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权利要求书2页 说明书14页

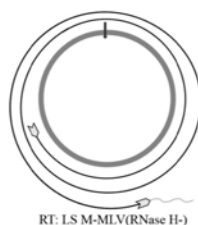
序列表16页 附图8页

(54) 发明名称

一种环形RNA全长鉴定方法及其试剂盒

(57) 摘要

本发明涉及分子生物学领域,涉及一种环形RNA全长鉴定方法及其试剂盒,包括以下步骤: S1. Splice junction序列分析和环形RNA全长序列的对比预测; S2. 设计CD Primers和Sjod Primers; S3. LS逆转录反应: 取0.1~1 μg抽提的总RNA加入N6 Random Primer, RNase-Free H₂O混合得反应液I; 然后向反应液I中加入5x LS RT Buffer, 将LS Enzyme Mix加入反应液I中, 得到cDNA; S4. PCR扩增和PCR产物分析; S5. Sanger测序和交叉分析对比序列。



1. 一种环形RNA全长鉴定方法,其特征在于,包括以下步骤:

S1. Splice junction序列分析和环形RNA全长序列的对比预测:首先在UCSC genome blast中对比,确认Splice junction序列对应的AG-GT剪切位点,然后在UCSC genome browser中对比,获得对应的基因组DNA序列,并在Ensembl中对比,获得预测的转录环形RNA全长序列;

S2. 设计CD Primers和Sjod Primers:使用软件设计引物在已知序列中搜索得到40bp的引物可选区,从数据库中获得环形RNA的序列和Splice junction序列,选用21~40bp作为正向引物,将1~20bp的序列反向互补后作为反向引物得CD Primers;将Splice junction位置的上游20bp和下游10bp共30bp序列输入引物设计软件中,搜索计算以使引物符合GC含量、Tm值常规的参数要求,从而得到Sjod的上游引物,所述Sjod的上游引物包含上述Splice junction位置的不少于上游13bp和不多于下游7bp的序列,接着根据上游引物的参数和位置使用软件自动设计得到一条Sjod下游引物,获得Sjod Primers;

S3. LS逆转录反应:抽提样品中的总RNA,取0.1~1 μ g抽提的总RNA加入N6 Random Primer, RNase-Free H₂O混合,在温度为60~70 $^{\circ}$ C反应5~10min,迅速冰浴2~3min,得反应液I;然后向反应液I中加入5x LS RT Buffer,将LS Enzyme Mix加入反应液I中,在温度为20~30 $^{\circ}$ C条件下反应5~10min,升温至50~60 $^{\circ}$ C条件下反应60~65min,再升温至80~90 $^{\circ}$ C条件下反应5~10min得到cDNA;所述LS Enzyme Mix包括逆转录酶LS M-MLV和RNase Inhibitor,所述逆转录酶LS M-MLV基因序列如SEQ ID NO.1;所述逆转录酶LS M-MLV删除了RNase H结构域;所述逆转录酶LS M-MLV突变体为 Δ N23/D108R/T306L/V433K/ Δ aa524-551;

S4. PCR扩增和PCR产物分析:使用步骤S2得到的CD Primers、Sjod Primers和步骤S3得到的cDNA进行扩增,得PCR产物,将PCR产物进行琼脂糖凝胶电泳分析,得直接扩增条带和滚环产物条带;

S5. Sanger测序和交叉分析对比序列:将步骤S4取得的直接扩增条带回收后直接进行Sanger测序,滚环产物条带回收后连接至pMD19T载体中进行Sanger测序;交叉对比CD Primers或Sjod Primers的直接扩增条带序列与滚环产物条带序列,所述直接扩增条带序列确认和验证Splice junction位置的序列,所述滚环产物条带序列中两个Splice junction位点之间为环形RNA的真实全长序列。

2. 根据权利要求1所述的环形RNA全长鉴定方法,其特征在于,所述步骤S3中逆转录中反应液I的组成包括:

实验材料体积

总RNA	0.1~1 μ g
N6 Random Primer	0.5 μ L
RNase-Free H ₂ O	Up to 14 μ L

所述步骤S3中LS逆转录中cDNA的组成包括:

实验材料体积

反应液I	14 μ L
LS Enzyme Mix	2 μ L
5 \times LS RT Buffer	4 μ L。

3. 根据权利要求1所述的环形RNA全长鉴定方法,其特征在于,所述步骤S3中取0.1~1 μ g抽提的总RNA加入N6 Random Primer,RNase-Free H₂O混合,在温度为65 $^{\circ}$ C反应5min,迅速冰浴2min,得反应液I。

4. 根据权利要求1所述的环形RNA全长鉴定方法,其特征在于,所述步骤S3中将LS Enzyme Mix加入反应液I中,在温度为25 $^{\circ}$ C条件下反应5min,升温至55 $^{\circ}$ C条件下反应60min,再升温至85 $^{\circ}$ C条件下反应5min得到cDNA。

一种环形RNA全长鉴定方法及其试剂盒

技术领域

[0001] 本发明涉及分子生物学领域,尤其是涉及一种环形RNA全长鉴定方法及其试剂盒。

背景技术

[0002] 环形RNA(circular RNAs, 环形RNAs)是一类具有闭合环状结构的RNA分子,在多物种中广泛存在,比线性RNA更稳定。

[0003] 目前研究多使用circBase等数据库及自有样品的高通量测序获得环形RNA信息,并筛选得到待研究的环形RNA后进行PCR检测、cDNA/gDNA分别扩增验证和RNase R消化等实验验证和确认其真实存在。但这些验证都是基于环形RNA的环化位点接头(Splice junction)序列进行的,缺乏对环化位点内部真实全长序列的鉴定验证,因此极易导致检测的真实准确性失真,特别是对于序列内部有多个外显子且存在可变剪切的情况。例如(Yibing Yang et al..Novel Role of FBXW7 Circular RNA in Repressing Glioma Tumorigenesis.J Natl Cancer Inst.2018 Mar 1;110(3))中通过PCR扩增和Sanger测序确定FBXW7的exon3和exon4经反向剪切形成620nt的环形RNA,而不是circBase数据库里收录hsa_circ_0001451的1227nt,可见不对环形RNA真实全长序列进行鉴定时极易导致基因识别错误、检测和验证失真。

[0004] 使用circBase等数据库及自有样品的高通量测序获得环形RNA信息中参考序列的注释也局限于技术本身和分析方法。1)高通量测序的reads长度在150nt左右,不能测到环形RNA的真实全长序列。2)环形RNA Junction reads的筛选鉴定和注释是mapping到参考基因组与GenBank数据集中分析的,仅通过已知线性基因的对比分析确定环形RNA全长的参考序列,且以对比匹配最高的转录本作为环形RNA的全长序列,无法区别鉴定外显子的可变剪切和线性基因与环形RNA可能不同的外显子组合。3)来自两条或更多pre-mRNA的剪切会因反式剪切(trans-splicing)形成tsRNA(trans-spliced RNA),这类tsRNA可能和环形RNA有相同的Splice Junction序列,导致环形RNA的筛选识别出现假阳性。

[0005] 因此急需开发一种环形RNA全长鉴定方法,对circBase已收录或新发现的环形RNA都进行全长鉴定以确定其真实的全长序列。

发明内容

[0006] 针对现有技术存在的不足,本发明的目的第一在于提供一种环形RNA全长鉴定方法,解决了环形RNA鉴定验证和研究中容易出现的识别错误、检测和验证失真等问题。

[0007] 为实现上述目的,本发明提供了如下技术方案:

[0008] 一种环形RNA全长鉴定方法,包括以下步骤:

[0009] S1.Splice junction序列分析和环形RNA全长序列的对比预测:首先在UCSC genome blast中对比,确认Splice junction序列对应的AG-GT剪切位点,然后在UCSC genome browser中对比,获得对应的基因组DNA序列,并在Ensembl中对比,获得预测的转录环形RNA全长序列;

[0010] S2.设计CD Primers和Sjod Primers:使用软件设计引物在已知序列中搜索得到40bp的引物可选区,从数据库中获得环形RNA的序列和Splice junction序列,选用21~40bp作为正向引物,将1~20bp的序列反向互补后作为反向引物得CD Primers;将Splice junction位置的上游20bp和下游10bp共30bp序列输入引物设计软件中,搜索计算以使引物符合GC含量、Tm值常规的参数要求,并使包含不少于上游13bp和不多于下游7bp的序列,从而得到Sjod的上游引物,接着根据上游引物的参数和位置使用软件自动设计得到一条Sjod下游引物,获得Sjod Primers;

[0011] S3.LS逆转录反应:抽提各类组织、细胞、血液、体液、外泌体、口腔拭子、肺泡灌洗液样品的总RNA,取0.1~1 μ g抽提的总RNA加入N6 Random Primer,RNase-Free H₂O混合,在温度为60~70℃反应5~10min,迅速冰浴2~3min,得反应液I;然后向反应液I中加入5x LS RT Buffer,将LS Enzyme Mix加入反应液I中,在温度为20~30℃条件下反应5~10min,升温至50~60℃条件下反应60~65min,再升温至80~90℃条件下反应5~10min得到cDNA;

[0012] S4.PCR扩增和PCR产物分析:使用步骤S2得到的CD Primers、Sjod Primers和步骤S3得到的cDNA进行扩增,得PCR产物,将PCR产物进行琼脂糖凝胶电泳分析,得直接扩增条带和滚环产物条带;

[0013] S5.Sanger测序和交叉分析对比序列。

[0014] 优选地,所述LS Enzyme Mix包括逆转录酶LS M-MLV (RNase H-) 和RNase Inhibitor,所述逆转录酶LS M-MLV (RNase H-) 突变体为 Δ N23/D108R/T306L/V433K/ Δ aa524-551,所述逆转录酶LS M-MLV (RNase H-) 基因序列如SEQ ID NO.1。

[0015] 优选地,所述步骤S3中逆转录中反应液I的组成包括:

实验材料	体积
总 RNA	Up to 13.5 μ L (0.1~1 μ g)
[0016] N6 Random Primer	0.5 μ L
RNase-Free H ₂ O	Up to 14 μ L

[0017] 所述步骤S3中LS逆转录中cDNA的组成包括:

实验材料	体积
反应液 I	14 μ L
[0018] LS Enzyme Mix	2 μ L
5 \times LS RT Buffer	4 μ L

[0019] 优选地,所述步骤S3中取0.1~1 μ g抽提的总RNA加入N6 Random Primer,RNase-Free H₂O混合,在温度为65℃反应5min,迅速冰浴2min,得反应液I。

[0020] 优选地,所述步骤S3中将LS Enzyme Mix加入反应液I中,在温度为25℃条件下反应5min,升温至55℃条件下反应60min,再升温至85℃条件下反应5min得到cDNA。

[0021] 优选地,所述PCR产物采用琼脂糖凝胶浓度为1.5~2%进行电泳分析。

[0022] 优选地,所述步骤S5中,将步骤S4取得的直接扩增条带回收后直接进行Sanger测序,滚环产物条带回收后连接至pMD19T载体中进行Sanger测序。

[0023] 优选地,所述步骤S5中,交叉对比CD Primers或Sjod Primers的直接扩增条带序

列与滚环产物条带序列,所述直接扩增条带序列确认和验证Splice junction位置的序列,所述滚环产物条带序列中两个Splice junction位点之间为环形RNA的真实全长序列。

[0024] 本发明的目的第二在于提供一种试剂盒,包括逆转录试剂和PCR扩增试剂,所述逆转录试剂包含LS Enzyme Mix、5×LS RT Buffer、N6 Random Primer和RNase-Free H₂O;所述PCR扩增试剂包含2×HS Taq Mix和RNase-Free H₂O。

[0025] 优选地,所述LS Enzyme Mix包含200U/μL LS M-MLV (RNase H⁻)、40U/μL RNase Inhibitor、RNase-Free H₂O和50%甘油;所述5×LS RT Buffer包含150mM pH8.3为Tris-HCl、375mM KCl、15mM MgCl₂、10mM dNTP和20mM DTT;所述2×HS Taq Mix包含2.5U/μL HS Taq Polymerase、10mM dNTP、125mM pH8.3为Tris-HCl、15mM MgCl₂、250mM KCl、500mM Glycine betaine、0.15%Tween-20、5%DMSO和10%甘油。

[0026] 本发明利用逆转录酶M-MLV的天然模板置换活性,通过点突变设计实现高度热稳定性和超强结合力,并删除RNase H结构域,避免逆转录过程中模板链的消化。改造优化的逆转录酶LS M-MLV (RNase H⁻)可以在55~60℃进行LS逆转录处理,能更好地打开环形RNA的二级结构,获得更高的得率和产量。天然模板置换活性和超强结合力的特性配合优化的反应体系与条件,并降低随机引物浓度,使对环形RNA模板逆转录时的链结合效率和逆转录效率大大增加,得到大量滚环逆转录的产物,即一条cDNA链中有多个Splice junction相连接,为PCR扩增得到环形RNA真实全长序列提供可能。

[0027] 本发明综合使用CD Primers和Sjod Primers两类反向引物,使用CD Primers扩增可能的环形RNA序列组合,同时参考Splice junction设计Sjod Primers以扩增特异的待鉴定环形RNA,两类引物的结果通过交叉对比和分析,能高效快速确定环形RNA的真实全长序列。其中CD Primers的PCR产物中包含一个Splice junction,Sjod Primers的直接扩增条带序列中包含一个Splice junction,Sjod Primers的滚环产物条带序列中包含两个Splice junction。CD Primers的PCR产物或Sjod Primers的直接扩增条带可以验证Splice junction位置的序列,Sjod Primers的滚环产物条带序列中两个Splice junction位点之间即为环形RNA的真实全长序列。

[0028] 由图2知,①为CD Primers的PCR产物示意线,②为Sjod Primers的直接扩增条带示意线,③为Sjod Primers的滚环产物条带示意线。

[0029] 与现有技术相比,本发明具有以下有益效果:

[0030] 本发明的环形RNA全长鉴定方法能对组织、细胞、血液、体液、外泌体、口腔拭子、肺泡灌洗液等各类样品抽提的总RNA直接进行鉴定,无需额外的RNase R消化等处理,简便易行,实验设计和分析方法标准规范,配套的全长鉴定试剂盒体系稳定,适用范围广,能使研究者更简单高效地获得环形RNA的真实全长序列。本发明的环形RNA全长鉴定方法能高效特异地鉴别鉴定环形RNA外显子的可变剪切以及线性基因与环形RNA不同的外显子组合,并能精确到单碱基的差异,最准确真实地获得环形RNA全长序列,保证环形RNA的识别、检测和验证精准可靠。

附图说明

[0031] 图1为本发明一种环形RNA全长鉴定方法的LS逆转录流程示意图;

[0032] 图2为本发明CD Primers或Sjod Primers和PCR产物的示意图;

- [0033] 图3为本发明环形RNAhsa_circ_0007928的Splice junction序列对应的AG-GT剪切位点；
- [0034] 图4为本发明环形RNAhsa_circ_0007928的PCR产物电泳检测图；
- [0035] 图5为226bp条带Sanger测序峰图；
- [0036] 图6为KFR1条带Sanger测序峰图；
- [0037] 图7为F2KR条带Sanger测序峰图；
- [0038] 图8为本发明环形RNAhsa_circ_0007928的测序结果交叉对比示意图；
- [0039] 图9为本发明环形RNArno_novel5139的Splice junction序列对应的AG-GT剪切位点；
- [0040] 图10为本发明环形RNArno_novel5139在Ensembl中对比结果示意图；
- [0041] 图11为本发明环形RNArno_novel5139的PCR产物电泳检测图；
- [0042] 图12为F2R2条带Sanger测序峰图；
- [0043] 图13为F1R1条带Sanger测序峰图；
- [0044] 图14为本发明环形RNArno_novel5139的测序结果交叉对比示意图；
- [0045] 图15为本发明环形RNAm9_circ_007585的Splice junction序列对应的AG-GT剪切位点；
- [0046] 图16为本发明环形RNA mm9_circ_007585在Ensembl中对比结果示意图；
- [0047] 图17为本发明环形RNAm9_circ_007585的PCR产物电泳检测图；
- [0048] 图18为本发明环形RNA F1R1条带Sanger测序峰图；
- [0049] 图19为F2KR条带Sanger测序峰图；
- [0050] 图20为本发明环形RNAm9_circ_007585的测序结果交叉对比示意图；

具体实施方式

- [0051] 以下结合附图及实施例,对本发明作进一步详细说明。
- [0052] 如本文所用,除非特别注明,其他实验方法都可采用本领域中的常规方法,例如参考《分子克隆实验指南(第四版)》(科学出版社,2017)。
- [0053] 所述LS Enzyme Mix包括逆转录酶LS M-MLV (RNase H-) 和RNase Inhibitor,所述逆转录酶LS M-MLV (RNase H-) 突变体为 Δ N23/D108R/T306L/V433K/ Δ aa524-551,所述逆转录酶LS M-MLV (RNase H-) 基因序列如SEQ ID NO.1;
- [0054] 其中N6 Random Primer为合成的寡核苷酸5' -N₆-3', 浓度50 μ M。
- [0055] 实施例1
- [0056] 在本实施例中,环形RNA参考circBase数据库中hsa_circ_0007928序列和Splice junction序列。
- [0057] 从circBase数据库中下载hsa_circ_0007928的参考序列389nt如SEQ ID NO.2;
- [0058] 从circBase数据库中获得hsa_circ_0007928的Splice junction序列100nt如下: 5' -CTGAAGGCATGGAGAAATTTTGTGAAGACATTGGTGTGAACCAGAAAAC-3' -5' -ATTTTCAGCTGAATC TCATCTCTCAACTGGCAAATATTCATAAGATC-3' 。
- [0059] 一种环形RNA全长鉴定方法,包括以下步骤:
- [0060] S1.Splice junction序列分析和环形RNA全长序列的对比预测:首先在UCSC

genome blast中对比,确认Splice junction序列对应的AG-GT剪切位点(参考图3),然后在UCSC genome browser中对比,获得对应的基因组DNA序列,并在Ensembl中对比,获得预测的转录环形RNA全长序列;

[0061] S2.设计CD Primers和Sjod Primers:利用Clone Mgr Suite软件对参考的389nt序列分别设计CD Primers和Sjod Primers,其中一些引物可以共用,将序列发送至生工生物进行合成,PAGE纯化。

[0062] CD Primers:

[0063] C7928-TZ-F1:TGCGGTCTTGCAGTTCTTCAGA

[0064] C7928-TZ-R1:GACTTCCTGTTTGGTGATCGTC

[0065] 扩增大小389bp,或389+n*389bp

[0066] C7928-TZ-F2:CCTGCCTCTGGAGATGATTTA

[0067] C7928-TZ-R2:GTCTTCTCTTTTCCTTGGTGGC

[0068] 扩增大小390bp,或390+n*389bp

[0069] Sjod Primers:

[0070] C7928-TZ-KF:GTTGAACCAGAAAACATTTTC

[0071] C7928-TZ-R1:GACTTCCTGTTTGGTGATCGTC

[0072] 扩增大小132bp,滚环产物扩增大小521bp

[0073] C7928-TZ-F2:CCTGCCTCTGGAGATGATTTA

[0074] C7928-TZ-KR:GAGTTCAGCTGAAAATGTTTTC

[0075] 扩增大小226bp,滚环产物扩增大小615bp

[0076] S3.RNA抽提和LS逆转录反应:使用Trizol Reagent抽提人食管癌细胞系ECA109的总RNA,然后进行LS逆转录处理。逆转录反应体系和程序如下:

[0077] ①按表1配置反应液,在温度为65℃反应5min,迅速冰浴2min。

[0078] 表1 LS逆转录步骤①

	试剂	体积
[0079]	ECA109 RNA	2.5 μL (1 μg)
	N6 Random Primer	0.5μL
	RNase-Free H ₂ O	11μL

[0080] ②按表2配置反应液,反应条件25℃反应5min,升温至55℃反应60min,再升温至85℃反应5min。

[0081] 表2 LS逆转录步骤②

	试剂	体积
[0082]	① 的反应液 I	14 μL
	LS Enzyme Mix	2 μL
	5× LS RT Buffer	4 μL

[0083] S4.PCR扩增和PCR产物分析:以ECA109cDNA为模板,使用四对引物分别进行PCR扩增,反应体系如表3所示。反应程序温度为95℃反应5min,40循环(95℃30s,58℃30s,72℃80s),温度为72℃反应5min,得PCR产物。

[0084] 表3 PCR扩增反应体系

	试剂	体积
	2× HS Taq Mix	25 μL
[0085]	ECA109 cDNA	1 μL
	Primer-F (10 μM)	2 μL
	Primer-R (10 μM)	2 μL
	RNase-Free H ₂ O	20 μL

[0086] 根据预测环形RNA长度和预期扩增的PCR产物大小,选用合适的琼脂糖凝胶浓度,预测环形RNA长度低于750nt时,使用2%的浓度,预测cirRNA长度大于750nt时,使用1.5%的浓度,对PCR产物进行琼脂糖凝胶电泳分析,根据条带大小分析辨别预期的直接扩增条带和滚环产物条带,结果见图4。

[0087] 结果显示F1/R1和F2/R2的扩增产物条带有较多杂带,KF/R1和F2/KR的产物条带大小符合预期,其中132bp和226bp为直接扩增条带,KFR1和F2KR为滚环产物条带。分别标记为KFR1、F2KR和226bp并回收。

[0088] S5.Sanger测序和交叉分析对比序列。

[0089] 回收直接扩增条带226bp并直接进行Sanger测序,结果验证hsa_circ_0007928的Splice junction序列与预期一致,测序峰图如5。

[0090] 回收滚环产物条带KFR1,连接至pMD19T载体中进行Sanger测序,得到测序序列如下,测序峰图如6,显示521bp条带内有C7928-TZ-KF和C7928-TZ-R1引物序列,并有两个环化剪切位点,两个剪切位点之间的序列即为hsa_circ_0007928的真实全长序列。下划线标记为目的基因的全长序列。

[0091] 如:

[0092] >GZ19011701145 (KFR1) M13-48_J_G11

[0093] TTGGCACGCCTGCCGTTTCGACGATTGTTGAACCAGAAAACATTTTCAGCTGAACTCT
CATCTCTCAAACTGGCAAATATTCATAAGATCTACCACACCCTTAATAAGCTGAACCTA
ACAGAAGACATTGGCCAAGACGATCACCAAACAGGAAGTCTGCGGTCTTGCAGTTCT
TCAGACTGCTTTAATAAAGTGATGCCACCAAGGAAAAAGAGAAGACCTGCCTCTGGA
GATGATTTATCTGCCAAGAAAAGTAGACATGATAGCATGTATAGAAAATATGATTCGACT
AGAATAAAGACTGAAGAAGAAGCCTTTTCAAGTAAAAGGTGCTTGGAAATGGTTCTATG

AATATGCAGGAACTGATGATGTTGTAGGCCCTGAAGGCATGGAGAAATTTTGTGAAGA
CATTGGTGTGTAACCCAGAAAACCTCTCATCTCTCAACACTGGCAAATATTCATAAGATC
 TACCACACCCTTAATAAGCTGAACCTAACAGAAGACATTGGCCAAG**ACGATCACAA**
ACAGGAAGTCAATCTCTGGAAGATCCGCGCGTACCGAGTTCTAATTCACTGGCCGTCG
 TTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGC
 [0094] ACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC
 CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCA
 TCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGC
 ATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGT
 CTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTC
 AGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGC

[0095] 回收滚环产物条带F2KR,连接至pMD19T载体中进行Sanger测序,得到测序序列如下,测序峰图如7,显示615bp条带内有C7928-TZ-F2和C7928-TZ-KR引物序列,并有两个环化剪切位点,两个剪切位点之间的序列即为hsa_circ_0007928的真实全长序列。加粗标记为引物序列,下划线标记为目的基因的全长序列。

[0096] 如:>GZ19011701148 (F2KR) M13-48_J_B12

AGGGCAGGAACATGATTACGCCAGTTTGCACGCCTGCCGTTTCGACGATT**CCTGCTCT**
GGAGATGATTTATCTGCCAAGAAAAGTAGACATGATAGCATGTATAGAAAATATGATTC
 GACTAGAATAAAGACTGAAGAAGAAGCCTTTTCAAGTAAAAGGTGCTTGGAAATGGTTC
 TATGAATATGCAGGAACTGATGATGTTGTAGGCCCTGAAGGCATGGAGAAATTTTGTGA
 AGACATTGGTGTGTAACCCAGAAAACATTTTCAGCTGAACTCTCATCTCTCAACACTGG
CAAATATTCATAAGATCTACCACACCCTTAATAAGCTGAACCTAACAGAAGACATTGGC
CAAGACGATCACAAACAGGAAGTCTGCGGTCTTGCAGTTCTTCAGACTGCTTTAATA
AAGTGATGCCACCAAGGAAAAAGAGAAGACCTGCCTCTGGAGATGATTTATCTGCCAA
 [0097] GAAAAGTAGACATGATAGCATGTATAGAAAATATGATTTCGACTAGAATAAAGACTGAAG
AAGAAGCCTTTTCAAGTAAAAGGTGCTTGGAAATGGTTCTATGAATATGCAGGAACTGAT
GATGTTGTAGGCCCTGAAGGCATGGAGAAATTTTGTGAAGACATTGGTGTGTAACCA
AAAACATTTTCAGCTGAACTCAATCTCTGGAAGATCCGCGCGTACCGAGTTCTAATTC
 ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAAT
 CGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCG
 ATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
 CTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGC
 TCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCT
 GACGGGC

[0098] 参见图8,交叉对比226bp条带Sanger测序得到的Splice junction序列和KFR1与F2KR条带Sanger测序得到的全长序列,分析得到hsa_circ_0007928的真实全长序列389nt如SEQ ID NO.3。

[0099] 实施例2

[0100] 高通量测序得到rno_novel5139的Splice junction序列;

[0101] S1.Splice junction序列分析和环形RNA全长序列的对比预测;

[0102] 已知rno_novel5139的Splice junction序列如下。

[0103] >rno_novel5139_junction_seq

[0104] ACTGGTGGCCATCCTGTTGTGAAGATCTTGAACCAGATGATTGTGCAT

[0105] 在UCSC genome blast中对比,确认rno_novel5139的Splice junction序列对应的AG-GT剪切位点如图9。

[0106] 在UCSC genome browser中对比,获得对应的基因组DNA序列如SEQ ID NO.4。

[0107] 参考图10,在Ensembl中对比,显示rno_novel5139与Nfatc3基因序列重叠,预测rno_novel5139包含两个外显子,其参考全长序列1301nt如SEQ ID NO.5。

[0108] S2.设计CD Primers和Sjod Primers:利用Clone Mgr Suite软件对参考的1301nt序列分别设计CD Primers和Sjod Primers,其中一些引物可以共用,将序列发送至生工生物进行合成,PAGE纯化。

[0109] CD Primers:

[0110] rno5139-YZ-F2:AACAGTATGGACCTGGACATT

[0111] rno5139-YZ-R1:TGTGGTAAGCCAAGTGATGAA

[0112] 扩增大小810bp,或 $810+n*1301$ bp

[0113] rno5139-YZ-F2:AACAGTATGGACCTGGACATT

[0114] rno5139-YZ-R2:ATACTGTTGATGCCAGGACTC

[0115] 扩增大小1309bp,或 $1309+n*1301$ bp

[0116] Sjod Primers:

[0117] rno5139-YZ-F1:CATCCTGTTGTGAAGATCTTG

[0118] rno5139-YZ-R1:TGTGGTAAGCCAAGTGATGAA

[0119] 扩增大小103bp,滚环产物扩增大小1404bp

[0120] S3.RNA抽提和LS逆转录反应:使用Trizol Reagent抽提大鼠肝脏组织的总RNA,然后进行LS逆转录处理。逆转录反应体系和程序如下:

[0121] 按表4配置反应液,反应条件 $65^{\circ}\text{C}5\text{min}$,迅速冰浴 2min 。

[0122] 表4 LS逆转录步骤①

	试剂	体积
[0123]	rno RNA	3.1 μL (1 μg)
	N6 Random Primer	0.5 μL
	RNase-Free H ₂ O	10.4 μL

[0124] 按表5配置反应液,反应条件 $25^{\circ}\text{C}5\text{min}$, $55^{\circ}\text{C}60\text{min}$, $85^{\circ}\text{C}5\text{min}$ 。

[0125] 表5LS逆转录步骤②

	试剂	体积
[0126]	② 的反应液	14 μL
	LS Enzyme Mix	2 μL
	5 \times LS RT Buffer	4 μL

[0127] S4.PCR扩增和PCR产物分析:

[0128] 以rno cDNA为模板,使用三对引物分别进行PCR扩增,反应体系如表6所示。反应程序95℃5min,40循环(95℃30s,58℃30s,72℃180s),72℃5min。

[0129] 表6PCR扩增反应体系

	试剂	体积
	2× HS Taq Mix	25 μL
[0130]	rno cDNA	1 μL
	Primer-F (10 μM)	2 μL
	Primer-R (10 μM)	2 μL
	RNase-Free H ₂ O	20 μL

[0131] 根据预测环形RNA长度和预期扩增的PCR产物大小,选用合适的琼脂糖凝胶浓度,预测环形RNA长度低于750nt时,使用2%的浓度,预测cirRNA长度大于750nt时,使用1.5%的浓度,对PCR产物进行琼脂糖凝胶电泳分析,根据条带大小分析辨别预期的直接扩增条带和滚环产物条带。

[0132] 电泳检测结果如图11,结果显示F2/R1扩增产物条带大小错误,可能是非特异扩增。F2/R2和F1/R1的产物条带大小符合预期,其中103bp为直接扩增条带,F2R2和F1R1为滚环产物条带。分别标记为F2R2和F1R1并回收。

[0133] 如图12,回收滚环产物条带F2R2并直接进行Sanger测序,结果验证rno_novel5139的Splice junction序列与预期一致。回收滚环产物条带F1R1,连接至pMD19T载体中进行Sanger测序,得到测序序列如下,测序峰图如图13,显示1404bp条带内有rno5139-YZ-F1和rno5139-YZ-R1引物序列,并有两个环化剪切位点,两个剪切位点之间的序列即为rno_novel5139的真实全长序列。加粗标记为引物序列,下划线标记为目的基因的全长序列。

[0134] >GZ18061302232 (5139-F1R1) M13+_-

TGGAAAATTGGACATGGATTACGCCAGTTTGCACGCCTGCCGTTTCGACGATT**CATCCT**
GTTGTGAAGATCTTGAACCAGATGATTGTGCATCCATTTACATCTTTAATGTAGACCCG
 CCTCCATCTACTTTAAATTCATCACTTGGCTTACCACATCATGGACTGCTGCAGTCTCAC
 TCTTCTGTTTTGTCACCATCATTTTCAGCTCCAAGGTTTCAAAAATTATGAAGGAACTGA
 TGATATTTCTGAATCTAAATATAGCTCATTAAAGTGGTCCTAAACCCTTTGAATGCCAAG
 TATCAAATTACATCCATCTCTCCTAACTGTCATCAAGAAACAGATGCTCATGAAGATGA
 CCTACATGTAAATGACCCAGAAAGGGAATATTGGAAAGGCCTTCTAGAGATCATCTCT
 ATCTCCCACCTTGAACCGTCCTACCGGGAATCTTCCCTTAGTCCTAGTCCTGCCAGCAGC
 GTTTCTTCTAGGAGTTGGTTCTCAGATGCATCTTCTTGTGAGTCTCTCTCACACATTTAT
 GACGATGTGGACTCAGAGTTGAATGAAGCTGCTGCACGATTTACTCTTGGCTCACCTCT
 GACTTCTCCAGGTGGCTCTCCAGGAGGTTGCCCTGGAGAAGAGTCCTGGCATCAACA
 GTATGGACCTGGACATTCCTTGTACCTAGGCAATCTCCTTGCCACTCTCCTAGATCCA
 GTATCACTGATGAGAATTGGCTGAGCCCCAGACCAGCCTCAGGACCCTCATCCAGGCC
 CACTTCTCCTTGTGGTAAACGACGGCACTCCAGTGCTGAAGTATGTTATGCTGGCTCTC
 TTTCACCCCATCACTCACCTGTTCCGTCCCCTGGTCACTCGCCTAGAGGGAGTGTA
 ACTGAAGATACCTGGCTCACTGCTCCTGTCCACACTGGATCAGGCCTCAGCCCTGCACCGT
 TTCCATTTCACTACTGTGTAGAGACTGACATCCCTTTGAAAACAAGGAAGACTTCTGA
 CGATCAAGCTGCCATACTACCAGGAAAATTAGAGGTCTGTTTCAGATGATCAAGGGAGC
 TTATCCCATCCCAGGAGACATCAGTAGATGATGGCCTTGGATCTCAGTATCCTTTAAAG
 AAAGATTCATCTGGTGACCAATTTCTTTCAGTTCCCTTCACCTTTTACCTGGAGCAAACC
 AAAGCCTGGCCACACTCCTATATTTTCGCACATCTTCATTACCTCCATTAGACTGGCCTTT
 ACCAACTCACTTTGGACAATGTGAATTGAAAATAGAAGTGCAACCTAAAACCTACCCAT
 AGAGCCCATTATGAAACTGAAGGTAGCCGAGGGCAGTGAAAGCCTCTACTGGTGGC
 CATCCTGTTGTGAAGATCTTGAACCAGATGATTGTGCATCCATTTACATCTTTAATGTAG
 ACCCGCCCCATCTACTTTAAAT**TCATCACTTGGCTTACCACA**AATCTCTGGAAGATC
 CGCGCGTACCGAGTTCTAATCACTGCCGTTT

[0136] S5. Sanger测序和交叉分析对比序列

[0137] 如图14,交叉对比F2R2条带Sanger测序得到的Splice junction序列和F1R1带Sanger测序得到的全长序列,分析得到rno_novel5139的真实全长序列1301nt如SEQ ID NO.6。

[0138] 实施例3

[0139] 从circBase数据库中获取mm9_circ_007585的参考序列和Splice junction序列;

[0140] S1.Splice junction序列分析和环形RNA全长序列的对比预测:从circBase数据库中下载mm9_circ_007585的参考序列449bp如下,如SEQ ID NO.7;

[0141] 从circBase数据库中获得mm9_circ_007585的Splice junction序列100bp如下:

[0142] 5'-TGGACAGCCTGGCTTGGCTACTCATTCTTCTGTAAACAGGGTCCTGGCAG-3' -5'-GAGGCTGCTGGAGTCTTCCCTCATTTTCATTATCCCGTTATGATGGAGCAG-3'

[0143] 在UCSC genome blast中对比,确认mm9_circ_007585的Splice junction序列对应的AG-GT剪切位点如图15。

[0144] 在UCSC genome browser中对比,获得对应的基因组DNA序列如下,如SEQ ID NO.8。

[0145] 如图16,在Ensembl中对比,显示mm9_circ_007585与Ambra1基因序列重叠,预测

mm9_circ_007585最多包含四个外显子,按最长序列预测其参考全长序列449nt如下,如SEQ ID NO.9。

[0146] S2.设计CD Primers和Sjod Primers:利用Clone Mgr Suite软件对参考序列分别设计CD Primers和Sjod Primers,其中一些引物可以共用,将序列发送至生工生物进行合成,PAGE纯化。

[0147] CD Primers:

[0148] mc7585-YZ-F1:AATCGGCTTCGTTCTTCCACCTCC

[0149] mc7585-YZ-R1:ATTCTGTTGGTAGCGCATGGAGC

[0150] 扩增大小452bp,或452+n*449bp

[0151] Sjod Primers:

[0152] mc7585-YZ-F2:CTGCACCTTCACTTGGACGATT

[0153] mc7585-YZ-KR:AAGACTCCAGCAGCCTCCTGC

[0154] 扩增大小149bp,滚环产物扩增大小598bp。

[0155] S3.RNA抽提和LS逆转录反应:使用Trizol Reagent抽提小鼠NC1469细胞系的总RNA,然后进行LS逆转录处理。逆转录反应体系和程序如下:

[0156] 按表7配置反应液,反应条件65℃5min,迅速冰浴2min。

[0157] 表7 LS逆转录步骤①

	试剂	体积
[0158]	NC1469 RNA	1.3 μ L (1 μ g)
	N6 Random Primer	0.5 μ L
	RNase-Free H ₂ O	12.2 μ L

[0159] 按表8配置反应液,反应条件25℃5min,55℃60min,85℃5min。

[0160] 表8 LS逆转录步骤②

	试剂	体积
[0161]	③ 的反应液	14 μ L
	LS Enzyme Mix	2 μ L
	5 \times LS RT Buffer	4 μ L

[0162] S4.PCR扩增和PCR产物分析:

[0163] 以NC1469 cDNA为模板,使用两对对引物分别进行PCR扩增,反应体系如表9所示。反应程序95℃5min,40循环(95℃30s,58℃30s,72℃90s),72℃5min。

[0164] 表9 PCR扩增反应体系

	试剂	体积
[0165]	2× HS Taq Mix	25 μL
	NC1469 cDNA	1 μL
	Primer-F (10 μM)	2 μL
	Primer-R (10 μM)	2 μL
	RNase-Free H ₂ O	20 μL

[0166] 根据预测环形RNA长度和预期扩增的PCR产物大小,选用合适的琼脂糖凝胶浓度,预测环形RNA长度低于750nt时,使用2%的浓度,预测cirRNA长度大于750nt时,使用1.5%的浓度,对PCR产物进行琼脂糖凝胶电泳分析,根据条带大小分析辨别预期的直接扩增条带和滚环产物条带。

[0167] 电泳检测结果如图17,结果显示F1/R1和F2/KR的产物条带大小符合预期,其中149bp为直接扩增条带,F2KR为滚环产物条带。分别标记为F1R1和F2KR并回收。

[0168] S5. Sanger测序和交叉分析对比序列

[0169] 如图18,回收F1R1条带并直接进行Sanger测序,结果验证mm9_circ_007585的Splice junction序列与预期一致。

[0170] 回收滚环产物条带F2KR,连接至pMD19T载体中进行Sanger测序,得到测序序列如下,测序峰图如图19,显示598bp条带内有mc7585-YZ-F2和mc7585-YZ-KR引物序列,并有两个环化剪切位点,两个剪切位点之间的序列即为mm9_circ_007585的真实全长序列。加粗标记为引物序列,下划线标记为目的基因的全长序列。

[0171] >GZ17122700658 (7585-F2KR) M13-47_J_C01

GGGGCATGCGTAGTGATTAGACTCGGTACGCGCGGATCTTCCAGAGATTCTGCAC
CTTCACTTGGACGATTTGTTCCAAGGCGTTTTTTTGGCTGCCTGAGTACTTGCCTTATGC
 TGGGATTTTTTCATGAACGTGGACAGCCTGGCTTGGCTACTCATTCTTCTGTAAACAGGG
 TCCTGGCAGGAGGCTGCTGGAGTCTTCCCTCATTTCATTATCCC GTTATGATGGAGCAG
GATCCAGAGAGCACCCAATTTACCCAGACCCAGCGAGATTATCTCCTGCTGCATACTAC
GCCCAGAGGATGATCCAGTATCTCTCAAGGAGAGACAGTATTCGCCAGCGCTCCATGC
GCTACCAACAGAATCGGCTTCGTTCTTCCACCTCCTCTTCTTCTCAGACAACCAGGGT
CCATCAGTAGAGGGAACCGACTTGGAATTTGAGGACTTTGAGGACAATGGTGACAGAT
CTAGGCACCGAGCTCCCCGAAATGCCCGAATGTCTGCACCTTCACTTGGACGATTTGTT
 [0172] CCAAGGCGTTTTTTTGGCTGCCTGAGTACTTGCCTTATGCTGGGATTTTTTCATGAACGTGG
ACAGCCTGGCTTGGCTACTCATTCTTCTGTAAACAGGGTCCTGGCAGGAGGCTGCTG
GAGTCTTAATCGTCGAACGGCAGGCGTGCAAACTTGGCGTAATCATGGTCATAGCTGT
 TTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATA
 AAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC
 ACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA
 CGCGCGGGGAGAGGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT
 CGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAT
 ACGGTTATCC

[0173] 如图20,交叉对比F1R1条带Sanger测序得到的Splice junction序列和F2KR条带Sanger测序得到的全长序列,分析得到mm9_circ_007585的真实全长序列449nt如SEQ ID NO.10。

[0174] 实施例4

[0175] 一种鉴定环形RNA全长序列的试剂盒,所述试剂盒包括逆转录试剂和PCR扩增试剂和使用说明,所述逆转录试剂包含LS Enzyme Mix、5×LS RT Buffer、N6 Random Primer和RNase-Free H₂O;所述PCR扩增试剂包含2×HS Taq Mix和RNase-Free H₂O。

[0176] 所述LS Enzyme Mix包含200U/μL LS M-MLV (RNase H⁻)、40U/μL RNase Inhibitor、RNase-Free H₂O和50%甘油;所述5×LS RT Buffer包含150mM pH8.3为Tris-HCl、375mM KCl、15mM MgCl₂、10mM dNTP和20mM DTT;所述2×HS Taq Mix包含2.5U/μL HS Taq Polymerase、10mM dNTP、125mM pH8.3为Tris-HCl、15mM MgCl₂、250mM KCl、500mM Glycine betaine、0.15%Tween-20、5%DMSO和10%甘油。

[0177] 使用说明给出了所述试剂盒的使用方法和鉴定环形RNA真实全长序列的标准化实验设计和分析方法,为全长鉴定中的逆转录、序列分析和全长序列的对比预测、引物设计、PCR扩增与电泳检测、sanger测序及序列分析,提供指导、指引或教导。

[0178] 本具体实施方式的实施例均为本发明的较佳实施例,并非依此限制本发明的保护

范围,故:凡依本发明的结构、形状、原理所做的等效变化,均应涵盖于本发明的保护范围之内。

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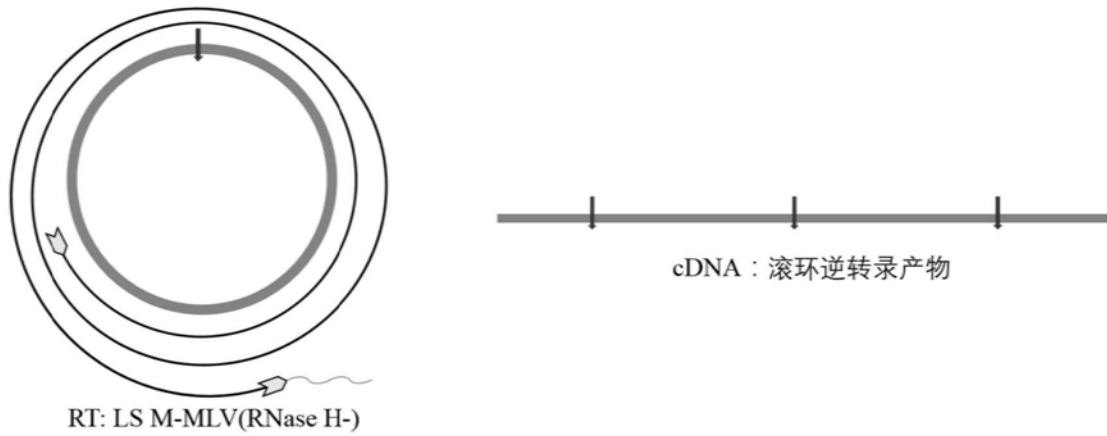


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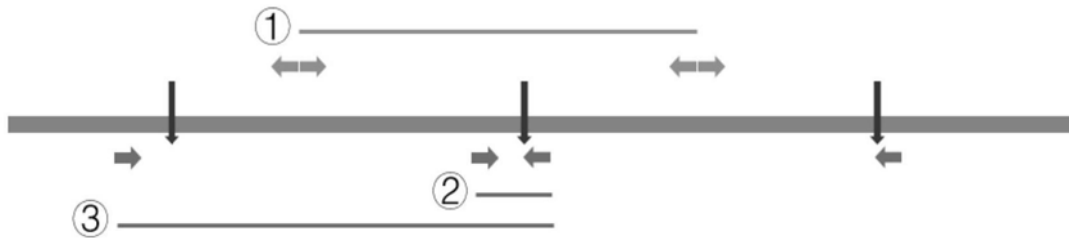


图2

Genomic chr4 :

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图3

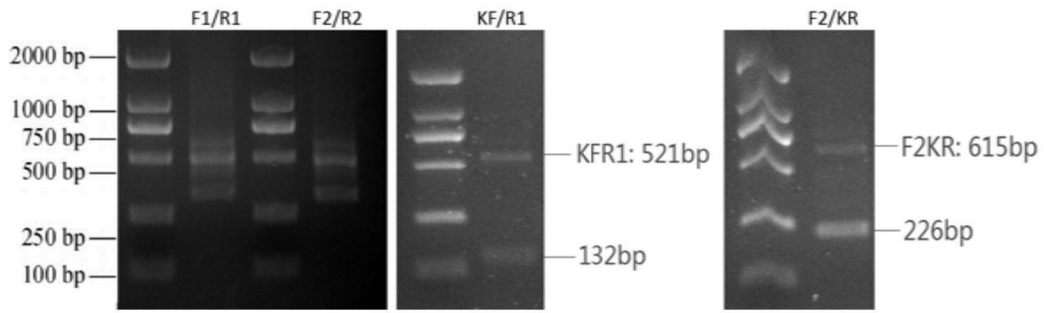


图4

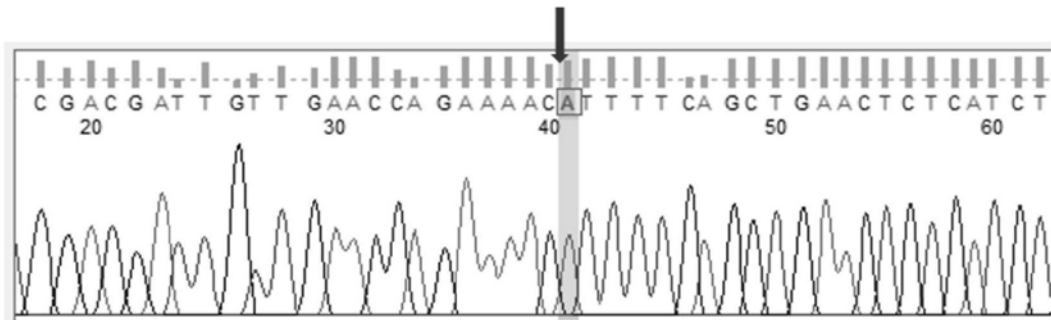


图5

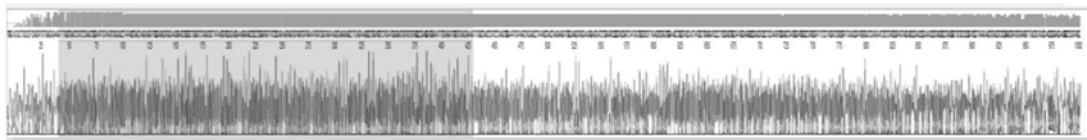


图6

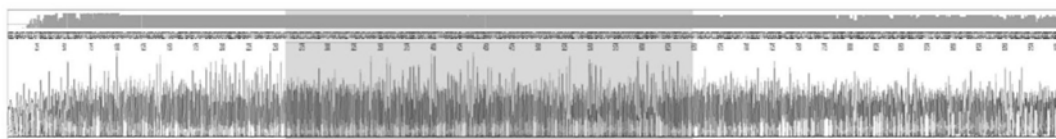


图7

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1 -----
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图8

Genomic chr19 :

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图9

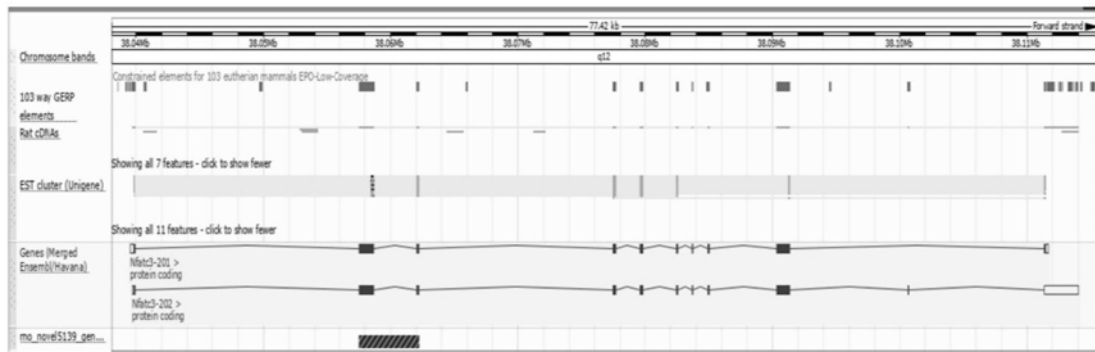


图10

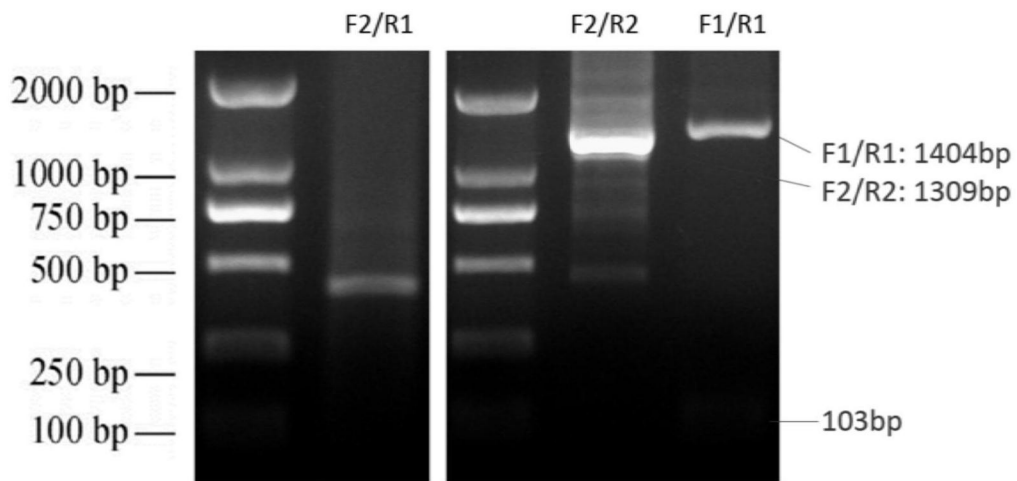


图11

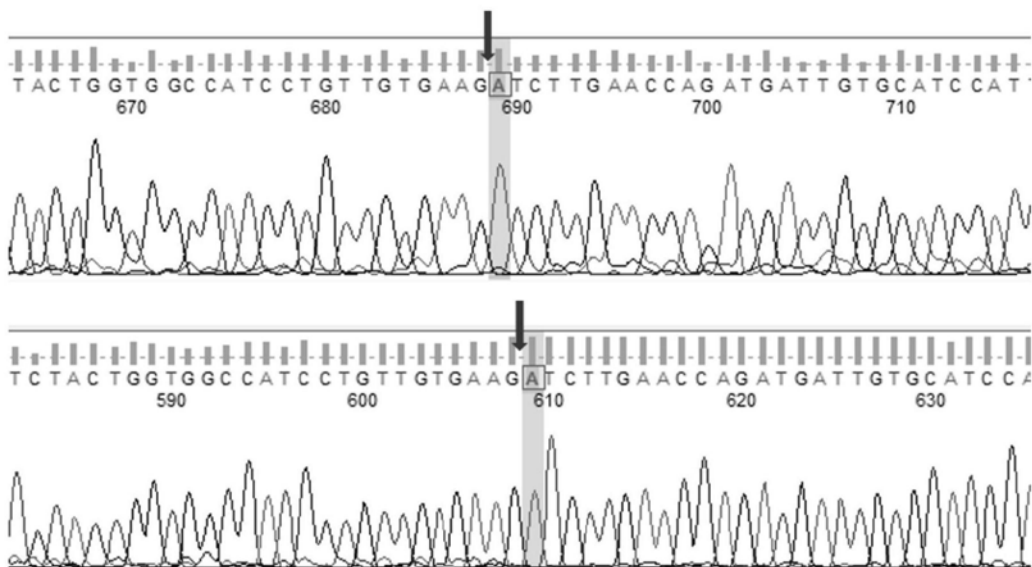


图12

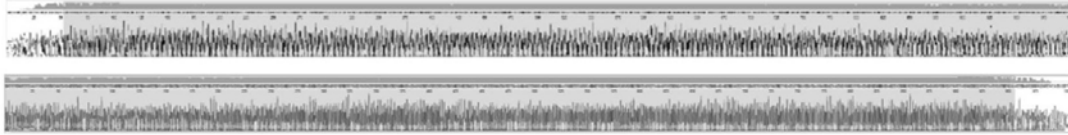


图13

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1302 -----

```

图14

Genomic chr3 :

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GATCCAGAGA GCACCCAATT TACCCAGACC CAGCGAGgta aggccaaaat 80713837
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aatctttagt tgactttcac atgtgattcc ttcttacagG CGTTTTTTCG 80732837
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图15

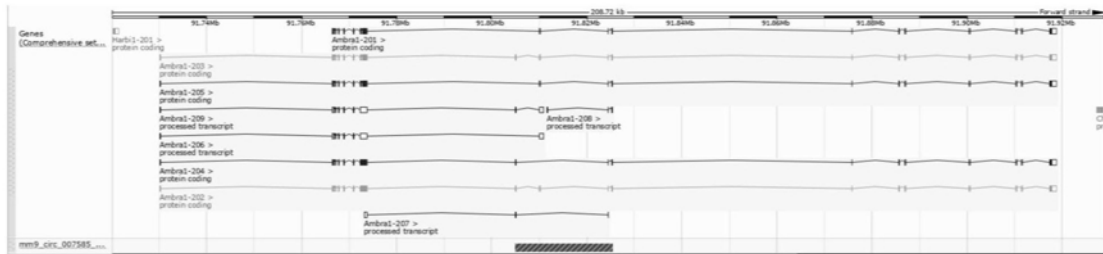


图16

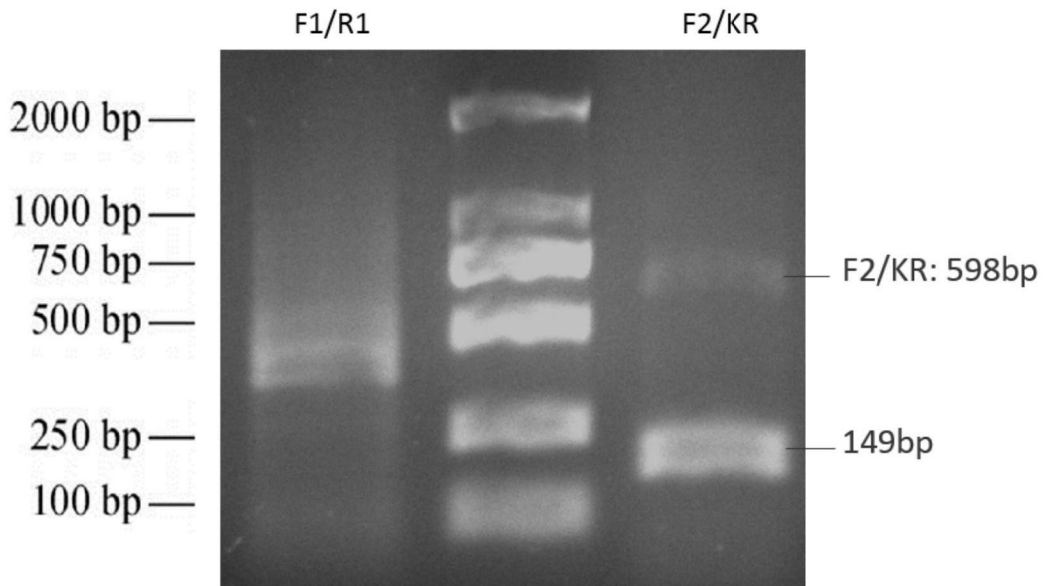


图17

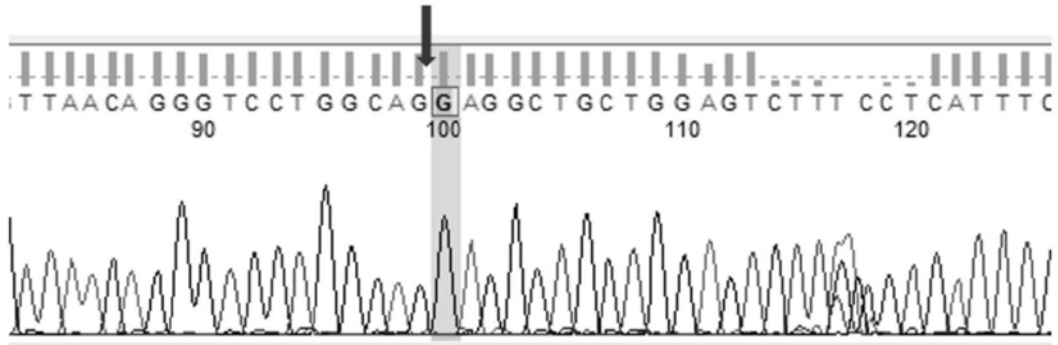


图18

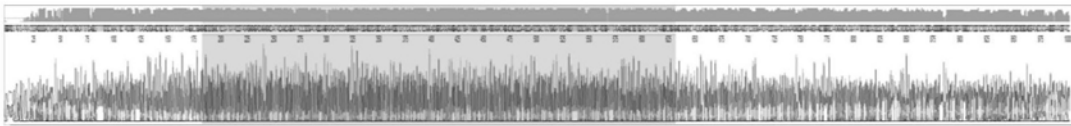


图19


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图20