.006	0.048
LRRN3	0.724	DPH3	0.648	0.845	0.039	0.008
LRRN3	0.724	E2F6	0.8	0.897	0.016	0.023
LRRN3	0.724	RFESD_SPATA9	0.815	0.895	0.014	0.043
HLA-DPB1	0.694	GOT2	0.702	0.859	0.032	0.017
VAMP2	0.811	SFRS9	0.841	0.97	0.003	0.018
JKAMP	0.752	LOC284757	0.834	0.916	0.031	0.011
JKAMP	0.752	SEC24A_SAR1B	0.679	0.898	0.038	0.002
JKAMP	0.752	SLC39A9	0.731	0.909	0.013	0.013
JKAMP	0.752	SFRS9	0.841	0.969	0	0.022
TCN1	0.755	AIG1	0.588	0.829	0.03	0.02
KPNA5	0.831	IRF4	0.759	0.941	0.041	0.017
CD63	0.645	SLC11A1	0.624	0.789	0.044	0.047
KLRK1_KLRC4	0.608	CCR4	0.44	0.758	0.011	0.012
ITK	0.646	ITGA4_CERKL	0.659	0.859	0.006	0.025
GOT2	0.702	HINT1	0.649	0.838	0.049	0.026
GOT2	0.702	ITGA4_CERKL	0.659	0.856	0.027	0.013
B3GAT3	0.605	EFCAB2	0.801	0.85	0.018	0.036
HIST1H4E	0.69	NF-E4	0.78	0.859	0.023	0.033
FGFBP2	0.698	PYHIN1	0.548	0.796	0.045	0.034
BPI	0.78	PPIF	0.683	0.833	0.033	0.05
BPI	0.78	AIG1	0.588	0.882	0.013	0.001
BPI	0.78	DPH3	0.648	0.865	0.036	0.012
BPI	0.78	S100B	0.703	0.906	0.011	0.008

BPI	0.78	CDC26	0.657	0.834	0.05	0.037
PPP2R5A_SNORA16	0.649	EAF2_HCG11_LOC	0.682	0.844	0.016	0.023
PPP2R5A_SNORA16	0.649	NA	0.682	0.818	0.048	0.018
PPP2R5A_SNORA16	0.649	EIF1AX_SCARNA9L	0.767	0.868	0.009	0.025
PPP2R5A_SNORA16	0.649	DPH3	0.648	0.812	0.047	0.014
PPP2R5A_SNORA16	0.649	TAF13	0.743	0.883	0.005	0.012
PPP2R5A_SNORA16	0.649	FSD1L_GARNL1	0.665	0.846	0.02	0.006
EAF2_HCG11_LOC	0.682	SEC24A_SAR1B	0.679	0.872	0.012	0.011
EAF2_HCG11_LOC	0.682	MTRR	0.66	0.845	0.046	0.007
EAF2_HCG11_LOC	0.682	KIAA0746	0.727	0.869	0.049	0.001
RCBTB2_LOC10013	0.578	NA	0.838	0.897	0.002	0.038
RCBTB2_LOC10013	0.578	PLEKHF2	0.85	0.924	0	0.044
SEC24A_SAR1B	0.679	TAF13	0.743	0.859	0.044	0.013
KLRD1	0.687	CCR4	0.44	0.799	0.029	0.003
KLRD1	0.687	PYHIN1	0.548	0.815	0.026	0.014
KLRD1	0.687	IGK@_IGKC_IGKV	0.664	0.818	0.018	0.037
SLC39A9	0.731	ZNF28	0.837	0.903	0.039	0.027
GIMAP7	0.618	DNAJC9_FAM149B1	0.759	0.89	0.003	0.013
HLA-DRA	0.669	HSP90AB1_HSP90A	0.735	0.865	0.006	0.047
DNAJC9_FAM149B1	0.759	HINT1	0.649	0.869	0.029	0.008
DNAJC9_FAM149B1	0.759	CENPK	0.781	0.922	0.003	0.045
DNAJC9_FAM149B1	0.759	ITGA4_CERKL	0.659	0.887	0.007	0.009
DNAJC9_FAM149B1	0.759	CTSL1_CTSLL3	0.697	0.856	0.03	0.028
NA	0.709	TRIM21	0.739	0.85	0.032	0.04
NA	0.709	NA	0.838	0.917	0.01	0.04
MTRR	0.66	TAF13	0.743	0.876	0.014	0.01
MTRR	0.66	FSD1L_GARNL1	0.665	0.859	0.014	0.007
MTRR	0.66	PLEKHF2	0.85	0.916	0.004	0.047
HIST1H3A	0.593	TYMS	0.761	0.899	0.001	0.015

HIST1H3A	0.593	HIST1H2BM	0.693	0.875	0.001	0.011
HIST1H3A	0.593	HIST1H3B	0.712	0.891	0.005	0.001
HIST1H3A	0.593	IGK@_IGKC_IGKV	0.664	0.777	0.04	0.046
TREML1	0.581	MYL9	0.472	0.717	0.028	0.006
TREML1	0.581	CMTM5	0.494	0.679	0.039	0.03
PDE3B	0.622	EIF1AX_SCARNA9L	0.767	0.844	0.025	0.026
PDE3B	0.622	TAF13	0.743	0.844	0.01	0.037
PDE3B	0.622	DLEU2_DLEU2L	0.785	0.867	0.005	0.043
PDE3B	0.622	E2F6	0.8	0.856	0.025	0.037
PDE3B	0.622	ATP5L_ATP5L2	0.797	0.878	0.006	0.033
PDE3B	0.622	CALM2_C2orf61	0.776	0.905	0.001	0.024
CENPK	0.781	IRF4	0.759	0.95	0.003	0.02
AMFR	0.582	E2F6	0.8	0.857	0.003	0.042
HSP90AB1_HSP90A	0.735	RFESD_SPATA9	0.815	0.887	0.026	0.041
HSP90AB1_HSP90A	0.735	SON	0.722	0.865	0.005	0.049
EIF1AX_SCARNA9L	0.767	CEP97	0.702	0.91	0.005	0.007
SFRS9	0.841	PLEKHA3	0.875	0.974	0.018	0.014
DPH3	0.648	KIAA0746	0.727	0.852	0.01	0.04
NF-E4	0.78	E2F6	0.8	0.906	0.022	0.041
NPCDR1	0.752	KLHL5	0.739	0.861	0.043	0.044
NPCDR1	0.752	SON	0.722	0.861	0.032	0.047
TAF13	0.743	CEP97	0.702	0.852	0.041	0.049
KIAA0746	0.727	FSD1L_GARNL1	0.665	0.848	0.046	0.017
ABCG1	0.669	RFESD_SPATA9	0.815	0.879	0.016	0.046
FAM118A	0.644	E2F6	0.8	0.876	0.017	0.02
E2F6	0.8	RASA4_RASA4P_R	0.645	0.861	0.031	0.023
S100B	0.703	MPO	0.705	0.856	0.029	0.018
CEP97	0.702	CALM2_C2orf61	0.776	0.895	0.003	0.043

Table 20

Ratios Mild ipSIRS Versus Shock ipSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
TLR5	0.769	NA	0.808	0.893	0.021	0.05
TLR5	0.769	DLEU2_DLEU2L	0.782	0.874	0.03	0.029
TLR5	0.769	NA	0.838	0.908	0.022	0.012
TLR5	0.769	ATP6V0D1_LOC100	0.701	0.859	0.018	0.017
VNN1	0.71	HIST1H4E	0.678	0.826	0.01	0.017
VNN1	0.71	SLC11A1	0.556	0.768	0.047	0.023
VNN1	0.71	CENPK	0.752	0.851	0.017	0.021
VNN1	0.71	ERGIC1	0.6	0.769	0.044	0.044
VNN1	0.71	SON	0.632	0.781	0.044	0.047
VNN1	0.71	PLEKHF2	0.692	0.864	0.002	0.011
VNN1	0.71	CALM2_C2orf61	0.687	0.848	0.003	0.016
UBE2J1	0.645	PLEKHF2	0.692	0.81	0.046	0.001
IMP3	0.742	GSR	0.723	0.864	0.027	0.013
IMP3	0.742	SLC39A9	0.736	0.873	0.012	0.025
ARG1	0.683	HMGB2	0.556	0.749	0.034	0.002
FAR2	0.746	VAMP2	0.834	0.923	0	0.046
FAR2	0.746	TRIM21	0.779	0.869	0.035	0.023
FAR2	0.746	ZNF28	0.797	0.883	0.018	0.022
FAR2	0.746	PPP1R2_PPP1R2P3	0.739	0.857	0.03	0.021
FAR2	0.746	ATP5L_ATP5L2	0.786	0.904	0.007	0.006
GNLY	0.792	GSR	0.723	0.851	0.05	0.041
OMG	0.709	C9orf72	0.573	0.784	0.028	0.022
OMG	0.709	JKAMP	0.554	0.793	0.023	0.007
OMG	0.709	HIST1H4E	0.678	0.801	0.047	0.037
OMG	0.709	CDS2	0.562	0.776	0.01	0.02

OMG	0.709	PLEKHF2	0.692	0.836	0.011	0.025
OMG	0.709	AIF1	0.719	0.83	0.021	0.031
OMG	0.709	CALM2_C2orf61	0.687	0.824	0.014	0.037
SLC37A3	0.653	HIST1H4E	0.678	0.802	0.024	0.02
BMX_HNRPDL	0.749	PLEKHF2	0.692	0.833	0.018	0.046
BMX_HNRPDL	0.749	CALM2_C2orf61	0.687	0.822	0.029	0.05
STOM	0.684	VAMP2	0.834	0.923	0	0.022
STOM	0.684	MINPP1	0.78	0.848	0.024	0.016
STOM	0.684	ATP5L_ATP5L2	0.786	0.865	0.005	0.034
TDRD9	0.735	AGTRAP	0.569	0.768	0.046	0.044
FAIM3	0.749	SLC15A2	0.733	0.861	0.01	0.026
FAIM3	0.749	SRXN1	0.7	0.834	0.015	0.049
CLEC4E	0.681	HIST1H4E	0.678	0.8	0.047	0.021
CLEC4E	0.681	ERGIC1	0.6	0.792	0.007	0.027
CLEC4E	0.681	PLEKHF2	0.692	0.819	0.011	0.038
CLEC4E	0.681	CALM2_C2orf61	0.687	0.823	0.007	0.033
IL18R1	0.715	SLC11A1	0.556	0.763	0.025	0.034
IL18R1	0.715	RRP12_LOC644215	0.569	0.76	0.014	0.035
TGFBR1	0.663	NA	0.838	0.909	0.001	0.024
FKBP5_LOC285847	0.685	HIST1H4E	0.678	0.804	0.022	0.016
FKBP5_LOC285847	0.685	PLEKHF2	0.692	0.823	0.008	0.024
FKBP5_LOC285847	0.685	CALM2_C2orf61	0.687	0.815	0.012	0.029
PLB1	0.651	EFCAB2	0.772	0.851	0.01	0.022
DSE	0.623	PLEKHF2	0.692	0.827	0.006	0.01
DSE	0.623	ARL17P1_ARL17	0.745	0.805	0.024	0.041
CAMK4	0.726	HDHD1A	0.647	0.804	0.048	0.035
DNAJC13	0.661	ARL17P1_ARL17	0.745	0.819	0.019	0.048
GSR	0.723	MINPP1	0.78	0.845	0.034	0.026
GSR	0.723	TRIM21	0.779	0.866	0.013	0.035

GSR	0.723	ZNF28	0.797	0.887	0.005	0.024
GSR	0.723	LY6G5B_CSNK2B	0.737	0.897	0.003	0.003
GSR	0.723	ZNF587_ZNF417	0.842	0.927	0.001	0.025
GSR	0.723	KDM6B_TMEM88	0.695	0.827	0.028	0.038
GSR	0.723	PLEKHF2	0.692	0.833	0.049	0.002
GSR	0.723	ATP6V0D1_LOC100	0.701	0.85	0.002	0.042
GSR	0.723	PPP1R2_PPP1R2P3	0.739	0.84	0.026	0.044
GSR	0.723	ATP5L_ATP5L2	0.786	0.878	0.004	0.035
SGMS2	0.752	ERGIC1	0.6	0.838	0.042	0.004
SGMS2	0.752	ATP5L_ATP5L2	0.786	0.878	0.005	0.046
B3GNT5_MCF2L2	0.692	EFCAB2	0.772	0.898	0.005	0.003
B3GNT5_MCF2L2	0.692	PLEKHF2	0.692	0.838	0.008	0.038
B3GNT5_MCF2L2	0.692	CALM2_C2orf61	0.687	0.829	0.012	0.033
GK3P_GK	0.729	DPH3	0.536	0.806	0.048	0.003
GK3P_GK	0.729	CALM2_C2orf61	0.687	0.842	0.009	0.038
PICALM	0.749	GIMAP7	0.827	0.888	0.019	0.04
PICALM	0.749	NA	0.808	0.887	0.012	0.035
PICALM	0.749	DLEU2_DLEU2L	0.782	0.911	0.009	0.002
HIST1H4C	0.638	ANAPC11	0.58	0.744	0.031	0.03
SLC15A2	0.733	ITK	0.736	0.856	0.049	0.004
SLC15A2	0.733	TRIM21	0.779	0.864	0.032	0.047
SLC15A2	0.733	PPP1R2_PPP1R2P3	0.739	0.86	0.012	0.025
SLC15A2	0.733	ATP5L_ATP5L2	0.786	0.873	0.014	0.029
VAMP2	0.834	CD63	0.722	0.945	0.026	0
VAMP2	0.834	SLC39A9	0.736	0.931	0.025	0
VAMP2	0.834	AREG	0.668	0.909	0.045	0
VAMP2	0.834	SFRS9	0.798	0.933	0.047	0.005
VAMP2	0.834	SRXN1	0.7	0.922	0.023	0
VAMP2	0.834	C4orf3	0.776	0.962	0.001	0.001

SMPDL3A	0.733	EFCAB2	0.772	0.883	0.008	0.042
SMPDL3A	0.733	TAF13	0.585	0.834	0.04	0.003
SMPDL3A	0.733	SON	0.632	0.809	0.007	0.04
SMPDL3A	0.733	TMEM62_SPCS2_L	0.629	0.81	0.035	0.024
SMPDL3A	0.733	PLEKHF2	0.692	0.857	0.014	0.021
JKAMP	0.554	PTGER2	0.616	0.731	0.047	0.032
SLC1A3	0.807	EFCAB2	0.772	0.902	0.046	0.008
SLC1A3	0.807	PPP1R2_PPP1R2P3	0.739	0.869	0.04	0.026
TCN1	0.726	FGFBP2	0.696	0.809	0.04	0.049
TCN1	0.726	PMS2CL_PMS2	0.581	0.79	0.024	0.006
TCN1	0.726	MYL9	0.6	0.777	0.05	0.033
ODZ1	0.733	HIST1H4E	0.678	0.825	0.02	0.025
KPNA5	0.845	SLC39A9	0.736	0.898	0.03	0.012
KPNA5	0.845	SFRS9	0.798	0.917	0.003	0.044
KPNA5	0.845	C4orf3	0.776	0.947	0.006	0.002
CD63	0.722	AGTRAP	0.569	0.82	0.025	0.004
CD63	0.722	TRIM21	0.779	0.863	0.022	0.044
CD63	0.722	ZNF28	0.797	0.873	0.007	0.034
CD63	0.722	LY6G5B_CSNK2B	0.737	0.856	0.015	0.048
CD63	0.722	NA	0.838	0.917	0.002	0.029
CD63	0.722	KDM6B_TMEM88	0.695	0.851	0.01	0.014
DDAH2	0.681	HIST1H4E	0.678	0.832	0.016	0.012
DDAH2	0.681	EFCAB2	0.772	0.851	0.028	0.017
DDAH2	0.681	AGTRAP	0.569	0.793	0.008	0.023
DDAH2	0.681	KDM6B_TMEM88	0.695	0.833	0.003	0.05
DDAH2	0.681	PLEKHF2	0.692	0.837	0.018	0.01
DDAH2	0.681	AIF1	0.719	0.822	0.021	0.044
ATP13A3	0.664	PLEKHF2	0.692	0.833	0.004	0.021
ITK	0.736	HDHD1A	0.647	0.812	0.037	0.022

ITK	0.736	TSHZ2	0.529	0.842	0.037	0
HIST1H4E	0.678	PPP2R5A_SNORA16	0.673	0.811	0.017	0.036
HIST1H4E	0.678	FOLR3_FOLR2	0.691	0.806	0.044	0.013
HIST1H4E	0.678	LGALS1	0.643	0.816	0.005	0.03
HIST1H4E	0.678	MTHFS	0.649	0.788	0.036	0.043
HIST1H4E	0.678	AP3B2	0.722	0.822	0.027	0.026
HIST1H4E	0.678	GSTO1	0.604	0.811	0.043	0.003
HIST1H4E	0.678	RETN	0.756	0.857	0.008	0.046
HIST1H4E	0.678	CD151	0.582	0.786	0.047	0.004
HIST1H4E	0.678	C4orf3	0.776	0.905	0	0.048
HIST1H4E	0.678	CDC26	0.519	0.792	0.018	0.001
FGFBP2	0.696	MKI67	0.667	0.793	0.032	0.045
ECHDC3	0.702	PLEKHF2	0.692	0.818	0.046	0.025
ECHDC3	0.702	CALM2_C2orf61	0.687	0.834	0.023	0.017
HSPC159	0.612	MINPP1	0.78	0.842	0.002	0.026
OLAH	0.723	DPH3	0.536	0.767	0.046	0.015
PPP2R5A_SNORA16	0.673	CENPK	0.752	0.851	0.025	0.004
PPP2R5A_SNORA16	0.673	MINPP1	0.78	0.846	0.014	0.03
PPP2R5A_SNORA16	0.673	PLEKHF2	0.692	0.849	0.012	0.003
PPP2R5A_SNORA16	0.673	CALM2_C2orf61	0.687	0.845	0.011	0.005
SEC24A_SAR1B	0.716	PLEKHF2	0.692	0.834	0.04	0.006
SLC39A9	0.736	NA	0.808	0.882	0.019	0.044
SLC39A9	0.736	ZNF28	0.797	0.896	0.019	0.003
SLC39A9	0.736	NA	0.838	0.91	0.006	0.016
SLC39A9	0.736	ZNF587_ZNF417	0.842	0.933	0.003	0.01
SLC39A9	0.736	ATP6V0D1_LOC100	0.701	0.846	0.017	0.031
SLC39A9	0.736	ATP5L_ATP5L2	0.786	0.882	0.03	0.006
EXOSC4	0.723	EFCAB2	0.772	0.856	0.043	0.04
EXOSC4	0.723	AGTRAP	0.569	0.791	0.035	0.023

EXOSC4	0.723	PLEKHF2	0.692	0.849	0.03	0.008
NA	0.808	C4orf3	0.776	0.899	0.026	0.029
HIST1H4L	0.596	CD24	0.721	0.807	0.01	0.032
LGALS1	0.643	CENPK	0.752	0.811	0.044	0.032
LGALS1	0.643	ZNF28	0.797	0.875	0.002	0.022
LGALS1	0.643	AIF1	0.719	0.844	0.012	0.002
PPIF	0.704	SRXN1	0.7	0.813	0.033	0.048
MTHFS	0.649	EFCAB2	0.772	0.825	0.034	0.047
MTHFS	0.649	PLEKHF2	0.692	0.813	0.026	0.025
MTHFS	0.649	CALM2_C2orf61	0.687	0.816	0.015	0.017
LCN2	0.679	PMS2CL_PMS2	0.581	0.745	0.032	0.047
AP3B2	0.722	AGTRAP	0.569	0.788	0.035	0.019
AP3B2	0.722	RRP12_LOC644215	0.569	0.781	0.047	0.023
AP3B2	0.722	AIF1	0.719	0.843	0.013	0.04
EFCAB2	0.772	RETN	0.756	0.867	0.029	0.044
EFCAB2	0.772	GALNT2	0.674	0.848	0.023	0.017
HIST1H2AA	0.769	DLEU2_DLEU2L	0.782	0.908	0.013	0.002
HIST1H3A	0.642	CD24	0.721	0.82	0.028	0.01
C22orf37	0.725	C4orf3	0.776	0.864	0.027	0.042
SLC39A8	0.646	PLEKHF2	0.692	0.832	0.005	0.022
SLC39A8	0.646	CALM2_C2orf61	0.687	0.794	0.019	0.047
AREG	0.668	CENPK	0.752	0.815	0.05	0.042
PTGER2	0.616	PLEKHF2	0.692	0.808	0.005	0.044
PMS2CL_PMS2	0.581	FSD1L_GARNL1	0.595	0.728	0.048	0.025
RETN	0.756	KDM6B_TMEM88	0.695	0.852	0.026	0.022
RETN	0.756	AIF1	0.719	0.856	0.026	0.019
PDE3B	0.582	CENPK	0.752	0.82	0.006	0.025
PDE3B	0.582	CALM2_C2orf61	0.687	0.81	0.003	0.041
CENPK	0.752	HDHD1A	0.647	0.816	0.037	0.036

CD24	0.721	HIST1H3C	0.558	0.82	0.036	0.001
CD24	0.721	MYL9	0.6	0.777	0.05	0.042
HDHD1A	0.647	MGST3	0.647	0.802	0.016	0.023
LRRFIP1	0.744	ZNF587_ZNF417	0.842	0.926	0.002	0.049
LRRFIP1	0.744	PPP1R2_PPP1R2P3	0.739	0.869	0.015	0.022
LRRFIP1	0.744	CALM2_C2orf61	0.687	0.881	0.011	0.001
SFRS9	0.798	NA	0.838	0.92	0.028	0.007
SFRS9	0.798	ZNF587_ZNF417	0.842	0.93	0.034	0.009
SFRS9	0.798	PLEKHA3	0.794	0.896	0.047	0.03
MINPP1	0.78	C4orf3	0.776	0.914	0.001	0.033
ZNF28	0.797	C4orf3	0.776	0.915	0.005	0.011
TAF13	0.585	FSD1L_GARNL1	0.595	0.776	0.016	0.012
THBS1	0.619	POLE2	0.708	0.773	0.026	0.039
HIST1H3B	0.488	HIST1H3C	0.558	0.732	0.008	0.015
ZRANB1	0.521	RFESD_SPATA9	0.697	0.761	0.003	0.043
FSD1L_GARNL1	0.595	RFESD_SPATA9	0.697	0.793	0.011	0.047
NA	0.838	C4orf3	0.776	0.915	0.012	0.013
UBE2F_C20orf194	0.622	POLE2	0.708	0.804	0.039	0.009
ZNF587_ZNF417	0.842	C4orf3	0.776	0.916	0.038	0.018
C4orf3	0.776	PLEKHA3	0.794	0.924	0.003	0.009
C4orf3	0.776	PLEKHF2	0.692	0.911	0.029	0
C4orf3	0.776	ATP6V0D1_LOC100	0.701	0.854	0.049	0.032
C4orf3	0.776	ATP5L_ATP5L2	0.786	0.905	0.019	0.004

Table 21

Ratios Severe ipSIRS Versus Shock ipSIRS

Gene 1 Name	Gene 1 AUC	Gene 2 Name	Gene 2 AUC	Ratio AUC	Ratio Signif to Gene 1	Ratio Signif to Gene 2
ACER3	0.724	GSR	0.554	0.804	0.014	0.027
ACER3	0.724	MTRR	0.552	0.842	0.017	0.001
CAMK4	0.777	PTGER2	0.653	0.841	0.036	0.014
GSR	0.554	SH3PXD2B	0.676	0.77	0.013	0.032
PICALM	0.612	SYNE2	0.678	0.799	0.029	0.05
SLC15A2	0.619	CCR4	0.693	0.797	0.041	0.038
TMEM144_LOC2855	0.578	PLIN2	0.434	0.652	0.028	0.048
MKI67	0.671	RETN	0.664	0.82	0.022	0.047
MME	0.671	CFD	0.554	0.767	0.022	0.036

[0294] Throughout this specification and claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers or steps but not the exclusion of any other integer or group of integers.

[0295] Persons skilled in the art will appreciate that numerous variations and modifications will become apparent. All such variations and modifications, which become apparent to persons skilled in the art, should be considered to fall within the spirit and scope that the invention broadly appearing before described.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1) Apparatus for identifying biomarkers, the apparatus including an electronic processing device that:
   a) uses reference data from a plurality of individuals to define a number of groups of individuals, the reference data including measurements of the activity of a plurality of reference biomarkers;
   b) uses a plurality of analysis techniques to identify a number of potential biomarkers from the plurality of reference biomarkers that are potentially useful for distinguishing the groups of individuals, allowing the potential biomarkers to be used in generating signatures for use in clinical assessments.
2) Apparatus according to claim 1, wherein the electronic processing device, for each analysis technique:
   a) using the analysis technique, identifies a number of reference biomarkers that best distinguish the groups of individuals;
   b) determines if the predictive performance of the identified reference biomarkers exceeds a predetermined threshold; and,
   c) in response to a successful determination, determines the identified reference biomarkers to be potential biomarkers.
3) Apparatus according to claim 2, wherein the number of reference biomarkers is at least one of:
   a) less than 10;
   b) more than 1;
   c) between 2 and 8; and,
   d) 5.
4) Apparatus according to claim 2 or claim 3, wherein the predetermined threshold is at least one of:
   a) at least 90%;
   b) at least 85%; and,
   c) at least 80%.
5) Apparatus according to any one of the claims 1 to 4, wherein the electronic processing device:
   a) adds potential biomarkers to a potential biomarker collection; and,
   b) removes the potential biomarkers from a reference biomarker collection.
6) Apparatus according to any one of the claims 1 to 5, wherein for each of a plurality of analysis techniques the electronic processing device repeatedly identifies reference biomarkers as potential biomarkers until the predictive performance of the identified reference biomarkers falls below the predetermined threshold.
7) Apparatus according to any of the claims 1 to 6, wherein the electronic processing device iteratively identifies potential biomarkers.

8) Apparatus according to any one of the claims 1 to 7, wherein the electronic processing device uses a number of iterations including at least one of:
   a) at least 100;
   b) at least 500;
   c) at least 1000;
   d) at least 2000; and,
   e) at least 5000.
9) Apparatus according to any one of the claims 1 to 8, wherein the electronic processing device repeatedly determines potential biomarkers until a predetermined number of potential biomarkers are identified.
10) Apparatus according to claim 9, wherein the predetermined number of potential biomarkers includes at least one of:
   a) at least 100;
   b) less than 500;
   c) about 200.
11) Apparatus according to any one of the claims 1 to 10, wherein the analysis techniques include at least one of:
   a) regression techniques;
   b) correlation analysis; and,
   c) a combination of regression and correlation techniques.
12) Apparatus according to any one of the claims 1 to 12, wherein the analysis techniques include:
   a) sparse PLS;
   b) random forest; and,
   c) support vector machines.
13) Apparatus according to any one of the claims 1 to 12, wherein the electronic processing device:
   a) removes a validation subgroup from the reference data prior to determining the potential biomarkers;
   b) determines the potential biomarkers using the reference data without the validation subgroup; and,
   c) uses the validation subgroup to validate at least one of:
      i) the potential biomarkers; and,
      ii) signatures including a number of the potential biomarkers.
14) Apparatus according to any one of the claims 1 to 13, wherein the processing system determines the number of groups by classifying the individuals using at least one of:
   a) an indication of a presence, absence, degree, stage or progression of a condition;
   b) phenotypic traits associated with the individuals;
   c) genetic information associated with the individuals;

d) biomarkers associated with the individuals.

15) Apparatus according to any one of the claims 1 to 14, wherein the processing system determines groups at least in part using input commands from a user.

16) Apparatus according to any one of the claims 1 to 15, wherein the reference data includes time series data indicative of the progression of a condition.

17) Apparatus according to claim 16, wherein the time series data is indicative of whether a condition that is at least one of:

a) improving;

b) worsening; and,

c) static.

18) Apparatus according to any one of the claims 1 to 17, wherein the reference data includes for each of the individuals an indication of at least one of:

a) an activity of each of the reference biomarkers;

b) a degree of a condition;

c) a stage of a condition

d) a presence of a condition;

e) an absence of a condition;

f) an indication of a condition progression;

g) phenotypic information;

h) genetic information; and,

i) a SOFA score.

19) Apparatus according to any one of the claims 1 to 18, wherein the electronic processing device identifies a number of potential biomarkers for use as signature biomarkers, the signature biomarkers being used in generating the signatures.

20) Apparatus according to claim 19, wherein the electronic processing device:

a) determines a clinical assessment; and,

b) identifies the signature biomarkers for the clinical assessment.

21) Apparatus according to any one of the claims 1 to 20, wherein the electronic processing device:

a) determines second groups of individuals relevant to the clinical assessment;

b) using a second analysis technique, identifies a number of the potential biomarkers that best distinguish the second groups of individuals;

c) determines if the predictive performance of the identified potential biomarkers exceeds a predetermined threshold; and,

d) in response to a successful determination, determines the identified potential biomarkers to be signature biomarkers.

22) Apparatus according to claim 21, wherein the electronic processing device, in response to an unsuccessful determination:

a) modifies parameters of the second analysis technique; and,

b) uses the second analysis technique to identify alternative potential biomarkers.

23) Apparatus according to claim 21 or claim 22, wherein the electronic processing device:
   a) determines if the identified potential biomarkers are to be excluded; and,
   b) in response to a successful determination:
      i) removes the potential biomarkers from a potential biomarker database; and,
      ii) uses the second analysis technique to identify alternative potential biomarkers for use as signature biomarkers.

24) Apparatus according to any one of the claims 21 to 23, wherein the second analysis technique includes at least one of:
   a) ordinal regression and,
   b) support vector machines.

25) Apparatus according to any one of the claims 1 to 24, wherein the signatures are indicative of:
   a) activities of each of a number of signature biomarkers; and,
   b) at least one of:
      i) a SOFA score; and,
      ii) a presence, absence, degree, stage or progression of a condition.

26) Apparatus according to any one of the claims 1 to 25, wherein the signatures are indicative of a presence, absence, degree, stage or progression of at least one of:
   a) infection-negative SIRS; and,
   b) infection-positive SIRS.

27) Apparatus according to any one of the claims 1 to 26, wherein activities of at least some of the potential biomarkers are indicative of at least one of:
   a) a presence, absence, degree, stage or progression of SIRS;
   b) a healthy diagnosis;
   c) a presence, absence, degree, stage, or progression of infection positive SIRS; and,
   d) a presence, absence, degree, stage or progression of infection negative SIRS.

28) Apparatus according to any one of the claims 1 to 27, wherein an activity of biomarkers are indicative of a level or abundance of a molecule selected from one or more of :
   a) A nucleic acid molecule;
   b) A proteinaceous molecule;
   c) An amino acid
   d) A carbohydrate;
   e) A lipid;
   f) A steroid;
   g) An inorganic molecule;
   h) An ion;
   i) A drug;
   j) A chemical;

k) A metabolite;
l) A toxin;
m) A nutrient;
n) A gas;
o) A cell;
p) A pathogenic organism; and,
q) A non-pathogenic organism.

29) A method for determining the likelihood of the presence or absence of a condition selected from a healthy condition (e.g., a normal condition or one in which inSIRS and inSIRS are absent), SIRS generally (i.e., not distinguishing between inSIRS or ipSIRS), inSIRS or ipSIRS, or to assess the likelihood of the presence, absence or risk of development of a stage of ipSIRS (e.g., a stage of ipSIRS with a particular severity), the method comprising: (1) correlating a reference IRS biomarker profile with the presence or absence, or degree of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; (2) obtaining an IRS biomarker profile of a sample from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile, wherein an individual IRS biomarker is an expression product of an IRS biomarker gene selected from the group consisting of: TLR5; CD177; VNN1; UBE2J1; IMP3; RNASE2//LOC643332; CLEC4D; C3AR1; GPR56; ARG1; FCGR1A//FCGR1B//FCGR1C; C11orf82; FAR2; GNLY; GALNT3; OMG; SLC37A3; BMX//HNRPDL; STOM; TDRD9; KREMEN1; FAIM3; CLEC4E; IL18R1; ACER3; ERLIN1; TGFBR1; FKBP5//LOC285847; GPR84; C7orf53; PLB1; DSE; PTGDR; CAMK4; DNAJC13; TNFAIP6; FOXD4L3//FOXD4L6//FOXD4//FOXD4L1//FOXD4L2//FOXD4L4//FOXD4L5; MMP9//LOC100128028; GSR; KLRF1; SH2D1B; ANKRD34B; SGMS2; B3GNT5//MCF2L2; GK3P//GK; PFKFB2; PICALM; METTL7B; HIST1H4C; C9orf72; HIST1H3I; SLC15A2; TLR10; ADM; CD274; CRIP1; LRRN3; HLA-DPB1; VAMP2; SMPDL3A; IFI16; JKAMP; MRPL41; SLC1A3; OLFM4; CASS4; TCN1; WSB2; CLU; ODZ1; KPNA5; PLAC8; CD63; HPSE; C1orf161; DDAH2; KLRK1//KLRC4; ATP13A3; ITK; PMAIP1; LOC284757; GOT2; PDGFC; B3GAT3; HIST1H4E; HPGD; FGFBP2; LRRC70//IPO11; TMEM144//LOC285505; CDS2; BPI; ECHDC3; CCR3; HSPC159; OLAH; PPP2R5A//SNORA16B; TMTC1; EAF2//HCG11//LOC647979; RCBTB2//LOC100131993; SEC24A//SAR1B; SH3PXD2B; HMGB2; KLRD1; CHI3L1; FRMD3; SLC39A9; GIMAP7; ANAPC11; EXOSC4; gene for IL-1beta-regulated neutrophil survival protein as set forth in GenBank Accession No. AF234262; INSIG1; FOLR3//FOLR2; RUNX2; PRR13//PCBP2; HIST1H4L; LGALS1; CCR1; TPST1; HLA-DRA;

CD163; FFAR2; PHOSPHO1; PPIF; MTHFS; DNAJC9//FAM149B1//RPL26; LCN2; EIF2AK2; LGALS2; SIAE; AP3B2; ABCA13; gene for transcript set forth in GenBank Accession No. AK098012; EFCAB2; HIST1H2AA; HINT1; HIST1H3J; CDA; SAP30; AGTRAP; SUCNR1; MTRR; PLA2G7; AIG1; PCOLCE2; GAB2; HS2ST1//UBA2; HIST1H3A; C22orf37; HLA-DPA1; VOPP1//LOC100128019; SLC39A8; MKI67; SLC11A1; AREG; ABCA1; DAAM2//LOC100131657; LTF; TREML1; GSTO1; PTGER2; CEACAM8; CLEC4A; PMS2CL//PMS2; RETN; PDE3B; SULF2; NEK6//LOC100129034; CENPK; TRAF3; GPR65; IRF4; MACF1; AMFR; RPL17//SNORD58B; IRS2; JUP; CD24; GALNT2; HSP90AB1//HSP90AB3P//HSP90AB2P; GLT25D1; OR9A2; HDHD1A; ACTA2; ACPL2; LRRFIP1; KCNMA1; OCR1; ITGA4//CERKL; EIF1AX//SCARNA9L//EIF1AP1; SFRS9; DPH3; ERGIC1; CD300A; NF-E4; MINPP1; TRIM21; ZNF28; NPCDR1; gene for protein FLJ21394 as set forth in GenBank Accession No. BC013935; gene for transcript set forth in GenBank Accession No. AK000992; ICAM1; TAF13; P4HA1//RPL17; C15orf54; KLHL5; HAL; DLEU2//DLEU2L; ANKRD28; LY6G5B//CSNK2B; KIAA1257//ACAD9//LOC100132731; MGST3; KIAA0746; HSPB1//HSPBL2; CCR4; TYMS; RRP12//LOC644215; CCDC125; HIST1H2BM; PDK4; ABCG1; IL1B; THBS1; ITGA2B; LHFP; LAIR1//LAIR2; HIST1H3B; ZRANB1; TIMM10; FSD1L//GARNL1; HIST1H2AJ//HIST1H2AI; PTGS1; gene for transcript set forth in GenBank Accession No. BC008667; UBE2F//C20orf194//SCLY; HIST1H3C; FAM118A; CCRL2; E2F6; MPZL3; SRXN1; CD151; HIST1H3H; FSD1L; RFESD//SPATA9; TPX2; S100B; ZNF587//ZNF417; PYHIN1; KIAA1324; CEACAM6//CEACAM5; APOLD1; FABP2; KDM6B//TMEM88; IGK@//IGKC//IGKV1-5//IGKV3D-11//IGKV3-20//IGKV3D-15//LOC440871//LOC652493//LOC100291464//LOC652694//IGKV3-15//LOC650405//LOC100291682; MYL9; HIST1H2BJ; TAAR1; CLC; CYP4F3//CYP4F2; CEP97; SON; IRF1; SYNE2; MME; LASS4; DEFA4//DEFA8P; C7orf58; DYNLL1; gene for transcript set forth in GenBank Accession No. AY461701; MPO; CPM; TSHZ2; PLIN2; FAM118B; B4GALT3; RASA4//RASA4P//RASA4B//POLR2J4//LOC100132214; CTSL1//CTSLL3; NP; ATF7; SPARC; PLB1; C4orf3; POLE2; TNFRSF17; FBXL13; PLEKHA3; TMEM62//SPCS2//LOC653566; RBP7; PLEKHF2; RGS2; ATP6V0D1//LOC100132855; RPIA; CAMK1D; IL1RL1; CMTM5; AIF1; CFD; MPZL2; LOC100128751; IGJ; CDC26; PPP1R2//PPP1R2P3; IL5RA; ARL17P1//ARL17; ATP5L//ATP5L2; TAS2R31; HIST2H2BF//HIST2H3D; CALM2//C2orf61; SPATA6; IGLV6-57; C1orf128; KRTAP15-1; IFI44; IGL@//IGLV1-44//LOC96610//IGLV2-23//IGLC1//IGLV2-18//IGLV5-45//IGLV3-25//IGLV3-12//IGLV1-36//IGLV3-27//IGLV7-46//IGLV4-3//IGLV3-16//IGLV3-19//IGLV7-43//IGLV3-22//IGLV5-37//IGLV10-54//IGLV8-61//LOC651536; gene for transcript set forth in GenBank Accession No. BC034024; SDHC; NFXL1; GLDC; DCTN5; and KIAA0101//CSNK1G1

30) A method according to claim 29, wherein the method determines the likelihood that SIRS or a healthy condition is present or absent in the subject, and wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with

the presence or absence of SIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from CD177, CLEC4D, BMX, VNN1, GPR84, ARG1, IL18R1, ERLIN1, IMP3, TLR5, UBE2J1, GPR56, FCGR1A, SLC1A3, SLC37A3, FAIM3, C3AR1, RNASE2, TNFAIP6, GNLY, OMG, FAR2, OLAH, CAMK4, METTL7B, B3GNT5, CLEC4E, MMP9, KREMEN1, GALNT3, PTGDR, TDRD9, GK3P, FKBP5, STOM, SMPDL3A, PFKFB2, ANKRD34B, SGMS2, DNAJC13, LRRN3, SH2D1B, C1orf161, HIST1H4C, IFI16, ACER3, PLB1, C9orf72, HMGB2, KLRK1, C7orf53, GOT2, TCN1, DSE, CCR3, CRIP1, ITK, KLRF1, TGFBR1, GSR, HIST1H4E, HPGD, FRMD3, ABCA13, C11orf82, PPP2R5A, BPI, CASS4, AP3B2, ODZ1, TMTC1, ADM, FGFBP2, HSPC159, HLA-DRA, HIST1H3I, TMEM144, MRPL41, FOLR3, PICALM, SH3PXD2B, DDAH2, HLA-DPB1, KPNA5, PHOSPHO1, TPST1, EIF2AK2, OR9A2, OLFM4, CD163, CDA, CHI3L1, MTHFS, CLU, ANAPC11, JUP, PMAIP1, GIMAP7, KLRD1, CCR1, CD274, EFCAB2, SUCNR1, KCNMA1, LGALS2, SLC11A1, FOXD4L3, VAMP2, ITGA4, LHFP, PRR13, FFAR2, B3GAT3, EAF2, HPSE, CLC, TLR10, CCR4, HIST1H3A, CENPK, DPH3, HLA-DPA1, ATP13A3, DNAJC9, S100B, HIST1H3J, 110, RPL17, C15orf54, LRRC70, IL5RA, PLA2G7, ECHDC3, HINT1, LCN2, PPIF, SLC15A2, PMS2CL, HIST1H2AA, CEACAM8, HSP90AB1, ABCG1, PDGFC, NPCDR1, PDK4, GAB2, WSB2, FAM118A, JKAMP, TREML1, PYHIN1, IRF4, ABCA1, DAAM2, ACPL2, RCBTB2, SAP30, THBS1, PCOLCE2, GPR65, NF-E4, LTF, LASS4, B4GALT3, RETN, TIMM10, IL1B, CLEC4A, SEC24A, RUNX2, LRRFIP1, CFD, EIF1AX, ZRANB1, SULF2, EXOSC4, CCDC125, LOC284757, ANKRD28, HIST1H2AJ, CD63, PLIN2, SON, HIST1H4L, KRTAP15-1, DLEU2, MYL9, FABP2, CD24, MACF1, GSTO1, RRP12, AIG1, RASA4, FBXL13, PDE3B, CCRL2, C1orf128, E2F6, IL1RL1, CEACAM6, CYP4F3, 199, TAAR1, TSHZ2, PLB1, UBE2F; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and (3) determining a likelihood of the subject having or not having the healthy condition or SIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

31) A method according to claim 29, wherein the method determines the likelihood that inSIRS, ipSIRS or a healthy condition is present or absent in the subject, and wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS, ipSIRS or the healthy condition, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, B3GAT3, CD300A, OCR1, PTGER2, LGALS1, HIST1H4L, AMFR, SIAE, SLC39A8, TGFBR1, GAB2, MRPL41, TYMS, HIST1H3B, MPZL3, KIAA1257, OMG, HIST1H2BM, TDRD9, C22orf37, GALNT3, SYNE2, MGST3, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, HSPB1, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, KREMEN1, IRS2, APOLD1, RBP7, DNAJC13, ERGIC1, FSD1L, TLR5, TMEM62, SDHC, C9orf72, NP, KIAA0746, PMAIP1, DSE, SMPDL3A,

DNAJC9, HIST1H3H, CDC26, CRIP1, FAR2, FRMD3, RGS2, METTL7B, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, IRF1, C7orf53, IGK@, RNASE2, FCGR1A, SAP30, PMS2CL, SLC11A1, AREG, PLB1, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, CPM, CCDC125, GPR56, PPP1R2, 110, ACPL2, HIST1H3A, C7orf58, IRF4, ANAPC11, HIST1H3J, KLRD1, GPR84, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, HSP90AB1, HPGD, IFI16, CD177, TAS2R31, CD163, B4GALT3, EIF1AX, CYP4F3, HIST1H2AA, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided).; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS, ipSIRS or a healthy condition the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile.

32) A method according to claim 29, wherein the method determines the likelihood that inSIRS or ipSIRS is present or absent in the subject, and wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having inSIRS or ipSIRS, wherein the reference biomarker profile evaluates at least one IRS biomarker selected from C11orf82, PLAC8, 132, INSIG1, CDS2, VOPP1, SLC39A9, FOXD4L3, WSB2, CD63, CD274, B3GAT3, CD300A, OCR1, JKAMP, TLR10, PTGER2, PDGFC, LGALS1, HIST1H4L, AGTRAP, AMFR, SIAE, 200, SLC15A2, SLC39A8, TGFBR1, DDAH2, HPSE, SUCNR1, MTRR, GAB2, P4HA1, HS2ST1, MRPL41, TYMS, RUNX2, GSTO1, LRRC70, HIST1H3B, RCBTB2, MPZL3, KIAA1257, AIG1, NEK6, OMG, HIST1H2BM, TDRD9, GALNT3, ATP13A3, C22orf37, SYNE2, ADM, MGST3, PDE3B, HIST1H3I, LOC284757, TRAF3, HIST1H3C, STOM, KLHL5, EXOSC4, C3AR1, KIAA0101, TNFRSF17, HAL, UBE2J1, GLT25D1, CD151, TPX2, PCOLCE2, HSPB1, EAF2, IMP3, PICALM, ACER3, IGL@, HIST1H2BJ, CASS4, ACTA2, PTGS1, KREMEN1, IRS2, TAF13, FSD1L, APOLD1, RBP7, DNAJC13, SEC24A, ERGIC1, FSD1L, TLR5, MKI67, TMEM62, CLEC4A, SDHC, C9orf72, NP, CLU, ABCA1, KIAA0746, PMAIP1, DSE, CMTM5, SMPDL3A, DNAJC9, HDHD1A, HIST1H3H, CDC26, ICAM1, LOC100128751, FAR2, CRIP1, MPZL2, FRMD3, CTSL1, METTL7B, RGS2, CLEC4E, MME, ABCA13, PRR13, HIST1H4C, RRP12, GLDC, ECHDC3, ITGA2B, C7orf53, IRF1, 268, IGK@, RNASE2, FCGR1A, UBE2F, SAP30, LAIR1, PMS2CL, SLC11A1, PLB1, AREG, PPIF, GSR, NFXL1, AP3B2, DCTN5, RPL17, PLA2G7, GALNT2, IGLV6-57, KLRF1, CHI3L1, ANKRD34B, OLFM4, 199, CPM, CCDC125, SULF2, LTF, GPR56, MACF1, PPP1R2, DYNLL1, LCN2, FFAR2, SFRS9, IGJ, FAM118B, 110, ACPL2, HIST1H3A, C7orf58, ANAPC11, HIST1H3J, IRF4, MPO, TREML1, KLRD1, GPR84, CCRL2, CAMK1D, CCR1, ZRANB1, KDM6B, TPST1, HINT1, DAAM2, PTGDR, FKBP5, CD24, HSP90AB1, HPGD, CEACAM8, DEFA4, IL1B, IFI16, CD177, KIAA1324, SRXN1, TAS2R31, CEACAM6, CD163, B4GALT3, ANKRD28, TAAR1, EIF1AX, CYP4F3, 314, HIST1H2AA, LY6G5B, LASS4 (where if a gene name is not provided then a SEQ ID NO. is provided); (2)

obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having inSIRS or ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

33) A method according to claim 29, wherein the method determines the likelihood that a stage of ipSIRS selected from mild sepsis, severe sepsis and septic shock is present or absent the subject, and wherein the method comprises: 1) providing a correlation of a reference IRS biomarker profile with the likelihood of having or not having the stage of ipSIRS, wherein the reference biomarker IRS biomarker profile evaluates at least one IRS biomarker selected from PLEKHA3, PLEKHF2, 232, SFRS9, ZNF587, KPNA5, LOC284757, GPR65, VAMP2, SLC1A3, ITK, ATF7, ZNF28, AIF1, MINPP1, GIMAP7, MKI67, IRF4, TSHZ2, HLA-DPB1, EFCAB2, POLE2, FAIM3, 110, CAMK4, TRIM21, IFI44, CENPK, ATP5L, GPR56, HLA-DPA1, C4orf3, GSR, GNLY, RFESD, BPI, HIST1H2AA, NF-E4, CALM2, EIF1AX, E2F6, ARL17P1, TLR5, SH3PXD2B, FAM118A, RETN, PMAIP1, DNAJC9, PCOLCE2, TPX2, BMX, LRRFIP1, DLEU2, JKAMP, JUP, ABCG1, SLC39A9, B3GNT5, ACER3, LRRC70, NPCDR1, TYMS, HLA-DRA, TDRD9, FSD1L, FAR2, C7orf53, PPP1R2, SGMS2, EXOSC4, TGFBR1, CD24, TCN1, TAF13, AP3B2, CD63, SLC15A2, IL18R1, ATP6V0D1, SON, HSP90AB1, CEACAM8, SMPDL3A, IMP3, SEC24A, PICALM, 199, CEACAM6, CYP4F3, OLAH, ECHDC3, ODZ1, KIAA0746, KIAA1324, HINT1, VNN1, C22orf37, FSD1L, FOLR3, IL1RL1, OMG, MTHFS, OLFM4, S100B, ITGA4, KLRD1, SLC39A8, KLHL5, KLRK1, MPO, PPIF, GOT2, LRRN3, HIST1H2AJ, CLU, LCN2, 132, CEP97, KLRF1, FBXL13, HIST1H3B, ANKRD34B, RPIA, HPGD, HIST2H2BF, GK3P (where if a gene name is not provided then a SEQ ID NO. is provided). ; (2) obtaining a sample IRS biomarker profile from the subject, which evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and (3) determining a likelihood of the subject having or not having the stage of ipSIRS based on the sample IRS biomarker profile and the reference IRS biomarker profile.

34) A method according to any one of claims 29 to 33, wherein an individual IRS biomarker is selected from the group consisting of: (a) a polynucleotide expression product comprising a nucleotide sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1-319, or a complement thereof; (b) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; (c) a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with at least a portion of the sequence set forth in SEQ ID NO: 320-619; (d) a polynucleotide expression product comprising a nucleotide sequence that hybridizes to the sequence

of (a), (b), (c) or a complement thereof, under medium or high stringency conditions; (e) a polypeptide expression product comprising the amino acid sequence set forth in any one of SEQ ID NO: 320-619; and (f) a polypeptide expression product comprising an amino acid sequence that shares at least 70% (or at least 71% to at least 99% and all integer percentages in between) sequence similarity or identity with the sequence set forth in any one of SEQ ID NO: 320-619.

35) A method according to any one of claims 29 to 34, wherein evaluation of the IRS markers includes determining the levels of individual IRS markers.

36) A method according to claim 35, comprising comparing the level of a first IRS biomarker in the sample IRS biomarker profile with the level of a second IRS biomarker in the sample IRS biomarker profile to provide a ratio and determining a likelihood of the presence or absence of the condition based on that ratio.

37) A method according to claim 36, wherein the determination is carried out in the absence of comparing the level of the first or second IRS biomarkers in the sample IRS biomarker profile to the level of a corresponding IRS biomarker in the reference IRS biomarker profile.

38) A method according to claim 36 or claim 37, wherein the first and second IRS biomarkers are selected from the IRS biomarkers listed in Example 6 and Tables 16 – 21.

39) A kit comprising one or more reagents and/or devices for use in performing the method of any one of claims 29 to 38.

40) A method for treating, preventing or inhibiting the development of inSIRS, ipSIRS or a particular stage of ipSIRS in a subject, the method comprising: (1) correlating a reference IRS biomarker profile with the presence or absence of a condition selected from a healthy condition, SIRS, inSIRS, ipSIRS, or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; (2) obtaining an IRS biomarker profile of a sample from a subject, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; (3) determining a likelihood of the subject having or not having the condition based on the sample IRS biomarker profile and the reference IRS biomarker profile, and administering to the subject, on the basis that the subject has an increased likelihood of having inSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of inSIRS, or administering to the subject, on the basis that the subject has an increased likelihood of having ipSIRS or a particular stage of ipSIRS, an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of ipSIRS or the particular stage of ipSIRS.

41) A method of monitoring the efficacy of a particular treatment regimen in a subject towards a desired health state (e.g., healthy condition), the method comprising: (1) providing a correlation of a reference IRS biomarker profile with the likelihood of

having a healthy condition; (2) obtaining a corresponding IRS biomarker profile of a subject having inSIRS, ipSIRS or a particular stage of ipSIRS after treatment with a treatment regimen, wherein a similarity of the subject's IRS biomarker profile after treatment to the reference IRS biomarker profile indicates the likelihood that the treatment regimen is effective for changing the health status of the subject to the desired health state.

42) A method of correlating a reference IRS biomarker profile with an effective treatment regimen for a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker, the method comprising: (a) determining a sample IRS biomarker profile from a subject with the condition prior to treatment, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker; and correlating the sample IRS biomarker profile with a treatment regimen that is effective for treating the condition.

43) A method of determining whether a treatment regimen is effective for treating a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, the method comprising: (a) correlating a reference biomarker profile prior to treatment with an effective treatment regimen for the condition, wherein the reference IRS biomarker profile evaluates at least one IRS biomarker; and (b) obtaining a sample IRS biomarker profile from the subject after treatment, wherein the sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker, and wherein the sample IRS biomarker profile after treatment indicates whether the treatment regimen is effective for treating the condition in the subject.

44) A method of correlating an IRS biomarker profile with a positive or negative response to a treatment regimen, the method comprising: (a) obtaining an IRS biomarker profile from a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS following commencement of the treatment regimen, wherein the IRS biomarker profile evaluates at least one IRS biomarker; and (b) correlating the IRS biomarker profile from the subject with a positive or negative response to the treatment regimen.

45) A method of determining a positive or negative response to a treatment regimen by a subject with a condition selected from inSIRS, ipSIRS or a particular stage of ipSIRS, the method comprising: (a) correlating a reference IRS biomarker profile with a positive or negative response to the treatment regimen, wherein the reference IRS biomarker profile evaluates at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) IRS biomarker; and (b) determining a sample IRS biomarker profile from the subject, wherein the subject's sample IRS biomarker profile evaluates for an individual IRS biomarker in the reference IRS biomarker profile a corresponding IRS biomarker and indicates whether the subject is responding to the treatment regimen.

46) A method according to claim 45, further comprising: determining a first sample IRS biomarker profile from the subject prior to commencing the treatment regimen, wherein the first sample IRS biomarker profile evaluates at least one IRS biomarker; and comparing the first sample IRS biomarker profile with a second sample IRS biomarker profile from the subject after commencement of the treatment regimen, wherein the second sample IRS biomarker profile evaluates for an individual IRS biomarker in the first sample IRS biomarker profile a corresponding IRS biomarker.

47) A method according to any one of claims 1 to 38, wherein the method is performed at least at 2-hour intervals.

48) A method according to any one of claims 1 to 38, wherein the method is performed at least at 4-hour intervals.

49) A kit according to claim 39, which is used at least at 2-hour intervals.

50) A kit according to claim 39, which is used at least at 4-hour intervals.

Figure 1

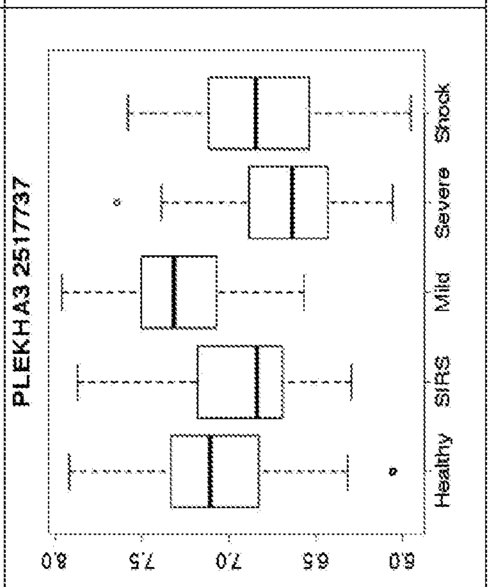
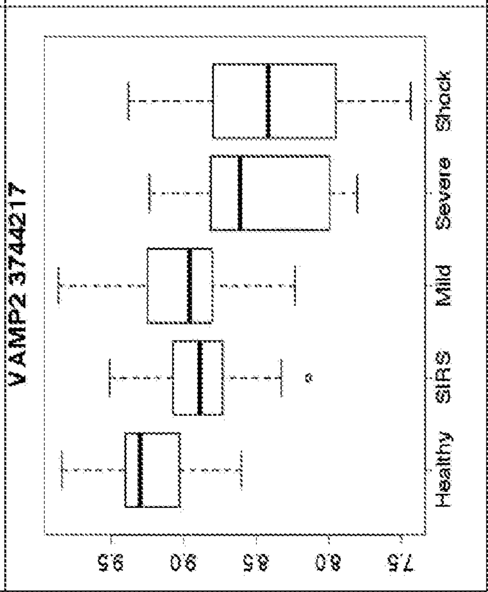


Figure 2



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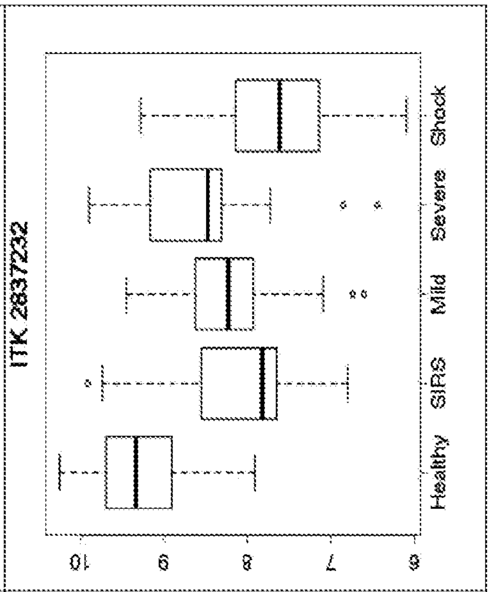

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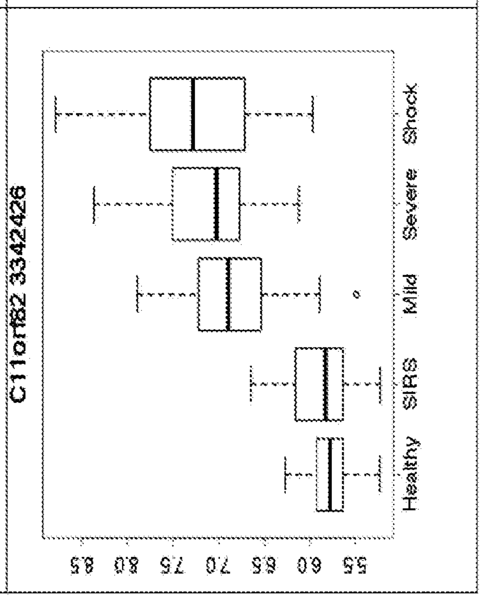

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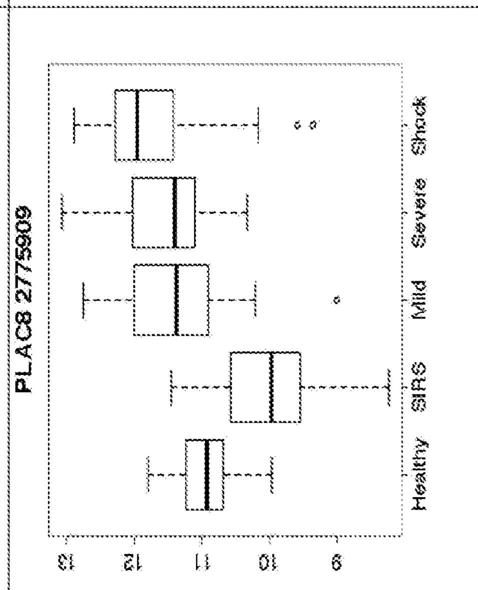
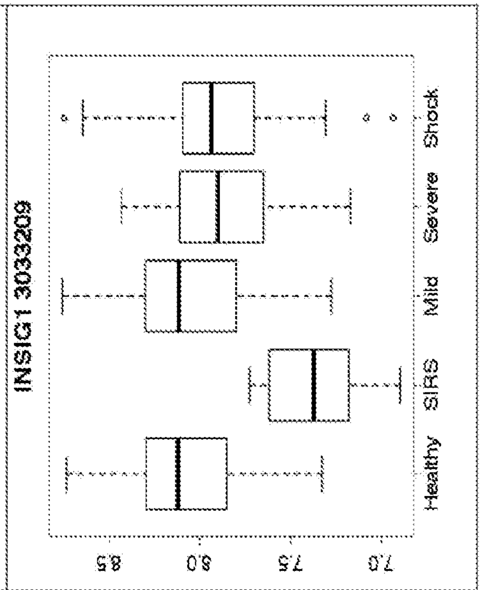


Figure 6



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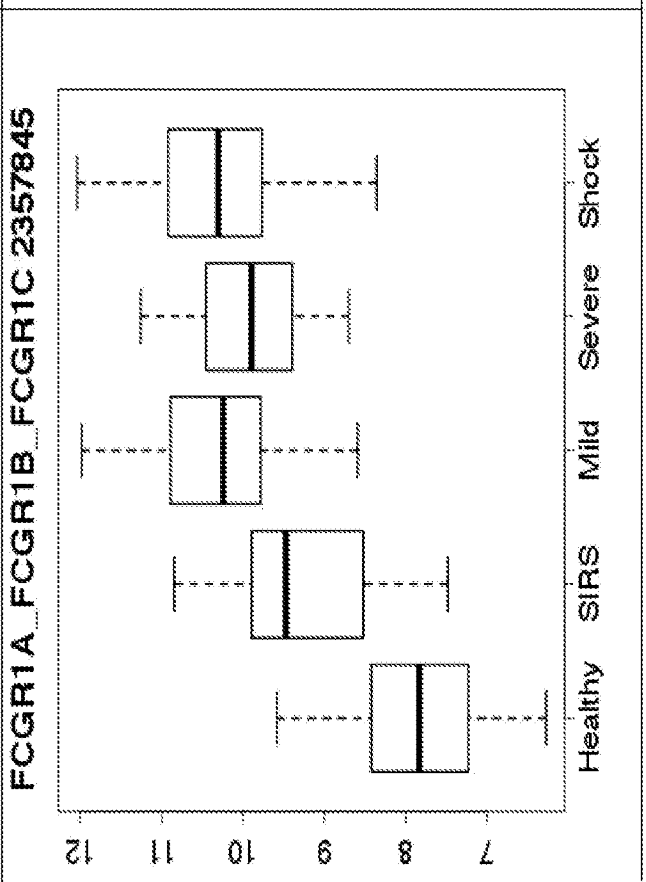
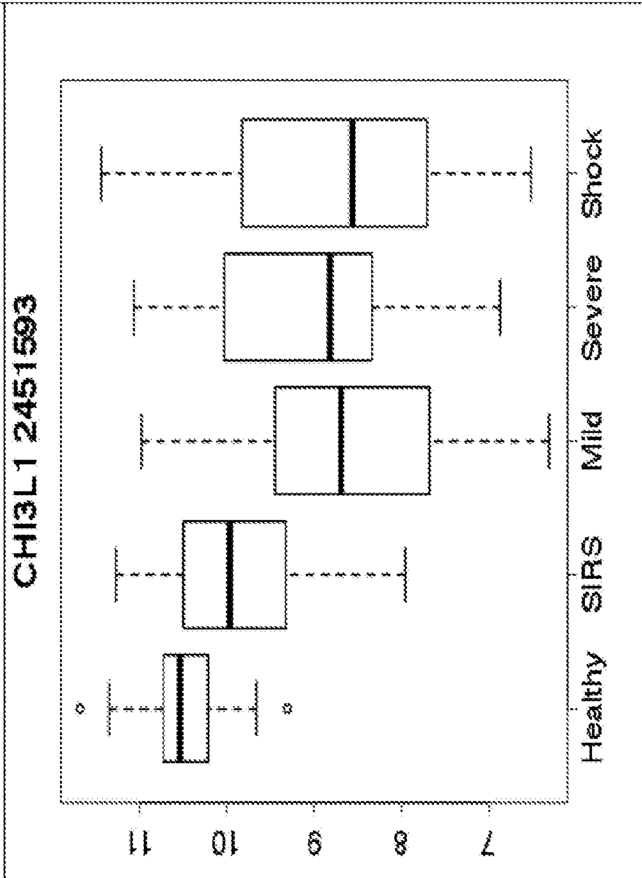


Figure 8



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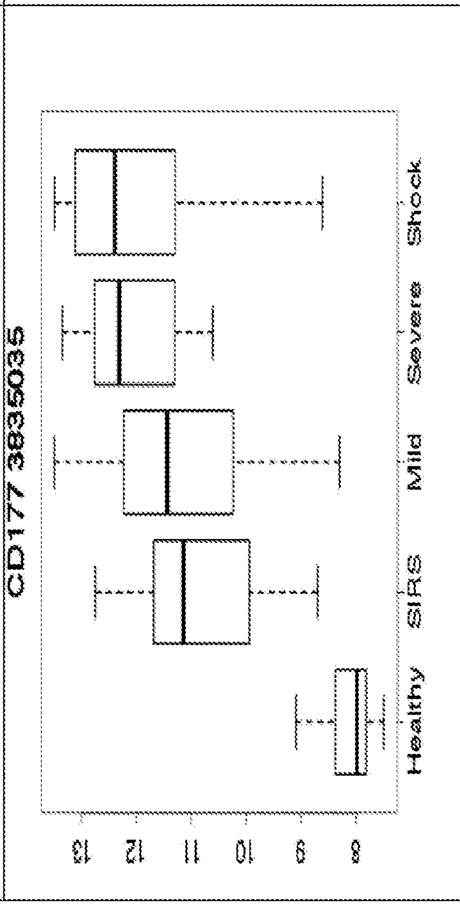

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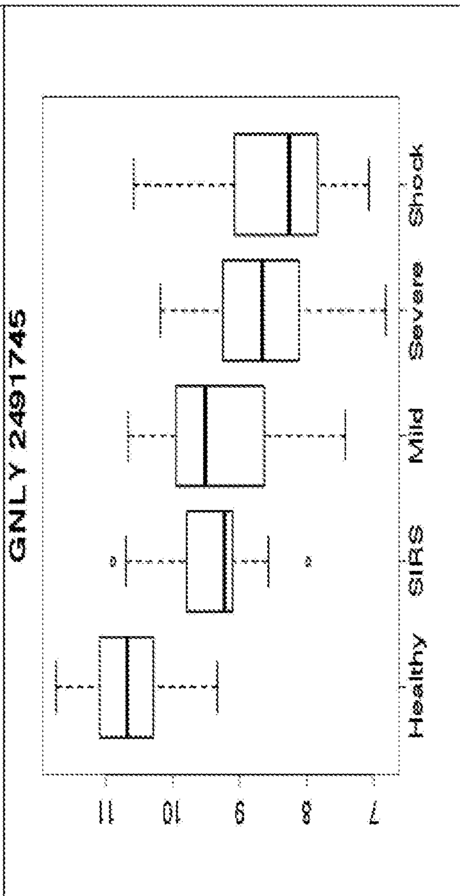

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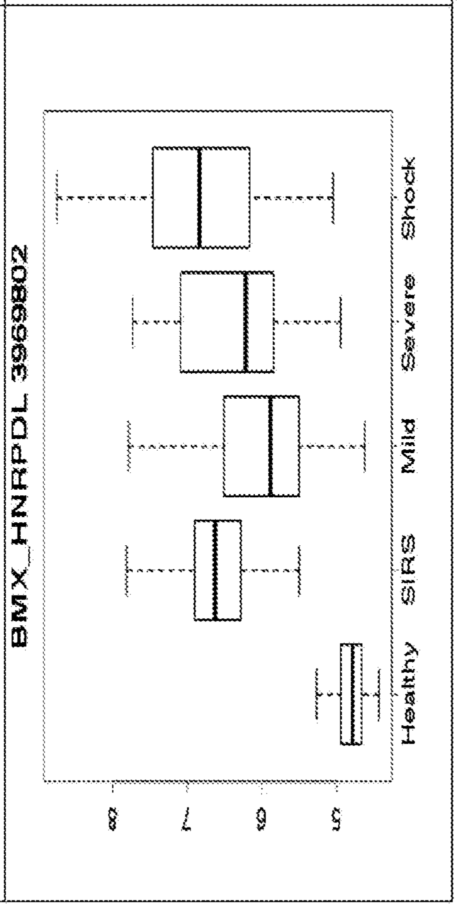

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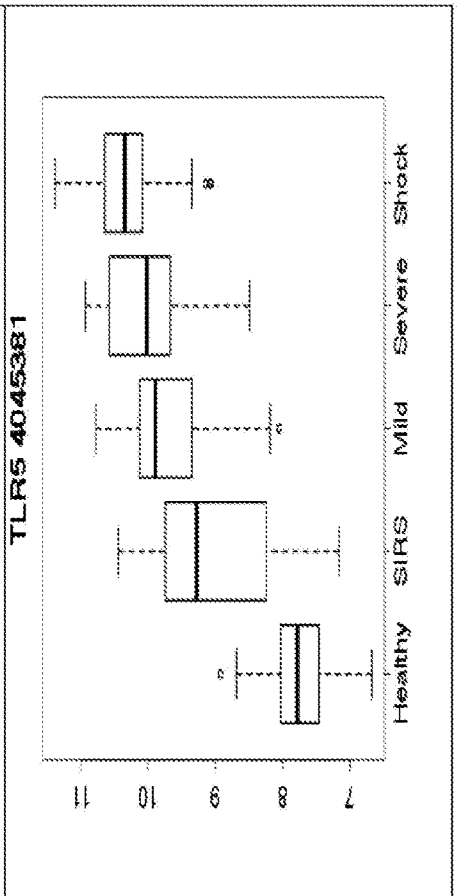


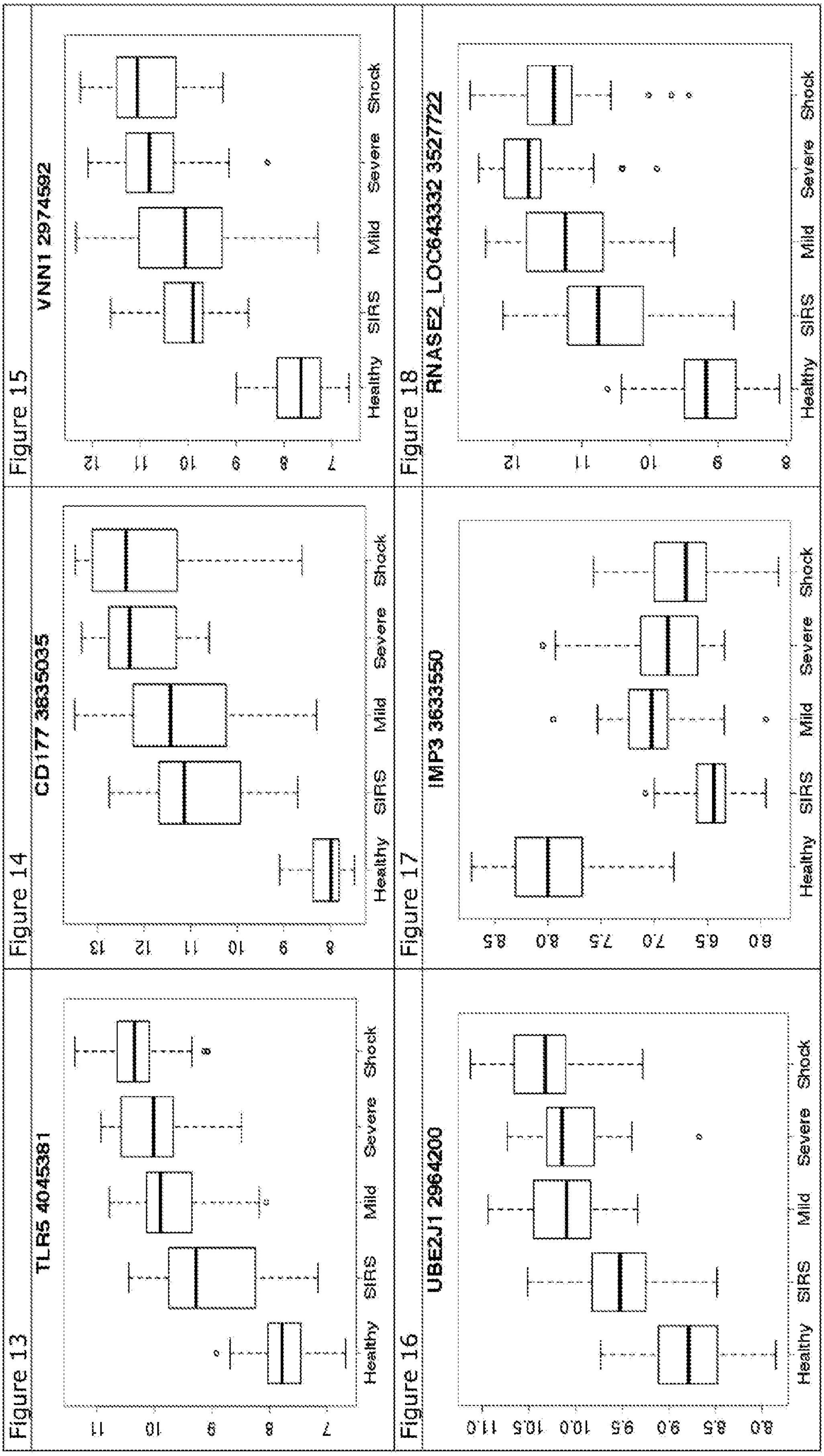
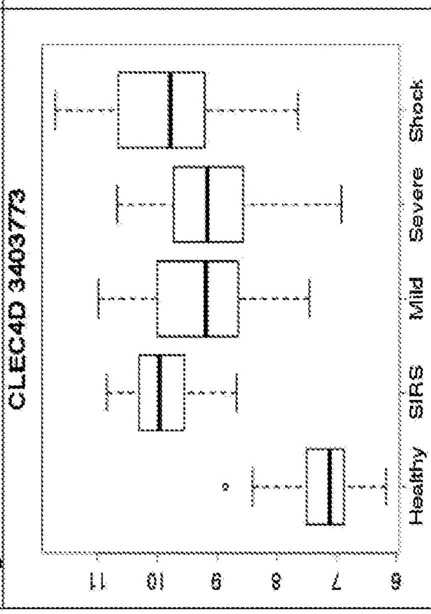


Figure 13
TLR5 4045381
Figure 14
CD177 3835035
Figure 15
VNN1 2974592
Figure 16
UBE2J1 2964200
Figure 17
IMP3 3633550
Figure 18
RNASE2_LOC643332 3527722
Healthy
SIRS
Mild
Severe
Shock

Figure 19



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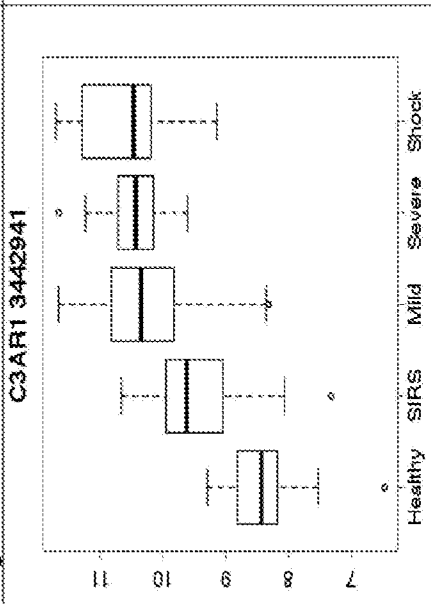

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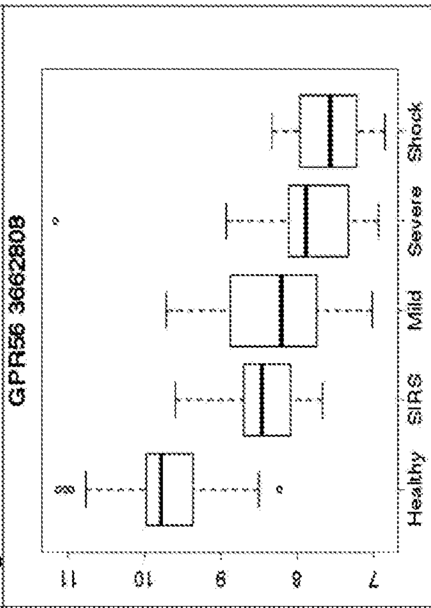

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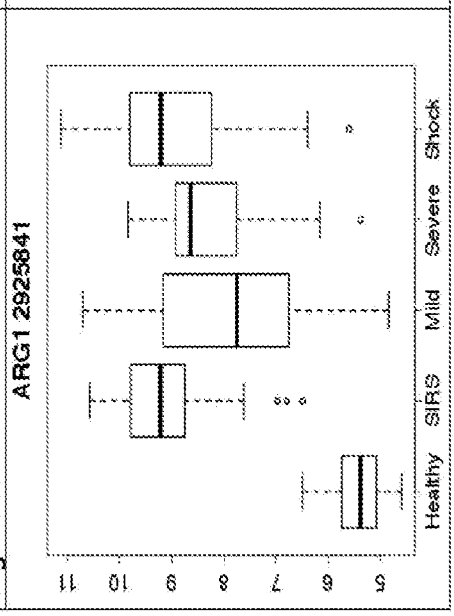

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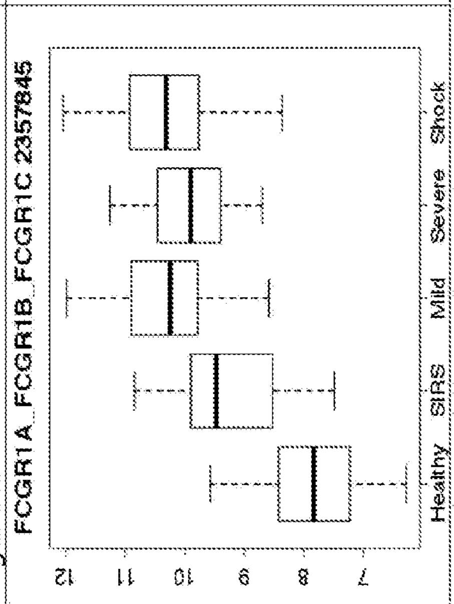

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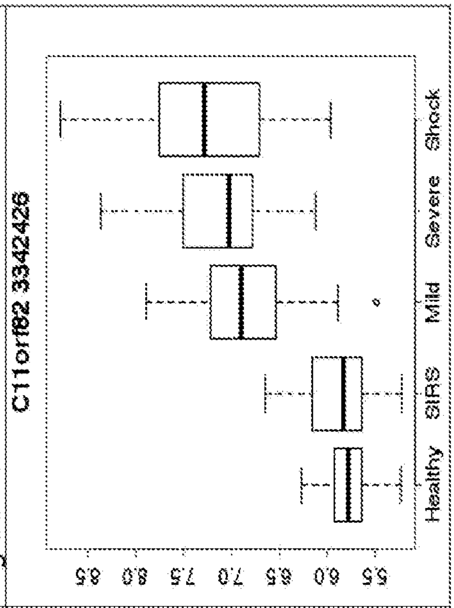

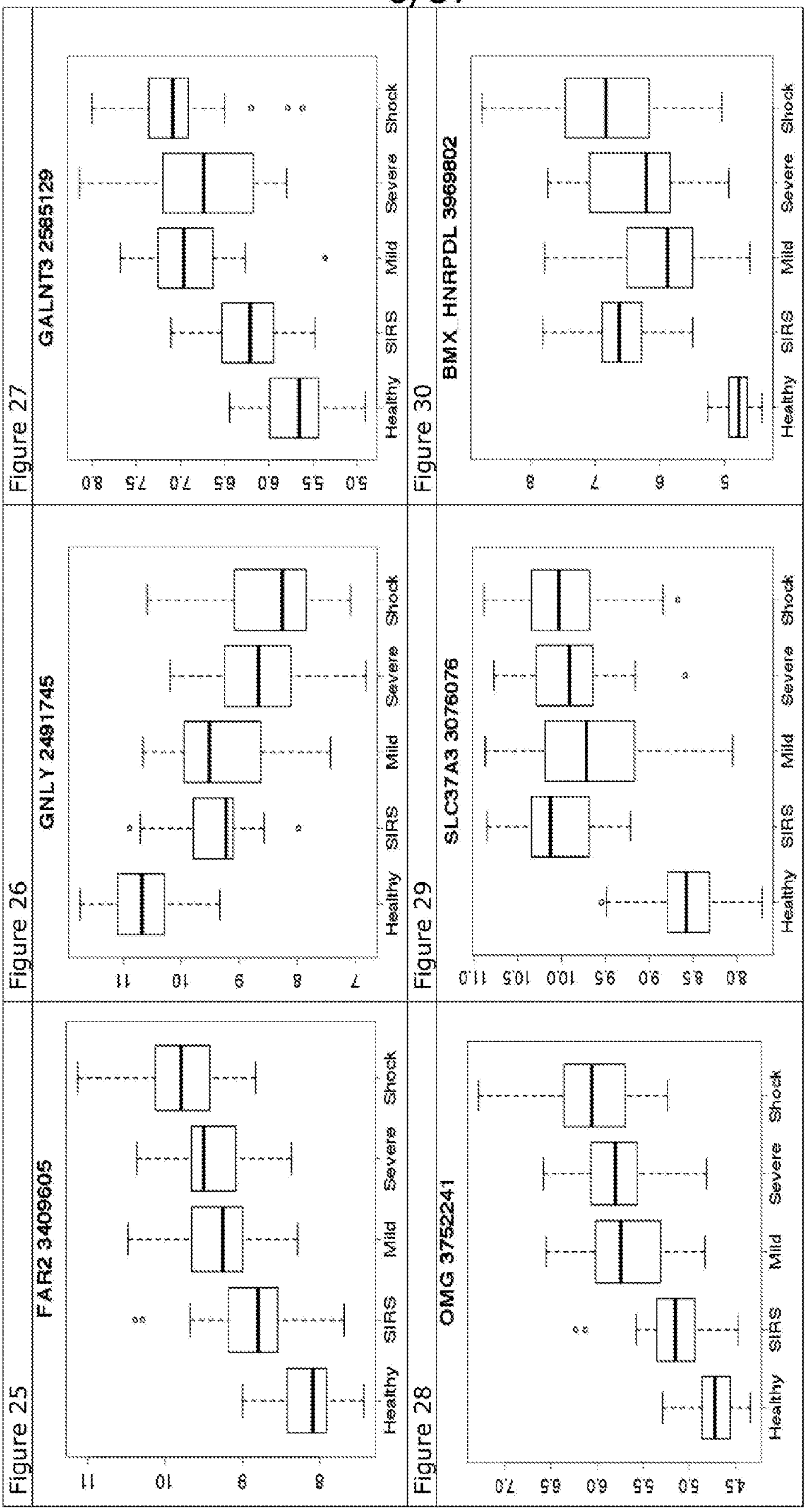
Figure 25
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Healthy SIRS Mild Severe Shock
Figure 26
GNLY 2491745
Healthy SIRS Mild Severe Shock
Figure 27
GALNT3 2585129
Healthy SIRS Mild Severe Shock
Figure 28
OMG 3752241
Healthy SIRS Mild Severe Shock
Figure 29
SLC37A3 3076076
Healthy SIRS Mild Severe Shock
Figure 30
BMX_HNRPDL 3969802
Healthy SIRS Mild Severe Shock

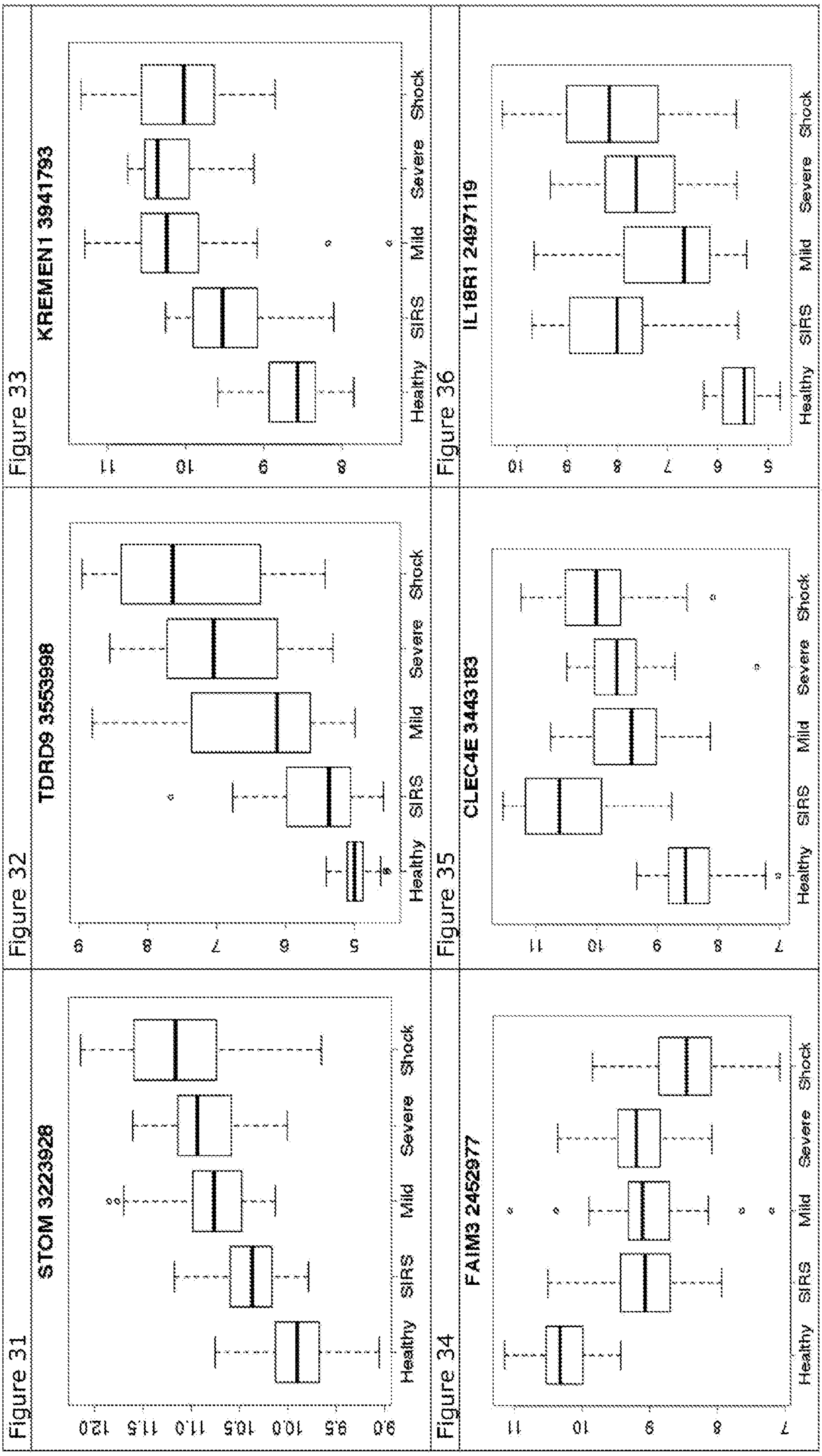


Figure 33

Figure 32

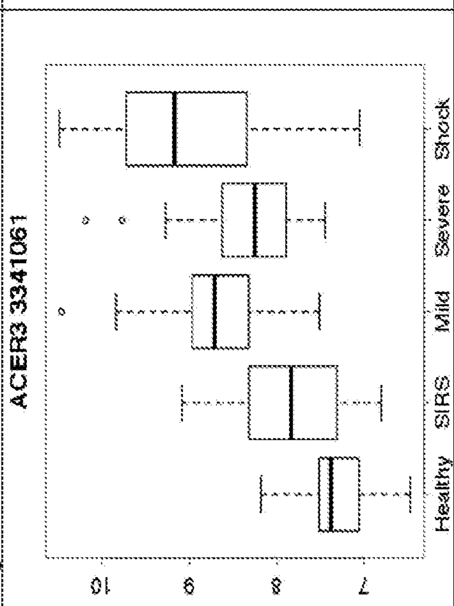
Figure 31

Figure 36

Figure 35

Figure 34

Figure 37



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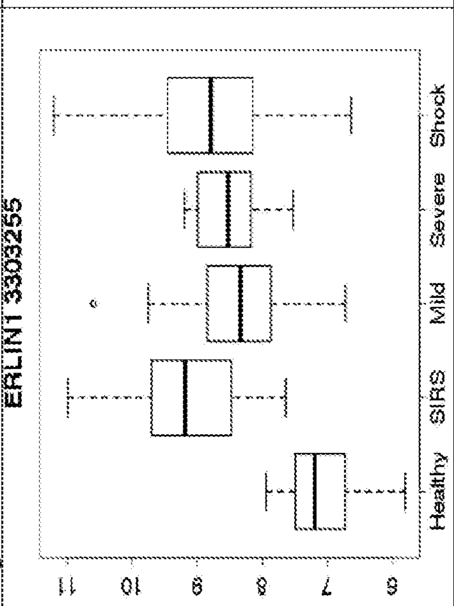

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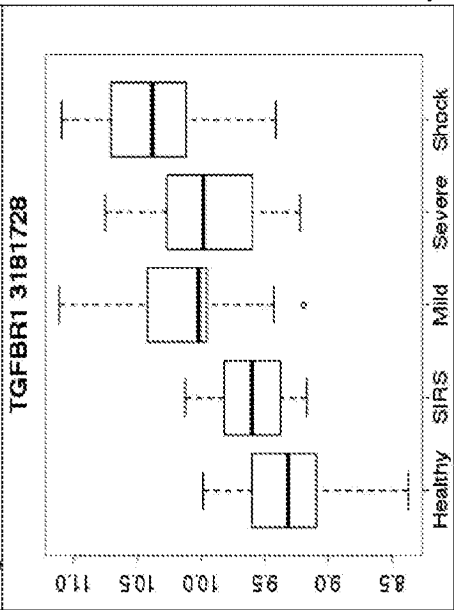

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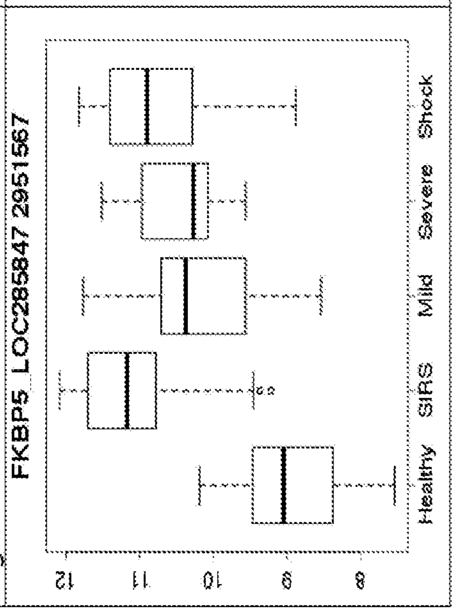

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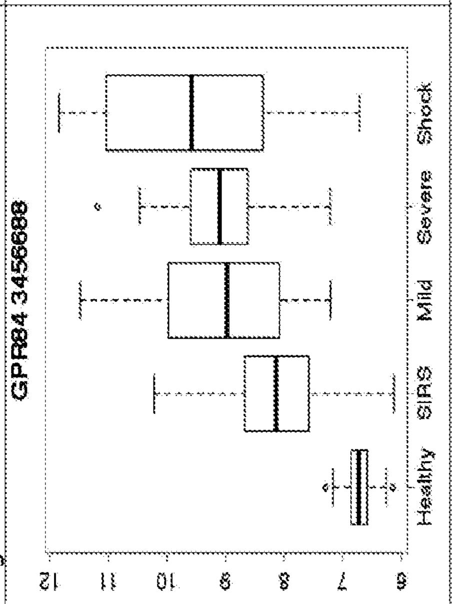

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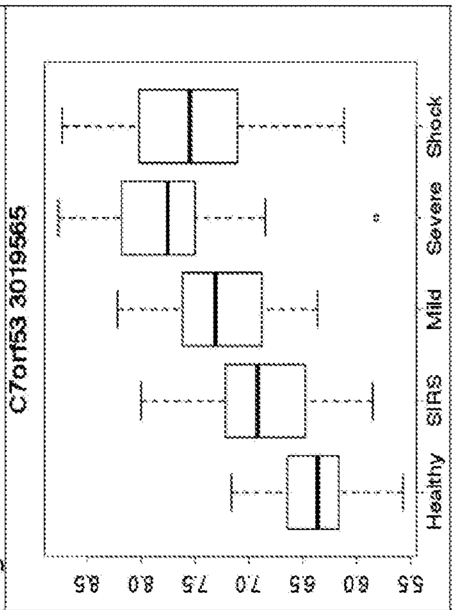
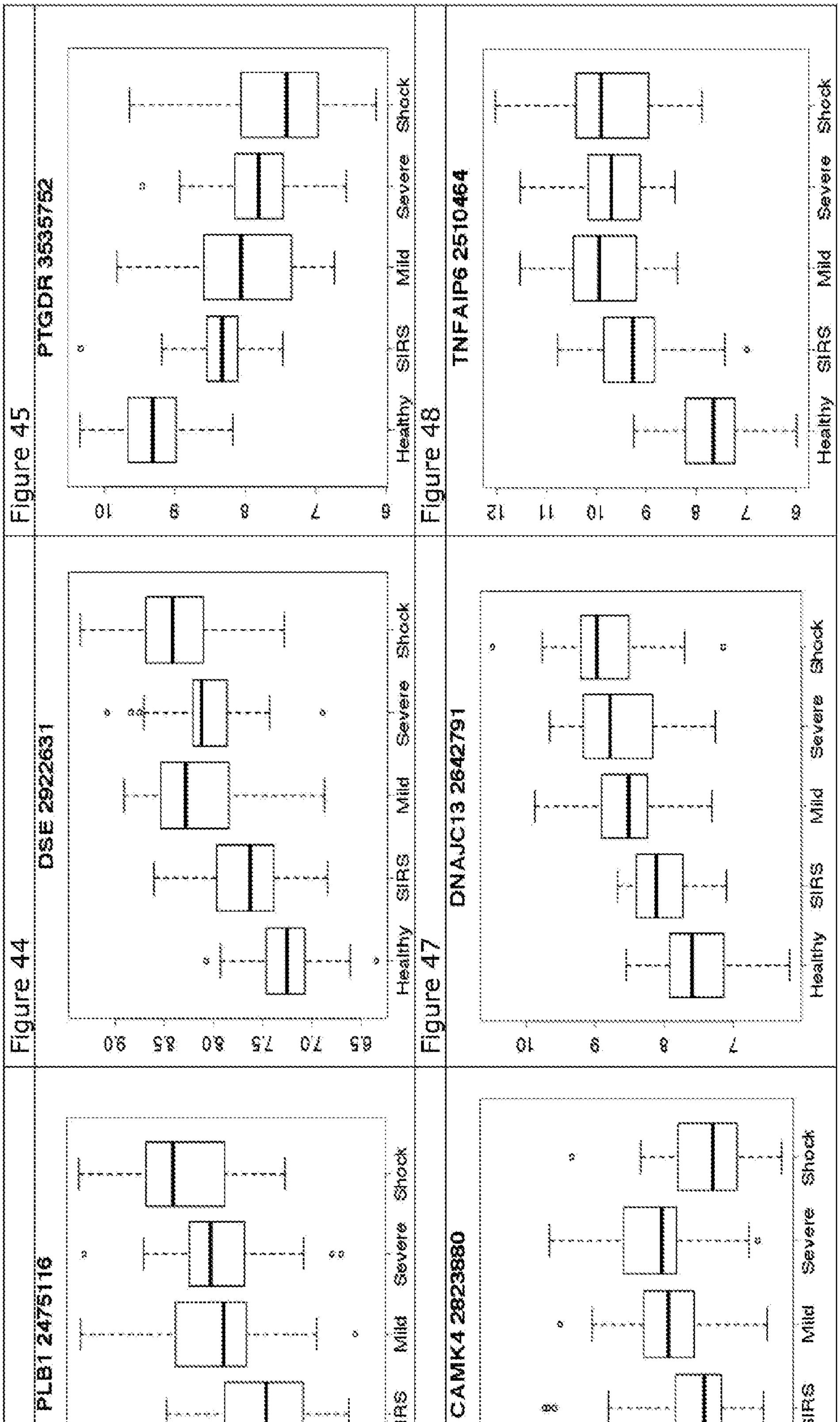


9/57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PLB1 2475116
Healthy SIRS Mild Severe Shock
Figure 44
DSE 2922631
Healthy SIRS Mild Severe Shock
Figure 45
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Healthy SIRS Mild Severe Shock
Figure 46
CAMK4 2823880
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Healthy SIRS Mild Severe Shock
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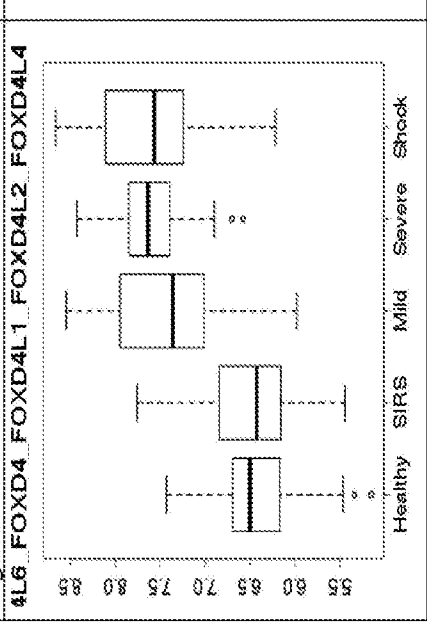
Healthy SIRS Mild Severe Shock

Figure 49



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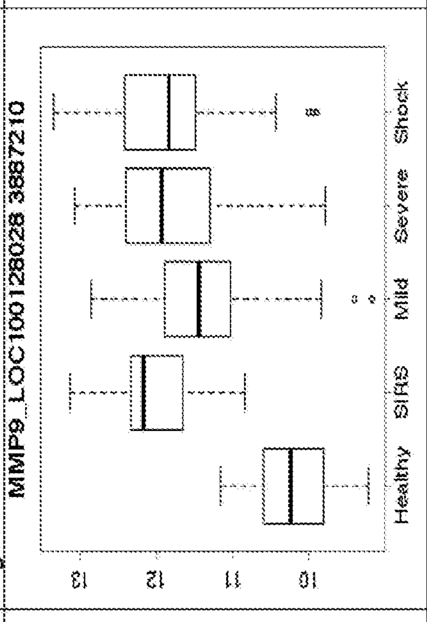

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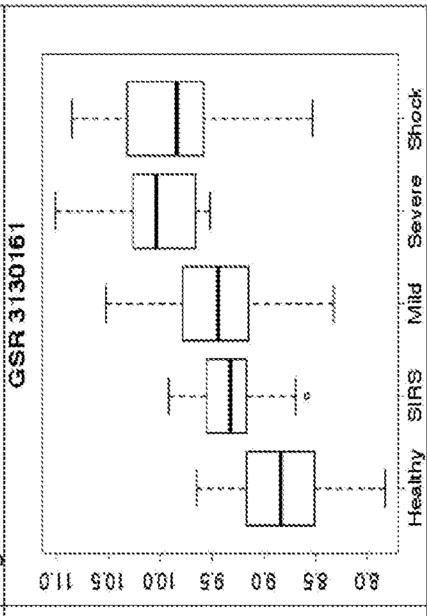

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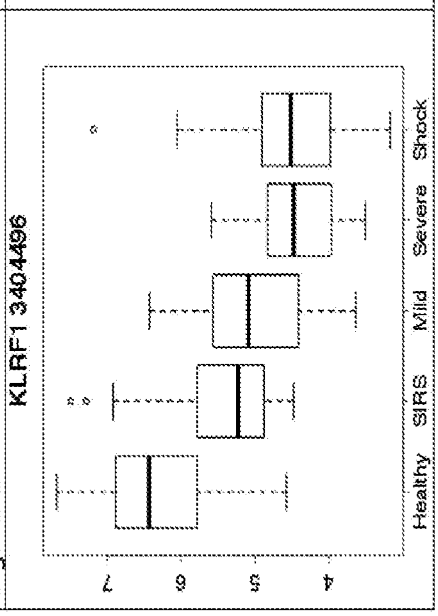

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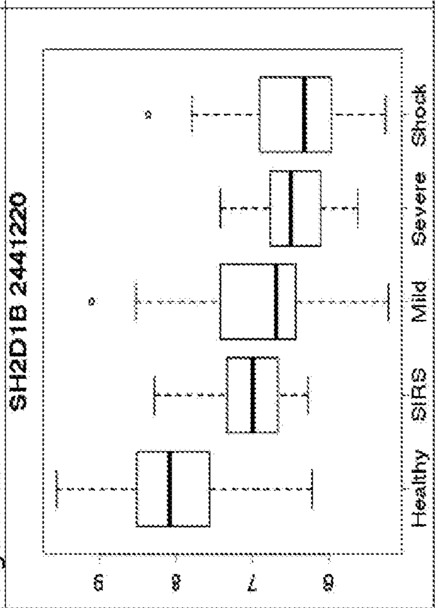

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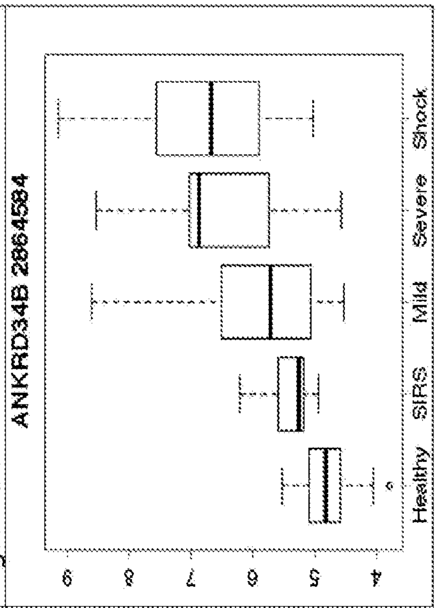


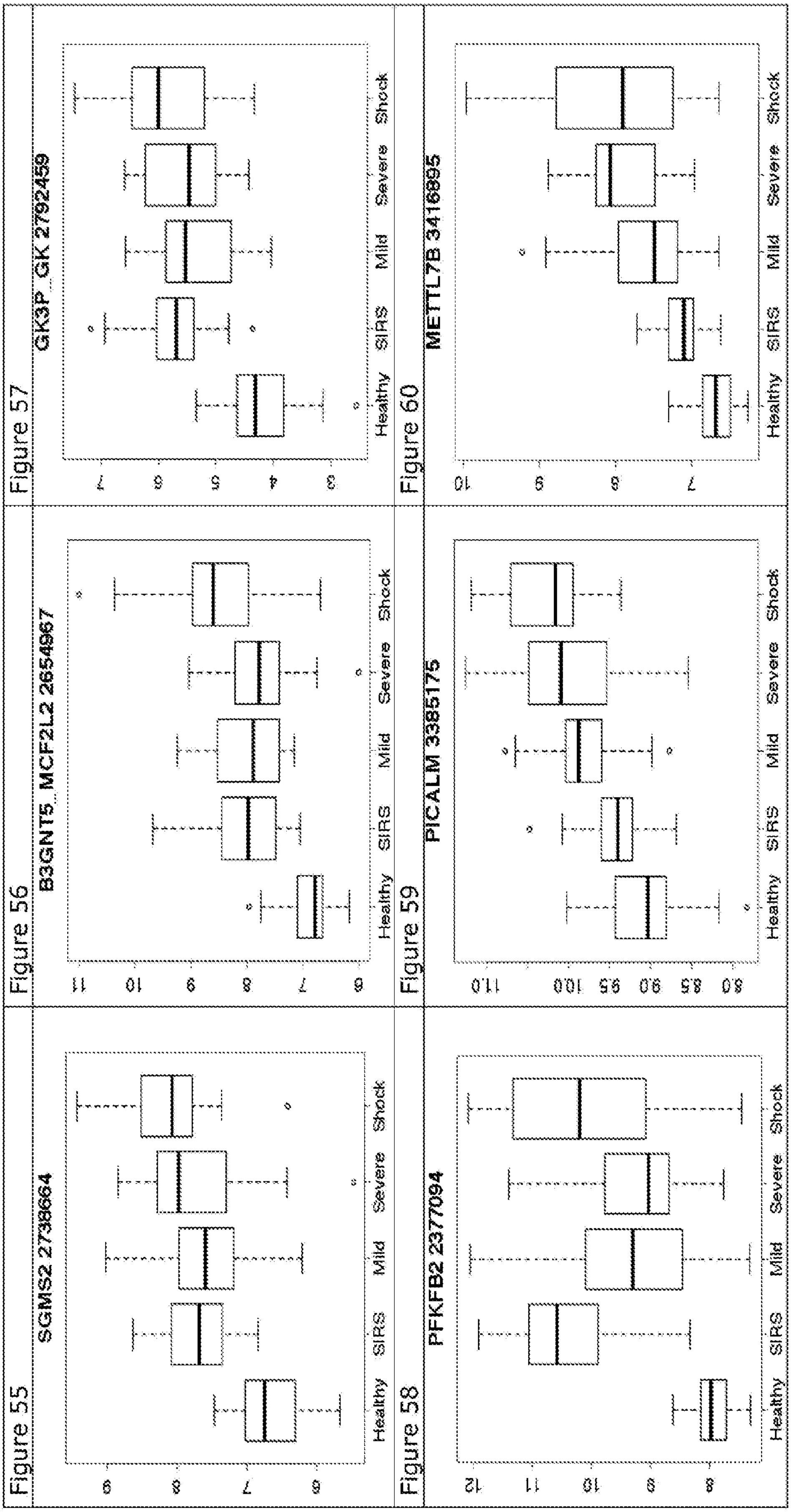


Figure 55

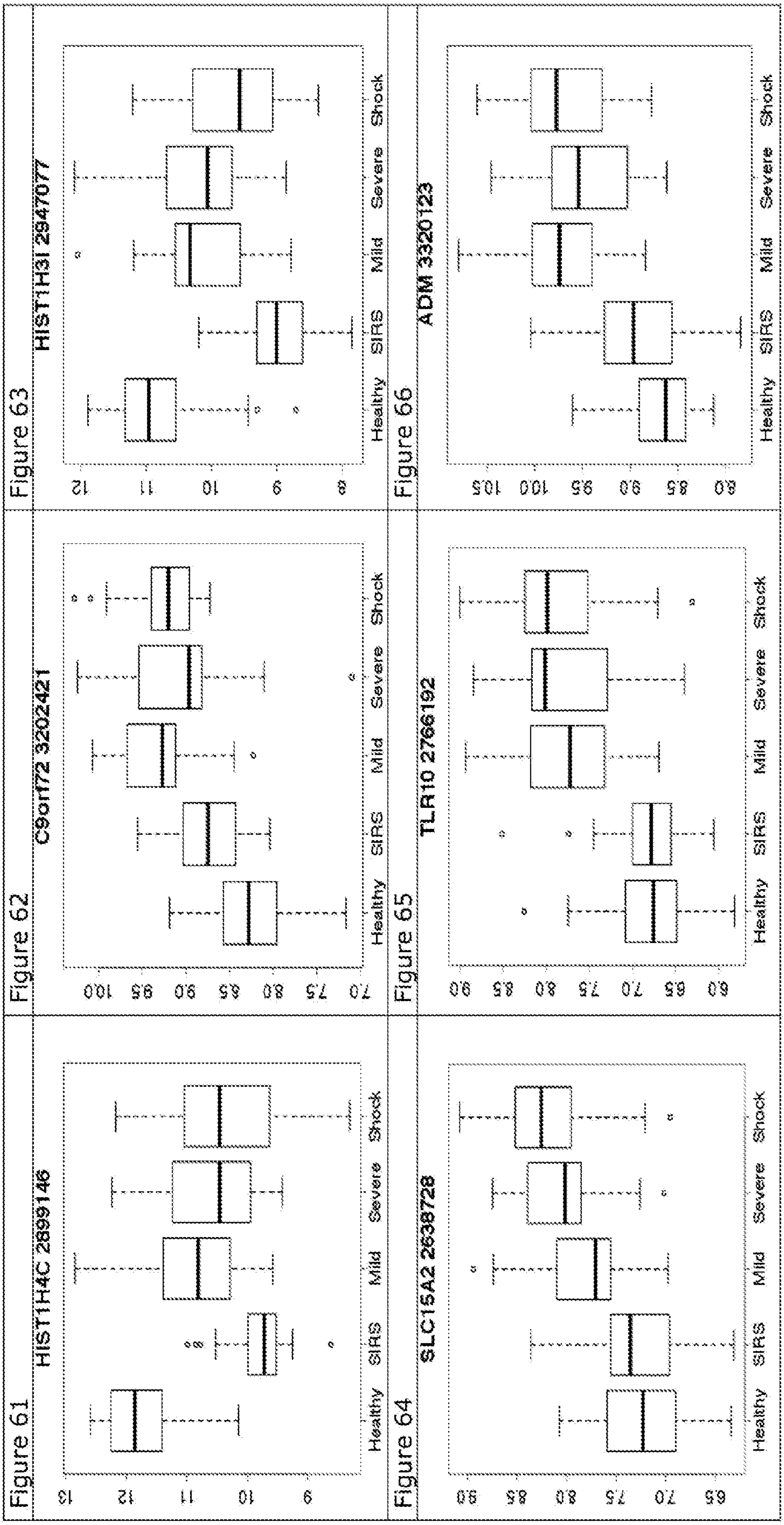
Figure 56

Figure 57

Figure 58

Figure 59

Figure 60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Healthy SIRS Mild Severe Shock
Figure 62
C9orf72 3202421
10.0 9.5 9.0 8.5 8.0 7.5 7.0
Healthy SIRS Mild Severe Shock
Figure 63
HIST1H3I 2947077
12 11 10 9 8
Healthy SIRS Mild Severe Shock
Figure 64
SLC15A2 2638728
9.0 8.5 8.0 7.5 7.0 6.5
Healthy SIRS Mild Severe Shock
Figure 65
TLR10 2766192
9.0 8.5 8.0 7.5 7.0 6.5 6.0
Healthy SIRS Mild Severe Shock
Figure 66
ADM 3320123
10.5 10.0 9.5 9.0 8.5 8.0
Healthy SIRS Mild Severe Shock

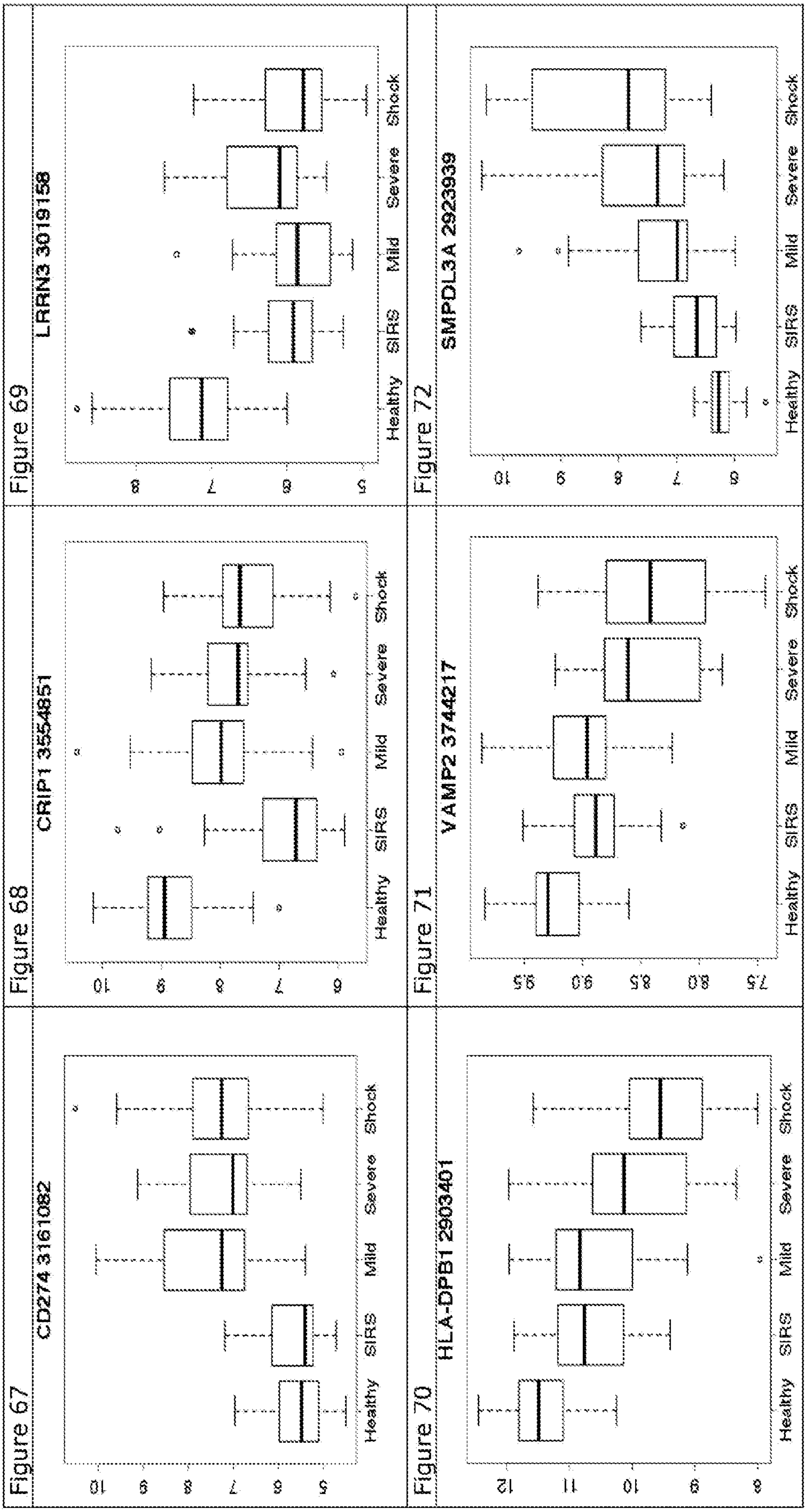
Figure 67
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Healthy SIRS Mild Severe Shock
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Healthy SIRS Mild Severe Shock
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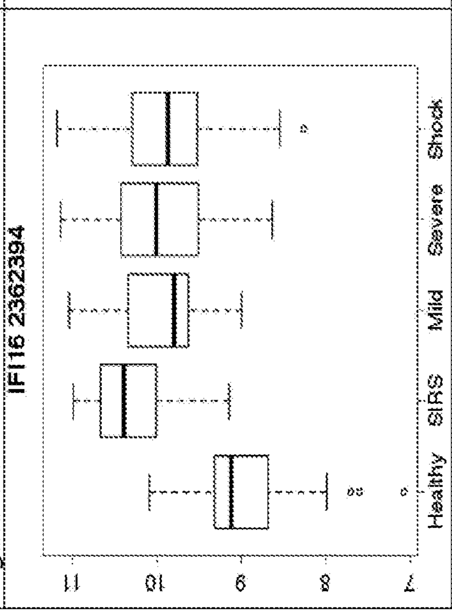
HLA-DPB1 2903401
Healthy SIRS Mild Severe Shock
Figure 71
VAMP2 3744217
Healthy SIRS Mild Severe Shock
Figure 72
SMPDL3A 2923939
Healthy SIRS Mild Severe Shock

Figure 73



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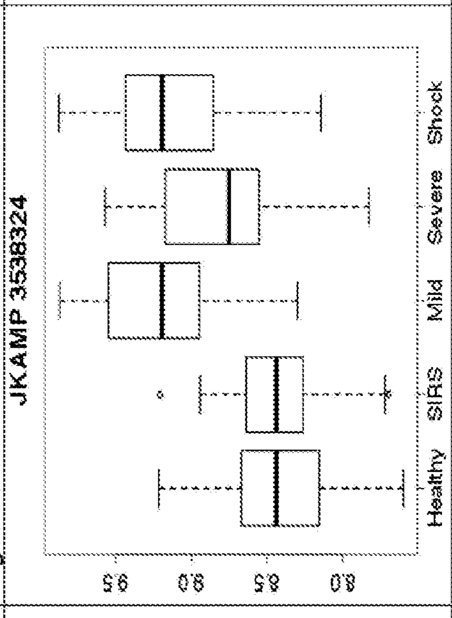

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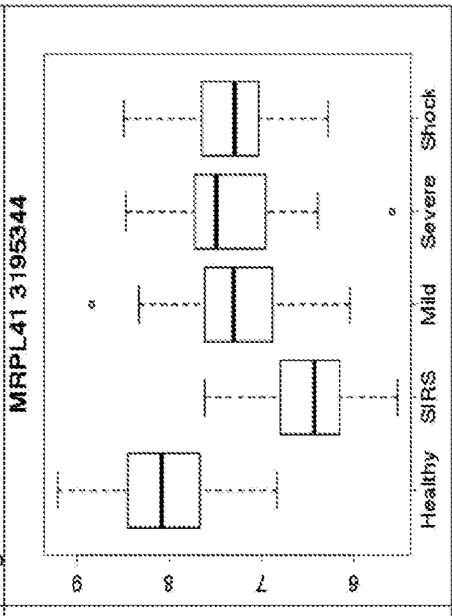

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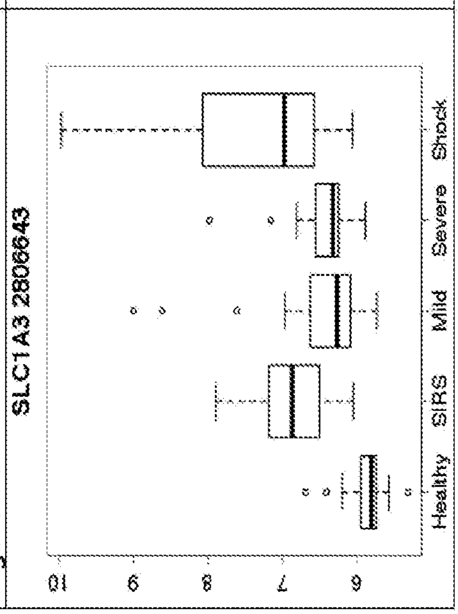

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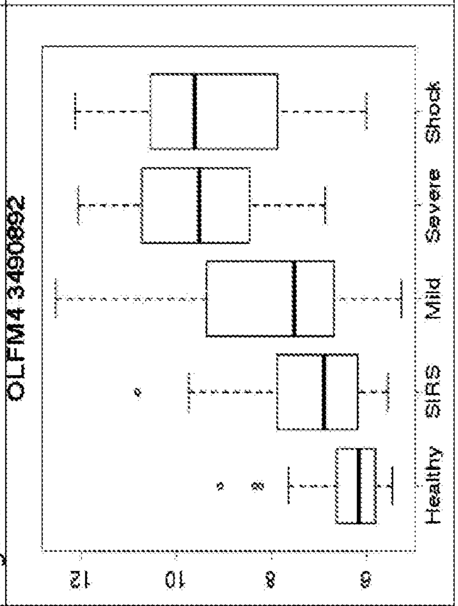

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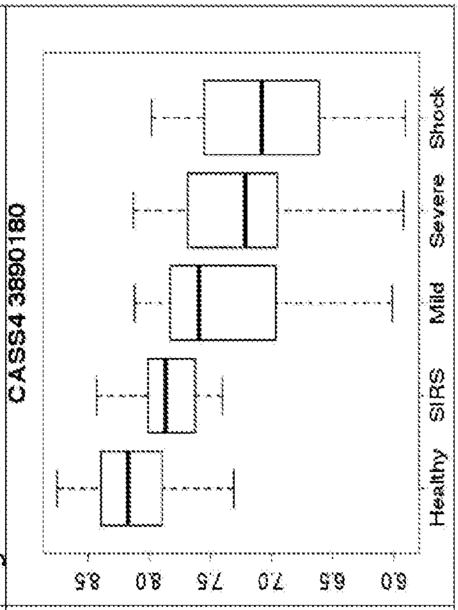

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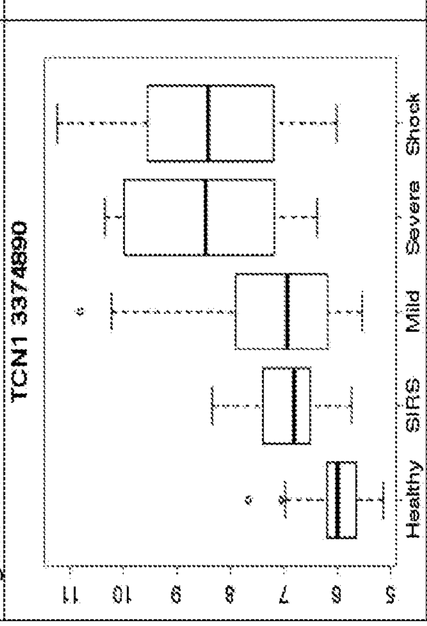

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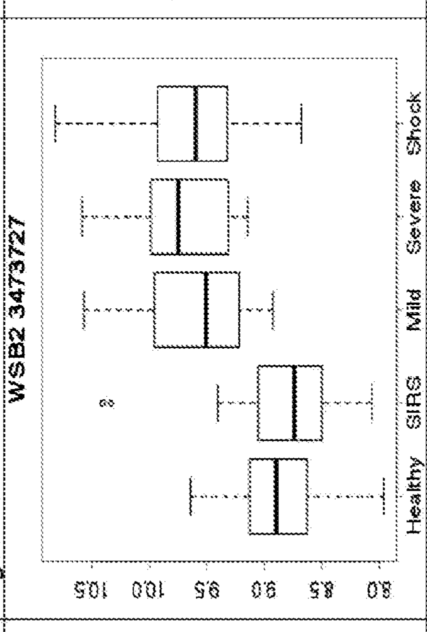

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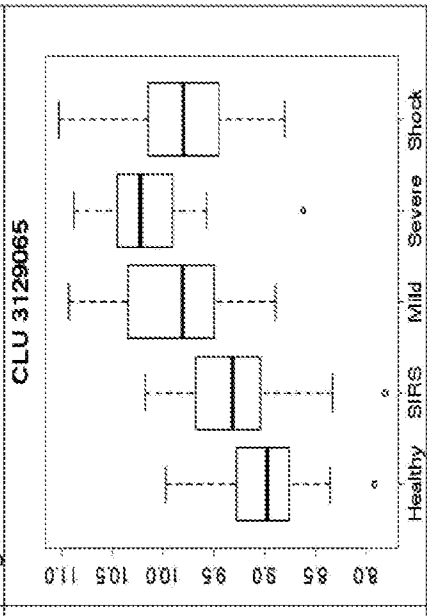

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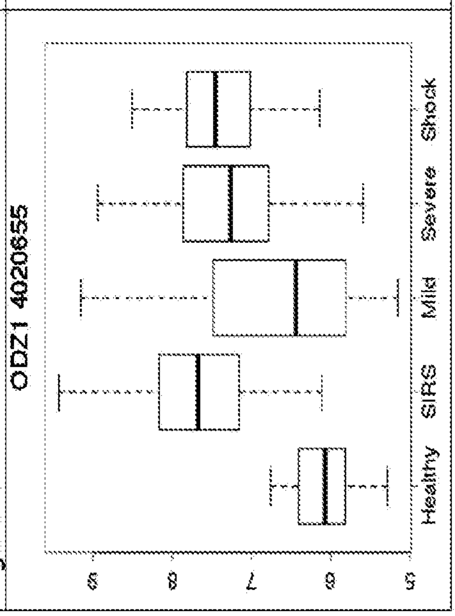

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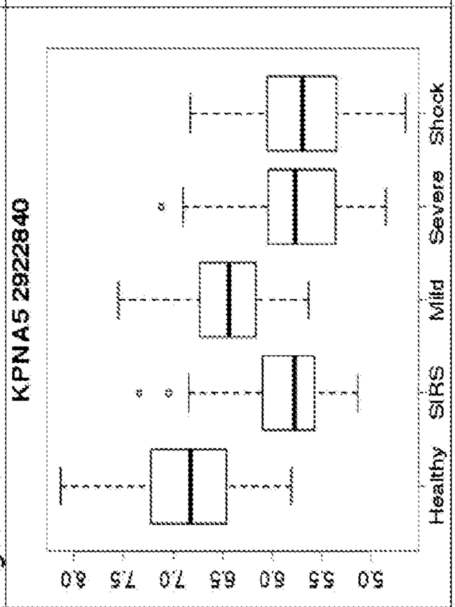

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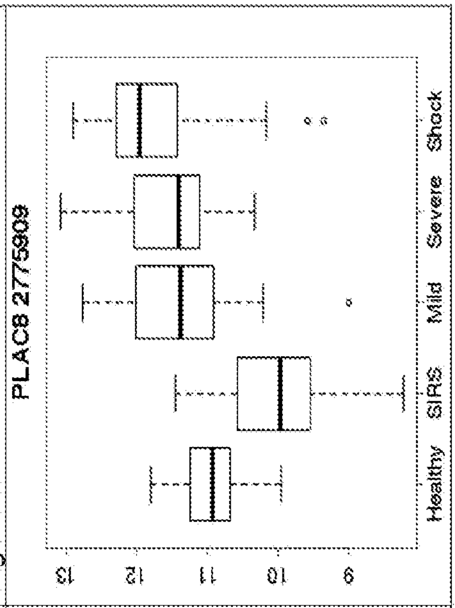

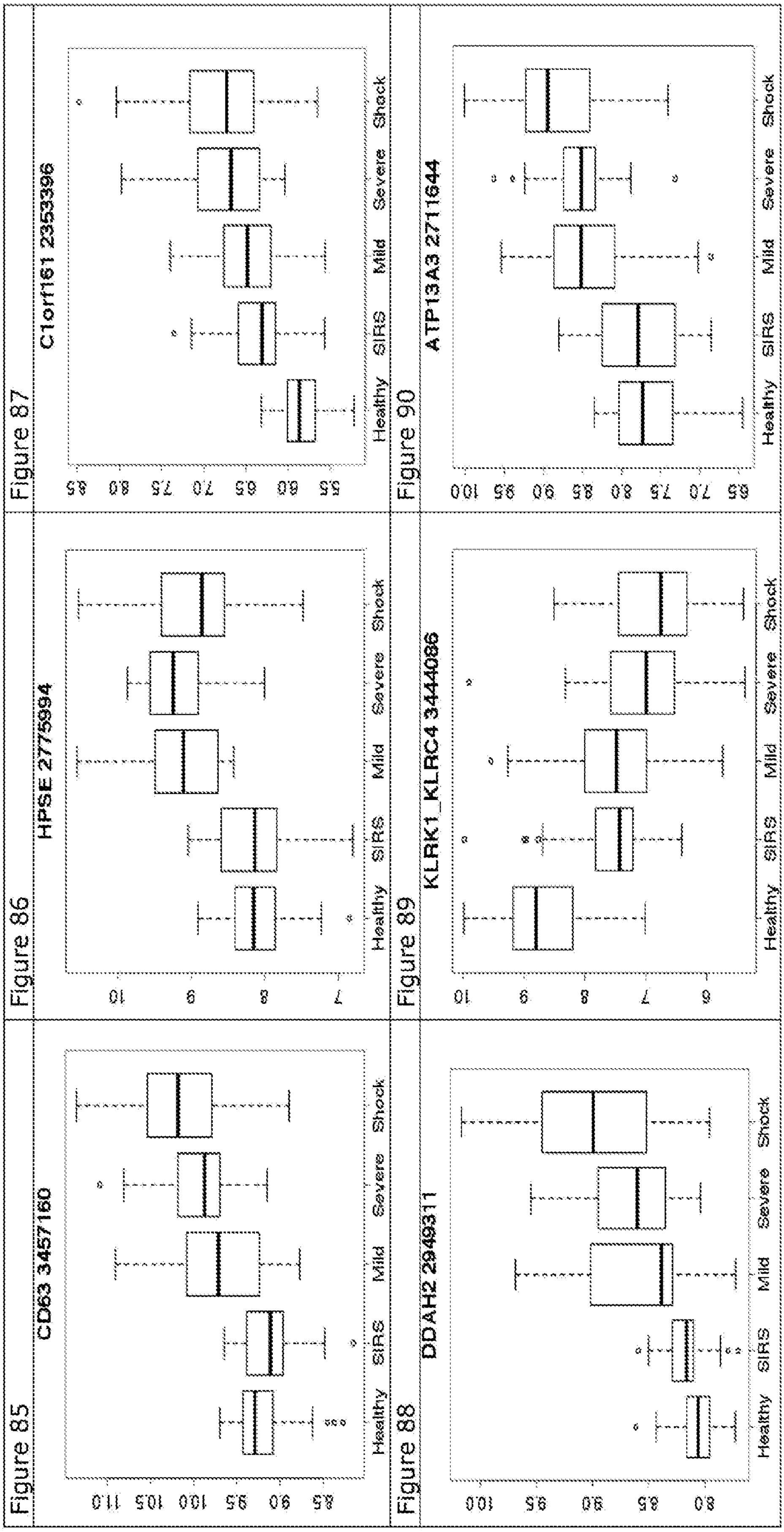
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CD63 3457160
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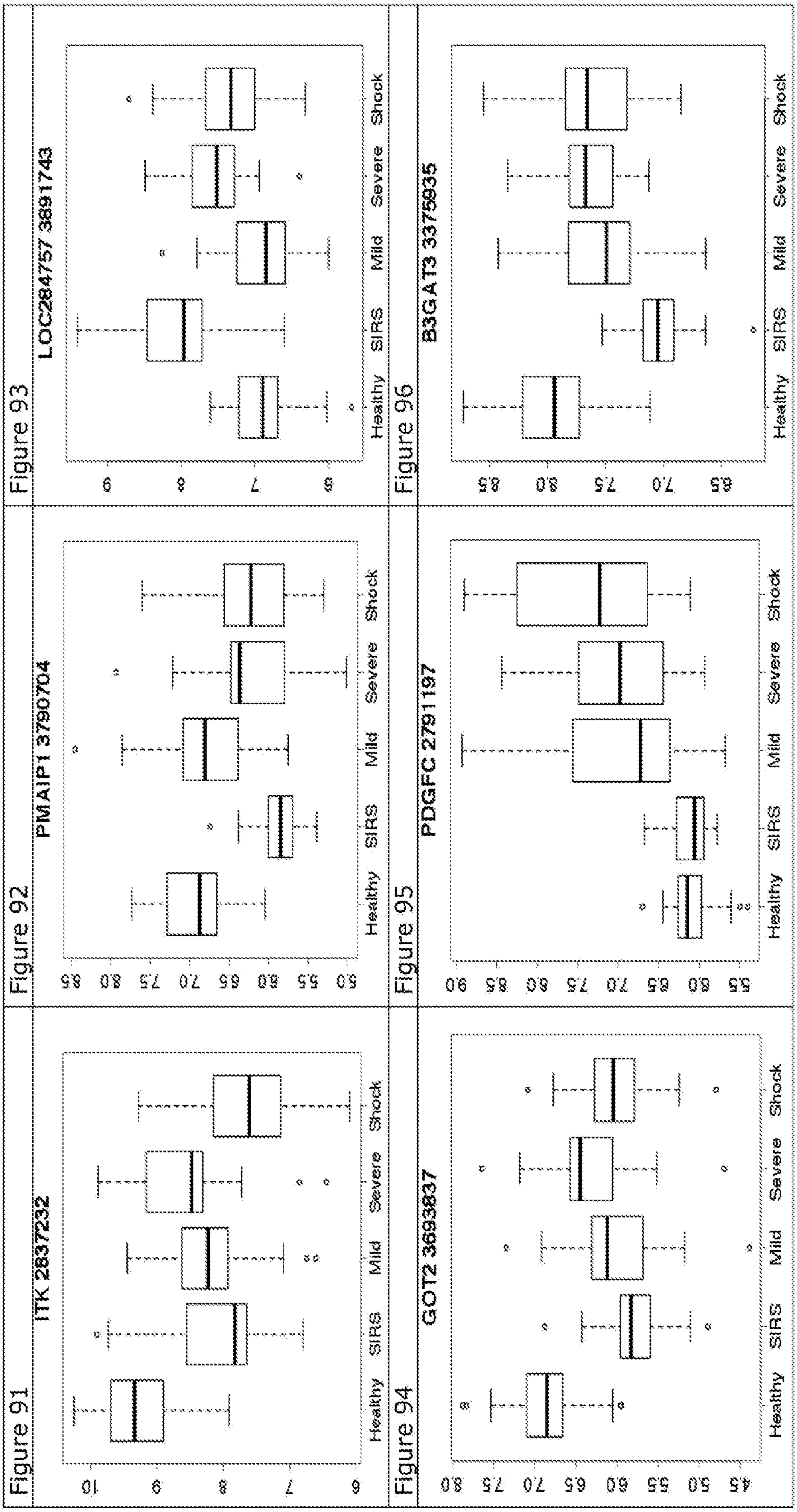
HPSE 2775994
Figure 87
C1orf161 2353396
Figure 88
DDAH2 2949311
Figure 89
KLRK1_KLRC4 3444086
Figure 90
ATP13A3 2711644
Healthy
SIRS
Mild
Severe
Shock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ITK 2837232
Healthy SIRS Mild Severe Shock
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PMAIP1 3790704
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Figure 94
GOT2 3693837
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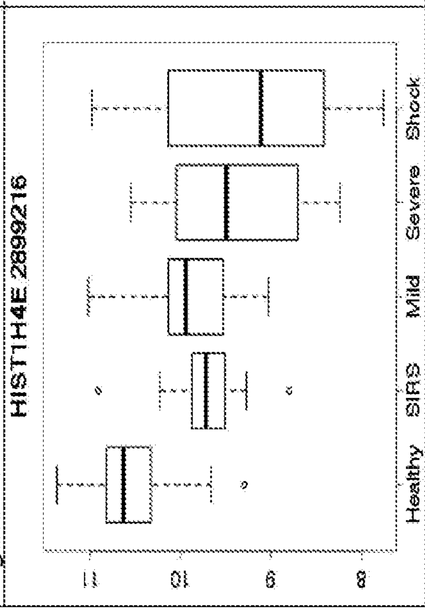
Healthy SIRS Mild Severe Shock

Figure 97



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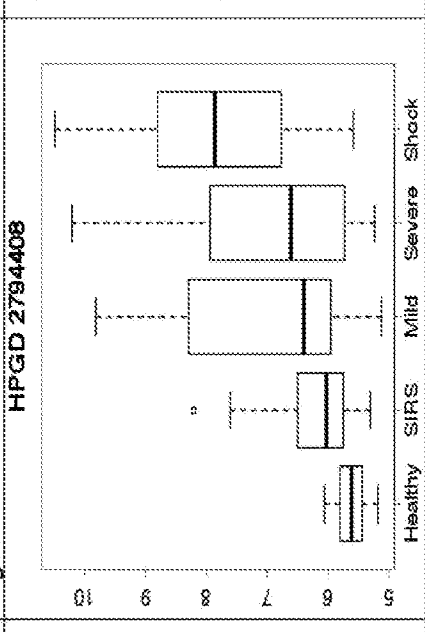

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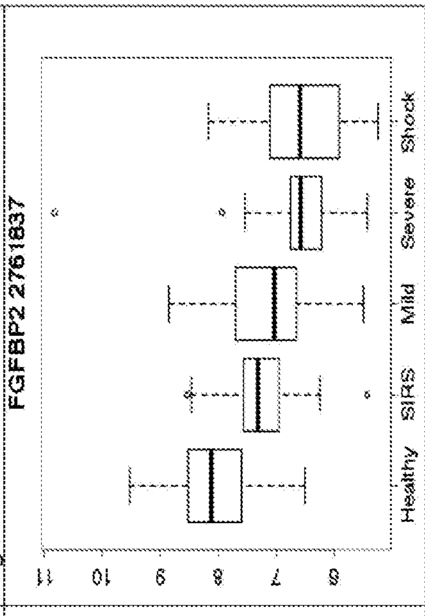

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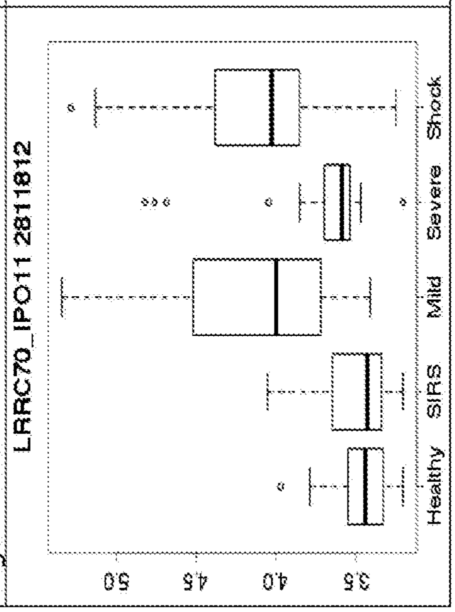

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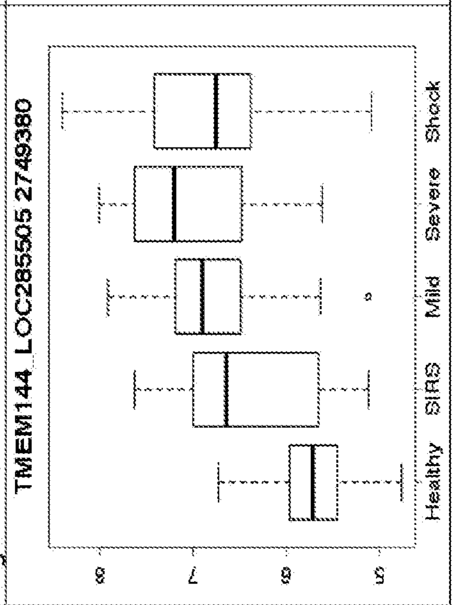

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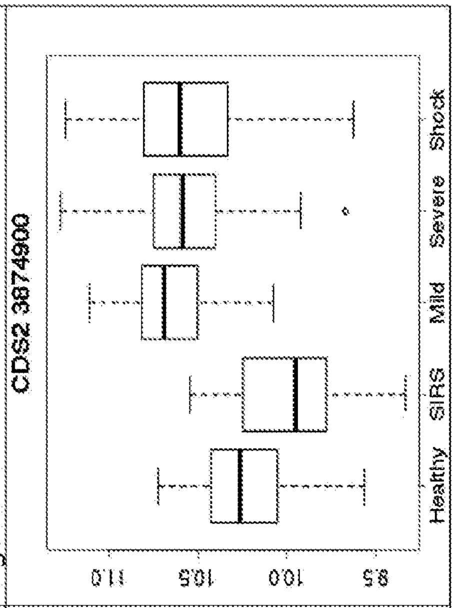

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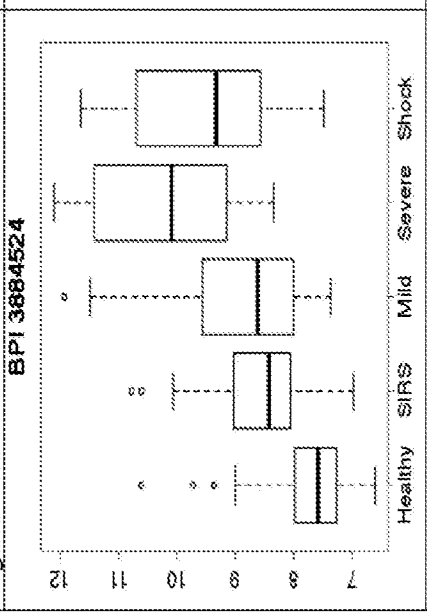

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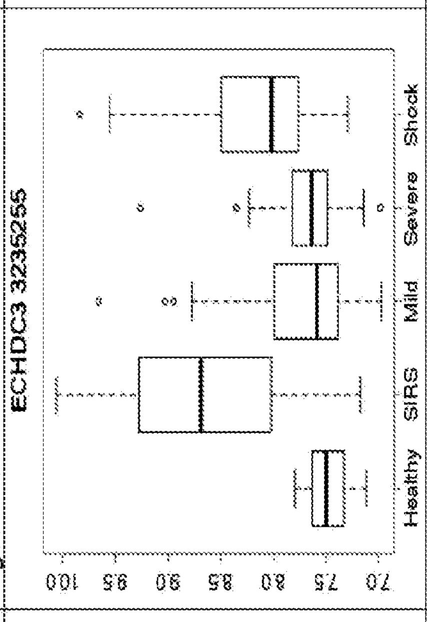

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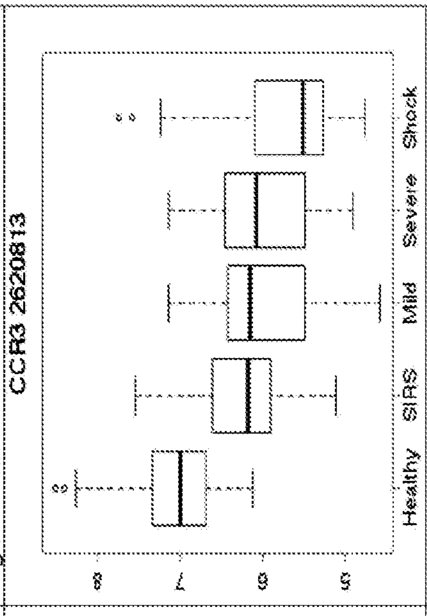

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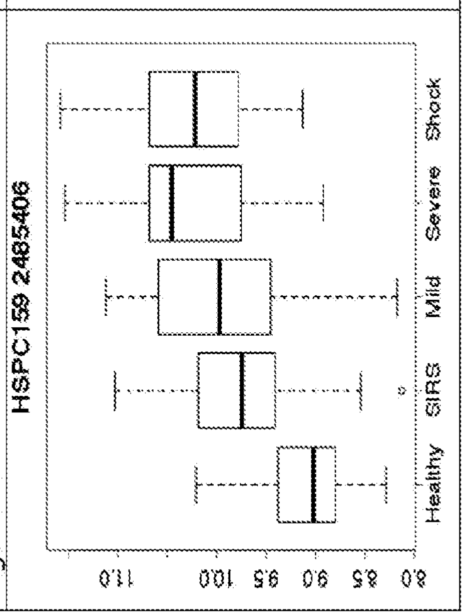

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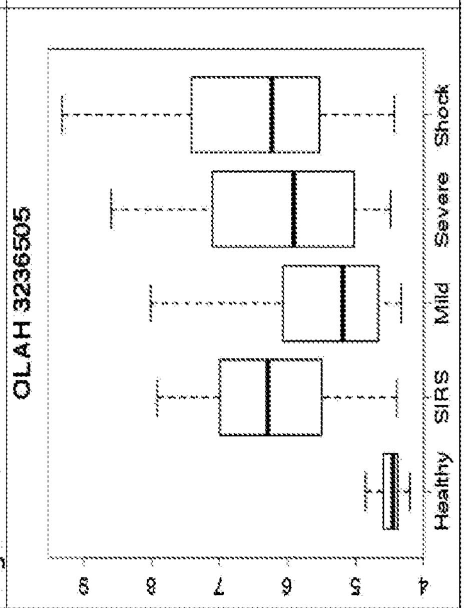

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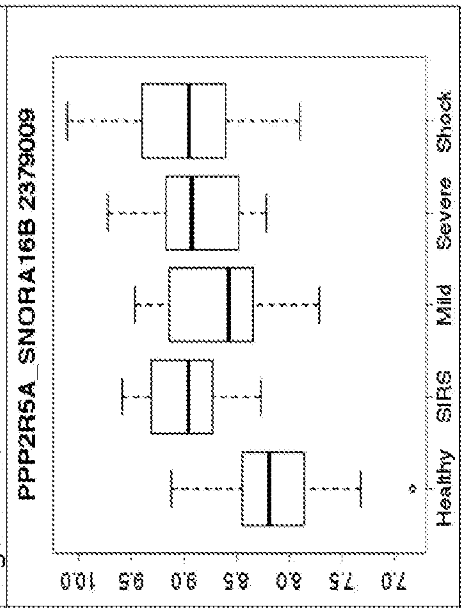

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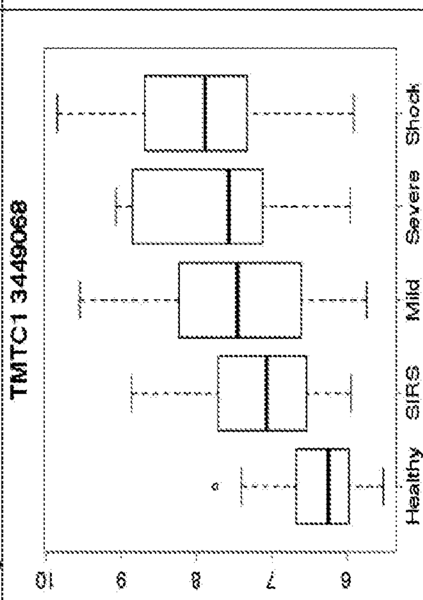

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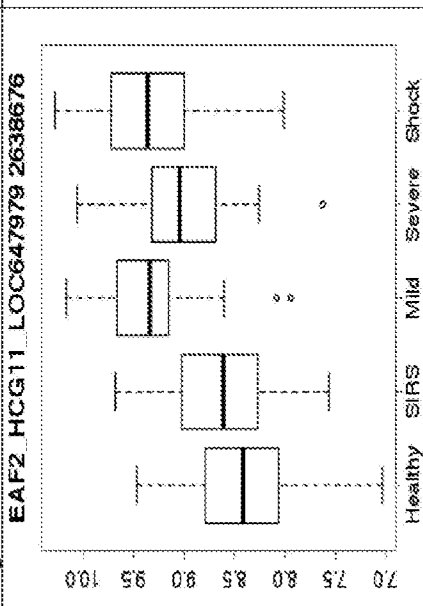

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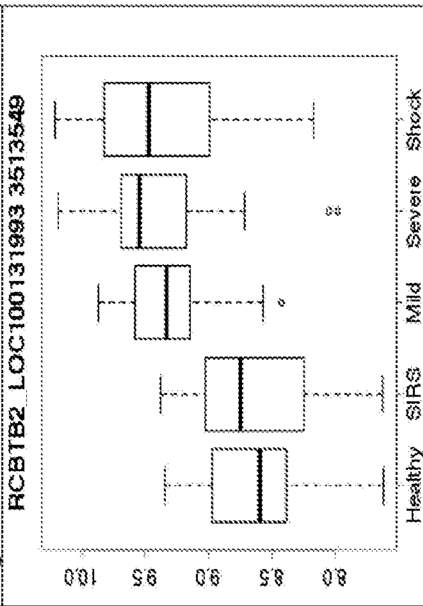

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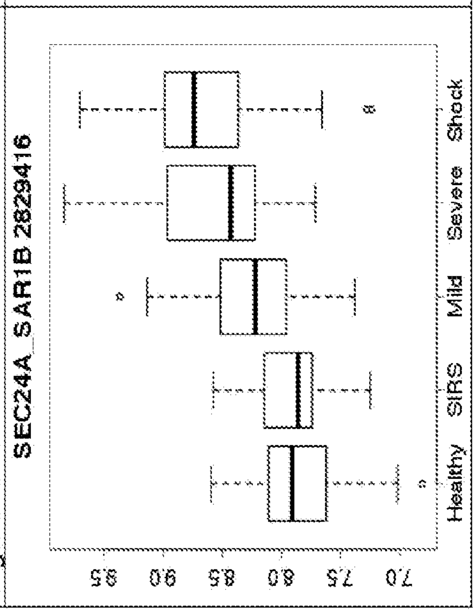

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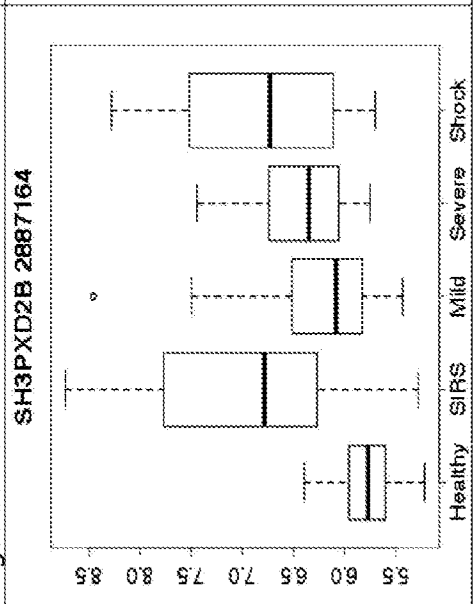

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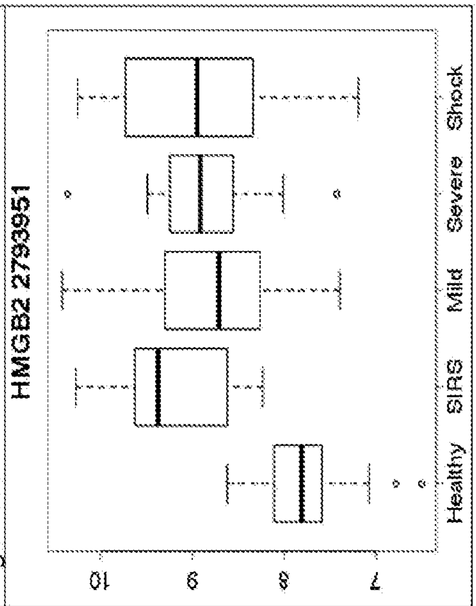

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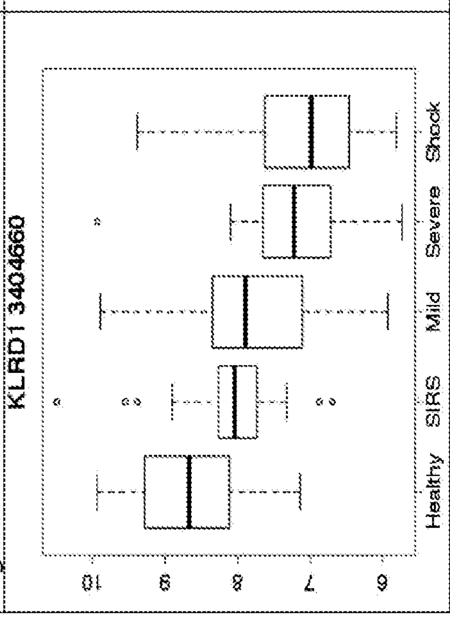

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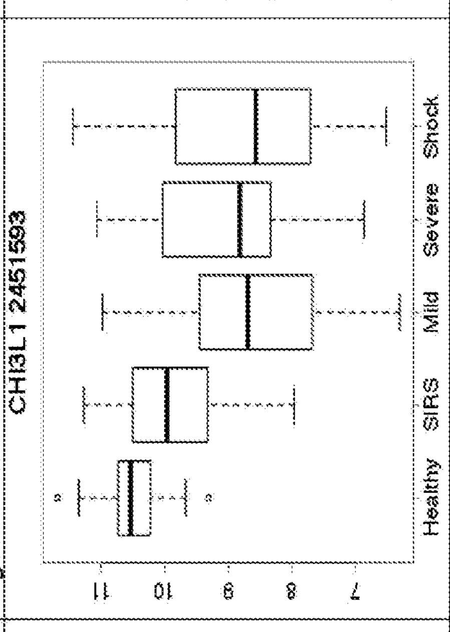

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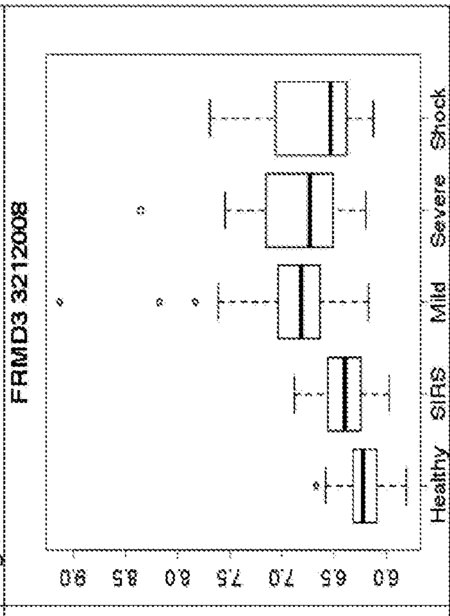

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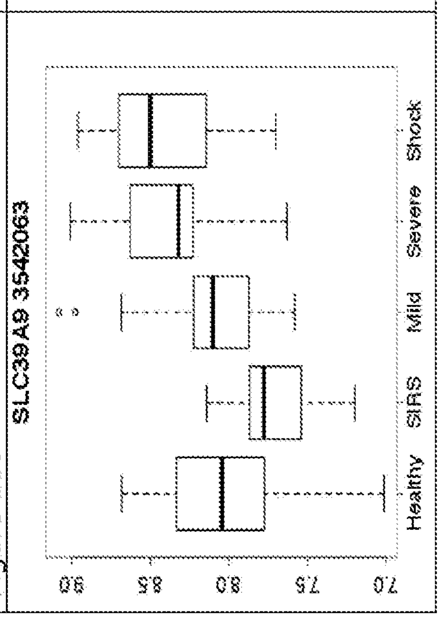

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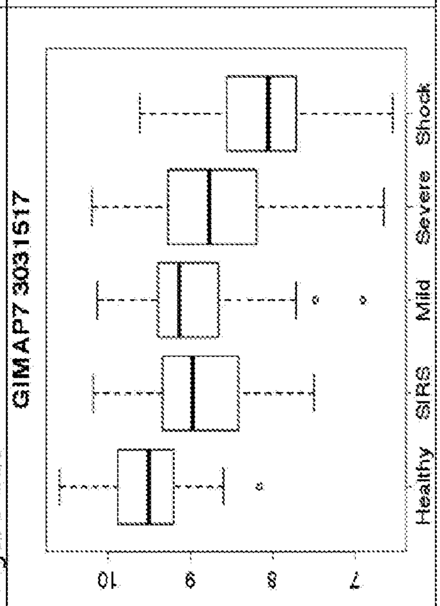

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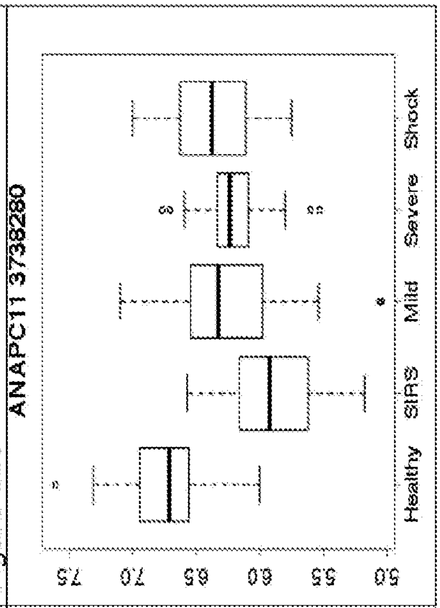

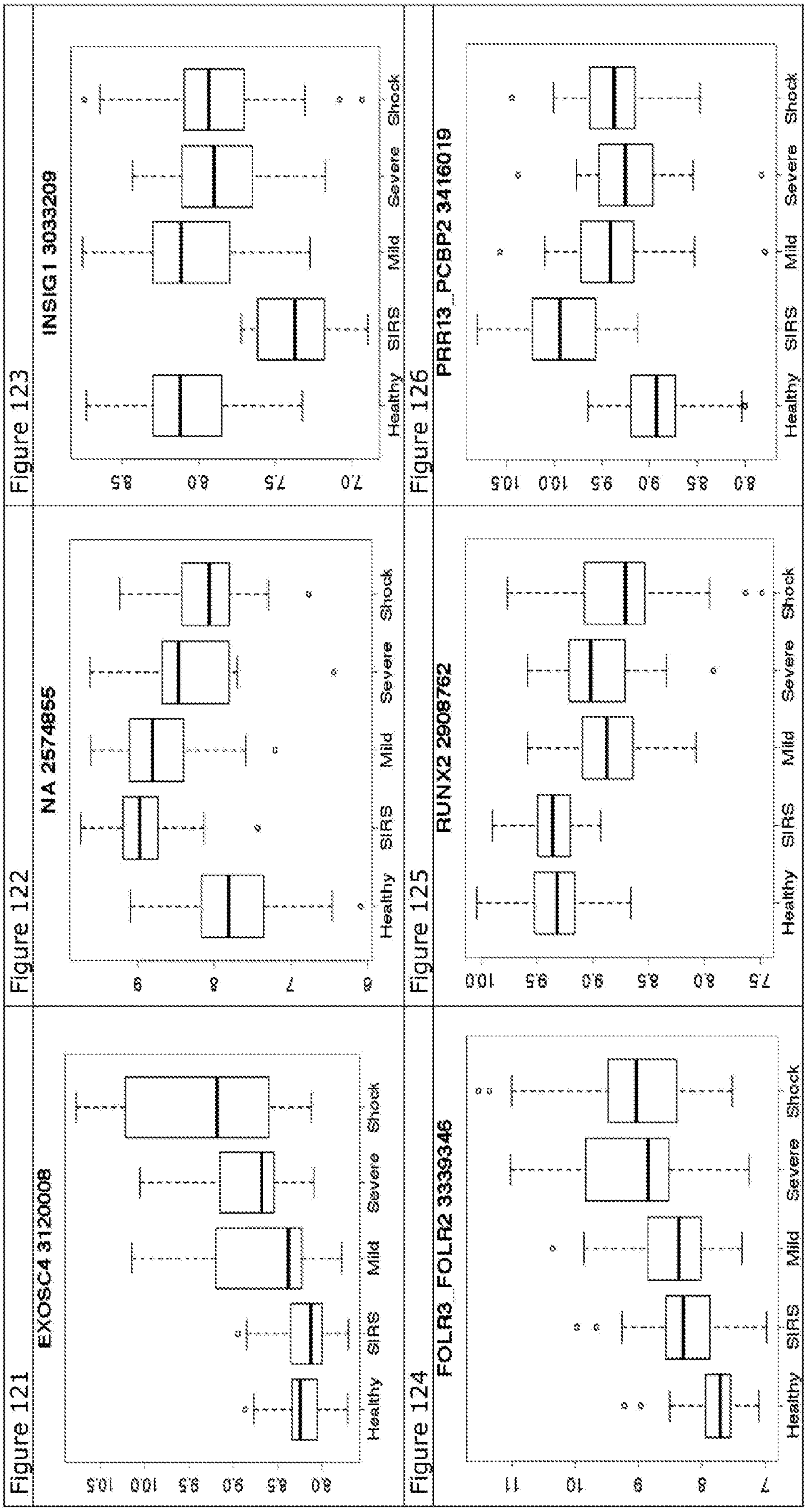
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Figure 124
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Figure 125
RUNX2 2908762
Figure 126
PRR13_PCBP2 3416019
Healthy
SIRS
Mild
Severe
Shock

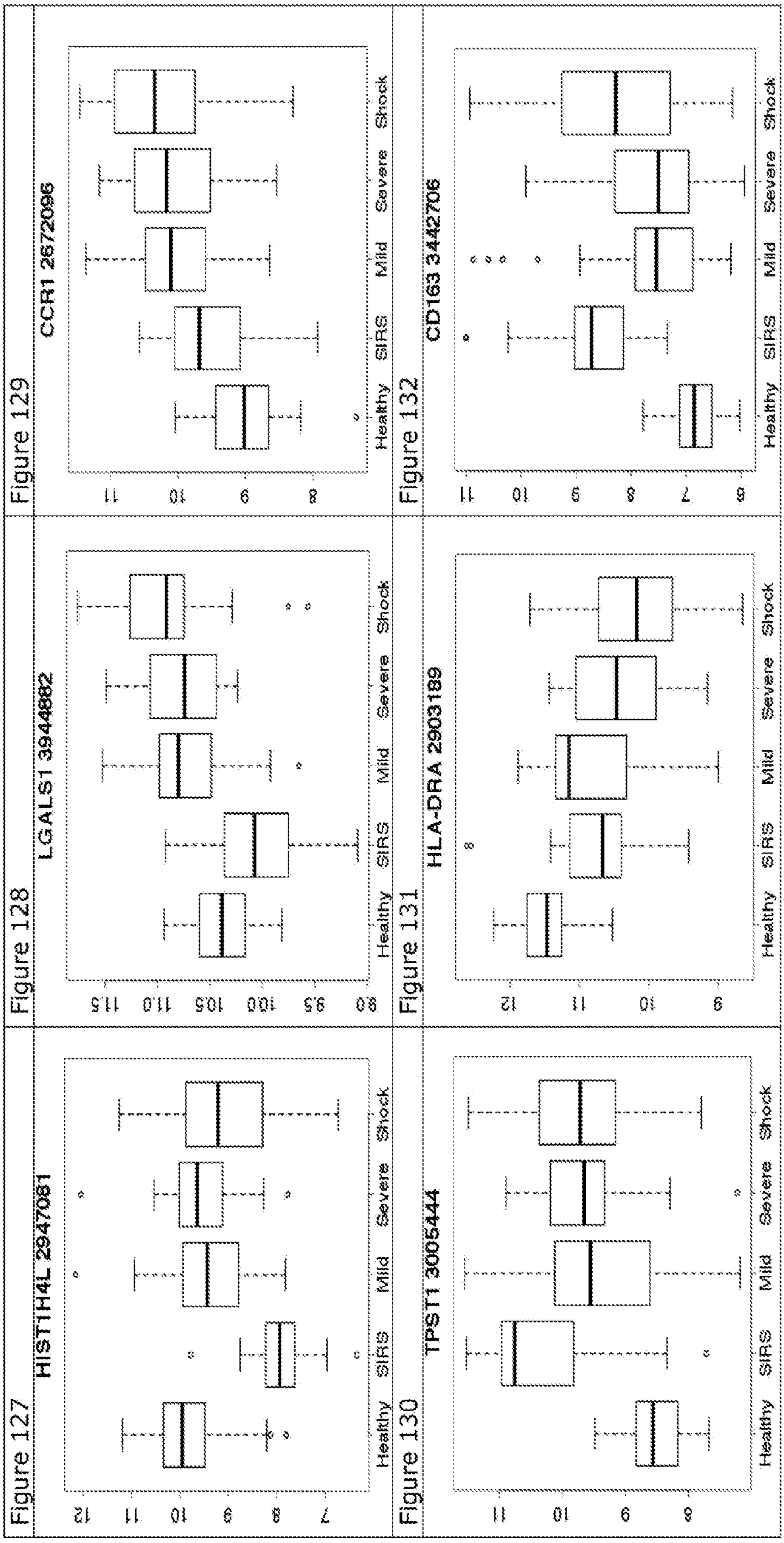

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Figure 128
Figure 129
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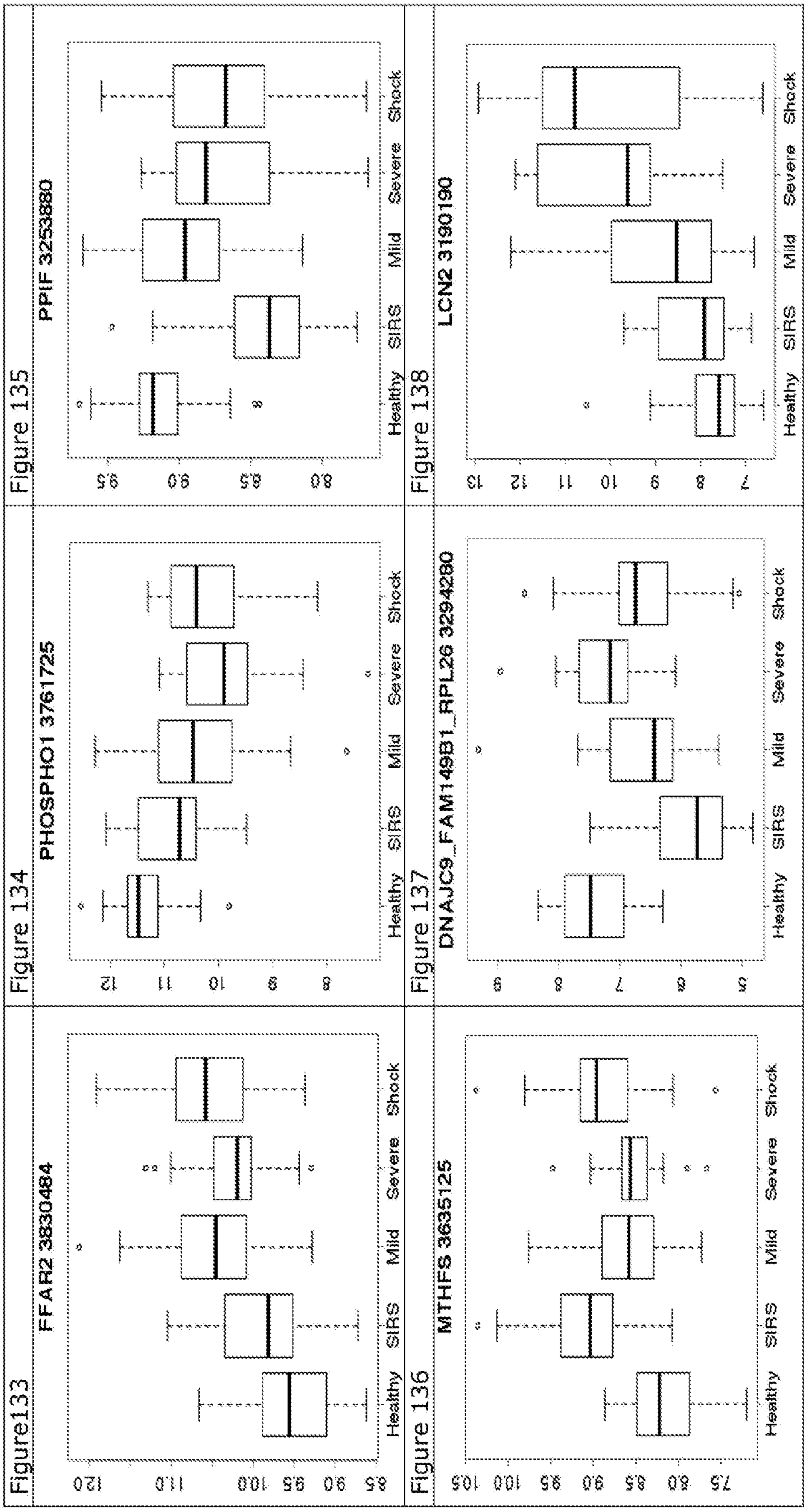
Figure 131
Figure 132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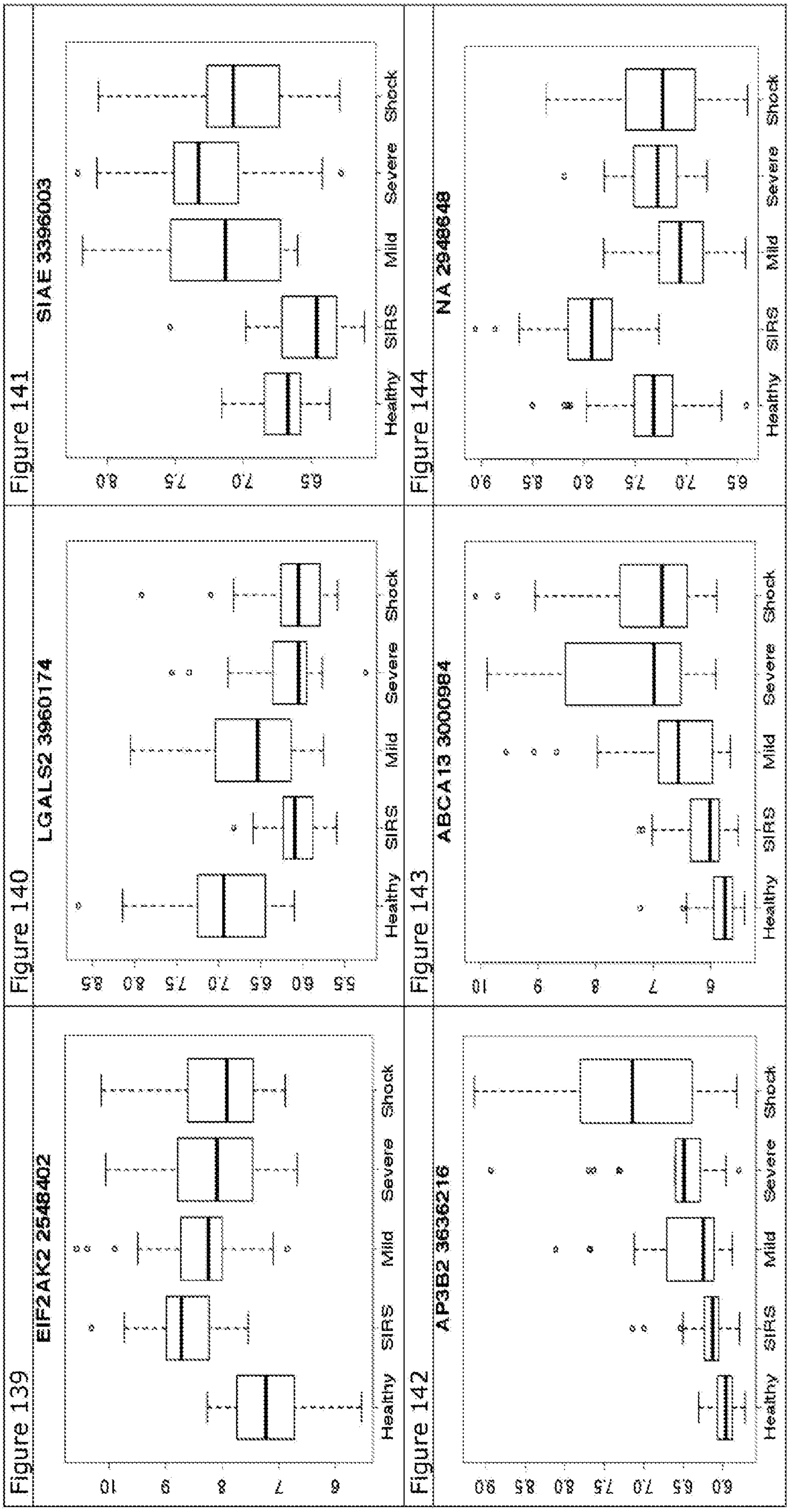
Mild
Severe
Shock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Mild
Severe
Shock

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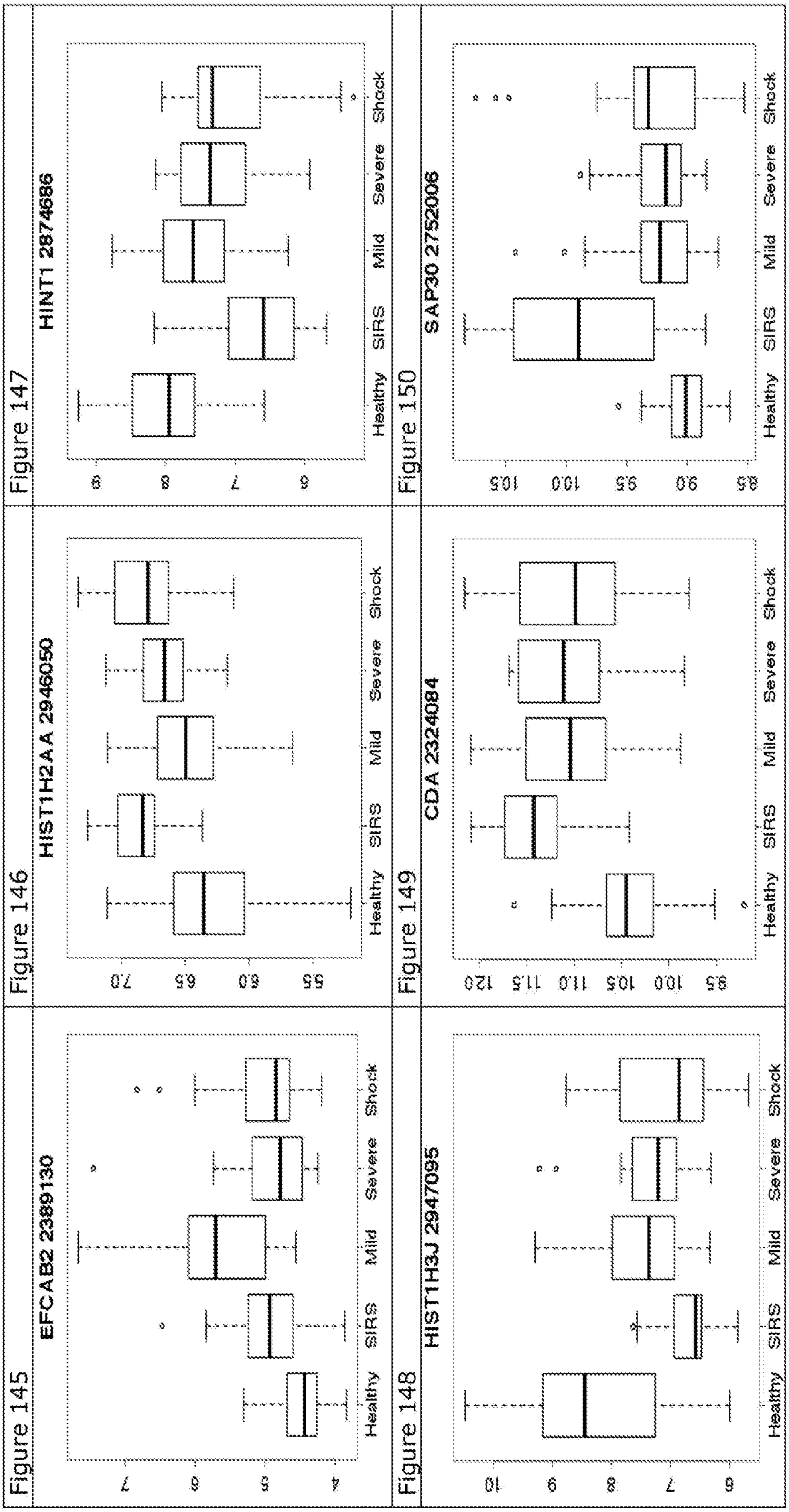

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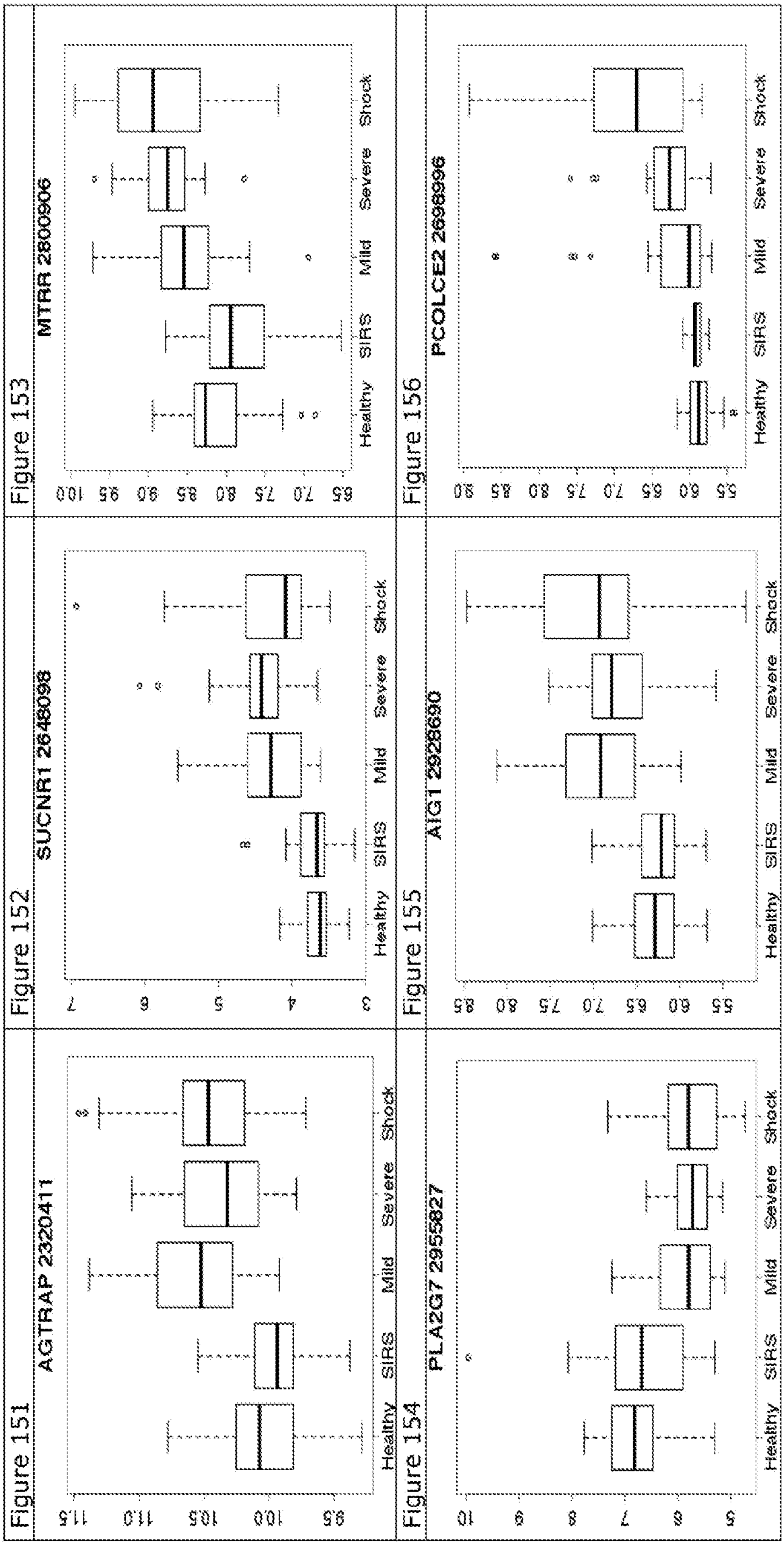
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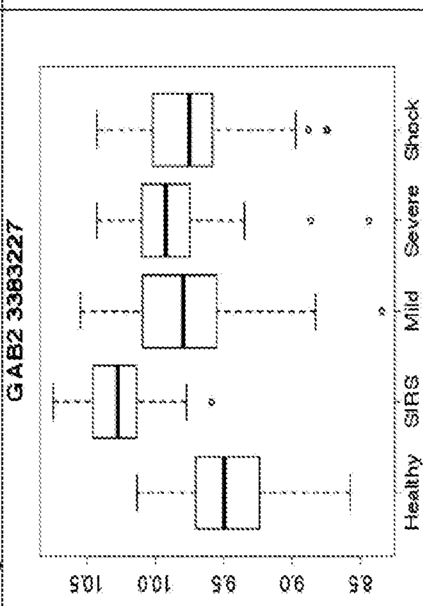
Healthy
SIRS
Mild
Severe
Shock

Figure 157



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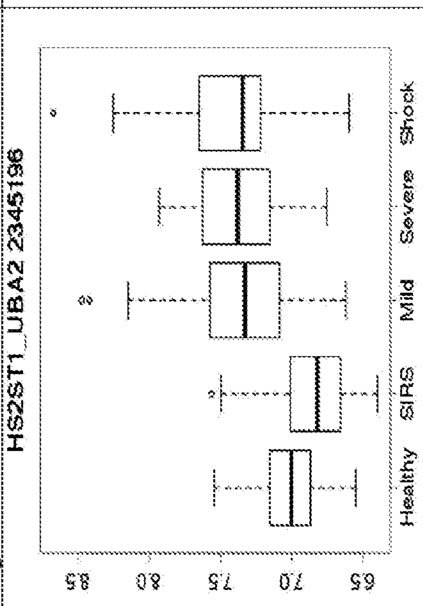

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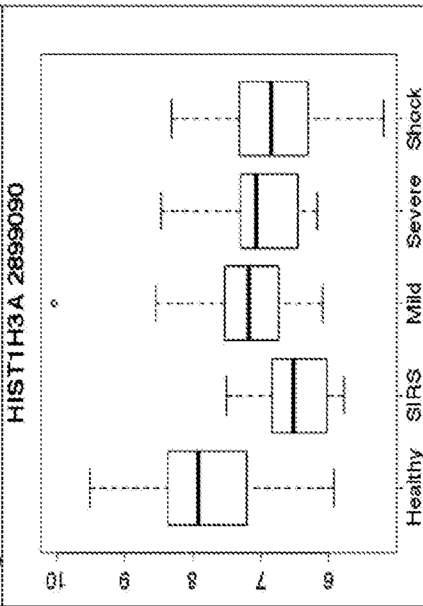

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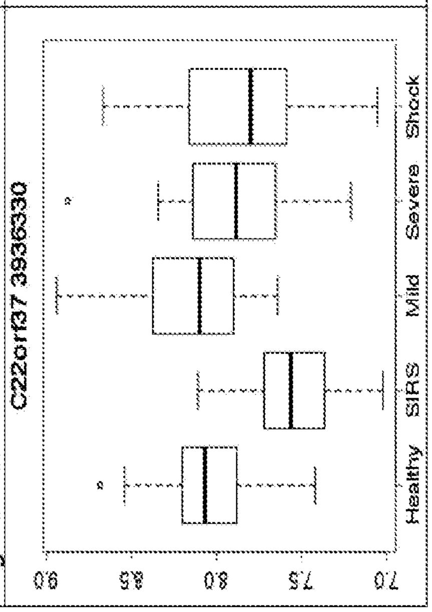

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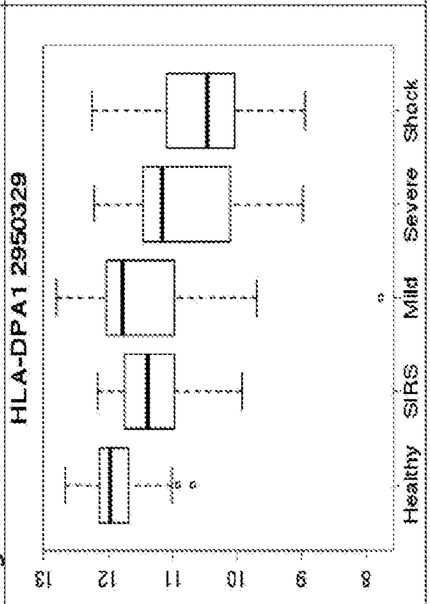

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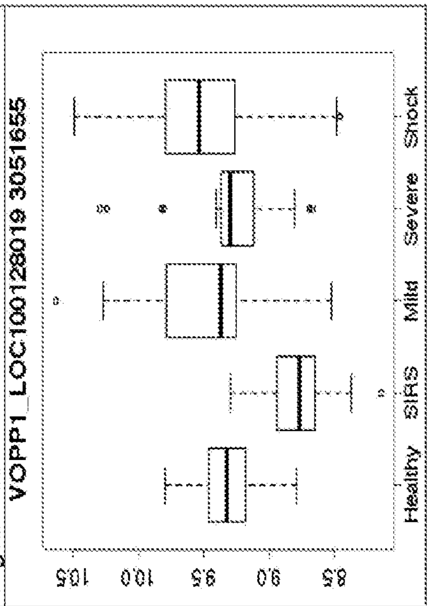

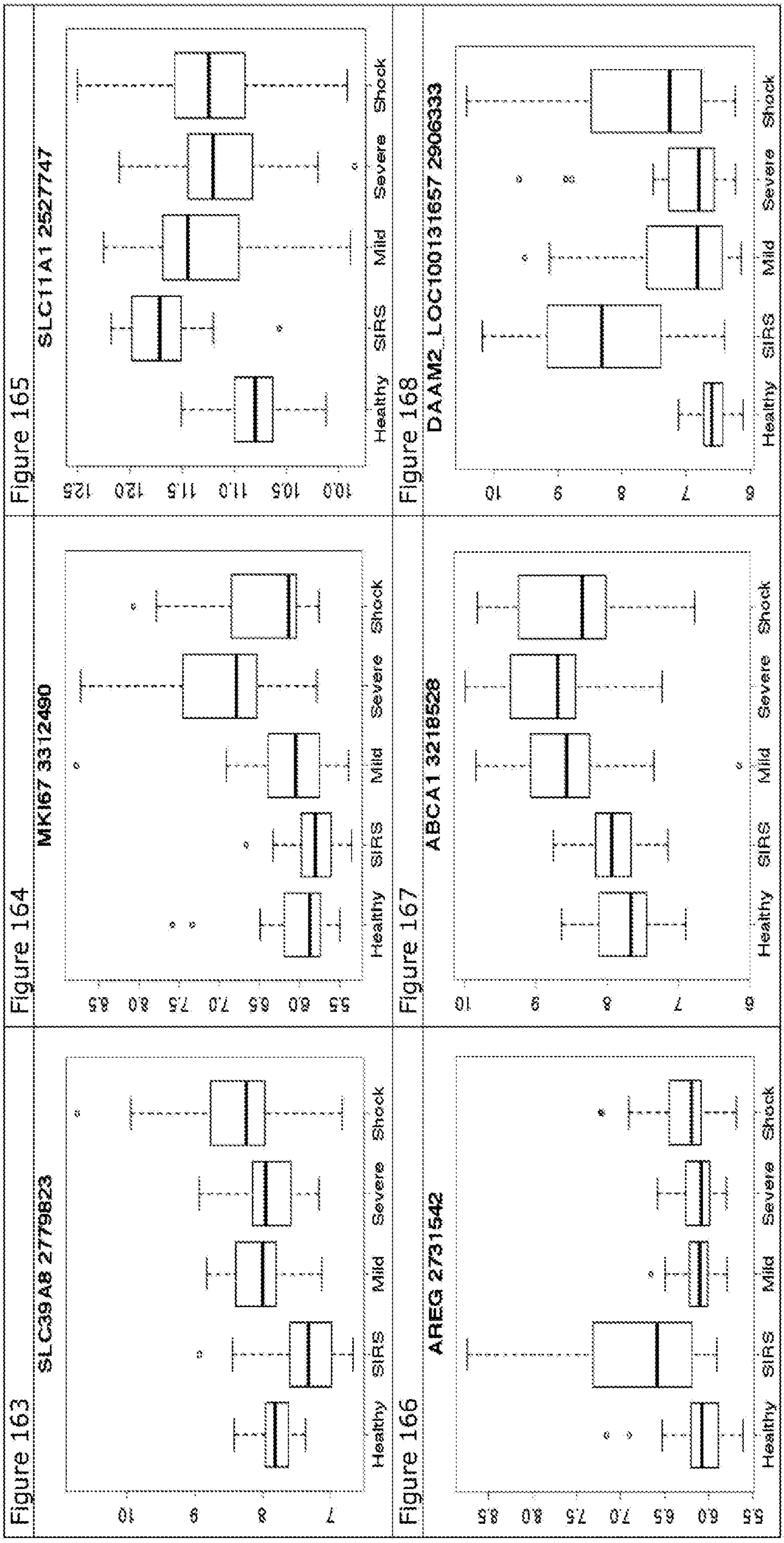
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Healthy
SIRS
Mild
Severe
Shock

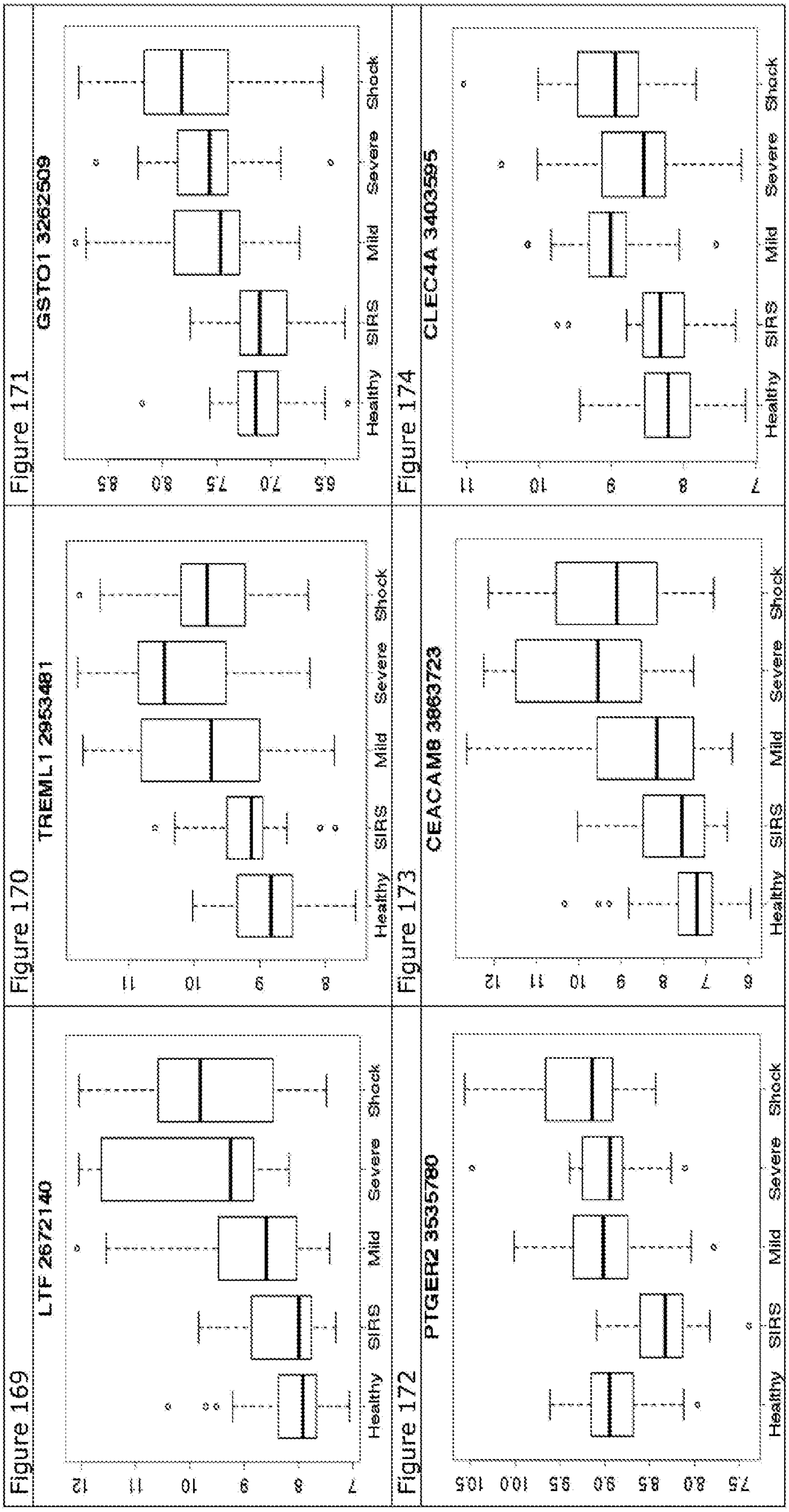

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Figure 170
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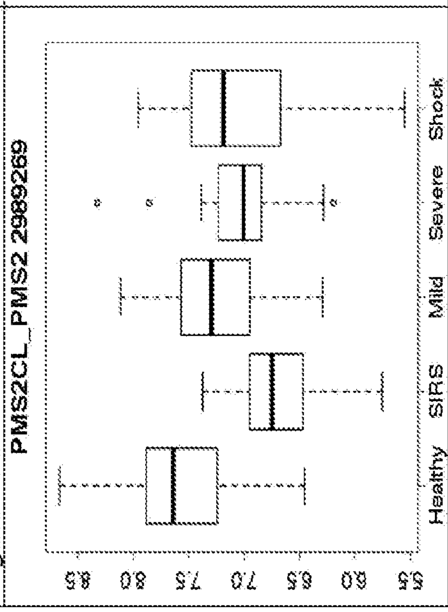
Figure 172
Figure 173
Figure 174

Figure 175



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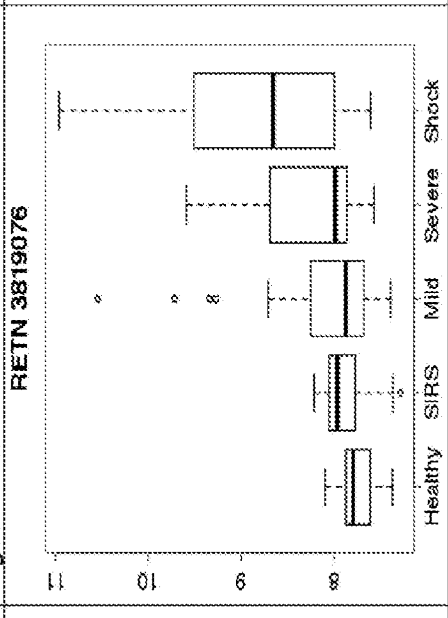

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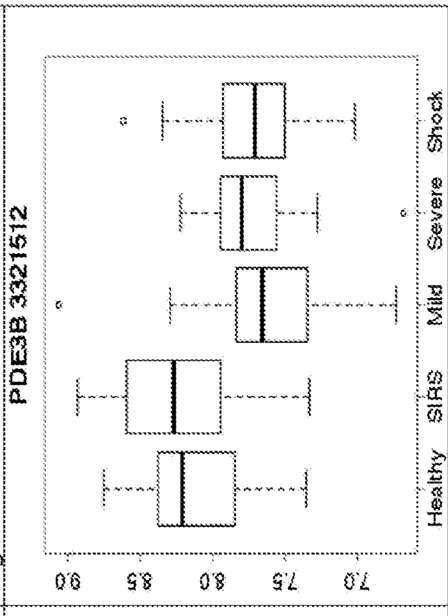

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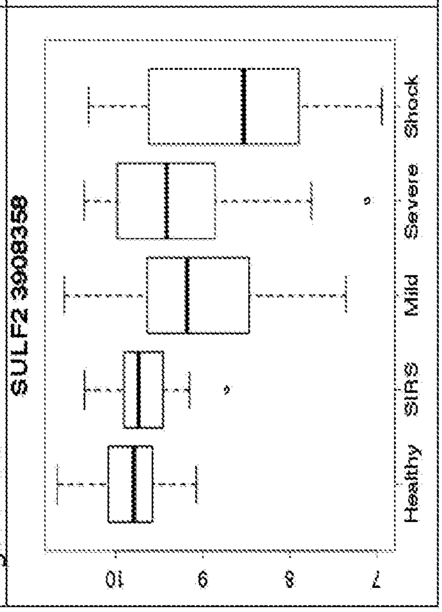

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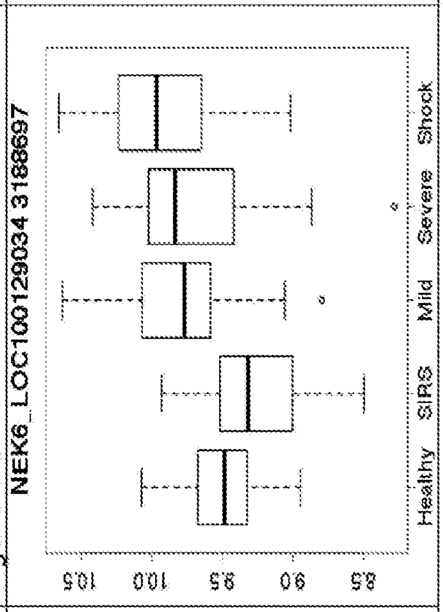

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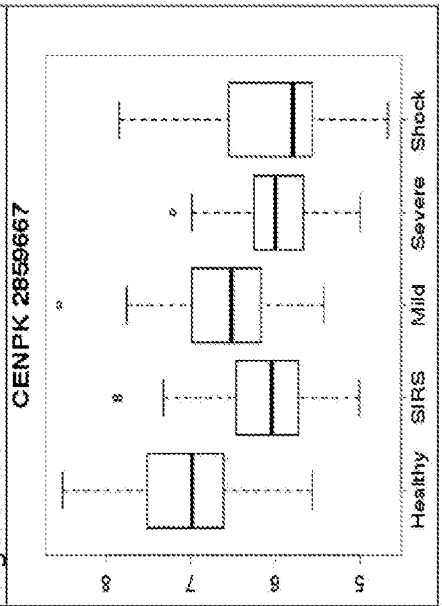

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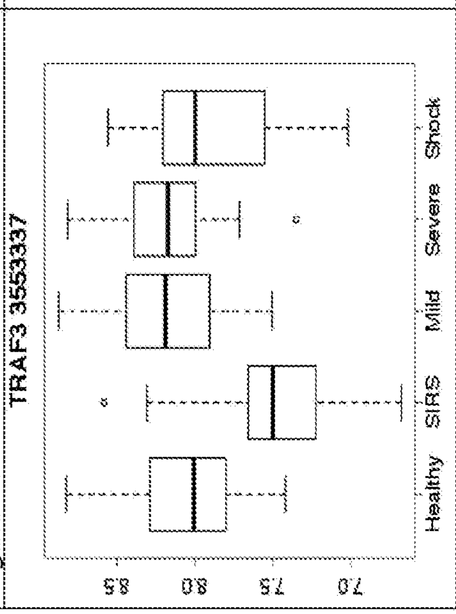

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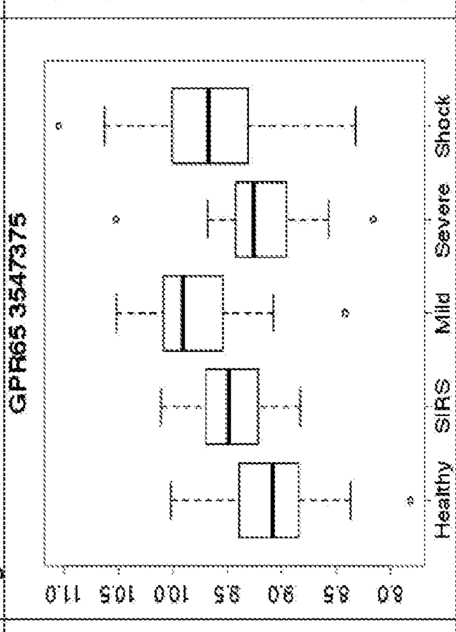

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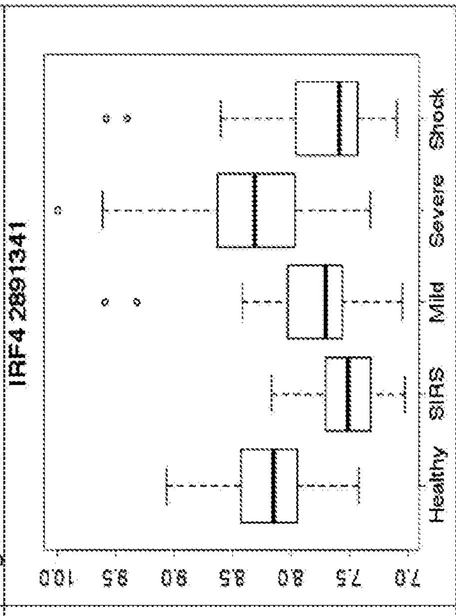

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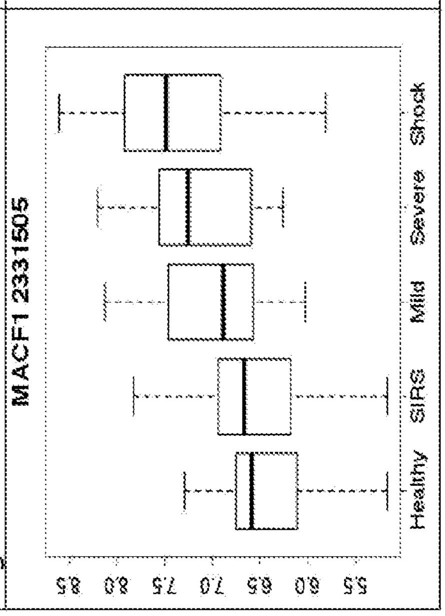

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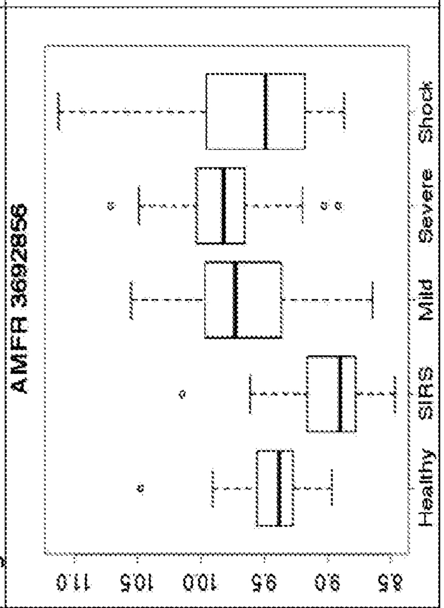

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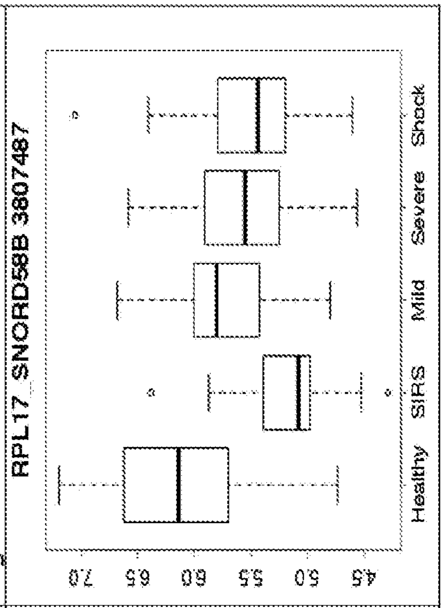

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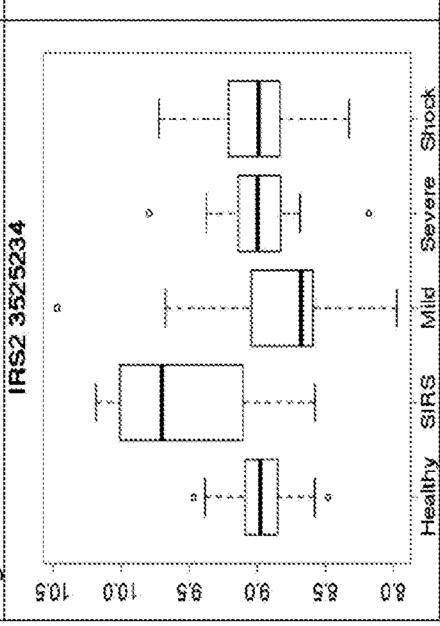

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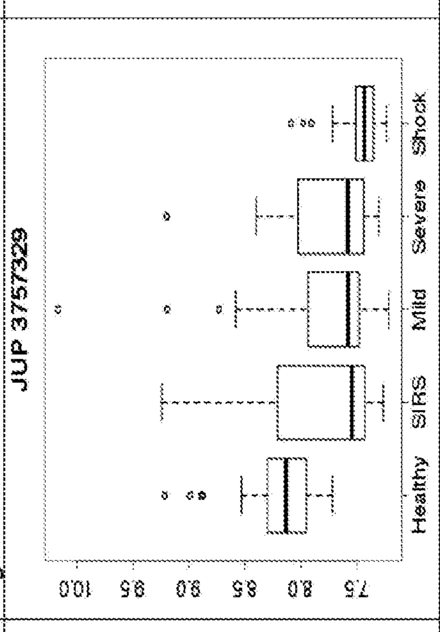

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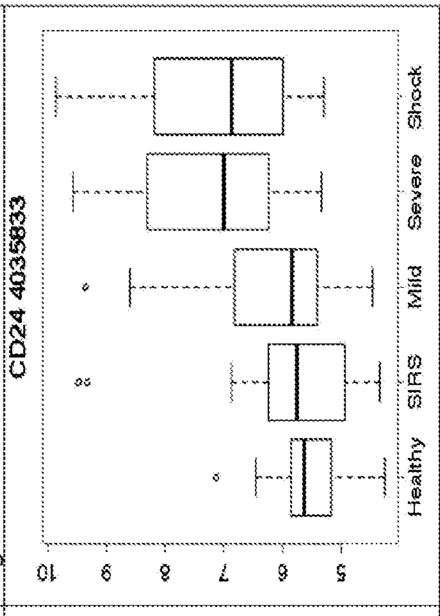

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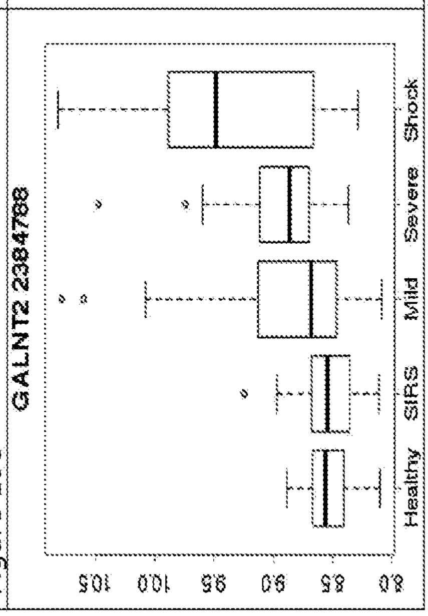
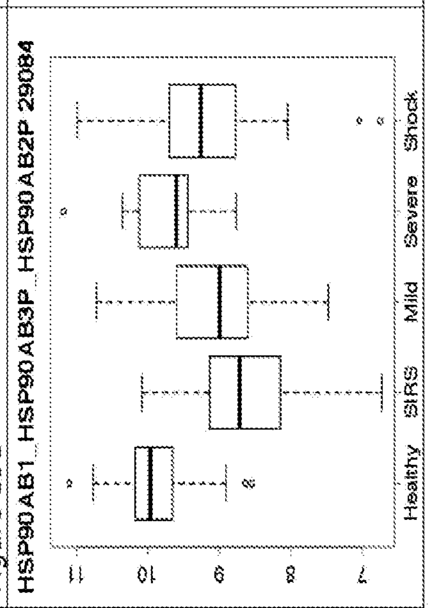


Figure 191



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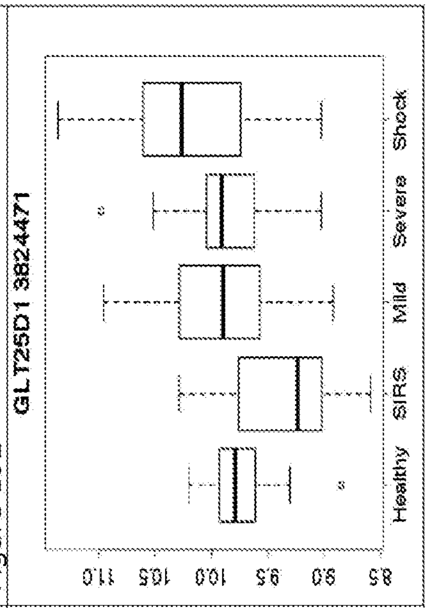

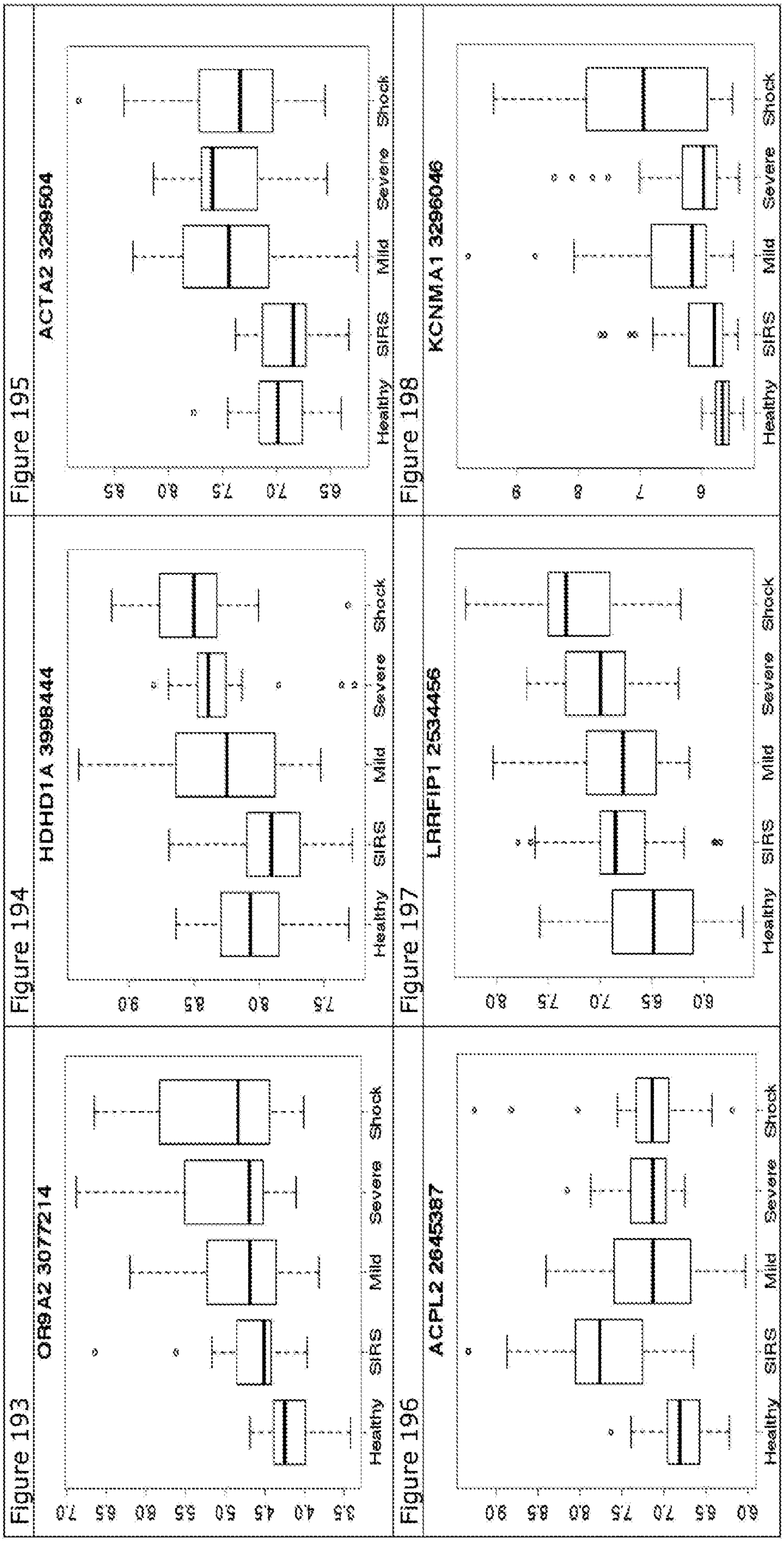
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Figure 196
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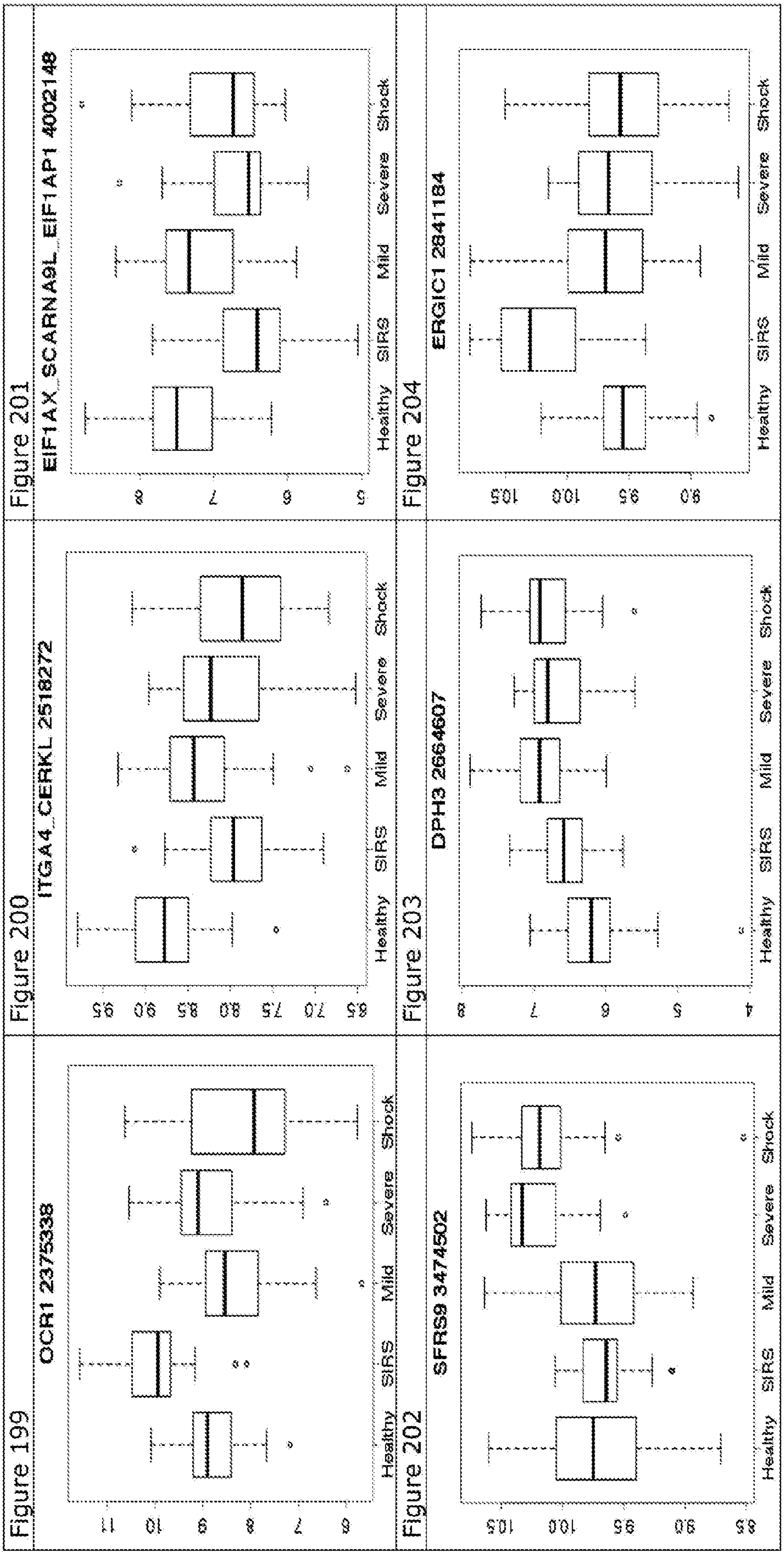
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Figure 204
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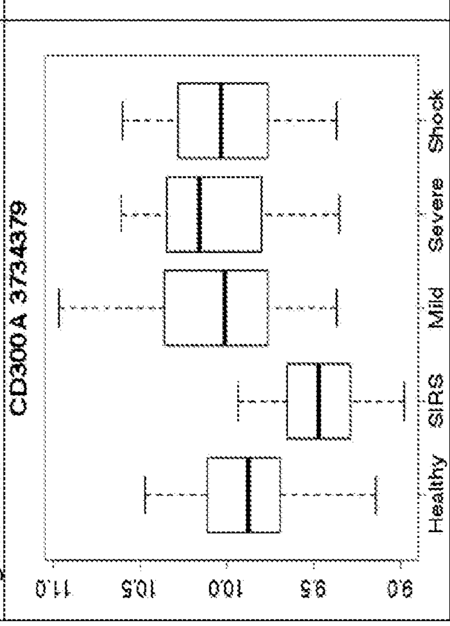
Healthy
SIRS
Mild
Severe
Shock

Figure 205



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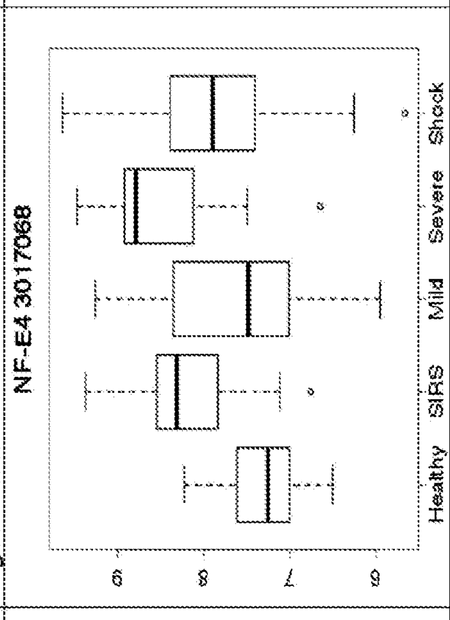

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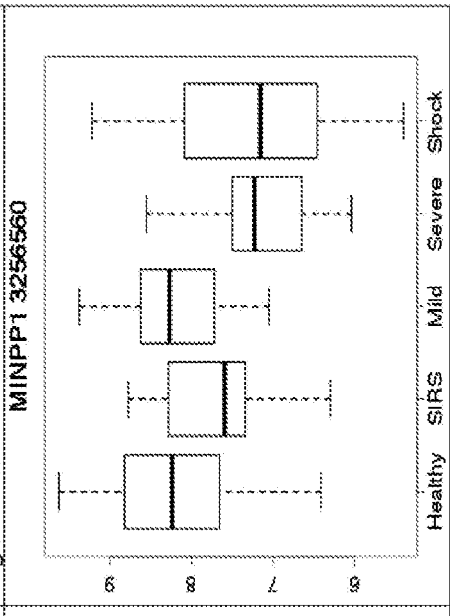

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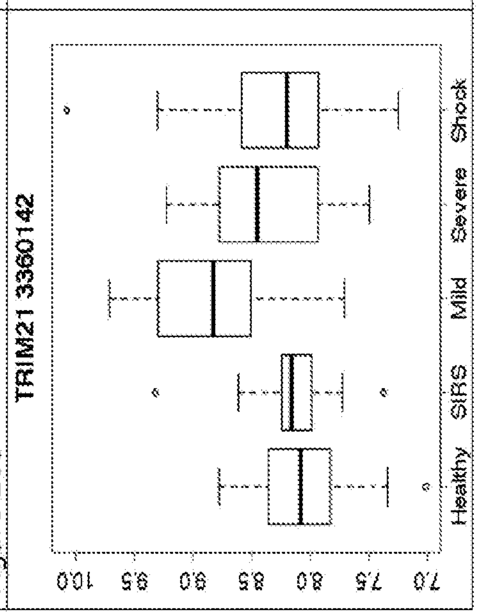

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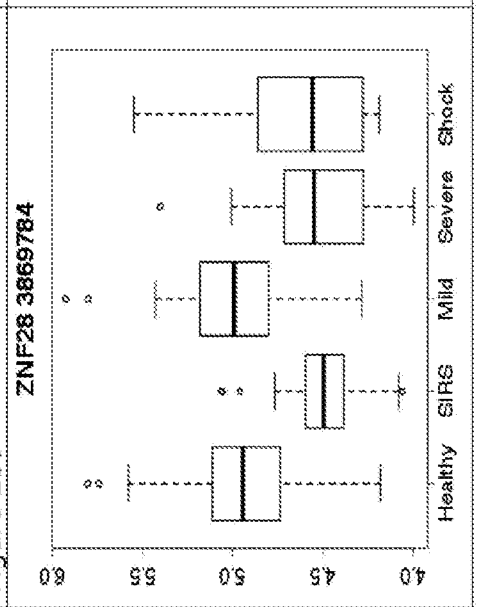

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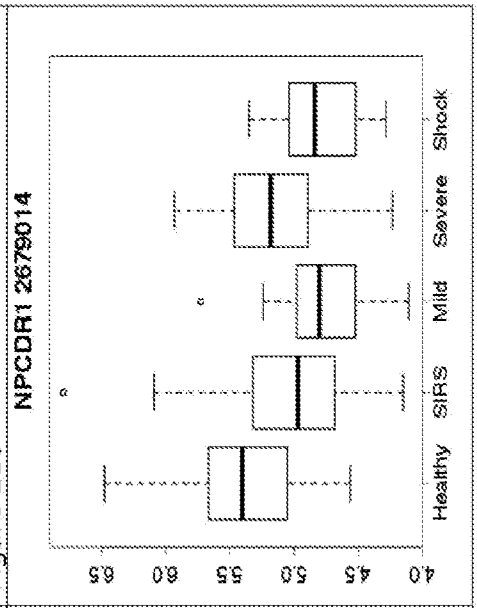

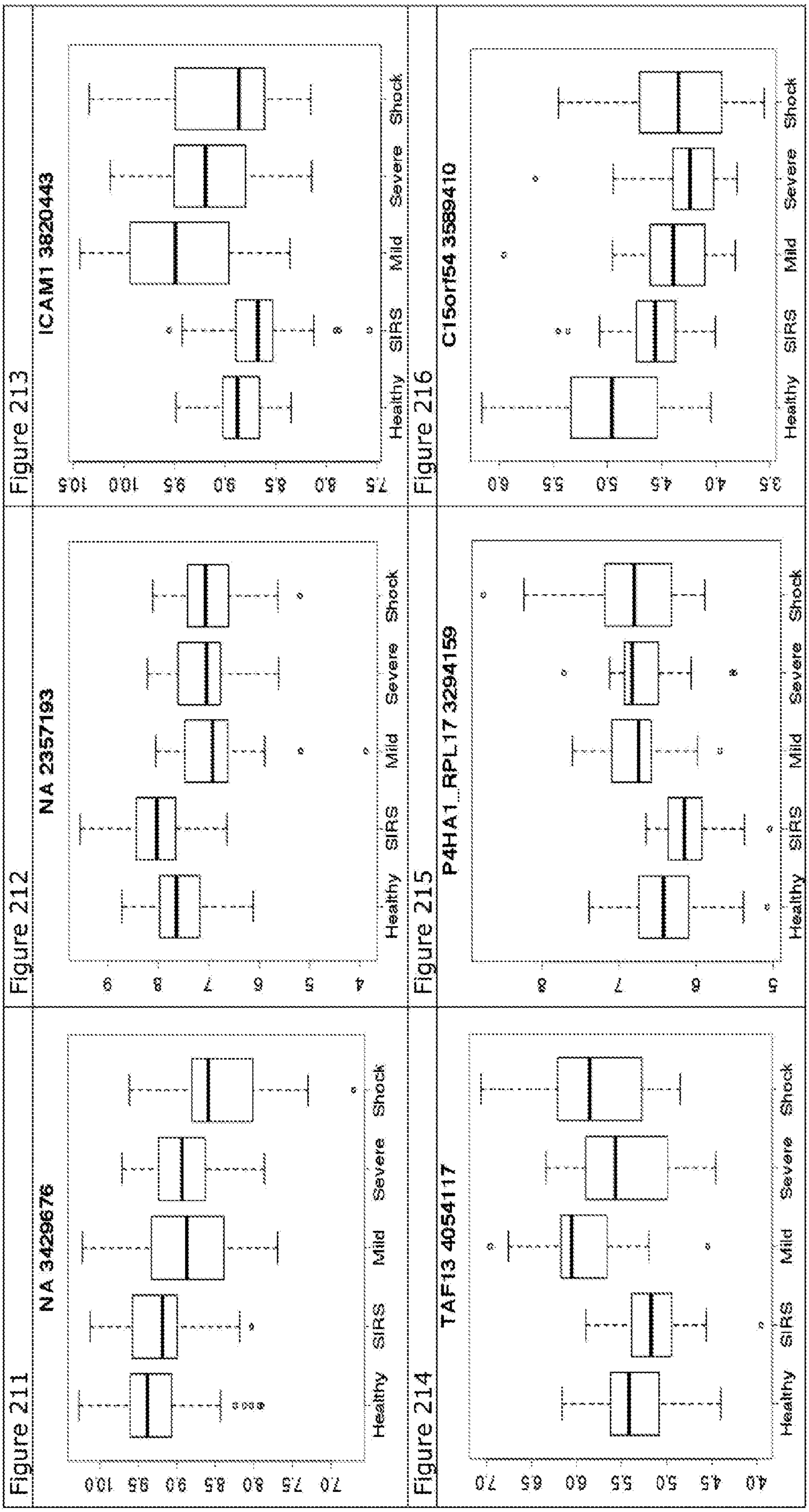
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Figure 216
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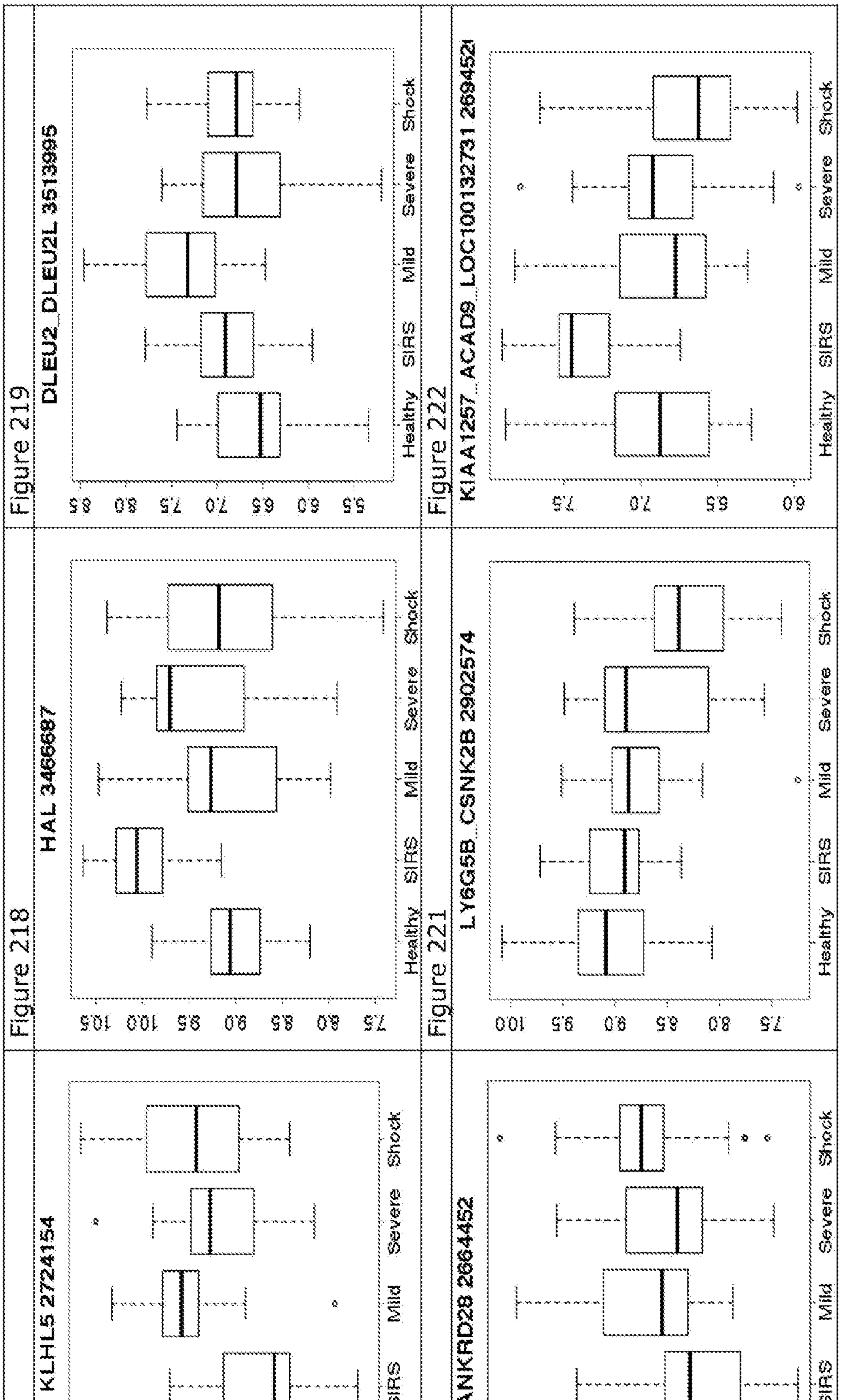
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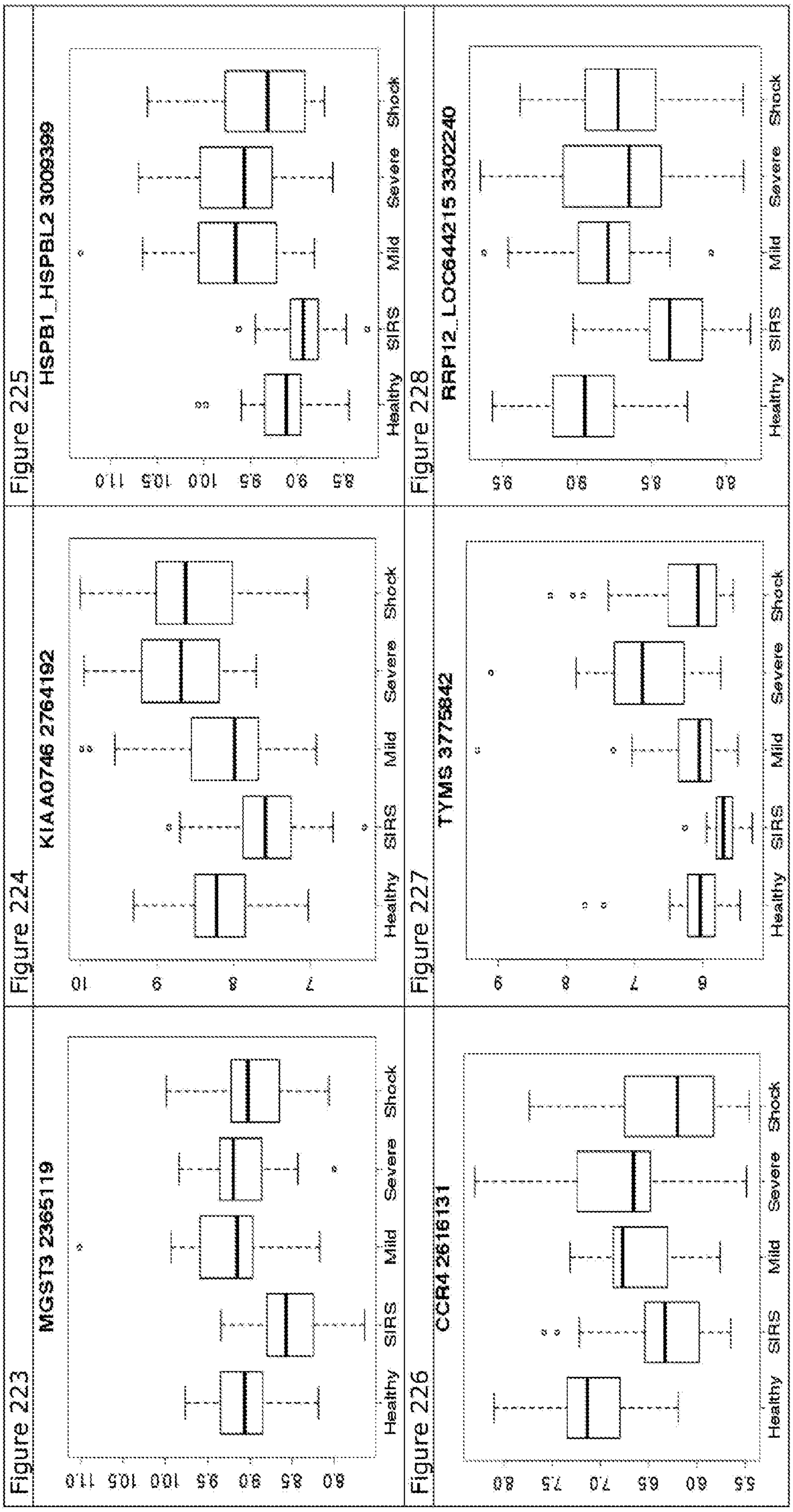
Severe
Shock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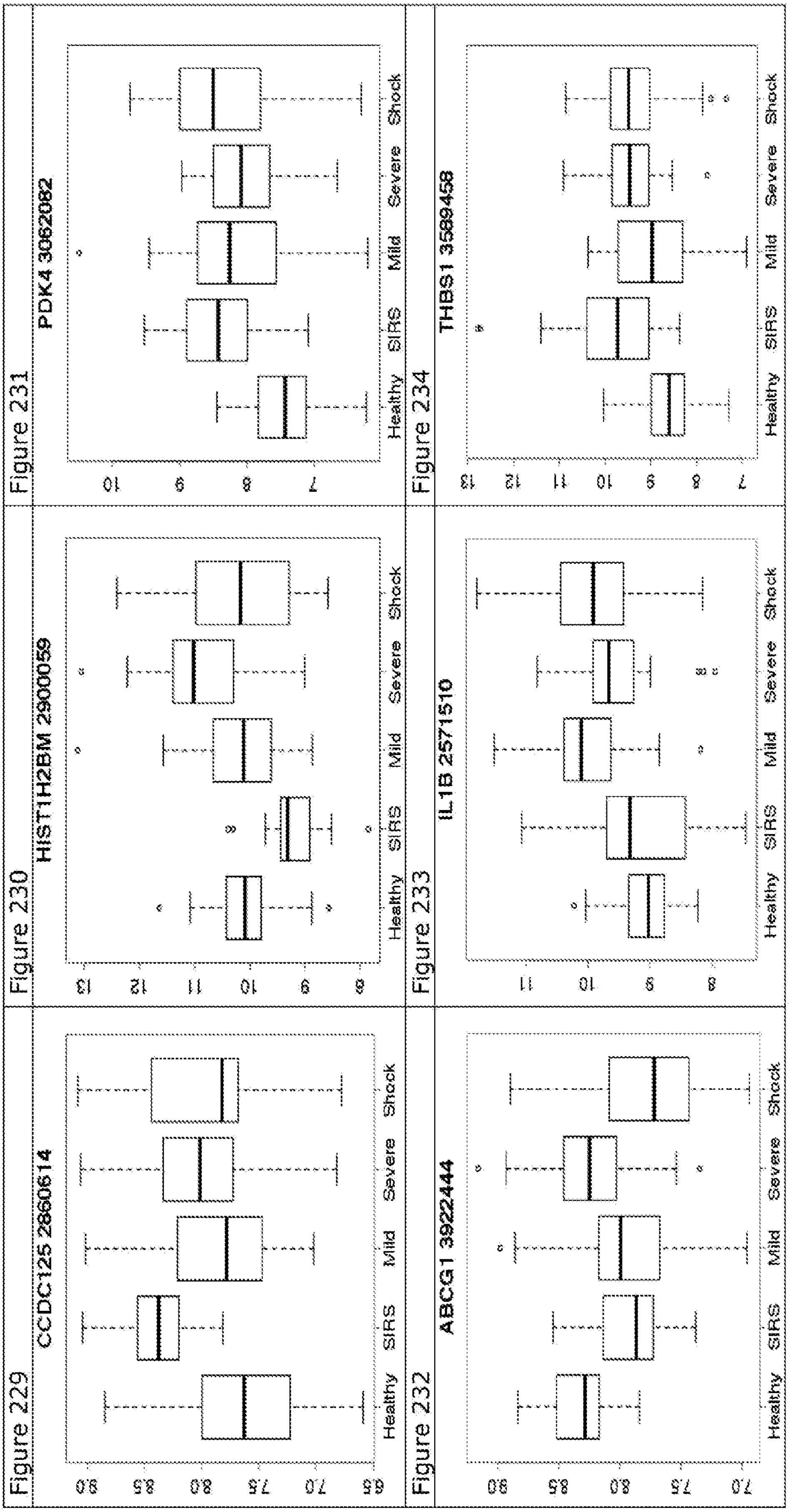
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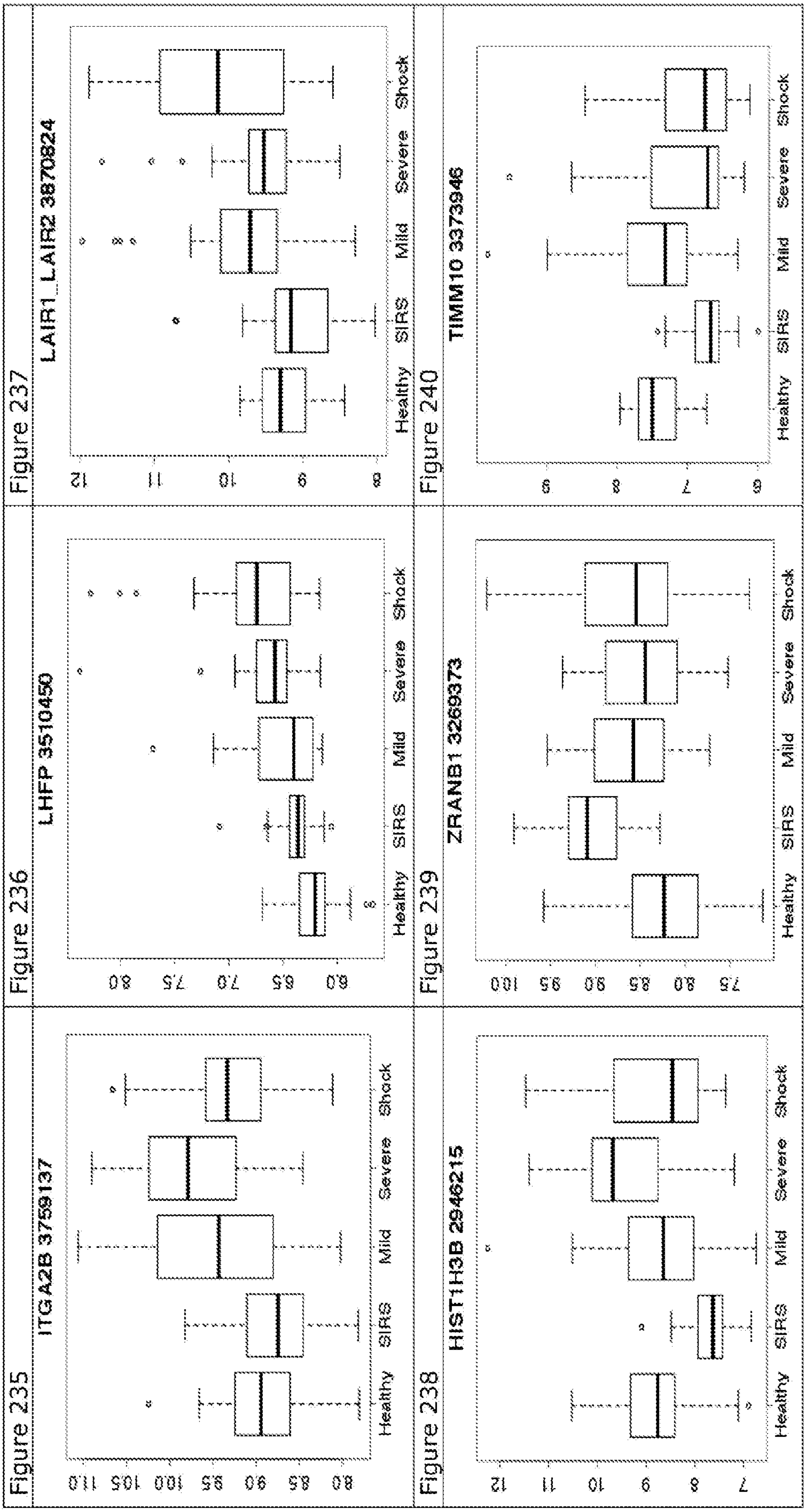
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Mild
Severe
Shock
Figure 236
LHFP 3510450
Figure 237
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Figure 238
HIST1H3B 2946215
Figure 239
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Figure 240
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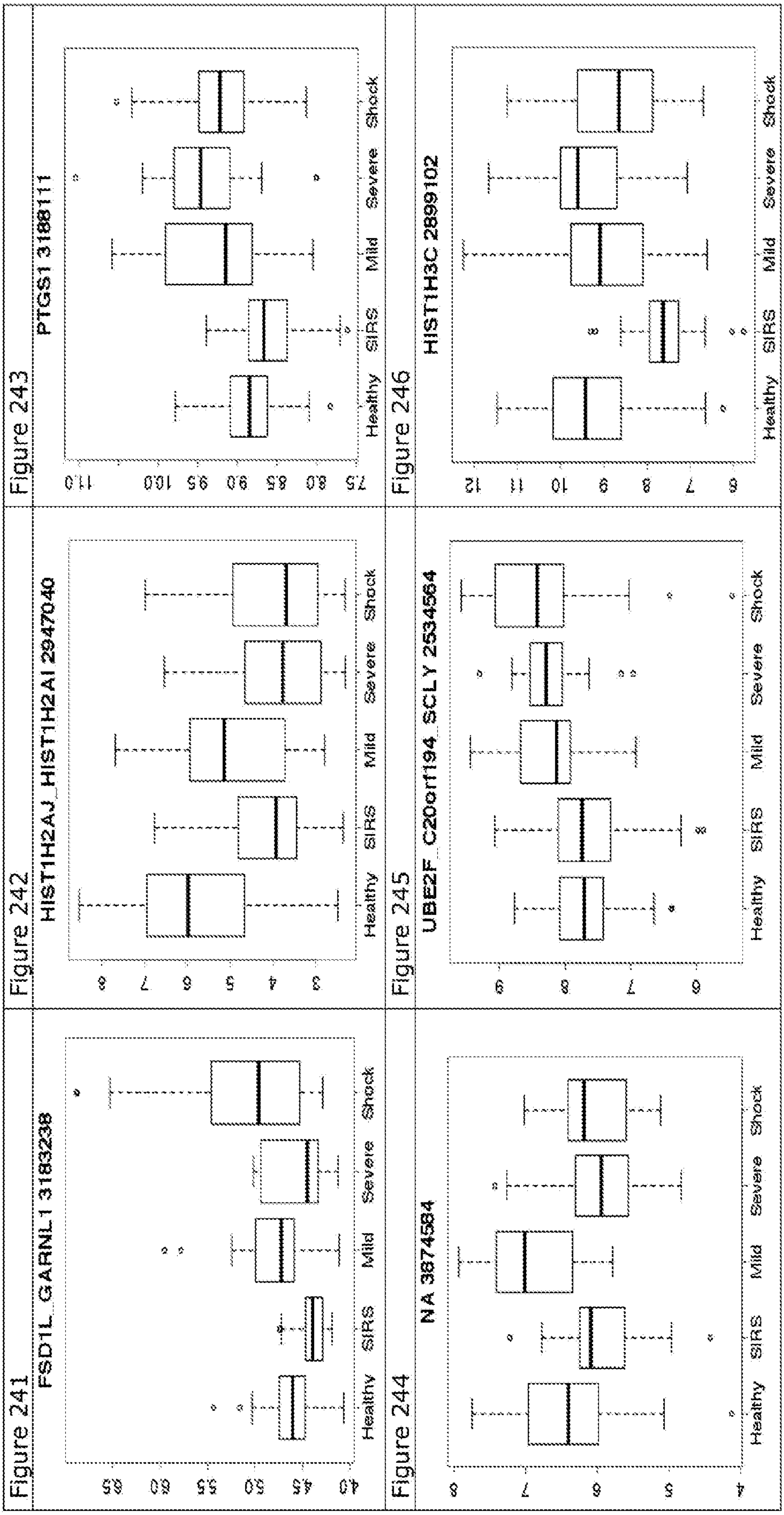
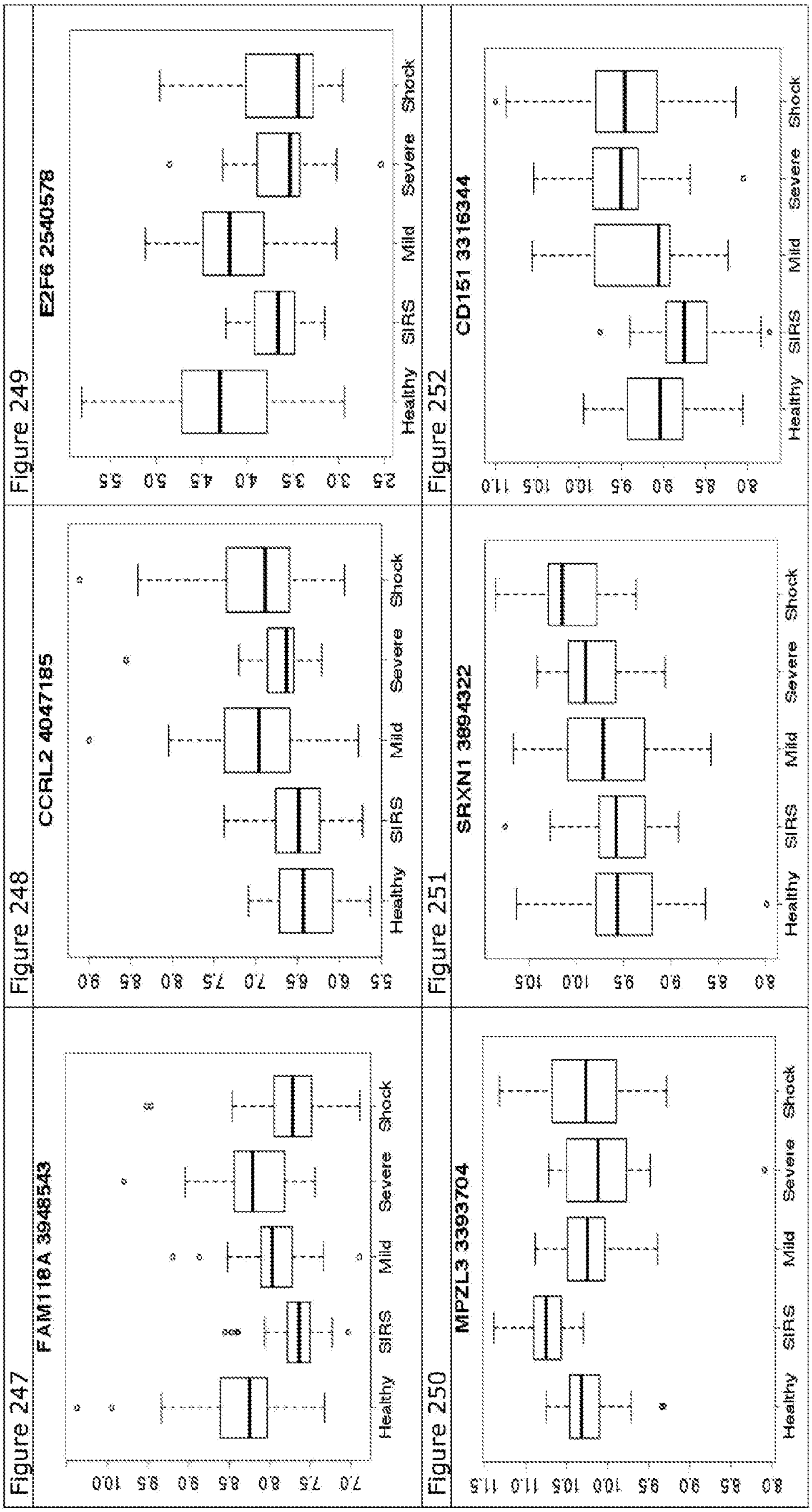


Figure 241 Figure 242 Figure 243 Figure 244 Figure 245 Figure 246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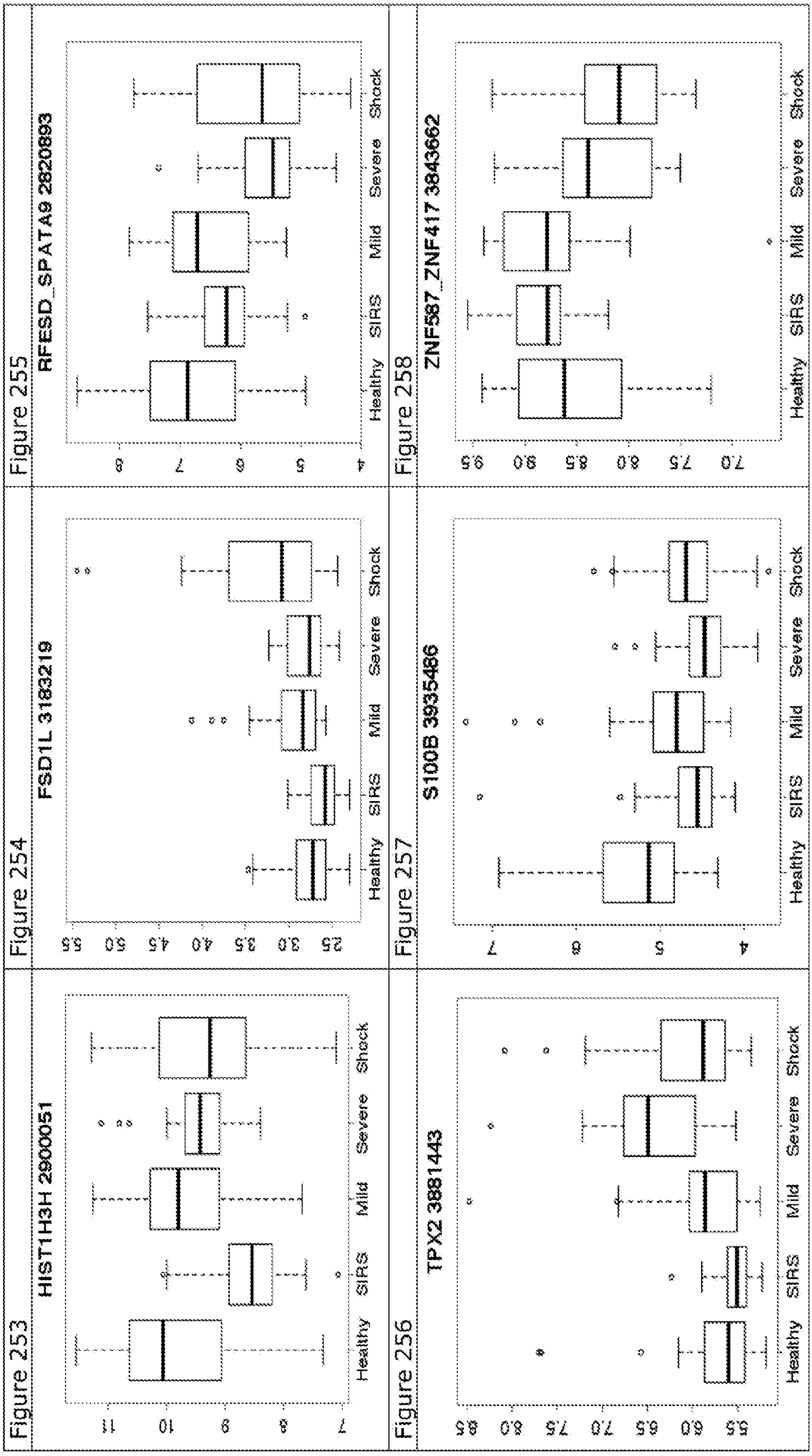
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Shock
Figure 255
RFESD_SPATA9 2820893
Healthy
SIRS
Mild
Severe
Shock
Figure 256
TPX2 3881443
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Severe
Shock
Figure 257
S100B 3935486
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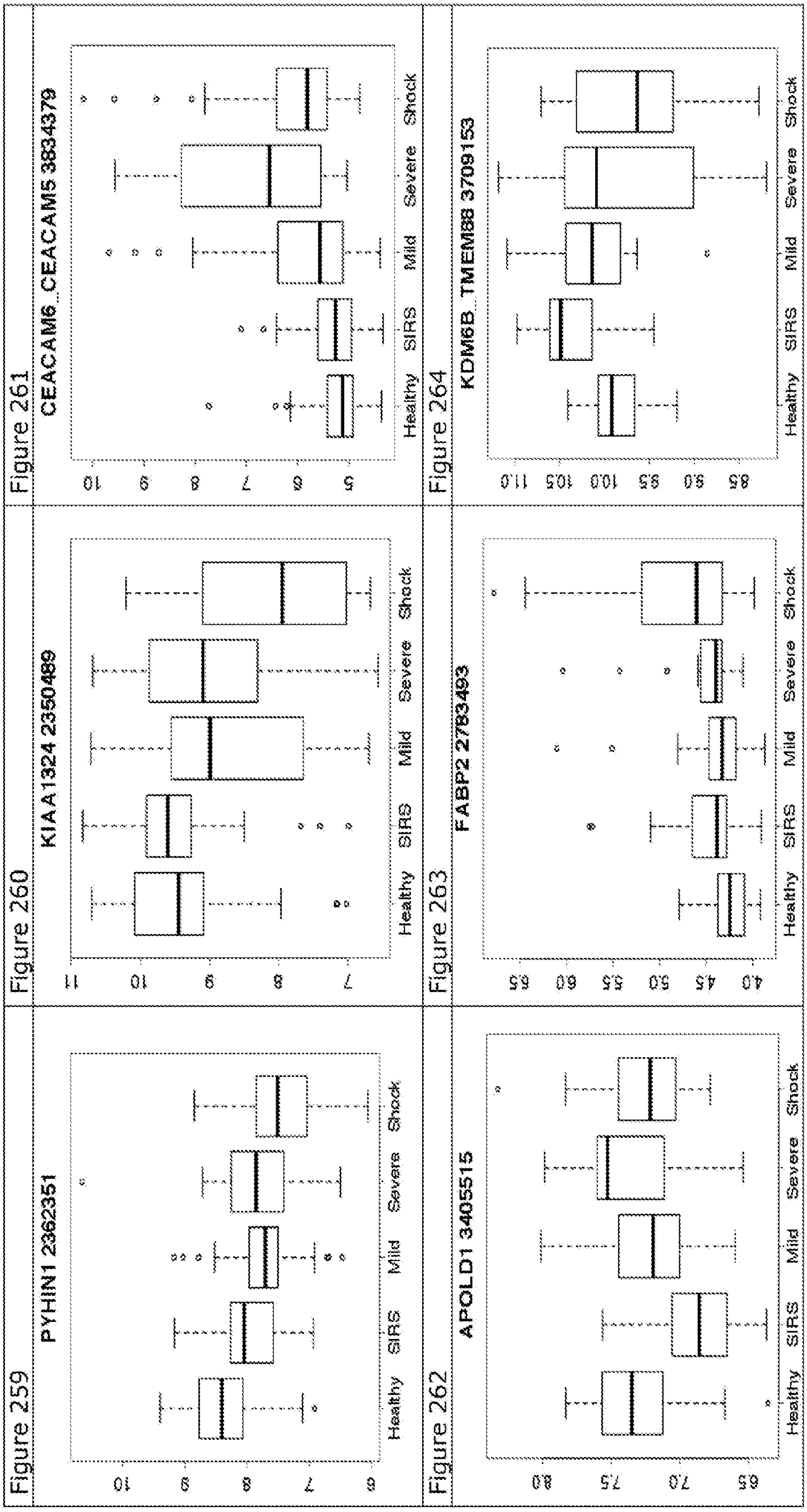
Shock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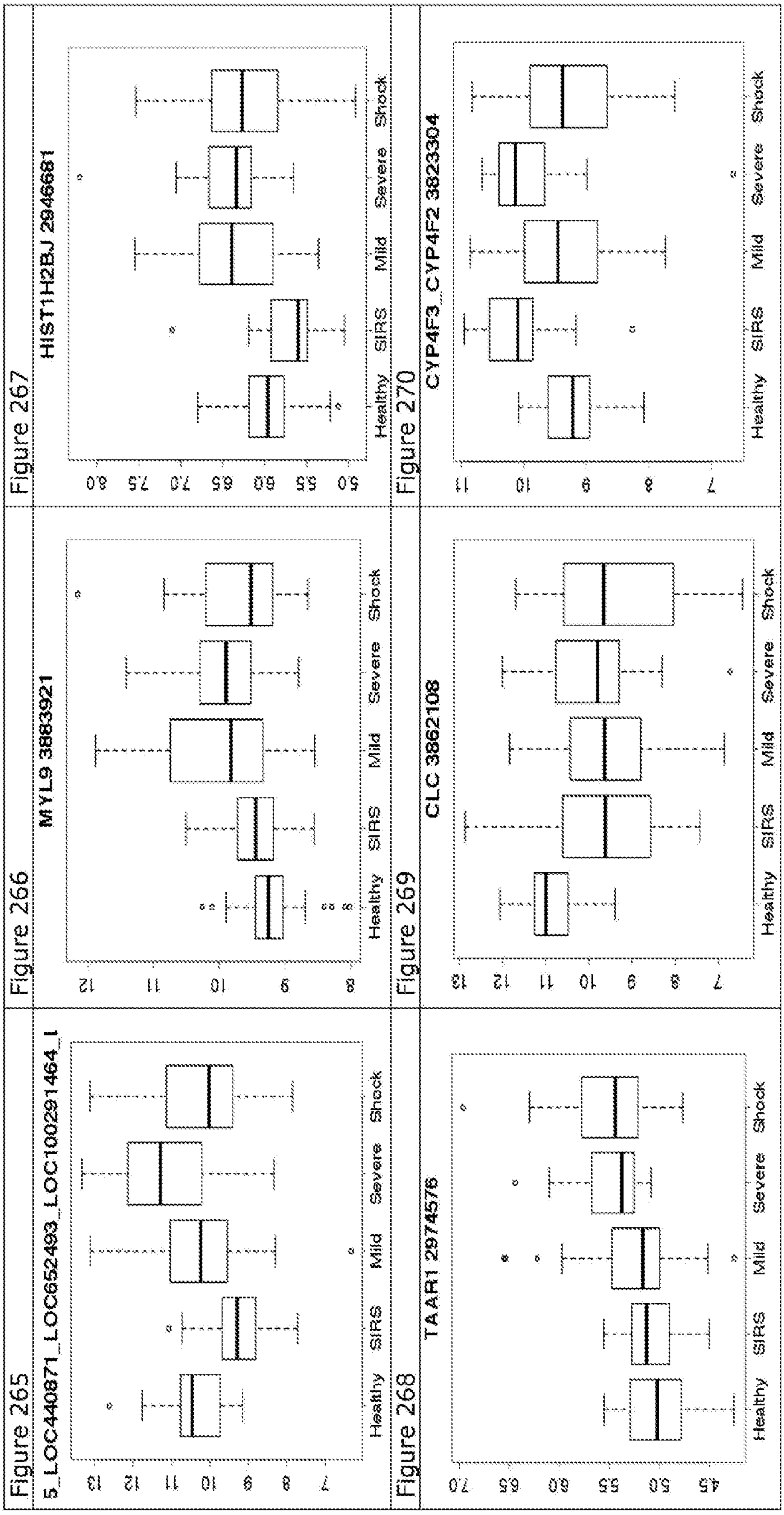
Severe
Shock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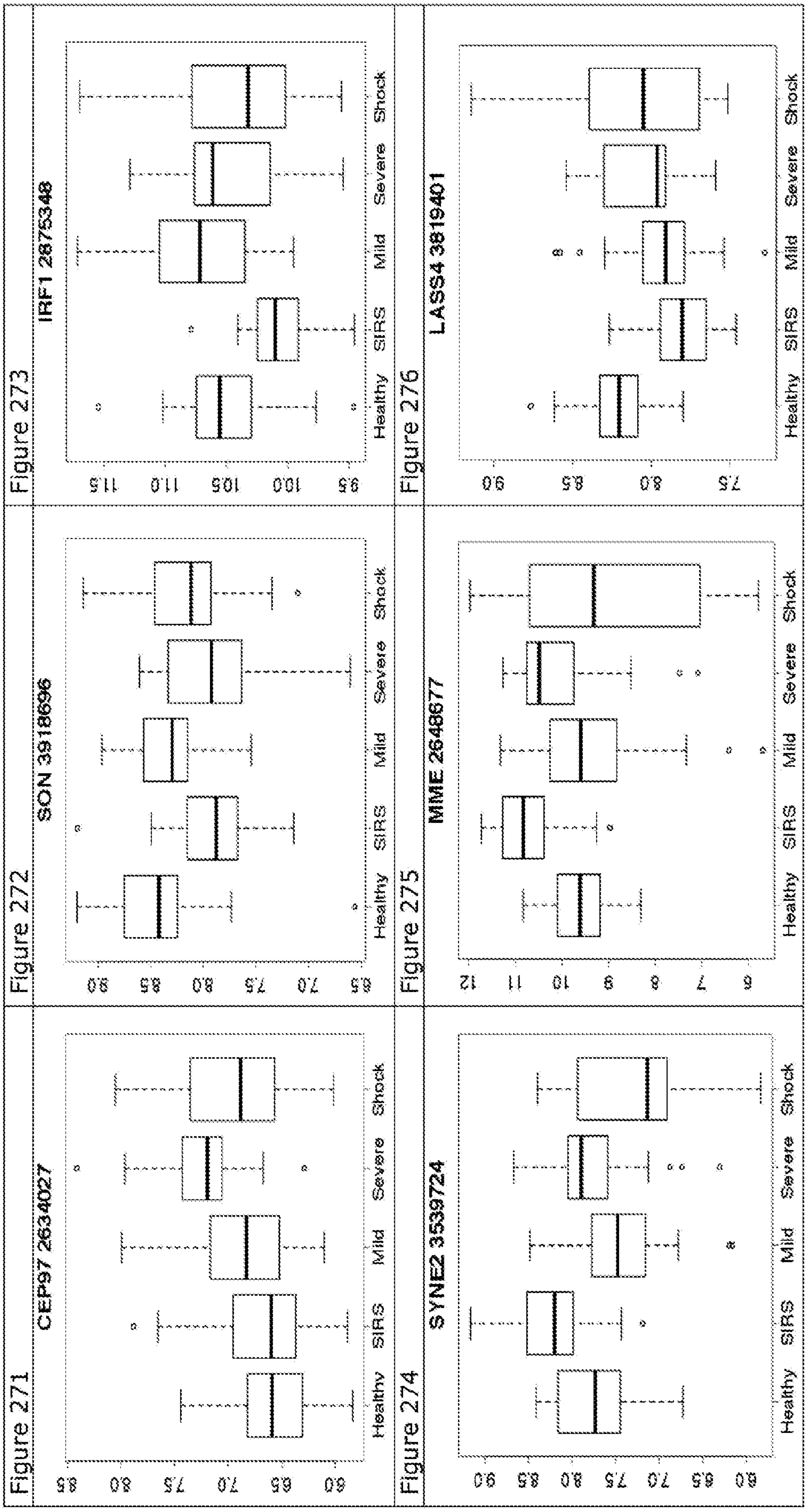
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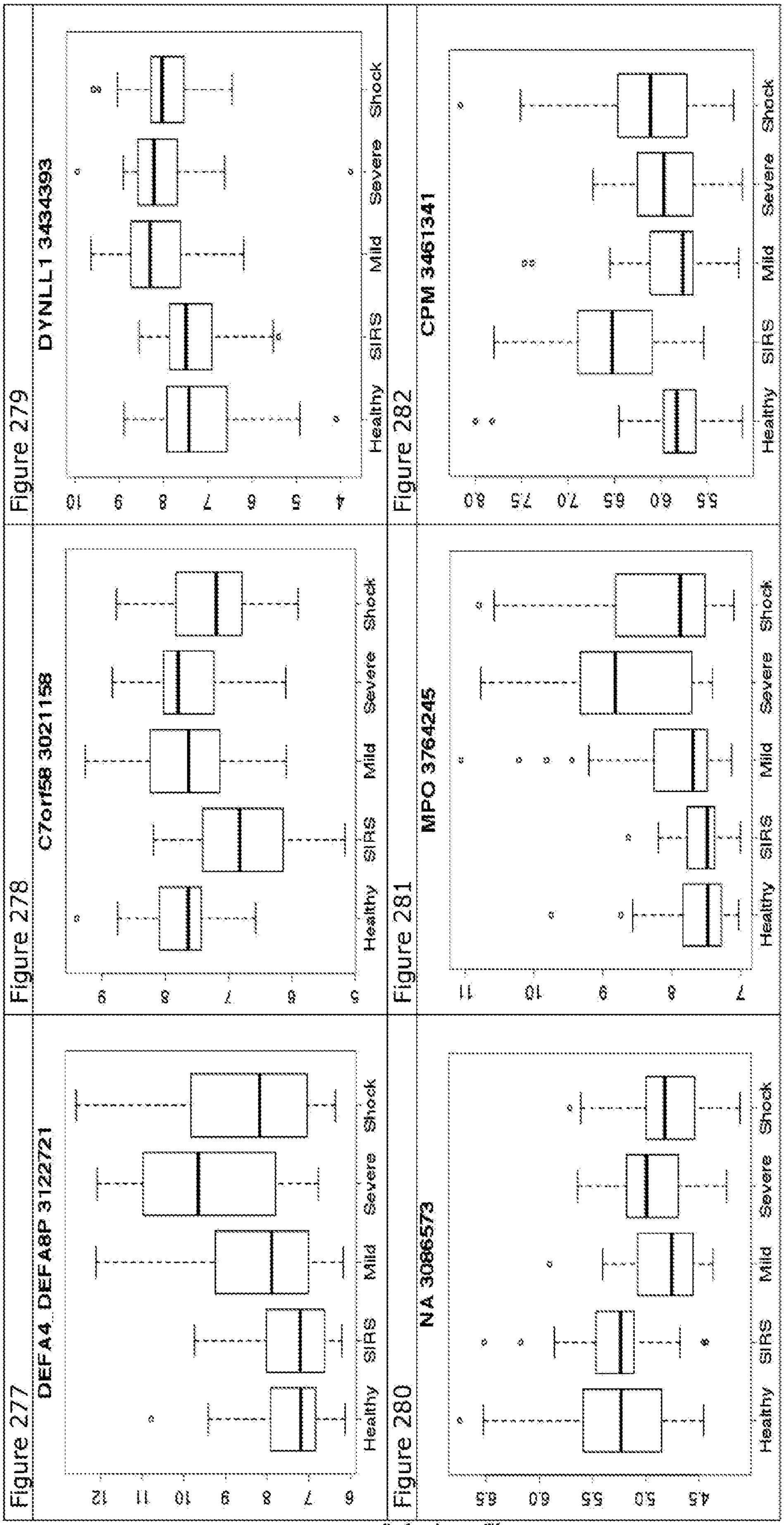
Shock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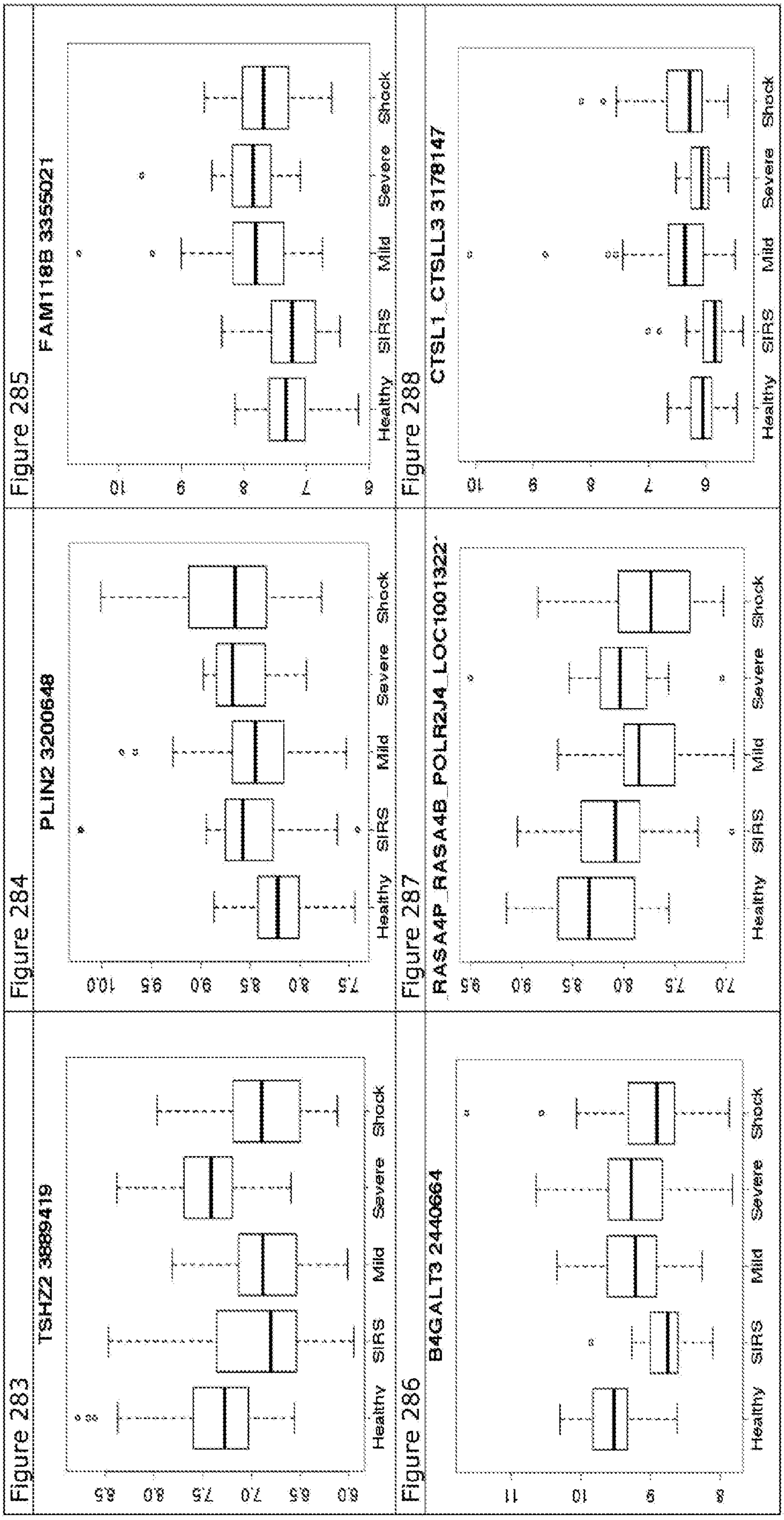
Mild
Severe
Shock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Healthy SIRS Mild Severe Shock
Figure 286
B4GALT3 2440664
Healthy SIRS Mild Severe Shock
Figure 287
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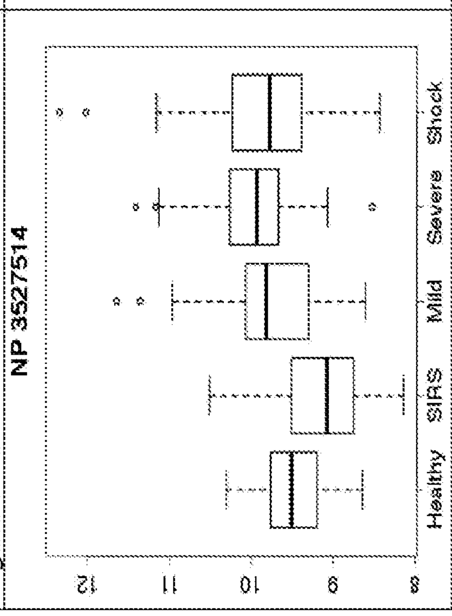
Figure 289



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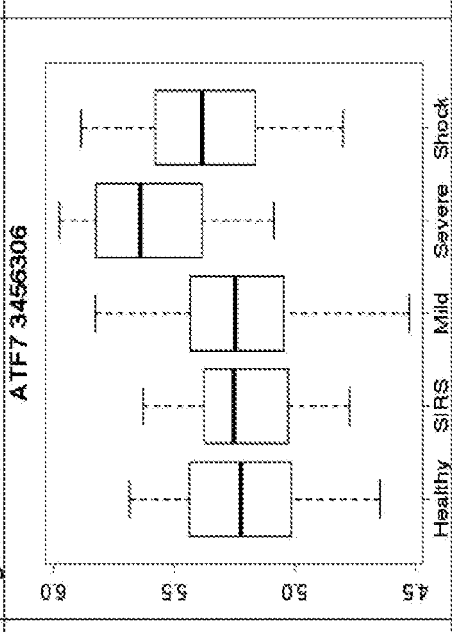

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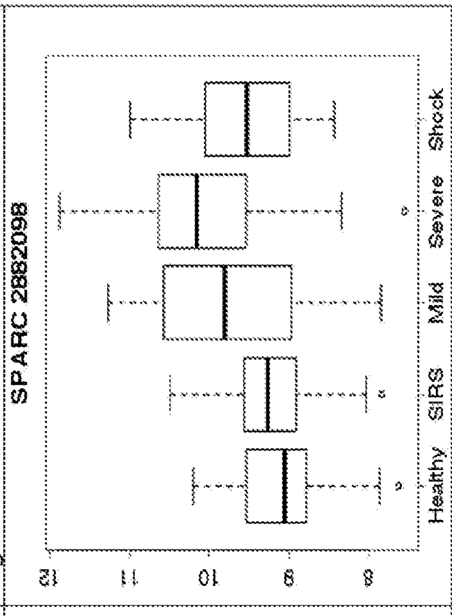

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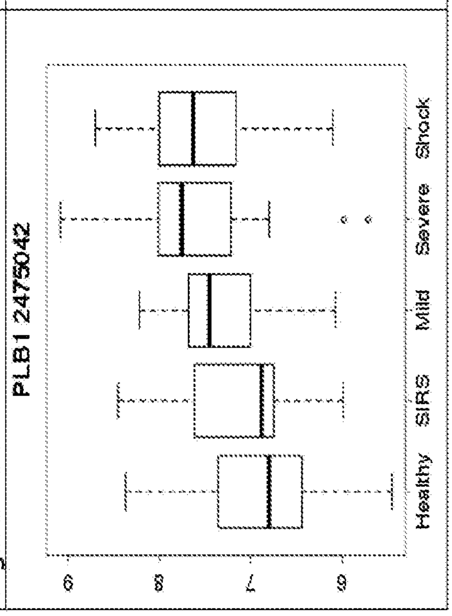

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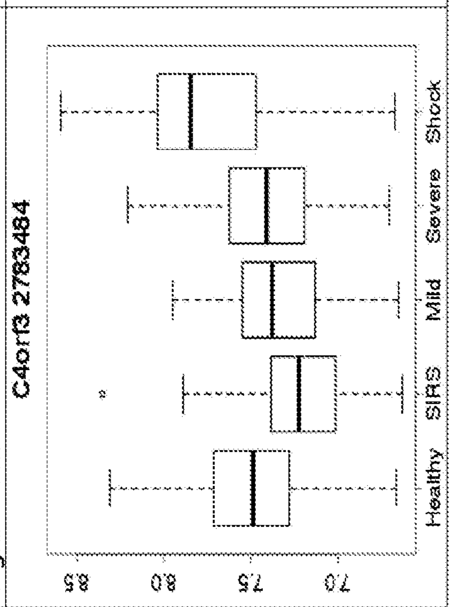

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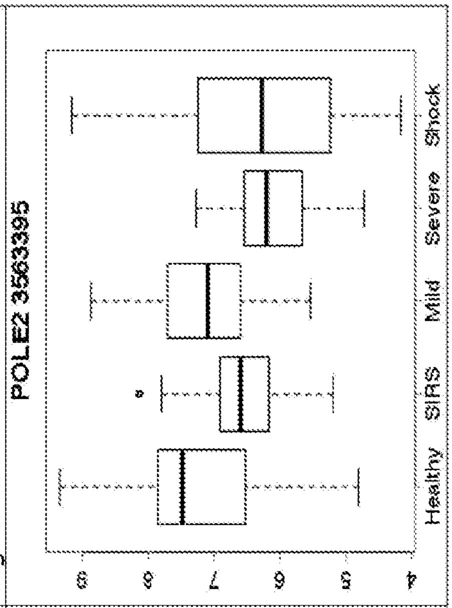

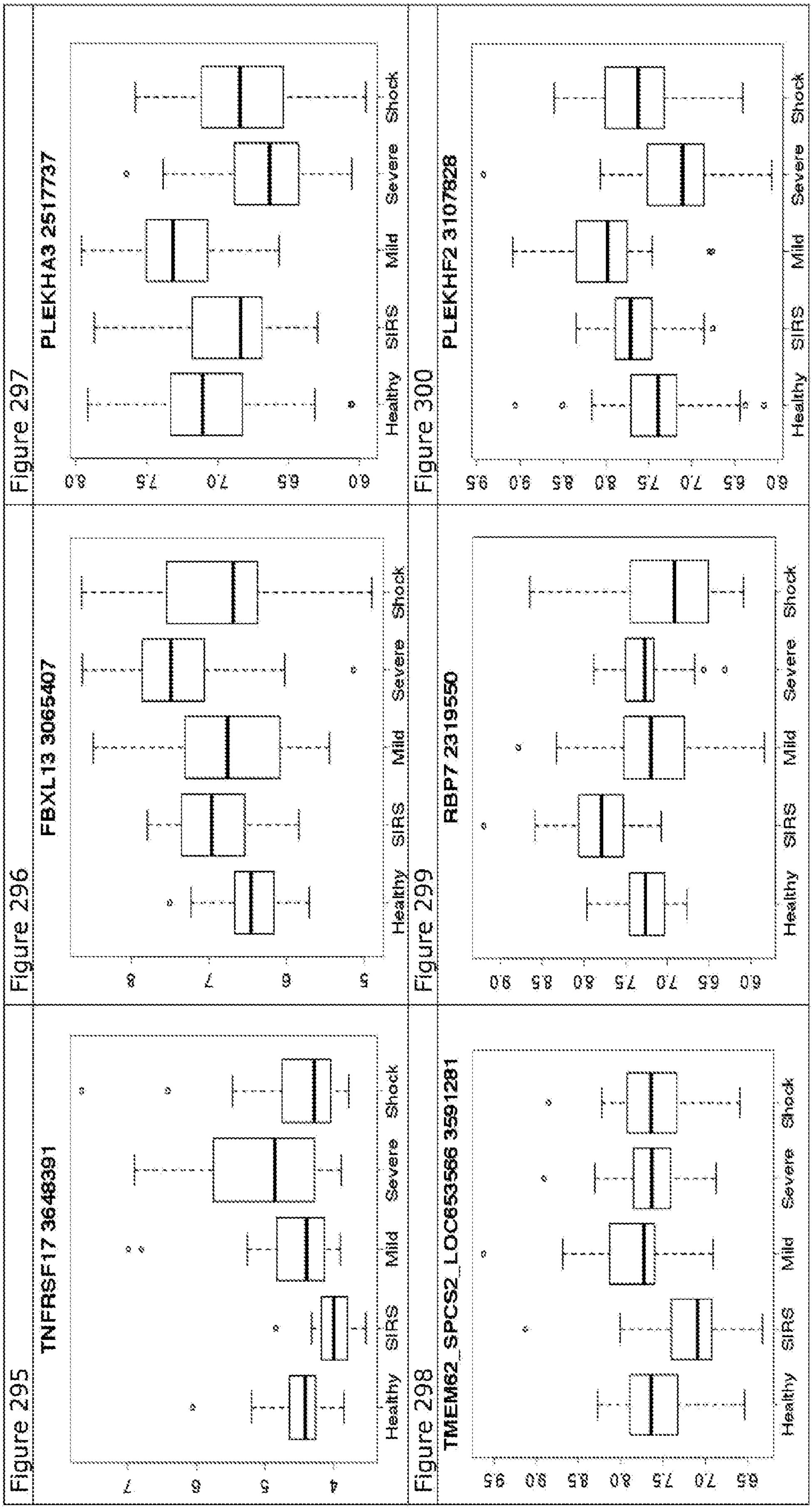

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RBP7 2319550
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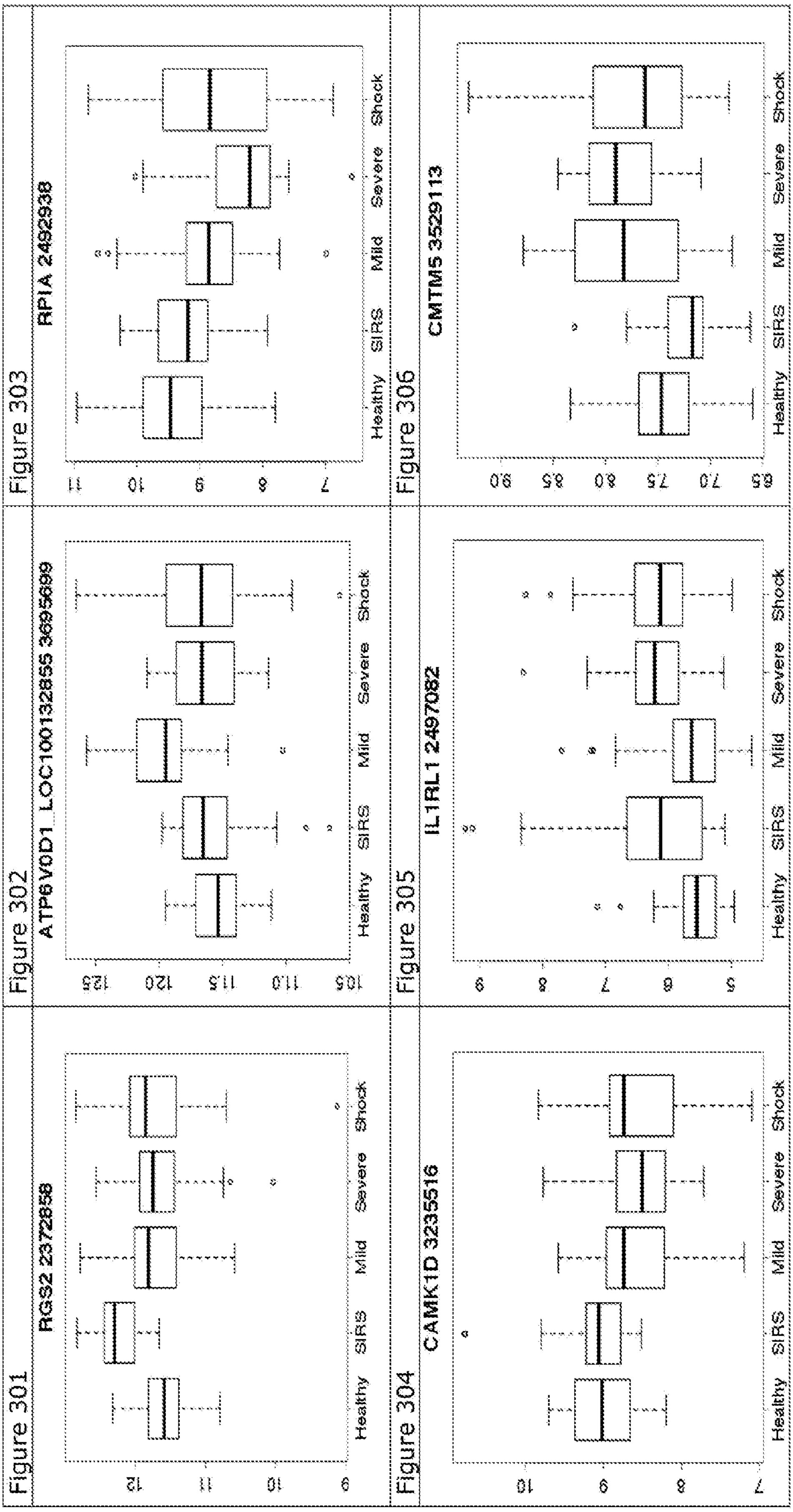
Healthy
SIRS
Mild
Severe
Shock



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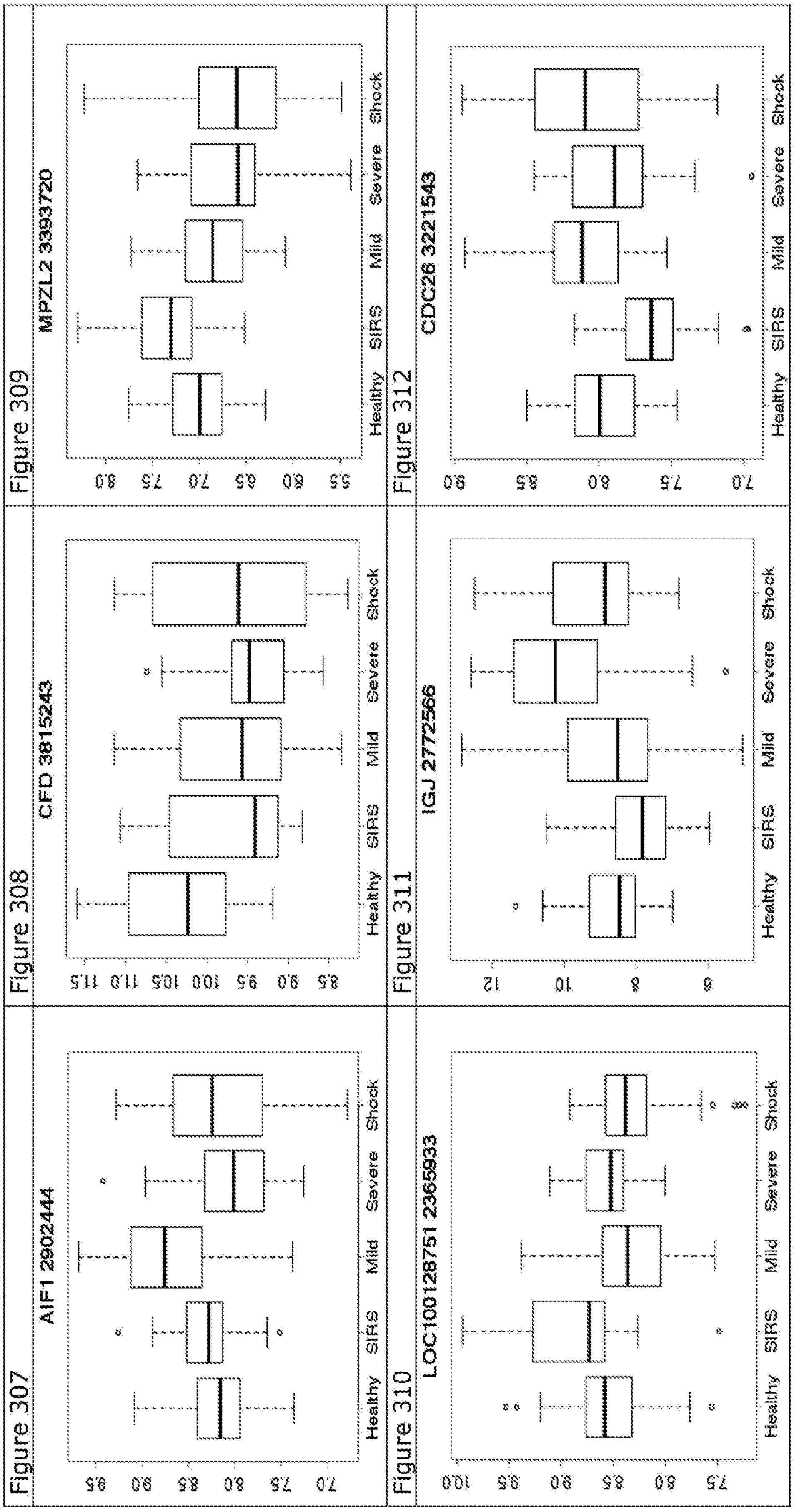
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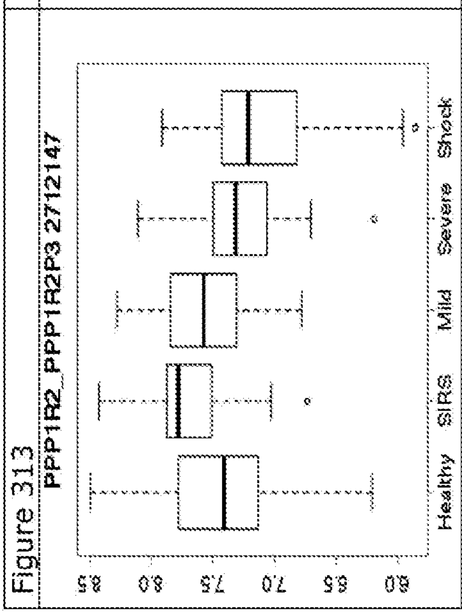
Shock



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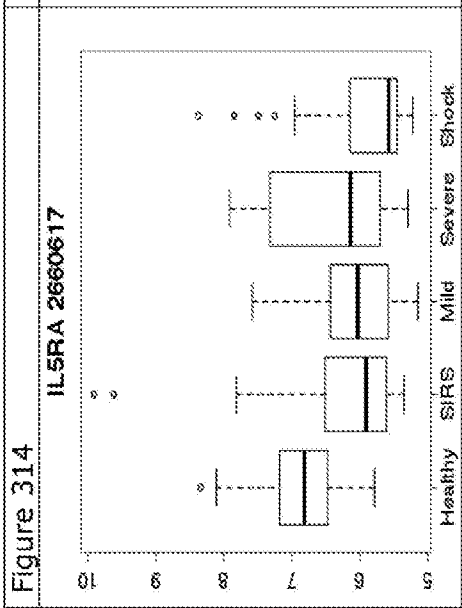

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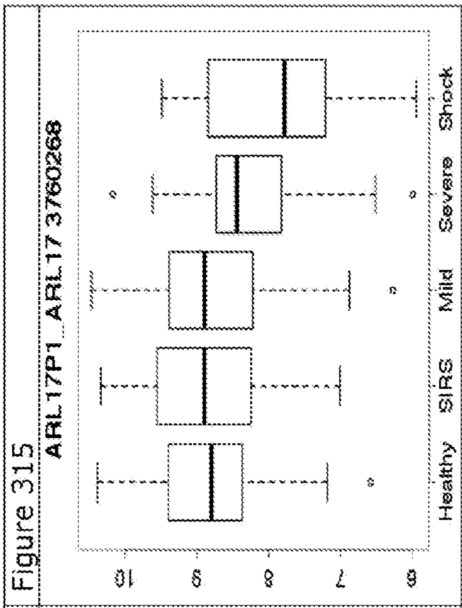

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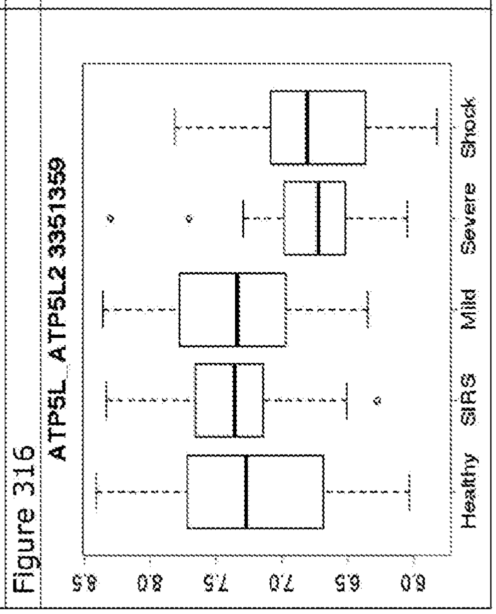

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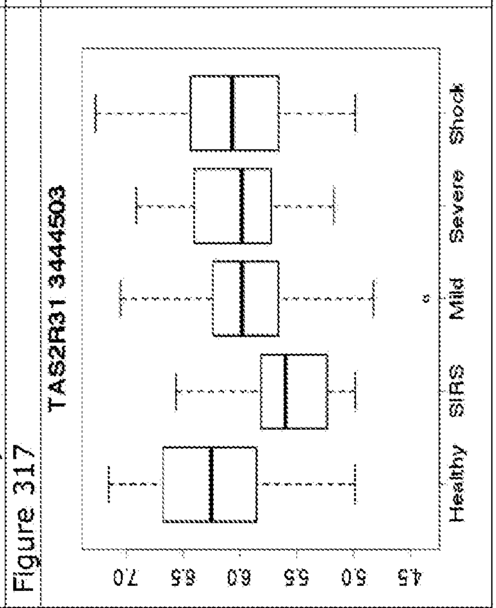

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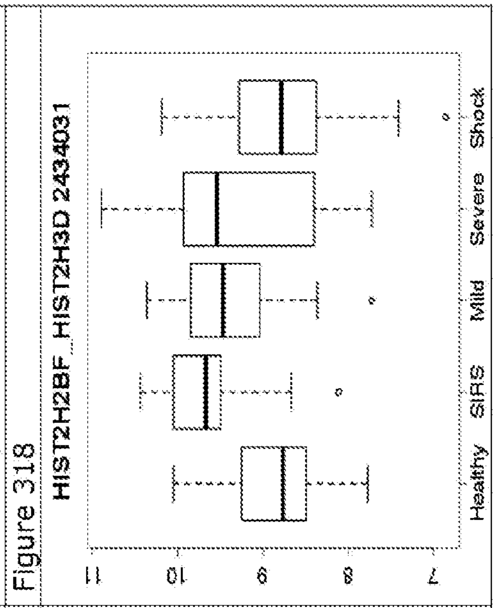
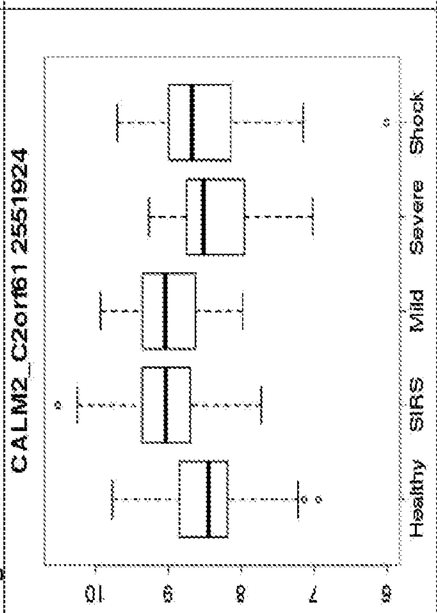


Figure 318

55/57

Figure 319



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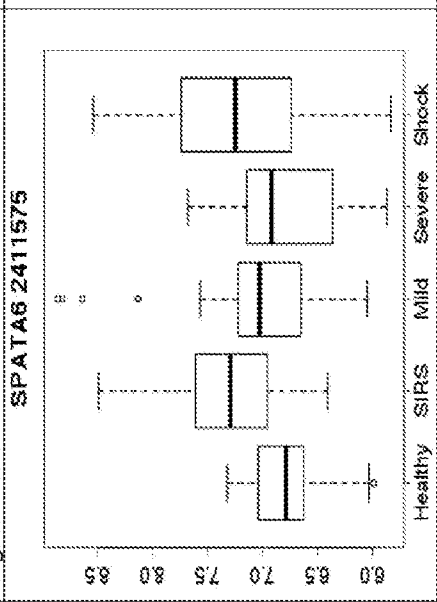

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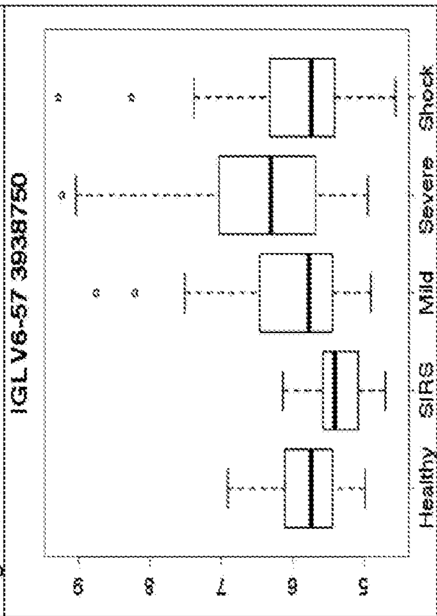

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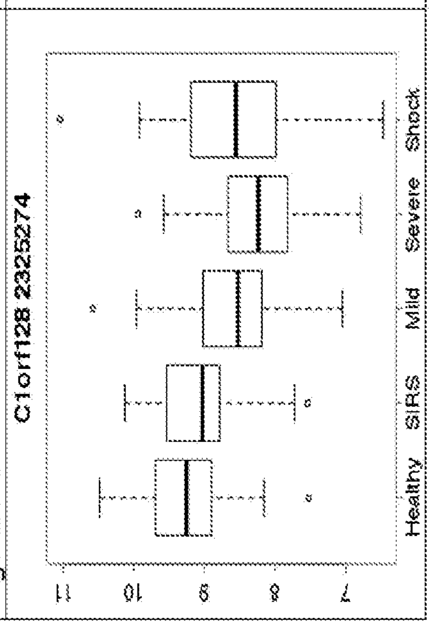

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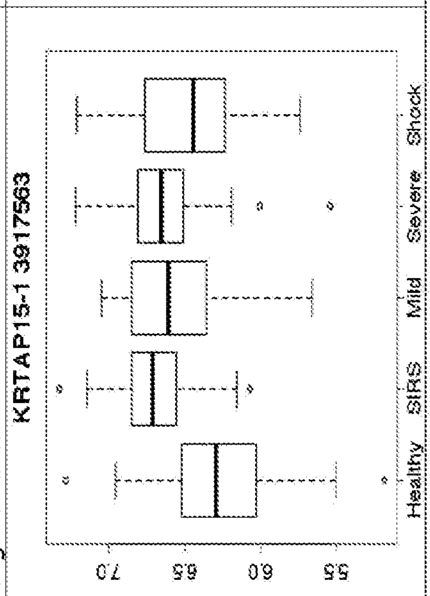

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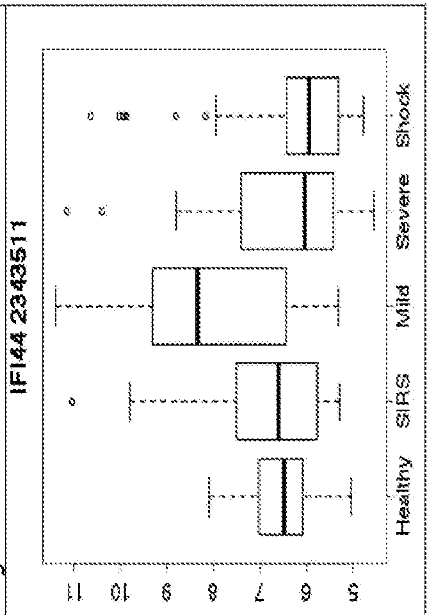

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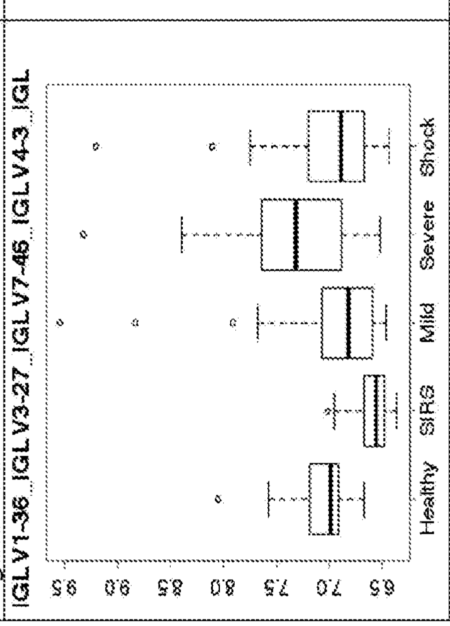

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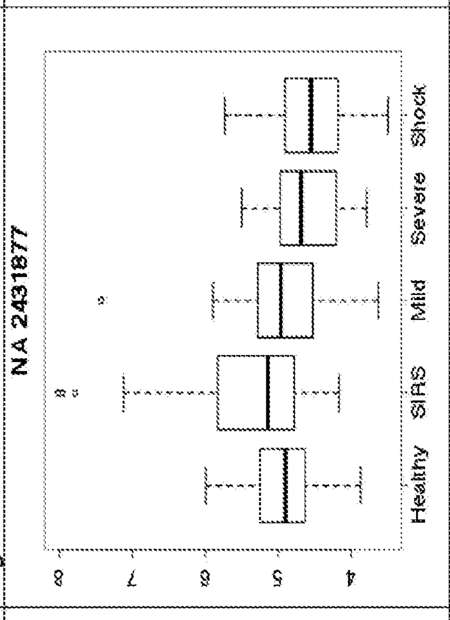

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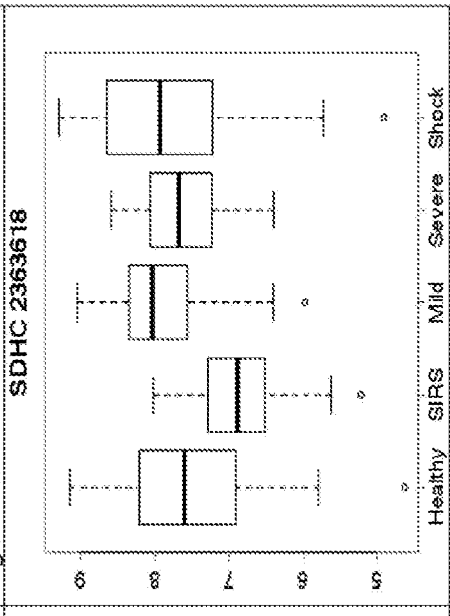

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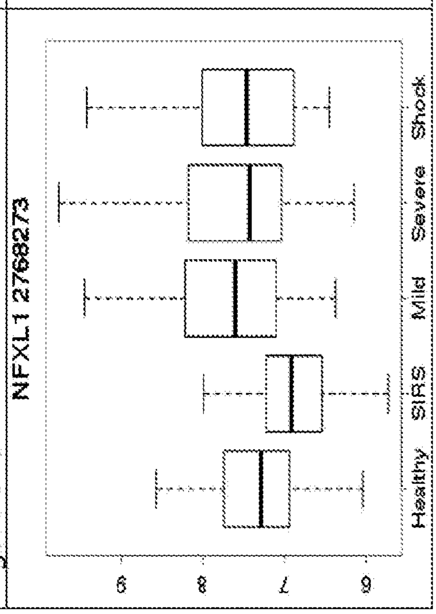

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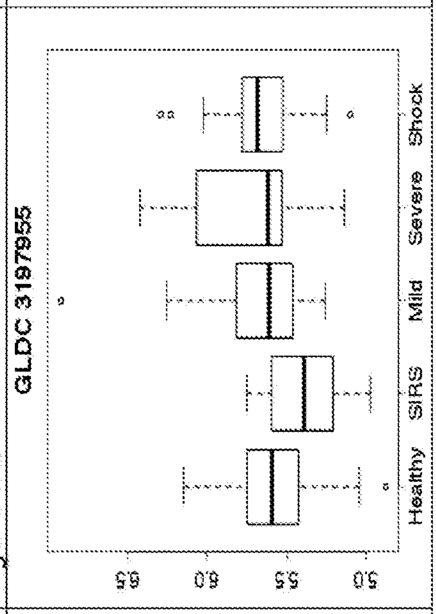

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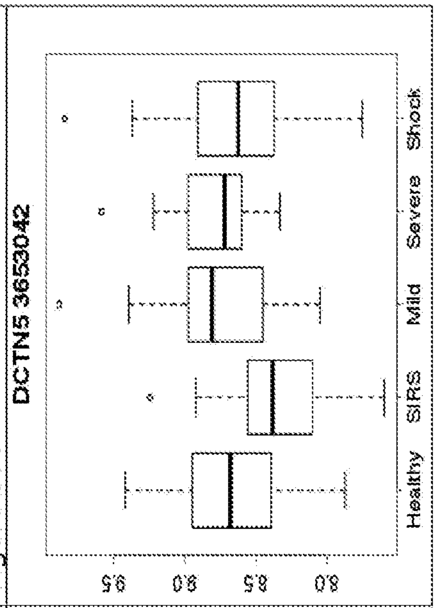

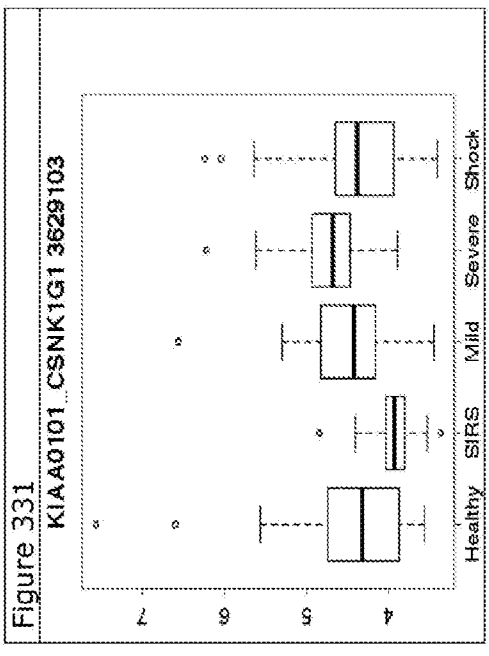
KIAA0101_CSNK1G1 3629103
7
6
5
4
Healthy
SIRS
Mild
Severe
Shock
Figure 331