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(54) Title: MARKERS OF ALTERATIONS IN THE Y CHROMOSOME AND USES THEREFOR

(57) Abstract: Novel sequence tagged sites (STSs), probes and primers useful, e.g., for detecting the presence or absence of an STS in a sample, and methods of using these STSs, probes and primers, e.g., in methods of detecting alterations in the Y chromosome are disclosed. These compositions are also useful in methods of diagnosing or aiding in the diagnosis and/or cause of reduced sperm count and in methods of predicting or aiding in the prediction of the likelihood of success of infertility treatments.

MARKERS OF ALTERATIONS IN THE Y CHROMOSOME AND USES THEREFOR

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application Serial No. 60/592,719 filed July 30, 2004, the entire disclosure of which is incorporated herein by reference.

GOVERNMENT SUPPORT

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BACKGROUND OF THE INVENTION

At least one in every ten couples of reproductive age is unable to bear children despite an extended period of unprotected sexual intercourse. In recent years, there has been an intensive search for genetic causes of infertility in both men and women. Spermatogenic failure is the most common form of male infertility, and here the most striking genetic findings have emerged from studies of the Y chromosome's long arm (Yq). It is now widely accepted that deletions in any one of three Yq regions - AZFa, AZFb, or AZFc - can severely diminish or extinguish sperm production. The number and type of Y chromosomal deletions in a male can have widely varying effects on the success of infertility treatments that a couple may choose to undergo. However, despite the region's biological and medical importance, efforts to develop physical maps have been stymied by the region's unusually repetitive sequence composition, and past studies have suggested that it would be difficult or impossible to identify single-copy DNA markers, localize deletion breakpoints, and accurately identify alterations of the Y chromosome.

SUMMARY OF THE INVENTION

The invention pertains in part to novel sequence tagged sites (STSs), to probes and primers useful, e.g., for detecting the presence or absence of an STS in a sample, and to methods of using these STSs, probes and primers, e.g., in methods of detecting alterations in the Y chromosome. These compositions are also useful in methods of diagnosing or aiding in the diagnosis and/or cause of reduced sperm count (oligospermia or azospermia) and in methods of predicting or aiding in the prediction of the likelihood of success of infertility treatments.

Described herein are results of the assessment and characterization of the human Y chromosome, particularly the AZFc region of the human Y chromosome. As a result of this work, important sequence landmarks of the Y chromosome, particularly AZFc, have been identified. In particular, STSs that can be used in evaluating Y chromosomal DNA for alterations, e.g., deletions such as microdeletions, have been identified; these alterations may be associated with reduced sperm count (e.g., azoospermia and/or oligospermia). The identified STSs and probes and primers therefor can be used in methods of analyzing Y chromosomal DNA for such alterations and for determining or confirming that a deletion or set of deletions is linked to (indicative of) reduced sperm count (azoospermia or severe oligospermia) in humans.

Accordingly, in some embodiments the invention pertains to a method of detecting an alteration in the human Y chromosome comprising assessing a nucleic acid sample from an individual to be tested for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, wherein the absence of one or more of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual. In one embodiment the AZFc region of the Y chromosome is altered. In a particular embodiment the alteration is a deletion in the Y chromosome, e.g., a deletion selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

In some embodiments the nucleic acid sample is a is a genomic DNA sample. In particular embodiments the sample is derived from blood, skin, sperm,

hair root, saliva or buccal cells, or from cells cultured from blood or skin. In other embodiments the individual to be tested is a male with reduced sperm count.

In a particular method of the invention, the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence. For example, said one or more probes can be immobilized on a solid support, such as a microarray.

In another method of the invention, the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence. For example, the primers selected from the group consisting of SEQ ID NOS: 21-60 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, and the primers selected from the group consisting of SEQ ID NOS: 109-204 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 61-108. Similarly, primers selected from the group consisting of SEQ ID NOS: 274-411 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 205-273, and the primers selected from the group consisting of SEQ ID NOS: 413-414 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 412.

Figures 5A-5F, 6A-6K and 7A-7P show the relationship between the primers of SEQ ID NOS 21-60 and 413-414 and the STSs of SEQ ID NOS: 1-20 and 412, respectively, the primers of SEQ ID NOS: 109-204 and the STSs of SEQ ID NOS: 61-108, and the primers of SEQ ID NOS: 274-411 and the STSs of SEQ ID NOS: 205-273, respectively. As used herein, a primer "corresponds" to an STS if it serves as a specific primer for that STS in an amplification reaction. For example, SEQ ID NOS: 21 and 22 are primers which serve as specific primers for SEQ ID NO: 1, and thus SEQ ID NOS: 21 and 22 are primers which correspond to the STS of SEQ ID NO: 1.

The invention also pertains to a method of predicting or aiding in the prediction of the likelihood of success of an infertility treatment of a male having reduced sperm count, comprising assessing a nucleic acid sample from said male for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, wherein the absence of one or more of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual, and determining the likelihood of success of a fertility treatment in view of the type of alteration present, if any.

In one embodiment the AZFc region of the Y chromosome is altered. In a particular embodiment the alteration is a deletion in the Y chromosome, e.g., a deletion selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

In some embodiments the nucleic acid sample is a genomic DNA sample. In particular embodiments the sample is derived from blood, skin, sperm, hair root, saliva or buccal cells, or from cells cultured from blood or skin. In other embodiments the individual to be tested is a male with reduced sperm count.

In a particular method of the invention, the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence. For example, said one or more probes can be immobilized on a solid support, such as a microarray.

In another method of the invention, the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence. For example, the primers selected from the group consisting of SEQ ID NOS: 21-60 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, and the primers selected from the group consisting of SEQ ID NOS: 109-204 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 61-108. Similarly, primers selected from the group consisting of SEQ ID NOS: 274-411 can

be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 205-273, and primers selected from the group consisting of SEQ ID NOS: 413-414 can be used to determine the presence or absence of a nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 412 .

The invention also pertains to an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21-60, 109-204, 274-411 and 413-414, as well as to an isolated nucleic acid molecule consisting of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412. The invention also pertains to nucleic acid probes capable of specifically hybridizing to a nucleic acid molecule selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, and to nucleic acid primers capable of serving as specific primers for amplification of a nucleic acid molecule selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412.

In another embodiment, the invention relates to a kit comprising one or more isolated nucleic acid molecules capable of serving as a specific primer for amplification of one or more nucleic acid molecules selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, amplification reagents, and instructions for using said nucleic acid molecules and reagents to detect the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412. In one embodiment the isolated nucleic acid molecules comprise or consist of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21-60, 109-204, 274-411 and 413-414.

In an additional embodiment, the invention relates to a kit comprising one or more isolated nucleic acid molecules capable of serving as a specific probe for one or more nucleic acid molecules selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, hybridization reagents, and instructions for using said nucleic acid molecules and reagents to detect the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the

group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412. For example, the nucleic acid molecules capable of serving as a specific probes may be selected from the group consisting of SEQ ID NOS: 21-60, 109-204, 274-411 and 413-414.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A-1B are a table listing landmark STSs and their Y chromosomal location.

Fig. 2 is a table showing plus/minus results for STSs distinguishing different types of Y chromosomal deletions. STSs are shown along the top, and deletions are shown down the left side. A minus ("-") indicates the absence of the indicated STS, while a filled-in square indicates the presence of the indicated STS.

Figs. 3A-3B are a table showing plus/minus results for a larger set of STSs distinguishing different types of Y chromosomal deletions. A minus ("-") indicates the absence of the indicated STS, while a filled-in square indicates the presence of the indicated STS.

Figs. 4A-4B are a table showing plus/minus results for a larger set of STSs distinguishing different types of Y chromosomal deletions. A minus ("-") indicates the absence of the indicated STS, while a filled-in square indicates the presence of the indicated STS.

Figs. 5A-5F show the nucleotide sequences of the STSs in Fig. 2 (SEQ ID NOS: 1-20 and 412), as well as the nucleotide sequences of probes and primers which can be used to identify the presence or absence of the corresponding STS (SEQ ID NOS: 21-60 and 413-414).

Figs. 6A-6K show the nucleotide sequences of the STSs in Figs. 3A-3B (SEQ ID NOS: 61-108), as well as the nucleotide sequences of probes and primers which can be used to identify the presence or absence of the corresponding STS (SEQ ID NOS: 109-204).

Figs. 7A-7P show the nucleotide sequences of the STSs in Figs. 4A-4B (SEQ ID NOS: 205-273), as well as the nucleotide sequences of probes and primers which can be used to identify the presence or absence of the corresponding STS (SEQ ID NOS: 274-411).

Fig. 8 is an abbreviated table showing plus/minus results distinguishing different types of deletions involving AZFc.

Fig. 9 shows a genealogical analysis of SFV patterns associated with b2/b3 and gr/gr deletions. In the SFV patterns, "C" indicates the cut variant described by Fernandes *et al.* (*N. Am J Hum Genet 74*:180–187 (2004)), "U" indicates the uncut variant, "B" indicates both variants, and "+" and "-" indicate the presence or absence, respectively, of the Y-DAZ3 variant. The order of SFVs is as shown in table 2 in the work of Fernandes et al. (2004): DAZ-SNV I, DAZ-SNV II, sY586 (DAZ-SNV III), DAZ-SNV IV, sY587 (DAZ-SNV V), DAZ-SNV VI, AZFc SFV 18 (assayed by Y-DAZ3), TTY4-SNV I, BPY2-SNV, GOLY-SNV I, and AZFc SFV 20 (AZFc-P1-SNV I) (Saxena *et al.*, *Genomics 67*:256–267 (2000); Kuroda-Kawaguchi *et al.*, *Nat Genet 29*:279–286 (2001); Fernandes *et al.*, *Mol Hum Reprod 8*:286–298 (2002); Fernandes *et al.*, *N. Am J Hum Genet 74*:180–187 (2004)). The genealogical tree of extant human Y chromosomes and the branch designations are from the studies by Underhill *et al.* (*Nat Genet 26*:358–361 (2000) and the Y-Chromosome Consortium (*Genome Res 12*:339–348 (2002)).

DETAILED DESCRIPTION OF THE INVENTION

A description of preferred embodiments of the invention follows.

Sequence tagged sites (STSs) are short sequences for which the exact location in the genome and order of bases are known. Because each is unique, STSs are helpful for chromosome placement of mapping and sequencing data and serve as landmarks on the physical map of the human genome. The primary sequence and presence or absence of alterations in the sequence of the Y chromosome, particularly deletions, are particularly difficult to determine due to the extensive blocks of sequence repeats within this region. As described herein, STSs have been identified which are uniquely suited for use in methods of detecting alterations in the Y chromosome. In particular, these STSs, individually or more preferably in combination, allow the detection of deletions in the Y chromosome which are difficult to detect and/or distinguish from other alterations in the Y chromosome using other markers and methods.

The ability to detect Y chromosomal alterations, e.g., deletions, and to differentiate between different types of alterations has significant implications for infertility treatment regimens. Infertility treatments can be invasive and the procedures, together with the accompanying stress, can impose a significant burden on both partners physiologically, emotionally and financially. In the end, in some instances these procedures do not result in successful pregnancies. The compositions and methods of the invention provide the couple with additional information which can inform their decision on whether to proceed with infertility treatments and which procedures are likely to be effective, based on the alterations, if any, detected in the male's Y chromosome. Many Y chromosomal deletions have known effects on the ability of the male to produce viable sperm. Using the methods and compositions of the invention it can be determined which, if any, of the described deletions are present in the male's Y chromosome and what the effect of the deletion(s) is on the ability to obtain viable sperm from the male. For example, if a p5/p1 Y chromosomal deletion is detected in the male, the likelihood of obtaining viable sperm from him is very low. This information can then guide the couple in determining which, if any, infertility treatments to pursue, rather than proceeding blindly with a course of action unlikely to produce results.

Thus, the invention pertains, in part, to a method of detecting an alteration in the human Y chromosome comprising assessing a nucleic acid sample from an individual to be tested for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412, wherein the absence of one or more of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual. While the presence or absence of a single nucleic acid molecule from this group can be informative, the greatest informational value is obtained when the presence or absence of multiple nucleic acid molecules is assessed in combination. That is, the greatest specificity of information can be obtained by assessing the pattern of presence and absence of particular markers. Preferred combinations will be apparent with reference to Figs. 2, 3A-3B, 4A-4B and 8.

For example, with reference to Fig. 2, assessment of the presence or absence of a single marker, e.g., sY1317, is informative in that the absence of this marker is expected only in AZFa, Xp->Xq(XG), Xp->(KALP,VCY), and Iso Yp (centromere) alterations. Thus, absence of this marker indicates that one of these alterations is present in the tested Y chromosome.

However, the pattern of presence or absence of a set of markers provides more specific information regarding the particular alteration present in the sample. For example, again with reference to Fig. 2, an AZFa deletion is indicated by the absence of markers sY1317 and sY1234 along with the presence of the other indicated markers. Thus, based on the additional markers assessed the type of alteration can be narrowed from a potential list of alterations (AZFa, Xp->Xq(XG), Xp->(KALP,VCY), and Iso Yp (centromere) alterations) to specific identification of an AZFa deletion. The same analytical framework can be applied to the other STSs shown in Figs. 2, 3A-3B, 4A-4B and 8.

Accordingly, preferred methods of the invention include the assessment of multiple STSs in combination. For example, one preferred combination of markers to be assessed is all or a subset of nucleic acid molecules comprising SEQ ID NOS: 1-20, SEQ ID NOS: 61-108, SEQ ID NOS: 205-273 or SEQ ID NO: 412. Particularly useful subsets of these markers will be apparent from review of Figs. 2, 3A-3B, 4A-4B and 8 and can be selected, for example, on the basis of the alteration to be assessed. For example, the control markers shown in the Figs. may be substituted or omitted in the judgment of the practitioner. In preferred embodiments the presence or absence of all of SEQ ID NOS: 1-20 or SEQ ID NOS: 1-20 and 412 is assessed, in other preferred embodiments the presence or absence of all of SEQ ID NOS: 61-108 is assessed, and in other preferred embodiments the presence or absence of all of SEQ ID NOS: 205-273 is assessed. Markers in addition to those described herein can also be assessed in conjunction with assessment of the markers described herein.

The Y chromosomal alteration to be detected (determined) can include any disruption of the chromosome, such as deletion of one or more nucleotides, addition of one or more nucleotides, or change in one or more nucleotides, including total

loss of the chromosome. In preferred embodiments the alteration detected is a deletion, and more preferably one of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8. The deletions shown in the Figs are referred to by their art-recognized names. For example, in Fig. 2 the AZFa deletion has been described in Sun *et al.*, *Hum. Mol. Genet.*, 9:2291-2296 (2000); the P5/proxP1 and P5/distP1 deletions have been described in Repping *et al.*, *J. Hum. Genet.*, 71:906-922 (2002); the gr/gr and b1/b3 deletions have been described in Repping *et al.*, *Nature Genetics*, 35:247-251 (2003); and the AFZc deletion has been described in Kuroda-Kawaguchi *et al.*, *Nature Genetics*, 29:279-286 (2001).

The nucleic acid sample from the individual to be tested will preferably be genomic DNA and can be obtained from any nucleic acid source. The sample will preferably comprise human nucleic acid molecules in a form suitable for hybridization to probes and primers of the invention or will be treated to render the nucleic acid molecules suitable for hybridiation prior to carrying out the methods of the invention. The nucleic acid molecules in the sample may be isolated, cloned or amplified. As used herein, an "isolated" nucleic acid molecule is intended to mean a nucleic acid molecule which is not flanked by DNA sequences which normally (in nature) flank the nucleic acid molecule. Thus, an isolated nucleic acid molecule can include a nucleic acid molecule which is biologically isolated or synthesized chemically or by recombinant means.

Methods of isolating cell and tissue samples (sources of nucleic acid molecules) are well known to those of skill in the art and include, but are not limited to, scrapings, aspirations, tissue sections, needle biopsies, and the like. Frequently the sample will be a "clinical sample" which is a sample derived from a patient, including sections of tissues such as frozen sections or paraffin sections taken for histological purposes. The sample can also be derived from supernatants (of cells) or the cells themselves from cell cultures, cells from tissue culture and other media in which it may be desirable to detect chromosomal abnormalities. In some cases, the nucleic acids may be amplified using standard techniques such as PCR, prior to carrying out the methods of the invention. The sample may be isolated nucleic acid molecules immobilized on a solid. The sample may also be prepared such that

individual nucleic acids remain substantially intact. Suitable sources include, but are not limited to, blood, skin, sperm, hair root, saliva or buccal cells, or cells cultured from blood or skin.

The nucleic acid sample will be obtained from a human male, typically from a human male who is part of a couple having difficulty conceiving a child. Even more typically the male will have been, at least preliminarily, determined to have a reduced sperm count. Reduced sperm count is understood to encompass both oligospermia and azoospermia, i.e., a sperm count of less than 20 million per ml, including total absence of sperm. Azoospermia is defined as a condition wherein the concentration of sperm in a semen sample is 0 to occasional sperm per ml, and oligospermia is defined as a condition wherein the concentration of sperm in a semen sample ranges from occasional to less than 20 million per ml.

The nucleic acid sequences of markers of the invention are shown in Figs. 5A-5F, 6A-6K and 7A-7P. In particular methods of the invention the presence or absence of the markers of the invention can be assessed (determined, analyzed) by any methods known in the art. In particular embodiments the presence or absence is determined by hybridization to specific probes and/or by amplification using specific primers. Based on the nucleic acid sequences of the markers shown in Figs. 5A-5F, 6A-6K and 7A-7P, suitable probes and primers can readily be designed by the skilled artisan.

In one embodiment, the presence or absence of one or more markers is determined by amplification using specific primers. One or more markers of the invention can be amplified using primer pairs that include or flank the marker sequence. Particularly preferred primers identified as specifically priming the markers of the invention are shown in Figs. 5A-5F, 6A-6K and 7A-7P. Other primers can readily be designed by the skilled artisan. For example, the primers selected from the group consisting of SEQ ID NOS: 21-60 can be used to determine the presence or absence of a corresponding nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, and the primers selected from the group consisting of SEQ ID NOS: 109-204 can be used to determine the presence or absence of a corresponding nucleic acid molecule

comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 61-108. Similarly, primers selected from the group consisting of SEQ ID NOS: 274-411 can be used to determine the presence or absence of a corresponding nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 205-273, and primers selected from the group consisting of SEQ ID NOS: 413-414 can be used to determine the presence or absence of a corresponding nucleic acid molecule comprising SEQ ID NO: 412.

Figures 5A-5F, 6A-6K and 7A-7P show the relationship between the primers of SEQ ID NOS 21-60 and 413-414 and the STSs of SEQ ID NOS: 1-20 and 412, respectively, the primers of SEQ ID NOS: 109-204 and the STSs of SEQ ID NOS: 61-108, and the primers of SEQ ID NOS: 274-411 and the STSs of SEQ ID NOS: 205-273, respectively. As used herein, a primer "corresponds" to an STS if it serves as a specific primer for that STS in an amplification reaction. For example, SEQ ID NOS: 21 and 22 are primers which serve as specific primers for SEQ ID NO: 1, and thus SEQ ID NOS: 21 and 22 are primers which correspond to the STS of SEQ ID NO: 1.

Suitable amplification methods include, but are not limited to: polymerase chain reaction, PCR (PCR Protocols, A Guide to Methods and Applications, ed. Innis, Academic Press, N.Y. (1990) and PCR Strategies (1995), ed. Innis, Academic Press, Inc., N.Y. (Innis)); ligase chain reaction (LCR) (Wu (1989) *Genomics 4*:560; Landegren (1988) *Science 241*:1077; Barringer (1990) *Gene 89*:117); transcription amplification (Kwoh (1989) *Proc. Natl. Acad. Sci. USA 86*:1173); and self-sustained sequence replication (Guatelli (1990) *Proc. Natl. Acad. Sci. USA, 87*:1874); Q Beta replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see Berger (1987) *Methods Enzymol. 152*:307-316, Sambrook, and Ausubel, as well as Mullis (1987) U.S. Pat. Nos. 4,683,195 and 4,683,202; Arnheim (1990) C&EN 36-47; Lomell (1989) *J. Clin. Chem. 35*:1826; Van Brunt (1990) *Biotechnology 8*:291-294; Wu (1989) *Gene 4*:560; Sooknanan (1995) *Biotechnology 13*:563-564. Methods for cloning *in vitro* amplified nucleic acids are described in Wallace, U.S. Pat. No. 5,426,039. Methods

of amplifying large nucleic acids are summarized in, e.g., Cheng (1994) *Nature 369*:684-685.

The presence or absence of amplification products for one or more markers can be analyzed to identify the presence or absence of one or more markers of the invention. That is, if an amplification product for a particular marker is detected, it can be concluded that that marker is present in the sample, and if an amplification product is not detected it can be concluded that the marker is not present in the sample.

In another method of the invention, the presence or absence of one or more markers of the invention is determined using nucleic acid probes which specifically hybridize to the markers of the invention. The terms "hybridizing specifically to" and "specific hybridization" and "selectively hybridize to," as used herein refer to the binding, duplexing, or hybridizing of a nucleic acid molecule preferentially to a particular nucleotide sequence under stringent conditions. The term "stringent conditions" refers to conditions under which a probe will hybridize preferentially to its target subsequence, and to a lesser extent to, or not at all to, other sequences. A "stringent hybridization" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization (e.g., as in array, Southern or Northern hybridizations) are sequence dependent, and are different under different environmental parameters. An extensive guide to the hybridization of nucleic acids is found in, e.g., Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes part I, chapt 2, "Overview of principles of hybridization and the strategy of nucleic acid probe assays," Elsevier, N.Y. ("Tijssen"). Generally, highly stringent hybridization and wash conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on an array or on a filter in a Southern

or northern blot is 42 °C using standard hybridization solutions (see, e.g., Sambrook), with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.15 M NaCl at 72 °C for about 15 minutes. An example of stringent wash conditions is a 0.2 x SSC wash at 65 °C for 15 minutes (see, e.g., Sambrook (1989) Molecular Cloning: A Laboratory Manual (2nd ed.) Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, NY ("Sambrook"). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1 x SSC at 45 °C for 15 minutes. An example of a low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6 x SSC at 40 °C for 15 minutes.

Nucleic acid hybridization assays can be performed in an array-based format. Arrays are a multiplicity of different "probe" or "target" nucleic acids (or other compounds) which hybridize with a sample nucleic acid. In an array format a large number of different hybridization reactions can be run essentially "in parallel." This provides rapid, essentially simultaneous, evaluation of a large number of loci. Methods of performing hybridization reactions in array based formats are also described in, e.g., Pastinen (1997) *Genome Res. 7*:606-614; Jackson (1996) *Nature Biotechnology 14*:1685; Chee (1995) *Science 274*:610; and WO 96/17958.

Many methods for immobilizing nucleic acids on a variety of solid surfaces are known in the art. A wide variety of organic and inorganic polymers, as well as other materials, both natural and synthetic, can be employed as the material for the solid surface. Illustrative solid surfaces include, e.g., nitrocellulose, nylon, glass, quartz, diazotized membranes (paper or nylon), silicones, polyformaldehyde, cellulose, and cellulose acetate. In addition, plastics such as polyethylene, polypropylene, polystyrene, and the like can be used. Other materials which may be employed include paper, ceramics, metals, metalloids, semiconductive materials, cermets or the like. In addition, substances that form gels can be used. Such materials include, e.g., proteins (e.g., gelatins), lipopolysaccharides, silicates, agarose and polyacrylamides. Where the solid surface is porous, various pore sizes may be employed depending upon the nature of the system.

In preparing the surface, a plurality of different materials may be employed, particularly as laminates, to obtain various properties. For example, proteins (e.g., bovine serum albumin) or mixtures of macromolecules (e.g., Denhardt's solution) can be employed to avoid non-specific binding, simplify covalent conjugation, enhance signal detection or the like. If covalent bonding between a compound and the surface is desired, the surface will usually be polyfunctional or be capable of being polyfunctionalized. Functional groups which may be present on the surface and used for linking can include carboxylic acids, aldehydes, amino groups, cyano groups, ethylenic groups, hydroxyl groups, mercapto groups and the like. The manner of linking a wide variety of compounds to various surfaces is well known and is amply illustrated in the literature. For example, methods for immobilizing nucleic acids by introduction of various functional groups to the molecules is known (see, e.g., Bischoff (1987) *Anal. Biochem., 164*:336-344; Kremsky (1987) *Nucl. Acids Res. 15*:2891-2910). Modified nucleotides can be placed on the target using PCR primers containing the modified nucleotide, or by enzymatic end labeling with modified nucleotides. Use of membrane supports (e.g., nitrocellulose, nylon, polypropylene) for the nucleic acid arrays of the invention is advantageous because of well developed technology employing manual and robotic methods of arraying targets at relatively high element densities. Such membranes are generally available and protocols and equipment for hybridization to membranes is well known.

Target elements of various sizes, ranging from 1 mm diameter down to 1 um can be used with these materials. Smaller target elements containing low amounts of concentrated, fixed probe DNA are used for high complexity comparative hybridizations since the total amount of sample available for binding to each target element will be limited. Thus it is advantageous to have small array target elements that contain a small amount of concentrated probe DNA so that the signal that is obtained is highly localized and bright. Such small array target elements are typically used in arrays with densities greater than 10.sup.4 /cm.sup.2. Relatively simple approaches capable of quantitative fluorescent imaging of 1 cm.sup.2 areas have been described that permit acquisition of data from a large number of target elements in a single image (see, e.g., Wittrup (1994) Cytometry 16:206-213).

Arrays on solid surface substrates with much lower fluorescence than membranes, such as glass, quartz, or small beads, can achieve much better sensitivity. Substrates such as glass or fused silica are advantageous in that they provide a very low fluorescence substrate, and a highly efficient hybridization environment. Covalent attachment of the target nucleic acids to glass or synthetic fused silica can be accomplished according to a number of known techniques (described above). Nucleic acids can be conveniently coupled to glass using commercially available reagents. For instance, materials for preparation of silanized glass with a number of functional groups are commercially available or can be prepared using standard techniques (see, e.g., Gait (1984) Oligonucleotide Synthesis: A Practical Approach, IRL Press, Wash., D.C.). Quartz cover slips, which have at least 10-fold lower autofluorescence than glass, can also be silanized.

Alternatively, probes can also be immobilized on commercially available coated beads or other surfaces. For instance, biotin end-labeled nucleic acids can be bound to commercially available avidin-coated beads. Streptavidin or anti-digoxigenin antibody can also be attached to silanized glass slides by protein-mediated coupling using e.g., protein A following standard protocols (see, e.g., Smith (1992) *Science 258*:1122-1126). Biotin or digoxigenin end-labeled nucleic acids can be prepared according to standard techniques. Hybridization to nucleic acids attached to beads is accomplished by suspending them in the hybridization mix, and then depositing them on the glass substrate for analysis after washing. Alternatively, paramagnetic particles, such as ferric oxide particles, with or without avidin coating, can be used.

In this embodiment of the invention, specific hybridization of a probe to one or more markers of the invention in a nucleic acid sample is indicative of the presence of that marker in the sample, and absence of specific hybridization of a probe to one or more markers of the invention in a nucleic acid sample is indicative of the absence of that marker in the sample.

In some embodiments of the invention, probes and primers of the invention are detectably labelled. The term "detectably labelled" as used herein refers to a nucleic acid attached to a detectable composition, i.e., a label. The detection can be

by, e.g., spectroscopic, photochemical, biochemical, immunochemical, physical or chemical means. For example, useful labels include ^{32}P, ^{35}S, ^{3}H, ^{14}C, ^{125}I, ^{131}I; fluorescent dyes (e.g., FITC, rhodamine, lanthanide phosphors, Texas red), electron-dense reagents (e.g. gold), enzymes, e.g., as commonly used in an ELISA (e.g., horseradish peroxidase, beta-galactosidase, luciferase, alkaline phosphatase), colorimetric labels (e.g., colloidal gold), magnetic labels (e.g. Dynabeads.TM.), biotin, dioxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available. The label can be directly incorporated into the nucleic acid molecule to be detected, or it can be attached to a probe or antibody which hybridizes or binds to the target.

In various embodiments, the labels may be coupled to the probes and primers in a variety of ways known to those of skill in the art. Methods of labeling nucleic acids are well known to those of skill in the art. In various embodiments, the nucleic acid probes are labeled using nick translation, PCR, or random primer extension (see, e.g., Sambrook). Preferred labels are those that are suitable for use in arrays and in situ hybridization. In one embodiment, the nucleic acid probes or primers of the invention are detectably labeled. Alternatively, a detectable label which binds to a hybridization product may be used. Such detectable labels include any material having a detectable physical or chemical property, such as those in the field of immunoassays. The particular label used is not critical to the present invention, so long as it does not interfere with hybridization of the probe or primer. However, probes directly labeled with fluorescent labels (e.g. fluorescein, Texas red, etc.) are preferred for chromosomal DNA hybridization. In a preferred embodiment, the label is detectible in as low copy number as possible to maximize the sensitivity of the assay and yet be detectible above any background signal. The label preferably has a highly localized signal. Thus, particularly preferred fluorescent labels include fluorescein-12-dUTP and Texas Red-5-dUTP.

The present invention also includes the nucleotide sequences described herein, and their complements, which are useful as hybridization probes or primers for an amplification method, such as polymerase chain reaction (PCR), to show the presence or absence of one or more markers of the present invention. Probes and

primers can have all or a portion of the nucleotide sequence (nucleic acid sequence) of the probes and primers specifically exemplified herein or all or a portion of their complements. For example, sequences shown in Figs 5A-5F, 6A-6K and 7A-7P can be used.

In addition, the invention pertains to isolated nucleic acid molecules consisting of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108, 205-273 and 412.

This invention also provides diagnostic kits for the detection of chromosomal abnormalities or alterations on the Y chromosome. In a preferred embodiment, a kit includes one or more probes for the markers of the invention. The kits can additionally include blocking nucleic acid (i.e., Cot-1 DNA) and instructional materials describing when and how to use the kit contents. The kits can also include one or more of the following: various labels or labeling agents to facilitate the detection of the probes, reagents for the hybridization including buffers, a metaphase spread, bovine serum albumin (BSA) and other blocking agents, tRNA, SDS sampling devices including fine needles, swabs, aspirators and the like, positive and negative hybridization controls and so forth.

The invention also provides diagnostic kits for the detection of chromosomal abnormalities or alterations on the Y chromosome using amplification methods. In a preferred embodiment, a kit includes one or more primers for the markers of the invention. The kits can additionally include amplification reagents and instructional materials describing when and how to use the kit contents. The kits can also include one or more of the following: various labels or labeling agents to facilitate the detection of the primers or amplification products, and sampling devices including fine needles, swabs, aspirators and the like, positive and negative hybridization controls and so forth.

The present invention is illustrated by the following exemplification, which is not intended to be limiting in any way. The teachings of all publication referenced herein are incorporated herein by reference in their entirety.

EXEMPLIFICATION

There has been a report of a novel deletion of part of the azoospermia factor c (AZFc [MIM 415000]) region of the human Y chromosome (Fernandes et al. 2004). This article reported that the deletion is found only in branchNof the Y-chromosome genealogical tree, occurs through one mutational pathway, is ~2.2 Mb in size, and has no effect on spermatogenesis. We, too, recently reported this deletion, which Fernandes et al. termed the "g1/g3" deletion and which we termed the "b2/b3" deletion (Repping et al. 2004). Our findings, however, differed from those of Fernandes et al. in several important particulars: (1) our screening of 1,563 men demonstrated that this deletion is not confined to branch N and that it has at least four independent origins; (2) our analysis revealed two mutational pathways, rather than one, that can generate the deletion, and we confirmed the existence of the inverted AZFc organizations that are the intermediate steps in these pathways; (3) on the basis of the reference sequence of the Y chromosome, we concluded that the size of the deletion is 1.8 Mb, rather than ~2.2 Mb; (4) using interphase FISH, we confirmed the amplicon organization that was postulated in the deletion and also identified three instances of duplication subsequent to the deletion; and (5) because of the possibility of a compensatory factor on Y chromosomes in branch N and because of the limited number of deletions outside this branch, we concluded that a possible effect of this deletion on risk of spermatogenic failure cannot be excluded (Repping et al. 2004).

Beyond these differences, however, the characterizations of this and other partial deletions of AZFc (Repping et al. 2003) highlight a more important question. At issue is the relative utility of sequence family variants (Saxena et al. 2000), compared with that of plus/minus STSs, for identification and differentiation of deletions involving AZFc. AZFc is composed entirely of amplicons —repeat units 115–678 kb in length that only differ by ~1 nt per 3,000 bp. These rare differences are called "sequence family variants" (SFVs). We previously relied on SFVs to map and sequence the AZFc region of one man's Y chromosome (Kuroda-Kawaguchi et al. 2001). The report by Fernandes et al. (2004) emphasized the use of SFVs in identification of the novel deletion, whereas our analysis relied on plus/minus STSs

for identification of the deletion, followed, in most instances, by confirmation with FISH.

Two observations led us to ask whether SFVs, as opposed to plus/minus STSs, offer the simpler and more robust means of detecting and distinguishing deletions in AZFc (see GenBank Web site for STSs and SFV assays). First, figures 1 and 4 in the report by Fernandes et al. (2004) indicated that negative results at the plus/minus STS sY1192 or 50f2/C combined with positive results at flanking STSs are sufficient to detect the deletion (table 1). Moreover, the b2/b3 deletion and other types of deletions involving AZFc can be distinguished by their plus/minus signatures, without the use of SFVs (table 1). Second, table 2 in the report by Fernandes et al. (2004) showed that the SFV patterns of undeleted chromosomes vary considerably among different branches of the Y chromosome genealogy and that the patterns also vary among individuals within branches. These observations suggested that the link between SFV patterns and particular types of deletions would likely not be consistent across the worldwide diversity of Y chromosomes.

The diversity of SFV patterns in undeleted chromosomes is not surprising, since AZFc is subject to large inversions, deletions, and duplications caused by ectopic homologous recombination between amplicons (Kuroda-Kawaguchi et al. 2001; Repping et al. 2003, 2004). Such events would rearrange the locations of particular variants and would blur the association between SFV patterns and particular types of deletions. The association would likely be further blurred by gene conversion, which frequently erases small sequence differences (i.e., SFVs) between amplicon copies on the Y chromosome (Rozen et al. 2003).

We experimentally investigated the consistency of SFV patterns in different types of deletions involving AZFc. First, using the SFVs employed by Fernandes et al. (2004), we typed 20 men reported elsewhere to have the b2/b3 deletion (Repping et al. 2004). These men represented branch N and three other branches of the Ychromosome genealogy (Fig. 9). Second, using the same SFVs, we typed 40 men reported elsewhere to have the gr/gr deletion, the other common deletion in that part of AZFc (Repping et al. 2003). These men represented 14 branches of the Y-chromosome genealogy (Fig. 9). The b2/b3 deletions outside branch N showed

diverse SFV patterns, and the gr/gr deletions showed even greater diversity. This greater diversity was likely due to the larger number of independent gr/gr deletions studied. Two branches, F*(xHK) and R1*x, contained numerous deletions and a high diversity of SFV patterns. In these branches, multiple independent deletion events probably account for the high diversity. By contrast, two other branches, D2b and N, contained numerous deletions but uniform SFV patterns. This uniformity is explained by the fact that all chromosomes in these branches descended from deleted founders (Repping et al. 2003, 2004; Fernandes et al. 2004). Thus, the chromosomes in each of these branches represent single-deletion events.

Our data also showed that the SFV patterns of b2/b3 and gr/gr deletions are not distinct from each other. For example, the b2/b3 pattern UUUCUU-CUUU (branch F*[xHK]) is more similar to the gr/gr pattern UUCCUU+CBUB (branch F*[xHK], four differences [underlined]) than to the b2/b3 pattern UBBBCU- CCUC (branch N, six differences). In another example, the gr/gr pattern UBBBCU-UBUB (branch R1*x) is more similar to the b2/b3 pattern UBBBCU-CUUC (branch I, three differences) than to the gr/gr pattern BCCCUB+CBCC (branch R1*x, 10 differences).

In conclusion, the SFV patterns of b2/b3 and gr/gr deletions vary widely and are not clearly distinct. SFVs can offer insight only if one knows the common SFV organizations in the genealogical branches represented by the Y chromosomes being tested. However, SFV organizations across the Y-chromosome genealogical tree are largely unknown, and SFV patterns vary even among individuals in the same branch. Just as important is that a large number of two-step assays are needed for SFV typing and for determining the Y-chromosome branch. By contrast, six simple plus/minus STSs distinguish between the deletions involving AZFc (Fig. 8). Thus, plus/minus STSs provide a straightforward means of identifying and distinguishing the deletions of part of AZFc, whereas, in most situations, SFVs do not.

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CLAIMS

What is claimed is:

1. A method of detecting an alteration in the human Y chromosome comprising assessing a nucleic acid sample from an individual to be tested for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108 and 205-273, wherein the absence of one or more of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual.

2. A method according to Claim 1, wherein the AZFc region of the Y chromosome is altered.

3. A method according to Claim 1, wherein the alteration is a deletion in the Y chromosome.

4. A method according to Claim 3, wherein the deletion is selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

5. A method according to Claim 1, wherein the nucleic acid sample is a genomic DNA sample.

6. A method according to Claim 1, wherein the individual to be tested is a male with reduced sperm count.

7. A method according to Claim 1, wherein the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence.

8. A method according to Claim 7, wherein said one or more probes are

immobilized on a solid support.

9. A method according to Claim 8, wherein said one or more probes are contained in a microarray.

10. A method according to Claim 1, wherein the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence.

11. A method according to Claim 1, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20.

12. A method according to Claim 11, wherein the presence or absence of the nucleic acid molecule is determined using one or more corresponding primers selected from the group consisting of SEQ ID NOS: 21-60.

13. A method according to Claim 1, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 61-108.

14. A method according to Claim 13, wherein the presence or absence of the nucleic acid molecule is determined using one or more corresponding primers selected from the group consisting of SEQ ID NOS: 109-204.

15. A method according to Claim 1, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 205-273.

16. A method according to Claim 15, wherein the presence or absence of the nucleic acid molecule is determined using one or more corresponding

primers selected from the group consisting of SEQ ID NOS: 274-411.

17. A method of predicting or aiding in the prediction of the likelihood of success of an infertility treatment of a male having reduced sperm count, comprising assessing a nucleic acid sample from said male for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108 and 205-273, wherein the absence of one or more of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual, and determining the likelihood of success of a fertility treatment in view of the type of alteration present, if any.

18. A method according to Claim 17, wherein the AZFc region of the Y chromosome is altered.

19. A method according to Claim 17, wherein the alteration is a deletion in the Y chromosome.

20. A method according to Claim 19, wherein the deletion is selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

21. A method according to Claim 17, wherein the nucleic acid sample is a genomic DNA sample.

22. A method according to Claim 17, wherein the individual to be tested is a male with reduced sperm count.

23. A method according to Claim 17, wherein the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence.

24. A method according to Claim 23, wherein said one or more probes are immobilized on a solid support.

25. A method according to Claim 24, wherein said one or more probes are contained in a microarray.

26. A method according to Claim 17, wherein the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence.

27. A method according to Claim 17, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20.

28. A method according to Claim 27, wherein the presence or absence of the nucleic acid molecule is determined using one or more corresponding primers selected from the group consisting of SEQ ID NOS: 21-60.

29. A method according to Claim 17, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 61-108.

30. A method according to Claim 29, wherein the presence or absence of the nucleic acid molecule is determined using one or more corresponding primers selected from the group consisting of SEQ ID NOS: 109-204.

31. A method according to Claim 17, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 205-273.

32. A method according to Claim 31, wherein the presence or absence of the

nucleic acid molecule is determined using one or more corresponding primers selected from the group consisting of SEQ ID NOS: 274-411.

33. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21-60, 109-204 and 274-411.

34. A kit comprising one or more isolated nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21-60, 109-204 and 274-411, amplification reagents, and instructions for using said nucleic acid molecules and reagents to detect the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-20, 61-108 and 205-273.

35. A method according to Claim 1 or 17, wherein the nucleic acid molecules assessed are those shown in Fig. 2.

36. A method according to Claim 1 or 17, wherein the nucleic acid molecules assessed are those shown in Fig. 3A-3B.

37. A method according to Claim 1 or 17, wherein the nucleic acid molecules assessed are those shown in Fig. 4A-4B.

38. A method of detecting an alteration in the human Y chromosome comprising assessing a nucleic acid sample from an individual to be tested for the presence or absence of one or more nucleic acid molecules comprising a nucleic acid sequence of SEQ ID NO: 412, wherein the absence of said nucleic acid sequences is indicative of an alteration in the human Y chromosome in the individual.

39. A method according to Claim 38, wherein the AZFc region of the Y chromosome is altered.

40. A method according to Claim 38, wherein the alteration is a deletion in the Y chromosome.

41. A method according to Claim 40, wherein the deletion is selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

42. A method according to Claim 38, wherein the nucleic acid sample is a genomic DNA sample.

43. A method according to Claim 38, wherein the individual to be tested is a male with reduced sperm count.

44. A method according to Claim 38, wherein the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence.

45. A method according to Claim 44, wherein said one or more probes are immobilized on a solid support.

46. A method according to Claim 45, wherein said one or more probes are contained in a microarray.

47. A method according to Claim 38, wherein the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence.

48. A method according to Claim 38, wherein the presence or absence of the nucleic acid molecule is determined using one or more primers selected from

the group consisting of SEQ ID NOS: 413-414.

49. A method of predicting or aiding in the prediction of the likelihood of success of an infertility treatment of a male having reduced sperm count, comprising assessing a nucleic acid sample from said male for the presence or absence of a nucleic acid molecule comprising SEQ ID NO: 412, wherein the absence of said nucleic acid sequence is indicative of an alteration in the human Y chromosome in the individual, and determining the likelihood of success of a fertility treatment in view of the type of alteration present, if any.

50. A method according to Claim 49, wherein the AZFc region of the Y chromosome is altered.

51. A method according to Claim 49, wherein the alteration is a deletion in the Y chromosome.

52. A method according to Claim 51, wherein the deletion is selected from the group consisting of the deletions shown in Figs. 2, 3A-3B, 4A-4B and 8.

53. A method according to Claim 49, wherein the nucleic acid sample is a genomic DNA sample.

54. A method according to Claim 49, wherein the individual to be tested is a male with reduced sperm count.

55. A method according to Claim 49, wherein the presence or absence of said one or more nucleic acid molecules is determined using one or more probes complementary to the nucleic acid sequence.

56. A method according to Claim 55, wherein said one or more probes are immobilized on a solid support.

57. A method according to Claim 56, wherein said one or more probes are contained in a microarray.

58. A method according to Claim 49, wherein the presence or absence of said one or more nucleic acid molecules is determined by amplification using one or more primers complementary to the nucleic acid sequence.

59. A method according to Claim 49, wherein the presence or absence of the nucleic acid molecule is determined using one or more primers selected from the group consisting of SEQ ID NOS: 413-414.

60. An isolated nucleic acid molecule comprising SEQ ID NO: 412.

61. A kit comprising one or more isolated nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS:413-414, amplification reagents, and instructions for using said nucleic acid molecules and reagents to detect the presence or absence of a nucleic acid molecule comprising SEQ ID NO: 412.

Landmark STSs

sY1247	Boundary of the 1st pseudoautosomal region
sY1248	Distal boundary of the distal part of X-transposed region
sY1240	100Kb deletion (compared to X) in the PCDH11Y intron
sY1241	Distal boundary of distal IR3
sY1242	Proximal boundary of distal IR3
sY605	Proximal boundary of the proximal part of X-transposed region
sY1219	Yp IR1 specific marker
sY1293	Distal boundary of major TSPY array
sY1250	Proximal boundary of major TSPY array
sY1243	Distal boundary of proximal IR3
sY1244	Proximal boundary of proximal IR3
sY1281	Proximal boundary of Yp major blue region
sY1280	rRNA pseudogene close to Yp centromere boundary
sY1200	Alpha-satellite/satelite 3 boundary in the middle of Y centromere
sY1251	Y centromere/Yq boundary
sY746	Proximal boundary of proximal AZFa 10Kb repeat unit
sY1064	Distal boundary of proximal AZFa 10Kb repeat unit
sY1065	Proximal boundary of distal AZFa 10Kb repeat unit
sY1066	Distal boundary of distal AZFa 10Kb repeat unit
sY1303	Proximal external boundary of P8
sY1223	Inner boundary 2 of P8
sY1222	Inner boundary 1 of P8
sY1274	Distal external boundary of P8
sY1312	P7 proximal outer boundary
sY1310	P7 proximal inner boundary
sY1311	P7 distal inner boundary
sY1304	P7 distal outer boundary
sY1275	P6 proximal outer boundary
sY1285	P6 proximal inner boundary
sY1286	P6 distal inner boundary
sY1276	P6 distal outer boundary
sY1264	P5 proximal outer boundary
sY1227	P5 inner boundary 1
sY1228	P5 inner boundary 2
sY1283	P5/P4 external boundary
sY1225	P4 proximal inner boundary
sY1226	P4 distal inner boundary
sY1287	P4 distal outer boundary
sY1252	DYZ19 proximal boundary
sY1253	DYZ19 distal boundary
sY1315	IR2 proximal boundary of proximal unit
sY1302	IR2 distal boundary of proximal unit
sY1279	IR2 distal boundary of proximal unit
sY1278	IR2 proximal boundary of distal unit
sY1294	IR2 proximal boundary of distal unit
sY1258	IR2 distal boundary of distal unit/ u1/b1 boundary/ P3 proximal outer boundary
sY1160	Blue/turquoise boundary (PRY intron)
sY1196	P3 proximal inner boundary
sY1197	P3 distal inner boundary
sY1572	P3 distal outer boundary (amplifies also b3 and b4)
sY1192	Yq IR1 specific (in u3)
sY1191	Yq IR1 specific (in u3)
sY1198	red/green
sY1307	P1/P2 inner boundary 1

Figure 1A

sY1308	P1/P2 inner boundary 2
sY1291	red/gray
sY1189	red/gray
sY1125	blue/gray
sY1054	blue/yellow
sY1292	P1.1 distal outer boundary
sY1289	P1.1/P1.2 inner boundary 1
sY1290	P1.1/P1.2 inner boundary 2
sY1257	P1.1 proximal outer boundary/chr15 transposition boundary
sY1206	green/yellow
sY1201	gray/white
sY1245	Proximal boundary of major heterochromatic region
sY1246	Proximal part of major heterochromatic region
sY1166	Marker between major heterochromatic region and 2nd pseudoautosomal region
sY1273	2nd pseudoautosomal boundary

sY602	BPY2
sY579	P1/P2 loop
sY639	CDY1
sY627	RBMY1

Figure 1B

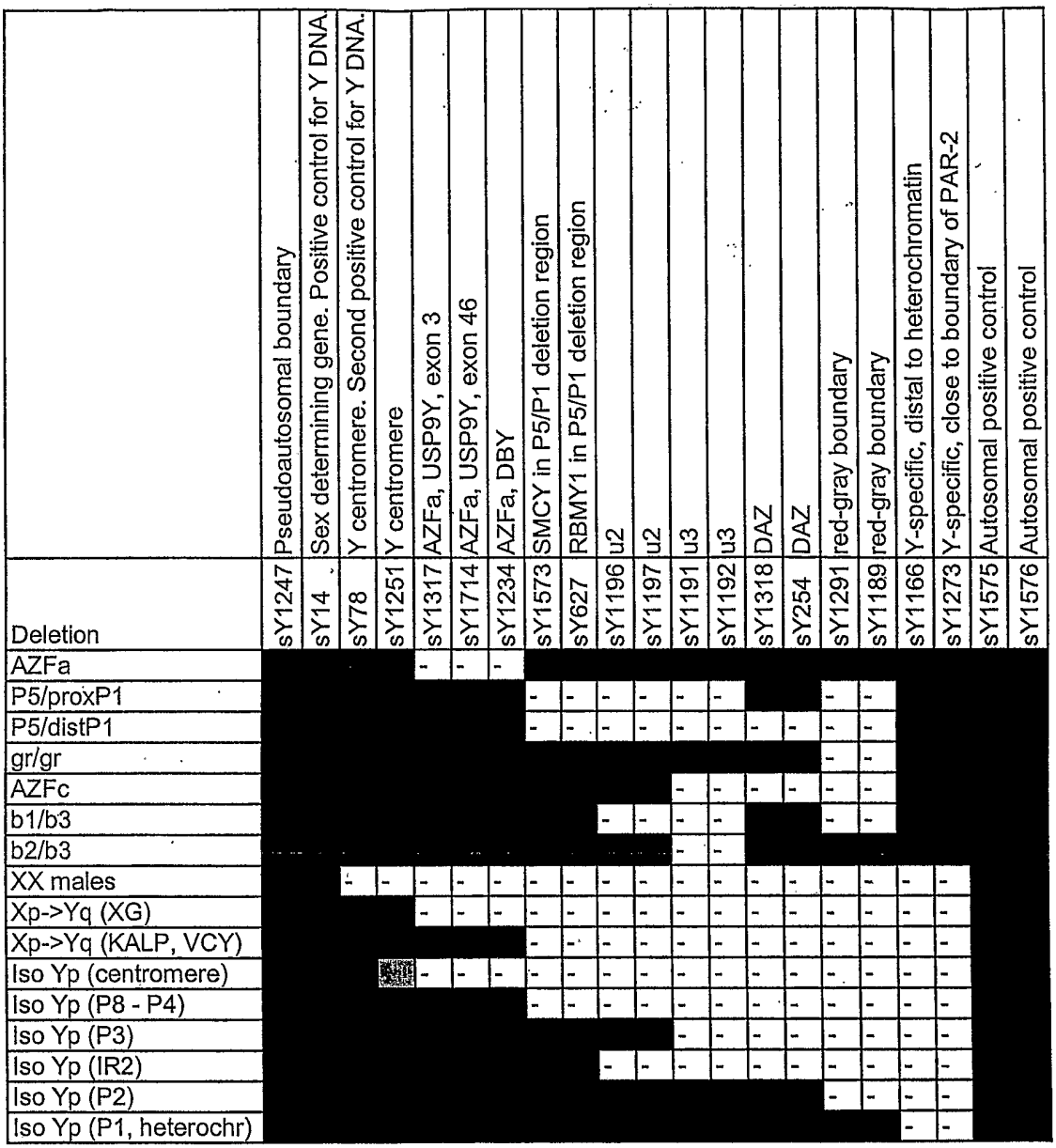
Deletion
sY1247 Pseudoautosomal boundary
sY14 Sex determining gene. Positive control for Y DNA
sY78 Y centromere. Second positive control for Y DNA.
sY1251 Y centromere
sY1317 AZFa, USP9Y, exon 3
sY1714 AZFa, USP9Y, exon 46
sY1234 AZFa, DBY
sY1573 SMCY in P5/P1 deletion region
sY627 RBMY1 in P5/P1 deletion region
sY1196 u2
sY1197 u2
sY1191 u3
sY1192 u3
sY1318 DAZ
sY254 DAZ
sY1291 red-gray boundary
sY1189 red-gray boundary
sY1166 Y-specific, distal to heterochromatin
sY1273 Y-specific, close to boundary of PAR-2
sY1575 Autosomal positive control
sY1576 Autosomal positive control
AZFa
P5/proxP1
P5/distP1
gr/gr
AZFc
b1/b3
b2/b3
XX males
Xp->Yq (XG)
Xp->Yq (KALP, VCY)
Iso Yp (centromere)
Iso Yp (P8 - P4)
Iso Yp (P3)
Iso Yp (IR2)
Iso Yp (P2)
Iso Yp (P1, heterochr)

Figure 2

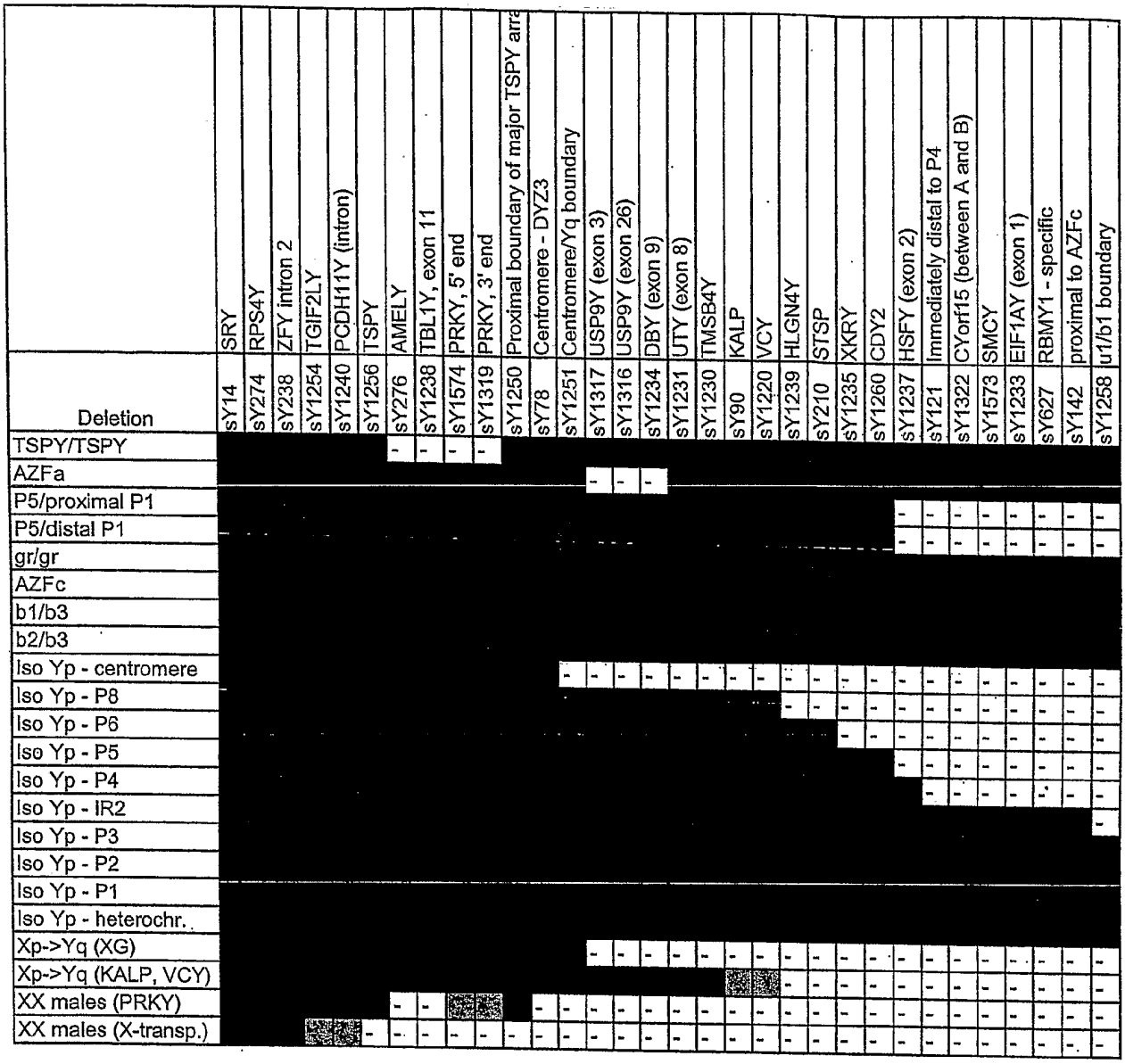
Deletion
sY14 SRY
sY274 RPS4Y
sY238 ZFY intron 2
sY1254 TGIF2LY
sY1240 PCDH11Y (intron)
sY1256 TSPY
sY276 AMELY
sY1238 TBL1Y, exon 11
sY1574 PRKY, 5' end
sY1319 PRKY, 3' end
sY1250 Proximal boundary of major TSPY arra
sY78 Centromere - DYZ3
sY1251 Centromere/Yq boundary
sY1317 USP9Y (exon 3)
sY1316 USP9Y (exon 26)
sY1234 DBY (exon 9)
sY1231 UTY (exon 8)
sY1230 TMSB4Y
sY90 KALP
sY1220 VCY
sY1239 HLGN4Y
sY210 STSP
sY1235 XKRY
sY1260 CDY2
sY1237 HSFY (exon 2)
sY121 Immediately distal to P4
sY1322 CYorf15 (between A and B)
sY1573 SMCY
sY1233 EIF1AY (exon 1)
sY627 RBMY1 - specific
sY142 proximal to AZFc
sY1258 u1/b1 boundary
TSPY/TSPY
AZFa
P5/proximal P1
P5/distal P1
gr/gr
AZFc
b1/b3
b2/b3
Iso Yp - centromere
Iso Yp - P8
Iso Yp - P6
Iso Yp - P5
Iso Yp - P4
Iso Yp - IR2
Iso Yp - P3
Iso Yp - P2
Iso Yp - P1
Iso Yp - heterochr.
Xp->Yq (XG)
Xp->Yq (KALP, VCY)
XX males (PRKY)
XX males (X-transp.)

Figure 3A

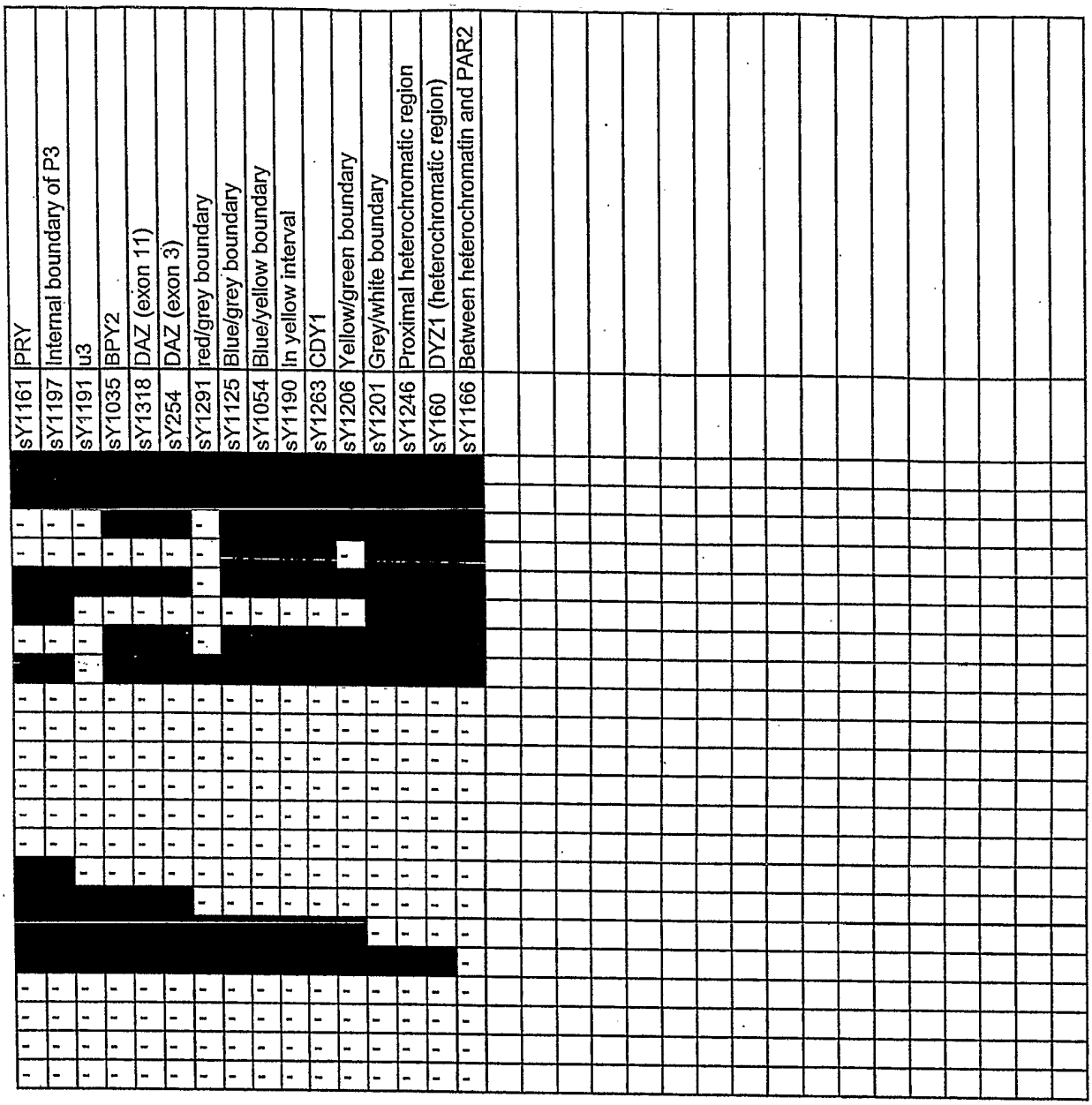
sY1161 PRY
sY1197 Internal boundary of P3
sY1191 u3
sY1035 BPY2
sY1318 DAZ (exon 11)
sY254 DAZ (exon 3)
sY1291 red/grey boundary
sY1125 Blue/grey boundary
sY1054 Blue/yellow boundary
sY1190 In yellow interval
sY1263 CDY1
sY1206 Yellow/green boundary
sY1201 Grey/white boundary
sY1246 Proximal heterochromatic region
sY160 DYZ1 (heterochromatic region)
sY1166 Between heterochromatin and PAR2

Figure 3B

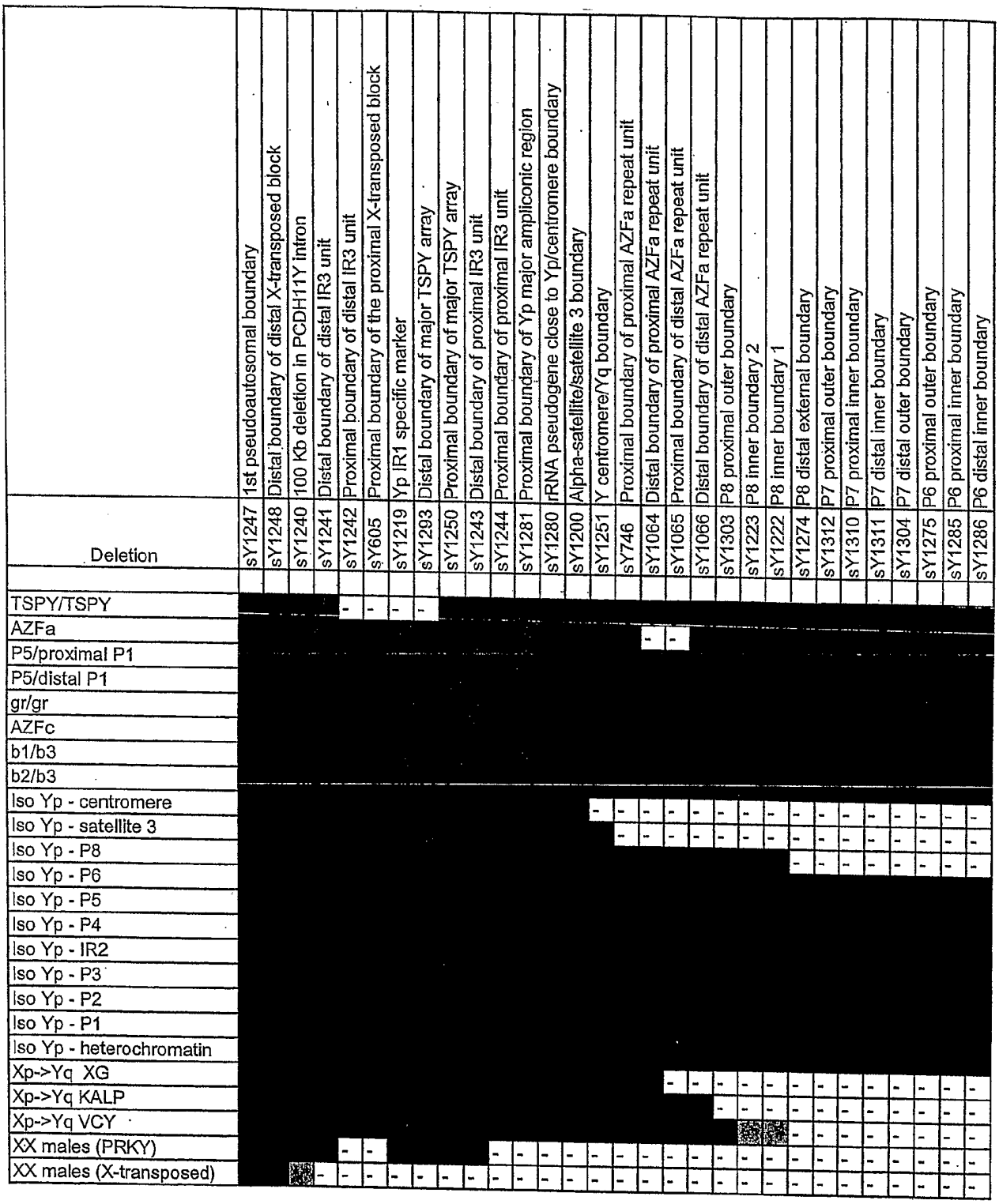
Deletion
sY1247 1st pseudoautosomal boundary
sY1248 Distal boundary of distal X-transposed block
sY1240 100 Kb deletion in PCDH11Y intron
sY1241 Distal boundary of distal IR3 unit
sY1242 Proximal boundary of distal IR3 unit
sY605 Proximal boundary of the proximal X-transposed block
sY1219 Yp IR1 specific marker
sY1293 Distal boundary of major TSPY array
sY1250 Proximal boundary of major TSPY array
sY1243 Distal boundary of proximal IR3 unit
sY1244 Proximal boundary of proximal IR3 unit
sY1281 Proximal boundary of Yp major ampliconic region
sY1280 rRNA pseudogene close to Yp/centromere boundary
sY1200 Alpha-satellite/satellite 3 boundary
sY1251 Y centromere/Yq boundary
sY746 Proximal boundary of proximal AZFa repeat unit
sY1064 Distal boundary of proximal AZFa repeat unit
sY1065 Proximal boundary of distal AZFa repeat unit
sY1066 Distal boundary of distal AZFa repeat unit
sY1303 P8 proximal outer boundary
sY1223 P8 inner boundary 2
sY1222 P8 inner boundary 1
sY1274 P8 distal external boundary
sY1312 P7 proximal outer boundary
sY1310 P7 proximal inner boundary
sY1311 P7 distal inner boundary
sY1304 P7 distal outer boundary
sY1275 P6 proximal outer boundary
sY1285 P6 proximal inner boundary
sY1286 P6 distal inner boundary
TSPY/TSPY
AZFa
P5/proximal P1
P5/distal P1
gr/gr
AZFc
b1/b3
b2/b3
Iso Yp - centromere
Iso Yp - satellite 3
Iso Yp - P8
Iso Yp - P6
Iso Yp - P5
Iso Yp - P4
Iso Yp - IR2
Iso Yp - P3
Iso Yp - P2
Iso Yp - P1
Iso Yp - heterochromatin
Xp->Yq XG
Xp->Yq KALP
Xp->Yq VCY
XX males (PRKY)
XX males (X-transposed)

Figure 4A

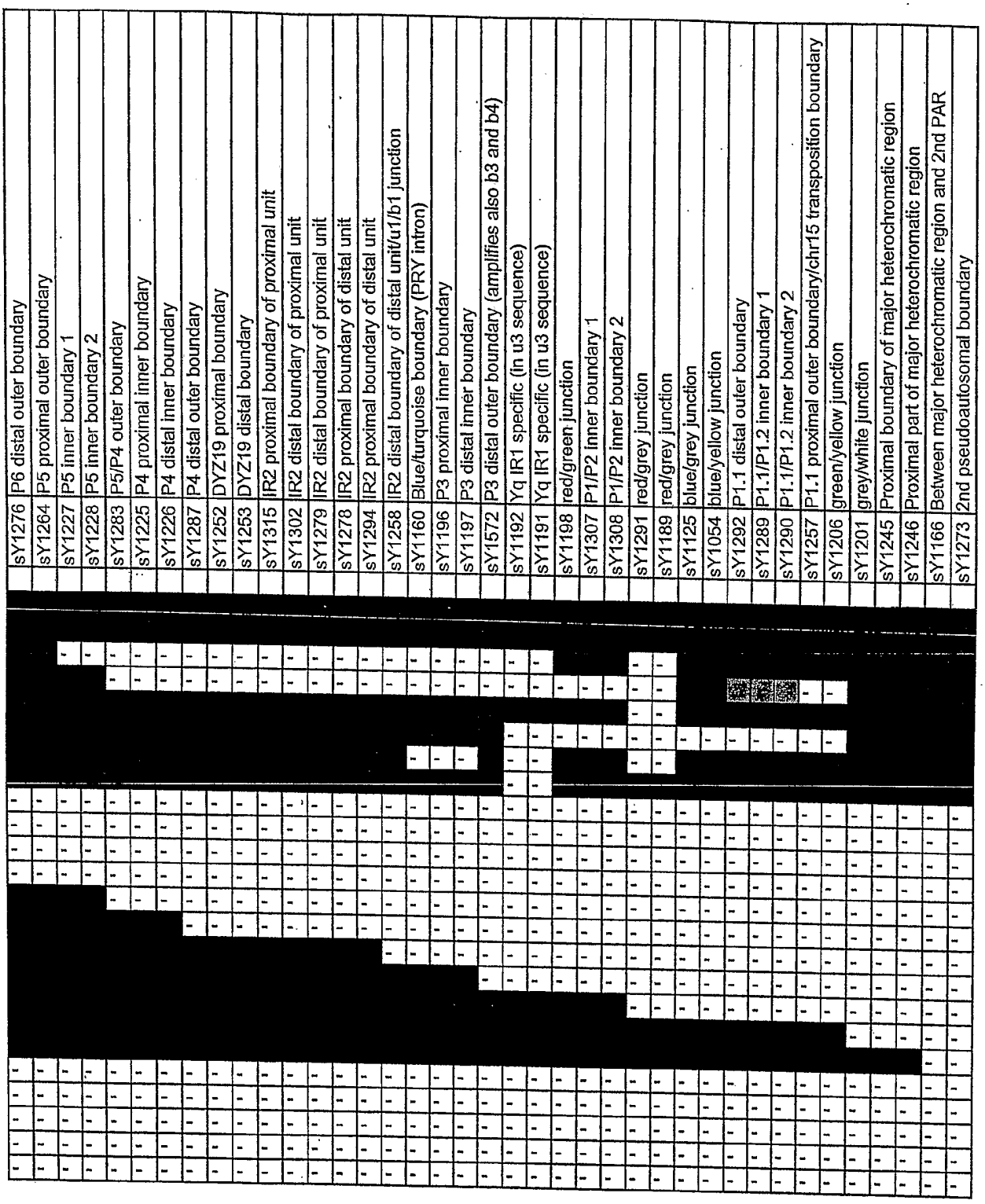
sY1276 P6 distal outer boundary
sY1264 P5 proximal outer boundary
sY1227 P5 inner boundary 1
sY1228 P5 inner boundary 2
sY1283 P5/P4 outer boundary
sY1225 P4 proximal inner boundary
sY1226 P4 distal inner boundary
sY1287 P4 distal outer boundary
sY1252 DYZ19 proximal boundary
sY1253 DYZ19 distal boundary
sY1315 IR2 proximal boundary of proximal unit
sY1302 IR2 distal boundary of proximal unit
sY1279 IR2 distal boundary of proximal unit
sY1278 IR2 proximal boundary of distal unit
sY1294 IR2 proximal boundary of distal unit
sY1258 IR2 distal boundary of distal unit/u1/b1 junction
sY1160 Blue/turquoise boundary (PRY intron)
sY1196 P3 proximal inner boundary
sY1197 P3 distal inner boundary
sY1572 P3 distal outer boundary (amplifies also b3 and b4)
sY1192 Yq IR1 specific (in u3 sequence)
sY1191 Yq IR1 specific (in u3 sequence)
sY1198 red/green junction
sY1307 P1/P2 inner boundary 1
sY1308 P1/P2 inner boundary 2
sY1291 red/grey junction
sY1189 red/grey junction
sY1125 blue/grey junction
sY1054 blue/yellow junction
sY1292 P1.1 distal outer boundary
sY1289 P1.1/P1.2 inner boundary 1
sY1290 P1.1/P1.2 inner boundary 2
sY1257 P1.1 proximal outer boundary/chr15 transposition boundary
sY1206 green/yellow junction
sY1201 grey/white junction
sY1245 Proximal boundary of major heterochromatic region
sY1246 Proximal part of major heterochromatic region
sY1166 Between major heterochromatic region and 2nd PAR
sY1273 2nd pseudoautosomal boundary

Figure 4B

STS sY1247
Forward primer: GAACTCTGCAAACCTCCTGG (SEQ ID NO: 21)
Reverse primer: TTTTGAGGCGGAGTCTCG (SEQ ID NO: 22)

Sequence:
GAACTCTGCAAACCTCCTGGATTTAGCAGGAGACAACATGAGGGTAATCACCCCGGCACCTGGACCCATT
AGATTAAGTCAATTTACTGAGGCTCCTGAGGATGATGCTCAGGACTCAGACCTTAGTTATAGATTAAAAG
AAGTTAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGATGGGCGGATCA
CGAGGTCAGGAGATCGAGACCATCTTGGCTAACACCGCGAAACCCCGTCTCTACTAAAAATACAAAAAAA
TCAGCCGGGCGTAGTGGCGGGCGCCTATAGTGCCAGCTACCCGGAGGCTGAGGCAGGAGAGTGGCGTGAA
CCCGGGAGGCGGCGCTTGCAGTGAGCTGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGAC
TCCGCCTCAAAA (SEQ ID NO: 1)

STS sY14
Forward primer: GAATATTCCCGCTCTCCGGA (SEQ ID NO: 23)
Reverse primer: GCTGGTGCTCCATTCTTGAG (SEQ ID NO: 24).
Sequence:
CTGTGCAAGAGAATATTCCCGCTCTCCGGAGAAGCTCTTCCTTCCTTTGCACTGAAAGCTGTAACTCTAA
GTATCAGTGTGAAACGGGAGAAAACAGTAAAGGCAACGTCCAGGATAGAGTGAAGCGACCCATGAACGCA
TTCATCGTGTGGTCTCGCGATCAGAGGCGCAAGATGGCTCTAGAGAATCCCAGAATGCGAAACTCAGAGA
TCAGCAAGCAGCTGGGATACCAGTGGAAAATGCTTACTGAAGCCGAAAAATGGCCATTCTTCCAGGAGGC
ACAGAAATTACAGGCCATGCACAGAGAGAAATACCCGAATTATAAGTATCGACCTCGTCGGAAGGCGAAG
ATGCTGCCGAAGAATTGCAGTTTGCTTCCCGCAGATCCCGCTTCGGTACTCTGCAGCGAAGTGCAACTGG
ACAACAGGTTGTACAGGGATGACTGTACGAAAGCCACACACTCAAGAATGGAGCACCAGCTAGGCCACTT
A (SEQ ID NO: 2)

STS sY78
Forward primer: TCCTTTTCCACAATAGACGTCA (SEQ ID NO: 25)
Reverse primer: GGAAGTATCTTCCCTTAAAAGCTATG (SEQ ID NO: 26)
Sequence:
ATCACAAAGAACTATGTCGGAATTCTTCTGTGTAGTTTTTATGTGAAGATATTTCCTTTTCCACAATAGA
CGTCAAAGTGATCCAGATATCCACTTGCAGATTCCACAAAAAGAGTGTTTCAAAAGTGCACAACCAAAAG
AAAGGTTCAACTAGGTGAGATGAATGCACACATCAGAAGGAAGTTTCTCAGAATGCTTCTGCATAGCTTT
TAAGGGAAGATACTTCCTTTTCCAACATAGGCCTCAAAGCA (SEQ ID NO: 3)

STS sY1251
Forward primer: GACTGGAGTGGAACGGTCTC (SEQ ID NO: 27)
Reverse primer: TCACTTCCCTCCGATTTTCT (SEQ ID NO: 28)
Sequence:
GACTGGAGTGGAACGGTCTCGAATGGAATGGAATGGATTGGAATGGAAAGGAATAGAATGGAATGGAATC
ATATGGAATGGAATGGAACAGAATGAGTCAAAACGGAATAGAATCAAGTGGAATGCAATCGAATGGAATG
GAATACAATGGACTCGAATGGAATGGATTCTAATGGAATAGAATATAATGGAATGGCATGGAATGGAATG
AAATAGCCAGCTCCCTGTGCAGGTGAAAATCCATGTATAACTTTTGACTCCCCAAAAGCTTAGTTACTTA
TCACCTACTGTTGACTAGAAGCCTGACTCGTAACATAGTCAAGTAATACACATTTTATATGTTATGTGTA
TTATATACTGTACTCTAACAAAAAGTAAGCTGAAGAAAGGAATATGTTATTAAGAAAATCGGAGGGAAGT
GA (SEQ ID NO: 4)

STS sY1317
Forward primer: GAGATTACAGGCATGCACCA (SEQ ID NO: 29)
Reverse primer: CCACACTTAGCCCACAGTCA (SEQ ID NO: 30)
Sequence:
GAGATTACAGGCATGCACCACCATGCCCAGACTCTTACTGGTCTTTTTAATATGTAAGACAGTGGTACCT
TTTTTCCTTTTAGGTTATGAAATGGTCTCTGCAAGATGTTTTGTCCTTGAATTGGAAATTTTTAAGGCTG
ATATATGCTGGTACTTCATCTTCTATATGTGGACTATAATTTCTTCCCTTAGGATAACTACATAAAGAGA
CAAAAAAAAGAAAAAAGAGCAAAGATCTGTGCTGTGTCAAGTATGACAGCCATCACTCATGGCTCTCCAG
TAGGAGGGAACGACAGCCAGGGCCAGGTTCTTGATGGCCAGTCTCAGCATCTCTTCCAACAGAACCAGGT

Figure 5A

AGGAGTAAGACTGTGTTGTTTGAGTAGTGTGAAATACAAAATTGTGAAACATGTCCTGAATGATTTGTA
AAGTAATCATAAAATATGTGGTTATTTTAAGTTACACGTGAAAAAAGTGACTGTGGGCTAAGTGTGG (SEQ II
NO: 5)

STS sY1234
Forward primer: TTACCCCTTTCACCCACTGA (SEQ ID NO: 31)
Reverse primer: CCATAAACTACACAAGGACGAACT (SEQ ID NO: 32)
Sequence:
TTACCCCTTTCACCCACTGAAAATAAGTTTGTAGATGTAATCTGCAAATTATAAAGAGAAAGTGATGAAT
TTTTAAAAACAATTGAAGTTTTGGGTTATGAATTTAAAATTATATTTATGTTTTAGGAAAATGGAAGGTA
TGGGCGCCGCAAACAATATCCAATATCCTTGGTTTTAGCCCCAACAAGAGAATTGGCTGTACAGATCTAT
GAGGAAGCCAGAAAAGTAAAATATTCATTTTAGTGATTATTGCTTTTCTTATTTGTCAAATGATGTTGTT
ATAGTCACTGACATGTTCTTTGCTTAAAGTTTTCCTACCGATCTAGAGTTCGTCCTTGTGTAGTTTATGG
SEQ ID NO: 6)

STS sY1573
Forward primer: AGGAATCATTTGAGGCCCTT (SEQ ID NO: 33)
Reverse primer: TGGAGTTCGGGTTCAAATTC (SEQ ID NO: 34)
Sequence:
AGGAATCATTTGAGGCCCTTGTGTACAAAAATGGTTACCAGAAGACTTTAAAAGAGTGGGAACAAATGAT
TGTGGTTTTCACTATCTTCATCCTTTACTGTGCCATAGTTACCAGGTCCTTACACTTTCTTCTAGGATTG
GCAGCCTCCTTTTGCAGTAGAAGTTGACAATTTCAGATTTACTCCTCGCGTCCAAAGGCTAAATGAACTG
GAGGTAAGATTGGGAGGCACACTTTTTTTAAAGGAATCTGATCTTTAATCTTGCCGTTGTAGTTTCATAA
TAATGTAGAACTTAAGTTTTGAAATCTAATGTATTGAATTTGAACCCGAACTCCA (SEQ ID NO: 7)

STS sY627
Forward primer: GCACCTGCCACGCATATAGT (SEQ ID NO: 35)
Reverse primer: GCAAACATGCTCACGATCAC (SEQ ID NO: 36)
Sequence:
GAGGAAAGCAGATATTTCCAAATAGTACTTAACTATTCATGCTTTAATGATAGCAGTAAAAATGTTTAAA
TGTAGTCCCACATATTATTTTACCAACCCTGCAGGGACCTCTCATGGTGCACCACCTGCAAGAGGGCCTC
GGATGTCTTATGGTGGAAGCACCTGCCACGCATATAGTAATACACGAGATAGATATGGCAGAAGTTGGGA
GAGTTACTCGAGCTGTGGTGATTTTCATTATTGTGATCGTGAGCATGTTTGCAGAAAAGACCAAAGGAAT
CCGCCTTCTCTGGGTAGGGTGCTCCCTGATCCTCGTGAAGCATATGGTAGCTCAAGTTATGTGGCATCTA
TAGTAGATGGTGGGGAGAGTCGATCTGAAAAAGGAGACTCGAGCAGATATTAAAGCAAGCATTGAAAGTA
ATAGTTATTGCATACCAATCCTTGTTTGCACATCAAAAATTGAAATGTTATTTCTGCATTGTTACCTGCA
TATTACTGAAAGAAACATGTTGGTTTTGTGGAGAGAGGTAGATACTAACTTCCTCCATGAATTTTTTGAG
GTATTCAAAGGAAAAGGAATTGTTTTCAAAGTAATTTCATACTTGTTGATGCTATTTGAAAAGTGTTTAG
ATGTAATATCTACCTTAAAATTTTCACAATAAAATTTGACAT (SEQ ID NO: 8)

STS sY1196
Forward primer: GTTGGCAACTTGCACTGCT (SEQ ID NO: 37)
Reverse primer: CCTTTCCTCTCAAAGTCCCC (SEQ ID NO: 38)
Sequence:
GTTGGCAACTTGCACTGCTCACTGCAGCCTCCTCTGCAGAGCTTCAAGTGATCCTCCGACTTCTCAGCTA
CTTGAGTAGCTACAGGCTCTCGCTATCAGAGCTAGTAGGCAATTTTTTTGTGTGTTTCTTTAATGGACAT
GGGTTTCCCCATGGTACCCAAGCTGGTCTCAAACTTGGGTTAAGTTAAGTTAAGATCTACCTCTCCCTCC
AAATCAGAGATAACCAGGCAACTTTAAGAACTAAAGTTGACTGTGGAGAAAATACTTAGACAGCCCTCTT
GGAACATCAGCCTGGTAATTGGTTAGAGCTCCTAGCTTAAGAGGTGAGAAAGACAGGTCACTTCTGGGCA
AGCTCTGGAACCTCACGATACTTGGGGACTTTGAGAGGAAAGG (SEQ ID NO: 9)

STS sY1197
Forward primer: TCATTTGTGTCCTTCTCTTGGA (SEQ ID NO: 39)
Reverse primer: CTAAGCCAGGAACTTGCCAC (SEQ ID NO: 40)
Sequence:
TCATTTGTGTCCTTCTCTTGGATTTACTAATTTACTAGTTAAGCTGTGTTATGTTCACTGGACATTTAAG

Figure 5B

ATTTTATAAATATCTATATTGCAATAGAGTCATTTCTGAGGTAGTAAGAATGTATTCTCCTTTCAACAGA
ACCTAATTGGAACCTGGTTTTATTACAAAGCCTTGTCTGAAATATCAAATACATTTAAGAATGATTTGCA
GAAAATCAGAGATAACCAGGCAACTTTAAGAACTAAAGTTGACTGTGGAGAAAATACTTAGACAGCCCTC
TTGGAACATCAGCCTGGTAATTGGTTAGAGCTCCTAGCTTAAGAGGTGAGAAAGACAGGTCACTTCTGGG
CAAGCTCTGGAACCTCACGATACTTGGGGACTTTGAGAGGAAAGGTATTCAACCAAGTGTATAGGTTCTG
AAAGGGAAGCCTGGTGGCAAGTTCCTGGCTTAG (SEQ ID NO: 10)

STS sY1191
Forward primer: CCAGACGTTCTACCCTTTCG (SEQ ID NO: 41)
Reverse primer: GAGCCGAGATCCAGTTACCA (SEQ ID NO: 42)
Sequence:
CTATCAGACACTATTTTGGCAATTTTATGTACCTAAACATGTTAAATAATCATGCTTACCATTTTTTCCA
GACGTTCTACCCTTTCGAGATTAGTTAATATGTTTACACACAGAGTTTTCTTTATAGGATTATAATTTAC
AATGTTTTCACAATTTTCTTAAACAGTCGACTTTATTTTATTTAACTTTAAGACAACTTTTTTATTCTTA
AGCAAAATACATAGTTATGCCTTATAATTTTTAACTAAAACCACTTTTTACCATTTTTATACACTTTTAT
GCAAATCCATGTTTAGCAGTTTTAATTACCTGTTATAACGGTAATTTTTAGCAATTTTTAACTTTAATGT
AAAGCCTATTACGTGTTTTTTATTTTGTTTTGTTTTGTTTTCTTTTTGAGACAGAGTCTTGCTCTCTCAT
CAGGCTAGAGTGTGGTAACTGGATCTCGGCTCACTGCAACCTCCACTTCTTGGATACAAGCGATTCTGCT
GCCTCAGCCTCCTGAGTAGCTTGGATTACAGACGCCTGCCACCACACCCAGCTAATTATTGTATTTTTAG
TAGGGAGGAGGTTTCACCATGTTTTCCAGGATTGTCTTGAT (SEQ ID NO: 11)

STS sY1192
Forward primer: ACTACCATTTCTGGAAGCCG (SEQ ID NO: 43)
Reverse primer: CTCCCTTGGTTCATGCCATT (SEQ ID NO: 44)
Sequence:
TTTTTAAAAATGAAAGATTATTCTTGTTTTCACTGTGAAGCACAATAACAATAAATTTTCCCCATTGGTA
CAAGTGAATGATTTACATGGTAAATTGATGTGCTTAACTACTACCATTTCTGGAAGCCGGATTTGATATA
AACTTATTTTGGGCTGGGCGCGGTGGCTCACGCCTGTAATCTCAGCAGTTTGGGAGGCCGAGGCAGGTGG
ATCACGAGGTCAGGAGATGGAGACCATGCTGGCTAACACAGTGAAACCCCGTCTCTACTAAATACACAAA
AAAATTAGCCGGGTGTAGTGGTGGGCGCCTGTGTTCCCAGCTACTCCGGAGGCTGAGGCAGGAGAATGGC
ATGAACCAAGGGAGCGGAGCTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTAGGCGACAGAGC
CAGACTCCGTCTTAAAAAAAAAAACAACAAAAAACTTATTTTGATAAACATGGCTTATGATACTTGATAA
TAAAATTAATAAAGATGTTGTTTTTATAAACATCAAATGTGAATAGCTGTTGTCATGGTTTAAAATGTCA
AAGGACAGCCTTTGAAAATTAAGATACTGATAACAGACATG (SEQ ID NO: 12).

STS sY1318
Forward primer: TGATATCAGGTGATGCGTCC (SEQ ID NO: 45)
Reverse primer: TGGCGTTAAGTAAACCTGGG (SEQ ID NO: 46)
Sequence:
TGATATCAGGTGATGCGTCCTCCTCGGCCTCCCAAAGTGCTGGGATTAGAGGTGTGAGCCACTGCTCCCA
GCCTCTTTTAGCATTTTTGCATTTCTTTGGAAATAAACTGATATGTTCATTAAACCATCAAAAGAAAAAC
CAAAACACACCCTTATTAAGAGTGAGTGAAAGAAAGAGTTGTCTTTACATTACTGAAAACTTCTGTGTTT
CAGAAATCTGTGGACCGAAGCATACAAATGGTGGTATCTTGTCTGTTTAATCCAGAGAAGAGACTGATAA
ATTCCGTTGTTACTCAAGATGACTGCTTCAAGGTATGAAAGGAATGGCATGCATAATTAAAAAGCACACT
TGTTCCCTCTCAAGTTAGCTGTTTTCCTTGTGGCACATGTATTTTGGGCTTTCTTAGAGGAATTTTTTTT
CTTTTTTTTTTTGTTTTGAGACGGAGTCTCCTCTGTCGCCCAGGCTGGAGTGCAGTGAGTGGCCCCATCTA
GGCTCACTGCAAGCTCCACCTCCCAGGTTTACTTAACGCCA (SEQ ID NO: 13)

STS sY254
Forward primer: GGGTGTTACCAGAAGGCAAA (SEQ ID NO: 47)
Reverse primer: GAACCGTATCTACCAAAGCAGC (SEQ ID NO: 48)
Sequence:
CCCAGTCTTCATCAGCTGCAGCTAGCCAAGGCTGGGTGTTACCAGAAGGCAAAATCGTGCTAAACACTG
TTTTTGTTGGTGGAATTGATGCTAGGATGGATGAACTGAGATTGGAAGCTGGTTTGGTAGATACGGTTCA
GTGAATTG (SEQ ID NO: 14)

Figure 5C

STS sY1251
Forward primer: TAAAAGGCAGAACTGCCAGG (SEQ ID NO: 49)
Reverse primer: GGGAGAAAAGTTCTGCAACG (SEQ ID NO: 50)
Sequence:
TAAAAGGCAGAACTGCCAGGTCTGTGTCTTATTTTCTTTGTCATTCTAATTTATCTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGG
ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTG
GGACTACAGGCGCCCGCCGCTACTCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTT
TTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGCACCTGGCCAAGTGTCTTCTTTTGAGAAGTGTCTGTTCATATACTTCACCCAC
TTTTTGATGGGGTTGTTTGTTTTTTTCTTGTAATTTTTGTTTGAGTTCATTGTAGATTCTGGATATTAGC
CCTTTGTCAGATGAGTACGTTGCAGAACTTTTCTCCC (SEQ ID NO: 15)

STS sY1189
Forward primer: TGGGCGAGGACTTTATGA (SEQ ID NO: 51)
Reverse primer: GGGGTCCCAGTTCCACTATT (SEQ ID NO: 52)
Sequence:
TGGGCGAGGACTTTATGACTAAAACACCAAAAGCAATGGCAACAAAAGCCAAAATTGACAAATGGGATCT
AATTAAACTAAAGAGCTTCCGCACAGCAAAATAAACCACTGTCAGAGTGAATAGGCAACCTACAGAATGG
GAGAAAAGTTCTGCAACGTACTCATCTGACAAAGGGCTAATATCCAGAATCTACAATGAACTCAAACAAA
AATTACAAGAAAAAAACAAACAACCCCATCAAAAAGTGGGTGAAGTATATGAACAGACACTTCTCAAAAG
AAGACACTTGGCCAGGTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGAT
CACGAGGTCAGGAGATCGAGACCATCCCGGCTAAAAACGGTGAAACCCCGTCTCTACTAAAAATACAAAA
AATTAGCCGGGAGTAGCGGCGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATGGCGT
GAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCCCGCCACTGCACTCCAGCCTGGGCGACAGAGTGA
GACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATAAATTAGAATGACAAAG
AAAATAAGACACAGACCTGGCAGTTCTGCCTTTTAAGGGCCAGCCTCAGCCTAGTCACCGTGAATCACAA
TTTCAGGTTCTGCGTCAGCGTGTCCCACCTTGGAAAATAGTGGAACTGGGACCCC (SEQ ID NO: 16)

STS sY1166
Forward primer: AGTCGGAGTCGGAGTGTGAT (SEQ ID NO: 53)
Reverse primer: ATTCCATTGCTTTCCATTGC (SEQ ID NO: 54)
Sequence:
AGGAATGGAATGGGATGGAGTGGAATGGAGTGGAGTGGAGTGCAGTGGAGTGGAGAGGAGTGGAATAGAG
TGGAATGGAATAGGATGTAATGGAATGTAGAGGAGTGGAGTGGAGTCGGAGTCGGAGTGTGATGGAATGT
AATGGAAAGGAATGGAATGCAATTGAATGCAAAGAAATGGAAAGTTGACATGTAATGTGACCTGAGATTG
TGCCACTGCACTCCAGCCTCTGTGACAGAGTGAGATCCTTTGGAAAGAAAGGAACGGAATGGTATGGAAT
GGAGTGGAGTAGAGTGGAGTGGAATGGAATGGAATGGAATGCAATGGAAAGCAATGGAATGCAATGGAAT
AGAATGCAGTGAAAAGGAAAGTTGACATGTAATGTGAGCAGAGATTGTGCCACTGCACTCCAGCCTGGGT
GACACAGTGATATCCTGTCAAAAGAAAGGAATGGAATGCAA (SEQ ID NO: 17)

STS sY1273
Forward primer: GAGCTGCAACATAACAGGCA (SEQ ID NO: 55)
Reverse primer: AGGGGAACATCACACTCTGG (SEQ ID NO: 56)
Sequence:
GAGCTGCAACATAACAGGCACTATAAATGAATGAATGGATAAAGACAGCACTGAAGAACTTGAAATTATA
GTTTACACATGTAAACAGTAACATAAATCTGAAGAAATAAAGTTTTTTTTTGTTGTTTTTTCGAGATGGA
GTCTCGCTCTGTCACCAGGCTGGAGTGCAGTGGTGCAATCTGGCCTCACTGCAACCTCCGCCTCCCGGGT
TCAAGCGATTCCCCTGCCTCAGCCTCAGCGTCCCAAGTAGCTAGGACTCCAGGCACGTGCCACTACGCCT
GGTTATTTTTCTTTCTTTCTTTTTATTGTATTTTAGTAGAGATGGGTTTCACTATATTGGCCAAGACGGT
CTCAATCTCCTGACCTTGTGATCTGCCTGCCTCATCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
CGGGCCTGGCCAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTTTATTATACTCTAAGTTTTAGGTTAC
ATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGACATGCTGGTGCGCTGCATCCACTAACTC
ATCATCTAGCATTAGGTATATCTCCCAATGCTATCCCTCCCCCTCCACCCACCCCACCACAGTCCCCAGA
GTGTGATGTTCCCCT (SEQ ID NO: 18)

Figure 5D

STS sY1575
Forward primer: AGATGTCCCAGATGCGTAGG (SEQ ID NO: 57)
Reverse primer: TTCAGGGGACTTAGGGATTCTT (SEQ ID NO: 58)
Sequence:
AGATGTCCCAGATGCGTAGGACAGAGTCATCTAGTCATCTTCCAGGGTTTAATCCTGGACTACTGGAAAC
AACTAGAAGTGAGAAAAGCGTCTGTGCTTTGCAGTGACCATTGTCCTGTCAGACAACCAATAAATGCTAT
CTTTCCTCTTTCAGGTTTTTCAGGGAAATCAAGACTCCTTCACACCTGTGGTGAACTCTCTAGACCCACC
GTTACTGACTCGCTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTT
CTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGCCACTGCAGCACCTGCCACTGCCGTCACCTCTCC
CTCCTCAGCTCCAGGGCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGCAGACACT
GCCTTGAAGCCTCCTGAATTAACTATCATCAGTCCTGCATTTCTTTGGTGGGGGGCCAGGAGGGTGCATC
CAATTTAACTTAACTCTTACCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACTAG
GCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTGAAAAGTTAGGCCTCTCAGAGTCACC
ACTTCCTCTGTTGTAGAAAAACTATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTCAGG
TTAAGCCTCATACGTTTAAAATAAAACTCTCAGTTGTTTATTATCCTGATCAAGCATGGAACAAAGCATG
TTTCAGGATCAGATCAATACAATCTTGGAGTCAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAG
AATACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGATATAATTATGTTATTTAGTC
ATTATGAGGGGCACATTCTTATCTCCAAAACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGA
ATCCCTAAGTCCCCTGAA (SEQ ID NO: 19)

STS sY1576
Forward primer: GTCTATGGGACCCTTGATGTTT (SEQ ID NO: 59)
Reverse primer: TGGTGGGGTGAATTCTTTG (SEQ ID NO: 60)
Sequence:
GTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTTTCTATGGTTAAGTTCATGTCATAGGAAGGGGAG
AAGTAACAGGGTACAGTTTAGAATGGGAAACAGACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGT
TTTAGTTTCTTTTATTTGCTGTTCATAACAATTGTTTTCTTTTGTTTAATTCTTGCTTTCTTTTTTTTTC
TTCTCCGCAATTTTTACTATTATACTTAATGCCTTAACATTGTGTATAACAAAAGGAAATATCTCTGAGA
TACATTAAGTAACTTAAAAAAAAACTTTACACAGTCTGCCTAGTACATTACTATTTGGAATATATGTGTG
CTTATTTGCATATTCATAATCTCCCTACTTTATTTTCTTTTATTTTTAATTGATACATAATCATTATACA
TATTTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACATATTGACCAAATCAGGGTAATTTTGCATT
TGTAATTTTAAAAAATGCTTTCTTCTTTTAATATACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTA
ATCTCTTTCTTTCAGGGCAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGT
GATAATTTCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGA
TGTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTATTTTATGGTTGGG
ATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTC
CCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCACCA
(SEQ ID NO: 20)

Figure 5E

STS sY1714
Forward primer: TGTGTGTGCACTTTCTCAAAAC (SEQ ID NO: 413)
Reverse primer: GCAAATTACTGCAAATAAACCAG (SEQ ID NO: 414)
Sequence:
TGTGTGTGCACTTTCTCAAAACACTTTATTCATATGGTACTTCTTCTCTTCAAATATAAAAATCAGATTGT
AAGTTCTTTTTTTTTTTTTAAAGATCCAGGTTTAAAAATGTCTACTTTTTGACCAACCTTACCCCATGGTT
TTAAATTTTTAATTGTTAATATTTGAAAAGTGTTACAATGCTGGTCTCTTTCACCCTCTTAGAATAATCAT
GTACATGGACAGCCATATACAGGACCAGCAGCACATCACTTGAACAACCCTCAGAAAACAGGCCAACGAAC
ACAAGAAAATTATGAAGGCAATGAAGAAGTATCCTCACCTCAGATGAAGGATCAGTGAAAAGCAATAATTA
ACTGCTTCCTTTATGACTATGCACTAAGGTCTTATAGTCCAAACTTTCTCTGTGTCTGGCTAGTATTGAAA
ACTAGATAAACTGCTCCAAACCAACATGGAGTAAAGAGCATATTCACTGGTTTATTTGCAGTAATTTGC
(SEQ ID NO: 412)

Figure 5F

STS sY14
Forward primer: GAATATTCCCGCTCTCCGGA (SEQ ID NO: 109)
Reverse primer: GCTGGTGCTCCATTCTTGAG (SEQ ID NO: 110)
Sequence:
CTGTGCAAGAGAATATTCCCGCTCTCCGGAGAAGCTCTTCCTTCCTTTGCACTGAAAGCTGTAACTCTAA
GTATCAGTGTGAAACGGGAGAAAACAGTAAAGGCAACGTCCAGGATAGAGTGAAGCGACCCATGAACGCA
TTCATCGTGTGGTCTCGCGATCAGAGGCGCAAGATGGCTCTAGAGAATCCCAGAATGCGAAACTCAGAGA
TCAGCAAGCAGCTGGGATACCAGTGGAAAATGCTTACTGAAGCCGAAAAATGGCCATTCTTCCAGGAGGC
ACAGAAATTACAGGCCATGCACAGAGAGAAATACCCGAATTATAAGTATCGACCTCGTCGGAAGGCGAAG
ATGCTGCCGAAGAATTGCAGTTTGCTTCCCGCAGATCCCGCTTCGGTACTCTGCAGCGAAGTGCAACTGG
ACAACAGGTTGTACAGGGATGACTGTACGAAAGCCACACACTCAAGAATGGAGCACCAGCTAGGCCACTT
A (SEQ ID NO: 61)

STS sY274
Forward primer: TTAAGGGGACAGTATTTCAACTTC (SEQ ID NO: 111)
Reverse primer: CCACATTTAAACTGAGTACAGTCC (SEQ ID NO: 112)
Sequence:
CCCATCTTGCACCTCTGAAGCTTAAGGGGACAGTATTTCAACTTCGGCCTTTTTTATAGGAGAATGAGCC
AAGCTCTGGTTACTTTACTTACTGTGTCTCTTTCCACACCTCCTAGGCAGGTTAAAAGCAGTGATAAGAG
AGAAGCTGGCAAACCTAGTTAGTCCTGAGAGCCCAAAGATACGGGAGAGAGGAAATGCAGCAGCTGATTA
AAAAACAAAAAAGTGGCTCCTCGAGTTCATTTATTGTACAGTTTCTGGAGTATTTCTGTCATCTTTTCAG
GGAGTTTTTCTGTCATCTGGCACTCTGTTTGTCCTTGTCATTTTCATATTTACCCAGAATTTGTCCTGAG
ACTTCAGAGGACTGTACTCAGTTTAAATGTGGAGTTTTTAATATCTTTTAA (SEQ ID NO: 62)

STS sY238
Forward primer: AACAAGTGAGTTCCACAGGG (SEQ ID NO: 113)
Reverse primer: GCAAAGCAGCATTCAAAACA (SEQ ID NO: 114)
Sequence:
TGGCAGACTGGCTAAACAGAAACCAAAGAAAAAGAGAAGACCTGATTCCAGGCAGTACCAAACAGGTGAG
TTCCACAGGGGTGTTATGATGGAGTTTTAGCTAGTAGGCCACATGTATTTTTATGTGTTGAATTTGAAAG
AAAAAATTTCAAAATTCAGTGATATTCATGAATGGTTTTCTTGGATAAGAAGAAACAGTTGTGCATCAAC
CATTCAGGAAAAAGAATTAAAATCCTCTGGTGATTTTAGTGAAAAGGAAAATAAATTTCTAAAATGTTAC
CTAACTTTAAGTGAACGAAATTACATGGATCTACTTATACTAGCATAAAGCAGGTATAATTTACCGAGAA
GTGGAAGAAGTACCTAGGTTATTTGTAGGACTGATTACTATCCTATGTTGTTTTGAATGCTGCTTTGCAT
ATTAAAATTTATTTATAGGTGCAGTTAAGCTTTACTGTTTGCATATATTTGGCTTGGAGTCAGTCACCAA
AGCAGAAATGCTGGACTTGATTTTTATGAGTTATTTGCTACACATTTCTAAATTCATGTTCTTTTGTCAC
TGCTTGATTGATTTTTTTTTTTAACTGGAGGGGGTGAGATTGGTTCATACTTAACCAAACCAGTTCTCTC
GATTAGGACATTATTATAACTCTTAACATTGAAAAGCAGTAAAAGGAATGTTAATAATTTAAAAGTATTT
GCCCACTAATGTTCAGAACACAAGCTTTAAAAAATTCATGAGGAGACCAGAAGTTTGATTAAGCACTCAT
ACTGCTTTCTTTTCCTTTCTTAG (SEQ ID NO: 63)

STS sY1254
Forward primer: GACCAATTTGTCTTTGTTGCG (SEQ ID NO: 115)
Reverse primer: GCTGCTGAAGTCGGCGTA (SEQ ID NO: 116)
Sequence:
GACCAATTTGTCTTTGTTGCGGATTTCTAACTGGTTTATCAATGCTCGCAGACGCATTCTCCCGGATATG
CTTCAACAGCGTAGAAACGACCCCATCATTGGCCACAAAACGGGCAAAGATGCCCATGCCACCCACCTGC
AGAGCACCGAGGCGTCTGTGCCGGCCAAGTCAGGGCCAGTGGTCCAGACAATGTACAAAGCCTGCCCCTG
TGGCCCTTGCCAAAGGGCCAGATGTCAAGAGAGAAGCAACCAGATCCGGAGTCGGCCCCTAGCCAGAAGC
TCACCGGAATAGCCCAGCCAAAGAAAAAGGTCAAGATTTCTATCACTTCCCCGTCTTCTCCAGAACTTGT
GTCTCCAGAGGAGTACGCCGACTTCAGCAGC (SEQ ID NO: 64)

STS sY1240
Forward primer: GGGTCCTAGATAGGCTCCAAG (SEQ ID NO: 117)
Reverse primer: TTCATGTTGGCAGTGATTGG (SEQ ID NO: 118)

Figure 6A

Sequence:
GGGTCCTAGATAGGCTCCAAGGAAACCAAATTACTTGAAGAAGCCTGAGATTATTCTTAAAGAAATATAG
ATTTCCTTGTATGTTTACAATGAATGAGTCTTATTTTTACATGCATGGAAGTATCACAGTCACTGGACAC
TGTATAATGAAAACTTACAAGTTCTCATTTTGAACAAGCTTCCTTTTTCCTTAGTTGACAAAATTATCCA
GGTTTCTTTTAGCATGTTCACAATTTCAGATTTTATACAATTACAAACTGAACTTTCCTTATAAACTGAT
TGTTATAGCTAATTTTTCCTAATAAAATTCAAATTAAGACAGCACCTGTGAATTCTATTTAGAGTTCTAT
TGATACTCAATGTAGCCAATCACTGCCAACATGAA (SEQ ID NO: 65)

STS sY1256
Forward primer: CCCAGTGAAGAATCGTCCAT (SEQ ID NO: 119)
Reverse primer: GCTAACAAGATGCACTGGGC (SEQ ID NO: 120)
Sequence:
CCCAGTGAAGAATCGTCCATTTCCAGAATCAATGAGAAGTAAAGCTGAAAATCATTCAGTTCAGTCTGTG
GCACTTGATTCCACGGCTGTCAACCCCACCGGCAGTCATCCCACCAACCCCATGAGATTGGGCTCCCTGA
ATGTGCGTCCTGGTCATCCTTGCCCCAAACCACAAAGGACTGTTTAGATTGATGGATTTCCTTAAGCTGT
TGCCCCATCAGACTTGTGTGTGCTTTTAGGGCCCAGTGCATCTTGTTAGC (SEQ ID NO: 66)

STS sY276
Forward primer: CCTACCGCATCAGTGAATTTC (SEQ ID NO: 121)
Reverse primer: TCTGTATGTGGAGTACACATGG (SEQ ID NO: 122)
Sequence:
TAGAACTCACATTCTCAGGCTATCAATGTTGACAGGATTGCTTTAGTGAGTCTATATTTCCTACCGCATC
AGTGAATTTCTGCATGGGATGAAAGTAAATTAAATCAAATGGATTCTAATATATCTTTCTCTTAAGGTGC
TCACCCCTTTGAAGTGGTACCAGAGCATGATAAGACCACCAGTATGTAGACATTTTGTTCTTTATTCCCT
GAAAATATTAGGCATGCATTTAAATTCCCATTTTAAGAAAATACCATGTGTACTCCACATACAGACACTA
ATGGGAAATTTAGTTTGTAAAAAATCATGTCTGTGTACACAGTTACAAATTTTTGCAAAGGAAAGATAAA
TACAATATTCCTATGGCCATAATGGCAAAGACAACACTGCTGCTTCTCTGGTTGGAGTCACGTGAGCCAA
(SEQ ID NO: 67)

STS sY1238
Forward primer: GGTGTGCTAACATTGCATGG (SEQ ID NO: 123)
Reverse primer: TTTGTTCCATTTCAGAGCGA (SEQ ID NO: 124)
Sequence:
GGTGTGCTAACATTGCATGGCACCAACTATTGCCTGAAGAACCCTCTGGACTTGGGATCCTGAGAGAGGC
TCTCTGAGCTTCTTTGGTGCTCCCACTCCTAAGCTGTTTTTCTGAGTTTGTATCTCTTTCTGGCCCTCAG
AGTGATGGAACACTATTGGCTATGGGTTCATATGATGGTTTCGCAAGAATATGGACAGAAAATGGTAAGT
CCTGCACCCCTCCTGCATGGGTCAGGTAAGAGGAGCTGCCATACATAACCCTTGATTGAACAGACCATGA
CAACAGAATCAACATGTTTGTTTTTACTAACAGGTAACCTGGCCAGCACCTTAGGCCAACATAAAGGCCC
CATCTTCGCTCTGAAATGGAACAAA (SEQ ID NO: 68)

STS sY1574
Forward primer: GGCTGTGCAGGTTGTTTCAT (SEQ ID NO: 125)
Reverse primer: GAGATTATGTCCTTTGCAGGAAC (SEQ ID NO: 126)
Sequence:
GGCTGTGCAGGTTGTTTCATAGGCAAACGTGGGCCATGCTGCTTTGTTGTTTTTCACTTTTTAATAATCG
CCATTCCGACTGGCATGAGATAACAACTCATTATGGTTTTCATGTACATTTCATTACCCAGGTATTGAGC
CTGGCATCCATTAGCTATTCTTCCTGATGCTCTCCTTCCCCCTGCGCCCCCTTACAACAGGCCCCAGAGT
GTGCTCTTCCCCACAATGTGTCCATGTGTTCTCATCGTTCAGCTCCCAATTATAAGTGAGAACATGCAGT
GTTTGGTTTTCTCTTCCTGTGTTAGTTTCCTGAGGATAACAGCTTCCAGCTTCATCCACGTTCCTGCAAA
GGACATAATCTC (SEQ ID NO: 69)

STS sY1319
Forward primer: ACCTGTCTGGGAAACACCTC (SEQ ID NO: 127)
Reverse primer: GAGCCCTACAACCAGCTTCA (SEQ ID NO: 128)
Sequence:

Figure 6B

ACCTGTCTGGGAAACACCTCATCTCTACAAAATACAAAAAAGTTAACTGGGCATGGTGGAGCATGCCTGT
AGTCTCAGCTACTCAGGAGGCTGAGATGAGAGGATCACTTGAGCCTGAGGAGGTCCAGGCCACAGTGATC
TGAGATCACACCATTGCCCTCCAGCCTGGGTGACAGAGTGAGACCCTGTTCCAAAAAAAAAAAAAAACCC
AAAAAACCTCAATGGCTTTTTGCTTTTGAAGGTGGTATGAAGAGAACGTCCACTTTAAGGCTTTAAAAGA
CAGTGAAGCTGGTTGTAGGGCTC (SEQ ID NO: 70)

STS sY1250
Forward primer: TTTTTCTAACCTTGCCTGCG (SEQ ID NO: 129)
Reverse primer: TGCAGAGAAGCAGCCTACAA (SEQ ID NO: 130)
Sequence:
TTTTTCTAACCTTGCCTGCGGTTTGCACCATTTATTACATTTTTCCAACAACCAAAGGTTGGCTTTGTAT
GTTTTACTAATTTTCTCTACATCATTATCCCCTCACTTTAGTTTTTCAGAATTGATTCTGTTGTTTCTGT
TCTAATTCTTTCTTTAAATATCTAGTACATTAATTTTCAAGTTGTAGAAACATTTGTCTATGAACTCCTA
TTGCAATATCACTTTTCCTGCTACCCACAAATTTAATCTGTAATATTTGCAGTACCATTAATTTCTATTA
TGAATTTATATTATGATAATCCATGAGTTGCTGAGAAATAGCTGTTATAATTTTGTTGTTCAATTCCCAT
TTAATTTTATTTTAACTTGTGCTAACTCAGTTGAAAATTCTTTACTAATTTTTTAAATCTCATATCAAGA
CTTTTATTCACATCAATTGTTCTATAAATGCTCCCTCCTTGAAGAACACTCTCTTGTAGGCTGCTTCTCT
GCA (SEQ ID NO: 71)

STS sY78
Forward primer: TCCTTTTCCACAATAGACGTCA (SEQ ID NO: 131)
Reverse primer: GGAAGTATCTTCCCTTAAAAGCTATG (SEQ ID NO: 132)
Sequence:
ATCACAAAGAACTATGTCGGAATTCTTCTGTGTAGTTTTTATGTGAAGATATTTCCTTTTCCACAATAGA
CGTCAAAGTGATCCAGATATCCACTTGCAGATTCCACAAAAAGAGTGTTTCAAAAGTGCACAACCAAAAG
AAAGGTTCAACTAGGTGAGATGAATGCACACATCAGAAGGAAGTTTCTCAGAATGCTTCTGCATAGCTTT
TAAGGGAAGATACTTCCTTTTCCAACATAGGCCTCAAAGCA (SEQ ID NO: 72)

STS sY1251
Forward primer: GACTGGAGTGGAACGGTCTC (SEQ ID NO: 133)
Reverse primer: TCACTTCCCTCCGATTTTCT (SEQ ID NO: 134)
Sequence:
GACTGGAGTGGAACGGTCTCGAATGGAATGGAATGGATTGGAATGGAAAGGAATAGAATGGAATGGAATC
ATATGGAATGGAATGGAACAGAATGAGTCAAAACGGAATAGAATCAAGTGGAATGCAATCGAATGGAATG
GAATACAATGGACTCGAATGGAATGGATTCTAATGGAATAGAATATAATGGAATGGCATGGAATGGAATG
AAATAGCCAGCTCCCTGTGCAGGTGAAAATCCATGTATAACTTTTGACTCCCCAAAAGCTTAGTTACTTA
TCACCTACTGTTGACTAGAAGCCTGACTCGTAACATAGTCAAGTAATACACATTTTATATGTTATGTGTA
TTATATACTGTACTCTAACAAAAAGTAAGCTGAAGAAAGGAATATGTTATTAAGAAAATCGGAGGGAAGT
GA (SEQ ID NO: 73)

STS sY1317
Forward primer: GAGATTACAGGCATGCACCA (SEQ ID NO: 135)
Reverse primer: CCACACTTAGCCCACAGTCA (SEQ ID NO: 136)
Sequence:
GAGATTACAGGCATGCACCACCATGCCCAGACTCTTACTGGTCTTTTTAATATGTAAGACAGTGGTACCT
TTTTTCCTTTTAGGTTATGAAATGGTCTCTGCAAGATGTTTTGTCCTTGAATTGGAAATTTTTAAGGCTG
ATATATGCTGGTACTTCATCTTCTATATGTGGACTATAATTTCTTCCCTTAGGATAACTACATAAAGAGA
CAAAAAAAAGAAAAAAGAGCAAAGATCTGTGCTGTGTCAAGTATGACAGCCATCACTCATGGCTCTCCAG
TAGGAGGGAACGACAGCCAGGGCCAGGTTCTTGATGGCCAGTCTCAGCATCTCTTCCAACAGAACCAGGT
AGGAGTAAGACTGTGTTGTTTTGAGTACTGTGAAATACAAAATTGTGAAACATGTCCTGAATGATTTGTA
AAGTAATCATAAAATATGTGGTTATTTTAAGTTACACGTGAAAAAAGTGACTGTGGGCTAAGTGTGG
(SEQ ID NO: 74)

STS sY1316
Forward primer: AAGGCAGGTCTGATGCATGT (SEQ ID NO: 137)

Figure 6C

Reverse primer: AAAGAAAGCTGCCTCATAGCA (SEQ ID NO: 138)
Sequence:
AAGGCAGGTCTGATGCATGTTTACTTTTACTTCCATTTCCACTTCTTTCACTAAGAGAAATATTTTGTTT
TCCTGATTATTCACTTTAATGTTCTGCCAGCACTTTTAATTATTTATTTCTTTTCTGCAGGCTTCAAGAT
ATATGCCTGATATTTGTGTAATTAGGGCTATACAGAAAATTATCTGGGCATCAGCATGTGGGGCATTAGG
ACTAGTTTTTAGCCCAAATGAAGAAATAACTAAAATTTATCAGATGGTAAGAATTATTACAGAAATAGAT
TTTTAAGAAAATGTTGCTTCATTGTACATGTGATTAAATTTTCATCATTTCTGTCACCTTATAGACCAAG
TCGCTTGTATCTAATGGTTTAAAATTTATTGCTACCTATAAATAAAATGAGAATATATTGTTTTATTTTG
GAAATAAAATACTCTAGAAGCCTGCTATGAGGCAGCTTTCTTT (SEQ ID NO: 75)

STS sY1234
Forward primer: TTACCCCTTTCACCCACTGA (SEQ ID NO: 139)
Reverse primer: CCATAAACTACACAAGGACGAACT (SEQ ID NO: 140)
Sequence:
TTACCCCTTTCACCCACTGAAAATAAGTTTGTAGATGTAATCTGCAAATTATAAAGAGAAAGTGATGAAT
TTTTAAAAACAATTGAAGTTTTGGGTTATGAATTTAAAATTATATTTATGTTTTAGGAAAATGGAAGGTA
TGGGCGCCGCAAACAATATCCAATATCCTTGGTTTTAGCCCCAACAAGAGAATTGGCTGTACAGATCTAT
GAGGAAGCCAGAAAAGTAAAATATTCATTTTAGTGATTATTGCTTTTCTTATTTGTCAAATGATGTTGTT
ATAGTCACTGACATGTTCTTTGCTTAAAGTTTTCCTACCGATCTAGAGTTCGTCCTTGTGTAGTTTATGG
(SEQ ID NO: 76)

STS sY1231
Forward primer: TTGCACCCGTAGTCAAATGT (SEQ ID NO: 141)
Reverse primer: ACCCACAACTCAAATCGTCT (SEQ ID NO: 142)
Sequence:
TTGCACCCGTAGTCAAATGTATGTTCCATAGTTTTAGCATTTGCGTATGTCTGACATTTTATATTATCCC
TACTTTTTGTTACTTTATTACATTAGACTGTATTGTAACTGATCTTTTCCCATGATCCATTGCAGTTCAA
TTTCATATTGCCCATTTGTATGAAACCCAGGTAAGTGTTTTAACTTAAGAACAAGAATGAAACAGTCACC
TATGCTTTAGATGAAATGAAATGTACTTGAAAATATCAGGCTTTAAATGAAATAAATATATTAGACGATT
TGAGTTGTGGGT (SEQ ID NO: 77)

STS sY1230
Forward primer: CTCTTCCAAGCCAGCCTTTA (SEQ ID NO: 143)
Reverse primer: AACCTTTGCAAGCCACATTC (SEQ ID NO: 144)
Sequence:
CTCTTCCAAGCCAGCCTTTAATTTTAAACGCTGTAATTAACAGTTCACAGGGGTCAAATTCCTTTATTCC
GGAACATTCCACTTTGAGAGGGATCTGTCCTCTTTGGTCCCCTGCGTTTTCAAATATTTGAGGAAAGGTG
TCGCCTCTTTTTCTGTGGAAAGAGGAAGCTCATGAGCGCGAAACAGCAGGGGACGGAGGGCGAGAAGGGC
TTTCTCAGGTTGCGGGTCGGAGGGCAGAAGCACAGTTCCCAGTACAGAGACCCGGACAGGTGGCTGTTTC
TCACGCTCACTTTGGATTGCTCCCTACGGCTTCCTCCGCAGCCATGTCTGACAAACCTGGTATGGCTGAG
ATCGAGAAATTCGATAAGTCGAAACTGAAGAAGACAGAAACGCAAGAGAAGAATCCATTGTCTTCCAAAG
AAAGTAAGCTCCGATCCTCCCCCATCTTTAGAAAGGCTGGAATGCGAGCGGGCGGTGGGAGGGCGGGAGA
CTGGGAGCTGCCACGGGAAGAATTCGGGAGGCAGGGGAGGGCGCTCAAGGAGCAGATAGTTGGTGAATGT
GGCTTGCAAAGGTT (SEQ ID NO: 78)

STS sY90
Forward primer: CAGTGCCCCATAACACTTTC (SEQ ID NO: 145)
Reverse primer: ATGGTAATACAGCAGCTCGC (SEQ ID NO: 146)
Sequence:
TGTACCGNAGTACAAACTTATCCATAGATTTAATACAAGCAGTGCCCCATAACACTTTCATAAGTCTCT
CTACCGTAGTCCTAACATTTTATACCATTCACTGAAACATACCAGCCAGGTTAGANCATAAAATGTGATG
TAAAACTTGTAAAACACCCAGCAGAGTGGNTGCTTCTTAGTAATCTTCCAGGCAGAGCGAGCTGCTGTAT
TACCATTGNGTATATTATTCCAACANGTTTNGTGTCCTGATTGCATCTNGCAGGGCAGGTGCTTCTGTCC
CCCACTGGCATGCATGNGGGGTTGATATTNAGGAAGATGGTGTAATCCACCCTACCTACCCATATACAAN
GCAGCAGAGCCTGGGGTGCAGAGCAGNTNTGCCCAGCCCCAAAGCCCACTTCCNTNTTTCCATAGCTCAC

Figure 6D

AGACTCATAGCTCCTNTTNACTNTGCTAACCTCCTACATGTATTANATTTTTTGGGGCCTGAATTAGCTC
CATGCTTGAATTGNCCTGGACAAAG (SEQ ID NO: 79)

STS sY1220
Forward primer: GAAGGGAGAAGCAGTTCGTG (SEQ ID NO: 147)
Reverse primer: CTCAGTGGTTCCTCCAGCTC (SEQ ID NO: 148)
Sequence:
GAAGGGAGAAGCAGTTCGTGGAGGGAGACGCGGGAAGAAAGGGGCTGCGACAAAGATGGCGGCCGTGACG
GCACCTGAGGCGGAGAGCGGGCCAGCGGCACCCGGCCCCAGCGACCAGCCCAGCCAGGAGCTCCCTCAGC
ACGAGCTGCCGCCGGAGGAGCCAGTGAGCGAGGGGACCCAGCACGACCCCCTGAGTCAGGAGAGCGAGCT
GGAGGAACCACTGAG (SEQ ID NO: 80)

STS sY1239
Forward primer: CCTAGCTCTCTTTTTCTTGCAG (SEQ ID NO: 149)
Reverse primer: CAAATATCGCCAGTGAGGCT (SEQ ID NO: 150)
Sequence:
CCTAGCTCTCTTTTTCTTGCAGAGACATCTTTCTCCCATCTCTGTCTGTTAGTACAGAGCTCTTATTCAG
CCACTAGCTCGGCCTTTCCTGCTTCAATTGTAATGCTTGTTCTGCCCGGGGACACACTATTGACAGCAGA
AACAATGAATTTCCTCCAAACCCGGCAATGTTGGTGGCTCTTGCATTCCTCTGGATGAGCGAATCTAGTT
GGGGGGTTCCCGAAGGGGAAGGCGCCTGGGCTTTCAATACATCCTCCTGAATCATACTGCGTTTCAGGTT
CCTTAGAAAAATTTGGATGTGTAAAAAGAACTCTTAACGGCGATGCAGGTCTTCCACAGCTAAGGTAGGT
GCAGTTTTAAGACGTGTCTTTCGCATATTATTATCCTTATTTTAAAAAGCCGTTTAAACAATTTGACTTG
CAGTGGCTCTCCAGCAAAGGAGGGAAAGCCTCACTGGCGATATTTG (SEQ ID NO: 81)

STS sY210
Forward primer: ATCACTTGGCAGCTTTTCC (SEQ ID NO: 151)
Reverse primer: GCACTGCAACTTTTATGCCT (SEQ ID NO: 152)
Sequence:
TCTCCATGAGGAGANTCAGGGATCCAGGTTGCTAATANCTTGTGCTTCTGTCATCTTAGTAGGTGGCCTT
CCCAATGGCATCCACAGGAGAAAAGAGTTGAAGGATCACTTGGCAGCTTTTCCTTACTTCACTGACCTAG
GGGTCACTTTGTAGAACAGGNCCCATGTCTCCACACTGACTTGACGTGGGGCTAAGAGGCAGTCTCCCCA
TATGTTCAGGAAGAAGAAAGTGAAACAGCCTTACTGAACACATAGAAGTGATTTTCCTACTGCAGGCAGT
GATTTTCAAATTTGTTTTAAAGCTGAGGNNTATTTCAGATGAAATTTTATGAGAAGCTAAGTATGTCAGA
GGCATAAAAGTTGCAGTGCTTGGGTGAACTGGAACAGAGGNC (SEQ ID NO: 82)

STS sY1235
Forward primer: GACACCATGGCTGGAGTTTT (SEQ ID NO: 153)
Reverse primer: GGATTGTATGTCCCACCTCG (SEQ ID NO: 154)
Sequence:
GACACCATGGCTGGAGTTTTCGAAAAGTGGAACTCATCTTCCTAGCAACACAAAAAATAATTCCAGCATG
GTGGGTAAGTATGGATGCTTATCTTAATCATGCTAGTATATGCTGCCATCAATTCTCCTGCTTGTCAGCA
GTGAAACTGCAGCTGTCAAATGAGGAATTGATAAGAGACACGAGGTGGGACATACAATCC (SEQ ID NO: 83)

STS sY1260
Forward primer: TTTCACTACACCAGTGGTGACC (SEQ ID NO: 155)
Reverse primer: CTGGCAGCAAATAACTTGCA (SEQ ID NO: 156)
Sequence:
TTTCACTACACCAGTGGTGACCAAATAGAAGAGGTTCATCCATACACAGAACCTGGTGAAGAGCTGGAGG
CAGAAAGAAGTGTCTATGTGGAGACGCAACTGAAACAAAGGTGGCACAGCAACTGTTCCAATCCCGTGTC
TTTCCTCATGGCTTCCCAGGAGTTTGAGGTTGAAGCTATTGTTGACAAAAGACAGGATAAAAATGGGAAT
ACACAGTATTTGGTTCGGTGGAAAGGTTATGACAAACAGGATGACACTTGGGAACCAGAGCAGCACCTCA
TGAACTGTGAAAAATGTGTACATGATTTTAATAGACGACAGACTGAAAAACAGAAAAAACTGACATGGAC
TACAACCAGTAGAATTTTTTCAAACAATGCCAGAAGAAGAACTTCCAGATCTACAAAAGCAAACTATTCT
AAGAACTCTCCTAAAACTCCAGTGACTGATAAACACCACAGGTCCAAAAACTGCAAGTTATTTGCTGCCA
G (SEQ ID NO: 84)

Figure 6E

STS sY1237
Forward primer: TAGAGCAGGGGCTAACATGG (SEQ ID NO: 157)
Reverse primer: ATGGGGACAGATGAATTTGC (SEQ ID NO: 158)
Sequence:
TAGAGCAGGGGCTAACATGGAGAATCATAATTCTGCCTTAGCTGCTGAAGCTAGTGAAGAAAGTTTATTT
TCAGCCTCTAAAAATTTAAATATGCCTCTAACAAGGGAATCTTCTGTCAGACAGATAATTGCAAATTCAT
CTGTCCCCAT (SEQ ID NO: 85)

STS sY121
Forward primer: AGTTCACAGAATGGAGCCTG (SEQ ID NO: 159)
Reverse primer: CCTGTGACTCCAGTTTGGTC (SEQ ID NO: 160)
Sequence:
AGTTCACAGAATGGAGCCTGGATTTTATAGGTCAGAAATTACCCTCAGAGTACACATTTAAGGGTCACA
GAGTGGTAATCATGGATAGAGTAACAAGTAAGAGTTACAGAGTAGGGATCTGAGATGGAAGACCAATCTG
AGGTTCACAGGTCAGAGTTCAGAAGAAAGAAGACCAAACTGGAGTCACAGG (SEQ ID NO: 86)

STS sY1322
Forward primer: TGGAAACATTCTCAACAGGGA (SEQ ID NO: 161)
Reverse primer: GGCATTTCTCGCATGAGTTT (SEQ ID NO: 162)
Sequence:
TGGAAACATTCTCAACAGGGAAACCCTACTAGACTTTGTAAAGCAAATAATGGAAAAGATACAGAACTTT
TTGAAGAATCATGGGAAATTTTTATAATTAAATAAATGCTAAAATTCTGTTTTGTGAAACATTTATGGGA
ATTATCACTGACAGTTTTTGTACACTTTCAAATAGTGTTAAAGCAGCAACTCCATGTTGTAAATGCACAA
AACAAATATTTAGTTAATAATCAACTCCAAGAATAAAGCTGTAACAATAATAGTTACTATTCTCTCATGT
GGTCCATATTTACCTCCACTTAGCTGGCATCTTCAAGTGCCACATACTTAGCAGCAGCCTGGCACCTTCT
GATATTTTGAGAAGCAGGAATCCCTGAGCATAAATGTAAATAGCTTAGAACTGTCCAAAAGCAAAGACAG
CAGAAAATAAAATTGTTGCTTGCTATGTTCAGGAAAGGAATGCTTCCATTGGATATGGAAGCCAGTCTCA
ATTGTTACATCAGCCTGAGGAAACTCATGCGAGAAATGCC (SEQ ID NO: 87)

STS sY1573
Forward primer: AGGAATCATTTGAGGCCCTT (SEQ ID NO: 163)
Reverse primer: TGGAGTTCGGGTTCAAATTC (SEQ ID NO: 164)
Sequence:
AGGAATCATTTGAGGCCCTTGTGTACAAAAATGGTTACCAGAAGACTTTAAAAGAGTGGGAACAAATGAT
TGTGGTTTTCACTATCTTCATCCTTTACTGTGCCATAGTTACCAGGTCCTTACACTTTCTTCTAGGATTG
GCAGCCTCCTTTTGCAGTAGAAGTTGACAATTTCAGATTTACTCCTCGCGTCCAAAGGCTAAATGAACTG
GAGGTAAGATTGGGAGGCACACTTTTTTTAAAGGAATCTGATCTTTAATCTTGCCGTTGTAGTTTCATAA
TAATGTAGAACTTAAGTTTTGAAATCTAATGTATTGAATTTGAACCCGAACTCCA (SEQ ID NO: 88)

STS sY1233
Forward primer: TCTCCGGTATCCTGATGGAG (SEQ ID NO: 165)
Reverse primer: AAATAGGGCATTCCCAGCTC (SEQ ID NO: 166)
Sequence:
TCTCCGGTATCCTGATGGAGTCTACTAGGTGTCAGTCATTTGGCCGTGCCTCAGCCGAAGAGAGGCGGGG
AAAAGCATCGTAATCAGCTGCGTCGCCTTTTGGTGACGCCAGAGAGTGCGCGTCAGCAGTTTATTAGAGA
GCTCTGTAGCCAGCCTCTTCTGCGCACCCACCTGCTGCATCTTAGTTCAGTCGGCTCTTAGAGTAGTAAC
CGCCAGAAAGGAGTCGGAAGAGGTCTCACGAGGCTGTCATCACCGCCATGCCCAAGAATAAAGGTACTGC
TGTAAGCCTCTGGGACTATACCTCGGCTTGCTCTGCCAGTAACCCCGACGCCTGTTCCAGGCCGCAGTGA
CTGTTCTAACGGCGGTACTGGCCACTGCGACCCCAGCACTGTGTTCGGGAAAGGAGCTGGGAATGCCCTA
TTT (SEQ ID NO: 89)

STS sY627
Forward primer: GCACCTGCCACGCATATAGT (SEQ ID NO: 167)
Reverse primer: GCAAACATGCTCACGATCAC (SEQ ID NO: 168)

Figure 6F

Sequence:
GAGGAAAGCAGATATTTCCAAATAGTACTTAACTATTCATGCTTTAATGATAGCAGTAAAAATGTTTAAA
TGTAGTCCCACATATTATTTTACCAACCCTGCAGGGACCTCTCATGGTGCACCACCTGCAAGAGGGCCTC
GGATGTCTTATGGTGGAAGCACCTGCCACGCATATAGTAATACACGAGATAGATATGGCAGAAGTTGGGA
GAGTTACTCGAGCTGTGGTGATTTTCATTATTGTGATCGTGAGCATGTTTGCAGAAAAGACCAAAGGAAT
CCGCCTTCTCTGGGTAGGGTGCTCCCTGATCCTCGTGAAGCATATGGTAGCTCAAGTTATGTGGCATCTA
TAGTAGATGGTGGGGAGAGTCGATCTGAAAAAGGAGACTCGAGCAGATATTAAAGCAAGCATTGAAAGTA
ATAGTTATTGCATACCAATCCTTGTTTGCACATCAAAAATTGAAATGTTATTTCTGCATTGTTACCTGCA
TATTACTGAAAGAAACATGTTGGTTTTGTGGAGAGAGGTAGATACTAACTTCCTCCATGAATTTTTTGAG
GTATTCAAAGGAAAAGGAATTGTTTTCAAAGTAATTTCATACTTGTTGATGCTATTTGAAAAGTGTTTAG
ATGTAATATCTACCTTAAAATTTTCACAATAAAATTTGACAT (SEQ ID NO: 90)

STS sY142
Forward primer: AGCTTCTATTCGAGGGCTTC (SEQ ID NO: 169)
Reverse primer: CTCTCTGCAATCCCTGACAT (SEQ ID NO: 170)
Sequence:
AAGCTTCTATTCGAGGGCTTCATGACCCCTGCAGGATGAGAAGCAGGTAGTCATATTTGGCTTCTGCTT
GGTAATCTAGCCTCTATTTCATTTCATCTGCATAGGCTTTTCATTGTGGAGGGGTTCTTTCATTGGGCTG
TTGCTAGATAAAGCTGTCTCTCACCACAGATTATTTAGATGTCAGGGATTGCAGAGAGCAAA (SEQ ID NO:
91)

STS sY1258
Forward primer: AACCCCATCTCTAGCAAAAATATG (SEQ ID NO: 171)
Reverse primer: TAGGTGACAGGGCAGGATTC (SEQ ID NO: 172)
Sequence:
AACCCCATCTCTAGCAAAAATATGAAAATTTGCTGGGCATGGTGGTGCACACCTGTAGTATGTTACAGTT
AATTGGGGGGCTCAGGCAGGAGAATTGTTTGAACCTGGGAGCCTGAGGCTGCAGTGAGCCAATATTGCAC
TATGTACTCTAGCCTGGGTGACAGAGCGAGACTCCAAATCAAAAATAATTATATAAATCTACAAATATGT
AAATAATAAATAAGGTATCCTTCATTTCAAGCATTTATTCTTTCTTTTTGCTTTTTTAGACACAGGGTCT
CCCTCTGTTGTCCAGCCTGGACTGCAGTGGCACCGTCAAGGCTCACTGCAGCCTCGAACTCCTGGGTTCA
AATGCACAAGCCTTCCATTTCAGCCTCCCAAGTAGTTGGGATTACAGACACACATCACTGTGCCCAACTT
TTGTGTTTGTGTGTGTGTGGTAGGGACAATGCTTTGGATATATTGTTCAGGCTGGTCTCAATCTCCCAGA
CCGAAATAATCCTCCTTCCCTGGCTTCCCAAAGTGTTGTGATTATAGCCGTGAGCCACTGAGTCTGGCAT
ATCTTTTCTCATTATGAGCGACATTCCACCTCACTGAGTCTGGCGTATCTTTTCTTGGTATCAGCGACAT
TCCACCTTCGCTCTATTAATTATTTTGAGATGTACAATAAATCATTATTAAGTGTAGTCATCCTGTGCCA
CTGAACACTAGATATTATTCCTTCTAAGCAAGTATAATTTAACCCACCCCCATCCCCTCTTTGATCCCTC
GCTTACCAGTTCACATTACTTGTATCAAAATATCACATGTATGCCAAAAGTATCTACAACTGTTAGGTAC
AAATTTTCATTCCCTTCCTCCTTCCCTCCCTTCCTTTCTTCCTTCCTGTCTTTCTTTCTTTTTGTCTCTG
TATCTTTTTCTCTCACTGATTTTTTTTTTTTTAAGAAAGAATCCTGCCCTGTCACCTA (SEQ ID NO: 92)

STS sY1161
Forward primer: CGACACTTTTGGGAAGTTTCA (SEQ ID NO: 173)
Reverse primer: TTGTGTCCAGTGGTGGCTTA (SEQ ID NO: 174)
Sequence:
ATCTATCGACACTTTTGGGAAGTTTCAGCCACTATTCATTTAAATATTCTTTTTTTCCCCATCTCACCTA
TTCCAGTGGGACTCCCATTATGAATATGTTGATATTCTTGATGGTGTCCCATGGAAACCTTAGTTTTGAT
CATTATTCTTGTTTCTCTTCCTTACACTGAACAATATCAAACAATCCATCTTCAAGTTGCCTCATTAGGC
ATTCCTGAGGCAGGCTAAGGCACCCTTCAGAGCTGTCAGTCTGCCTAAGCAGAGGAAAATGGTACAGGCA
GAGCCTTCCTGGTATAGGGAAAAATGCTGCCTGTAATAAGCCACCACTGGACACAAAAATATAGATGATA
GGGCCCTTTTGGGCAGTCTCTAAGGTTGGGTTCCACAGAAGAAGTCATTTT (SEQ ID NO: 93)

STS sY1197
Forward primer: TCATTTGTGTCCTTCTCTTGGA (SEQ ID NO: 175)
Reverse primer: CTAAGCCAGGAACTTGCCAC (SEQ ID NO: 176)
Sequence:

Figure 6G

TCATTTGTGTCCTTCTCTTGGATTTACTAATTTACTAGTTAAGCTGTGTTATGTTCACTGGACATTTAAG
ATTTTATAAATATCTATATGGCAATAGAGTCATTTCTGAGGTAGTAAGAATGTATTCTCCTTTCAACAGA
ACCTAATTGGAACCTGGTTTTATTACAAAGCCTTGTCTGAAATATCAAATACATTTAAGAATGATTTGCA
GAAAATCAGAGATAACCAGGCAACTTTAAGAACTAAAGTTGACTGTGGAGAAAATACTTAGACAGCCCTC
TTGGAACATCAGCCTGGTAATTGGTTAGAGCTCCTAGCTTAAGAGGTGAGAAAGACAGGTCACTTCTGGG
CAAGCTCTGGAACCTCACGATACTTGGGGACTTTGAGAGGAAAGGTATTCAACCAAGTGTATAGGTTCTG
AAAGGGAAGCCTGGTGGCAAGTTCCTGGCTTAG (SEQ ID NO: 94)

STS sY1191
Forward primer: CCAGACGTTCTACCCTTTCG (SEQ ID NO: 177)
Reverse primer: GAGCCGAGATCCAGTTACCA (SEQ ID NO: 178)
Sequence:
CTATCAGACACTATTTTGGCAATTTTATGTACCTAAACATGTTAAATAATCATGCTTACCATTTTTTCCA
GACGTTCTACCCTTTCGAGATTAGTTAATATGTTTACACACAGAGTTTTCTTTATAGGATTATAATTTAC
AATGTTTTCACAATTTTCTTAAACAGTCGACTTTATTTTATTTAACTTTAAGACAACTTTTTTATTCTTA
AGCAAAATACATAGTTATGCCTTATAATTTTTAACTAAAACCACTTTTTACCATTTTTATACACTTTTAT
GCAAATCCATGTTTAGCAGTTTTAATTACCTGTTATAACGGTAATTTTTAGCAATTTTTAACTTTAATGT
AAAGCCTATTACGTGTTTTTTATTTTGTTTTGTTTTGTTTTCTTTTTGAGACAGAGTCTTGCTCTCTCAT
CAGGCTAGAGTGTGGTAACTGGATCTCGGCTCACTGCAACCTCCACTTCTTGGATACAAGCGATTCTGCT
GCCTCAGCCTCCTGAGTAGCTTGGATTACAGACGCCTGCCACCACACCCAGCTAATTATTGTATTTTTAG
TAGGGAGGAGGTTTCACCATGTTTTCCAGGATTGTCTTGAT (SEQ ID NO: 95)

STS sY1035
Forward primer: TCAGTCCACCTATGTGCTGG (SEQ ID NO: 179)
Reverse primer: ATTCCTTTCCTTGGGTGGAT (SEQ ID NO: 180)
Sequence:
CTCACCTCGACACTGAGCCAGTGATACAGCATAATCTCATTTGTATGCTGGGCCTAGTCAGAAGAGTCAC
TTCACCCGGGTACAGTTTCACATAATATGTCAGCAAGCCCACTATGGACAGGGAAGAAAAAAGAGAGGAC
AGTCAGTCCACCTATGTGCTGGACTCCGCAATATGTAACAACCCTCTCTCTTGGTAGAGTCTAGAATATG
AAGGAGAGTCACATCATGTAGGTTTTTCAATCAGCGGTATGTCACAATTTGTTTGCTGAGCAAGGCTCAG
GCAGGAGGTGAGAATCACATTACCTAGATGTTAAGCCAAACAATATTTCACAATGTCTTCTGGGTGCAGG
ACACTGTCAGAAGAGACAAATCCTCTAGCTTATAGACCCATAGATATGTGATAATATCCCCTTTTGGCAG
GGTCCAGACAGAAGAGACACATTATGATTCTAACACAGTGATATGTTACAATCCACCCAAGGAAAGGAAT
TTAAGCCAAATAGTCTCAACACCTAAGCACTATGCCTATTAATAGGCCAAATCCCCTTGTCTTTGAGAGT
GACATTATAAACTCTGAGCTGGGTGTGTATATGAGAGTAAC (SEQ ID NO: 96)

STS sY1318
Forward primer: TGATATCAGGTGATGCGTCC (SEQ ID NO: 181)
Reverse primer: TGGCGTTAAGTAAACCTGGG (SEQ ID NO: 182)
Sequence:
TGATATCAGGTGATGCGTCCTCCTCGGCCTCCCAAAGTGCTGGGATTAGAGGTGTGAGCCACTGCTCCCA
GCCTCTTTTAGCATTTTTGCATTTCTTTGGAAATAAACTGATATGTTCATTAAACCATCAAAAGAAAAAC
CAAAACACACCCTTATTAAGAGTGAGTGAAAGAAAGAGTTGTCTTTACATTACTGAAAACTTCTGTGTTT
CAGAAATCTGTGGACCGAAGCATACAAATGGTGGTATCTTGTCTGTTTAATCCAGAGAAGAGACTGATAA
ATTCCGTTGTTACTCAAGATGACTGCTTCAAGGTATGAAAGGAATGGCATGCATAATTAAAAAGCACACT
TGTTCCCTCTCAAGTTAGCTGTTTTCCTTGTGGCACATGTATTTTGGGCTTTCTTAGAGGAATTTTTTTT
CTTTTTTTTTTGTTTTGAGACGGAGTCTCCTCTGTCGCCCAGGCTGGAGTGCAGTGAGTGGCCCCATCTA
GGCTCACTGCAAGCTCCACCTCCCAGGTTTACTTAACGCCA (SEQ ID NO: 97)

STS sY254
Forward primer: GGGTGTTACCAGAAGGCAAA (SEQ ID NO: 183)
Reverse primer: GAACCGTATCTACCAAAGCAGC (SEQ ID NO: 184)
Sequence:
CCCAGTCTTCATCAGCTGCAGCTAGCCAAGGCTGGGTGTTACCAGAAGGCAAAATCGTGCTAAACACTG
TTTTTGTTGGTGGAATTGATGCTAGGATGGATGAACTGAGATTGGAAGCTGGTTTGGTAGATACGGTTCA

Figure 6H

GTGAATTG (SEQ ID NO: 98)

STS sY1291
Forward primer: TAAAAGGCAGAACTGCCAGG (SEQ ID NO: 185)
Reverse primer: GGGAGAAAAGTTCTGCAACG (SEQ ID NO: 186)
Sequence:
TAAAAGGCAGAACTGCCAGGTCTGTGTCTTATTTTCTTTGTCATTCTAATTTATCTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGG
ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTG
GGACTACAGGCGCCCGCCGCTACTCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTT
TTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGCACCTGGCCAAGTGTCTTCTTTTGAGAAGTGTCTGTTCATATACTTCACCCAC
TTTTTGATGGGGTTGTTTGTTTTTTTCTTGTAATTTTTGTTTGAGTTCATTGTAGATTCTGGATATTAGC
CCTTTGTCAGATGAGTACGTTGCAGAACTTTTCTCCC (SEQ ID NO: 99)

STS sY1125
Forward primer: GTGGGGGTTTCACATTATGG (SEQ ID NO: 187)
Reverse primer: GGTCACAGACTCACATTTAAGCA (SEQ ID NO: 188)
Sequence:
TGGGTTAGTGGATTTTGGGAGGCAGATGTGGAGATATAAAATGGGGCTAGATTATAGAGAATCTTCAAAG
TTAGCAAAGTTAAGATTTTGTGTAATAGGCAGTAGAGAGCTTGTGTAAGCTTTTTTATTCGAGATGAGCC
ATCTTGCAGACCACTGCTTAAGAAGACTGACTGTGGCAGTTTGCAGTGTGGAAGGGGGAAAGATGGTGAA
AGCTCCAAGTAGGAGGCTAGGGCTGCCATTCGTGGGTAAGATGAAGAGGACCAAGACAGTAGAGATGATA
TATAGATAATTGTAACCAAATCAGGAGTAATTGTTGGAACAGCATAACACATTTACATATTTGCTGATGT
AATTACTCAAGGGTCATATCATAAAAAGGGGTGGGGGTTTCACATTATGGAAACCTTGGAATTCTCTGTC
TTACGGTGGAAGACAGAACCCAGTGTAGTGTAGACAAAAGTCTAATTTTAATTCCCAGAGAAAGACTGAT
ATCTTATGGGACAAATTAGTATATTCCCATTCCTAATAATGGTGTACCTAGCTGGTGGGTAATTGCAGGC
TTTCAACCTCCAGTTCATCTTCATGAGATCAATGTTGATTCAGAACAATAAGTGTCAGGTCTATGACACC
TTTAAAGTTATGCTTAAATGTGAGTCTGTGACCACTAATGAATGACTACAGTTGTTTCATGACTTGCTAA
ACATACCTGGTTTTTCACAAGCAATAGATTTTTGAAGGAGAGGTATTCACAGTGGGTGCTAGGAAGATAC
ACACATTAATTCTGTAGAATTTAGCTAAAAT (SEQ ID NO: 100)

STS sY1054
Forward primer: ACCTAAGGGAACCCAGGAGA (SEQ ID NO: 189)
Reverse primer: CGACACTTTTGGGAAGTTTCA (SEQ ID NO: 190)
Sequence:
ACCTAAGGGAACCCAGGAGAACAGTGATTCAAAATTGAAAATATCAATAAAAATGTATGAATTATTTTGA
AAAATGAAATCAATAATCTGTAACTAGAAGGACTGAATAGCATGTGTGAGCATGTAGAAAGCCTAATGAG
GCAACTTGAAGATGGATTGTTTGATATTGTTCAGTGTAAGGAACAAGAAGAGAAACAAGAATAATGATCA
AAACTAAGGTTTCCATGGGACACCATCAAGAATATCAACATATTCATAATGGGAGTCCCACTGGAATAGG
TGAGATGGGGAAAAAAAGAATATTTAAATGAATAGTGGTTGAAACTTCCCAAAAGTGTCG (SEQ ID NO: 101)

STS sY1190
Forward primer: TTGTGAAATGGTGGTGATGG (SEQ ID NO: 191)
Reverse primer: CTGATTTGGAAACTCGTCCC (SEQ ID NO: 192)
Sequence:
TTGTGAAATGGTGGTGATGGTTGCACAATGTGAGCATAGTTAATGCCACTGAACTATACACTCAATAATG
TTTGGAGTGGTAAATTTTTTATGTATGTTTTTCCACATACAACAAAAGCTTCCTCAGAAGTCCTCCTAAT
AGTTCCATGTGTGATGAAAGAAGACAATTCTCTGTTATCATGAGTAGAATCCTATTTATTTATTCATGCT
GGTATACACACTCCTAGCTCTTCTACACGAACAGCATGATCTCATGAAGCATAATGAGTCCCTTCTCACC
TGGCCCATTTGTGCTTTTTTCCATCATTCCATTCTGCTAATCAACTCACTATCTACCCGCTACAAACCAC
TGTAAATTACAGGTCTGTTTACTGTCTCTGTAGACATTTCTTCTCTGTTATGTAATAGAAATGAAATCAT
ACAGTATGTCATCGCTTCAGACCAGCTTTTATCACTTAGCTTTATGTATGCCTGATACATCCATGGCTTT
GCATGGCTTCATAAATCATTCCTTTCTTTTGATGAATAGTATTTCCTTTTATGAATTTACCTGGCCTGGT
TAATATTGAAGGGCATCCTGATTCCTTAAAGTATTTGGCCATTGTCAAGAGAGCAGTTACACATAAATGC

Figure 6I

CTGTGGTTATTGTTTAGGGACGAGTTTCCAAATCAG (SEQ ID NO: 102)

STS sY1263
Forward primer: TTAAGGAGCTTGCCTCATACAATC (SEQ ID NO: 193)
Reverse primer: TAGAGCTTGCAAGAAGAGTCTGTT (SEQ ID NO: 194)
Sequence:
TTAAGGAGCTTGCCTCATACAATCCAATTGTACTGGAAGAATGTAAGGCCCTCGTTCGCTGTAATATTAA
GTTGGAGTTGGAACAGGCCAATGAGAGAGAGTGTGAGGTGCTGAGGAAGATCTGGAGCTCAGCCCAAGGG
ATAGAATCCATGTTAAAGTATGTTGAAAATAAAATTGATGAGTTTTAATTGTCAGTCTGTCTGCTCAGGA
CACAAGAACTAAGGGGCAACAAATGCATCATGAGTTGCAAGATGCCCTAATCCATCTTCATAGCCCAAAA
CAATTTCACCCATAGCTAAGGCTTGGAAACAGAACTGGAAATGTCCAAGCTATGTATTTAAATTATCACA
TCATTTTTAAGCACTGTAGCTTTACAAGGAGTAACAAAACAGCCTCTTTGCCCAAATGTGATTATTTTAT
GCACACCTAAGCCCAAATATAAAAACAGACTCTTCTTGCAAGCTCTA (SEQ ID NO: 103)

STS sY1206
Forward primer: ATTGATCTCCTTGGTTCCCC (SEQ ID NO: 195)
Reverse primer: GACATGTGTGGCCAATTTGA (SEQ ID NO: 196)
Sequence:
CTGCGAAGAGAACTCTTCCTTACCCTTGGTCACGATAAGTATCTTTCTCTACAAACAAACTACTTCTGGG
CTTTCTGTGGCATTTTGGATATCTCTGAACAGCAGTTAAAGAGATTGGTGCTCTAACTTCACGAAAATAC
AGGAGGCAGAGATTGATCTCCTTGGTTCCCCCGCTTGCTGTCCTCTACGTTGGTTAGAAAAATTTGGTCA
AAGATGAAATCCACACTGGGAAGGCTCAGGTTGACTTTAGAAGATATGCTTGATTAAAAATGGTTTTTTT
TTTTTTTTGGTTCCATTACATTCTATGAGGAGGCAAGGAGGCAGGTCAACAGGTAGTGATCATTCAGCAA
GGTATATTAATGCCATAAACAAACAACACAGTACACAATGGTCTTGTGTTAACCTCACCTATACAAACTG
AGAGAGGCATTGAGCTTATCCTGGTCAAATTTTTTAATTTAGTGTGTTAAAAAAATCTTATAGCATAAAC
ATAAATTAAGAATTTTCCTGAATAGAAGTCACTGGTCAAATTGGCCACACATGTCTCTTCTATAAACAAA
ACTCCAGAATATATGGCAATGTCTAAAGAATTCTTGGTAAA (SEQ ID NO: 104)

STS sY1201
Forward primer: CCGACTTCCACAATGGCT (SEQ ID NO: 197)
Reverse primer: GGGAGAAAAGTTCTGCAACG (SEQ ID NO: 198)
Sequence:
CCGACTTCCACAATGGCTGAACTAGTTTACAGTCCCACCAACAGTGTAAAAGTGTTCTTATTTCTCCACA
TCCTCTCCAGCACCTGTTGTTTCCTGACTTTTTAATGATCGCCATTCTAACTGGTGTGAGATGGTATCTC
ATTGTGGTTTTGATTTGCATTTCTCTGATGGCCAGTGATGGTGAGCATTTTTTTCATGTGTTTTTTGGCTG
CATAAGTGTCTTCTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTG
CAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCC
CAAGTAGCTGGGACTACAGGCGCCCGCCACTACTCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGG
TTTCACCGTTTTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAG
TGCTGGGATTACAGGCGTGAGCCACCGCACCTGGCCAAGTGTCTTCTTTTGAGAAGTGTCTGTTCATATA
CTTCACCCACTTTTTGATGGGGTTGTTTGTTTTTTTCTTGTAATTTTTGTTTGAGTTCATTGTAGATTCT
GGATATTAGCCCTTTGTCAGATGAGTACGTTGCAGAACTTTTCTCCC (SEQ ID NO: 105)

STS sY1246
Forward primer: ATCGTTTTGAATGGCGTCAA (SEQ ID NO: 199)
Reverse primer: CTGCACCACTCCAATCCAA (SEQ ID NO: 200)
Sequence:
ATCGTTTTGAATGGCGTCAAATGAAATGGCATGGAAGGCAGTGAATTGGAGTGGAGTGGAATAGAGAGGA
ATGAATTGGAATGGAGTGTAGTGGAATAGAGTGGATTCCAGTGGAGTGGAGTGGATTGGATTGGAATGGA
ATGGAATAGATTGGATTGGAGTGGTGCAG (SEQ ID NO: 106)

STS sY160
Forward primer: TACGGGTCTCGAATGGAATA (SEQ ID NO: 201)
Reverse primer: TCATTGCATTCCTTTCCATT (SEQ ID NO: 202)
Sequence:

Figure 6J

TACGGGTCTCGAATGGAATAAAAATATATGGAATGGAATGCAATGNAACGGAATCGAATGTCATAGAAT
GTAATGCAATGCAAAAACATGGAATCCAAAATCATTGACTGGAAAGGCTGGGTGTCGAAAGGAATTGACT
CCAATGGAATGGAATCGAATGGAATGGAAGTGAATAGAATCGAACTAAATCGAATGGAATGGAATTGATA
GGAACGGAATGGAAAGGAATGCAATGA (SEQ ID NO: 107)

STS sY1166
Forward primer: AGTCGGAGTCGGAGTGTGAT (SEQ ID NO: 203)
Reverse primer: ATTCCATTGCTTTCCATTGC (SEQ ID NO: 204)
Sequence:
AGGAATGGAATGGGATGGAGTGGAATGGAGTGGAGTGGAGTGCAGTGGAGTGGAGAGGAGTGGAATAGAG
TGGAATGGAATAGGATGTAATGGAATGTAGAGGAGTGGAGTGGAGTCGGAGTCGGAGTGTGATGGAATGT
AATGGAAAGGAATGGAATGCAATTGAATGCAAAGAAATGGAAAGTTGACATGTAATGTGACCTGAGATTG
TGCCACTGCACTCCAGCCTCTGTGACAGAGTGAGATCCTTTGGAAAGAAAGGAACGGAATGGTATGGAAT
GGAGTGGAGTAGAGTGGAGTGGAATGGAATGGAATGGAATGCAATGGAAAGCAATGGAATGCAATGGAAT
AGAATGCAGTGAAAAGGAAAGTTGACATGTAATGTGAGCAGAGATTGTGCCACTGCACTCCAGCCTGGGT
GACACAGTGATATCCTGTCAAAAGAAAGGAATGGAATGCAA (SEQ ID NO: 108)

Figure 6K

STS sY1247
Forward primer: GAACTCTGCAAACCTCCTGG (SEQ ID NO: 274)
Reverse primer: TTTTGAGGCGGAGTCTCG (SEQ ID NO: 275)
Sequence:
GAACTCTGCAAACCTCCTGGATTTAGCAGGAGACAACATGAGGGTAATCACCCCGGCACCTGGACCCATT
AGATTAAGTCAATTTACTGAGGCTCCTGAGGATGATGCTCAGGACTCAGACCTTAGTTATAGATTAAAAG
AAGTTAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGATGGGCGGATCA
CGAGGTCAGGAGATCGAGACCATCTTGGCTAACACCGCGAAACCCCGTCTCTACTAAAAATACAAAAAAA
TCAGCCGGGCGTAGTGGCGGGCGCCTATAGTGCCAGCTACCCGGAGGCTGAGGCAGGAGAGTGGCGTGAA
CCCGGGAGGCGGCGCTTGCAGTGAGCTGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGAC
TCCGCCTCAAAA (SEQ ID NO: 205)

STS sY1248
Forward primer: GTGGGTGCATGATGTACTGC (SEQ ID NO: 276)
Reverse primer: CCGTTAACCAACGAGTGGAT (SEQ ID NO: 277)
Sequence:
GTGGGTGCATGATGTACTGCGTTGGATTCAGTTTGCCAGTATTTTATTGAGAATTTTTGCATCAATGTTC
ATCAGGGATATTGGCCTGATGTTTTCTTTTTTGTTGTGTATTTGCCAGGTTTTGGTATCAGAATGATGCT
GACCTCATAGAAGAAGGGAGTGGTTTCTCCTTTTCAGTAGTTTGGAATAGTATCAGAAGAAAGGGTATCA
GCTTTTCTCTGTACTTCTGGTCCCCAGAATAATGGTCCCCAACTCCATCCCAGTTACTGTGAATGCCATT
ATTTCATTCCTGTTTATGGCTGAGTAGTATTCCATGGTATAAATGTATAGCACATTTTCTTTATCCACTC
GTTGGTTAACGG (SEQ ID NO: 206)

STS sY1240
Forward primer: GGGTCCTAGATAGGCTCCAAG (SEQ ID NO: 278)
Reverse primer: TTCATGTTGGCAGTGATTGG (SEQ ID NO: 279)
Sequence:
GGGTCCTAGATAGGCTCCAAGGAAACCAAATTACTTGAAGAAGCCTGAGATTATTCTTAAAGAAATATAG
ATTTCCTTGTATGTTTACAATGAATGAGTCTTATTTTTACATGCATGGAAGTATCACAGTCACTGGACAC
TGTATAATGAAAACTTACAAGTTCTCATTTTGAACAAGCTTCCTTTTTCCTTAGTTGACAAAATTATCCA
GGTTTCTTTTAGCATGTTCACAATTTCAGATTTTATACAATTACAAACTGAACTTTCCTTATAAACTGAT
TGTTATAGCTAATTTTTCCTAATAAAATTCAAATTAAGACAGCACCTGTGAATTCTATTTAGAGTTCTAT
TGATACTCAATGTAGCCAATCACTGCCAACATGAA (SEQ ID NO: 207)

STS sY1241
Forward primer: AGGCTACTGTGAATCACGCC (SEQ ID NO: 280)
Reverse primer: GTGCATGTGTTCCCTTTGTG (SEQ ID NO: 281)
Sequence:
AGGCTACTGTGAATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTAAGACCTTGTTTCTATCTCTGTT
TCTCTCTGTCTCTCTCACACACACAGACACACACAAATAAAGGGAAAGATATTCATTAACAATCTCCAGT
TGTAATTGCTTTATAATGATATCTTAATCTTGAAATGAATTACTTAGATTTACATAAAATAGGCACATCT
AGCTGTGGTAAGGATACACTGTTCATTTAGTATGGAGCCAGCACAGAAATGGGAGAAAGACAGTTGTAGA
GAAACTGTCAAGGGAATTCAAGTCCCCAAAACCCCAGCTAAGCAGCGTGAAGAAGTAGAATAGCTGGGGG
AATGGCGCAGCTTGCTGTTTTTTGGTGCTGGTTATGACCAAACCTTAGAAAAAGCATCATACTGTGATGA
AATCAGCCACATAGACCAGTGGAACAGAAGAGAGAGCCCACATGTATTCAACTACTTTTTGACGAGGGCA
CAAAGGGAACACATGCAC (SEQ ID NO: 208)

STS sY1242
Forward primer: CGTCGGTATTTTACGACACG (SEQ ID NO: 282)
Reverse primer: GCATTTGTTTTTCATGTGCG (SEQ ID NO: 283)
Sequence:
CGTCGGTATTTTACGACACGGAAGAATATAACATATACATCGGTATTTTACGACACCGACGATTATAACA
GATACGTCGGTATTTTACGACACCGACGAATATAACATATACGTCGGTATTTTACGGCACCTACGAATAT
AACATATACATTGGTATTTTACGACACCCCACCCCCCAAAAAAAGGCGTCACATTTACATAAACATAATT
ATCTTAAAAGCCAGTATAATTTTAATTTTATTGTAGTCATCACCTTCAGACTTTATTTTGGAGAAGTGAT

Figure 7A

TACGGAAATCTGAAATATCAAGGCCTGATGAGAACACTTAAATTAACCACACTCCAGAAGTCCAAATCTG
AAAAGCAAAGATGTTTCTGATATAATAGTCTAAATTCTGCATTTCCTCTCTATTGGGCAGTATGATATTG
CGCACATGAAAAACAAATGC (SEQ ID NO: 209)

STS sY605
Forward primer: ACCTCCGAAGACTGAACCAG (SEQ ID NO: 284)
Reverse primer: CCCTTGAGTCCACAGAGTCC (SEQ ID NO: 285)
Sequence:
TACACCTCCGAAGACTGAACCAGGAAGAAGCTGAATCCCTGAATACACTAATAACAAGTTCTGAAATTGA
GGCAGTAATAAATAATCTACCAACCAAAAAAGCTCAAGACCAGATGGATTTCCCGATCCATCTTCTATTC
TATTCTATTCTATTCATTATTCTAATTGAAGCAACACAATAATTATAAACCAAACACAGGATGTTCTCAC
TTAGAAGTGGGAGCTATGCTATGAGGATGCAAATGAATAAGAATGATGTAATGGACTCTGTGGACTCAAG
GGGGAAGGTGGGAGGGGGTGAGAGATAAAAGGGTACACATTGGGTTCAGTGTACACTGCTTGGGTGATGG
GTGCACCAAAATCACAGAAATCACCACTAAAAACTTATCCATGTAACCAAACACTACCTGTTTCCC
(SEQ ID NO: 210)

STS sY1219
Forward primer: CCAGACGTTCTACCCTTTCG (SEQ ID NO: 286)
Reverse primer: CTCCCTTGGTTCATGCCATT (SEQ ID NO: 287)
Sequence:
CCAGACGTTCTACCCTTTCGAGATTAGTTAATATGTTTACACACAGAGTTTTCTTTATAGGATTATAATT
TACAATGTTTTCACAATTTTCTTAAACAGTCCACTTTATTTTATTTAACTTTAAGACAACTTTTTTATTC
TTAAGCAAAATACATAGTTATGCCTTATAATTTTTAACTAAAACCACTTTTTACCATTTTTATACACTTT
TATGCAAATCCATGTTTAGCAGTAGTGGGCGCCTGTATTCCCAGCTACTCCAGAGGCTGAGGCAGGAGAA
TGGCATGAACCAAGGGAG (SEQ ID NO: 211)

STS sY1293
Forward primer: TCCCCTCAGCCATCTGTATT (SEQ ID NO: 288)
Reverse primer: GGCCCACCTGAGTAATGGTA (SEQ ID NO: 289)
Sequence:
TCCCCTCAGCCATCTGTATTCTGGATTTCAGGATATCACTTTTAGCCTGTGATCCCAACATGGACTACAT
GGGATCACAGGCTACCCCATGGGTATCATGACTACCCCATGTGTTTACTGGCACTCTTTAAACCATAATT
TGATTGAACGGGAAACTGAGTAGTTTTCAATTAAGTACCTACTTGCATTTTTAGGCCATTGCTGATGAAA
CAGATTTTTTTAAATAGTCATTAGCAAATAGCCCATAAATAGGTAGTTATAAGAATATAACAGATGACAA
AACGACTGTGGCCAGACAAATCAACTACTGTCTGTCACCTAAGCTTCTATTTCCAACACATAATTTACAT
ATATCTAGCCTATTATTTCCTTCCTTTTCCCCAGACCTAGCATTTCCACAAGGGGCAAATAAGAAAAAGA
ATTTAACACCCCCCATATAAAGTACAAACAGTAATCTGAAAAGAACCACAAGGGAAAAAAATTCAAAATT
TACAACTATCTACCCTAAAAGAAGCTGAAAGTCCCTCAAAAACTTTCTAGAGGCCATGTCCTTCTATTAC
AAAAATGATCATAAGAACTGCAGGAGTAGAAGAATAAAAATGCATCTTAAAACTTGCTAAACACTTCAAG
TCTCCCATAAGAATTGTAATGGAAAATGGATCAGTCAGCAGTTTTTTCCATACAATTATGAACGAATTAT
ATTTCCTCATACACAGATTTGTTTTTTCAATATTCTAAGGAATTAACTTTTATACTAATAGTAGGTGATG
TAAGAAAGCAGGCCTTTATCAAGATAACTGACACTGGATGTCCATACCATTACTCAGGTGGGCC
SEQ ID NO: 212)

STS sY1250
Forward primer: TTTTTCTAACCTTGCCTGCG (SEQ ID NO: 290)
Reverse primer: TGCAGAGAAGCAGCCTACAA (SEQ ID NO: 291)
Sequence:
TTTTTCTAACCTTGCCTGCGGTTTGCACCATTTATTACATTTTTCCAACAACCAAAGGTTGGCTTTGTAT
GTTTTACTAATTTTCTCTACATCATTATCCCCTCACTTTAGTTTTTCAGAATTGATTCTGTTGTTTCTGT
TCTAATTCTTTCTTTAAATATCTAGTACATTAATTTTCAAGTTGTAGAAACATTTGTCTATGAACTCCTA
TTGCAATATCACTTTTCCTGCTACCCACAAATTTAATCTGTAATATTTGCAGTACCATTAATTTCTATTA
TGAATTTATATTATGATAATCCATGAGTTGCTGAGAAATAGCTGTTATAATTTTGTTGTTCAATTCCCAT
TTAATTTTATTTTAACTTGTGCTAACTCAGTTGAAAATTCTTTACTAATTTTTTAAATCTCATATCAAGA
CTTTTATTCACATCAATTGTTCTATAAATGCTCCCTCCTTGAAGAACACTCTCTTGTAGGCTGCTTCTCT

Figure 7B

GCA (SEQ ID NO: 213)

STS sY1243
Forward primer: ATCTGCACACTTGGGTAGGC (SEQ ID NO: 292)
Reverse primer: GAGGAAATGCAGAATTTGGG (SEQ ID NO: 293)
Sequence:
ATCTGCACACTTGGGTAGGCAAGGCAGGTAGATTACCAGATGTCAGAAGTTCAGGACCAGCCTGGTCAAC
ATAGTGAAACCCCATCTCTACTAAATATTCAAAAATTAGCCAGGTATGGTGGCAAGTGCCTGGAATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATTAGTTGAACCCATGAGGTGGAGGTTGCAGTAAGCCAATATCA
GACCACTGCAATCCAGCCTGGGCCACAAGAGCAAAACTTTTTCTCCACCCCACCCCCCCAAAAAAGGCGT
CACATTTACATAAACATAATTATCTTAAAAGCCAGTATAATTTTAATTTTATTGTAGTCATCACCTTCAG
ACATTGTTTATTTTGGAGAAGTGATTATGGAAATCTGAAATATCAAGGCCTGATGAGAATACTTAAATTA
ACCACACTCCAGAAGTCCAAATCTGAAAAGCAAAGATGTTTCTGATATAATAGCCCAAATTCTGCATTTC
CTC (SEQ ID NO: 214)

STS sY1244
Forward primer: GCTACTTGTGAATCACGCCA (SEQ ID NO: 294)
Reverse primer: TGCATATTTCGAAGCATTGTC (SEQ ID NO: 295)
Sequence:
GCTACTTGTGAATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTAAGACCTTGTTTCTATCTCTGTTT
CTCTCTGTCTCTCTCACACACACAGACACACACAAATAAAGGGAAAGATATTCATTAACAATCTCCAGTT
GTAATTGCTTTATAATGATATCTTAATCTTGAAATGAATTACTTAGATTTACATAAAATAGGCACATCTA
GCTGTGGTAAGGATACACTGTTCATTTAGTATGGAGCCAGCACAGAAATGGGAGAAAGACAGTTGTAGAG
AAACTGTCAAGGGAATTCACCAATTCCTGCCTCCCAGCAGCTGGGACAGAGGGTTACATGGCCAGGGCAT
AATCCACACTCCGCAGAAGGAATACACATGTGGAATAGAGTGAGATTAGTGTTACCACTCTCCTATTTCT
AAAATCTAATTTTAGGTTTTTAGGAATATGCTTGAGAAATTCAGTATCTTCAATTCTGAGACAATGCTTC
GAAATATGCA (SEQ ID NO: 215)

STS sY1281
Forward primer: TGCTCCTCCTTCTCACGTTT (SEQ ID NO: 296)
Reverse primer: TCCCGTACATGTCTTGTTGC (SEQ ID NO: 297)
Sequence:
TGCTCCTCCTTCTCACGTTTCTCCTGCCGCTCTAATCCCGCCTTGGCCATGAAGGAAATCGTGCTCACGC
AGGCCGGGCAGTGCGGGAACCAGATTGGCGCCAAGGTTGTATTTGACTCCCTAAAATTTAAAATTTTGTA
TGAGAGAAAAATACCTCAAAGTCAAAAGTCAACAGACTGGGGAAATAGATCTGCAACATACATGACAGAC
AAAAAGCTAATTTGGGATATATATATACACATATATATACAGACACACATATATATACACACACATATAC
ATACATACATATAAATATATATACATATAAATATATATAGAGATAGATAGATATATGTAAATATCCATTT
TTTTTGTTTTTTTTTTTTTTTGGTGAACAAGTGAAAGGAAGTTTATTGTGTTTGGTACATATATCTGTTT
CTGTTTTCCATACAAGCACATCAACCACAAGACTTACAGAGCACAATGGAATAATAATCACAAAATATTT
AAAGATATAAAAAGACCTAACAATTCCAATCATAAGCAAGTCCCTCATACAGGACATAAACCACAAAAGC
AACAAGACATGTACGGGA (SEQ ID NO: 216)

STS sY1280
Forward primer: CCATCCTCACGACTTGGACT (SEQ ID NO: 298)
Reverse primer: AAGGCAGATTTTTGAATGGG (SEQ ID NO: 299)
Sequence:
CCATCCTCACGACTTGGACTCCTGGCTCATCCTCGTGAGGCCCGGAGGCCGCTTTCTACCTACATGGTTG
ATCCTACCAGAACCATATGCTTGTCTCAAAGATTAAGCCATACATGTCTAAGTACGCAGGGCCGGTCCAG
TGAAACTGCAAATGGCTCATTAAATCAGTTATGGTTCTTTTGGTCACTCGCTCCTCTCCTAATTGGAAAA
CTGTGGTAATTCTAAATCTAATACATGCCAAAGGGCGCTGACCCCCTTCGCGGGGAAGATGCGTGCATTT
ATCAGATCAAAACCAACCCAGTCAGCCCCTCTCCAGCCCCGGCCGGAGGGTCAGGTGCCACCAGCTTTTG
TGACACTAGATAACCTCAGGCCAATGGCATGCCCCCAGTGGCAGCGACGACCCATTCAAAAATCTGCCTT
(SEQ ID NO: 217)

STS sY1200

Figure 7C

Forward primer: TGGAATACCCTGGATTGGAA (SEQ ID NO: 300)
Reverse primer: CTTATGCCTCAAATCGCTCC (SEQ ID NO: 301)
Sequence:
TGGAATACCCTGGATTGGAATAGAGTGGAATCGAAAGGAATGGAATGGAATGGAGTGCATTGGAGTGGAG
TGGATTGGAGTGGAATGGAATGGGACGAAATGGAATGCAGTGTAGTGGACTGGAGCACTTTGACGCCTAT
GGTGGAAAGGGAAATATATTCACATAAAACCTAGACAGAAGCATTCTGAGAAACTTCTGTGTGATTTGTT
CATTCTTCTCACAGAGTTGAACCTTTCTTTTTATTGAACAGATTGGAAAAACTCTTTTTGCAGAATCTGC
AAGTGGACATATGGAGCGATTTGAGGCATAAG (SEQ ID NO: 218)

STS sY1251
Forward primer: GACTGGAGTGGAACGGTCTC (SEQ ID NO: 302)
Reverse primer: TCACTTCCCTCCGATTTTCT (SEQ ID NO: 303)
Sequence:
GACTGGAGTGGAACGGTCTCGAATGGAATGGAATGGATTGGAATGGAAAGGAATAGAATGGAATGGAATC
ATATGGAATGGAATGGAACAGAATGAGTCAAAACGGAATAGAATCAAGTGGAATGCAATCGAATGGAATG
GAATACAATGGACTCGAATGGAATGGATTCTAATGGAATAGAATATAATGGAATGGCATGGAATGGAATG
AAATAGCCAGCTCCCTGTGCAGGTGAAAATCCATGTATAACTTTTGACTCCCCAAAAGCTTAGTTACTTA
TCACCTACTGTTGACTAGAAGCCTGACTCGTAACATAGTCAAGTAATACACATTTTATATGTTATGTGTA
TTATATACTGTACTCTAACAAAAAGTAAGCTGAAGAAAGGAATATGTTATTAAGAAAATCGGAGGGAAGT
GA (SEQ ID NO: 219)

STS sY746
Forward primer: TTGACTGCTTATTCTACACAAGGC (SEQ ID NO: 304)
Reverse primer: CAGGGGAAATTGGGTTTT (SEQ ID NO: 305)
Sequence:
TTGACTGCTTATTCTACACAAGGCAATTTCACATTAATTAATGCATGTAATCCTCATAGCTTCTCTGTAA
AGTAGACACTGGTTTTCCTCATTTTACACATGAAGAAACCAAATCACAGGAACATCTCCATGATGATATT
GGAACAGGAATTAAAAGAAATTAAAGAGTGTGTAAGCAAAAACTCAGTTGTTTGTAGGAAAACCCAATTT
CCCCTG (SEQ ID NO: 220)

STS sY1064
Forward primer: GGGTCGGTGCACCTAAATAA (SEQ ID NO: 306)
Reverse primer: TGCACTAAAGAGTGATAATAAATTCTG (SEQ ID NO: 307)
Sequence:
GGGTCGGTGCACCTAAATAATTAAATAATTCCTCCTCAACCCCTAGGTCTCTCTGATTCCTTAATTATCC
TGCTGCAAATACTCAGAATTTATTATCACTCTTTAGTGCA (SEQ ID NO: 221)

STS sY1065
Forward primer: TCAGGTACTGTGATGCCGTT (SEQ ID NO: 308)
Reverse primer: TGAAGAGGACACAAAGGGAAA (SEQ ID NO: 309)
Sequence:
TCAGGTACTGTGATGCCGTTAGTTTTGTTTGTTTTGCTCAGAGTTGCTTTGGCTCTTTGGTCTCTATCAG
TTTCATACAAATTTTAGTATTTTTTTTTCTATTTCTATTGAAAATAACATTGATATTTTGATACAGACTG
CATTGAATCTGTAGATGGCTTCTAGTAGTATGGTCATTTTAATGATGTCAATTCTTTTGATCAATGACAT
GCAATGTTTTTCCCTTTGTGTCCTCTTCA (SEQ ID NO: 222)

STS sY1066
Forward primer: TCACAGCTCAGTTCTTTGGG (SEQ ID NO: 310)
Reverse primer: TGTCCATGTTGGATGAGGAA (SEQ ID NO: 311)
Sequence:
TCACAGCTCAGTTCTTTGGGTGTTAATCTGACTGGGTCGGTGCACCTAAATAATTAAATAATTCCTCCTC
AACCCCTAGGTCTCTCTGATTCCTTAATTATCCTGCTGCATTTCCTCATCCAACATGGACA (SEQ ID NO:
223)

STS sY1303

Figure 7D

Forward primer: CCTTTTTGCAACTGTGGAGA (SEQ ID NO: 312)
Reverse primer: AGCTGGGTATTCCATCGTGA (SEQ ID NO: 313)
Sequence:
CCTTTTTGCAACTGTGGAGACAAGAAGTAGATTTCATATTTCCATATATTAGAAATACACAGGACTTTTC
TGTATATAGTAGAATTTACTATATACAAATATACATAAATATATGTAAGTAAAATATACAATTATATTTA
TTGTAGGCAAACCTATGTATTTATATATGAAATATATAAATACAAACATACAAATATGGAATTTATCTTT
ATATATAAAATACATAAATATGAATATATATGAATATATATTATATATACACACTTTAGTAATACACAGG
TCTTTTCTATGTATACTAGAACCTACCATATATTTATATATTAACATGTATTTTCATATTTTTATATTTA
TATATAGATTGTATATAGAAATATTGATATATAGATATATATTTTATATATAAATATCTATATAAAACAT
ATTTATATGTATATATTATATATAATCATTTATTTTAGAAGTTAAGGTGTTATGATTGTTGAAGCATGGT
TCACAGGCAAAAAGAGAAAGGAAATTATCACTTTTAGAAGAATAAAGTACAAAATTATCACGATGGAATA
CCCAGCT (SEQ ID NO: 224)

STS sY1223
Forward primer: ATCTAGAATTGGGCCTTGCC (SEQ ID NO: 314)
Reverse primer: TGGGGAACGTTGCCTAAC (SEQ ID NO: 315)
Sequence:
ATCTAGAATTGGGCCTTGCCTTCCCACTAGCCACAACATCAGTACTCTCTGCATTCATGTCTCTGTCCTA
ATGATATCTTACTCACTAAGGGAGGAAGGGCTTACCTTATCTTATCCTGCTTCTGGCCCCATAAGTGTTA
TTCCATAAAATCTTGTTAACAACAGAATTGGGATTTAAATCTGTTTTGAAACCTAGTTAATATGTCTTGC
CCACCTGTCTATGTCATAAACAAAGACAACTATTATTAAAACAACAACAATACAATGTTTCTTACTTCCA
AACACAAATACGTATCCATTCAAAAAACTAGTAATTAAGTATGCACTACACGTTAGGCAACGTTCCCCA
SEQ ID NO: 225)

STS sY1222
Forward primer: TGAAATGTAAAACCGTGGACA (SEQ ID NO: 316)
Reverse primer: TGGGGAACGTTGCCTAAC (SEQ ID NO: 317)
Sequence:
TGAAATGTAAAACCGTGGACATTTGGAAAAGAAAATGATCCTACACAATATTTATTAAAACTTCCTCCCT
GAGATTGTTTTTCCAAAAATAAGTAATGTGTGTGGCAAAAAAGTTAAGAGAATTTCAGGGTTACAATCTT
GTTAACAACAGAATTGGGATTTAAATCTGTTTTGAAACCTAGTTAATATGTCTTGCCCACCTGTCTATGT
CATAAACAAAGACAACTATTATTAAAACAACAACAATACAATGTTTCTTACTTCCAAACACAAATACGTA
TCCATTCAAAAAACTAGTAATTAAGTATGCACTACACGTTAGGCAACGTTCCCCA (SEQ ID NO: 226)

STS sY1274
Forward primer: AGGGTCCCCTCCCTACAAT (SEQ ID NO: 318)
Reverse primer: GAGACCCCTGCTTGAACAAT (SEQ ID NO: 319)
Sequence:
AGGGTCCCCTCCCTACAATCTAATATAATTAAGAAGAAAAATTCAAAGTAGAGCAATATCTATCTACTTG
AAAAAAGCCTTTTTGCAACTGAGGAGACAAAAAGTACATTTCATATTTCCATATATTAGAAAGACACAGG
TCCTTTATATAGTAGAATTCACTGTATACAAATGTATAGAAACATATGTAAATAAAATGTAATATACAAC
TATATTTACTGTATACAAAGCTATATATAATATATATTTACATATAAATATATAAATACAAATATAGGAA
TATGGATTATATATTTATATGTAATAGAAATATAAATATATATTGATATAGATGATATATATCTGTTAGA
AATACGCAGGTCTTTTCTATAAATACTGGAACCTACTATATAAATGTATATATTAATATATGTGTTTTCT
TATGATTTGTAGATTATATATAGAAATATTTATATATTTTATGTATAAATACATATATAAACAATTATTC
ATATATGATATATAATCATTTATTTTAGAGGGTAAGCTGTTAGTATTGTTCAAGCAGGGGTCTC
(SEQ ID NO: 227)

STS sY1312
Forward primer: GGCCCCGTAGGTCTATACAA (SEQ ID NO: 320)
Reverse primer: GGTCATGACTTGCCATGTTG (SEQ ID NO: 321)
Sequence:
GGCCCCGTAGGTCTATACAAAGCCAACTTCTGTGAAAAACAGTGTTGATGCTTCAACAGTGATTCCTATT
CTTGGCTCCACATTAGAATGACCCAAGGAGCTCTTTGTGTAAAATGCTGATGTAAAGGACACCTCCTTAA
AGCAATAAAACCGATGCTGACCTTGATTTACAATGTGCAGCTATAGTTGAGAGCCACTTGCCTAGAGGAG

Figure 7E

ATCTTCTCAATCTTAAATCTGCATGGGAACTTCCTTCTTATCTTGTTAACATGTAGGGTCTAATTAACTC
AGTCTGTGGTGAAGACTTGAAATTCTGCATTTCTAACAACCTCCTTGGAGGACAAAGCTGACCAGTCCTG
GAGTAGTGTGGTTGAGTTTTGGCAACATTGAGATTACTCACACAACTCGATTTTTAAGTGCTTCAGTATG
TGTTTATATGTGTCCTCTTTTTATCTTTATTAATTATTCACAGAGCATTCAACAGAACACCAACATGGCA
AGTCATGACC (SEQ ID NO: 228)

STS sY1310
Forward primer: TCCAAGCATATAGTTGCCCC (SEQ ID NO: 322)
Reverse primer: TCTTTCACTGCACATGGAGC (SEQ ID NO: 323)
Sequence:
TCCAAGCATATAGTTGCCCCCAATTCTTTAATTTCTTCTGGCTAGAAAAGCCATAGGCTTTCTATATGAA
TTTTAGCTGAAGTGTTAATTGAGATGTATATTCTGGCTAAAATCTGTAAGAATGGAAACTTCAAAATTGT
GGTTTGTTTTATCCAGGTACCAACTTCCCTCCAAAATCAGCCCGCTTGTATTTACTTTCTTCTGACTTCA
GATAGTTGATTTGCGTCTCTTCCCCAGATTTTATTCTTATTACCTGAGCATTTGTTGGTGCAGTATTGGC
TTCACTGGACACACAGAAGTGAAATTCCTGAACTGAACTTCTACAGAATTTGATACTTAATTAAGCAAAA
ATCAGAGAGTGATGAACTACATGCAAGATAAATATGCCTATCAGAGATTCTGGGGCACATTCGAGTGTGC
TCCATGTGCAGTGAAAGA (SEQ ID NO: 229)

STS sY1311
Forward primer: AGAAAACTTGCAATGCAGGAG (SEQ ID NO: 324)
Reverse primer: ACTGCACCAACAAATGCTCA (SEQ ID NO: 325)
Sequence:
AGAAAACTTGCAATGCAGGAGTAGGTTTATGTTTCCTCTGCATCAGTCATTTGAGAGAAATATCTTTAAA
TATGAAATTGCAAAACCGAATCCTGTTTGTGTCTTTGTCTTTGATAATGTTCAAATATCAAGGCTCATAA
GTATGATCTTCAACAAAAAGGAGCATAATGGAAAAAACTGCAATATCTTTTGAAGATTTTTAACTCAGGC
TGGGCACAGTGGCCCATGCCTGTAATCCTAGCAGTTCTGGAGGGCAACCTGGGTGAATCTGCTGAGGTTA
GAAGTTTGAAATCAGTTTCTCTTGTGGTTTGTTTTATCCAGGTACCAACTTCCCTCCAAAATCAGCCCGC
TTGTATTTACTTTCTTCTGACTTCAGATAGTTGATTTGCGTCTCTTCCCCAGATTTTATTCTTATTACCT
GAGCATTTGTTGGTGCAGT (SEQ ID NO: 230)

STS sY1304
Forward primer: GCTCCACATTAGAATGACCCA (SEQ ID NO: 326)
Reverse primer: GGAAAAATATTGTGACCCCCA (SEQ ID NO: 327)
Sequence:
GCTCCACATTAGAATGACCCAAGGAGCTCTTTGTGTAAAATGCTGATGTAAAGGACACCTCCTTAAAGCA
ATAAAACCGATGCTGACCTTGATTTACAATGTGCAGCTATAGTTGAGAGCCACTTGCCTAGAGGAGATCT
TCTCAATCTTAATTCTGCATGGAACTTCATTGTATTTCTCACATATATCACATGTTCATGGGGGAAAAAA
TGAAAAAGAATTGTGAACTATAAAGTACTCCACATTTTACATACAAAAACATCCTGAATATATGTTGAGG
TTAGCAGGAAGAAATCATCTCTTACTCCTTAAGATTGGAATCTACAGAGGGAAGAATACCTTATGTCTTA
AAAATAATATTTTGGACACATAGCAAATTTCAAATCCAGCTTTATTTTTTGAAGAATTAAATGGGGGTCA
CAATATTTTTCC (SEQ ID NO: 231)

STS sY1275
Forward primer: TTGCAACATTGCACTTGTAGG (SEQ ID NO: 328)
Reverse primer: ATGATTCTGGTCTTGGTGCC (SEQ ID NO: 329)
Sequence:
TTGCAACATTGCACTTGTAGGAATTTGGAGATGTCCTAAGTGGTTAACTCTATTGAAAGAGTCACATAAG
TGCATAGGATATTTCTGCTCTCTGATGACCTATAGCTATTTAGACAATGTAGATAAATATACAGGCTCAG
CCACAACGTGTTCTCAAGATATTTTGTTTGGCAGGAAACTACATTTCAGGGCATTAACTACAATGCATGT
AACGGGGTGAAATAGTTGAAATGATGCTGAAAGAGGAATTTTGCTTTCCTTTCTTTAATTTGTTATCAGT
AGTATACTGTTTGATATCAGTTTCAACTATAAGAGCATGCTGGGGAACCGAATTGCCTTTGAAATAGTGC
CCAGGTTTTGAGAGTAGCTCTTGGGTAGCACAGGCACCAAGACCAGAATCAT (SEQ ID NO: 232)

STS sY1285
Forward primer: CCTATCTCTGCATGGCCTGT (SEQ ID NO: 330)

Figure 7F

Reverse primer: AAGGCAAGTTTTGGAGCAGA (SEQ ID NO: 331)
Sequence:
CCTATCTCTGCATGGCCTGTTTTTTCATAGCTTATGATTATAGAGCAAGGATTAATACAGTATTGGAATA
AAGAGTAATTGTTACAAACTAACGATTAATGATATCCATATACGATCATATCTATGATCTATGTCTAGTA
TAACTCTTGTTGTTTTATACAGTTTATTATAATAGAACAGCTCACGCCCTCTGTCTCTTGCCTCTGAAAC
TAGGTGGCTTGCTACCCACACTCTCCCACAACCCATGGGAATTGTGGGAGCCACAATTCAAGATGAGATT
TGGGTGGGGACACAGACAAATCATATCAAAGGTTAAACAGCACACTTGTTCTTCAAGTTGCCCACTTGAG
TCTTTTCCAAGCATACTTTCCTTTTTTTCGTGTCTTAAAGCCTTTTTAAATAAACTTCTCTGCTCCAAAA
CTTGCCTT (SEQ ID NO: 233)

STS sY1286
Forward primer: ATCTCACATGGTGCCAGACA (SEQ ID NO: 332)
Reverse primer: AAGGCAAGTTTTGGAGCAGA (SEQ ID NO: 333)
Sequence:
ATCTCACATGGTGCCAGACAAGAGAAGTGAACGTGTGCAGGGAAACTAACCTTTATAAAATAATCAGATC
TCATGAGTCTTATTCACTACCATGAGAGCAGCATGGGAAAGACCGACTCCCATGAATTAATTACTTCCAC
TGGGGCCCTCCCACAACCCATGGGAATTGTGGGAGCCACAATTCAAGATGAGATTTGGGTGGGGACACAG
ACAAATCATATCAAAGGTTAAACAGCACACTTGTTCTTCAAGTTGCCCACTTGAGTCTTTTCCAAGCATA
CTTTCCTTTTTTTCGTGTCTTAAAGCCTTTTTAAATAAACTTCTCTGCTCCAAAACTTGCCTT
(SEQ ID NO: 234)

STS sY1276
Forward primer: TGCACTTGTAGGAATTTGGA (SEQ ID NO: 334)
Reverse primer: AAAACAGACATATATACACATACACTG (SEQ ID NO: 335)
Sequence:
TGCACTTGTAGGAATTTGGAGATGTCCTAAGTGGTTAACTCTATTGAAAGGGTCACATAAGTGCATAGGA
TATTTCTGCTCTCTGATGACCTATAGCTATTTAGACAATGTAGATAAATATACAAGCTCAGCCACAACGT
GTTCTCAAGATATTTTGTTTGGCAGGAAACTACATTTCAGGGCATTAACTACAATGCATGTAACGGGGTG
AAATAGTTGAAATGATGCTGAAAGACAAAAGTTTCTGCTGTGCCAGAAACTTTCTGAGCCGCTATAGTTT
AGGGCTGTCTGATTTTGGAATCTTTGATCAATTAAACTCTGTTAAATTTAATATACTGAAAGTTTTTATT
TTAACAATAGTATACATATATATATACAGTGTATGTGTATATATGTCTGTTTT (SEQ ID NO: 235)

STS sY1264
Forward primer: GGCTTAAACTTGGGAGGGTG (SEQ ID NO: 336)
Reverse primer: GCACTTCAAACCGAGGCTTA (SEQ ID NO: 337)
Sequence:
GGCTTAAACTTGGGAGGGTGTATGTGTCCAGGAATTTATCCATTTCTTTTAGATTTTCTAGTGTATTTGC
ATAGAGGTGTTCAGAGTATTATCTGATGATCAGCAATGATATTCCCTATGTCATTTTTTATTGCATCTAT
GTGATTTTTCTCTCTTTTCTTCTTTGTTAGTCTGGCTAGTGGTCTATCTATATTGTTGATCTTTTCAAAA
AACCAGCTTACGGATTTATTGATTTTTGAAAGGTTTTTGTGTCTCTGTCTTCTTCAGTTCTGCTCTGATC
ATAGTTATTTTATGTCTTCTGCTAGGTTTTGTATTCGTTTGCTCTCACTAAACTAGTTCTTTTAATTTTG
ATGTTAGGGTGTCAATTTTAGATCTTTCCTGCTTTCTCTTTTGGGCATTTAGTGCTATCAGTTTTTCTCT
AAACACCACTTTAAATGTGTCTCAGAGTTTGTGGCACATTGTGGTTGGTGGCCTGGAGAGACATTGGTCA
AAAATACAAACTTTTAGTTAAACAGGAAGAATAACTCAAAGAAATCTATTGTACAACATAGTGGCATCAC
ACTATGTTAAGGGTCTAACACTACCTGATACAATGTTATATCTAATAACAACGTATTGTACTCTTGAAAA
TGGCTACAATAATAGATTTAAGTGTTCTAACATTAAATAAATGAAAAGTATATAATGTAGTGCATGTTAA
TTAGCTTGAAATGAATACATATTTCAAAGAGGTCTTAAAAAGCACCATCCTAGACATTTAATTATAAGAA
TAAGCCTCGGTTTGAAGTGC (SEQ ID NO: 236)

STS sY1227
Forward primer: GCAAAGTTCTTGCACTGTGTTT (SEQ ID NO: 338)
Reverse primer: TTGTGGCCTGTGGTGTAGAA (SEQ ID NO: 339)
Sequence:
GCAAAGTTCTTGCACTGTGTTTTTTAGCTACATCAGGACATTTATGTTTTCCTCTAAACTAGTTATAATC
ATAATTATTACTATTTTTGAGACGGAGTCTCACTCTGTCACCAGCCTGAAGTGCAGTGGTGTCAACTCAG

Figure 7G

CTCACTTCAACCTCCACCTCCCGTGGATTCAGCTGCTCTTAGCTGAGACTACATAGCGGGCCATCTTGGC
ACCCTAAAGTGAAGCCTGAGCTGTCCAACCATGGAGTAAATGTAGAGAGCCTAATCGACATAGTATAGTT
GCTTCTTCACACAACTCTTTCTACACCACAGGCCACAA (SEQ ID NO: 237)

STS sY1228
Forward primer: GCAAAGTTCTTGCACTGTGTTT (SEQ ID NO: 340)
Reverse primer: AAAGGAAACCTTGAGCAGGA (SEQ ID NO: 341)
Sequence:
GCAAAGTTCTTGCACTGTGTTTTTTAGCTACATCAGGACATTTATGTTTTCCTCTAAACTAGTTATAATC
ATAATTATTACTATTTTTGAGACGGAGTCTCACTCTGTCACCAGAGAGCTTCTGGAAATCTGAACTTATA
GATTATCCTAGACAATTGTGTGCATATAAAACCAGACATTAATCATTTTAAACGTCTAAGAATATGTACG
TGTTTTTGCTTTGTTTTGAAGCAAGTTTCTGCATTTAATCATGTGTAAAGAATTTTAGCTTATTAAATAG
AATATAATCTAAGTTAATCTAAAAAGCACACTTTATGACCATAAAAACTTAGATATTTCTACCTAAATGA
TTCCATGATTGACTAATCCTGCTCAAGGTTTCCTTT (SEQ ID NO: 238)

STS sY1283
Forward primer: GGTTTTGTATTCGTTTGCTCTCA (SEQ ID NO: 342)
Reverse primer: TGCAATGAAATGAGAACCCA (SEQ ID NO: 343)
Sequence:
GGTTTTGTATTCGTTTGCTCTCACTAAACTAGTTCTTTTAATTTTGATGTTAGGGTGTCAATTTTAGATC
TTTCCTGCTTTCTCTTTTGGGCATTTAGTGCTATCAGTTTTTCTCTAAACACCATTTTAAATGTGTCTCA
GAGTTTGTGACACATTGTGTCTTCATTCTTATTGGTTTCAAAGAACATCTTTATTTCTACCTTATTTCAG
TATTTACCCAGCAATGATTTACAGCCTGCTCCTAAATGTTCAGTTTCTATGTAGTTGTGCAGGTTTGTGT
GAGTTTCTGAATCCTGGGTTCTCATTTCATTGCA (SEQ ID NO: 239)

STS sY1225
Forward primer: GTCAGGAGGCTTAGGAAGGC (SEQ ID NO: 344)
Reverse primer: CTGGGATTACTGGCAAGGAC (SEQ ID NO: 345)
Sequence:
GTCAGGAGGCTTAGGAAGGCTAAGTAAAAATATTTTAAATCTGTTTTGTCAGAGACTAGGAATGCAATTT
CCCTTTATTTCTTTCCTTAAAACTATCGCTAGTGTGACTGAATAACTGAATTTTTAATCTATGCTTAATA
AACTACATGTGCATAATGACTACCATACAGGGTAGCATAATTCTAAGGTACATGGCTGGTATCTGTTGCT
TAACTCTTACTACCAAAGGAAATTTCTGGCTTGAAGGGATATTAAGAAACAATCTACGGGCCACGCATGA
TGGTCCTTGCCAGTAATCCCAG (SEQ ID NO: 240)

STS sY1226
Forward primer: GTGCTGTTAAGCACCATCCA (SEQ ID NO: 346)
Reverse primer: CTGGGATTACTGGCAAGGAC (SEQ ID NO: 347)
Sequence:
GTGCTGTTAAGCACCATCCAGTATGACTCGCTGTGAAAATTGAAATGTTTGTATCTATGTTGTTGACTGT
GGTAGGTACTAGCCTCATGTGGCTATTGAGCACTTGAAATTTGGCTAGTGTGACTGAATAACTGAATTTT
TAATCTATGCTTAATAAACTACATGTGCATAATGACTACCATACAGGGTAGCATAATTCTAAGGTACATG
GCTGGTATCTGTTGCTTAACTCTTACTACCAAAGGAAATTTCTGGCTTGAAGGGATATTAAGAAACAATC
TACGGGCCACGCATGATGGTCCTTGCCAGTAATCCCAG (SEQ ID NO: 241)

STS sY1287
Forward primer: GCAACATAGATGGACCCAGAA (SEQ ID NO: 348)
Reverse primer: ATAGCAAAGAGCCTCCCAGA (SEQ ID NO: 349)
Sequence:
GCAACATAGATGGACCCAGAAAATATTATGTTAAGTCAAATAAGCCAGGCACACAAAGACAGATACTACA
TAATCTCATTTATACCTAGAAATAAAAGCAGTCAAACTTACAGAAGCATAGAGTAAAGGGGTGGTTAACA
GTAAAGGTTCATTGGTTTCAAAGAACAACTTTATTTCTACCTTATTTCATTATTTACCCAGCAATGATTT
ACAGCCTGCTCCTAAATGTTCAGTTTCTATGTAGTTGTGCAGGTTTGTGTGAGTTTCTGAATCCTGGGTT
CTCATTTCATTGCACTGTGGTCTGGGAGGCTCTTTGCTAT (SEQ ID NO: 242)

Figure 7H

STS sY1252
Forward primer: CCATCTCCTGACCTCGTGAT (SEQ ID NO: 350)
Reverse primer: TCATTTTTGCAGTGAGCGAG (SEQ ID NO: 351)
Sequence:
CCATCTCCTGACCTCGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCA
CGCCCAGGCATAGAGGCACTTTTAACCATAAATGAACACTGTTATGATTTGTATTACCACAGTATCATTA
TTCTGTCCTGTTTGCCTTACATTTTATTTATTTATTATACTGTAAGTTCTGGGATACATGTGCAGAATGT
GCAGGTTTGTTACAGAGATATATGCTTGTTTGCTGCACCTGTCAGTTTTTCATCTACATTAGGTATTTCT
CCTAATGCTATTCCCTGTTAGGTCCCCACCCTCCAACAGTCTCCAGTGTTTGATGTTCCCCTCCCTATGT
CCATGTATTCTCATTTTACAACTCCCACCTATGAGTGAGAAATTGCAGTGTTTGTGTGTTTGGAACTTAT
TCCTTCCAGTGGGTTTGTGGTCTCGCTCACTGCAAAAATGA (SEQ ID NO: 243)

STS sY1253
Forward primer: CTGGCAGGTTCATGGTCTTT (SEQ ID NO: 352)
Reverse primer: AGCCCAACATCACCAACCA (SEQ ID NO: 353)
Sequence:
CTGGCAGGTTCATGGTCTTTCTCACTTCAAGAATGAAGCTGCAGACCTTACTGGTGAGTGTTGCAGCACT
TAAATGTGTTATGTCCAGGGTTTGTTCCTTCATATGTGTCCATAGTTTCTTCCTTCTGGCTGGTTCATGG
TCTTGCTCACTTCAAGAATGAAGCTGCAGACCTTAGTGGTGAGTGTCTGCTAAAAACAATGTAAAAATAT
GTGTCTGCTAAAAACAGTTTAAAAGTGTTCCTCTTTCTCCACAGCCTTGCCAGCATCAGTTGTTTCCTGA
CCTTTTAATAATCTCCACTATGACTGGTGTGAGATGATCTCTCATCGTCGTTTTGATTTGCATTTCTCTG
ATGGTTGGTGATGTTGGGCT (SEQ ID NO: 244)

STS sY1315
Forward primer: TCGGGTTCAACAGATTCTCC (SEQ ID NO: 354)
Reverse primer: TTTTCTACAGGCCACAGCAA (SEQ ID NO: 355)
Sequence:
TCGGGTTCAACAGATTCTCCTGCCTCAGCCTCCCAAATAGCTAGGATTACAGGAACCTGCCAACACACAG
ATAATTTTTGAATATTTAGTAGAGATGAGGTTTCACCATGTTGACCAGGCTGGATTTGAACTTCTGACAT
CTGGTAATCCACCAGCCTTGGCCTCCCAAGGGGATTACAGGAGTGAACCACCCCGTGTGTGGTTAAAACA
TATACATAAACATATACATAAGAACTGTTTACAAAAATTGCTGTGGCCTGTAGAAAA (SEQ ID NO: 245)

STS sY1302
Forward primer: CAATGGCATTCACTGTGAACA (SEQ ID NO: 356)
Reverse primer: CTTGAAACTCCTCCAGCTGG (SEQ ID NO: 357)
Sequence:
CAATGGCATTCACTGTGAACACTAGACAAAGCTCACAGCTCAGGCCTGGTAGCTTGAGAAGAGCGCATGT
GCATTCGGAAGGCAGGCACAGGCGCCCAAATATCAGATCTGTGAGCCTTCCTAAGCAGAGGAAAATGCTA
CAGGCAGAGCCAGCCTGGTATCTGGAGAAAGGCTTTCTGCGATAACGCACTATGGGACCCTGTAAGTCTC
AACCTTAGGGCTCCGTCGGGCCATTTTTGTGGCCTGGTCCAGCTGGAGGAGTTTCAAG (SEQ ID NO: 246)

STS sY1279
Forward primer: CATGCAGAAGATCATCCACGTA (SEQ ID NO: 358)
Reverse primer: CAGACAAGTTATTGAAGGTAGCCA (SEQ ID NO: 359)
Sequence:
CATGCAGAAGATCATCCACGTACTGGAGCAAAACGCAGCATAGGTCTTTGGTGGGGAACTTTTGGAGGTC
TCAAGCCAGCACCTCTCCTGAAGATGGTGGGTGAGTGCTTAAACCCTTGGAGAAGCAGGATTCAAGTGTA
CTGAGTGGTGACACCTAACCCCGGATCTTTCTTCCCACTGGAAGGCAAACAGTTTCTGGCTCTCAGGAGA
TAGTCTGATGCTAAATAAGGTGTCCTTCAGGTCTAGGCAAGTGAACCACCTGTCCTCAGCTGACAATAAC
CCAACAATGTGTATGGGTTAGGTACTGTTGGATGTAAAGTCACTGTAGTGTGACTGACCAAGCACAAGTC
CTGTACTTGCCTGTAGTCCTCAGTCCCTGGCTTAGGAACAGGCAGGAGGGGAGTGTTCCATGGCGACTGA
CAAGGGACTATAATTCCAAAGGCTCTGAGGCATTTGAGATGAACCTGGCTACCTTCAATAACTTGTCTG
(SEQ ID NO: 247)

STS sY1278

Figure 7I

Forward primer: GCACTGAAGGTGTTTCACGA (SEQ ID NO: 360)
Reverse primer: TCTCAAATGCCAGAGAGCCT (SEQ ID NO: 361)
Sequence:
GCACTGAAGGTGTTTCACGATGGTGATGGATCCAGGCTGTGTATGGGTTAGGTACTGTTGGATGTAAAGT
CACTGTAGTGTGATTGACTAAGAACAAGTCCTGTATTGGCCTGTAGTCCTTGGTCCCTGGCTTGAGAACA
GGCAAGAGGGGAGTGTTCCATGGTGACTGACAAGGGACTATAATTCCAAAGGCTCTCTGGCATTTGAGA
(SEQ ID NO: 248)

STS sY1294
Forward primer: TTCTTCAGGTTGGCTCACG (SEQ ID NO: 362)
Reverse primer: CTGTCAGCTCTGTCTGGCAT (SEQ ID NO: 363)
Sequence:
TTCTTCAGGTTGGCTCACGTCTGCCCTCTCCTAGGATCATGGGACTCTCCCGTGATCCCACAGAGAAAAC
AGCCAGAATCCACCACCTATGCACCTCCACGGAGGTCTCCTTCTCCACCAAGCCACAGGGACTTGCTGCT
ATGCAATGGTGGCATTCATTGTGATGCCAGACAGAGCTGACAG (SEQ ID NO: 249)

STS sY1258
Forward primer: AACCCCATCTCTAGCAAAAATATG (SEQ ID NO: 364)
Reverse primer: TAGGTGACAGGGCAGGATTC (SEQ ID NO: 365)
Sequence:
AACCCCATCTCTAGCAAAAATATGAAAATTTGCTGGGCATGGTGGTGCACACCTGTAGTATGTTACAGTT
AATTGGGGGGCTCAGGCAGGAGAATTGTTTGAACCTGGGAGCCTGAGGCTGCAGTGAGCCAATATTGCAC
TATGTACTCTAGCCTGGGTGACAGAGCGAGACTCCAAATCAAAAATAATTATATAAATCTACAAATATGT
AAATAATAAATAAGGTATCCTTCATTTCAAGCATTTATTCTTTCTTTTTGCTTTTTTAGACACAGGGTCT
CCCTCTGTTGTCCAGCCTGGACTGCAGTGGCACCGTCAAGGCTCACTGCAGCCTCGAACTCCTGGGTTCA
AATGCACAAGCCTTCCATTTCAGCCTCCCAAGTAGTTGGGATTACAGACACACATCACTGTGCCCAACTT
TTGTGTTTGTGTGTGTGTGGTAGGGACAATGCTTTGGATATATTGTTCAGGCTGGTCTCAATCTCCCAGA
CCGAAATAATCCTCCTTCCCTGGCTTCCCAAAGTGTTGTGATTATAGCCGTGAGCCACTGAGTCTGGCAT
ATCTTTTCTCATTATGAGCGACATTCCACCTCACTGAGTCTGGCGTATCTTTTCTTGGTATCAGCGACAT
TCCACCTTCGCTCTATTAATTATTTTGAGATGTACAATAAATCATTATTAAGTGTAGTCATCCTGTGCCA
CTGAACACTAGATATTATTCCTTCTAAGCAAGTATAATTTAACCCACCCCCATCCCCTCTTTGATCCCTC
GCTTACCAGTTCACATTACTTGTATCAAAATATCACATGTATGCCAAAAGTATCTACAACTGTTAGGTAC
AAATTTTCATTCCCTTCCTCCTTCCCTCCCTTCCTTTCTTCCTTCCTGTCTTTCTTTCTTTTTGTCTCTG
TATCTTTTTCTCTCACTGATTTTTTTTTTTTTAAGAAAGAATCCTGCCCTGTCACCTA (SEQ ID NO: 250)

STS sY1160
Forward primer: GGTGTCCCATGGAAACCTTA (SEQ ID NO: 366)
Reverse primer: TTACAGGCAGCATTTTTCCC (SEQ ID NO: 367)
Sequence:
ATCTATCGACACTTTTGGGAAGTTTCAGCCACTATTCATTTAAATATTCTTTTTTTCCCCATCTCACCTA
TTCCAGTGGGACTCCCATTATGAATATGTTGATATTCTTGATGGTGTCCCATGGAAACCTTAGTTTTGAT
CATTATTCTTGTTTCTCTTCCTTACACTGAACAATATCAAACAATCCATCTTCAAGTTGCCTCATTAGGC
ATTCCTGAGGCAGGCTAAGGCACCCTTCAGAGCTGTCAGTCTGCCTAAGCAGAGGAAAATGGTACAGGCA
GAGCCTTCCTGGTATAGGGAAAAATGCTGCCTGTAATAAGCCACCACTGGACACAAAAATATAGATGATA
GGGCCCTTTTGGGCAGTCTCTAAGGTTGGGTTCCACAGAAGAAGTCATTTT (SEQ ID NO: 251)

STS sY1196
Forward primer: GTTGGCAACTTGCACTGCT (SEQ ID NO: 368)
Reverse primer: CCTTTCCTCTCAAAGTCCCC (SEQ ID NO: 369)
Sequence:
GTTGGCAACTTGCACTGCTCACTGCAGCCTCCTCTGCAGAGCTTCAAGTGATCCTCCGACTTCTCAGCTA
CTTGAGTAGCTACAGGCTCTCGCTATCAGAGCTAGTAGGCAATTTTTTTGTGTGTTTCTTTAATGGACAT
GGGTTTCCCCATGGTACCCAAGCTGGTCTCAAACTTGGGTTAAGTTAAGTTAAGATCTACCTCTCCCTCC
AAATCAGAGATAACCAGGCAACTTTAAGAACTAAAGTTGACTGTGGAGAAAATACTTAGACAGCCCTCTT
GGAACATCAGCCTGGTAATTGGTTAGAGCTCCTAGCTTAAGAGGTGAGAAAGACAGGTCACTTCTGGGCA

Figure 7J

AGCTCTGGAACCTCACGATACTTGGGGACTTTGAGAGGAAAGG (SEQ ID NO: 252)

STS sY1197
Forward primer: TCATTTGTGTCCTTCTCTTGGA (SEQ ID NO: 370)
Reverse primer: CTAAGCCAGGAACTTGCCAC (SEQ ID NO: 371)
Sequence:
TCATTTGTGTCCTTCTCTTGGATTTACTAATTTACTAGTTAAGCTGTGTTATGTTCACTGGACATTTAAG
ATTTTATAAATATCTATATGGCAATAGAGTCATTTCTGAGGTAGTAAGAATGTATTCTCCTTTCAACAGA
ACCTAATTGGAACCTGGTTTTATTACAAAGCCTTGTCTGAAATATCAAATACATTTAAGAATGATTTGCA
GAAAATCAGAGATAACCAGGCAACTTTAAGAACTAAAGTTGACTGTGGAGAAAATACTTAGACAGCCCTC
TTGGAACATCAGCCTGGTAATTGGTTAGAGCTCCTAGCTTAAGAGGTGAGAAAGACAGGTCACTTCTGGG
CAAGCTCTGGAACCTCACGATACTTGGGGACTTTGAGAGGAAAGGTATTCAACCAAGTGTATAGGTTCTG
AAAGGGAAGCCTGGTGGCAAGTTCCTGGCTTAG (SEQ ID NO: 253)

STS sY1572
Forward primer: CTCAAACTCCCAGACCGAAA (SEQ ID NO: 372)
Reverse primer: GGCAAGTGAGGAATCATTTCA (SEQ ID NO: 373)
Sequence:
CTCAAACTCCCAGACCGAAATAATCCTCCTTCCCTGGCTTCCCAAAGTGTTGTGATTATAGCCGTGAGCC
ACTGAGTCTGGCATATCTTTTCTCATTATGAGCGACATTCCACCTCACTGAGTCTGGCGTATCTTTTCTT
GGTATCAGCGACATTCCACCTTCGCTCTATTAATTATTTTGAGATGTACAATAAATCATTATTAAGTGTA
GTCATCCTGTGCCACTGAACACTAGATATTATTCCTTCTAAGCAAGTATAATTTAACCCACCCCCATCCC
CTCTTTGATCCCTCGCTTACCAGTTCACATTACTTGTATCAAAATATCACATGTATGCCAAAAATACCTA
CAACTTTTACGTACAAATTTTTTAAATAAGTAAAAATTAATAAAAAAGGGTATCTCCAACAAAGTGATAA
AATAGGAGGCTCTAATTTGTTCCTCCATCCACAAATGCAACAAATAAAGAGCCACACCCACATCAATTCC
CTATGAGATAAACTTACAAACAAGTTGGGATACTCTTGCATGTAGGGTTATGAAAATACTTACTTAAAAA
AAGGTAAGAAAAACTGAATCATGATCTTTTTCTAGCGTTTATCTCTGACACATTGCCCTAGAATCAATAG
GGAACTGTTATTTCACAGCTTCTCTCAGAGAACTGAAGTATTAATCCACATATGTAAAGCCCCAGCTGTT
AACAGCTGCTTCTCAATGAAATGATTCCTCACTTGCC (SEQ ID NO: 254)

STS sY1192
Forward primer: ACTACCATTTCTGGAAGCCG (SEQ ID NO: 374)
Reverse primer: CTCCCTTGGTTCATGCCATT (SEQ ID NO: 375)
Sequence:
TTTTTAAAAATGAAAGATTATTCTTGTTTTCACTGTGAAGCACAATAACAATAAATTTTCCCCATTGGTA
CAAGTGAATGATTTACATGGTAAATTGATGTGCTTAACTACTACCATTTCTGGAAGCCGGATTTGATATA
AACTTATTTTGGGCTGGGCGCGGTGGCTCACGCCTGTAATCTCAGCAGTTTGGGAGGCCGAGGCAGGTGG
ATCACGAGGTCAGGAGATGGAGACCATGCTGGCTAACACAGTGAAACCCCGTCTCTACTAAATACACAAA
AAAATTAGCCGGGTGTAGTGGTGGGCGCCTGTGTTCCCAGCTACTCCGGAGGCTGAGGCAGGAGAATGGC
ATGAACCAAGGGAGCGGAGCTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTAGGCGACAGAGC
CAGACTCCGTCTTAAAAAAAAAAACAACAAAAAACTTATTTTGATAAACATGGCTTATGATACTTGATAA
TAAAATTAATAAAGATGTTGTTTTTATAAACATCAAATGTGAATAGCTGTTGTCATGGTTTAAAATGTCA
AAGGACAGCCTTTGAAAATTAAGATACTGATAACAGACATG (SEQ ID NO: 255)

STS sY1191
Forward primer: CCAGACGTTCTACCCTTTCG (SEQ ID NO: 376)
Reverse primer: GAGCCGAGATCCAGTTACCA (SEQ ID NO: 377)
Sequence:
CTATCAGACACTATTTTGGCAATTTTATGTACCTAAACATGTTAAATAATCATGCTTACCATTTTTTCCA
GACGTTCTACCCTTTCGAGATTAGTTAATATGTTTACACACAGAGTTTTCTTTATAGGATTATAATTTAC
AATGTTTTCACAATTTTCTTAAACAGTCGACTTTATTTTATTTAACTTTAAGACAACTTTTTTATTCTTA
AGCAAAATACATAGTTATGCCTTATAATTTTTAACTAAAACCACTTTTTACCATTTTTATACACTTTTAT
GCAAATCCATGTTTAGCAGTTTTAATTACCTGTTATAACGGTAATTTTTAGCAATTTTTAACTTTAATGT
AAAGCCTATTACGTGTTTTTTATTTTGTTTTGTTTTGTTTTCTTTTTGAGACAGAGTCTTGCTCTCTCAT
CAGGCTAGAGTGTGGTAACTGGATCTCGGCTCACTGCAACCTCCACTTCTTGGATACAAGCGATTCTGCT

Figure 7K

GCCTCAGCCTCCTGAGTAGCTTGGATTACAGACGCCTGCCACCACACCCAGCTAATTATTGTATTTTTAG
TAGGGAGGAGGTTTCACCATGTTTTCCAGGATTGTCTTGAT (SEQ ID NO: 256)

STS sY1198
Forward primer: AAAGGCAGAACTGCCAGG (SEQ ID NO: 378)
Reverse primer: CCAACTCTAGGAGGAGGGCT (SEQ ID NO: 379)
Sequence:
AAAGGCAGAACTGCCAGGTCTGTGTCTTATTTTCTTTGTCATTCTAATTTATCTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAG
TGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAA
GTAGCTGGGACTACAGGCGCCCGCCGCTACGCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTT
CCCCGTTTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCT
GGGATTACAGGCGTGAGCCACCGCGCCCGGCCTCTAATTTATCTTTTGGTATGGAGAGCAGAAAACAGTC
TGAGGATGTGACAGCCCTCCTCCTAGAGTTGG (SEQ ID NO: 257)

STS sY1307
Forward primer: GACAACACCACCGTACTCCA (SEQ ID NO: 380)
Reverse primer: CAGGGGCAGCATTTACAGAT (SEQ ID NO: 381)
Sequence:
GACAACACCACCGTACTCCAGCCTAGCTGACAGAACGAGACCTGTCTCTTAAAAACGGAACAAAACAAAA
TAAAACTTGTTGACTGACTAGGTATTGGAAATAACAAAAAAGGTTTCCCTCCACTTCCTTCCTTTTTTTA
AAAATTATGTATATTATCTCTGTGCCTGGTTTTTCTTTATTCCATGATTTTCCTTTGACTGTATTCTCTT
CTTTAGTCCTTTCAGTTCCTTGTACTTGCTAATGCAGGCTGAAATGCTAGCTAGAGGTACATAAAGTTTT
TGCCAAAAGGGTTTTGAAATTGTGGACTTTTTTTTTTTTCAGTCAATGCCACGTAAGTCACAGAAAAAAA
AAAAATCCTTCATGAGGAAAAAAGAAACATTTCACCCGCTCCTTTTTGTGGTGATCAGAGATTGATTAAT
TTAGTTTTGCATTAATCAAGTTGTCATCAGAACCTTCCCTGCTAATCTGTAAATGCTGCCCCTG
(SEQ ID NO: 258)

STS sY1308
Forward primer: GGTCTGCTGCACCTTCATTT (SEQ ID NO: 382)
Reverse primer: CAGGGGCAGCATTTACAGAT (SEQ ID NO: 383)
Sequence:
GGTCTGCTGCACCTTCATTTTAGCCAATTTCACCCATTTGGAATGGGTGTATTTACTCAATGCCTGTACC
CTCATTGTATCTAGGAAGTTACTAACTTACTTTTGATTTTACAGGCTCATACGTGAGACTTGCCTTGTCT
CAGGTGAGACTTTGAACTTGGACTTTTGGGTGAAATGTTGGAACCTGGACCCAATGCTAGCTAGAGGTAC
ATAAAGTTTTTGCCAAAAGGGTTTTGAAATTGTGGACTTTTTTTTTTTTCAGTCAATGCCACGTAAGTCAC
AGAAAAAAAAAAAATCCTTCATGAGGAAAAAAGAAACATTTCACCCGCTCCTTTTTGTGGTGATCAGAGA
TTGATTAATTTAGTTTTGCATTAATCAAGTTGTCATCAGAACCTTCCCTGCTAATCTGTAAATGCTGCCC
CTG (SEQ ID NO: 259)

STS sY1291
Forward primer: TAAAAGGCAGAACTGCCAGG (SEQ ID NO: 384)
Reverse primer: GGGAGAAAAGTTCTGCAACG (SEQ ID NO: 385)
Sequence:
TAAAAGGCAGAACTGCCAGGTCTGTGTCTTATTTTCTTTGTCATTCTAATTTATCTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGG
ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTG
GGACTACAGGCGCCCGCCGCTACTCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTT
TTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGCACCTGGCCAAGTGTCTTCTTTTGAGAAGTGTCTGTTCATATACTTCACCCAC
TTTTTGATGGGGTTGTTTGTTTTTTTCTTGTAATTTTTGTTTGAGTTCATTGTAGATTCTGGATATTAGC
CCTTTGTCAGATGAGTACGTTGCAGAACTTTTCTCCC (SEQ ID NO: 260)

STS sY1189
Forward primer: TGGGCGAGGACTTTATGA (SEQ ID NO: 386)

Figure 7L

Reverse primer: GGGGTCCCAGTTCCACTATT (SEQ ID NO: 387)
Sequence:
TGGGCGAGGACTTTATGACTAAAACACCAAAAGCAATGGCAACAAAAGCCAAAATTGACAAATGGGATCT
AATTAAACTAAAGAGCTTCCGCACAGCAAAATAAACCACTGTCAGAGTGAATAGGCAACCTACAGAATGG
GAGAAAAGTTCTGCAACGTACTCATCTGACAAAGGGCTAATATCCAGAATCTACAATGAACTCAAACAAA
AATTACAAGAAAAAAACAAACAACCCCATCAAAAAGTGGGTGAAGTATATGAACAGACACTTCTCAAAAG
AAGACACTTGGCCAGGTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGAT
CACGAGGTCAGGAGATCGAGACCATCCCGGCTAAAAACGGTGAAACCCCGTCTCTACTAAAAATACAAAA
AATTAGCCGGGAGTAGCGGCGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATGGCGT
GAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCCCGCCACTGCACTCCAGCCTGGGCGACAGAGTGA
GACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATAAATTAGAATGACAAAG
AAAATAAGACACAGACCTGGCAGTTCTGCCTTTTAAGGGCCAGCCTCAGCCTAGTCACCGTGAATCACAA
TTTCAGGTTCTGCGTCAGCGTGTCCCACCTTGGAAAATAGTGGAACTGGGACCCC (SEQ ID NO: 261)

STS sY1125
Forward primer: GTGGGGGTTTCACATTATGG (SEQ ID NO: 388)
Reverse primer: GGTCACAGACTCACATTTAAGCA (SEQ ID NO: 389)
Sequence:
TGGGTTAGTGGATTTTGGGAGGCAGATGTGGAGATATAAAATGGGGCTAGATTATAGAGAATCTTCAAAG
TTAGCAAAGTTAAGATTTTGTGTAATAGGCAGTAGAGAGCTTGTGTAAGCTTTTTTATTCGAGATGAGCC
ATCTTGCAGACCACTGCTTAAGAAGACTGACTGTGGCAGTTTGCAGTGTGGAAGGGGGAAAGATGGTGAA
AGCTCCAAGTAGGAGGCTAGGGCTGCCATTCGTGGGTAAGATGAAGAGGACCAAGACAGTAGAGATGATA
TATAGATAATTGTAACCAAATCAGGAGTAATTGTTGGAACAGCATAACACATTTACATATTTGCTGATGT
AATTACTCAAGGGTCATATCATAAAAAGGGGTGGGGGTTTCACATTATGGAAACCTTGGAATTCTCTGTC
TTACGGTGGAAGACAGAACCCAGTGTAGTGTAGACAAAAGTCTAATTTTAATTCCCAGAGAAAGACTGAT
ATCTTATGGGACAAATTAGTATATTCCCATTCCTAATAATGGTGTACCTAGCTGGTGGGTAATTGCAGGC
TTTCAACCTCCAGTTCATCTTCATGAGATCAATGTTGATTCAGAACAATAAGTGTCAGGTCTATGACACC
TTTAAAGTTATGCTTAAATGTGAGTCTGTGACCACTAATGAATGACTACAGTTGTTTCATGACTTGCTAA
ACATACCTGGTTTTTCACAAGCAATAGATTTTTGAAGGAGAGGTATTCACAGTGGGTGCTAGGAAGATAC
ACACATTAATTCTGTAGAATTTAGCTAAAAT (SEQ ID NO: 262)

STS sY1054
Forward primer: ACCTAAGGGAACCCAGGAGA (SEQ ID NO: 390)
Reverse primer: CGACACTTTTGGGAAGTTTCA (SEQ ID NO: 391)
Sequence:
ACCTAAGGGAACCCAGGAGAACAGTGATTCAAAATTGAAAATATCAATAAAAATGTATGAATTATTTTGA
AAAATGAAATCAATAATCTGTAACTAGAAGGACTGAATAGCATGTGTGAGCATGTAGAAAGCCTAATGAG
GCAACTTGAAGATGGATTGTTTGATATTGTTCAGTGTAAGGAACAAGAAGAGAAACAAGAATAATGATCA
AAACTAAGGTTTCCATGGGACACCATCAAGAATATCAACATATTCATAATGGGAGTCCCACTGGAATAGG
TGAGATGGGGAAAAAAAGAATATTTAAATGAATAGTGGTTGAAACTTCCCAAAAGTGTCG (SEQ ID NO: 263)

STS sY1292
Forward primer: TGCCTGCCTCTGTAGACTCTG (SEQ ID NO: 392)
Reverse primer: TTCAGGTATACCAATCAGATGTCAC (SEQ ID NO: 393)
Sequence:
TGCCTGCCTCTGTAGACTCTGCCTGTGGGGGCAGGGCATAGCCAAACAAAAGGCAGCAGAAACCTATGCA
GACTTAAATATCTCTGTCTGACAGCTTTGAAGAAAATAGTGGTTCTCCCAGCACGCAGCTTGAAATCTCA
GAACAGACAGACTGCCTCTTCAAGTGGGTCCCTGAACCCCACATAGCCTAACTGGGAGGCACCCCCCAGT
AGCTGCAGACTGACACCTCACATGGCTGGGTACTCCTCTGAGGCAAAACTTCCAGAGGAACAATCAGCCA
GCAACATTTGCTGTTCACCAATATCTGCTGTTCTGCAGGCTCCGCCGCTGATACCCAGGGAAACAGGGTC
TGGAGTGGACCTCCAGCAAACTCCAACAGACCTGCAGCTGAGGGTCCTGACTGTTAGAAGGAAAACTAAC
AAACAGAAAGGACATCCACACCAAAACCCCATCTGTATGTCACCGTCATCAAAGACCAAAGGTAGATAAA
ACCACAAAGATTGGGAAAAAACAGAGCAGAAAAACTGGAAACTCTAAAAATCAGAACACCTCTCCTCCTC
CAAATGAACGCAGCTCCTTACCAGCAGTGGAACAAAGCTGGATGGAGAATGACTTTGACGTGTTGAAAGA
AGAAGGTTTCAGATGATCAAACTACTCCGAGCTAAAGGAGGAAGTTCGAACCCATGGCAAAGGAGCTGAA

Figure 7M

AACCTTGAAAAAAAAAATTAGATGAATGGCTAACTAGAATAACCAAAGCAGAGAAGCCCTTAAAGGACCT
GATGGAGCTGAAAACCATGGCACGAGAACTACGTGATGAACGCACAAGCCTCATTAGCCGATTTGATCAA
CTGGAAGAAAGGGTATCAGTGATGTAAGATTAAATGAATGAAATGAAGTGAGAAGAGAAGTTAAGAGAAA
AAAGAATAAAAAGAAATGAACAAAGCCTCCAAAAAATTTGGGACTATGTGAAAAGACCAAAGTGACATCT
GATTGGTATACCTGAA (SEQ ID NO: 264)

STS sY1289
Forward primer: TGTGCCACAGAAAACCAA (SEQ ID NO: 394)
Reverse primer: CCCATTTTGTAGGTTGCTTG (SEQ ID NO: 395)
Sequence:
TGTGCCACAGAAAACCAATTTTAAAAAACATACTCTCAGCTCTACTTAGTAAAAAATGAAAAAATTAATG
GTCATACTGCCCAAGGTAATTTATAGATTCAATGCCATCCCCATCAAGCTACCAAAGACTTTCTTCACTG
AATTGGAAAAAACTATTTTAAAGTTCATATAGAACCAAAAAAGAGCCCACATCACCAAGTCAATCCTAAG
CCAAAAGAACAAAGCTGGAGGCATCACGCTACCTGACTTCAAACTATACTACAAGGCTACAGTAACCAAA
ACAGCATGGTACTGGTACCAAAACAGAGATATAGATTAATGGAACAGAAAATAATGCCGCATATCTACAA
CTATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGGATTCCCTACTTAATAAATGGTGC
GGGGAAAACTGGCTAGCCATAGGTAGAAAGCTGAAACTGGATCCCTTCCTTACGCCTTACACAAAAATTA
ATTCAAGATGTATTAAAGACTTAAGCGTTAGACCTGAAACCATAAAAACCCGAGAAGAAAACCTAGGCAT
TACCATCCAGGACATAGGCATGGGCAAGGACTTCATGTCTAAAACACCAAAAGCAATGGCAACAAAAGCC
AAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTCTGCACAGCAAAAGAAACTACCATCAGAGTGA
ACAAGCAACCTACAAAATGGG (SEQ ID NO: 265)

STS sY1290
Forward primer: TGAGCTTAGACCCGGAAAG (SEQ ID NO: 396)
Reverse primer: TGTCCTGGATGGTAATGCC (SEQ ID NO: 397)
Sequence:
TGAGCTTAGACCCGGAAAGCTCTGGATGCAAGGCTCAGTCCTCTCTTCTGCAGAAAAGAGTCATGACCTA
ATACTCTAGCCAGCTGCCCAGAGCCTTCTGTAATCCTAAACTGGCTAGCCATAGGTAGAAAGCTGAAACT
GGATCCCTTCCTTACGCCTTACACAAAAATTAATTCAAGATGTATTAAAGACTTAAGCGTTAGACCTGAA
ACCATAAAAACCCGAGAAGAAAACCTAGGCATTACCATCCAGGACA (SEQ ID NO: 266)

STS sY1257
Forward primer: AACAATCAGCCAGCAACATT (SEQ ID NO: 398)
Reverse primer: TACATGTGCCTACCACCACG (SEQ ID NO: 399)
Sequence:
AACAATCAGCCAGCAACATTTGCTGTTCACCAATATCTGCTGTTCTGCAGGCTCCGCCGCTGATACCCAG
GGAAACAGGGTCTGGAGTGGACCTCCAGCAAACTCCAACAGACCTGCAGCTGAGGGTCCTGACTGTTAGA
AGGAAAACTAACAAACAGAAAGGACATCCACACCAAAACCCCATCTGTATGTCACCGTCATCAAAGACCA
AAGGTAGATAAAACCACAAAGATTGGGAAAAAACAGAGCAGAAAAACTGGAAACTCTAAAAATCAGAGCA
AGCACTATGGGAGGCCATGGCAGGTGGATCACCTGAGGACAGGAGTTTGAGACCAGCCTGGCCAACATGG
TGAAATTCTGTCTCTACTAAAAGTACAAAAATTAGCCGGGCGTGGTGGTAGGCACATGTA (SEQ ID NO: 267)

STS sY1206
Forward primer: ATTGATCTCCTTGGTTCCCC (SEQ ID NO: 400)
Reverse primer: GACATGTGTGGCCAATTTGA (SEQ ID NO: 401)
Sequence:
CTGCGAAGAGAACTCTTCCTTACCCTTGGTCACGATAAGTATCTTTCTCTACAAACAAACTACTTCTGGG
CTTTCTGTGGCATTTTGGATATCTCTGAACAGCAGTTAAAGAGATTGGTGCTCTAACTTCACGAAAATAC
AGGAGGCAGAGATTGATCTCCTTGGTTCCCCCGCTTGCTGTCCTCTACGTTGGTTAGAAAAATTTGGTCA
AAGATGAAATCCACACTGGGAAGGCTCAGGTTGACTTTAGAAGATATGCTTGATTAAAAATGGTTTTTTT
TTTTTTTTGGTTCCATTACATTCTATGAGGAGGCAAGGAGGCAGGTCAACAGGTAGTGATCATTCAGCAA
GGTATATTAATGCCATAAACAAACAACACAGTACACAATGGTCTTGTGTTAACCTCACCTATACAAACTG
AGAGAGGCATTGAGCTTATCCTGGTCAAATTTTTTAATTTAGTGTGTTAAAAAAATCTTATAGCATAAAC
ATAAATTAAGAATTTTCCTGAATAGAAGTCACTGGTCAAATTGGCCACACATGTCTCTTCTATAAACAAA
ACTCCAGAATATATGGCAATGTCTAAAGAATTCTTGGTAAA (SEQ ID NO: 268)

Figure 7N

STS sY1201
Forward primer: CCGACTTCCACAATGGCT (SEQ ID NO: 402)
Reverse primer: GGGAGAAAAGTTCTGCAACG (SEQ ID NO: 403)
Sequence:
CCGACTTCCACAATGGCTGAACTAGTTTACAGTCCCACCAACAGTGTAAAAGTGTTCTTATTTCTCCACA
TCCTCTCCAGCACCTGTTGTTTCCTGACTTTTTAATGATCGCCATTCTAACTGGTGTGAGATGGTATCTC
ATTGTGGTTTTGATTTGCATTTCTCTGATGGCCAGTGATGGTGAGCATTTTTTCATGTGTTTTTTGGCTG
CATAAGTGTCTTCTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTG
CAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCC
CAAGTAGCTGGGACTACAGGCGCCCGCCACTACTCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGG
TTTCACCGTTTTTAGCCGGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAG
TGCTGGGATTACAGGCGTGAGCCACCGCACCTGGCCAAGTGTCTTCTTTTGAGAAGTGTCTGTTCATATA
CTTCACCCACTTTTTGATGGGGTTGTTTGTTTTTTTCTTGTAATTTTTGTTTGAGTTCATTGTAGATTCT
GGATATTAGCCCTTTGTCAGATGAGTACGTTGCAGAACTTTTCTCCC (SEQ ID NO: 269)

STS sY1245
Forward primer: ATTCCACTCCATTCCACTGC (SEQ ID NO: 404)
Reverse primer: TAATGTCATGGCCTCCCTTC (SEQ ID NO: 405)
Sequence:
ATTCCACTCCATTCCACTGCGCTCCATTCCTCTCCACTCCATCGTATTCCATTTTTTCCCATTCCATTCC
ATTCCACTCCTTTCCACTCTGCTCCACTCCACTCCTCTCCATTCAATTCTATTCCACCCCATTCCTTTCC
ACTCCATTCTACTCCACTCCACTTCACTGTATTCCATTTGATTTCATTCAATGCCATTCGAATCCATTTG
ATTCGATTCCATTCGATTCCATTTGATTTCATTTTTATGTATGGTAGATATACATAAAATATATATGTTT
GAATATACATCAATTTCTATGTAATAAACATGTATATCGCCGTTATGTTTTGCCAGACAGTGATCAAAGC
ACTTTCTTCCCAAAGATAGATGAATTCTACTGTTCTCCCAAATATTTGTTAGCTTCTAAAATATACACAT
TTTGCTATCATATATACCAGGTTGGTGGGCAGGTGTGGTGTTTCATGCCTGTAATCCCAGGACTTTGGAA
GGGAGGCCATGACATTA (SEQ ID NO: 270)

STS sY1246
Forward primer: ATCGTTTTGAATGGCGTCAA (SEQ ID NO: 406)
Reverse primer: CTGCACCACTCCAATCCAA (SEQ ID NO: 407)
Sequence:
ATCGTTTTGAATGGCGTCAAATGAAATGGCATGGAAGGCAGTGAATTGGAGTGGAGTGGAATAGAGAGGA
ATGAATTGGAATGGAGTGTAGTGGAATAGAGTGGATTCCAGTGGAGTGGAGTGGATTGGATTGGAATGGA
ATGGAATAGATTGGATTGGAGTGGTGCAG (SEQ ID NO: 271)

STS sY1166
Forward primer: AGTCGGAGTCGGAGTGTGAT (SEQ ID NO: 408)
Reverse primer: ATTCCATTGCTTTCCATTGC (SEQ ID NO: 409)
Sequence:
AGGAATGGAATGGGATGGAGTGGAATGGAGTGGAGTGGAGTGCAGTGGAGTGGAGAGGAGTGGAATAGAG
TGGAATGGAATAGGATGTAATGGAATGTAGAGGAGTGGAGTGGAGTCGGAGTCGGAGTGTGATGGAATGT
AATGGAAAGGAATGGAATGCAATTGAATGCAAAGAAATGGAAAGTTGACATGTAATGTGACCTGAGATTG
TGCCACTGCACTCCAGCCTCTGTGACAGAGTGAGATCCTTTGGAAAGAAAGGAACGGAATGGTATGGAAT
GGAGTGGAGTAGAGTGGAGTGGAATGGAATGGAATGGAATGCAATGGAAAGCAATGGAATGCAATGGAAT
AGAATGCAGTGAAAAGGAAAGTTGACATGTAATGTGAGCAGAGATTGTGCCACTGCACTCCAGCCTGGGT
GACACAGTGATATCCTGTCAAAAGAAAGGAATGGAATGCAA (SEQ ID NO: 272)

STS sY1273
Forward primer: GAGCTGCAACATAACAGGCA (SEQ ID NO: 410)
Reverse primer: AGGGGAACATCACACTCTGG (SEQ ID NO: 411)
Sequence:
GAGCTGCAACATAACAGGCACTATAAATGAATGAATGGATAAAGACAGCACTGAAGAACTTGAAATTATA
GTTTACACATGTAAACAGTAACATAAATCTGAAGAAATAAAGTTTTTTTTTGTTGTTTTTTCGAGATGGA

Figure 7O

GTCTCGCTCTGTCACCAGGCTGGAGTGCAGTGGTGCAATCTGGCCTCACTGCAACCTCCGCCTCCCGGGT
TCAAGCGATTCCCCTGCCTCAGCCTCAGCGTCCCAAGTAGCTAGGACTCCAGGCACGTGCCACTACGCCT
GGTTATTTTTCTTTCTTTCTTTTTATTGTATTTTAGTAGAGATGGGTTTCACTATATTGGCCAAGACGGT
CTCAATCTCCTGACCTTGTGATCTGCCTGCCTCATCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
CGGGCCTGGCCAAGTTGTTGTTGTTGTTGTTGTTGTTGTTTTTATTATACTCTAAGTTTTAGGTTAC
ATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGACATGCTGGTGCGCTGCATCCACTAACTC
ATCATCTAGCATTAGGTATATCTCCCAATGCTATCCCTCCCCCTCCACCCACCCCACCACAGTCCCCAGA
GTGTGATGTTCCCCT (SEQ ID NO: 273)

Figure 7P

Plus/Minus-STS Results Distinguishing Different Types of Deletions Involving *AZFc*

	Result at STS[a]					
Deletion	sY142	sY1197	sY1191, sY1192, and/or 50f2/C	sY1291	sY1206	sY1201
b2/b3[b]	+	+	−	+	+	+
gr/gr	+	+	+	−	+	+
b1/b3	+	−	−	−	+	+
b2/b4[c]	+	+	−	−	−	+
None	+	+	+	+	+	+

[a] + = present; − = absent.
[b] Termed the "g1/g3" deletion by Fernandes et al. (2004).
[c] "Classical" *AZFc*.

Note.-See Kuroda-Kawaguchi, T., et al., "The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men," *Nat. Genet.*, 29:279–286 (2001); Repping S., et al., "Polymorphism for a 1.6-Mb deletion of the human Y chromosome persists through balance between recurrent mutation and haploid selection," *Nat. Genet.*, 35:247–251 (2003); Skaletsky H., et al., "The malespecific region of the human Y chromosome is a mosaic of discrete sequence classes," *Nature*, 423:825–837 (2003); Fernandes S., et al., "A large AZFc deletion removes DAZ3/DAZ4 and nearby genes from men in Y haplogroup N," *Am. J. Hum. Genet.*, 74:180–187 (2004); Repping S., et al., "A family of human Y chromosomes has dispersed throughout northern Eurasia despite a 1.8-Mb deletion in the azoospermia factor c region," *Genomics*,(advance online publication) (2004).

Figure 8

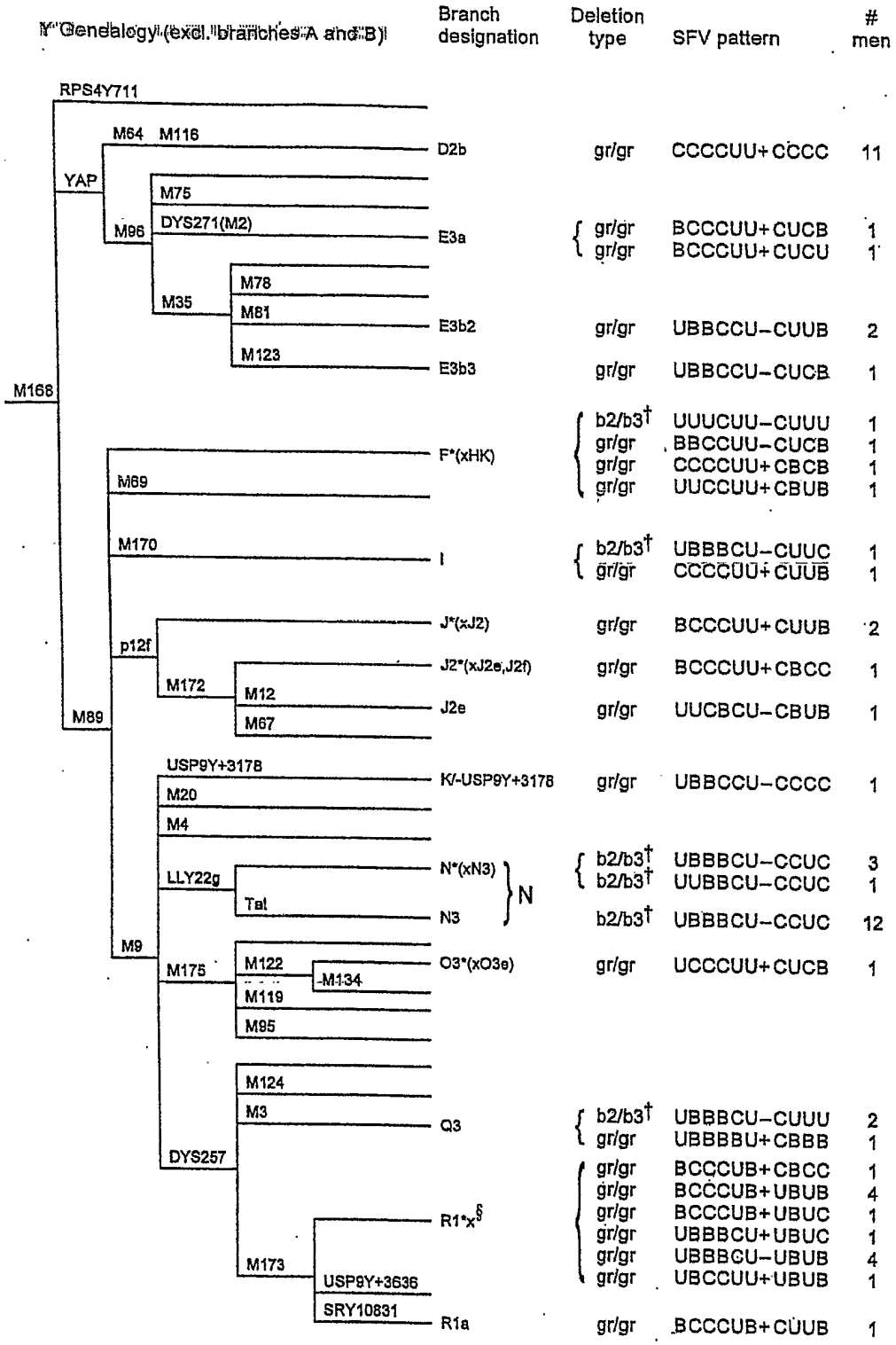
Y Genealogy (excl. branches A and B)
Branch designation
Deletion type
SFV pattern
men
RPS4Y711
M64
M116
YAP
M75
M96
DYS271(M2)
M76
M35
M81
M123
M168
M69
M170
M89
p12f
M172
M12
M67
USP9Y+3178
M20
M4
LLY22g
Tat
M9
M175
M122
M134
M119
M95
M124
M3
DYS257
M173
USP9Y+3636
SRY10831
D2b
E3a
E3b2
E3b3
F*(xHK)
I
J*(xJ2)
J2*(xJ2e,J2f)
J2e
K/-USP9Y+3178
N*(xN3)
N3
N
O3*(xO3e)
Q3
R1*x§
R1a
gr/gr CCCCUU+CCCC 11
gr/gr BCCCUU+CUCB 1
gr/gr BCCCUU+CUCU 1
gr/gr UBBCCU-CUUB 2
gr/gr UBBCCU-CUCB 1
b2/b3† UUUCUU-CUUU 1
gr/gr BBCCUU-CUCB 1
gr/gr CCCCUU+CBCB 1
gr/gr UUCCUU+CBUB 1
b2/b3† UBBBCU-CUUC 1
gr/gr CCCCUU+CUUB 1
gr/gr BCCCUU+CUUB 2
gr/gr BCCCUU+CBCC 1
gr/gr UUCBCU-CBUB 1
gr/gr UBBCCU-CCCC 1
b2/b3† UBBBCU-CCUC 3
b2/b3† UUBBCU-CCUC 1
b2/b3† UBBBCU-CCUC 12
gr/gr UCCCUU+CUCB 1
b2/b3† UBBBCU-CUUU 2
gr/gr UBBBBU+CBBB 1
gr/gr BCCCUB+CBCC 1
gr/gr BCCCUB+UBUB 4
gr/gr BCCCUB+UBUC 1
gr/gr UBBBCU+UBUC 1
gr/gr UBBBCU-UBUB 4
gr/gr UBCCUU+UBUB 1
gr/gr BCCCUB+CUUB 1

Figure 9