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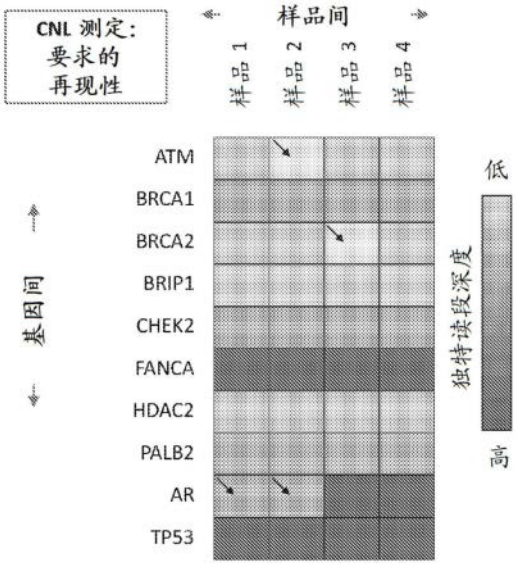
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(54)发明名称

用于检测DNA样品中基因组拷贝变化的方法

(57)摘要

本发明包括可用于检测细胞基因组DNA或无细胞DNA(cfDNA)的样品内的突变、SNP、易位、倒位、缺失、拷贝数变化或其他遗传变异的组合物和方法。在一些实施方案中,本发明的组合物和方法提供了极高水平的分辨率,其特别可用于检测来自生物样品(例如血液)的总cfDNA的一小部分中的拷贝数变异。



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1.用于从包含DNA片段的测试样品产生DNA文库的多种组合物,其中所述多种组合物包含一组衔接子,每种衔接子包含:

(i)扩增区,

(ii)样品标签区,和

(iii)锚定区;

其中所述的一组衔接子的每种衔接子的样品标签区包含多核苷酸序列,其中所述多核苷酸序列识别所述测试样品,并且其中所述多核苷酸序列识别独特DNA文库片段。

2.如权利要求1所述的多种组合物,其中所述的一组衔接子的每种衔接子包含选自独特样品标签区池的样品标签区,其中在所述独特样品标签区池的所有样品标签区中,包含所述样品标签区内的至少三个核苷酸的任何连续序列不是保守的。

3.如权利要求1所述的多种组合物,其中所述的一组衔接子的每种衔接子包含选自独特样品标签区池的样品标签区,其中所述独特样品标签区池选自多个池,并且其中所述池对所述测试样品是独特的。

4.包含多个DNA文库片段的DNA文库,其中所述DNA文库由测试样品产生,其中所述DNA文库片段各自包含衔接子和DNA片段,

其中所述衔接子选自一组衔接子并且包含:

(i)扩增区,

(ii)样品标签区,和

(iii)锚定区;

其中所述样品标签区包含多核苷酸序列,其中所述多核苷酸序列识别所述测试样品,并且其中所述多核苷酸序列识别独特DNA文库片段。

5.一组衔接子,其独特地识别包含DNA片段的测试样品,其中所述的一组衔接子的每种衔接子包含:

(i)扩增区,

(ii)样品标签区,和

(iii)锚定区;

其中所述样品标签区包含多核苷酸序列,其中所述多核苷酸序列识别所述测试样品,并且其中所述多核苷酸序列识别所述测试样品的独特DNA片段。

6.一种用于对来自包含多个DNA片段的测试样品的DNA靶区域进行遗传分析的方法,所述方法包括:

(a)通过使所述测试样品与一组衔接子接触来产生包含多个DNA文库片段的DNA文库,所述一组衔接子包含独特样品标签区池,其中所述DNA文库片段各自包含来自所述测试样品的DNA片段和衔接子,其中所述的一组衔接子的每种衔接子包含:

(i)扩增区;

(ii)包含多核苷酸序列的样品标签区,其中所述多核苷酸序列识别所述测试样品,并且其中所述多核苷酸序列识别独特DNA文库片段;和

(iii)锚定区;

以及

(b)对包含所述DNA靶区域的DNA文库片段进行定量遗传分析以检测指示疾病状态的遗

传变化。

7.如权利要求6所述的方法,包括使所述DNA文库与特异性结合所述DNA靶区域的多个捕获探针接触,从而在所述捕获探针和包含所述DNA靶区域的DNA文库片段之间形成复合物。

8.一种用于对来自测试样品的DNA靶区域进行遗传分析的方法,其包括:

(a)生成包含多个DNA文库片段的基因组DNA文库,其中所述DNA文库片段中的每一个包含来自所述测试样品的基因组DNA片段和衔接子;

(b)使所述基因组DNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的所述DNA文库片段之间形成复合物;以及

(c)对包含所述DNA靶区域的基因组DNA片段进行定量遗传分析;

其中所述衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;

其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;

其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;

其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段;并且

其中进行所述遗传分析以检测指示疾病状态的遗传变化。

9.一种用于高灵敏地检测拷贝数增加和拷贝数丢失的方法,其包括:

(i).测定针对捕获探针的RGD;

(ii).通过将针对所述捕获探针的RGD转换成探针特异性归一化读段计数,对实验组中所有样品中针对所述捕获探针的RGD进行归一化;

(iii).计算每个探针特异性归一化读段计数的近似拷贝数值;并且

(iv).对于针对靶向特异性基因的所有探针的近似拷贝数值取平均值。

10.一种用于测量染色体稳定性的方法,其包括:

(i).设计和验证一种或多种染色体稳定性探针的组,其中所述染色体稳定性探针均匀分布在人染色体上;

(ii).使用所述一种或多种染色体稳定性探针对患者样品进行靶向测序;

(iii).针对每种染色体探针测定近似拷贝数值;

(iv).测定患者样品的基因组表型,其中所述患者样品中针对一种或多种染色体探针的拷贝数值的波动表明基因组不稳定性。

用于检测DNA样品中基因组拷贝变化的方法

[0001] 相关申请的引用

[0002] 本申请是申请号为201780059053.2的中国专利申请的分案申请,并且要求2016年8月25日提交的美国临时专利申请号62/379,593和2017年4月4日提交的美国临时专利申请号62/481,538的优先权,将其各自通过引用以其全文并入本文。

[0003] 关于序列表的声明

[0004] 与本申请相关的序列表以文本格式代替纸质副本提供,并且特此通过引用并入本说明书中。包含序列表的文本文件的名称是CLFK_005_02WO_ST25。该文本文件为2,238KB,创建于2017年8月24日并通过EFS-Web以电子方式提交。

技术领域

[0005] 本发明总体上涉及用于生物样品例如直接组织活检或外周血的定量遗传分析的组合物和方法。特别地,本发明涉及用于检测生物样品的靶特异性拷贝数变化以及遗传表征和分析的方法。

[0006] 发明背景

[0007] 越来越明显的是,大多数(如果不是全部)最常见的人类癌症是人类基因组疾病。认为体细胞突变在个体的一生中会积累,其中一些体细胞突变会增加携带它们的细胞发展成肿瘤的可能性。由于积累的突变事件的错误组合,癌症前期生长失去了约束(这种约束能遏制不受控制的增殖)并且产生的细胞团块成为癌症。导致癌症所必需的且足以导致癌症的突变群通常统称为“驱动突变”。最近的密集分子分析中出现的主题之一是曾经被认为是一种单一的组织特异性疾病的癌症实际上是一组相关疾病,其中每种疾病都有独特的分子病理学。人类基因组计划为癌症的全基因组分析奠定了基础。

[0008] 基因拷贝数变化是生物多样性的基本驱动因素。在进化的背景下,基因的重复和功能的分化是物种多样性的公认驱动因素。在人类疾病的背景下,体细胞内的基因丢失和基因扩增是诸如癌症的患病组织的标志。某些治疗剂特异性地作用于具有这些基因组增加和/或丢失突变的细胞,然而,这些拷贝数变异的鉴定是困难的,因为这些突变通常仅存在于患病细胞或癌细胞的DNA中而在身体的其他细胞中不存在。虽然患病组织或细胞是突变DNA的主要来源,但通过活检获取DNA是侵入性的、有风险的并且通常是不可能的。观察到垂死的肿瘤或癌细胞将其小片DNA(称为无细胞DNA或循环DNA)释放至血流中,这允许开发能够用侵入性较小的技术诸如血液样品进行的基因测试。然而,从样品中分离无细胞DNA只能获得少量DNA,并且只有总DNA的一部分携带与所述疾病相关的突变。例如,在癌症基因组学的背景下,诊断上明显的肿瘤突变通常仅以显著小于50%的低等位基因频率发现。这与常规SNP基因分型形成对比,常规SNP基因分型中的等位基因频率通常为约100%、50%或0%。

[0009] 因此,需要能够检测特定靶基因座中的基因拷贝数变化的基因组技术。

发明内容

[0010] 检测cfDNA中罕见突变的方法先前已在国际PCT公开号WO 2016/028316中描述。然

而,这些技术仍然缺乏在极低等位基因频率下检测最罕见拷贝数丢失的必需灵敏度。本文提供了用于检测靶特异性拷贝数变化的组合物和方法,其适用于若干样品类型,包括直接组织活检、外周血以及特别是cfDNA。本文所述的组合物和方法的灵敏度足以检测出只存在于总DNA的一小部分中的拷贝数变化。

[0011] 本发明尤其包括可用于检测细胞基因组DNA(例如,来自组织活检样品)或cfDNA(例如,来自血液样品)的样品内的突变、SNP、易位、倒位、缺失、拷贝数变化或其他遗传变异的组合物和方法。特别地,本发明的组合物和方法提供了极高水平的分辨率,其特别可用于检测来自生物样品(例如血液)的总cfDNA的一小部分中的拷贝数变异。

[0012] 具体的实施方案涉及用于对来自测试样品的DNA靶区域进行遗传分析的方法,其包括:(a)生成包含多个DNA文库片段的基因组DNA文库,其中所述DNA文库片段中的每一个包含来自所述测试样品的基因组DNA片段和衔接子;(b)使所述基因组DNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成复合物;以及(c)对包含所述DNA靶区域的基因组DNA片段进行定量遗传分析;其中所述衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段;并且其中进行所述遗传分析以检测指示疾病状态的遗传变化。

[0013] 在一些实施方案中,所述指示疾病状态的遗传变化选自单核苷酸变异(SNV)、长度小于40个核苷酸的插入、长度小于40个核苷酸的DNA区域的缺失和/或拷贝数变化。在具体实施方案中,所述指示疾病状态的遗传变化是拷贝数变化。在一些实施方案中,所述测试样品是组织活检。在各种实施方案中,所述组织活检取自肿瘤或怀疑为肿瘤的组织。在某些实施方案中,所述基因组DNA是无细胞DNA(cfDNA)或细胞DNA。在具体实施方案中,所述基因组DNA是从所述测试样品分离的cfDNA;并且其中所述测试样品是选自由以下组成的组的生物样品:羊水、血液、血浆、血清、精液、淋巴液、脑脊液、眼内液、尿液、唾液、粪便、粘液和汗液。

[0014] 在某些实施方案中,由以下步骤获得所述基因组DNA片段,其包括:(i)从所述测试样品分离细胞DNA;以及(ii)使所述细胞DNA片段化以获得所述基因组DNA片段。在具体实施方案中,步骤(ii)是通过使所述细胞DNA与至少一种消化酶接触来进行的。在一些实施方案中,步骤(ii)是通过对所述细胞DNA施加机械应力来进行的。在某些实施方案中,通过超声处理所述细胞DNA来施加所述机械应力。

[0015] 在具体实施方案中,所述样品标签还包含有助于鉴定独特基因组DNA片段的独特分子标识符(UMI)。

[0016] 在一些实施方案中,所述扩增区的长度在10与50个核苷酸之间。在具体实施方案中,所述扩增区的长度在20与30个核苷酸之间。在某些实施方案中,所述扩增区的长度为25个核苷酸。

[0017] 在一些实施方案中,所述样品标签的长度在5与50个核苷酸之间。在具体实施方案中,所述样品标签的长度在5与15个核苷酸之间。在某些实施方案中,所述样品标签的长度为8个核苷酸。在一些实施方案中,UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。

[0018] 在某些实施方案中,所述UMI倍增器的长度在1与5个核苷酸之间。在具体实施方案中,所述UMI倍增器的长度为3个核苷酸,并且包含64个可能的核苷酸序列中的一个。

[0019] 在一些实施方案中,所述锚定区的长度在1与50个核苷酸之间。在具体实施方案中,所述锚定区的长度在5与25个核苷酸之间。在某些实施方案中,所述锚定区的长度为10个核苷酸。

[0020] 本发明的具体实施方案涉及以下方法,其中生成包含多个DNA文库片段的基因组DNA文库的步骤(a)包括将所述基因组DNA片段附接至多个衔接子。在某些实施方案中,在将所述基因组DNA片段与多个衔接子附接之前,对所述基因组DNA片段进行末端修复。在具体实施方案中,所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。

[0021] 在某些实施方案中,所述多个衔接子中的每个衔接子的样品标签区包含在2与1,000个核苷酸序列之间的一个核苷酸序列。在具体实施方案中,所述多个衔接子中的每个衔接子的样品标签区包含在50与500个核苷酸序列之间的一个核苷酸序列。在各种实施方案中,所述多个衔接子中的每个衔接子的样品标签区包含在100与400个核苷酸序列之间的一个核苷酸序列。在一些实施方案中,所述多个衔接子的每个衔接子的样品标签区包含在200与300个核苷酸序列之间的一个核苷酸序列。在某些实施方案中,所述多个衔接子中的每个衔接子的样品标签区的长度为8个核苷酸。在一些实施方案中,所述核苷酸序列中的每个序列与240个核苷酸序列中的任何其他序列相隔的汉明距离为至少二。

[0022] 在具体实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。在一些实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍增器。在某些实施方案中,所述多个衔接子中的每个衔接子的所述UMI倍增器的长度在1与5个核苷酸之间。在一些实施方案中,所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸。

[0023] 在具体实施方案中,所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0024] 在一些实施方案中,所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;所述多个衔接子中的每个衔接子的样品标签区的长度为8个核苷酸;每个样品标签的核苷酸序列与所述多个衔接子的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二;所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器;所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸;并且每个可能的核苷酸序列的UMI倍增器与所述多个衔接子的每个样品标签区配对;所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个;并且给定序列的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0025] 本发明的具体实施方案涉及一种方法,其中将基因组DNA片段与多个衔接子附接的步骤包括:(i)将包含锚定区的至少一部分的寡核苷酸附接至每个基因组DNA片段,其中包含锚定区的至少一部分的寡核苷酸是DNA双链体,所述DNA双链体包含与配偶体链双链化的5'磷酸化附接链,其中所述配偶体链通过在其3'端的化学修饰而被阻止附接,并且其中所述附接链附接至所述基因组DNA片段;(ii)使与包含所述锚定区的至少一部分的寡核苷酸附接的基因组DNA片段与编码所述多个衔接子中的每个衔接子核苷酸序列的全长衔接子

序列的DNA寡核苷酸接触;以及(iii)在适合于DNA连接的条件下,使所述基因组DNA片段和编码所述全长衔接子序列的DNA寡核苷酸与T4多核苷酸激酶、Taq DNA连接酶和全长Bst聚合酶接触;从而将所述多个衔接子附接至所述基因组DNA片段。在一些实施方案中,所述基因组DNA片段是cfDNA。在某些实施方案中,分析DNA靶区域的拷贝数变化。

[0026] 在具体实施方案中,对包含所述DNA靶区域的基因组DNA片段进行定量遗传分析的步骤(c)包括对在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成的复合物进行纯化。在某些实施方案中,步骤(c)包括对在捕获探针与包含DNA靶区域的DNA文库片段之间形成的复合物进行纯化,从而预形成包含来自所述基因组DNA文库的目标区域的DNA文库片段的引物延伸和/或扩增。在一些实施方案中,步骤(c)包括对在捕获探针与包含DNA靶区域的DNA文库片段之间形成的复合物进行纯化,从而预形成包含来自所述基因组DNA文库的目标区域的DNA文库片段的引物延伸和扩增。在某些实施方案中,步骤(c)包括对所述包含DNA靶区域的DNA文库片段进行DNA测序,以生成多个测序读段。

[0027] 在一些实施方案中,本发明涉及一种方法,其中所述基因组分析包括测定目标DNA区域中的拷贝数变化,并且其中步骤(c)对所述包含DNA靶区域的基因组DNA片段进行定量遗传分析包括测定源自所述测试样品的基因组DNA文库中存在的目标区域的拷贝数,以及将其与源自参考样品的基因组DNA文库中存在的目标区域的拷贝数进行比较,其中所述参考样品包含已知拷贝数目的DNA靶区域。

[0028] 在一些实施方案中,测定所述目标区域中的拷贝数包括对包含DNA靶区域的DNA文库片段进行DNA测序,以生成多个测序读段,其中每个测序读段包含独特分子标识元件(UMIE)。在一些实施方案中,所述UMIE包含来自所述衔接子和至少一部分所述基因组DNA序列的测序信息。在一些实施方案中,包含相同UMIE的测序读段被鉴定为独特基因组序列(UGS)。

[0029] 在一些实施方案中,测定所述拷贝数的方法还包括针对与所述基因组DNA文库接触的所述捕获探针中的每一个测定原始基因组深度(RGD)。在一些实施方案中,测定RGD包括测定与一组样品重复中的每个捕获探针序列相关联的UGS的平均数目。在一些实施方案中,与高度可变数目的UGS相关联的捕获探针被鉴定为噪声探针并且从进一步的计算中去除。在一些实施方案中,测定RGD还包括计算样品的RGD,其包括计算所述样品中针对所有捕获探针的所有RGD的数值平均值。在一些实施方案中,在计算样品的RGD中不包括针对噪声探针的RGD值。

[0030] 在一些实施方案中,通过将针对每个捕获探针的RGD转换成探针特异性归一化读段计数将实验组中所有样品中针对捕获探针的RGD归一化,其包括(i)使样品中的每个捕获探针RGD乘以归一化常数,其中所述归一化常数包括任何实数;以及(ii)使(i)的乘积除以对于相应样品计算的RGD;或(iii)使(i)的乘积除以从探针子集计算的平均RGD。在一些实施方案中,所述探针子集是对照探针组。

[0031] 在一些实施方案中,将所述探针特异性归一化读段计数转换成拷贝数值,其包括(i)在源自女性的样品中使针对常染色体和/或X连锁区的探针的探针特异性归一化读段计数乘以2;(ii)在源自男性的样品中使针对Y连锁和/或X连锁区的探针的探针特异性归一化读段计数乘以1;(iii)对实验中的所有样品的(i)和/或(ii)的乘积取平均值;以及(iv)使(i)和/或(ii)的乘积除以(iii)的平均值。在一些实施方案中,对于针对靶向特异性基因的

所有探针的近似拷贝数值取平均值。

[0032] 在一些实施方案中,本发明涉及一种用于高灵敏地检测拷贝数增加和拷贝数丢失的方法,其包括(i)测定针对捕获探针的RGD;(ii)通过将针对所述捕获探针的RGD转换成探针特异性归一化读段计数,对实验组中所有样品中针对捕获探针的RGD进行归一化;(iii)计算针对每个探针特异性归一化读段计数的近似拷贝数值;(iv)对于针对靶向特异性基因的所有探针的近似拷贝数值取平均值。

[0033] 在一些实施方案中,本发明涉及一种用于测量染色体稳定性的方法,其包括(i)设计和验证一种或多种染色体稳定性探针的组,其中所述染色体稳定性探针均匀分布在人染色体上;(ii)使用所述一种或多种染色体稳定性探针对患者样品进行靶向测序;(iii)针对每种染色体探针测定近似拷贝数值;(iv)测定患者样品的基因组表型,其中所述患者样品中针对一种或多种染色体探针的拷贝数值的波动表明基因组不稳定性。

[0034] 在一些实施方案中,本发明涉及治疗有需要的受试者中的癌症的方法,其中所述受试者已根据权利要求62所述的方法被鉴定为具有去稳定化的基因组,其中治疗所述癌症的所述方法包括给予药学有效量的PARP抑制剂。

[0035] 在一些实施方案中,本发明涉及一种方法,其中所述基因组分析包括测定目标DNA区域中的拷贝数变化,并且其中步骤(c)对所述包含DNA靶区域的基因组DNA片段进行定量遗传分析包括测定源自所述测试样品的基因组DNA文库中存在的目标区域的拷贝数,以及将其与源自参考样品的基因组DNA文库中存在的目标区域的拷贝数进行比较,其中所述参考样品包含已知拷贝数目的DNA靶区域。在一些实施方案中,所述目标区域是基因或所述基因的一部分。在具体实施方案中,所述基因与疾病有关。在某些实施方案中,所述疾病是癌症。在各种实施方案中,所述基因是BRCA2、ATM、BRCA1、BRIP1、CHEK2、FANCA、HDAC2和/或PALB2。

[0036] 具体实施方案涉及包含多个DNA文库片段的基因组DNA文库,其中所述DNA文库片段中的每一个包含衔接子和基因组DNA片段;其中所述衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;并且其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段。在一些实施方案中,所述样品标签还包含独特分子标识符(UMI),其中UMI有助于鉴定独特基因组DNA片段。在具体实施方案中,所述扩增区的长度在10与50个核苷酸之间。在具体实施方案中,所述扩增区的长度为25个核苷酸。在具体实施方案中,所述样品标签的长度在5与50个核苷酸之间。在某些实施方案中,所述样品标签的长度为8个核苷酸。在一些实施方案中,UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。在具体实施方案中,所述UMI倍增器的长度在1与5个核苷酸之间。在某些实施方案中,所述锚定区的长度在1与50个核苷酸之间。在一些实施方案中,所述锚定区的长度为10个核苷酸。在具体实施方案中,所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。在一些实施方案中,所述样品标签中的每个核苷酸序列与所述样品的核苷酸序列中的任何其他序列相隔的汉明距离为至少二。在某些实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。在具体实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍

增器。在一些实施方案中,所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。在一些实施方案中,所述基因组DNA片段是cfDNA。

[0037] 在某些实施方案中,所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;所述多个衔接子中的每个衔接子的样品标签区的长度为8个核苷酸,所述多个衔接子中的每个衔接子的样品标签区包含核苷酸序列,所述核苷酸序列与所述多个衔接子的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二,所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器,所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸,并且每个可能的核苷酸序列的UMI倍增器与所述多个衔接子的每个样品标签区配对,所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且给定序列的每个样品区仅与给定序列的四个锚定区中的一个配对。在一些实施方案中,所述基因组DNA片段是cfDNA。

[0038] 某些实施方案涉及多个基因组DNA文库,其包含多于一个本文所述的基因组文库。在一些实施方案中,属于所述多个基因组DNA文库的基因组DNA文库的样品标签区的核酸序列不同于属于所述多个基因组DNA文库的其他基因组DNA文库的样品标签区的核酸序列。在具体实施方案中,属于所述多个基因组DNA文库的基因组DNA文库的扩增区的核酸序列与属于多个基因组DNA文库的其他基因组DNA文库的扩增区的核酸序列相同。

[0039] 某些实施方案涉及一种用于无细胞DNA(cfDNA)的DNA靶区域的遗传分析的方法,其包括:(a)生成如本文所述的DNA文库;(b)使cfDNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成复合物;并且(c)对包含所述DNA靶区域的cfDNA片段进行定量遗传分析;从而对所述DNA靶区域进行遗传分析。

[0040] 某些实施方案涉及一种预测、诊断或监测受试者中遗传疾病的方法,其包括:(a)从所述受试者获得测试样品;(b)从所述测试样品分离基因组DNA;(c)生成包含多个DNA文库片段的DNA文库,其中所述DNA文库片段中的每一个包含来自所述测试样品的基因组DNA片段和衔接子;(d)使cfDNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成复合物;以及(e)对cfDNA克隆文库中与所述遗传疾病相关的一个或多个靶基因座进行定量遗传分析,其中所述一个或多个靶基因座中的一个或多个遗传病变的鉴定或检测是对于所述遗传疾病的进展的预后、诊断或监测。在具体实施方案中,所述定量遗传分析包括DNA测序以生成多个测序读段。

[0041] 具体实施方案涉及用于生成基因组DNA文库的编码独特基因组DNA片段的特征和测试样品的特征的衔接子组,其中所述衔接子组中的每个衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;并且其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段。在一些实施方案中,所述样品标签还包含独特分子标识符(UMI),其中UMI有助于鉴定独特基因组DNA片段。在各种实施方案中,所述扩增区的长度在10与50个核苷酸之间。在某些实施方案中,所述扩增区的长度为25个核苷酸。在具体实施方案中,所述样品标签的长度在5与50个核苷酸之间。在一些实施方

案中,所述样品标签的长度为8个核苷酸。在具体实施方案中,UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。在一些实施方案中,所述UMI倍增器的长度在1与5个核苷酸之间。在具体实施方案中,所述锚定区的长度在1与50个核苷酸之间。在一些实施方案中,所述锚定区的长度为10个核苷酸。在某些实施方案中,所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。

[0042] 在一些实施方案中,所述样品标签中的每个核苷酸序列与所述衔接子组的样品标签中的任何其他核苷酸序列相隔的汉明距离为至少二。在各种实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。在具体实施方案中,所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍增器。

[0043] 在一些实施方案中,所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。如权利要求75所述的衔接子组,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;其中每个衔接子的样品标签区的长度为8个核苷酸;其中所述样品标签的每个核苷酸序列与所述衔接子组的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二,其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸,其中所述UMI倍增器包含64个可能的核苷酸序列中的一个,并且其中所述64个可能的核苷酸序列中每一个的UMI倍增器与所述多个衔接子的每个样品标签区配对,其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个;并且其中给定序列的每个样品区仅与给定序列的四个锚定区中的一个配对。

附图说明

[0044] 图1示出了拷贝数丢失(CNL)测定的框架。每个基因(行)显示出特征性的独特读段值,此处用阴影表示。每个样品(列)都在同一组基因中被询问。

[0045] 图2示出了展示CNL测定信号的驱动器的图。

[0046] 图3示出了展示对无细胞DNA(cfDNA)进行的说明性CNL测定的步骤的图。

[0047] 图4A至图4E示出了说明性第一代衔接子(图4A和图4B)和本发明的衔接子(图4C至图4E)的图。图4A示出了第一代衔接子设计。图4B示出了在第一代衔接子中,存在249个可能的序列标签的集合,长度为5个核苷酸(nt)的每个序列标签附接至单个锚定序列。图4C示出了第二代衔接子的图。图4D示出了应用于单个样品的说明性衔接子组,其由四组8mer标签序列组成,其中每组具有60个成员。每组60个标签特定针对四个锚定序列中的一个。图4E示出了47nt衔接子的说明性DNA序列。

[0048] 图5A至图5B示出了展示在样品标签内移动UMI倍增器的位置可以增加独特样品标签的数目的图。

[0049] 图6A和图6B示出了展示针对CNL测定构建基因组文库的过程的图。图6A示出了10nt锚定序列附接至基因组片段的3'端的步骤。图6B示出了将全长基因组衔接子退火至初始锚定序列的步骤。

[0050] 图7显示了到CNL文库中的DNA输入。示出了琼脂糖凝胶图像,其中标记物的大小(bp)在左侧示出。

[0051] 图8A至图8C示出了通过CNL分析测定的八个样品中测量的基因拷贝的常规盒须图。

[0052] 图9A至图9B示出了Log_{10} P值图,其将片段化基因组样品的CNL测量中的与正常值的显著偏差定量化。顶部的SNP百分比示出了存在于ΔATM和ΔBRCA2样品中的罕见杂合SNP的低等位基因频率。

[0053] 图10A至图10B示出了Log_{10} P值图,其将掺有片段化基因组DNA的cfDNA样品的CNL测量中的与正常值的显著偏差定量化。顶部的SNP百分比示出了存在于ΔATM和ΔBRCA2样品中的罕见杂合SNP的低等位基因频率。

[0054] 图11A至图11D示出了靶向杂交捕获平台。图11A示出了通过添加衔接子序列将cfDNA转化成基因组文库,所述衔接子序列为每个基因组克隆提供通用的单引物PCR扩增序列、样品多路复用标签和独特分子标识符。图11B示出了与靶特异性捕获探针杂交的变性扩增基因组和引物延伸。图11C示出了不对称配对端测序的示意图。图11D示出了来自典型靶向捕获序列运行的377,711,020个Illumina NextSeq读段的映射统计。98.5%的读段映射至其预期靶标。在去重复后,20.40%的读段(77,053,048)源自独特基因组克隆。

[0055] 图12A至图12H示出了来自池1-3的衔接子寡核苷酸的序列。

[0056] 图13A至图13H示出了来自池4-6的衔接子寡核苷酸的序列。

[0057] 图14A至图14I示出了来自池7-9的衔接子寡核苷酸的序列。

[0058] 图15A至图15H示出了来自池10-12的衔接子寡核苷酸的序列。

[0059] 图16A至图16H示出了来自池13-15的衔接子寡核苷酸的序列。

[0060] 图17A至图18H示出了来自池16-18的衔接子寡核苷酸的序列。

[0061] 图18A至图18H示出了来自池19-21的衔接子寡核苷酸的序列。

[0062] 图19A至图19H示出了来自池22-24的衔接子寡核苷酸的序列。

[0063] 图20A至图20H示出了来自池25-27的衔接子寡核苷酸的序列。

[0064] 图21A至图21H示出了来自池28-30的衔接子寡核苷酸的序列。

[0065] 图22A至图22H示出了来自池31-32的衔接子寡核苷酸的序列。

[0066] 图23A至图23C示出了TP53基因的靶向测序。图23A示出了捕获探针的BedFile展示。图23B示出了在0到8000个独特读段的范围内的每个基础位置处的覆盖深度。图23C示出了已知TP53剪接变体的UCSC基因模型展示。较厚的矩形区域代表TP53编码的蛋白质的氨基酸编码区。

[0067] 图24A至图24C示出了16个样品中针对单个探针TP53r10_1的原始和归一化的独特读段密度。图24A示出了对于16个独立样品在通过“去重复”去除冗余读段之后通过探针TP53r10_1所得的原始独特读段捕获数目。图24B示出了对于所有16个样品的2596个捕获探针的独特读段的总体平均值。图24C示出了16个样品中的归一化独特读段深度(计算如下:[来自探针TP53r10_1的样品n独特读段×常数÷来自样品n的总体平均独特读段/探针])。

[0068] 图25示出了任何给定TP53探针内所有16个样品的归一化独特读段计数的一般一致性,尽管探针之间有显著平均深度变化。所有16个样品的归一化独特读段计数显示为紧密间隔的条形图的“柱”;示出了靶向TP53的所有45个探针的结果。用箭头突出显示两个表现出“噪声”计数行为的探针。来自此类探针的计数通常在随后的拷贝数分析中显示为异常值。

[0069] 图26展示了2596个探针的广泛组的归一化逐探针独特读段计数的样品间一致性。示出了来自三个代表性样品的散点图。每个点代表不同的探针。x轴是16个样品中每个探针的归一化平均独特读段深度。y轴是对于三个不同单独样品的每个探针的归一化独特读段深度。一致的逐探针独特读段计数支持染色体拷贝变异的定量分析。

[0070] 图27A至图27C展示了来自健康女性和男性供体和来自晚期前列腺癌症患者的cfDNA的拷贝数分析。图27A示出了来自健康女性供体的cfDNA的分析。x轴是靶向来自所有22个常染色体的区域的一系列对照探针、靶向X连锁AR基因的一系列探针以及靶向TP53基因的编码区的一系列探针。Y轴示出了每个探针的计算倍性。通过将观察到的独特读段计数针对一系列已知倍性的对照样品进行归一化,计算每个探针的近似值([样品_Z的探针_Y的独特读段计数]×2÷[多个对照样品的探针_Y的平均独特读段计数])。图27B展示了X连锁AR基因在健康男性中显示出单倍体拷贝数。图27C展示了来自晚期前列腺癌症患者的cfDNA的拷贝数分析,并示出了对照探针中非常明显的非整倍性、AR基因扩增和TP53基因丢失的证据。

[0071] 图28示出了相对于对照样品,前列腺患者cfDNA文库的全基因组非整倍性分析。示出了通过染色体分类的239个对照探针中的每一个的近似倍性。患者2号染色体探针显示一致的拷贝丢失,并且大多数5号染色体探针显示拷贝增加。对于许多但非全部的患者对照探针,观察到近似倍性的显著偏差。

[0072] 图29示出了拷贝数丢失检测的分析验证。将来自永生化系NA02718(单等位基因ΔATM)和来自NA09596(单等位基因ΔBRCA2)的基因组DNA以16%掺入来自NA12878的“黄金标准”基因组DNA中,产生相当于8%双等位基因缺失低等位基因频率。在靶向测序和CNV分析之后,对两个靶基因的逐探针倍性取平均值。示出了两个未受干扰的对照基因BRIP1和HDAC2用于比较。

具体实施方式

[0073] A.概述

[0074] 本发明尤其包括可用于检测细胞基因组DNA(例如,来自组织活检样品)或cfDNA(例如,来自血液样品)的样品内的突变、SNP、易位、倒位、缺失、拷贝数变化或其他遗传变异的组合物和方法。本发明的组合物和方法特别适用于以精确的分辨率检测来自生物样品(例如血液)的cfDNA中非常难以检测的拷贝数变异。特别地,本发明的一些实施方案涉及一种用于通过以下方式检测来自测试样品的DNA靶区域的拷贝数的方法:通过生成由附接至衔接子的基因组DNA片段构成的基因组DNA文库、用多个捕获探针捕获DNA靶区域、分离包含所述DNA靶区域的DNA文库片段以及对所述DNA靶区域进行定量遗传分析,从而测定DNA靶区域的拷贝数。本文所述的衔接子允许鉴定正在测序的单独DNA片段,以及所述样品或基因组DNA来源的特征。

[0075] 本发明部分地考虑适用于几种样品类型的用于检测靶特异性拷贝数变化的组合物和方法,其包括但不限于直接组织活检和外周血。在癌症基因组学,并且特别在用于分析实体瘤的无细胞DNA(cfDNA)测定的上下文中,肿瘤DNA的量通常是整个DNA的非常小的部分。此外,在基因组DNA测定并且特别在拷贝数变化可能仅存在于来自样品的总基因组DNA的一部分中的基因组DNA测定(例如cfDNA测定)中,难以检测出拷贝数丢失。例如,从癌症患

者中提取的大多数无细胞DNA将源自正常来源并具有二倍体拷贝数(除了男性受试者中的X连锁基因)。在癌症患者中,源自肿瘤的DNA的部分通常具有低等位基因频率,例如这样的患者,其中从血浆中提取的循环DNA的2%源自肿瘤。肿瘤抑制基因(例如,乳腺癌中的BRCA1)的一个拷贝的丢失意味着缺乏可检测的基因组片段的低等位基因频率为1%。在这种情况下,改造的拷贝数丢失测定必须能够区分100个拷贝(正常)与99个拷贝(杂合基因丢失)。因此,具体的实施方案考虑到本发明的方法和组合物允许以足够的分辨率检测拷贝数变化,以在低等位基因频率下即使在cfDNA的情况下也能检测拷贝数变化。

[0076] 为了达到这种区分水平,本发明提供了新型样品衔接子设计。本发明的衔接子被设计成包含对成功的拷贝数丢失测定性能而言至关重要的特征,其包括(i)跨衔接子的均匀的性能;(ii)大量独特分子标识符(UMI);(iii)高效附接;以及(iv)样品多路复用的适应性。例如,本发明的衔接子提供以下项:

[0077] 跨衔接子的均匀的性能:生物信息学分析通常会研究样品内探针性能和样品间探针性能。因此,预期跨样品的衔接子池之间的任何性能波动将负面地影响CNL分析所需的检测细微变化的能力。在本发明中,这种性能均匀性通过具有全部在每个样品标签池中得以表示的多个锚定标签和增加用于鉴定基因组片段的独特样品标签序列的一个UMI倍增器来实现,在所述多个锚定标签中固定的样品标签区(用于鉴定样品和基因组片段)被随机选择用于每个池。

[0078] 大量独特分子标识符(UMI):虽然从分子生物学的角度来看,衔接子必须在功能上等效,但它们必须具有能加强对独特基因组片段的鉴定的大量独特序列标签(≥10,000)。在本文背景中,"加强"意味着每个基因组克隆片段具有特定的一对片段化位点,其对应于基因组序列中双链DNA被切割的位置。该切割位点用于区分独特基因组克隆,因为每个克隆可能具有不同的切割位点。然而,在具有数千个独立克隆的文库中,独特衍生的片段通常具有完全相同的切割位点。共用相同切割位点的基因组克隆(即片段)可以相对于源自相同样品的其他克隆序列而被分类为独特的或冗余的。通过附接能引入高度多样性的序列标签的衔接子,共用相同切割位点的不同基因组克隆更可能被鉴定为独特的。在该系统中,UMI是通过样品标签区与UMI倍增器的组合产生的。UMI和所述切割位点的组合产生了独特分子标识符元件(UMIE),其有助于将序列读段分类为冗余读段或独特读段。具体实施方案考虑到UMI倍增器可以包含更长或更短的序列来增加或降低整体UMI复杂性。

[0079] 高效附接:衔接子必须高效附接至基因组片段。在大多数肿瘤学应用中,可用的细胞DNA或cfDNA的量是有限的,因此这些基因组片段向基因组文库克隆的转化必须是高效的。为了实现这一点,在本发明的一些方面,本文所述的衔接子系统将约25%至约50%或更多的基因组输入片段转化到基因组文库克隆中。

[0080] 样品多路复用的适应性:通常,必须有不同衔接子组的池,其中组中的每个独特衔接子附接至不同的样品。同时,所述衔接子组中的每个成员必须具有与所述组中的所有其他成员基本上相同的行为(从序列计数的角度)。为了实现这一点,在一些实施方案中,样品标签区在任何其他可能的样品标签组合之间的汉明距离为2,从而减少了读段被错误地分配至错误样品的机会。在一些实施方案中,每组衔接子被分成与特定锚定区配对的池,从而允许进一步降低样品解复用中出错的可能性。例如,在汉明距离为2的8mer标签中,可能序列的总数为16,384。

[0081] 在具体实施方案中,提供了预先指定的衔接子寡核苷酸池。这种预先指定的池用于表示单个样品。也就是说,X个衔接子寡核苷酸(在上面给出的例子中为16,384个衔接子寡核苷酸)的每个池中的每个衔接子序列与用于鉴定其他样品的每个其他池中的每个衔接子序列不同。本领域技术人员将认识到对于衔接子寡核苷酸可能的不同预先指定的池的数目将取决于样品标签和/或UMI倍增器的长度。

[0082] 因此,在某些实施方案中,衔接子包含序列,即样品标签和相邻和/或所包含的UMI倍增器,其代表或鉴定样品并且独特地鉴定基因片段。这与本领域中使用的当前系统形成鲜明对比,所述系统使用随机生成的标签来鉴定所述序列,并使用单独的条形码或测序仪索引以允许多路复用。

[0083] 用于检测从样品获得的DNA内的靶特异性拷贝数变化的说明性实施方案示于图3中。当图3由cfDNA生成DNA文库时,该说明性程序可以与来自其他来源的DNA(例如片段化的细胞DNA)一起使用。如图3所示,收集cfDNA(上图)。接下来,通过将本发明的基因组文库衔接子(灰色圆圈)与基因组DNA缀合,由cfDNA生成基因组文库。用识别感兴趣的基因组区域的捕获探针(黑色圆圈)捕获基因组DNA片段。对目标基因组DNA进行测序,并进行数据分析以对目标基因组DNA进行拷贝丢失分析和/或表征。

[0084] 除非特别相反地指出,否则本发明的具体实施方案的实践将采用本领域技术范围内的化学、生物化学、有机化学、分子生物学、微生物学、重组DNA技术、遗传学、免疫学和细胞生物学的常规方法,为了说明的目的下文中描述了其中许多方法。此类技术在文献中得到充分解释。参见例如,Sambrook,等人,Molecular Cloning:A Laboratory Manual(第3版,2001);Sambrook,等人,Molecular Cloning:A Laboratory Manual(第2版,1989);Maniatis等人,Molecular Cloning:A Laboratory Manual(1982);Ausubel等人,Current Protocols in Molecular Biology(John Wiley和Sons,2008年7月更新);Short Protocols in Molecular Biology:A Compendium of Methods from Current Protocols in Molecular Biology,Greene Pub.Associates and Wiley-Interscience;Glover,DNA Cloning:A Practical Approach,第I和II卷(IRL Press,Oxford,1985);Anand,Techniques for the Analysis ofComplex Genomes,(Academic Press,New York,1992);Transcription and Translation(B.Hames和S.Higgins编,1984);Perbal,A Practical Guide to Molecular Cloning(1984);以及Harlow和Lane,Antibodies,(Cold Spring Harbor Laboratory Press,Cold Spring Harbor,N.Y.,1998)。

[0085] B.定义

[0086] 除非另外定义,本文所用的全部技术术语和科学术语具有与本发明所属领域的普通技术人员通常所理解的相同意义.尽管在发明的实施和测试中可以使用任何相似于或等效于本文中所述那些的方法和材料,本文描述了组合物、方法和材料的优选实施方案。出于本发明的目的,以下术语定义如下。

[0087] 冠词“一个”、“一种”和“所述”在本文中用于指代该冠词的一个或多于一个(即至少一个)语法对象。举例来说,“一种元件”意指一种元件或多于一种元件。

[0088] 替代方案(例如,“或”)的使用应理解为意指替代方案中的一个、两个或任何组合。

[0089] 术语“和/或”应理解为意指替代方案中的一个或两个。

[0090] 如本文所用,术语“约”或“近似”是指与参考数量、水平、值、数目、频率、百分比、尺

寸、大小、量、重量或长度相比变化多达15%、10%、9%、8%、7%、6%、5%、4%、3%、2%或1%的数量、水平、值、数目、频率、百分比、尺寸、大小、量、重量或长度。在一个实施方案中，术语“约”或“近似”是指在参考数量、水平、值、数目、频率、百分比、尺寸、大小、量、重量或长度周围±15%、±10%、±9%、±8%、±7%、±6%、±5%、±4%、±3%、±2%或±1%的数量、水平、值、数目、频率、百分比、尺寸、大小、量、重量或长度范围。

[0091] 在整个说明书中，除非上下文另有要求，否则词语“包含”(“comprise”、“comprises”和“comprising”)应被理解为暗示包含所述步骤或元件或步骤或元件的组但不排除任何其他步骤或元件或步骤或元件的组。在具体实施方案中，术语“包括”、“具有”、“含有”和“包含”同义使用。

[0092] “由……组成”意味着包括并限于短语“由……组成”之后的任何内容。因此，短语“由……组成”表示所列出的元件是必需的或强制性的，并且不存在其他元件。

[0093] “基本上由……组成”意味着包括在该短语之后列出的任何元件，并且限于不干扰或有助于本公开中针对所列元件指定的活动或行动的其他元件。因此，短语“基本上由……组成”表示所列元件是必需的或强制性的，但是没有其他元件是任选的且可以存在或可以不存在，这取决于它们是否影响所列元件的活动或行动。

[0094] 在本说明书中引用“一个实施方案”、“实施方案”、“具体实施方案”、“相关实施方案”，“某个实施方案”、“附加的实施方案”或“另外的实施方案”或其组合意味着结合该实施方案描述的特定特征、结构或特性被包括在本发明的至少一个实施方案中。因此，在整个说明书中各个地方出现的前述短语不一定都指的是相同的实施方案。此外，具体特征、结构或特性可以在一个或多个实施方案中以任何合适的方式组合。

[0095] 如本文所用，术语“分离的”意指这样的物质，所述物质大体上或基本上不含在它的天然状态下通常伴随它的组分。在具体实施方案中，术语“获得的”或“衍生的”与“分离的”同义使用。

[0096] 如本文所用，术语“DNA”是指脱氧核糖核酸。在各种实施方案中，术语DNA指基因组DNA、重组DNA、合成DNA或cDNA。在一个实施方案中，DNA是指基因组DNA或cDNA。在具体实施方案中，DNA包含“靶区域”。本文考虑的DNA文库包括由RNA(例如RNA表达文库)构建的基因组DNA文库和cDNA文库。在各种实施方案中，DNA文库包含一个或多个附加的DNA序列和/或标签。

[0097] 术语“靶基因座”和“DNA靶区域”在本文中可互换使用，并且是指DNA序列内的目标区域。在各种实施方案中，在靶基因座上进行靶向遗传分析。在具体实施方案中，DNA靶区域是与以下相关的基因区域：具体遗传状态、遗传病症、遗传疾病；胎检；遗传嵌合、亲子鉴定；预测对药物治疗的反应；诊断或监测医疗病症；微生物组分析；病原体筛查；或器官移植监测。在另外的实施方案中，DNA靶区域是与特定人染色体(如特定的常染色体或X连锁染色体)或其区域(例如，独特染色体区域)相关的DNA序列。

[0098] 如本文所用，术语“循环DNA”、“循环无细胞DNA”和“无细胞DNA”通常可互换使用并且是指这样的DNA，它是细胞外DNA、已从细胞中排出的DNA或已从坏死或凋亡细胞中释放的DNA。该术语通常与“细胞基因组DNA”或“细胞DNA”形成对比，后者在本文中可互换使用，并且是指这样的基因组DNA(即核酸酶)，它包含在细胞内并且只有通过裂解或以其他方式破坏细胞的完整性才可用于分子生物学技术，如本文所述的那些技术。

[0099] 本文所用的“受试者”、“个体”或“患者”包括表现出可用本文考虑的组合物检测或鉴定的病症症状的任何动物。合适的受试者包括实验室动物(如小鼠、大鼠、兔子或豚鼠)、农场动物(如马、牛、羊、猪)和家畜或宠物(如猫或狗)。在具体实施方案中,受试者是哺乳动物。在某些实施方案中,受试者是非人灵长类动物,并且在优选的实施方案中,受试者是人。

[0100] 如本文所用,术语“配对的”当关于两个不同多核苷酸序列或包含不同多核苷酸序列的DNA区域使用时,意味着两个不同多核苷酸序列或包含不同多核苷酸序列的DNA区域存在于相同的多核苷酸上。例如,如果DNA的特定样品标签区被称为与DNA的特定扩增区配对,则意味着所述样品标签区和扩增标签存在于相同的DNA多核苷酸分子上。

[0101] C.拷贝数分析方法

[0102] 在各种实施方案中,提供了用于DNA靶区域DNA的拷贝数分析的方法。在某些实施方案中,通过生成各自含有基因组DNA片段和衔接子的DNA文库片段的基因组DNA文库、分离含有DNA靶区域的DNA文库片段以及对DNA靶区域进行定量遗传分析来进行拷贝数分析。“定量遗传分析”意指通过任何分子生物学技术进行的分析,所述技术能够量化DNA(例如,基因、基因座、目标靶区域等)的变化,包括但不限于DNA突变、SNP、易位、缺失和拷贝数变异(CNV)。在某些实施方案中,定量遗传分析通过测序例如新一代测序进行。

[0103] 新一代DNA测序(NGS)非常适合两种诊断应用。首先是大规模的DNA序列测定。在目前的情况下,这种能力使得能够搜索罕见的、可操作的变体,所述变体指导有效的治疗决策。第二种是对基因拷贝数计数。数百万个独立序列的输出使得能够在全基因组范围内精确测量基因拷贝数。从母体血液样品进行胎儿三体性的非侵入性产前检测的出现证明了这种能力。RNAseq(即使用NGS进行基因表达分析的技术)是另一个例子,但输入是RNA(cDNA)而不是基因组DNA。Samorodnitsky等人J Mol Diagn.2015年1月;17(1):64-75等人描述了当前捕获方法的比较。

[0104] 本发明将NGS计数能力扩展到靶向杂交捕获方法的领域。本文描述的方法至少部分地因为它们具有以下四个品质而对拷贝数变异的检测有效:

[0105] (a)本方法区分独特克隆与冗余克隆。扩增的基因组DNA文库片段的NGS测序产生多个单独NGS读段,每个读段包含与特定人基因组序列连接的衔接子编码的序列信息。这些元件定义了每个克隆的特征。因为通过PCR扩增捕获的基因组区域,所以在随后的NGS分析中多次遇到相同的克隆并不罕见。源自单个克隆和捕获过程的读段组被称为“冗余读段”。基于由独特分子标识元件(UMIE)提供的测序信息,两个或更多个冗余读段被鉴定为冗余读段。UMIE是指来自衔接子标签的序列信息和基因组DNA序列的起点的组合。包含相同UMIE的两个或更多个读段被鉴定为冗余读段。冗余读段被分组在一起,并且从冗余读段的家族组装单个代表性共有序列。该共有序列被称为“独特读段”或“独特基因组序列”(UGS)。每个独特读段代表来自原始DNA样本的单独克隆。鉴定和分组冗余克隆家族以及生成代表该家族的单个独特读段的过程被定义为“去重复”。用于创建基因组文库的衔接子具有非常深的独特样品标签信息库(每个衔接子具有15,360个密码)。当与每个捕获的基因组克隆的精确映射坐标(其相对于捕获探针可以跨越>100个不同位置)一起应用时,在基因组文库中生成并随后通过靶特异性捕获探针检索的每个独特克隆具有与包含相同捕获环境的所有其他独特克隆区分开来的极高可能性。区分独特克隆与冗余克隆的能力是本文所述方法的核心。

[0106] (b)用于创建基因组文库的衔接子在不产生衔接子之间拷贝数计数的可变性的情

况下允许样品多路复用。拷贝数测定的中心基础是同时分析已全部在单个测序运行中处理的样品组。这允许将阳性和阴性对照与临床样品一起包括在内。先前衔接子设计迭代的主要问题引起相同对照样品中基因拷贝计数的微妙变化,从而实际上设置信噪比不确定性阈值,其在基于血液的实体肿瘤基因分型测定中太高而不具有临床应用性。本发明克服了这个问题并且显著降低了信噪比阈值,使得在≤2%低等位基因频率时能检测到单拷贝基因丢失。这种改进的信号识别使得本发明的方法在循环肿瘤DNA测定中具有显著的临床实用性。

[0107] (c)本文使用的专有靶向杂交捕获方法必须在所有靶标上产生高度统一的“中靶”读段覆盖。依赖于对独特基因组片段计数以估计拷贝数的方法(如本文所述的方法)在遇到所有可能的独特片段方面必须实现接近饱和。接近饱和只能通过过采样来实现,也就是说,收集超过最终遇到的独特读段数量的测序读段。为了实用性、可扩展性和经济性,靶向杂交捕获文库中的独特读段必须显示出足够的均匀性,使得<10倍中靶读段过采样,并且优选<4倍中靶读段过采样将捕获靶基因座处>90%的独特中靶读段。

[0108] (d)靶向杂交捕获方法(参见美国专利公开号2014-0274731)必须具有高中靶捕获率。为了实用性、可扩展性和经济性,换言之是为了成为本公开相对于本领域其他技术的区别性特征,所述方法必须实现>90%、优选>95%的中靶读段。由于中靶映射率超过95%,对于中靶读段的4至10倍过采样的要求和对于整体过采样的要求是相同的。

[0109] 在一些实施方案中,样品中存在的DNA靶区域的拷贝数通过定量遗传分析确定。在一些实施方案中,通过比较样品中存在的DNA靶区域的拷贝量并将其与具有已知拷贝数的一个或多个样品中存在的DNA靶区域的量进行比较来确定DNA靶区域的拷贝数。

[0110] 具体实施方案考虑到本文所述的组合物和方法特别适用于检测基因组DNA样品中的拷贝数变化,其中样品中总基因组DNA的仅一部分具有拷贝数变化。例如,样品例如无细胞DNA的样品中可能存在显著的肿瘤突变,所述肿瘤突变以显著小于50%(例如,在0.1%至>20%的范围内)的低等位基因频率存在,这与常规SNP基因分型(其中等位基因频率通常为约100%、50%或0%)不同。本领域技术人员将认识到,本发明的组合物和方法还可用于检测其他类型的突变,包括单核苷酸变异(SNV)、短(例如,少于40个碱基对(bp))插入和缺失(indel)、和基因组重排,其包括致癌基因融合。

[0111] 在某些实施方案中,本文描述的本发明的组合物和/或方法可用于、能够、适合于和/或能检测、鉴定、观察和/或揭示一个或多个DNA靶区域的拷贝数变化,所述一个或多个DNA靶区域存在于少于约20%、少于约19%、少于约18%、少于约17%、少于约16%、少于约15%、少于约14%、少于约13%、少于约12%、少于约11%、少于约10%、少于约9%、少于约8%、少于约7%、少于约6%、少于约5%、少于约4%、少于约3%、少于约2%、少于约1%、少于约0.5%、少于约0.2%或少于约0.1%的来自样品的总基因组DNA中。在一些实施方案中,本发明的方法可用于、能够、适合于和/或能检测、鉴定、观察和/或揭示一个或多个DNA靶区域的拷贝数变化,所述一个或多个DNA靶区域存在于在约0.01%至约100%、约0.01%至约50%和或约0.1%至约20%的来自样品的总基因组DNA中。

[0112] 具体实施方案由图1中所示的概念框架表示。在图1中,每个基因由一行表示,并且每个患者样品表示为一列。在任何给定的基因组DNA样品中,对于每个单独基因计数的片段的数目将具有一些可变性,并且对于任何给定的目标DNA区域(例如基因),拷贝数的扰动被

检测为相对于针对其他样品中DNA靶区域的归一化计数的显著片段计数偏差。这种测定要求样品内的逐基因片段计数特征是可再现的,并且还要求逐样品计数特征具有高度可比性。两种测定要求都需要优异的信噪比计数鉴别。

[0113] 一些实施方案考虑到有助于增加信噪比的测定元件是基因组输入、探针数目和测序深度,如图2所示。

[0114] 在具体实施方案中,用于cfDNA遗传分析的方法包括:生成和扩增cfDNA文库、测定cfDNA文库中基因组当量的数目;并对一个或多个基因组靶基因座进行定量遗传分析。

[0115] 具体实施方案考虑到本文所述的任何方法和组合物可有效地用于使用基因组DNA(例如细胞或cfDNA)来有效地分析、检测、诊断和/或监测遗传状态、遗传病症、遗传疾病、遗传嵌合、胎儿诊断、亲子鉴定、微生物组分析、病原体筛查以及器官移植监测,其中样品中总基因组DNA的全部或仅部分具有目标特征,例如遗传病变、突变、单核苷酸变异(SNV)。在一些实施方案中,目标特征是与疾病或病症相关的遗传特征。例如,样品例如cfDNA的样品中可能存在显著的肿瘤突变,所述肿瘤突变以明显小于50%(例如,在0.1%至>20%的范围内)的低等位基因频率存在,这与常规SNP基因分型(其中等位基因频率通常为约100%、50%或0%)不同。

[0116] 在某些实施方案中,本文描述的本发明的组合物和/或方法可用于、能够、适合于和/或能检测、鉴定、观察和/或揭示一个或多个DNA靶区域的遗传病变,所述一个或多个DNA靶区域存在于少于约20%、少于约19%、少于约18%、少于约17%、少于约16%、少于约15%、少于约14%、少于约13%、少于约12%、少于约11%、少于约10%、少于约9%、少于约8%、少于约7%、少于约6%、少于约5%、少于约4%、少于约3%、少于约2%、少于约1%、少于约0.5%、少于约0.2%或少于约0.1%的来自样品的总基因组DNA中。在一些实施方案中,本发明的方法可用于、能够、适合于和/或能检测、鉴定、观察和/或揭示一个或多个DNA靶区域的遗传病变,所述一个或多个DNA靶区域存在于在约0.01%至约100%、约0.01%至约50%和或约0.1%至约20%的来自样品的总基因组DNA中。

[0117] 1.生成DNA文库

[0118] 在具体实施方案中,本文考虑的遗传分析方法包括生成DNA文库,包括用一种或多种末端修复酶处理cfDNA或片段化的细胞基因组DNA以生成末端修复的DNA,并将一个或多个衔接子附接至末端修复的DNA的各端以生成DNA文库。基因组DNA

[0119] 在具体实施方案中,本文考虑的方法和组合物被设计为使用基因组DNA作为分析物来有效地分析、检测、诊断和/或监测拷贝数变化。在某些实施方案中,通过从测试样品(例如生物样品如组织活检)获得的基因组DNA生成基因组DNA文库来进行拷贝数分析。在某些实施方案中,基因组DNA是循环或无细胞DNA。在一些实施方案中,基因组DNA是细胞基因组DNA。

[0120] 在某些实施方案中,基因组DNA是从组织样品或取自组织的活检获得,所述组织包括但不限于骨髓、食道、胃、十二指肠、直肠、结肠、回肠、胰腺、肺、肝、前列腺、脑、神经、脑膜组织、肾组织、子宫内膜组织、宫颈组织、乳房、淋巴结、肌肉和皮肤。在某些实施方案中,组织样品是肿瘤或疑似肿瘤的活检。在具体实施方案中,肿瘤是癌性的或怀疑是癌性的。在具体实施方案中,组织样品包括癌细胞或怀疑具有癌性的细胞。

[0121] 从细胞或从由细胞构成的生物组织中纯化基因组DNA的方法是本领域公知的,并

且技术人员将根据组织和获得组织的条件识别最佳程序或商业试剂盒。一些实施方案考虑到从组织中纯化细胞DNA将需要细胞破碎或细胞裂解以暴露其中的细胞DNA,例如通过化学和物理方法,如混合、研磨或超声处理组织样品;通过添加也用于细胞裂解的洗涤剂或表面活性剂去除膜脂质,任选例如通过添加蛋白酶去除蛋白质;去除RNA,例如通过添加RNase;以及例如从在细胞裂解步骤中使用的洗涤剂、蛋白质、盐和试剂中纯化DNA。DNA纯化可以通过例如采用乙醇或异丙醇的沉淀进行;通过苯酚-氯仿萃取进行。

[0122] 在具体实施方案中,从组织和/或细胞获得的细胞DNA在获得、生成、制备、形成和/或产生如本文所述的基因组DNA文库之前和或期间被片段化。本领域技术人员将理解存在几种适合于DNA片段化的技术,并且本领域技术人员能够识别和鉴定适合于为了生成用于DNA测序(其包括但不限于新一代测序)的基因组DNA文库的目的片段化细胞DNA的技术。某些实施方案考虑到通过包括但不限于物理片段化、酶促片段化和化学剪切的方法可以将细胞DNA片段化成对于生成文库而言合适的和/或足够的长度的片段。

[0123] 物理片段化可包括但不限于声学剪切、超声处理和流体动力学剪切。在一些实施方案中,细胞DNA通过物理片段化进行片段化。在具体实施方案中,通过声学剪切或超声处理将细胞DNA片段化。具体实施方案考虑到声学剪切和超声处理是用于剪切细胞DNA的常用物理方法。Covaris®仪器(Woburn,MA)是一种用于将DNA破坏为100bp-5kb bp的声学装置。Covaris还制造管(gTubes),它将样品处理为6-20kb以用于Mate-Pair文库。Bioruptor®(Denville,NJ)是一种用于剪切染色质、DNA和破坏组织的超声装置。可以将少量DNA剪切至150个碱基-1kb长度。来自Digilab(Marlborough,MA)的Hydroshear利用水动力来剪切DNA。雾化器(Life Tech,Grand Island,NY)也可用于使用压缩空气雾化液体,从而在几秒钟内将DNA剪切成100个碱基-3kb片段。雾化成本低,但该过程可导致原始样品中损失约30%的细胞DNA。在某些实施方案中,细胞DNA通过超声处理片段化。

[0124] 酶促片段化可以包括但不限于用限制性内切核酸酶(例如DNase I)处理或用非特异性核酸酶处理。在一些实施方案中,细胞DNA通过酶促片段化进行片段化。在具体实施方案中,通过用限制性内切核酸酶处理将细胞DNA片段化。在一些实施方案中,通过用非特异性核酸酶处理将细胞DNA片段化。在某些实施方案中,通过用转座酶处理将细胞DNA片段化。某些实施方案考虑到将细胞DNA剪切成小片的酶促方法包括DNAse I、麦芽糖结合蛋白(MBP)-T7 Endo I和非特异性核酸酶创伤弧菌(Vvn)New England Biolabs(Ipswich,MA)片段化酶的组合以及Nextera标记技术(Illumina,San Diego,CA)。非特异性核酸酶和T7 Endo的组合协同作用以产生非特异性切口和反切口,从而生成从切口位点解离8个核苷酸或更少核苷酸的片段。标记使用转座酶来同时将衔接子片段化并插入双链DNA上。

[0125] 化学片段化可包括用热和二价金属阳离子处理。在一些实施方案中,基因组DNA通过化学片段化进行片段化。具体实施方案考虑到化学剪切更常用于长RNA片段而不是基因组DNA的分解。化学片段化通常通过用二价金属阳离子(镁或锌)热消化DNA来进行。可以通过增加或减少孵育时间来调节DNA片段的长度。

[0126] 在具体实施方案中,本文考虑的方法和组合物被设计为使用无细胞DNA(cfDNA)作为分析物来有效地分析、检测、诊断和/或监测拷贝数变化。cfDNA的大小分布范围为约150bp至约180bp片段。cfDNA的片段化可能是核酸内切和/或核酸外切活性的结果,并且呈

现出对cfDNA的准确、可靠和稳健的分析的强大挑战。分析cfDNA的另一个挑战是它在血流中的半衰期短,约15分钟。不希望受任何特定理论的约束,本发明部分地考虑到cfDNA的分析类似于“液体活检”并且是当前生物过程的实时快照。

[0127] 此外,由于cfDNA不存在于细胞内,并且可以从包括但不限于生物流体和粪便样品的许多合适的来源获得,因此不受困扰新一代测序分析的现有限制(如直接获取被分析的组织)。

[0128] 作为在具体实施方案中从中分离cfDNA的合适来源的生物流体的说明性例子包括但不限于羊水、血液、血浆、血清、精液、淋巴液、脑脊液、眼内液、尿液、唾液、粘液和汗液。在具体实施方案中,生物流体是血液或血浆。

[0129] 在某些实施方案中,市售的试剂盒和技术人员已知的其他方法可用于直接从受试者的生物流体或从先前获得的和任选稳定的生物样品例如通过冷冻和/或添加包括但不限于EDTA、EGTA或对二价阳离子有特异性的其他螯合剂的酶螯合剂来分离cfDNA。

[0130] (a)生成末端修复的cfDNA

[0131] 在具体实施方案中,生成基因组DNA文库包括分离的cfDNA或片段化细胞DNA的末端修复。片段化的cfDNA或细胞DNA由末端修复酶处理以生成具有平端、5’-突出端或3’-突出端的末端修复的cfDNA。在一些实施方案中,例如末端修复酶可以产生。在一些实施方案中,末端修复的cfDNA或细胞DNA含有平端。在一些实施方案中,末端修复的细胞DNA或cfDNA被处理成含有平端。在一些实施方案中,末端修复的cfDNA或细胞DNA的平端被进一步修饰以含有单个碱基对突出端。在一些实施方案中,含有平端的末端修复的cfDNA或细胞DNA可被进一步处理以含有腺嘌呤(A)/胸腺嘧啶(T)突出端。在一些实施方案中,含有平端的末端修复的cfDNA或细胞DNA可被进一步处理以含有作为单碱基对突出端的腺嘌呤(A)/胸腺嘧啶(T)突出端。在一些实施方案中,末端修复的cfDNA或细胞DNA具有非模板化的3’突出端。在一些实施方案中,末端修复的cfDNA或细胞DNA被处理以含有3’突出端。在一些实施方案中,末端修复的cfDNA或细胞DNA用末端转移酶(TdT)处理以含有3’突出端。在一些实施方案中,可以通过TdT添加G尾部。在一些实施方案中,使用通过任何已知的限制酶(例如用酶Sau3A等)的部分消化,将末端修复的cfDNA或细胞DNA处理成含有突出端。

[0132] (b)将衔接子分子附接至末端修复的cfDNA

[0133] 在具体实施方案中,生成cfDNA文库包括将一个或多个衔接子附接至末端修复的cfDNA的各端。本发明部分地考虑了衔接子模块,其被设计为在cfDNA文库中容纳大量基因组当量。衔接子模块被配置成测量cfDNA文库中存在的基因组当量的数目,并且通过扩展被配置成测量用于鉴定序列突变的测序测定的灵敏度。

[0134] 如本文所用,术语“衔接子”和“衔接子模块”可互换使用,并且是指包含至少三种元件的多核苷酸:扩增区、样品标签区和锚定区。在具体实施方案中,衔接子包含扩增区、样品标签区和锚定区。在一些实施方案中,衔接子还包含独特分子标识符(UMI)。在具体实施方案中,衔接子包含一个或多个扩增区、一个或多个样品标签区、一个或多个UMI和/或一个或多个锚定区。在一些实施方案中,衔接子以从5’到3’的顺序包含扩增区、样品标签区、UMI和锚定区。在具体实施方案中,衔接子以从5’到3’的顺序包含扩增区、样品标签区、UMI和锚定区。在某些实施方案中,UMI被包含在样品标签区内,并且衔接子以从5’到3’的顺序包含扩增区、整合的样品标签/UMI区和锚定区。

[0135] 如本文所用,术语“扩增区”是指衔接子分子的元件,其包含能够充当PCR扩增的引物识别位点的多核苷酸序列。在具体实施方案中,衔接子包含扩增区,其包含用于基因组DNA文库的单引物扩增的一个或多个引物识别序列。在一些实施方案中,扩增区包含基因组DNA文库的单引物扩增的一个、两个、三个、四个、五个、六个、七个、八个、九个、十个或更多个引物识别序列。

[0136] 在一些实施方案中,扩增区的长度在约5与50个核苷酸之间、10与45个核苷酸之间、15与40个核苷酸之间或20与30个核苷酸之间。在一些实施方案中,扩增区为10个核苷酸、11个核苷酸、12个核苷酸、13个核苷酸、14个核苷酸、15个核苷酸、16个核苷酸、17个核苷酸、约18个核苷酸、19个核苷酸、20个核苷酸、21个核苷酸、22个核苷酸、23个核苷酸、24个核苷酸、25个核苷酸、26个核苷酸、27个核苷酸、28个核苷酸、29个核苷酸、30个核苷酸、31个核苷酸、32个核苷酸、33个核苷酸、34个核苷酸、35个核苷酸、36个核苷酸、37个核苷酸、38个核苷酸、39个核苷酸或40个核苷酸或更多。在具体实施方案中,所述扩增区的长度为25个核苷酸。

[0137] 如本文所用,术语“样品标签”或“样品标签区”可互换使用,并且是指衔接子的元件,所述元件包含独特地鉴定特定DNA片段以及衍生出它的样品的多核苷酸序列。

[0138] 在某些实施方案中,样品标签区的长度在3与50个核苷酸之间、3与25个核苷酸之间或5与15个核苷酸之间。在一些实施方案中,样品标签区的长度为3个核苷酸、4个核苷酸、5个核苷酸、6个核苷酸、7个核苷酸、8个核苷酸、9个核苷酸、10个核苷酸、约11个核苷酸、12个核苷酸、13个核苷酸、14个核苷酸、15个核苷酸、16个核苷酸、17个核苷酸、18个核苷酸、19个核苷酸或20个核苷酸或更多。

[0139] 在某些实施方案中,衔接子包含UMI倍增器,其中UMI倍增器的长度为至少1、至少2、至少3、至少4、至少5、至少6、至少7、至少8、至少9或至少10个核苷酸。

[0140] 在某些实施方案中,UMI倍增器的每个核苷酸位置可以包含腺嘌呤、鸟嘌呤、胞嘧啶或胸腺嘧啶中的任何一种。因此,在一些实施方案中,包含n个核苷酸的UMI倍增器可以包含n^4个可能的核苷酸序列中的任何一种。在一些实施方案中,UMI倍增器的长度为一个核苷酸并且包含四个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为两个核苷酸并且包含十六个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为三个核苷酸并且包含64个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为四个核苷酸并且包含256个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为五个核苷酸并且包含1,024个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为六个核苷酸并且包含4,096个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为七个核苷酸并且包含16,384个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为八个核苷酸并且包含65,5336个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为九个核苷酸并且包含262,144个可能序列中的一个。在一些实施方案中,UMI倍增器的长度为十个或更多个核苷酸并且包含1,048,576或更多个可能序列中的一个。

[0141] 在具体实施方案中,衔接子包含UMI倍增器,其中UMI倍增器与样品标签区相邻或包含在样品标签区内(图5A)。与样品标签相邻或包含在样品标签内的UMI倍增器的说明性例子在图5B中示出。在图5B中,示出了8-mer样品标签区,其具有相邻的UMI倍增器(顶部和底部行)或并入样品标签内的UMI倍增器(中间7行)。在一些实施方案中,该衔接子包含长度

为八个核苷酸的样品标签和长度为三个核苷酸的UMI倍增器,并且包含64个可能序列中的一个,并且其中UMI倍增器与样品标签区相邻或包含在样品标签区内。在一些实施方案中,相同的过程将全长衔接子附接至基因组片段的另一端。

[0142] 在具体实施方案中,衔接子模块包含一个或多个锚定序列。如本文所用,“锚定区”和“锚定序列”可互换使用,并且是指与配偶体寡核苷酸杂交的核苷酸序列。在一些实施方案中,锚定区包含以下三个特性:(1)每个锚定序列是两个或更多个锚定序列的家族的一部分,所述锚定序列共同表示延伸内每个位点处的四个可能的DNA碱基中的每一个;这一特征(平衡的碱基表示)可用于在具体实施方案中校准测序读段中的正确碱基调用;(2)每个锚定序列仅由四个可能碱基中的两个组成,并且这两个碱基被特别选择为相同数目的A+C或相同数目的G+T;仅由两个碱基形成的锚定序列降低了锚定序列参与二级结构形成的可能性,这将阻碍正常的衔接子功能;以及(3)因为每个锚定序列由相同数目的A+C或G+T组成,所以每个锚定序列与四个一组中的每个其他锚定序列具有大致相同的解链温度和双链体稳定性。

[0143] 在一些实施方案中,锚定序列的长度在1与50个核苷酸之间。在一些实施方案中,锚定序列的长度在4与40个核苷酸之间。在某些实施方案中,所述锚定区的长度在5与25个核苷酸之间。在具体实施方案中,锚定区的长度为至少4个核苷酸、至少6个核苷酸、至少8个核苷酸、至少10个核苷酸、至少12个核苷酸、至少14个核苷酸或至少16个核苷酸。在具体实施方案中,所述锚定区的长度为10个核苷酸。

[0144] 在具体实施方案中,附接步骤包括将衔接子模块附接/连接至末端修复的cfDNA或细胞DNA以生成“标记的”基因组DNA文库。在一些实施方案中,使用单个衔接子模块。在一些实施方案中,使用两个、三个、四个或五个衔接子模块。在一些实施方案中,将具有相同序列的衔接子模块附接至片段化的末端修复的DNA的各端。

[0145] 在一些实施方案中,将多个衔接子种类附接至末端修复的细胞或无细胞基因组DNA片段。多个衔接子中的每一个可以包含用于cfDNA或细胞DNA文库的扩增的一个或多个扩增区、用于cfDNA或细胞基因组DNA片段的鉴定和单独样品的鉴定的一个或多个样品标签区以及用于DNA测序的一个或多个序列。

[0146] 在一些实施方案中,将多个衔接子种类附接至样品的末端修复的细胞或无细胞基因组DNA片段,并且所述多个衔接子全部包含具有相同核苷酸序列的扩增区。

[0147] 在某些实施方案中,来自样品的基因组DNA与包含样品标签序列的多个衔接子附接,所述样品标签序列全部不同于附接至来自其他样品的基因组DNA片段的衔接子中的样品标签区的其他序列。

[0148] 在具体实施方案中,多个衔接子种类附接至来自样品的末端修复的细胞或无细胞基因组DNA片段,并且所述多个衔接子全部包含含有以下的一个或多个样品标签区:在2与10,000个核苷酸序列之间的一个核苷酸序列、在5与5,000个核苷酸序列之间的一个核苷酸序列、在25与1,000个核苷酸序列之间的一个核苷酸序列、在50与500个核苷酸序列之间的一个核苷酸序列、在100与400个核苷酸序列之间的一个核苷酸序列或在200与300个核苷酸序列之间的一个核苷酸序列。在一些实施方案中,每个衔接子的样品标签区的长度为8个核苷酸,并且所述多个衔接子中的每个样品标签区包含240个核苷酸序列中的一个。

[0149] 在某些实施方案中,将多个衔接子种类附接至来自样品的末端修复的细胞或无细

胞基因组DNA片段,并且所述多个衔接子的样品标签区包含汉明距离彼此相差1、2、3、4或大于4的核苷酸序列。在具体实施方案中,所述汉明距离为2。

[0150] 在具体实施方案中,附接至样品的基因组DNA片段的多个衔接子的样品标签区的长度为8个核苷酸,并且包含汉明距离彼此相差2的240个核苷酸序列中的一个。

[0151] 在某些实施方案中,样品标签区用于鉴定单独基因组DNA片段以及用于鉴定单独样品,即基因组文库来源。例如,当附接至样品的多个衔接子的样品标签具有240个可能序列中的一个时,每个样品被鉴定为具有240个可能标签中的一个,并且每个样品接收一组240个标签,这些标签与任何其他样品相隔的汉明距离为二(意味着需要两个碱基变化来将一种标签更改为另一种)。这些相同的标签用于枚举克隆多样性,因此它们也充当序列标签,即用于鉴定基因组DNA片段。为了进一步增加可能序列标签的多样性,可以添加UMI倍增器。例如,可以将UMI倍增器添加至包含由3个碱基的64种可能组合组成的3个核苷酸的衔接子区域。另外,多个衔接子可以包含多于一个锚定序列。例如,多个衔接子可以含有同时使用的4个不同的锚定序列。在样品解复用期间也可以使用这些锚定序列来减少错误。

[0152] 图4示出了第一代衔接子(图4A和图4B)与本发明的衔接子(图4C至图4E)之间的说明性比较。图4A和图4B示出了第一代衔接子的例子,其长度为40nt并且由离散的PCR扩增序列、序列标签和样品标签组成。这里,样品由固定序列(序列标签)鉴定,所述固定序列存在于用于从样品生成DNA文库的所有衔接子上。通过单独且不同的序列(序列标签)鉴定单独基因组片段。图4C至图4E示出了来自本发明的衔接子的说明性例子。显示的说明性衔接子的长度为47个核苷酸,并且序列标签与样品标签组合。存在附加的3nt序列,即UMI倍增器,其由3个碱基的64种可能组合组成。10nt锚定序列是四个不同的相异序列中的一个。

[0153] 因此,在说明性例子(参见图4C至图4E)中,与单个样品组合使用的衔接子组包含240个样品标签序列,其可以被分成四组样品标签序列,每组包含60种标签(每种核苷酸为一组:A、C、T和G)。因此,每组60个标签针对四个锚定序列中的一个是特异性的。总的来说,每个样品可以有240种可能样品标签配置的一个池。具体地,在这种情况下,240个样品标签序列被分成四组60个序列,其中每组涉及特定的锚定区。因此,样品ID不仅涉及来自八个核苷酸样品标签的序列信息,还涉及相关的锚定序列信息。此外,读段内序列的位置是固定的,因此样品标签和锚定序列必须在测序读段内具有固定位置,以通过包含过滤器以供下游考虑。此外,包含UMI倍增器将序列标签多样性从240增加至240×64=15,360种可能的序列标签。

[0154] 本文考虑的一个或多个衔接子的附接可以通过本领域普通技术人员已知的方法进行。在具体实施方案中,将本文考虑的一个或多个衔接子附接至包含平端的末端修复的cfDNA。在某些实施方案中,将本文考虑的一个或多个衔接子附接至末端修复的cfDNA,所述cfDNA包含适合于所用附接方法的互补端。在某些实施方案中,将本文考虑的一个或多个衔接子附接至包含3'突出端的末端修复的cfDNA。

[0155] 在一些实施方案中,将基因组DNA片段附接至多个衔接子包括将末端修复的cfDNA或细胞DNA片段附接至含有至少一部分锚定区的寡核苷酸的步骤。在一些实施方案中,寡核苷酸含有整个锚定区。在具体实施方案中,寡核苷酸是包含与配偶体链双链化的5'磷酸化附接链的DNA双链体,其中所述配偶体链通过在其3'端的化学修饰而被阻止附接,并且其中所述附接链附接至所述基因组DNA片段。在某些实施方案中,与至少一部分锚定区附接的

DNA片段随后与编码全长衔接子序列的DNA寡核苷酸退火。在具体实施方案中,将一种或多种多核苷酸激酶、一种或多种DNA连接酶和/或一种或多种DNA聚合酶添加至编码全长衔接子序列的基因组DNA片段和DNA寡核苷酸中。在一些实施方案中,多核苷酸激酶是T4多核苷酸激酶。在一些实施方案中,DNA连接酶是Taq DNA连接酶。在某些实施方案中,DNA聚合酶是Taq聚合酶。在具体实施方案中,DNA聚合酶是全长Bst聚合酶。

[0156] 图6示出了将多个衔接子附接至修复的DNA片段的3'端的说明性方法。在第一步中,将锚定序列附接至基因组片段的3'端。在该步骤中,锚部分是DNA双链体,其中十个核苷酸5'磷酸化的"附接链"与在其3'端通过化学修饰被阻止附接的八个核苷酸"配偶体链"双链化。锚双链体在磷酸化/封闭端是平端的,因此可以附接至平端的基因组片段。在下一步骤中,将编码完整衔接子序列的寡核苷酸池退火至初始锚定序列。T4多核苷酸激酶、Taq DNA连接酶和全长Bst聚合酶的组合作用如对于顶部链所示经由连接附接该寡核苷酸,并通过DNA聚合在底部链上延伸初始锚定序列以完成全长衔接子序列。可以使用相同的过程将全长衔接子附接至基因组片段的5'端。

[0157] 2.DNA文库扩增

[0158] 在具体实施方案中,本文考虑的遗传分析方法包括基因组DNA文库(例如细胞DNA文库或cfDNA文库)的扩增,以生成DNA克隆文库或DNA克隆的文库,例如cfDNA克隆文库或cfDNA克隆的文库,或者细胞DNA克隆文库或细胞DNA克隆的文库。DNA文库的每个分子包含附接至末端修复的DNA片段的各端的衔接子,并且每个衔接子包含一个或多个扩增区。在一些实施方案中,将不同的衔接子附接至末端修复的cfDNA的不同端。在具体实施方案中,将不同的衔接子附接至末端修复的细胞DNA的不同端。

[0159] 在一些实施方案中,将相同的衔接子附接至DNA片段的两端。相同的衔接子附接至末端修复的DNA的两端允许采用单个引物序列的PCR扩增。在具体实施方案中,衔接子附接的cfDNA文库的一部分将使用采用单个引物序列驱动扩增的标准PCR技术进行扩增。在一个实施方案中,单个引物序列为约25个核苷酸,任选地在标准离子强度条件下预计Tm≥55℃。

[0160] 在具体实施方案中,皮克的初始基因组DNA文库(例如细胞DNA文库或cfDNA文库)被扩增成微克的DNA克隆,这意味着10,000倍的扩增。扩增产物的量可以使用本领域已知的方法测量,例如在Qubit 2.0或Nanodrop仪器上定量来测量。

[0161] 3.测定基因组当量的数目

[0162] 在各种实施方案中,基因组DNA的遗传分析方法包括测定DNA克隆文库中基因组当量的数目。如本文所用,术语"基因组当量"是指每个文库中基因组拷贝的数目。本文考虑的组合物和方法遇到的重要挑战是达到足够的测定灵敏度以检测和分析罕见的遗传突变或遗传序列的差异。为了在逐样品基础上确定测定灵敏度值,通过测量测序文库中存在的基因组当量的数目来测量每个样品中存在的不同和有区别的序列的数目。为了建立灵敏度,必须测量每个样品文库的基因组当量的数目。

[0163] 基因组当量的数目可以在进行测序后通过qPCR测定或通过使用基于生物信息学的计数来测定。在临床样品的工艺流程中,基因组当量的qPCR测量用作DNA文库(例如cfDNA文库或基因组DNA文库)的QC步骤。该步骤在序列分析之前建立了对测定灵敏度的期望值,并且允许从分析中排除样品,条件是该样品相应的DNA克隆文库缺乏所需的基因组当量深度。最终,基于生物信息学的基因组当量计数也用于鉴定每个给定DNA克隆文库的基因组当

量,并因此鉴定测定灵敏度和假阴性估计。

[0164] 经验qPCR测定和统计计数测定应该具有良好的相关性。在测序未能揭示DNA克隆文库中的序列深度的情况下,可能需要重新处理DNA克隆文库和/或附加的测序。

[0165] 在一个实施方案中,使用定量PCR(qPCR)测定来测定细胞DNA或cfDNA克隆文库中的基因组当量。在具体实施方案中,使用已知浓度的标准文库来构建标准曲线,并且将来自qPCR测定的测量值拟合至得到的标准曲线,并且从所述拟合推导出基因组当量的值。本发明人已发现包括一个与基因组中的共同序列特异性地杂交的引物(例如重复序列)和另一个结合衔接子中引物结合位点的引物的"基于重复"的qPCR测定与仅使用衔接子特异性引物(存在于cfDNA克隆的两端)的方法相比,测量到的基因组当量增加8倍。通过基于重复的测定测量的基因组当量的数目提供了更一致的文库间性能以及在测序运行中基因组当量的qPCR估计与生物信息学计数的标签当量之间更好的比对。

[0166] 适用于本文考虑的基于重复的基因组当量测定的重复的说明性例子包括但不限于:短散布核元件(SINE),例如Alu重复;长散布核元件(LINE),例如LINE1、LINE2、LINE3;微卫星重复元件,例如短串联重复(STR),简单序列重复(SSR);以及哺乳动物广泛散布重复(MIR)。

[0167] 在一个实施方案中,所述重复是Alu重复。

[0168] 4.定量遗传分析

[0169] 在各种实施方案中,用于基因组DNA(例如基因组细胞或cfDNA)的遗传分析的方法包括DNA文库克隆的一个或多个靶基因座的定量遗传分析。定量遗传分析包括以下步骤中的一个或多个或全部:捕获包含靶基因座的DNA克隆;捕获的靶向基因座的扩增;对扩增的捕获靶向基因座进行测序;以及生成的序列读段的生物信息学分析。如本文所用,术语"DNA文库克隆"是指DNA文库片段,其中衔接子和基因组DNA片段的组合产生独特DNA序列(例如,可以区别于另一个DNA文库克隆的DNA序列)。

[0170] (a)捕获靶基因座

[0171] 本发明部分地考虑了捕获探针模块,其被设计为保持较大探针的效率和可靠性,但最小化包含较小DNA片段的基因组DNA文库(例如cfDNA克隆文库)中的无信息序列生成。如本文所用的"捕获探针"或"捕获探针模块"可互换使用,并且是指包含捕获探针序列和尾序列的多核苷酸。在具体实施方案中,捕获探针模块序列或其部分充当一个或多个测序引物的引物结合位点。

[0172] 在具体实施方案中,捕获探针模块包含捕获探针。如本文所用,"捕获探针"是指能够与特异性DNA靶区域杂交的区域。在一些实施方案中,捕获探针与由细胞DNA构建的基因组DNA文库一起使用。在具体实施方案中,捕获探针与由cfDNA构建的基因组DNA文库一起使用。因为cfDNA的平均大小为约150至约170bp并且是高度片段化的,所以某些实施方案所涉及的本文考虑的组合物和方法包括使用高密度和相对短的捕获探针来询问目标DNA靶区域。在一些实施方案中,捕获探针能够与以均匀密度分布在所有染色体区段上的DNA靶区域杂交。一组这样的捕获探针在本文中称为"染色体稳定性探针"。染色体稳定性探针用于询问全基因组范围的拷贝数变异,以提供染色体拷贝数(例如,染色体倍性)的全基因组测量。

[0173] 使用高密度捕获探针的一个特别关注点是通常使用特定的"序列规则"设计捕获探针。例如,在设计捕获探针时通常排除冗余序列的区域或显示出极端碱基组成偏差的区

域。然而,本发明人已经发现捕获探针设计规则缺乏灵活性基本上不影响探针性能。相反,严格根据位置约束选择的捕获探针提供中靶序列信息;显示出极少的脱靶和不可映射的读段捕获;并且产生统一的、有用的中靶读段,只有少数例外。此外,紧密探针间距的高冗余度大大补偿了偶尔性能较差的捕获探针。

[0174] 在具体实施方案中,靶区域被多个捕获探针靶向,其中任何两个或更多个捕获探针被设计为与靶区域在彼此10个核苷酸内、在彼此15个核苷酸内、在彼此20苷酸内、在彼此25个核苷酸内、在彼此30个核苷酸内、在彼此35个核苷酸内、在彼此40个核苷酸内、在彼此45个核苷酸内或在彼此50个核苷酸或更多个核苷酸内以及在所有中间的核苷酸长度内结合。

[0175] 在一个实施方案中、捕获探针为约25个核苷酸、约26个核苷酸、约27个核苷酸、约28个核苷酸、约29个核苷酸、约30个核苷酸、约31个核苷酸、约32个核苷酸、约33个核苷酸、约34个核苷酸、约35个核苷酸、约36个核苷酸、约37个核苷酸、约38个核苷酸、约39个核苷酸、约40个核苷酸、约41个核苷酸、约42个核苷酸、约43个核苷酸、约44个核苷酸或约45个核苷酸。

[0176] 在一个实施方案中,捕获探针为约100个核苷酸、约200个核苷酸、约300个核苷酸、约400个核苷酸或约100个核苷酸。在另一个实施方案中,捕获探针为约100个核苷酸至约500个核苷酸、约200个核苷酸至约500个核苷酸、约300个核苷酸至约500个核苷酸或约400个核苷酸至约500个核苷酸或其任何中间范围。

[0177] 在具体实施方案中,捕获探针为60个核苷酸。在另一种实施方案中,捕获探针基本上小于60个核苷酸,但与靶向相同DNA靶区域的60个核苷酸捕获探针相比,可比较地、相当地或更好地杂交。在某个实施方案中,捕获探针为40个核苷酸。

[0178] 在某些实施方案中,捕获探针模块包含尾序列。如本文所用,术语“尾序列”是指捕获探针模块的5’端的多核苷酸,它在具体实施方案中可充当引物结合位点。在具体实施方案中,测序引物结合尾区中的引物结合位点。

[0179] 在具体实施方案中,尾序列为约5至约100个核苷酸、约10至约100个核苷酸、约5至约75个核苷酸、约5至约50个核苷酸、约5至约25个核苷酸或约5至约20个核苷酸。在某些实施方案中,第三区域为约10至约50个核苷酸、约15至约40个核苷酸、约20至约30个核苷酸或约20个核苷酸或任何中间数目的核苷酸。

[0180] 在具体实施方案中,尾序列为约30个核苷酸、约31个核苷酸、约32个核苷酸、约33个核苷酸、约34个核苷酸、约35个核苷酸、约36个核苷酸、约37个核苷酸、约38个核苷酸、约39个核苷酸或约40个核苷酸。

[0181] 在各种实施方案中,捕获探针模块包含结合对的特定成员,使得能够分离和/或纯化与捕获探针杂交的标记和/或扩增的基因组DNA文库(例如,细胞或cfDNA文库)的一个或多个捕获片段。在具体实施方案中,捕获探针模块与生物素或另一种合适的半抗原(例如二硝基苯酚、地高辛)缀合。

[0182] 在各种实施方案中,捕获探针模块与标记的和任选扩增的DNA文库杂交以形成复合物。在一些实施方案中,多功能捕获探针模块基本上与DNA文库中的特异性基因组靶区域杂交。

[0183] 杂交(“Hybridization”或“hybridizing”)条件可以包括任何反应条件,其中两个

核苷酸序列形成稳定的复合物;例如,标记的DNA文库和捕获探针模块形成稳定的标记DNA文库-捕获探针模块复合物。这种反应条件是本领域公知的,并且本领域技术人员将理解,这样的条件可以适当地并且在本发明的范围内改变,例如,较短长度的捕获探针的情况下降低退火温度。当捕获探针复合物的第二区域显示出与标记的DNA文库的区域100%、99%、98%、97%、96%、95%、94%、93%、92%、91%、90%、89%、88%、85%、80%、75%或70%序列同一性、同源性或互补性时,可发生大量杂交。

[0184] 在具体实施方案中,捕获探针为约40个核苷酸,并且最佳退火温度为约44℃至约47℃。

[0185] 在某些实施方案中,本文考虑的方法包括分离标记的cfDNA文库-捕获探针模块复合物。在具体实施方案中,用于分离DNA复合物的方法是本领域技术人员公知的,并且本领域技术人员认为合适的任何方法都可以与本发明的方法一起使用(Ausubel等人,Current Protocols in Molecular Biology,2007-2012)。在具体实施方案中,使用生物素-链霉亲和素分离技术分离复合物。

[0186] 在具体实施方案中,考虑从分离的标记DNA文库片段-捕获探针模块复合物中去除单链3'-端。在某些实施方案中,所述方法包括3'-5'外切核酸酶酶促处理分离的标记DNA文库-多功能捕获探针模块复合物以去除单链3'端。

[0187] 在某些其他实施方案中,所述方法包括利用分离的标记DNA文库片段作为模板,进行多功能捕获探针的5'-3′DNA聚合酶延伸。

[0188] 在某些其他实施方案中,所述方法包括通过5'FLAP内切核酸酶、DNA聚合和通过DNA连接酶的切口闭合的协同作用产生杂交捕获探针分离的标记DNA靶分子,例如标记的cfDNA靶分子或标记的细胞DNA靶分子。

[0189] 多种酶可用于分离的标记DNA文库-多功能捕获探针模块复合物的3'-5'外切核酸酶酶促处理。在具体实施方案中可以使用的显示出3'-5'外切核酸酶酶活性的合适酶的说明性例子包括但不限于:T4或外切核酸酶I、III、V(还参见,Shevelev IV,Hübscher U.,Nat Rev Mol Cell Biol.3(5):364-76(2002))。在具体实施方案中,包含3'-5'外切核酸酶活性的酶是T4聚合酶。在具体实施方案中,可以使用显示出3'-5'外切核酸酶酶活性并且能够进行引物模板延伸的酶,其包括例如T4或外切核酸酶I、III、V(同上)。

[0190] 在一些实施方案中,本文考虑的方法包括对上文和本文其他地方讨论的经3'-5'外切核酸酶酶促处理的复合物进行测序和/或PCR。在具体实施方案中,复制捕获探针分子的尾部以生成杂交核酸分子。在一个实施方案中,生成的杂交核酸分子包含能够与捕获探针模块和捕获探针模块尾序列的互补体杂交的靶区域。

[0191] 在特定的实施方案中,遗传分析包括a)将一个或多个捕获探针模块与多个基因组DNA文库克隆中的一个或多个靶基因座杂交,以形成一个或多个捕获探针模块-DNA文库克隆复合物;b)从a)分离一个或多个捕获探针模块-DNA文库克隆复合物;c)酶促处理来自步骤b)的一个或多个分离的捕获探针模块-DNA文库克隆复合物;d)对来自c)的经酶促处理的复合物进行PCR,其中复制捕获探针分子的尾部以生成扩增的杂交核酸分子,其中扩增的杂交核酸分子包含能够与捕获探针和捕获探针模块尾序列的互补体杂交的靶基因组基因座中的靶序列;以及e)对来自d)的经扩增的杂交核酸分子进行定量遗传分析。

[0192] 在具体实施方案中,考虑了用于测定特异性靶基因座的拷贝数的方法,其包括:a)

将一个或多个捕获探针模块与多个DNA文库克隆中的一个或多个靶基因座杂交,以形成一个或多个捕获探针模块-DNA文库克隆复合物;b)从a)分离一个或多个捕获探针模块-DNA文库克隆复合物;c)酶促处理来自步骤b)的一个或多个分离的捕获探针模块-DNA文库克隆复合物;d)对来自c)的经酶促处理的复合物进行PCR,其中复制捕获探针分子的尾部以生成扩增的杂交核酸分子,其中扩增的杂交核酸分子包含能够与捕获探针和捕获探针模块尾序列的互补体杂交的靶基因组基因座中的靶序列;e)对d)中的经扩增的杂交核酸分子进行PCR扩增;以及f)量化e)中的PCR反应,其中量化允许测定特异性靶区域的拷贝数。

[0193] 在一个实施方案中,步骤c)的酶促处理包括使用具有3'-5'外切核酸酶活性的酶对来自b)的一个或多个捕获探针模块-DNA文库克隆复合物进行3'-5'外切核酸酶酶促处理,以去除单链3'端;通过5'FLAP内切核酸酶、DNA聚合和通过DNA连接酶的切口闭合的协同作用产生一个或多个杂交捕获探针模块-cfDNA文库克隆分子;或使用复合物中分离的DNA克隆作为模板进行捕获探针的5'-3'DNA聚合酶延伸。

[0194] 在一个实施方案中,步骤c)的酶促处理包括使用复合物中分离的DNA克隆作为模板进行捕获探针的5'-3'DNA聚合酶延伸。

[0195] 在具体实施方案中,PCR可以使用本领域技术人员公知的任何标准PCR反应条件进行。在某些实施方案中,e)中的PCR反应使用两个PCR引物。在一个实施方案中,e)中的PCR反应使用第一PCR引物,其与靶基因座内的重复杂交。在具体实施方案中,e)中的PCR反应使用第二PCR引物,其与靶基因座/尾连接处的杂交核酸分子杂交。在某些实施方案中,e)中的PCR反应使用与靶基因座杂交的第一PCR引物和与靶基因座/尾连接处的扩增的杂交核酸分子杂交的第二PCR引物。在具体实施方案中,第二引物与靶基因座/尾连接杂交,使得引物的至少一个或多个核苷酸与靶基因座杂交,并且引物的至少一个或多个核苷酸与尾序列杂交。

[0196] 在某些实施方案中,对从步骤e)获得的扩增的杂交核酸分子进行测序,并将序列水平地比对,即彼此比对但不与参考序列比对。在具体实施方案中,步骤a)至e)用一个或多个捕获探针模块重复一次或多次。捕获探针模块可以相同或不同,并且被设计为靶向靶基因座的cfDNA链。在一些实施方案中,当捕获探针不同时,它们在标记的cfDNA克隆文库中的靶基因座内的重叠或相邻靶序列处杂交。在一个实施方案中,使用高密度捕获探针策略,其中多个捕获探针与靶基因座杂交,并且其中所述多个捕获探针中的每一个在与标记的DNA克隆文库中的靶基因座杂交的任何其他捕获探针的约5、10、15、20、25、30、35、40、45、50、100、200bp或更多长度内(包括所有中间距离)与靶基因座杂交。

[0197] 在一些实施方案中,所述方法可以使用每个靶基因座的两个捕获探针模块进行,其中一个与靶区域上游的"Watson"链(非编码或模板链)杂交,并且一个与靶区域下游的"Crick"链(编码或非模板链)杂交。

[0198] 在具体实施方案中,本文考虑的方法可以进一步用任何数目的捕获探针模块进行多次,例如每个靶基因座的2、3、4、5、6、7、8、9或10个或更多个捕获探针模块,任何数目的所述捕获探针模块以任意组合与Watson或Crick链杂交。在一些实施方案中,获得的序列可以彼此比对以鉴定许多差异中的任何差异。

[0199] 在某些实施方案中,使用一个或多个捕获探针模块询问多个靶基因座,例如在单个反应中询问100、200、300、400、500、600、700、800、900、1000、1500、2000、2500、3000、

3500、4000、4500、5000、10000、50000、100000、500000个或更多个。

[0200] (b)测序

[0201] 在具体实施方案中,定量遗传分析包括如本文其他地方所述对多个杂交核酸分子进行测序,以生成足够的测序深度以获得多个独特测序读段。术语“独特读段”或“独特基因组序列”(UGS)在本文中可互换使用,并通过将单独冗余读段分组为“家族”来鉴定。冗余读段是如下序列读段,其共用相同的UMIE(例如,在基因组序列内共用相同的读段密码和相同DNA序列起始位置)并且源自单个附接事件,因此是彼此的经扩增衍生的“同胞”。代表冗余读段家族的单个共有序列作为独特读段或UGS继续使用。每个独特读段或UGS被视为独特附接事件。对应于特定捕获探针的独特读段的总和被称为针对该特定捕获探针的“原始基因组深度”(RGD)。每个捕获探针产生一组独特读段,它通过分组为家族从总读段计算得出。然后将给定样品的独特读段(例如,样品的原始基因组深度)计算为在逐探针的基础上观察到的所有独特读段的平均值。独特读段是重要的,因为每个独特读段必须源自独特基因组DNA克隆。每个独特读段代表基因组DNA的单倍体当量的输入和分析。独特读段的总和是分析的单倍体基因组的总和。反过来,分析的基因组数目限定了测序测定的灵敏度。作为非限制性例子,如果平均独特读段计数是100个基因组当量,那么该特定测定具有能够检测100个中的一个突变读段或1%的灵敏度。任何低于此的观察结果都是不可靠的。

[0202] 从用于计算样品平均值的数据组排除存在明显拷贝数变化的情况(例如,噪声探针的例子)。在本文中,“噪声探针”是指在大的相同样品组中捕获高度可变数目的独特读段(例如,12-16个样品重复中的高度可变数目的独特读段)的探针。在一些实施方案中,与样品的独特读段的平均数目相比,与噪声探针相关的独特读段的数目增加了50%或更多。在一些实施方案中,与样品的独特读段的平均数目相比,与噪声探针相关的独特读段的数目减少了50%或更多。在一些实施方案中,在特定分析中使用的约2%至约4%的探针被鉴定为噪声探针,并且从计算中排除以测定给定样品的独特读段的平均数目。

[0203] 在一些实施方案中,测序读段被鉴定为“中靶读段”或“脱靶读段”。中靶读段具有基因组DNA序列,其位于用于产生基因组文库的捕获探针附近。在一些实施方案中,其中每个基因组序列与特异性捕获探针物理连接并且其中基因组区段和捕获探针的序列均被确定为统一的信息片段,中靶读段被定义为起始坐标位于相应捕获探针的3’端的400bp内且更通常位于200bp内的任何基因组序列。脱靶读段被定义为具有如下基因组序列,所述基因组序列相对于捕获探针在≥500个碱基对(并且更通常映射至完全不同的染色体)的位置处与参考基因组比对。

[0204] 在具体实施方案中,定量遗传分析包括源自多个样品的杂交核酸分子的多重测序。

[0205] 在各种实施方案中,定量遗传分析包括获得一个或多个或多个标记的DNA文库克隆,每个克隆包含第一DNA序列和第二DNA序列,其中第一DNA序列包含靶向基因座中的序列且第二DNA序列包含捕获探针序列;在一个或多个克隆上进行配对端测序反应并获得一个或多个测序读段或在所述一个或多个克隆上进行测序反应,其中获得大于约100、200、300、400、500个或更多个核苷酸的单个长测序读段,其中所述读段足以鉴定第一DNA序列和第二DNA序列;以及根据测序读段的探针序列对一个或多个克隆的测序读段进行排序或聚类。

[0206] (c)生物信息学分析

[0207] 在各种实施方案中,定量遗传分析还包括测序读段的生物信息学分析。生物信息学分析排除了在没有用于测序的化合物或方法的情况下进行的任何纯粹的心理分析。在某些实施方案中,生物信息学分析包括但不限于:序列比对;基因组当量分析;单核苷酸变异(SNV)分析;基因拷贝数变异(CNV)分析;测量染色体拷贝数;以及检测遗传病变。在具体实施方案中,生物信息学分析可用于量化cfDNA克隆文库中分析的基因组当量数目;检测靶基因座的遗传状态;检测靶基因座中的遗传病变;以及测量靶基因座内的拷贝数波动。

[0208] 可以在序列读段与一种或多种人参考DNA序列之间进行序列比对。在具体实施方案中,测序比对可用于检测靶基因座中的遗传病变,包括但不限于检测核苷酸转换或颠换、核苷酸插入或缺失、基因组重排、拷贝数变化或基因融合。检测作为因果或预后指标的遗传病变可用于诊断、预后、治疗和/或监测特定遗传病症或疾病。

[0209] 本文还考虑了用于序列比对分析的方法,其可以在不需要与参考序列比对的情况下进行,这在本文中称为水平序列分析。可以对通过本文考虑的方法或任何其他方法生成的任何序列进行这种分析。在具体实施方案中,序列分析包括对通过本文考虑的方法获得的读段进行序列比对。

[0210] 在一个实施方案中,在进行测序之后,使用基于生物信息学的计数来测定cfDNA克隆文库中的基因组当量。每个测序读段与特定捕获探针相关,并且分配至每个捕获探针的读段的集合被解析成组。在一组中,读段集在基因组序列内共用相同的读段密码和相同的DNA序列起始位置。这些单独读段被分组为“家族”,并且代表该家族的单个共有序列作为“独特读段”继续使用。构成家族的所有单独读段都源自单个附接事件,因此,它们是彼此的扩增衍生的“同胞”。每个独特读段被认为是独特的附接事件,并且独特读段的总和被认为等于所分析的基因组当量的数目。

[0211] 随着独特克隆的数目接近可能的序列组合的总数,概率规定相同的密码和起始位点组合将通过独立事件创建,并且这些独立事件将不适当地分组在单个家族中。最终结果将是低估了所分析的基因组当量,并且罕见突变读段可能作为测序错误被丢弃,因为它们与具有相同标识符的野生型读段重叠。

[0212] 在具体实施方案中,为了提供cfDNA克隆文库的准确分析,分析的基因组当量数目是可能的独特克隆数目的约1/10、约1/12、约1/14、约1/16、约1/18、约1/20、约1/25或更少。应该理解,以上概述的程序仅仅是说明性的而非限制性的。

[0213] 在一些实施方案中,可能需要增加待分析的基因组当量的数目。为了增加基因组当量的深度,考虑了至少两种解决方案。第一种解决方案是每个样品使用多于一个衔接子组。通过组合衔接子,可以成倍地扩大可能克隆的总数,从而扩大基因组输入的舒适极限。第二种解决方案是将读段密码扩大1、2、3、4或5个或更多个碱基。与每个其他读段密码相差至少2个碱基的可能读段密码的数目以$4^{(n-1)}$放大,其中n是读段密码内的碱基数目。因此,在非限制性例子中,如果读段密码是5个核苷酸且$4^{(5-1)}=256$;因此,对于每个附加的碱基,包含附加的碱基将可用的库扩大了四倍。

[0214] 在一个实施方案中,定量遗传分析包括测序读段的生物信息学分析以鉴定罕见的单核苷酸变异(SNV)。

[0215] 新一代测序的固有错误率为约0.02-0.02%,这意味着从1/200到1/500的碱基调用不正确。为了检测在低于此频率发生的变异和其他突变,例如以1/1000的序列的频率,有

必要使用分子注释策略。作为非限制性例子,使用靶向序列捕获技术分析5000个独特分子将生成(在>50,000个读段的充分测序深度下)5000个独特读段的集合,其中每个独特读段属于全部具有相同读段密码的读段"家族"。在家族中发生的SNV是成为罕见变异的候选者。当在多于一个家族中观察到相同的变异时,它是成为在起始样品中存在的罕见变异的非常强大的候选者。相反,在家族中偶尔发生的变异可能是测序错误,并且在一个且仅一个家族中发生的变异是罕见的或者是离体发生的碱基改变(例如,DNA碱基的氧化或PCR引入的错误)的结果。

[0216] 在一个实施方案中,检测SNV的方法包括根据测定所需的目标灵敏度引入10倍多的基因组输入(基因组或基因组当量)。在一个非限制性例子中,如果所需的灵敏度是2%(2/100),那么实验靶标是2000个基因组的输入。

[0217] 在具体实施方案中,测序数据的生物信息学分析用于检测或鉴定与以下相关的SNV:遗传状态、病症或疾病,遗传嵌合,胎检,亲子鉴定,预测对药物治疗的反应,诊断或监测医疗病症,微生物组分析,病原体筛查以及监测器官移植。

[0218] 在各种实施方案中,提供了用于拷贝数测定分析的方法,包括获得一个或多个或多个克隆,每个克隆包含第一DNA序列和第二DNA序列,其中第一DNA序列包含靶向基因座中的序列且第二DNA序列包含捕获探针序列。在相关的实施方案中,在一个或多个克隆上进行配对端测序反应,并获得一个或多个测序读段。在另一个实施方案中,在一个或多个克隆上进行测序反应,其中获得大于约100个核苷酸的单个长测序读段,其中所述读段足以鉴定第一DNA序列和第二DNA序列。可以根据测序读段的探针序列对一个或多个克隆的测序读段进行排序或聚类。

[0219] 拷贝数分析包括但不限于检查在给定基因组DNA样品中发生的特定基因或突变的拷贝数的分析,并且还可以包括定量测定给定基因的拷贝数或给定样品中的序列差异。在具体实施方案中,拷贝数分析用于检测或鉴定与以下相关的基因扩增:遗传状态、病症或疾病,胎检,遗传嵌合,亲子鉴定,预测对药物治疗的反应,诊断或监测疫疗病症,微生物组分析,病原体筛查,以及监测器官移植。

[0220] 在一些实施方案中,拷贝数分析用于测量染色体不稳定性。在这样的实施方案中,使用包含染色体稳定性探针的捕获探针组来测定所有染色体组中均匀密度下的拷贝数变异。对每个染色体稳定性探针进行拷贝数分析,然后将染色体稳定性探针根据其染色体靶标进行排序。这允许基因组中拷贝数丢失或增加的可视化,并且可以充当染色体稳定性的量度。

[0221] 在具体实施方案中,测序数据的生物信息学分析用于检测或鉴定靶基因座中的一个或多个序列或遗传病变,包括但不限于检测核苷酸转换或颠换、核苷酸插入或缺失、基因组重排、拷贝数变化或基因融合。检测作为因果或预后指标的遗传病变可用于诊断、预后、治疗和/或监测特定遗传病症或疾病。在一个实施方案中,遗传病变与以下相关:遗传状态、病症或疾病,胎检,遗传嵌合,亲子鉴定,预测对药物治疗的反应,诊断或监测医疗病症,微生物组分析,病原体筛查和监测器官移植。

[0222] D.定量CNL测定的临床应用

[0223] 在各种实施方案中,本发明考虑了通过检测目标区域中的突变、SNP、易位、倒位、缺失、拷贝数变化或其他基因变异来检测、鉴定、预测、诊断或监测受试者中的病症或疾病

的方法。

[0224] E.定量遗传分析的临床应用

[0225] 在各种实施方案中,本发明考虑了检测、识别、预测、诊断或监测受试者中的病症或疾病的方法。

[0226] 在具体实施方案中,检测、鉴定、预测、诊断或监测受试者中的遗传状态、病症或疾病的方法包括对DNA克隆文库中的一个或多个靶基因座进行定量遗传分析,以检测或鉴定一个或多个靶基因座处的序列变化。在一些实施方案中,所述变化是拷贝数变化。

[0227] 在一个实施方案中,检测、鉴定、预测、诊断或监测遗传状态、病症或疾病的方法包括从受试者的生物样品分离或获得细胞DNA或cfDNA;用一种或多种末端修复酶处理细胞DNA或cfDNA以生成末端修复的DNA;将一个或多个衔接子附接至末端修复的DNA的各端以生成基因组DNA文库;扩增DNA文库以生成DNA克隆文库;测定DNA克隆文库中的基因组当量数目;以及对DNA克隆文库中的一个或多个靶基因座进行定量遗传分析,以检测或鉴定序列的变化,例如一个或多个靶基因座处的SNP、易位、倒位、缺失或拷贝数变化。

[0228] 在具体实施方案中,检测、鉴定、预测、诊断或监测遗传状态或遗传病症或疾病(其选自由以下组成的组:遗传疾病;遗传嵌合;胎检;亲子鉴定;亲子鉴定;预测对药物治疗的反应;诊断或监测医疗病症;微生物组分析;病原体筛查;和器官移植监测)的方法包括从受试者的生物样品分离或获得基因组DNA;用一种或多种末端修复酶处理DNA以生成末端修复的DNA;将一个或多个衔接子附接至末端修复的DNA的各端以生成基因组DNA文库;扩增基因组DNA文库以生成DNA克隆文库;测定DNA克隆文库中的基因组当量数目;以及对DNA克隆文库中的一个或多个靶基因座进行定量遗传分析,以检测或鉴定一个或多个靶基因座处的序列中的核苷酸转换或颠换、核苷酸插入或缺失、基因组重排、拷贝数变化或基因融合。

[0229] 可用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的遗传疾病的说明性例子包括但不限于癌症、阿尔茨海默病(APOE1)、腓骨肌萎缩症、Leber遗传性视神经病变(LHON)、Angelman综合征(UBE3A,泛素-蛋白连接酶E3A)、Prader-Willi综合征(15号染色体中的区域)、β-地中海贫血(HBB,β-球蛋白)、戈谢病(I型)(GBA,葡糖脑苷脂酶)、囊性纤维化(CFTR上皮氯通道)、镰状细胞病(HBB,β-球蛋白)、泰-萨克斯病(HEXA,己糖胺酶A)、苯丙酮尿症(PAH,苯丙氨酸水解酶)、家族性高胆固醇血症(LDLR,低密度脂蛋白受体)、成人多囊肾病(PKD1,多囊蛋白)、亨廷顿病(HDD,亨廷顿蛋白)、I型神经纤维瘤病(NF1,NF1肿瘤抑制基因)、肌强直性营养不良(DM,蔷仁米)、结节性硬化症(TSC1,马铃薯球蛋白)、软骨发育不全(FGFR3,成纤维细胞生长因子受体)、脆性X综合征(FMR1,RNA结合蛋白)、杜氏肌肉营养不良(DMD,肌萎缩蛋白)、A型血友病(F8C,凝血因子VIII)、Lesch-Nyhan综合征(HPRT1,次黄嘌呤鸟嘌呤核糖基转移酶1)和肾上腺脑白质营养不良(ABCD1)。

[0230] 可用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的癌症的说明性例子包括但不限于:B细胞癌、例如多发性骨髓瘤、黑色素瘤、乳腺癌、肺癌(如非小细胞肺癌或NSCLC)、支气管癌症、结直肠癌、前列腺癌、胰腺癌、胃癌、卵巢癌、尿膀胱癌、脑或中枢神经系统癌症、外周神经系统癌症、食道癌、宫颈癌、子宫或子宫内膜癌、口腔癌或咽癌、肝癌、肾癌、睾丸癌、胆道癌、小肠或阑尾癌、唾液腺癌、甲状腺癌、肾上腺癌、骨肉瘤、软骨肉瘤、血液组织癌、腺癌、炎性肌纤维母细胞瘤、胃肠道间质瘤(GIST)、结肠癌、多发性骨髓瘤(MM)、骨髓增生异常综合征(MDS)、骨髓增殖性疾病(MPD)、急性淋巴细胞白血病(ALL)、急性粒细胞

白血病(AML)、慢性粒细胞白血病(CML)、慢性淋巴细胞白血病(CLL)、真性红细胞增多症、霍奇金淋巴瘤、非霍奇金淋巴瘤(NHL)、软组织肉瘤、纤维肉瘤、粘液肉瘤、脂肪肉瘤、骨肉瘤、脊索瘤、血管肉瘤、内皮肉瘤、淋巴管肉瘤、淋巴管内皮肉瘤、滑膜瘤、间皮瘤、尤文氏肉瘤、平滑肌肉瘤、横纹肌肉瘤、鳞状细胞癌、基底细胞癌、腺癌、汗腺癌、皮脂腺癌、乳头状癌、乳头状腺癌、髓样癌、支气管癌、肾细胞癌、肝细胞瘤、胆管癌、绒毛膜癌、精原细胞瘤、胚胎性癌、维尔姆斯瘤、膀胱癌、上皮癌、神经胶质瘤、星形细胞瘤、成神经管细胞瘤、颅咽管瘤、室管膜瘤、松果体瘤、血管母细胞瘤、听神经瘤、少突神经胶质瘤、脑膜瘤、神经母细胞瘤、视网膜母细胞瘤、滤泡性淋巴瘤、弥漫性大B细胞淋巴瘤、套细胞淋巴瘤、肝细胞癌、甲状腺癌、胃癌、头颈癌、小细胞癌、原发性血小板增多症、不明原因的髓样化生、嗜酸性粒细胞增多症、系统性肥大细胞增生症、熟悉嗜酸性粒细胞增多症、慢性嗜酸性粒细胞白血病、神经内分泌癌、类癌肿瘤等。

[0231] 在一个实施方案中,遗传病变是在Cosmic数据库中注释的病变(病变和序列数据可在线获得,并且可从Cosmic网站的Cancer Gene Census部分下载)或在癌症基因组图谱中注释的病变(病变和序列数据可在线获得,并且可从The Cancer Genome Atlas网站下载)。

[0232] 具有可采用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的与癌症相关的一种或多种遗传病变的基因的说明性例子包括但不限于ABCB1、ABCC2、ABCC4、ABCG2、ABL1、ABL2、AKT1、AKT2、AKT3、ALDH4A1、ALK、APC、AR、ARAF、ARFRP1、ARID1A、ATM、ATR、AURKA、AURKB、BCL2、BCL2A1、BCL2L1、BCL2L2、BCL6、BRAF、BRCA1、BRCA2、Clorf144、CARD11、CBL、CCND1、CCND2、CCND3、CCNE1、CDH1、CDH2、CDH20、CDH5、CDK4、CDK6、CDK8、CDKN2A、CDKN2B、CDKN2C、CEBPA、CHEK1、CHEK2、CRKL、CRLF2、CTNNB1、CYP1B1、CYP2C19、CYP2C8、CYP2D6、CYP3A4、CYP3A5、DNMT3A、DOT1L、DPYD、EGFR、EPHA3、EPHA5、EPHA6、EPHA7、EPHB1、EPHB4、EPHB6、EPHX1、ERBB2、ERBB3、ERBB4、ERCC2、ERG、ESR1、ESR2、ETV1、ETV4、ETV5、ETV6、EWSR1、EZH2、FANCA、FBXW7、FCGR3A、FGFR1、FGFR2、FGFR3、FGFR4、FLT1、FLT3、FLT4、FOXP4、GATA1、GNA11、GNAQ、GNAS、GPR124、GSTP1、GUCY1A2、HOXA3、HRAS、HSP90AA1、IDH1、IDH2、IGF1R、IGF2R、IKBKE、IKZF1、INHBA、IRS2、ITPA、JAK1、JAK2、JAK3、JUN、KDR、KIT、KRAS、LRP1B、LRP2、LTK、MAN1B1、MAP2K1、MAP2K2、MAP2K4、MCL1、MDM2、MDM4、MEN1、MET、MITF、MLH1、MLL、MPL、MRE11A、MSH2、MSH6、MTHFR、MTOR、MUTYH、MYC、MYCL1、MYCN、NF1、NF2、NKX2-1、NOTCH1、NPM1、NQO1、NRAS、NRP2、NTRK1、NTRK3、PAK3、PAX5、PDGFRA、PDGFRB、PIK3CA、PIK3R1、PKHD1、PLCG1、PRKDC、PTCH1、PTEN、PTPN11、PTPRD、RAF1、RARA、RB1、RET、RICTOR、RPTOR、RUNX1、SLC19A1、SLC22A2、SLCO1B3、SMAD2、SMAD3、SMAD4、SMARCA4、SMARCB1、SMO、SOD2、SOX10、SOX2、SRC、STK11、SULT1A1、TBX22、TET2、TGFBR2、TMPRSS2、TNFRSF14、TOP1、TP53、TPMT、TSC1、TSC2、TYMS、UGT1A1、UMPS、USP9X、VHL和WT1。

[0233] 在具体实施方案中,遗传病变包括核苷酸转换或颠换、核苷酸插入或缺失、基因组重排、拷贝数变化或基因融合。

[0234] 在一个实施方案中,遗传病变是基因融合,其将ALK基因的3'编码区与另一基因融合。

[0235] 在一个实施方案中,遗传病变是基因融合,其将ALK基因的3'编码区与EML4基因融合。

[0236] 可以用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的适合于胎检的病症的说明性例子包括但不限于:唐氏综合征(21三体)、爱德华氏综合征(18三体)、Patau综合征(13三体)、克氏综合征(XXY)、Triple X综合征、XYY综合征、8三体、16三体、特纳综合征(XO)、罗伯逊易位、迪乔治综合征和Wolf-Hirschhorn综合征。

[0237] 可以用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的适合于亲子鉴定的等位基因的说明性例子包括但不限于以下中的16种或更多种:D20S1082、D6S474、D12ATA63、D22S1045、D10S1248、D1S1677、D11S4463、D4S2364、D9S1122、D2S1776、D10S1425、D3S3053、D5S2500、D1S1627、D3S4529、D2S441、D17S974、D6S1017、D4S2408、D9S2157、釉原蛋白、D17S1301、D1GATA113、D18S853、D20S482和D14S1434。

[0238] 可以用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的适合于预测药物治疗反应的基因的说明性例子包括但不限于以下基因中的一种或多种:ABCB1(ATP结合盒、亚家族B(MDR/TAP)、成员1)、ACE(血管紧张素I转化酶)、ADH1A(醇脱氢酶1A(I类)、α多肽)、ADH1B(醇脱氢酶IB(I类)、β多肽),ADH1C(醇脱氢酶1C(I类)、γ多肽),ADRB1(肾上腺素能,β-1-,受体),ADRB2(肾上腺素能,β-2-,受体,表面)、AHR(芳基碳氢化合物受体)、ALDH1A1(醛脱氢酶1家族,成员A1)、ALOX5(花生四烯酸5-脂氧合酶)、BRCA1(乳腺癌1,早发)、COMT(儿茶酚-O-甲基转移酶)、CYP2A6(细胞色素P450,家族2,亚家族A,多肽6)、CYP2B6(细胞色素P450,家族2,亚家族B,多肽6)、CYP2C9(细胞色素P450,家族2,亚家族C,多肽9)、CYP2C19(细胞色素P450,家族2,亚家族C,多肽19)、CYP2D6(细胞色素P450,家族2,亚家族D,多肽6)、CYP2J2(细胞色素P450,家族2,亚家族J,多肽2)、CYP3A4(细胞色素P450,家族3,亚家族A,多肽4)、CYP3A5(细胞色素P450,家族3,亚家族A,多肽5)、DPYD(二氢嘧啶脱氢酶)、DRD2(多巴胺受体D2)、F5(凝血因子V)、GSTP1(谷胱甘肽S-转移酶pi)、HMGCR(3-羟基-3-甲基戊二酰基-辅酶A还原酶)、KCNH2(钾电压门控通道,亚家族H(eag相关),成员2)、KCNJ11(钾内向整流通道,亚家族J,成员11)、MTHFR(5,10-亚甲基四氢叶酸还原酶(NADPH))、NQO1(NAD(P)H脱氢酶,醌1)、P2RY1(嘌呤能受体P2Y,G蛋白偶联,1)、P2RY12(嘌呤能受体P2Y,G蛋白偶联,12)、PTGIS(前列腺素I2(前列环素)合酶)、SCN5A(钠通道,电压门控,V型,α(长QT综合征3))、SLC19A1(溶质载体家族19(叶酸转运蛋白),成员1)、SLCO1B1(溶质载体有机阴离子转运蛋白家族,成员1B1)、SULT1A1(磺基转移酶家族,细胞溶质,1A,偏选苯酚,成员1)、TPMT(硫嘌呤S-甲基转移酶)、TYMS(胸苷酸合成酶)、UGT1A1(UDP葡糖醛酸基转移酶1家族,多肽A1)、VDR(维生素D(1,25-二羟基维生素D3)受体)、VKORC1(维生素K环氧化物还原酶复合物,亚基1)。

[0239] 可用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的医学病症的说明性例子包括但不限于:中风、短暂性脑缺血发作、创伤性脑损伤、心脏病、心脏病发作、心绞痛、动脉粥样硬化和高血压。

[0240] 可用本文考虑的组合物和方法筛查的病原体的说明性例子包括但不限于:细菌、真菌和病毒。

[0241] 可用本文考虑的组合物和方法筛查的细菌物种的说明性例子包括但不限于:分枝杆菌属物种、肺炎球菌属物种、埃希氏菌属物种、弯曲菌属物种、棒状杆菌属物种、梭菌属物种、链球菌属物种、葡萄球菌属物种、假单胞菌属物种、志贺氏菌属物种、密螺旋体属物种或沙门氏菌属物种。

[0242] 可用本文考虑的组合物和方法筛查的真菌物种的说明性例子包括但不限于:曲霉属物种、芽生菌属物种、假丝酵母属物种、球孢子虫属物种、隐球菌属物种、肤癣菌、癣属物种、毛癣菌属物种、小孢子癣菌属物种、镰刀菌属物种、组织胞浆菌属物种、毛霉亚门(Mucoromycotina)物种、肺孢子虫属物种、孢子丝菌属物种、突脐蠕孢属物种或枝孢属物种。

[0243] 可用本文考虑的组合物和方法筛查的病毒的说明性例子包括但不限于:甲型流感(如H1N1、H1N2、H3N2和H5N1(禽流感))、乙型流感、丙型流感病毒、甲型肝炎病毒、乙型肝炎病毒、丙型肝炎病毒、丁型肝炎病毒、戊型肝炎病毒、轮状病毒、诺瓦克病毒组的任何病毒、肠道腺病毒、细小病毒、登革热病毒、猴痘、单链病毒、狂犬病毒等狂犬病病毒、拉各斯蝙蝠病毒、Mokola病毒、Duvenhage病毒、欧洲蝙蝠病毒1和2以及澳大利亚蝙蝠病毒、Ephemerovirus、水泡病毒属、水泡性口炎病毒(VSV)、疱疹病毒(如单纯疱疹病毒1型和2型、水痘带状疱疹、巨细胞病毒、Epstein-Bar病毒(EBV)、人类疱疹病毒(HHV)、人类疱疹病毒6型和8型)、莫洛尼鼠白血病病毒(M-MuLV)、莫洛尼鼠肉瘤病毒(MoMSV)、Harvey鼠肉瘤病毒(HaMuSV)、鼠乳腺瘤病毒(MuMTV)、长臂猿白血病病毒(GaLV)、猫白血病病毒(FLV)、泡沫病毒属、Friend鼠白血病病毒、鼠干细胞病毒(MSCV)和Rous肉瘤病毒(RSV)、HIV(人类免疫缺陷病毒;包括HIV 1型和HIV 2型)、visna-maedi病毒(VMV)病毒、山羊关节炎-脑炎病毒(CAEV)、马传染性贫血病毒(EIAV)、猫免疫缺陷病毒(FIV)、牛免疫缺陷病毒(BIV)和猿猴免疫缺陷病毒(SIV)、乳头瘤病毒、鼠γ疱疹病毒、沙粒病毒(如阿根廷出血热病毒、玻利维亚出血热病毒、萨比亚相关出血热病毒、委内瑞拉出血热病毒、拉沙热病毒)、马丘波病毒、淋巴细胞性脉络丛脑膜炎病毒(LCMV)、Bunyaviridiae如克里米亚-刚果出血热病毒、汉坦病毒、引起伴有肾综合征的出血热的病毒、裂谷热病毒、包括埃博拉出血热和马尔堡出血热的丝状病毒科(丝状病毒)、包括Kaysanur Forest疾病病毒的黄病毒科、鄂木斯克出血热病毒、引起森林脑炎的病毒和副粘病毒科(如Hendra病毒和Nipah病毒)、大天花和小天花(天花)、甲病毒(如委内瑞拉马脑炎病毒、东部马脑炎病毒、西部马脑炎病毒)、SARS相关冠状病毒(SARS-CoV)、西尼罗河病毒和引起脑炎的任何病毒。

[0244] 可以用本文考虑的组合物和方法检测、鉴定、预测、诊断或监测的适合于监测移植接受者中器官移植的基因的说明性例子包括但不限于以下基因中的一种或多种:HLA-A、HLA-B、HLA-C、HLA-DR、HLA-DP和HLA-DQ。

[0245] 在具体实施方案中,生物信息学分析用于量化cfDNA克隆文库中分析的基因组当量的数目;检测靶基因座中的遗传变异;检测靶基因座内的突变;检测靶基因座内的遗传融合;或测量靶基因座内的拷贝数波动。

[0246] F.伴随诊断

[0247] 在各种实施方案中,提供了遗传疾病的伴随诊断,其包括:从受试者的生物样品分离或获得基因组DNA;用一种或多种末端修复酶处理DNA以生成末端修复的DNA;将一个或多个衔接子附接至末端修复的DNA的各端以生成DNA文库;扩增DNA文库以生成DNA克隆文库;测定DNA克隆文库中的基因组当量的数目;以及对DNA克隆文库中与遗传疾病相关的一种或多种生物标志物进行定量遗传分析,其中检测到或未检测到一种或多种生物标志物中的至少一种表明所述受试者是否应该对该遗传疾病进行治疗。在一些实施方案中,DNA是cfDNA。在具体实施方案中,DNA是细胞DNA。

[0248] 如本文所用,术语“伴随诊断”是指与特定抗癌疗法相关的诊断测试。在具体实施方案中,诊断方法包括检测与生物样品相关的生物标志物中的遗传病变,从而允许快速鉴定患者应该或不应该用抗癌疗法治疗。

[0249] 抗癌疗法包括但不限于手术、放疗、化疗、抗癌药物和免疫调节剂。

[0250] 抗癌药物的说明性例子包括但不限于:烷化剂如噻替哌和环磷酰胺(CYTOXAN™);烷基磺酸盐如白消安、英丙舒凡和哌泊舒凡;氮丙啶类如benzodopa、卡波醌、meturedopa和uredopa;乙烯亚胺和methylamelamine,包括六甲蜜胺,三乙烯三聚氰胺、三乙烯磷酰胺、三乙烯硫代磷酰胺和trimethylolomelamine resume;氮芥如苯丁酸氮芥、萘氮芥、氯磷酰胺、雌莫司汀、异环磷酰胺、氮芥、盐酸甲氧氮芥、美法仑、新恩比兴、苯芥胆甾醇、泼尼氮芥、曲洛磷胺、乌拉莫司汀;亚硝基脲如卡莫司汀、氯脲霉素、福莫司汀、洛莫司汀、尼莫司汀、雷莫司汀;抗生素如aclacinomysin、放线菌素、authramycin、重氮丝氨酸、博来霉素、cactinomycin、卡里奇霉素、carabicin、洋红霉素、嗜癌菌素、色霉素、更生霉素、道诺霉素、地托比星、6-二氮-5-氧-L-正亮氨酸、阿霉素及其聚乙二醇化制剂、表柔比星、依索比星、伊达比星、麻西罗霉素、丝裂霉素、霉酚酸、诺加霉素、橄榄霉素、培洛霉素、potfiromycin、嘌呤霉素、三铁阿霉素、罗多比星、链黑菌素、链脲霉素、杀结核菌素、乌苯美司、新制癌菌素、佐柔比星;抗代谢物如甲氨蝶呤和5-氟尿嘧啶(5-FU);叶酸类似物如二甲叶酸、甲氨蝶呤、蝶罗呤、三甲曲沙;嘌呤类似物如氟达拉滨、6-巯嘌呤、硫咪嘌呤、硫鸟嘌呤;嘧啶类似物如安西他滨、阿扎胞苷、6-氮尿苷、卡莫氟、阿糖胞苷、双脱氧尿苷、去氧氟尿苷、依诺他滨、氟尿苷、5-FU;雄激素如卡普睾酮、屈他雄酮丙酸酯、环硫雄醇、美雄烷、睾内酯;抗肾上腺,如氨鲁米特、米托坦、曲洛司坦;叶酸补充剂如亚叶酸;醋葡醛内酯;醛磷酰胺糖苷;氨基乙酰丙酸;安吖啶;bestrabucil;比生群;edatraxate;defofamine;地美可辛;亚丝醌;elformithine;依利醋铵;依托格鲁;硝酸镓;羟基脲;香菇多糖;氯尼达明;米托胍腙;米托蒽醌;莫哌达醇;硝基可润;喷司他丁;苯来美特;吡柔比星;podophyllinic acid;2-乙基酰肼;甲基苄肼;PSK®;雷佐生;西佐喃;锗螺胺;细交链孢菌酮酸;三亚胺醌;2,2',2”-三氯三乙胺;乌拉坦;长春地辛;达卡巴嗪;甘露醇氮芥;二溴甘露醇;二溴卫矛醇;哌泊溴烷;gacytosine;阿拉伯糖苷(“Ara-C”);环磷酰胺;噻替哌;紫杉烷,例如紫杉醇(TAXOL®,Bristol-Myers Squibb Oncology,Princeton,N.J.)和多西紫杉醇(TAXOTERE®.,Rhne-Poulenc Rorer,Antony,France);苯丁酸氮芥;吉西他滨;6-硫鸟嘌呤;巯嘌呤;甲氨蝶呤;铂类似物如顺铂和卡铂;长春碱;铂;依托泊苷(VP-16);异环磷酰胺;丝裂霉素C;米托蒽醌;长春新碱;长春瑞滨;诺维本;米托蒽醌;替尼泊苷;氨基蝶呤;希罗达;伊班膦酸钠;CPT-11;拓扑异构酶抑制剂RFS 2000;二氟甲基鸟氨酸(DMFO);视黄酸衍生物,如Targretin™(蓓萨罗丁)、Panretin™(阿利维a酸);ONTAK™(地尼白介素);esperamicins;卡培他滨;以及上述的任何药学上可接受的盐、酸或衍生物。该定义还包括用于调节或抑制激素对癌症的作用的抗-激素剂如抗雌激素,包括例如它莫昔芬、雷洛昔芬、芳香化酶抑制4(5)-咪唑、4-羟基三苯氧胺、曲沃昔芬、keoxifene、LY117018、奥那司酮和托瑞米芬(Fareston);和抗雄激素如氟他胺、尼鲁米特、比卡鲁胺、亮丙瑞林和戈舍瑞林;以及上述的任何药学上可接受的盐、酸或衍生物。

[0251] 免疫调节剂的说明性例子包括但不限于:环孢菌素、他克莫司、曲培莫司、吡美莫

司、西罗莫司、依罗莫司、拉氟莫司、拉喹莫德和咪喹莫特以及其类似物、衍生物、盐、离子和复合物。

[0252] 在一些实施方案中,抗癌药物可包括聚ADP核糖聚合酶(PARP)抑制剂。PARP抑制剂的说明性例子包括但不限于奥拉帕尼(AZD-2281)、卢卡帕利(AG014699或PF-01367338)、尼雷帕利(MK-4827)、他佐帕利(BMN-673)、维利帕利(ABT-888)、CEP 9722、E7016、BGB-290、3-氨基苯甲酰胺。

[0253] 本申请还涉及以下实施方案:

[0254] 实施方案1.一种用于对来自测试样品的DNA靶区域进行遗传分析的方法,其包括:

[0255] (a)生成包含多个DNA文库片段的基因组DNA文库,其中所述DNA文库片段中的每一个包含来自所述测试样品的基因组DNA片段和衔接子;

[0256] (b)使所述基因组DNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的所述DNA文库片段之间形成复合物;以及

[0257] (c)对包含所述DNA靶区域的基因组DNA片段进行定量遗传分析;

[0258] 其中所述衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;

[0259] 其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;

[0260] 其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;

[0261] 其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段;并且

[0262] 其中进行所述遗传分析以检测指示疾病状态的遗传变化。

[0263] 实施方案2.如实施方案1所述的方法,其中所述指示疾病状态的遗传变化选自单核苷酸变异(SNV)、长度小于40个核苷酸的插入、长度小于40个核苷酸的DNA区域的缺失和/或拷贝数变化。

[0264] 实施方案3.如实施方案1所述的方法,其中所述指示疾病状态的遗传变化是拷贝数变化。

[0265] 实施方案4.如实施方案1-3中任一项所述的方法,其中所述测试样品是组织活检。

[0266] 实施方案5.如实施方案4所述的方法,其中所述组织活检取自肿瘤或怀疑为肿瘤的组织。

[0267] 实施方案6.如实施方案1-3中任一项所述的方法,其中所述基因组DNA是无细胞DNA(cfDNA)或细胞DNA。

[0268] 实施方案7.如实施方案6所述的方法,其中所述基因组DNA是从所述测试样品分离的cfDNA;并且其中所述测试样品是选自由以下组成的组的生物样品:羊水、血液、血浆、血清、精液、淋巴液、脑脊液、眼内液、尿液、唾液、粪便、粘液和汗液。

[0269] 实施方案8.如实施方案1-5中任一项所述的方法,其中通过包括以下的步骤获得所述基因组DNA片段:

[0270] (i)从所述测试样品分离细胞DNA;

[0271] (ii)使所述细胞DNA片段化以获得所述基因组DNA片段。

[0272] 实施方案9.如实施方案8所述的方法,其中步骤(ii)是通过使所述细胞DNA与至少一种消化酶接触来进行的。

[0273] 实施方案10.如实施方案8所述的方法,其中步骤(ii)是通过对所述细胞DNA施加机械应力来进行的。

[0274] 实施方案11.如实施方案10所述的方法,其中通过超声处理所述细胞DNA来施加所述机械应力。

[0275] 实施方案12.如前述实施方案中任一项所述的方法,其中所述样品标签还包含有助于鉴定独特基因组DNA片段的独特分子标识符(UMI)。

[0276] 实施方案13.如前述实施方案中任一项所述的方法,其中所述扩增区的长度在10与50个核苷酸之间。

[0277] 实施方案14.如前述实施方案中任一项所述的方法,其中所述扩增区的长度在20与30个核苷酸之间。

[0278] 实施方案15.如前述实施方案中任一项所述的方法,其中所述扩增区的长度为25个核苷酸。

[0279] 实施方案16.如前述实施方案中任一项所述的方法,其中所述样品标签的长度在5与50个核苷酸之间。

[0280] 实施方案17.如实施方案16所述的方法,其中所述样品标签的长度在5与15个核苷酸之间。

[0281] 实施方案18.如实施方案16所述的方法,其中所述样品标签的长度为8个核苷酸。

[0282] 实施方案19.如实施方案12-18中任一项所述的方法,其中所述UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。

[0283] 实施方案20.如实施方案19所述的方法,其中所述UMI倍增器的长度在1与5个核苷酸之间。

[0284] 实施方案21.如实施方案19所述的方法,其中所述UMI倍增器的长度为3个核苷酸,并且包含64个可能的核苷酸序列中的一个。

[0285] 实施方案22.如前述实施方案中任一项所述的方法,其中所述锚定区的长度在1与50个核苷酸之间。

[0286] 实施方案23.如实施方案22所述的方法,其中所述锚定区的长度在5与25个核苷酸之间。

[0287] 实施方案24.如实施方案22或23所述的方法,其中所述锚定区的长度为10个核苷酸。

[0288] 实施方案25.如前述实施方案中任一项所述的方法,其中步骤(a)包括将所述基因组DNA片段附接至多个衔接子。

[0289] 实施方案26.如实施方案25所述的方法,其中在将所述基因组DNA片段与多个衔接子附接之前,对所述基因组DNA片段进行末端修复。

[0290] 实施方案27.如实施方案25所述的方法,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。

[0291] 实施方案28.如实施方案26或27所述的方法,其中所述多个衔接子中的每个衔接子的样品标签区包含在2与1,000个核苷酸序列之间的一个核苷酸序列。

[0292] 实施方案29.如实施方案28所述的方法,其中所述多个衔接子中的每个衔接子的样品标签区包含在50与500个核苷酸序列之间的一个核苷酸序列。

[0293] 实施方案30.如实施方案28所述的方法,其中所述多个衔接子中的每个衔接子的样品标签区包含在100与400个核苷酸序列之间的一个核苷酸序列。

[0294] 实施方案31.如实施方案28所述的方法,其中所述多个衔接子中的每个衔接子的样品标签区包含在200与300个核苷酸序列之间的一个核苷酸序列。

[0295] 实施方案32.如实施方案28所述的方法,其中所述多个衔接子中的每个衔接子的样品标签区的长度为8个核苷酸。

[0296] 实施方案33.如实施方案28-32中任一项所述的方法,其中所述核苷酸序列中的每个序列与240个核苷酸序列的任何其他序列相隔的汉明距离为至少二。

[0297] 实施方案34.如实施方案26-33中任一项所述的方法,其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。

[0298] 实施方案35.如实施方案26-34中任一项所述的方法,其中所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍增器。

[0299] 实施方案36.如实施方案34或35所述的方法,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度在1与5个核苷酸之间。

[0300] 实施方案37.如实施方案36所述的方法,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸。

[0301] 实施方案38.如实施方案26-37所述的方法,其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0302] 实施方案39.如实施方案25或26所述的方法,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;

[0303] 其中所述多个衔接子中的每个衔接子的样品标签区的长度为8个核苷酸,其中每个样品标签的核苷酸序列与所述多个衔接子的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二,

[0304] 其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸,并且其中每个可能的核苷酸序列的UMI倍增器与所述多个衔接子的每个样品标签区配对,

[0305] 其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0306] 实施方案40.如实施方案25-39中任一项所述的方法,其中将所述基因组DNA片段与多个衔接子附接的步骤包括:

[0307] (i)将包含锚定区的至少一部分的寡核苷酸附接至每个基因组DNA片段,其中所述包含锚定区的至少一部分的寡核苷酸是DNA双链体,所述DNA双链体包含与配偶体链双链化的5’磷酸化附接链,其中所述配偶体链通过在其3’端的化学修饰而被阻止附接,并且其中所述附接链附接至所述基因组DNA片段;

[0308] (ii)使与包含所述锚定区的至少一部分的寡核苷酸附接的基因组DNA片段与编码所述多个衔接子中的每个衔接子核苷酸序列的全长衔接子序列的DNA寡核苷酸接触;并且

[0309] (iii)在适合于DNA连接的条件下,使所述基因组DNA片段和编码所述全长衔接子

序列的DNA寡核苷酸与T4多核苷酸激酶、Taq DNA连接酶和全长Bst聚合酶接触;

[0310] 从而将所述多个衔接子附接至所述基因组DNA片段。

[0311] 实施方案41.如实施方案25-40中任一项所述的方法,其中所述基因组DNA片段是cfDNA。

[0312] 实施方案42.如实施方案25-41中任一项所述的方法,其中分析所述DNA靶区域的拷贝数变化。

[0313] 实施方案43.如前述实施方案中任一项所述的方法,其中步骤(c)包括对所述捕获探针与包含所述DNA靶区域的所述DNA文库片段之间形成的复合物进行纯化。

[0314] 实施方案44.如前述实施方案中任一项所述的方法,其中步骤(c)包括对在所述捕获探针与包含所述DNA靶区域的所述DNA文库片段之间形成的复合物进行纯化,从而预形成包含来自所述基因组DNA文库的目标区域的DNA文库片段的引物延伸和/或扩增。

[0315] 实施方案45.如前述实施方案中任一项所述的方法,其中步骤(c)包括对在所述捕获探针与包含所述DNA靶区域的所述DNA文库片段之间形成的复合物进行纯化,从而预形成包含来自所述基因组DNA文库的目标区域的所述DNA文库片段的引物延伸和扩增。

[0316] 实施方案46.如前述实施方案中任一项所述的方法,其中步骤(c)包括对包含所述DNA靶区域的所述DNA文库片段进行DNA测序,以生成多个测序读段。

[0317] 实施方案47.如前述实施方案中任一项所述的方法,其中其中基因组分析包括测定目标DNA区域中的拷贝数变化,并且其中步骤(c)包括:

[0318] (i).测定源自所述测试样品的基因组DNA文库中存在的目标区域的拷贝数,并且

[0319] (ii).将步骤(i)中测定的拷贝数与源自参考样品的基因组DNA文库中存在的目标区域的拷贝数进行比较,其中所述参考样品包含已知拷贝数目的所述DNA靶区域。

[0320] 实施方案48.如实施方案47所述的方法,其中测定所述目标区域中的拷贝数包括对包含所述DNA靶区域的所述DNA文库片段进行DNA测序,以生成多个测序读段,其中每个测序读段包含独特分子标识元件(UMIE)。

[0321] 实施方案49.如实施方案48所述的方法,其中所述UMIE包含来自所述衔接子和至少一部分所述基因组DNA序列的测序信息。

[0322] 实施方案50.如实施方案49所述的方法,其中包含相同UMIE的测序读段被鉴定为独特基因组序列(UGS)。

[0323] 实施方案51.如实施方案47-50中任一项所述的方法,其还包括针对与所述基因组DNA文库接触的所述捕获探针中的每一个测定原始基因组深度(RGD)。

[0324] 实施方案52.如实施方案51所述的方法,其中测定所述RGD包括测定与一组样品重复中的每个捕获探针序列相关联的UGS的平均数目。

[0325] 实施方案53.如实施方案52所述的方法,其中与高度可变数目的UGS相关联的捕获探针被鉴定为噪声探针并且从进一步的计算中去除。

[0326] 实施方案54.如实施方案52所述的方法,其还包括计算样品的RGD,其包括计算所述样品中针对所有捕获探针的所有RGD的数值平均值。

[0327] 实施方案55.如实施方案52所述的方法,其中在计算样品的RGD中不包括针对噪声探针的RGD值。

[0328] 实施方案56.如实施方案51-55中任一项所述的方法,其中通过将针对每个捕获探

针的RGD转换成探针特异性归一化读段计数将实验组中所有样品中针对所述捕获探针的RGD归一化,其包括

[0329] (i)使样品中的每个捕获探针RGD乘以归一化常数,其中所述归一化常数包括任何实数;以及

[0330] (ii)使(i)的乘积除以针对相应样品计算的RGD;或

[0331] (iii)使(i)的乘积除以从探针子集计算的平均RGD。

[0332] 实施方案57.如实施方案56所述的方法,其中所述探针子集是对照探针组。

[0333] 实施方案58.如实施方案57所述的方法,其中将所述探针特异性归一化读段计数转换成拷贝数值,其包括

[0334] (i)在源自女性的样品中使针对常染色体和/或X连锁区的探针的探针特异性归一化读段计数乘以2;

[0335] (ii)在源自男性的样品中使针对Y连锁和/或X连锁区的探针的探针特异性归一化读段计数乘以1;

[0336] (iii)对实验中的所有样品的(i)和/或(ii)的乘积取平均值;并且

[0337] (iv)使(i)和/或(ii)的乘积除以(iii)的平均值。

[0338] 实施方案59.如实施方案58所述的方法,其中对于针对靶向特异性基因的所有探针的近似拷贝数值取平均值。

[0339] 实施方案60.一种用于高灵敏地检测拷贝数增加和拷贝数丢失的方法,其包括:

[0340] (i).测定针对捕获探针的RGD;

[0341] (ii).通过将针对所述捕获探针的RGD转换成探针特异性归一化读段计数,对实验组中所有样品中针对所述捕获探针的RGD进行归一化;

[0342] (iii).计算每个探针特异性归一化读段计数的近似拷贝数值;并且

[0343] (iv).对于针对靶向特异性基因的所有探针的近似拷贝数值取平均值。

[0344] 实施方案61.一种用于测量染色体稳定性的方法,其包括:

[0345] (i).设计和验证一种或多种染色体稳定性探针的组,其中所述染色体稳定性探针均匀分布在人染色体上;

[0346] (ii).使用所述一种或多种染色体稳定性探针对患者样品进行靶向测序;

[0347] (iii).针对每种染色体探针测定近似拷贝数值;

[0348] (iv).测定患者样品的基因组表型,其中所述患者样品中针对一种或多种染色体探针的拷贝数值的波动表明基因组不稳定性。

[0349] 实施方案62.一种治疗有需要的受试者中的癌症的方法,其中所述受试者已根据实施方案61所述的方法被鉴定为具有去稳定化的基因组,其中治疗所述癌症的所述方法包括给予药学有效量的PARP抑制剂。

[0350] 实施方案63.如前述实施方案中任一项所述的方法,其中所述目标区域是基因或所述基因的一部分。

[0351] 实施方案64.如实施方案63所述的方法,其中所述基因与疾病有关。

[0352] 实施方案65.如实施方案64所述的方法,其中所述疾病是癌症。

[0353] 实施方案66.如实施方案63所述的方法,其中所述基因是BRCA2、ATM、BRCA1、BRIP1、CHEK2、FANCA、HDAC2和/或PALB2。

[0354] 实施方案67.一种包含多个DNA文库片段的基因组DNA文库,其中所述DNA文库片段中的每一个包含衔接子和基因组DNA片段,

[0355] 其中所述衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;

[0356] 其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;

[0357] 其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;并且

[0358] 其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段。

[0359] 实施方案68.如实施方案67所述的基因组DNA文库,其中所述样品标签还包含独特分子标识符(UMI),其中所述UMI有助于鉴定独特基因组DNA片段。

[0360] 实施方案69.如实施方案67或68所述的基因组DNA文库,其中所述扩增区的长度在10与50个核苷酸之间。

[0361] 实施方案70.如实施方案69所述的基因组DNA文库,其中所述扩增区的长度为25个核苷酸。

[0362] 实施方案71.如前述实施方案中任一项所述的基因组DNA文库,其中所述样品标签的长度在5与50个核苷酸之间。

[0363] 实施方案72.如实施方案71所述的基因组DNA文库,其中所述样品标签的长度为8个核苷酸。

[0364] 实施方案73.如实施方案67-72中任一项所述的基因组DNA文库,其中所述UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。

[0365] 实施方案74.如实施方案73所述的基因组DNA文库,其中所述UMI倍增器的长度在1与5个核苷酸之间。

[0366] 实施方案75.如前述实施方案中任一项所述的基因组DNA文库,其中所述锚定区的长度在1与50个核苷酸之间。

[0367] 实施方案76.如实施方案75所述的基因组DNA文库,其中所述锚定区的长度为10个核苷酸。

[0368] 实施方案77.如实施方案67-76中任一项所述的基因组DNA文库,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。

[0369] 实施方案78.如实施方案67-77中任一项所述的基因组DNA文库,其中所述样品标签的每个核苷酸序列与所述样品的核苷酸序列的任何其他序列相隔的汉明距离为至少二。

[0370] 实施方案79.如实施方案67-78中任一项所述的基因组DNA文库,其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。

[0371] 实施方案80.如实施方案67-78中任一项所述的基因组DNA文库,其中所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍增器。

[0372] 实施方案81.如实施方案67-78中任一项所述的基因组DNA文库,其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0373] 实施方案82.如实施方案67所述的基因组DNA文库,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;

[0374] 其中所述多个衔接子中每个衔接子的样品标签区的长度为8个核苷酸,其中所述多个衔接子中每个衔接子的样品标签区包含核苷酸序列,所述核苷酸序列与所述多个衔接子的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二;

[0375] 其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸,并且其中每个可能的核苷酸序列的UMI倍增器与所述多个衔接子的每个样品标签区配对;

[0376] 其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个;并且

[0377] 其中给定序列的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0378] 实施方案83.如实施方案67-82中任一项所述的基因组DNA文库,其中所述基因组DNA片段是cfDNA。

[0379] 实施方案84.多个基因组DNA文库,其包含多于一个根据实施方案67-83中任一项所述的基因组文库。

[0380] 实施方案85.如实施方案84所述的多个基因组DNA文库,其中属于所述多个基因组DNA文库的基因组DNA文库的样品标签区的核酸序列不同于属于所述多个基因组DNA文库的其他基因组DNA文库的样品标签区的核酸序列。

[0381] 实施方案86.如实施方案84或85所述的多个基因组DNA文库,其中属于所述多个基因组DNA文库的基因组DNA文库的扩增区的核酸序列与属于多个基因组DNA文库的其他基因组DNA文库的扩增区的核酸序列相同。

[0382] 实施方案87.一种用于无细胞DNA(cfDNA)的DNA靶区域的遗传分析的方法,其包括:

[0383] (a)生成如实施方案67-86中任一项所述的DNA文库;

[0384] (b)使所述cfDNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成复合物;以及

[0385] (c)对包含所述DNA靶区域的cfDNA片段进行定量遗传分析;

[0386] 从而进行所述DNA靶区域的遗传分析。

[0387] 实施方案88.一种预测、诊断或监测受试者中的遗传疾病的方法,其包括:

[0388] (a)从所述受试者获得测试样品;

[0389] (b)从所述测试样品分离基因组DNA;

[0390] (c)生成包含多个DNA文库片段的DNA文库,其中所述DNA文库片段中的每一个包含来自所述测试样品的基因组DNA片段和衔接子;

[0391] (d)使所述cfDNA文库与特异性地结合DNA靶区域的多个捕获探针接触,从而在所述捕获探针与包含所述DNA靶区域的DNA文库片段之间形成复合物;以及

[0392] (e)对cfDNA克隆文库中与所述遗传疾病相关的一个或多个靶基因座进行定量遗传分析,其中所述一个或多个靶基因座中的一个或多个遗传病变的鉴定或检测是对于所述遗传疾病的进展的预后、诊断或监测。

[0393] 实施方案89.如实施方案87或88所述的方法,其中所述定量遗传分析包括DNA测序以生成多个测序读段。

[0394] 实施方案90.一组用于生成基因组DNA文库的编码独特基因组DNA片段的特征和测试样品的特征的衔接子,其中所述衔接子组中的每个衔接子是包含扩增区、样品标签区和锚定区的DNA多核苷酸;

[0395] 其中所述扩增区包含能够充当PCR扩增的引物识别位点的多核苷酸序列;

[0396] 其中所述样品标签包含编码所述独特文库DNA片段的特征且编码所述测试样品的特征的多核苷酸序列;并且

[0397] 其中所述锚定区包含编码所述测试样品的特征的多核苷酸序列,并且其中所述锚定区能够附接至所述基因组DNA片段。

[0398] 实施方案91.如实施方案90所述的衔接子组,其中所述样品标签还包含独特分子标识符(UMI),其中所述UMI有助于鉴定独特基因组DNA片段。

[0399] 实施方案92.如实施方案90或91所述的衔接子组,其中所述扩增区的长度在10与50个核苷酸之间。

[0400] 实施方案93.如实施方案90-92中任一项所述的衔接子组,其中所述扩增区的长度为25个核苷酸。

[0401] 实施方案94.如前述实施方案中任一项所述的衔接子组,其中所述样品标签的长度在5与50个核苷酸之间。

[0402] 实施方案95.如实施方案94所述的衔接子组,其中所述样品标签的长度为8个核苷酸。

[0403] 实施方案96.如实施方案90-95中任一项所述的衔接子组,其中所述UMI倍增器与所述样品标签区相邻或包含在所述样品标签区内。

[0404] 实施方案97.如实施方案96所述的衔接子组,其中所述UMI倍增器的长度在1与5个核苷酸之间。

[0405] 实施方案98.如实施方案90-97所述的衔接子组,其中所述锚定区的长度在1与50个核苷酸之间。

[0406] 实施方案99.如实施方案98所述的衔接子组,其中所述锚定区的长度为10个核苷酸。

[0407] 实施方案100.如实施方案90-99中任一项所述的衔接子组,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列。

[0408] 实施方案101.如实施方案100所述的衔接子组,其中所述样品标签的每个核苷酸序列与所述衔接子组的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二。

[0409] 实施方案102.如实施方案90-101中任一项所述的衔接子组,其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器。

[0410] 实施方案103.如实施方案90-101中任一项所述的衔接子组,其中所述多个衔接子中的每一个包含与所述样品标签区相邻的UMI倍增器。

[0411] 实施方案104.如实施方案103所述的衔接子组,其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个,并且其中给定序列中的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0412] 实施方案105.如实施方案90-104中任一项所述的衔接子组,其中所述多个衔接子中的每个衔接子的扩增区包含相同的核苷酸序列;

[0413] 其中每个衔接子的样品标签区的长度为8个核苷酸,其中所述样品标签的每个核苷酸序列与所述衔接子组的样品标签的任何其他核苷酸序列相隔的汉明距离为至少二;

[0414] 其中所述多个衔接子中的每一个包含与所述样品标签区相邻或包含在所述样品标签区内的UMI倍增器,其中所述多个衔接子中的每个衔接子的所述UMI倍增器的长度为三个核苷酸,其中所述UMI倍增器包含64个可能的核苷酸序列中的一个,并且其中所述64个可能的核苷酸序列中的每一个的UMI倍增器与所述多个衔接子的每个样品标签区配对;

[0415] 其中所述多个衔接子中的每个衔接子的锚定标签区包含四个核苷酸序列中的一个;并且

[0416] 其中给定序列的每个样品区仅与给定序列的四个锚定区中的一个配对。

[0417] 本说明书中引用的所有出版物、专利申请和授权专利均通过引用并入本文,如同每个单独的出版物、专利申请或授权专利被特别且单独地指出通过引用并入。特别地,国际PCT公开号WO 2016/028316的全部内容通过引用特别并入。

[0418] 尽管为了清楚理解的目的已经通过说明和例子的方式详细地描述了前述发明,但是根据本发明的教导,本领域普通技术人员将容易明白,可以在不脱离所附权利要求的精神或范围的情况下对其进行某些改变和修改。仅通过说明的方式而不是通过限制的方式,提供以下实施例。本领域技术人员将容易地认识到各种非关键参数,它们可以被改变或修改以产生基本类似的结果。

[0419] 实施例

[0420] 实施例1:含有片段化基因组DNA的混合物的样品的拷贝数分析

[0421] 生成片段化的基因组DNA的精细混合物,其含有源自掺入片段化野生型人gDNA样品中的ΔATM或ΔBRCA2永生化人样品的DNA。这种样品类型的优点是可以小心控制化合物,并且样品可用性是基本上无限制的。

[0422] 从健康志愿者捐献的全血样品中纯化野生型人类女性基因组DNA。从Coriell储存库获得从具有覆盖整个ATM基因(NA09596,ΔATM)的杂合缺失的永生化细胞分离的基因组DNA和带有BRCA2(NA02718,ΔBRCA2)杂合缺失的单独样品。重要的是,这些样品显示在其余基因组中具有正常的倍性。ΔATM样品源自男性供体,因此在X连锁AR基因的拷贝数方面也是半合子的。无细胞DNA(cfDNA)获自女性或男性来源的健康供体血浆样品。对于文库构建,使用Covaris仪器在200bp的设置下对基因组DNA进行超声处理,然后使用"双侧"DNA珠粒纯化进一步选择大小。文库输入DNA样品显示在图7中。

[0423] 将片段化和cfDNA样品的适当组合混合至确定的百分比,进行末端修复并转化为基因组文库。将约500ng的每个文库组合在八个样品的组中,并与含有2304个DNA探针的拷贝数丢失(CNL)前列腺探针池杂交。在样品处理之后,在Illumina NextSeq NGS仪器上对每组8个样品进行测序,深度为约4.8亿个过滤读段;这相当于6000万个读段/样品。约95%的读段具有合理的样品ID标签并与人参考基因组进行比对,其中约98%映射至预期的靶基因座。总体测序深度被测量为每个探针每个输入基因组的读段数目(计算如下:靶读段(6千万)除以平均基因组深度(2500),再除以探针计数(2400)),其为每个探针每个基因组约10个读段。拷贝数损失分析的图形表示如图1所示。拷贝数扰动用箭头突出显示。(样品1,5%男性DNA在女性DNA中;样品2,5%ΔATM DNA(男性)在女性DNA中;样品3,5%ΔBRCA2 DNA(女性)在女性DNA中;样品4,纯女性DNA)。

[0424] CNL调用者鉴定冗余读段并将它们压缩成单个共有读段,然后将其在每个探针位置量化。该信息进一步压缩为逐基因拷贝数平均值。最后,统计显著性被分配至每个CNL测量中检测到的偏差;这以图形方式显示为统计显著性的$\log_{10}$P值。

[0425] 图8示出了片段化和混合的基因组文库中AR(图8B)和ATM(图8C)基因的拷贝数测定的盒须图。由于ΔATM样品是男性,AR基因(X连锁,半合子)和ATM基因都表现出CNL行为。正如预期的那样,测量的拷贝变异的量级是适度的。图9B所示的统计分析表明观察到的拷贝波动是统计学上显著的。此外,在预测显示出均匀拷贝特征的剩余基因中观察到非常小的显著波动。这些值与针对各种基因组混合物预测的频率相关性良好。图10示出了在主要为cfDNA的样品中也容易观察到统计学上显著的拷贝波动,在所述样品中少量掺加来自异性的cfDNA或少量添加片段化gDNA。这些值与针对各种基因组混合物预测的频率相关性良好。用片段化的gDNA和用cfDNA观察到的结果是可比较的,从而证明了测定的完整性并且表明完整性将转化为临床样品。

[0426] 这些数据证明了测定系统检测出基因拷贝数的细微变化低至2%的低等位基因频率的能力。虽然所展示的实施例的重点在于拷贝数丢失,但该技术同样适用于拷贝数增加的检测,包括通过染色体臂复制和焦点扩增发生的基因拷贝的增加。该测定法还保留了检测其他类型基因组变异的能力,包括SNV、indel和基因融合(染色体重排)。重要的是,这些数据表明所述方法可以应用于源自血浆的基因组DNA,也可以应用于源自其他来源(例如组织和其他身体来源)的基因组DNA。

[0427] 实施例2:来自健康供体和癌症患者的cfDNA的拷贝数分析

[0428] 以下实施例说明了在基因组文库构建和杂交后处理过程中添加的分子特征用于生成拷贝数分析的方式。使用Qiagen Circulating Nucleic Acids Extraction试剂盒(Qiagen,Hilden,Germany)从十六名健康供体和一名去势抗性前列腺癌症患者的血浆中提取DNA。使用Qubit荧光计(Thermo Fisher,Waltham,MA)和相应的hsDNA定量试剂盒量化双链DNA的产量。使用凝胶电泳在2%琼脂糖凝胶上进行大小分析,其中PCR标志物作为大小标准(New England Biolabs,Ipswich,MA)。取决于来自样品的cfDNA的产量,约40-100ng的cfDNA用于文库构建。

[0429] 文库构建的基本特征如图11A至图11C所示。首先将cfDNA去磷酸化,然后在两步过程中将其修复成平端。然后将由磷酸化的连接链和惰性配偶体链组成的短的10nt锚定序列与cfDNA连接。用于产生一组四个锚定序列的八种寡核苷酸显示在表1中。

[0430] 表1:连接锚定寡核苷酸

[0431]

寡聚物 ID	核酸序列	SEQ ID NO:
配偶体链 o 连接链寡聚物 o_16-1	GTATGCC[3-dA-Q]*	1

[0432]

配偶体链 o 连接链寡聚物 o_16-2	AGCGTTA[3-dC-Q]*	2
配偶体链 o 连接链寡聚物 o_16-3	TCGACAT[3-dG-Q]*	3
配偶体链 o 连接链寡聚物 o_16-4	CATCAGG[3-dT-Q]*	4
连接链寡聚物_16-1	/5Phos/TGG CAT ACG T**	5
连接链寡聚物_16-2	/5Phos/GTA ACG CTA G**	6
连接链寡聚物_16-3	/5Phos/CAT GTC GAT C**	7
连接链寡聚物_16-4	/5Phos/ACC TGA TGC A **	8

[0433] *[3-d(A,C,G,或T)-Q]表示其中羟基位于核糖环的2'位置的修饰碱基

[0434] **/5Phos/表示5'磷酸基团化学加成至5'碱基位置

[0435] 通过添加退火至锚定序列的全长衔接子序列完成衔接子结构。图12至图22中示出了三十二组衔接子序列,每组由240个成员构成。这些衔接子附接至cfDNA,并通过多核苷酸激酶、DNA聚合酶和DNA连接酶的协同作用延伸,以生成基因组文库。作为测序前质量控制步骤,通过qPCR对所得基因组文库的覆盖深度进行量化。然后扩增基因组文库并与靶向特异性基因的探针组杂交(图11B)。杂交后,使用探针的引物延伸来复制捕获的基因组序列和附接的衔接子中编码的信息(图11C)。使用标准新一代分析软件的后测序分析的一个例子显示在图11D中。该分析在包含32个样品(28个癌症患者样品和4个野生型对照)的测序运行中进行,并且其显示了测序读段的总体分布。

[0436] 本文描述的靶向杂交捕获平台的核心特征是它提供多种类型的基因组信息。捕获探针的一个基本功能是在高覆盖深度的靶区域提供突变检测。该功能由捕获探针的序列背景、密度和放置决定,并采用TP53基因示于图23中(TP53探针序列示于下表2中)。同样重要的是,靶向杂交捕获平台测定在未检测到显著突变的区域中生成了相等覆盖深度的读出。这些数据对医生和患者至关重要,因为他们在未检测到有害突变的情况下增加了统计显著性。

[0437] 表2:TP53探针

[0438]

名称	序列	SEQ ID NO:
TP53_1	GGCACAGACCCTCTCACTCATGTGATGTCATCTCTCCTCC	7689
TP53_2	ATGGGGGTGGGAGGCTGTCAGTGGGGAACAAGAAGTGGAG	7690
TP53_3	GTCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAGTTT	7691
TP53_4	CCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAA	7692
TP53_5	TCATGCTGGATCCCCACTTTTCCTCTTGCAGCAGCCAGAC	7693
TP53_6	GTTGGGGTGGGGGTGGTGGGCCTGCCCTTCCAATGGATCC	7694
TP53_7	CAGTTTCCATAGGTCTGAAAATGTTTCCTGACTCAGAGGG	7695
TP53_8	CTGCCATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCC	7696
TP53_9	GCAGAGACCTGTGGGAAGCGAAAATTCCATGGGACTGACT	7697
TP53_10	CTGGGGGGCTGGGGGGCTGAGGACCTGGTCCTCTGACTGC	7698
TP53_11	GCAGGGGGATACGGCCAGGCATTGAAGTCTCATGGAAGCC	7699
TP53_12	GTGGCCCCTGCACCAGCAGCTCCTACACCGGCGGCCCCTG	7700
TP53_13	GGGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGA	7701
TP53_14	CCGTGCAAGTCACAGACTTGGCTGTCCCAGAATGCAAGAA	7702
TP53_15	CCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGG	7703
TP53_16	CCAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGC	7704
TP53_17	TAGGTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGG	7705
TP53_18	TGCTTTATCTGTTCACTTGTGCCCTGACTTTCAACTCTGT	7706
TP53_19	CCTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGC	7707
TP53_20	TTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGT	7708
TP53_21	CCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCC	7709
TP53_22	GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGA	7710

[0439]

TP53_23	CATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCA	7711
TP53_24	CCAGGGTCCCCAGGCCTCTGATTCCTCACTGATTGCTCTT	7712
TP53_25	GAGGGCCACTGACAACCACCCTTAACCCCTCCTCCCAGAG	7713
TP53_26	CCTCAGGCGGCTCATAGGGCACCACCACACTATGTCGAAA	7714
TP53_27	AGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACT	7715
TP53_28	CTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTG	7716
TP53_29	GAGGCAAGCAGAGGCTGGGGCACAGCAGGCCAGTGTGCAG	7717
TP53_30	CCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTC	7718
TP53_31	ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCG	7719
TP53_32	GGACAGGTAGGACCTGATTTCCTTACTGCCTCTTGCTTCT	7720
TP53_33	CTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCCTGCTTG	7721
TP53_34	TCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACG	7722
TP53_35	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCT	7723
TP53_36	GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGG	7724
TP53_37	TCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTC	7725
TP53_38	TGCCTCAGATTCACTTTTATCACCTTTCCTTGCCTCTTTC	7726
TP53_39	GGCATTTTGAGTGTTAGACTGGAAACTTTCCACTTGATAA	7727
TP53_40	CCTGAAGGGTGAAATATTCTCCATCCAGTGGTTTCTTCTT	7728
TP53_41	CCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCA	7729
TP53_42	CATCTTTTAACTCAGGTACTGTGTATATACTTACTTCTCC	7730
TP53_43	ATGGCTTTCCAACCTAGGAAGGCAGGGGAGTAGGGCCAGG	7731
TP53_44	CCTGGAGTGAGCCCTGCTCCCCCCTGGCTCCTTCCCAGCC	7732
TP53_45	TCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCA	7733

[0440] 捕获探针与捕获的基因组序列的连接(图11C)也有助于测量每个探针位置处的基因组深度。测量了与所述实验中使用的每个捕获探针相关的独特读段的数目(图24)。图24中所示的数据源自测序运行,其中分析了16个健康供体cfDNA样品。计算了在TP53基因中的一个探针位置处的每个样品中遇到的独特读段的深度(原始独特读段计数示于图24A中)。每个样品包含独特的文库深度,如独特读段的广泛的样品间分布所反映的。还计算了所述实验中所有2596个捕获探针的独特读段深度的总体平均值(图24B)。值得注意的是,通过对所有探针测量的总体独特读段深度将在图24C中显示的单个探针位点处观察到的读段深度进行归一化,揭示了归一化独特读段的均匀密度。这些数据表明,选择用于分析的特定探针的捕获性能在样品间是均匀的,并且与每个单独文库的基因组深度成正比。

[0441] 将相同的归一化功能应用于图23中所示的45个TP53特异性探针(归一化数据示于图25中)。而图23示出了所有探针对TP53编码区的测序深度的总贡献,图25示出了由每个单独探针检索的归一化深度。对于任何给定的探针,由每个单独探针检索的归一化深度通常在样品间是一致的,但是当将一个探针与另一个探针进行比较时则有些变化。几个因素决定了探针之间观察到的后归一化捕获深度的差异,最重要的是探针相对于彼此的位置以及探针与基因组重复区域的接近程度。并非所有探针都显示出均匀的捕获行为;捕获性能不一致的两个探针在图25中用箭头突出显示。然而,这些数据表明这种探针是罕见的且易于鉴定。因此,它们可以从下游拷贝数分析中排除。

[0442] 图25中通过45TP53靶向探针显示出的均匀的捕获性能是本文描述的靶向杂交捕获平台的一般特征。在图26中,对于在该实验中分析的所有16个正常cfDNA文库,计算一组2596个捕获探针中的每个探针的平均捕获深度。然后使用散点图分析将平均值与三个代表性样品单独比较。每个点代表不同的探针并且它在图上的位置是x轴上的平均值与y轴上的单独样品的比较。大多数探针的紧对角线分布反映了大多数探针的高度相关的独特读段捕获性能(对于全部三个图,R^2相关性≥0.95)。重要的是,逐探针测序深度的一致性支持在拷贝数测量中使用靶向杂交捕获平台。

[0443] 关于拷贝数,探针数据的最直接的处理是进一步将在常染色体中发生的调整的基因组深度值针对二倍体平均值“2”进行归一化。对于X连锁基因座在女性中发生的探针值也是如此。对于正常男性中的X连锁和Y连锁区域,平均拷贝值适当地设置为“1”。将该数值转换应用于一组染色体对照探针(靶向选择所有22个常染色体上的基因座的239个探针,表3)、靶向X连锁的AR基因的一组199个探针以及45个上文详细考虑的TP53特异性探针(图27A和图27B)。每个点代表单独探针的值。除了不常见的“噪声”探针外,预计区域中的绝大多数单独探针计数为二倍体所具有的值,即约“2”。健康男性中的AR基因的探针波动,平均值接近预期的“1”。

[0444] 表3:染色体对照探针

[0445]

名称	序列	SEQ ID NO:
Chr_1_1	GTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACA	7734
Chr_1_2	ATCCAAGGGGAGGAGATCAGTGCCCCTATTTGTATCGCAC	7735
Chr_1_3	ACTTACTGAAGCAAGAACCTCATCAAGCTGCCTCCCACCA	7736
Chr_1_4	AGTTTGTGATCCTCCTGTGGGCAACCTCAGCAGTCTGGTT	7737
Chr_1_5	GGAGAGCGGAGCTGCTCAGAGCTTGGCCAGGTTCTAAGTG	7738
Chr_1_6	GACTGTGGCAATGAGGCAGCTAAGTGGTTCACCAACTTCT	7739
Chr_1_7	GGTGTATTTTGACAACGGTGGACCCAGACACTGGAGTCAT	7740
Chr_1_8	GTTGGTCTATTCTTGCGGTTGTAAAAGTGGCCCAGAGTGA	7741
Chr_1_9	GTGAGCCTTCTCTCACCATTCTGTCCAAAATAGCAGCCCT	7742
Chr_1_10	CAGCCTAGATATGATTCCTCACTACCCTGTTCCATGGTTC	7743
Chr_1_11	AAAGAATGTGTTGGCTCATGATCAGACTTGAGCACTTGGG	7744
Chr_1_12	CCTAGGCTGTTGCTGCTGGACCTGTTTGTGCTTCATCACA	7745
Chr_2_1	CAGTTGACCCTTCAGCCACAGGGGTTTGAACTTTGAAGGA	7746
Chr_2_2	AGGACCTGAGTATGCACGTTTTGGTATACTGGGTAGGGGT	7747
Chr_2_3	TATCAGCTGGGATGGTCCGGTCAGCAGCATTACCCTGTTT	7748
Chr_2_4	TGCCTGCTCAGCCCAGATTTCAGTCATGCTGGCCATAAAC	7749
Chr_2_5	CTGGGGGGTGAGGTTTGAGGTTTGAGTGTGGGATGTGAGG	7750
Chr_2_6	CCAGCTTTTTCAGAAGCTGGGAAAGTAATAACCCGTGTTG	7751
Chr_2_7	CCCAGCGCCCGTGGCTTTGGCTCCTCAGTCCCATTTAAAT	7752
Chr_2_8	TATACCACCAAGTCTACCTACTGCCTGCACATGCTATGGC	7753
Chr_2_9	GGTCAATCCGGCACTACTGGTTGTCCAAAGGGAGGTTACT	7754
Chr_2_10	AATCAAACATCAGGACCGCCCACAGCACAGGTCAATGAAC	7755
Chr_2_11	GTGTCTCCTGGAGGTGCATGGGTGGTTTTGAACTTCATTG	7756
Chr_2_12	GACCCATGTAAGGGGTTGGGTTATGTTCTCCTTTTGCCCA	7757
Chr_2_13	TCACTGACATGCGAAGCTGGGAACGAGAAAATGCACATCC	7758
Chr_2_14	TCCTACAGTGCTTAGGGATGAATCTGGCAAAGAAGGATGC	7759
Chr_2_15	GAAAGCAGTCCTTACCACAAGAAGACCCCGATGTGGTGGT	7760
Chr_2_16	ATTGCTCACTGGCTGGCTTGCATTTGGTATGCGATTGGGA	7761
Chr_2_17	GTCCCTGGGACCATCTGTGCATTGTTCTTGTAACTGGAAA	7762
Chr_2_18	GACCGAATGGCGAACGCAGTGAATAGATCAGGAGGGAAAA	7763

[0446]

Chr_3_1	GAAGGAATGGAGTGGAACAGATAGGGGTGAGGGAATAACG	7764
Chr_3_2	CCACTGCCATCCTCAGAGGGAGATTCACAAGTCTCACAAT	7765
Chr_3_3	ATCCAGGCTTCATGTTCAAATGCAATGGCCCTTGCCCCAT	7766
Chr_3_4	AAATTTCCCCTGGCTCCCTACTGCTTTGCAGGCCAAGTAA	7767
Chr_3_5	ACCTTAAAGACGGGCCCACATCTCTTTGGATGGGATTAGG	7768
Chr_3_6	GGGCTTCGGTTTTGGCGAAGGTGCTCACAATCTTGATATC	7769
Chr_3_7	TGAGCTGTCCTTCATGCCTGCATTTCCCATGTCTGTCTTC	7770
Chr_3_8	ATCTTTATCCAGGGCTACCAGTGGTGGGTCCAAAATGACT	7771
Chr_3_9	TACAGGTGAAGGATGTCAACGAGTTTGCTCCCACCTTCAA	7772
Chr_3_10	GCTGTTGTGACGGAGGGCAAGATCTATGACAGCATTCTGC	7773
Chr_3_11	AATGAAGGGGATTCAAGCCTTGCCACCGACTTACAGGAAG	7774
Chr_3_12	TGTGAGCGTACTTTCTCCCCCAGGTTGAAGAGGAATGAGT	7775
Chr_4_1	ATTCCAAGTCCAGGTCCCAAATCTATCAGTACCGGCTGGC	7776
Chr_4_2	GACACAGAGTGCATGAAGACCGTTCAAATATGTCAGGGAC	7777
Chr_4_3	CATGAGTCCTTCTATGACTCCCTCTCAGACATGCAGGAAG	7778
Chr_4_4	TTTTTAGGAGACAGGTACCCACTGTCTGGTGACGAGGACT	7779
Chr_4_5	CCTTCTGTTGAGTCGCTAGGAGATGCCTCAGTTCAACAAT	7780
Chr_4_6	GACAGAAACTTCATACCCAAGAGCTGCTTTCTCAGCTGGA	7781
Chr_4_7	CAGGCAACTTTGGCAAGACCAAGTCAGCCTTCTCATCTCT	7782
Chr_4_8	CCCTTGCTACCATCACTGTTGTCATCTGTGCTTGCATTCC	7783
Chr_5_1	AGGTCTCACTCCAACTGCCCCTGTATTAGAGCTAGGCTGC	7784
Chr_5_2	GAAACCATGCGGGATTCATCTTTGTCAGAGTGGAGCGGCA	7785
Chr_5_3	TATGAAATTAGGCGGTGGTTGGACGTGACTGTGTGTTGAC	7786
Chr_5_4	TGAAACTTGCATGACATACTGCGGCTGCCCATTCACTAGG	7787
Chr_5_5	TGCTTCTTGTTTATAACTCCCCTGGCCACCATCTCGGGCT	7788
Chr_5_6	ATTCCCTCTCATTTGTGGTTGGTGGCTGGATATCTGTTCC	7789
Chr_5_7	AGCATCAGCATTTCCCTGTGGACTTACCTCTCTCAGTAGT	7790
Chr_5_8	AAAATTTAAAGGTCGGCGGTAAGGCTGAAAGCCAACAGGC	7791
Chr_5_9	GAGTGTGTCGGTCAGAAGGAACACCTGAGAAACCGCTTTA	7792
Chr_5_10	CATAGCAAATACCTGTCGCTGAGCCAGGAGTAAAGTCTGG	7793
Chr_5_11	AAGAGGCTCTGAGCTCTTGATAGAGGTTACATGGGGAGCA	7794
Chr_5_12	GGAGACAACTTAGGAGGTTATCTAGACCATTCCCGCCTTC	7795
Chr_5_13	GTGTTTCCTCCCAGCATGCACTTTGTGGCTGCCTTTCTTT	7796
Chr_5_14	TGGCTTGTGTAGCGTGTTTCATTTTGGAACCTTGGAGCCG	7797
Chr_5_15	GACACCTCTGGTGCAGTTTTGAGGCTGGCCGGGAAGGGAT	7798
Chr_5_16	GTTTCAGATCTTGCAATGGGAGGGATCGACTCGGCCCTTT	7799
Chr_5_17	TGCCTAAATCAGAAATGGGCTACTTCCCTTGGCCACATCC	7800
Chr_5_18	CAATCTACCACCTCAAGGTTCACGCGTGGATTCTACACCT	7801

[0447]

Chr_6_1	GAGTTTTTCTTTCAGGTAGTCTGAGATGGCCCGCACCAAG	7802
Chr_6_2	TACTATAAAGAAGGCACCTCTAGGCTTGGCAAGCACACGT	7803
Chr_6_3	GGCAGATTCGATGGGACTTTAGACACTTGCTTTGCTCCCT	7804
Chr_6_4	CAAATGTCCCCATGCAAACATGTCCCGCACTGTGTGGTAA	7805
Chr_6_5	ACATGTGTAATCTTCTTCTCCTAGGGCGGCAGAACTCATG	7806
Chr_6_6	CCCGAGGAAAGCTCCTCTTTGCTGACTGTAATGTACTGCA	7807
Chr_6_7	GAGGACAGCATTCGCATATCAGGTCGAAATTTCTCCGCGA	7808
Chr_6_8	GTCCAGCTTTCATCCTTGATCCTGCTACTCTAGGCTCTCC	7809
Chr_6_9	ACTGATGGTGTTCACTTGCACCATCAGGTCTGATGGAGGA	7810
Chr_6_10	AATTGGTTCACAAAGCGTCGGGTGATCCAGTAACAGTCGA	7811
Chr_6_11	CAGAACTCTGCTCTAACGCCAAGCCTTCAATATGTCTTCG	7812
Chr_7_1	CAATTCTTACCATCCACAAAATGGATCCAGACAACTGTTC	7813
Chr_7_2	ACTACACCTCAGATATATTTCTTCATGAAGACCTCACAGT	7814
Chr_7_3	TGCTATAGACGCACAAACGACCGCGAGCCACAAATCAAGC	7815
Chr_7_4	CCATGACTTATGTGCAGCTTGCGCATCCAGGGGTAGATCT	7816
Chr_7_5	AGGAGTTGGTGGCTAAACCGCTGACTTTTCTATTGCAGAC	7817
Chr_7_6	GAAATATAACAGGACCAGAAGTGGCTCGCAGGAGACTCAT	7818
Chr_7_7	TAGCCAGACAGAAGGCGGACACTGATGATACCTCAAGACT	7819
Chr_7_8	GTTTGCCACCAGCGAAGAGAGCCATCCTGGTAGAATTGGA	7820
Chr_7_9	GGAGATATGCACTTGCCCTTTGGTAATCCTGCTCCTTCTG	7821
Chr_7_10	AAAACTAACCAGTAAGTACAGGGAGGGACCGAGAGGCATC	7822
Chr_7_11	AAGAACACCAGTCCATAAAGACGCATGTCCGGTGATGCCT	7823
Chr_7_12	AATCTGTTTAGACTGAGCAACTGTGCCAGCAGAGGGACCT	7824
Chr_8_1	AAGATGGCGAAGGTCTCAGAGCTTTACGATGTCACTTGGG	7825
Chr_8_2	CCATGCCTGCCAGCTGATAAGATTTGGTTACCTTTCCATG	7826
Chr_8_3	GCTGCAAGAAAGCGTAAGATTGCCATTCGAAAAGCCCAGG	7827
Chr_8_4	ATGCAGGAGTACAATGTGGGCATGTCCACCCTCTACGACA	7828
Chr_8_5	AGAACGGCTTTGCTGTCTTCCGGCAAACCTATGGTTCTGA	7829
Chr_8_6	TGGCTTTGGCGCTTTAAGGCCAGACACGGCATTAAAAAGC	7830
Chr_8_7	GCAGGCAGAGAAAGATGGCTTTAGAAACCTCTTCCCCACC	7831
Chr_8_8	TCAGCTGTGGCCATTGGTGGATCTCATCCTTAGTACTAGT	7832
Chr_8_9	CCATGGTTCTGTGAGACTGGTAGAAAGCACAGACCCCTTA	7833
Chr_9_1	AATGTGCTTATCACTCGTGATGGGGTCCTGAAGCTGGCAG	7834
Chr_9_2	AGGGTCTCATTTTAAGACAGCTTGATTTGAGGGTGAGGGG	7835
Chr_9_3	CAGTTGCAAACCATACTTCCTTCAGCCCAGTCCTGTCTAT	7836
Chr_9_4	GTCTAAGGGCATCTTACCTCCAAGAACTGCTTGAGGCGTA	7837
Chr_9_5	TACCTAGGGAATGACCACTAAGCACCATCTCCGTCACTCT	7838
Chr_9_6	GGAAGAGAGGAGGGTCATCCAGTCAGTTTTGCAGGAATCT	7839

[0448]

Chr_9_7	TGCTGCAGTGTCGGAAGAAACCTACCTGCGTTTCTTAGAA	7840
Chr_9_8	CATCATACCTATGGCATAGCCATCAGGGCACTGCAGTTTG	7841
Chr_9_9	TATATCTCACGTGACCGAGGATGGGTCGTGGGCATTCACA	7842
Chr_9_10	GAAATGGCCATCTATAGGTGGGAACCACTCCAGTGTCACA	7843
Chr_10_1	GGAAACCTTTCAGTCTCTACTAGAAGCGCGGAGAGAACTC	7844
Chr_10_2	TCTGGCCGGCATTCATTTAAGGCCTAAGGATGAAGGCGGT	7845
Chr_10_3	AGATACCCTATCGTTCCTTATCTCAGCGAAACAACTCCCC	7846
Chr_10_4	CGCAACTCCTCCAGATCGCAGTGGTGCTTCTTCACTTTCA	7847
Chr_10_5	TGATTCCATGGTTGCCCGTATACTCCATAAGGCGGTACTT	7848
Chr_10_6	ATACCATATCCGGCTTGGTTAGGAGGAGGTATTACAGGGG	7849
Chr_10_7	GTACCTGTTAACCCAGACGCAATTCCTCCACAGTACACAG	7850
Chr_11_1	ATGTGACACTTGCATCCAGGGAGGTCACCATCTGTGTATG	7851
Chr_11_2	CTAGGTCCTGAAGAGGTGGCAAGGAACCAGGACAGAACAT	7852
Chr_11_3	TCTGTCATTGGTGACGCCATCTAGACTCTTGGCTTTGGGA	7853
Chr_11_4	AAGGTATAGAGCTGGGCGGCTTTCCTCGTTATAGGTGGAG	7854
Chr_11_5	CTCCTACGTAGCCGGGTAGAAACTTATGGCAGAAGTCAGG	7855
Chr_11_6	TGGATTCCCAGGGTTAATTGTGACCCATTGCAGGAAGGTG	7856
Chr_11_7	AATGCTGTCCTACTATGGTCTGTACCTGTCCCAGAGGTGG	7857
Chr_11_8	GTGCACCTGGAGAGCATACAGGGCACTGACTTGTAGATCA	7858
Chr_11_9	TTCCATCTCGCATAACCTGCCCCTAAACTCTTCTCGGTTC	7859
Chr_11_10	ATGAAGGCCTGCTTTGAGTTATCAGATAGGAAGGGGCCAG	7860
Chr_11_11	AGGTCATGTCCCGCTTTTGGCTGAACCTAGTTTTGCCCAA	7861
Chr_12_1	CTGCATTCTCCATGAGTAGAGTACGAGCCTCATGTTGGTA	7862
Chr_12_2	AAGGCTGTCTTCACCAACTGGGTAGGTGTGGATCAAGACC	7863
Chr_12_3	CTGACTTTGGTGTTGGGGAGTCGGTGGTCCTTCTTCCATT	7864
Chr_12_4	ACTGCAGAGGACCAGACTGGGAAAACAACGATATGGCAGG	7865
Chr_12_5	CCTGGCTTAGAAGTCTGGCCGGTCCTTCTTCAGCTTCTTA	7866
Chr_12_6	AATCTCAGAAAGAGTTCCTGGGACCATGGCAAATGGTGGC	7867
Chr_12_7	ACATTATATCCGGTCCAGGAATATCTGGCTCAGGCTGGGT	7868
Chr_12_8	AAGCACAGGAAATGTGCCTCACACGACTTCACATGCCCTT	7869
Chr_12_9	GGGGGCTTTGCGGGAAGAGGGGACTAAACAACCCTTCTGT	7870
Chr_12_10	AAAAGAAATGCGATCAGCGCAACCCATCCGGTGTGGCGCT	7871
Chr_12_11	GGCAGTGGTACCATGACATACTTAGCAGAGATGGACTACA	7872
Chr_13_1	ATTTCCCATGCGAGAGGTAGCTTGCCCAGGCTGTTGGATA	7873
Chr_13_2	TTCCATGCCGAGTCCTGATGGAAACTAGCACTGAAAGACC	7874
Chr_13_3	TCACGGGAGCTTCCTTCACTGAGTTCTGCGAATCTGAAGC	7875
Chr_13_4	TTTCCAGAGATGAAGCACTACCCAGTCTTACCCAAGTTCG	7876
Chr_13_5	CCACCGAGAACAGTGATGAAGGACTTAAAGTGAGAGATGG	7877

[0449]

Chr_13_6	GTTCACTCGTCGGTTTTTCACCAACCACAGACTAGCCTCA	7878
Chr_13_7	ACGCAGCTGTGTTGAGTGCACAGGAAGCTCTTAGGGTTAA	7879
Chr_13_8	TCTCAGTGAACAGAGGGCTCACTGAGAGGACTTTGAATAC	7880
Chr_13_9	ATGGCACAGGCCACATACTGGAATGAATGACGGGCTTCAT	7881
Chr_13_10	TGCTGCTTGATGGTGGCATCACTGTCCCCTCATTCCATGA	7882
Chr_14_1	GGACACATGTGGACAGTGTGAAACCTCAGAACACTAACCC	7883
Chr_14_2	AAGTTCTTATCCTTAGGGACCCAGCGGAGACCTTGGTTCT	7884
Chr_14_3	CGACGATGCCTGGGAATAGGATCCATGGGATTGATGAGAA	7885
Chr_14_4	GGGAGCCATGAAGATTTCTCCCAGCTCCTGAGGAACTTTG	7886
Chr_14_5	TCTGGTCCTCAAGTCCTCAGCTGTAGAAGTTCTCATTGCG	7887
Chr_14_6	TGCCAACCCTGGAAACTGGCTTGTGTGTCCACAACAGAAA	7888
Chr_15_1	TAGGTGACAGCACTGTCCTTTCCCTGCCATTTGCAGGGAA	7889
Chr_15_2	TTCTTCTAGATGGCAGACATTGTTGAGGCCTCCCGTACCT	7890
Chr_15_3	AGAGAGCTGCGAGACAAGACTTGGAGTGCGACAAGATTTC	7891
Chr_15_4	TTCAATCAGGTACTCCGAGTTCCCTTGGAGGCCAAAAGGA	7892
Chr_15_5	AGGAATATGGGGTCCATCTGAGACTCGCAAGTGATGATAC	7893
Chr_15_6	GATCTCCAGGACCAGCTCTCAGAAATGCACGATGAACTGG	7894
Chr_15_7	ACAGTGTGATGGAGCAGCAGTCCAAGTTCATCCTCCAAGA	7895
Chr_15_8	AAGATGACAGGATCCAGGAAACAAGACGCATGGGCCAGAA	7896
Chr_15_9	AAAGAGTGGGTCTGTTAATAATCAGGCCGAGACCACCAGC	7897
Chr_15_10	CACCCTTGTTCGTGGCCCTTGCTTGGTAAACTGGTATCCA	7898
Chr_15_11	CCCAAGTATGGGTGAGGATGCTAGAAATGCCCACATAATG	7899
Chr_15_12	AAGACTGTCATTGGTAGGTCATGATCCTTGGCAGCATGAC	7900
Chr_16_1	GTGGGGACGGTCATTATCAGCTTTCTGGACACACAGACAG	7901
Chr_16_2	TGAGAGGCCAAAGAATATCAGTTGACTCTGGATCAGGGGC	7902
Chr_16_3	GAGGCTTTTTAGGGCAGCGAGAAAACGGGAACTTCATTCC	7903
Chr_16_4	AGGACTTCTCTGGACCTGTGCCTCAACTACTCACCTGGAT	7904
Chr_16_5	TGGCCACAAATGTTGCCTCCAGCTGCTCAATGTTCTCCAA	7905
Chr_16_6	CTGGCATTGGTGAGTAATAGGAGCCAGACGGGTCTGTGTT	7906
Chr_16_7	ATACTTACCTGCACGAGAATGAGTTTGGAGCGCAAGGGGG	7907
Chr_16_8	TTCCCCCAGAGACTCTGTCCACTATGGACATTAAAATGTG	7908
Chr_16_9	GTGCTACCCTCCTCCCTTCAGGTTATGTGGTCCAGGCTTT	7909
Chr_16_10	TAAGTGGAACAACATTCCCTTCATTATAGCCCTTCGTGGG	7910
Chr_16_11	GCAACGTCAACAACTACTACGTGCACAAGCGCCTCTACTG	7911
Chr_17_1	GCGGATGTCGTTATGGGACAGGTACAAGTAGATAAGTTGC	7912
Chr_17_2	GTGGTCACCATCTCTTCAAACCATTTGGACTGGGCCTGGT	7913
Chr_17_3	AAGCCAAGGAGTTCTGAGAGAGCTTAGCTAAGTTCTTCGC	7914
Chr_17_4	TTTTTTAGTACCCCAGTGTGTAAGACCAACTGAGGGTGGC	7915

[0450]

Chr_17_5	GTTGTCATTGGGGCTATAGACATAAGCACCTTCCGGAATC	7916
Chr_17_6	CTGAGTGTGCGAGGGGAAGATATTGGTGAAGACCTGTTCT	7917
Chr_17_7	GTCAGACCCTGTCCTCGTCTCCTTTACCTTGTCTCGATTT	7918
Chr_17_8	TAAACTATGCTCGCCACCACTCAGCACTCACCTCTTGGGC	7919
Chr_17_9	GGCAACTTCCTGAGACAGATCGGTAAAAACAACCCCTTCT	7920
Chr_17_10	TCAACTGTATTTCATCAGAGAGATGTGGCTTTCCCAGACA	7921
Chr_17_11	GTTTCCCTCATGTTCCCCCAGGTTCTGTCAGGTGAAGCTG	7922
Chr_18_1	TTAACCCATCTCTACCCGTCCTGTGTCAAGAACGGAGGCT	7923
Chr_18_2	CTGCCCAAAATAGAAACCGAGGTTCTCCGTGACCTACATC	7924
Chr_18_3	TTCCTTTGCAGTAACAGCGGGAACATGAAGCCGCCACTCT	7925
Chr_18_4	TGGTTTGCCAGTTCAGACACCCAGCCAAATTGCCCTCTCA	7926
Chr_18_5	TAGTGCAGCTGGCTTTGAGCCTGTTCCCGAATGTTCAGAT	7927
Chr_18_6	AGGGTAATAGCACCAAGCTCTAGTCTACCCACCTCTCTGA	7928
Chr_18_7	CCGCATCTCTGGAGTAGGAATTGATCAGCCACCATATGGG	7929
Chr_18_8	CTATGAGCATACTGGGGAGGGAAACCTCTAAGCGGAACTT	7930
Chr_18_9	AAAAACCTGCAGGAAGGAGACCTGAATGCAACTGTGGGTC	7931
Chr_18_10	CAGGTGCTCCAAACCTTCCAGTCTATGTTGTAGATTGCAG	7932
Chr_18_11	GCCATACTAACCTACTTCTCCTTGAAGCTCTTGGCCCATC	7933
Chr_19_1	ACTGTGAGATAGCCCTCATCATCTTCAACAGCGCCAACCG	7934
Chr_19_2	AGATACACGGTCACAGACGCCATGTGTTGTGGCTTCTGCA	7935
Chr_19_3	CACATCCTCTCACCTTTTCCGAAGGTTGCAGCTCCTTCTC	7936
Chr_19_4	TCTGTCTCACCGGTCCCTTCATTCCTAGGCAACTGTAGAT	7937
Chr_19_5	ATATCATGGTCTGTATCCCCCAGGTACCTTGACACAGGCC	7938
Chr_19_6	CTCTCCGCCTTTCTTTAGACCTGAGCATGCAGAATTCCGA	7939
Chr_19_7	AAGGCATTTAAATGGGACAGCGTCCCATGCGTGACTTCTC	7940
Chr_19_8	TCTTTCTAACAGACGAACAGCCTACACCTACAACCCCGAG	7941
Chr_19_9	GTCCCAGCCCAAAAGCATCTTGGGTAAGGATTTGGGATCA	7942
Chr_19_10	GTTGTTCTGGGCCAGTGTTAGTTGCTCACATGTCCTGTCT	7943
Chr_19_11	AACATGCCTCTTAGTCCTGGGCCATACCTTAGCCTTGTGC	7944
Chr_20_1	TAACCTCCAAAAGAGGTACCCATTGGCGCTCAACCGAATT	7945
Chr_20_2	CTATATCTCCGACTATGCCTTCTTGGGCACTGCACTGCTG	7946
Chr_20_3	TCTAGATGGAAGCTGTATCCAAGGATGCTCCGGAATGTTG	7947
Chr_20_4	ATCTTCTCTGCCTGCCGCACTAGCTTCTTGGTGACTTCTC	7948
Chr_20_5	ATCGAGTTGTCGAGCCCCATGATTCGACACCAAGATCCCA	7949
Chr_20_6	AGGTGCTTGTTTTACTCTCTCCAGGTGATGATGCCAGGGA	7950
Chr_20_7	GTGCACTGTCAGATCTTGGAAACGGCCAAAGGATTTTTCC	7951
Chr_20_8	CATTTTGCAGGAGGCTGCTAATTAAGGCTGAGGGCCATCA	7952
Chr_20_9	TCAATGGTAGACTGGAGTACCTTGCCAGGGCAGAGAAAAA	7953

[0451]

Chr_20_10	CTCCTCCAGGAGCTGGCAGCATCAAGACCCCACTTCGCTT	7954
Chr_21_1	AAATAATAGCAGGCGTTGAGATGTCCCTTCCCCAGCACTC	7955
Chr_21_2	AAGTCTGACAGCATCTGCTTGAACTGAGGCACAGTGATGG	7956
Chr_21_3	ATTCGTGATGGCGCTCATTTCCATAAAGGACGACAGGTCA	7957
Chr_21_4	GAAGAGTGAATTCCCGCTTCTGCGCCAACATTCTGTTTCC	7958
Chr_21_5	ACAGGTGAAGTCTTTGCGTGCCTCCCTGTTGGACTCAAAT	7959
Chr_21_6	TAATGATATTCTGGCACAAGGAGCAGAGCCCCTCTTCTTC	7960
Chr_21_7	AGACCCAGCCTACCTGCATGATCTCTTGTACAGCTTTGCA	7961
Chr_21_8	TCATGGAACATGGGCCTTGCAAAGGGGTCAAGATCACAAC	7962
Chr_21_9	GTCAAAAAGGTCCAATCAGCTAGAGACTAGGCCAGACCCA	7963
Chr_22_1	TGTGACCACCCTAAAGGGAGGGCAGAAGCCGAGTCACCCT	7964
Chr_22_2	ACGCCTCCACCTGCTGCTAGGACTCCCCTCCCAAACAAAG	7965
Chr_22_3	CACAGTCTAGACCCTGATGGGCGATCTCAGTAGTGCTGTT	7966
Chr_22_4	CCTATCAACGTGCAAGTGGGATTTGTCTCCACTGGCTTTC	7967
Chr_22_5	GAAAATCATTCCCCATTCTGCAGGATCCGTTCCCCTGGCA	7968
Chr_22_6	AGTGGGACATACCAACTTGATGAGGCAGTTGTGCGAGTTC	7969
Chr_22_7	GTAAACAGCTGTCTTCTTACCCTACAGATCATTGGGCAGG	7970
Chr_22_8	CAGAAGGATACTAGAATGGAATGTCCTGCGTGACGAAAGC	7971
Chr_22_9	AGTTCACATCTGATTCTCCTATGGCTGCTAGGCTCCAGGA	7972

[0452] 值得注意的是,当使用健康样品作为归一化对照对从去势抗性前列腺癌症患者的血浆级分收集的cfDNA应用相同分析时,出现了三个突出特征(图27C)。首先,所有对照探针都显示出有噪声的计数行为。其次,所有AR探针的计数从正常值“1”显著升高至约“5”的放大值。在晚期前列腺癌症患者中始终观察到AR基因的扩增。第三,TP53探针计数越紧密聚集,其平均值与“2”的预期值相比更接近“1”。这可能反映了源自肿瘤组织的循环DNA部分中拷贝数丢失导致的TP53的一个或两个等位基因的失活。

[0453] 这些数据表明本发明方法包括三个重要的核型分析方面。即,本文描述的方法检测广义的染色体非整倍性、特异性的靶向基因的拷贝增加和相同特异性的靶向基因中的拷贝丢失。这些结果进一步表明,本文描述的方法和平台可以指导精确疗法的使用,因为所有这三种基因组异常在癌症中经常发生。

[0454] 测量了相对于健康对照(褐色点)的去势抗性前列腺癌症患者样品(蓝点)的广义染色体非整倍性(图28)。在该分析中,该实验中使用的所有239个对照探针的近似倍性是根据它们的染色体靶标排序的。对于一些染色体(例如,1号染色体和22号染色体),在患者与对照样品之间观察到类似的倍性值“2”。在其他情况下,观察到两个样品之间的偏差。由这些实验提供的关于总体基因组倍性的信息程度受所用对照探针的数量和密度的限制。然而,这些数据表明,以均匀密度覆盖所有染色体区段的更密集的探针组可以结合本发明的附加的独特特征使用。此类分析将提供染色体拷贝数的更高分辨率的全基因组测量。

[0455] 这些数据进一步突出了本发明作为精确治疗指南的能力。例如,在同源重组修复中具有基因组缺陷的肿瘤通常表现出高度不稳定的染色体倍性,并且具有这种肿瘤的患者是PARP酶复合物抑制剂的良好候选者(参见Popova等人,Genome Biol.2009;10(11):

R128)。与寻求对肿瘤进行基因分型的大多数测序测定不同,本文所述的测定使用测序来检测作为肿瘤表型的去稳定的染色体倍性,即使驱动该表型的因果突变仍然隐藏于靶向分析之外。

[0456] 检测从实体瘤脱落的DNA中基因缺失的能力尤其重要。肿瘤抑制基因的突变和缺失是癌症基因组中的常见事件;此外,具有肿瘤抑制基因的种系缺失的个体在以后的生活中特别容易患上癌症。液体活检拷贝数丢失(CNL)测定的诊断价值与其灵敏度成正比。为了确定本文所述发明的检测下限,将实施例1中描述的永生化细胞系系统地稀释成"瓶中基因组"参考细胞系NA12878。一种细胞系具有ATM的单拷贝缺失(单等位基因丢失),另一细胞系具有BRCA2的单拷贝缺失。该实验包括四个纯NA12878的对照样品和八个含有16%的每个单等位基因缺失细胞系的掺杂样品(图29)。出于报告目的,这对应于双等位基因丢失的8%低等位基因频率。靶向特异性基因的所有探针和两个附加的未缺失的对照基因的平均值示于图29中。ATM和BRCA2的拷贝丢失仅限于掺加样品。对数据的附加计算处理揭示了低至2%低等位基因频率的双等位基因缺失的确信拷贝丢失调用。该灵敏度表明,本发明不需要专门考虑以在标准的基于血液的基因分型测定中常规地包括拷贝丢失调用。

[0457] 这些数据证明了使用探针特异性基因组捕获数据来分析拷贝数,包括靶基因组基因座的拷贝数增加和拷贝数丢失。另外,本文所述的发明已显示具有检测单核苷酸变异、插入和单个核苷酸至数千个碱基对范围的缺失以及由异常突变过程的染色体重排产生的基因融合的灵敏能力(参见PCT公开号WO 2016/028316;和美国专利公开号2014-0274731)。所有这些突变过程都可以促进正常组织向肿瘤性癌症的转化,并且随着精确疗法的不断出现,对这些患病基因组特征的准确诊断将成为精准医学日益不可或缺的特征。

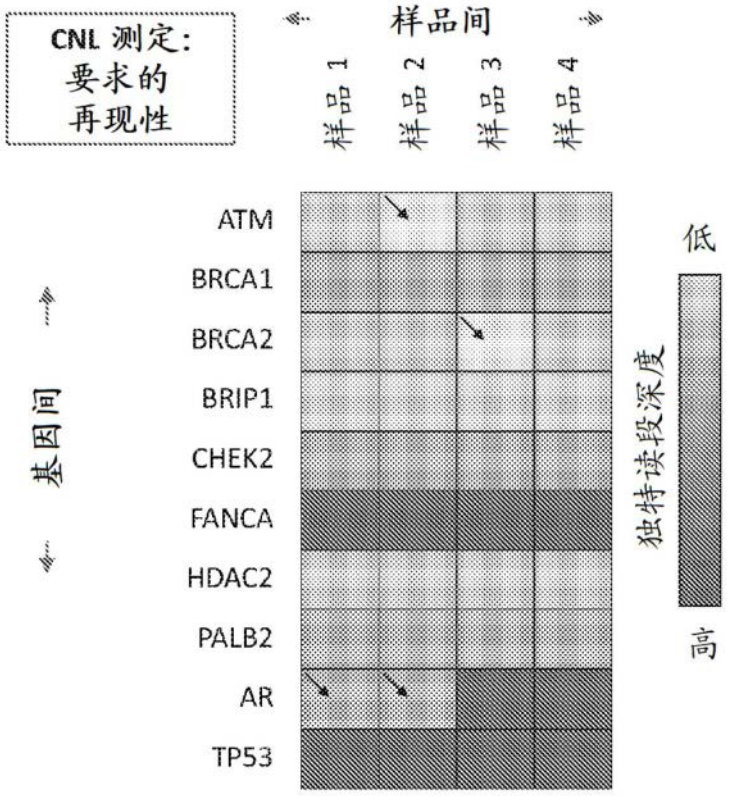

CNL 测定:
要求的
再现性
样品间
样品 1
样品 2
样品 3
样品 4
基因间
ATM
BRCA1
BRCA2
BRIP1
CHEK2
FANCA
HDAC2
PALB2
AR
TP53
独特读段深度
低
高

图1

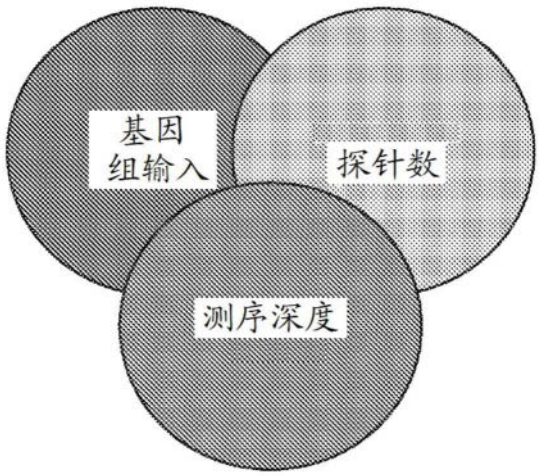

基因
组输入
探针数
测序深度

图2

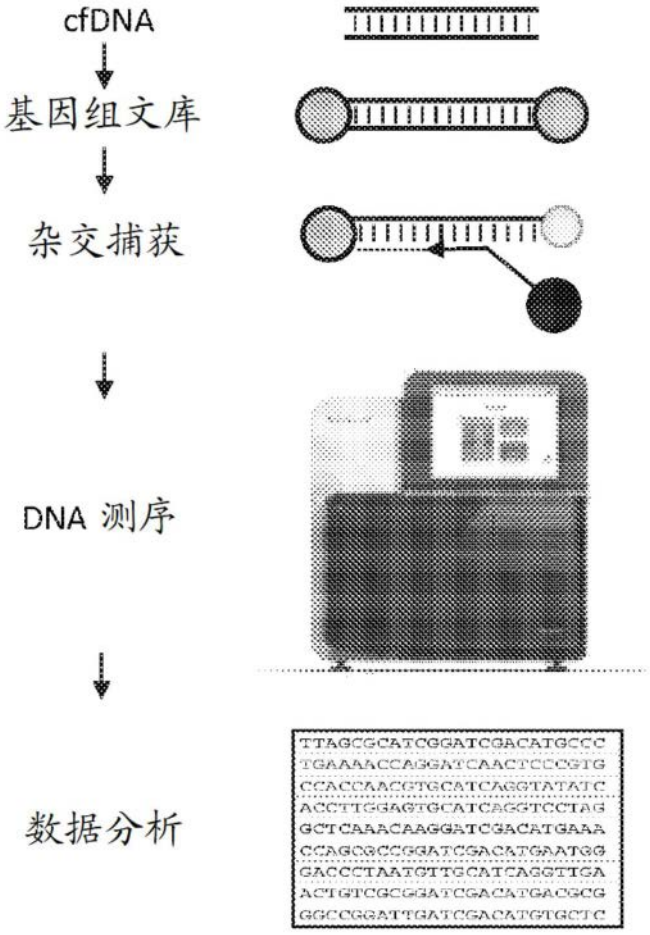

cfDNA
基因组文库
杂交捕获
DNA 测序
数据分析
TTAGCGCATCGGATCGACATGCCC
TGAAAACCAGGATCAACTCCCGTG
CCACCAACGTGCATCAGGTATATC
ACCTTGGAGTGCATCAGGTCCTAG
GCTCAAACAAGGATCGACATGAAA
CCAGCGCCGGATCGACATGAATGG
GACCCTAATGTTGCATCAGGTTGA
ACTGTCGCGGATCGACATGACGCG
GGCCGGATTGATCGACATGTGCTC

图3

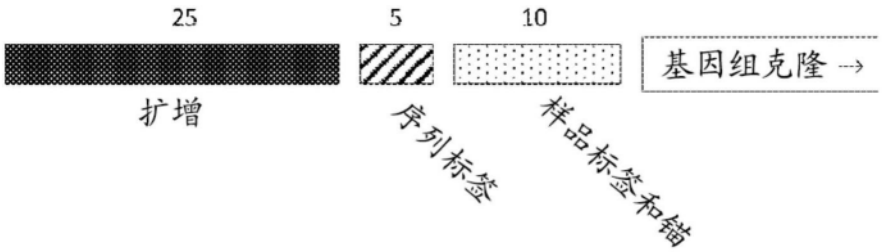

25
5
10
基因组克隆
扩增
序列标签
样品标签和锚

图4A

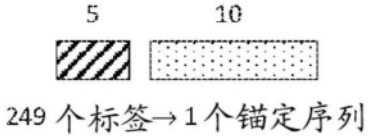

5
10
249 个标签→1 个锚定序列

图4B

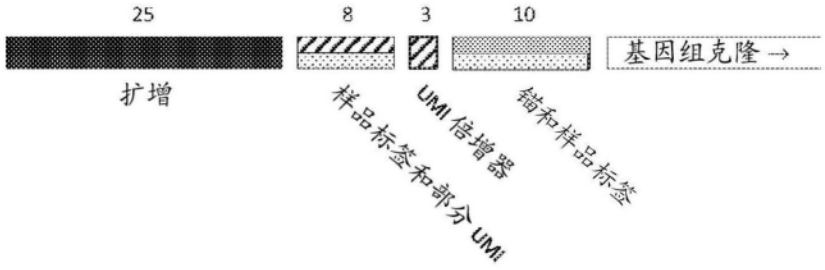


图4C

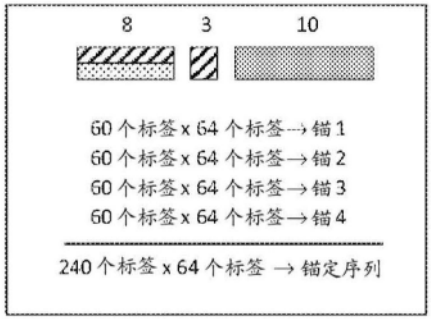


图4D



图4E

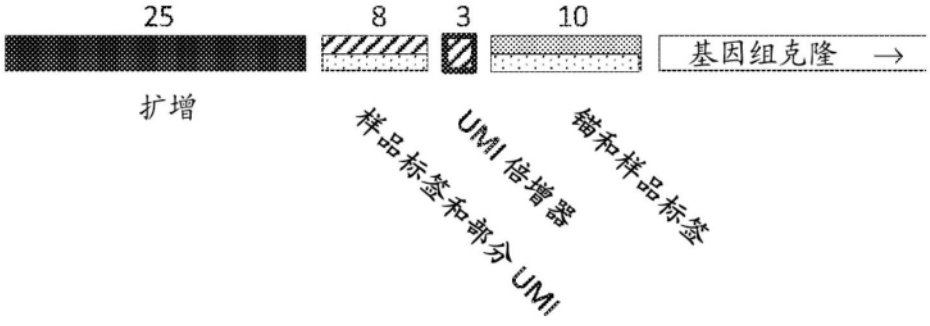


图5A

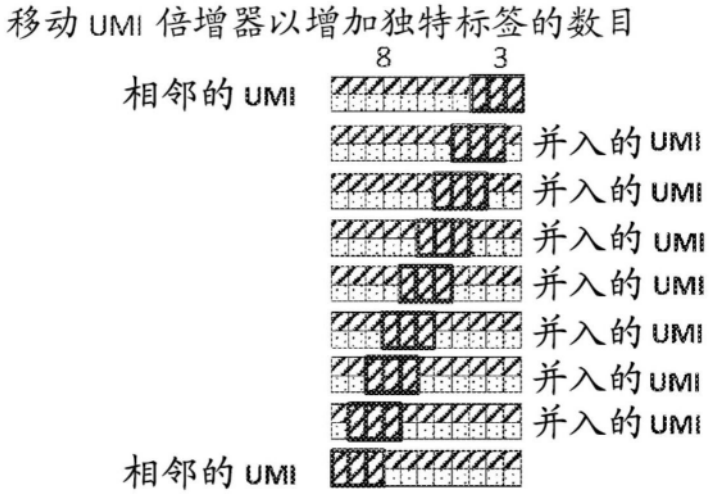

移动 UMI 倍增器以增加独特标签的数目
8
3
相邻的 UMI
并入的 UMI
并入的 UMI
并入的 UMI
并入的 UMI
并入的 UMI
并入的 UMI
并入的 UMI
相邻的 UMI

图5B

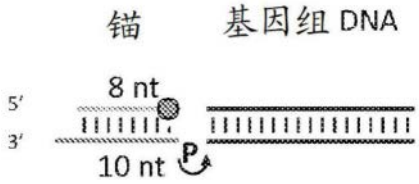

锚
基因组 DNA
8 nt
5′
3′
10 nt
P

图6A

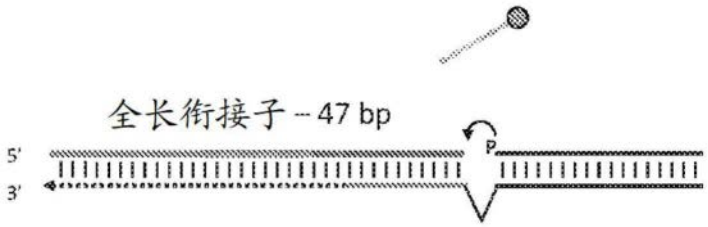

全长衔接子－47 bp
5′
3′
P

图6B

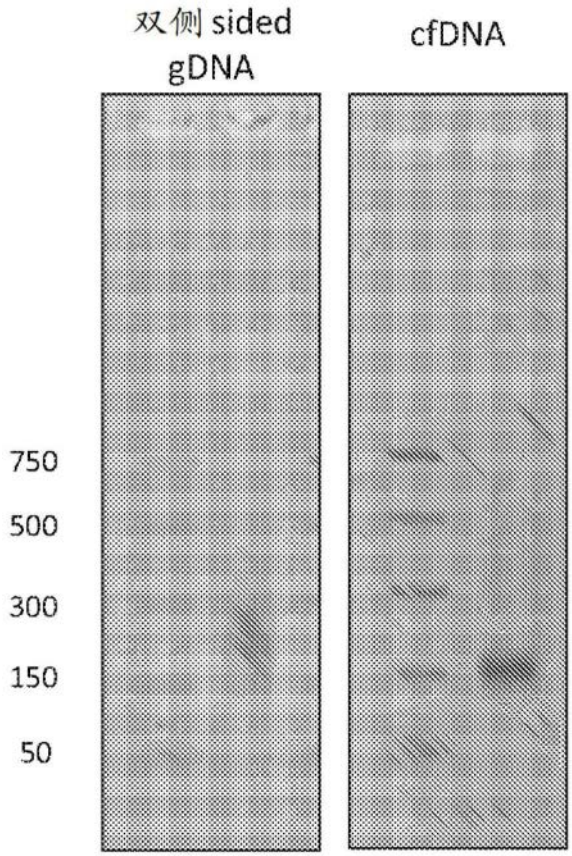


图7

样品	输入
样品 1	女性 gDNA + 8% BRCA2 缺失
样品 2	女性 gDNA + 4% BRCA2 缺失
样品 3	女性 gDNA + 2% BRCA2 缺失
样品 4	纯女性 gDNA
样品 5	女性 gDNA + 8% ATM 缺失
样品 6	女性 gDNA + 4% ATM 缺失
样品 7	女性 gDNA + 2% ATM 缺失
样品 8	纯女性 gDNA

图8A

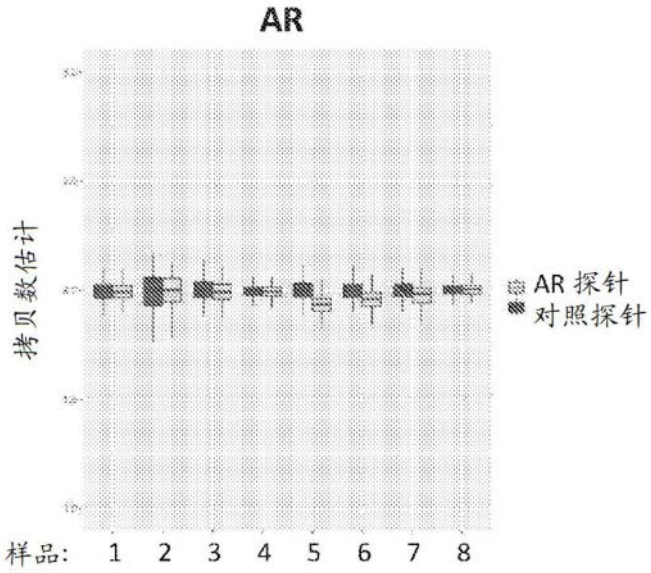

AR
拷贝数估计
AR 探针
对照探针
样品: 1 2 3 4 5 6 7 8

图8B

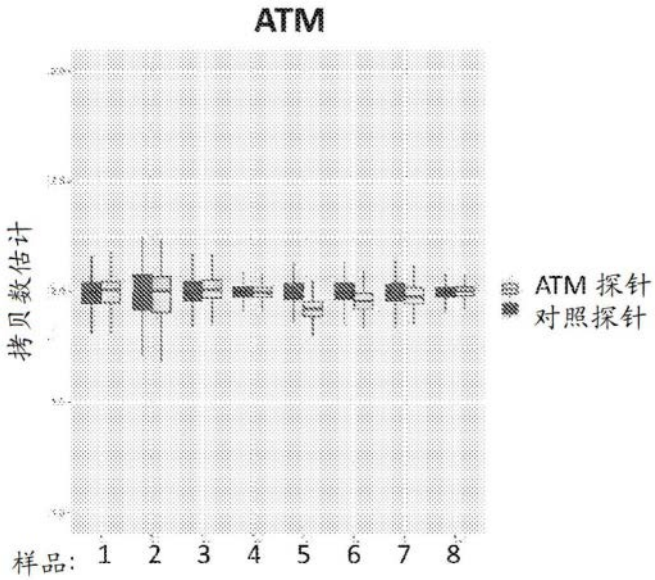

ATM
拷贝数估计
ATM 探针
对照探针
样品: 1 2 3 4 5 6 7 8

图8C

样品	输入
样品1	女性 gDNA + 8% BRCA2 缺失
样品2	女性 gDNA + 4% BRCA2 缺失
样品3	女性 gDNA + 2% BRCA2 缺失
样品4	纯女性 gDNA
样品5	女性 gDNA + 8% ATM 缺失
样品6	女性 gDNA + 4% ATM 缺失
样品7	女性 gDNA + 2% ATM 缺失
样品8	纯女性 gDNA

图9A

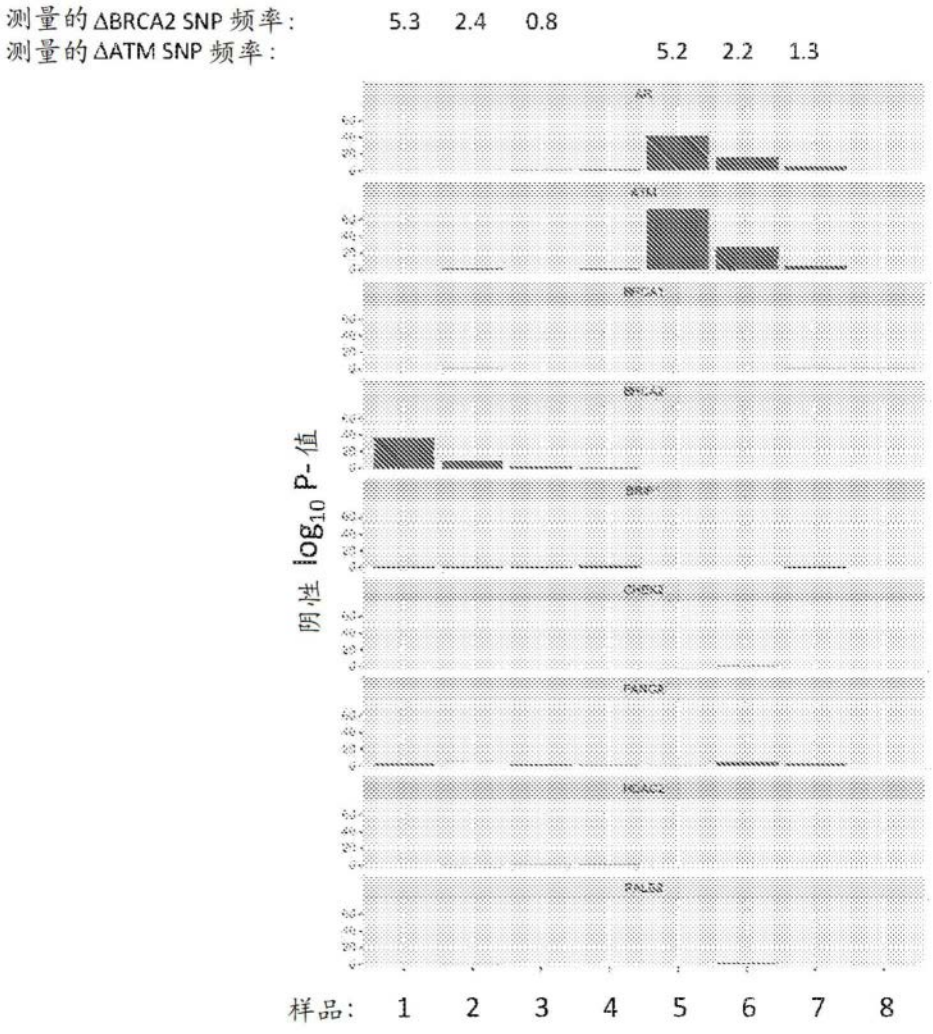


图9B

样品	输入
样品 1	F_cfDNA + 10% M_cfDNA
样品 2	F_cfDNA + 5% M_cfDNA
样品 3	纯 F_cfDNA
样品 4	纯 F_cfDNA
样品 5	F_cfDNA + 10% ATM
样品 6	F_cfDNA + 5% ATM
样品 7	F_cfDNA + 10% BRCA2
样品 8	F_cfDNA + 5% BRCA2

图10A

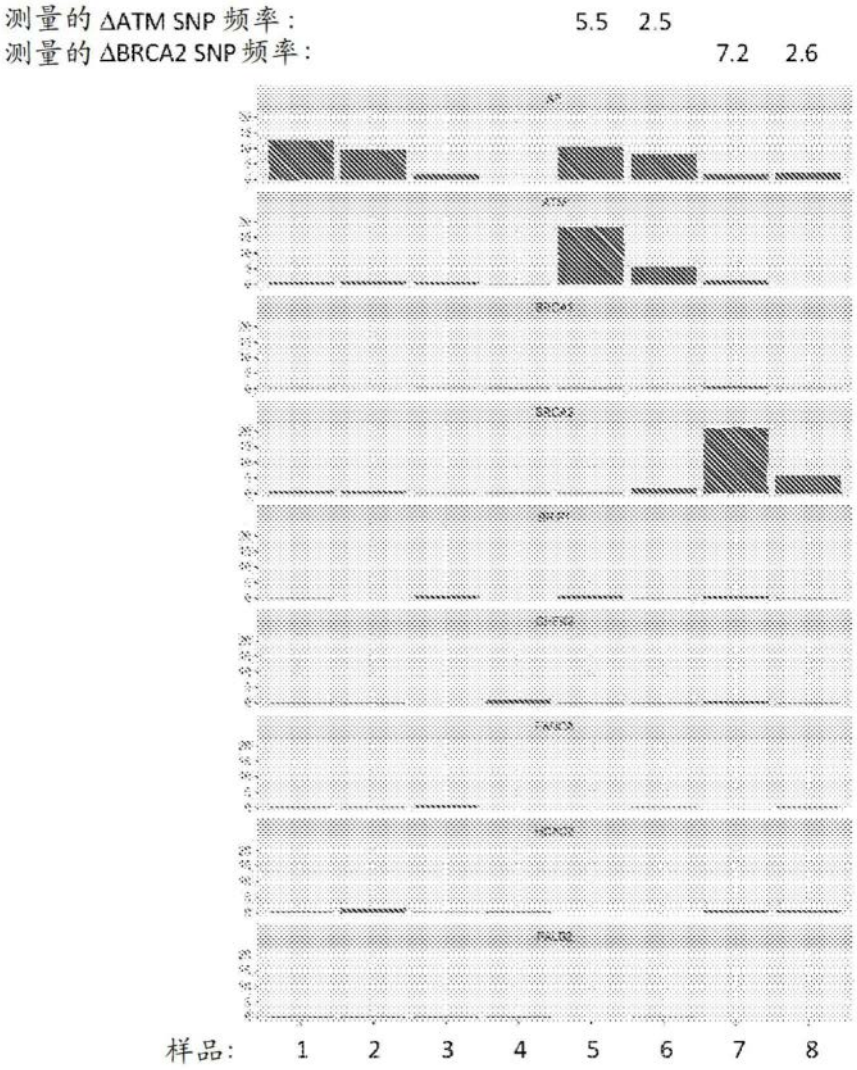


图10B

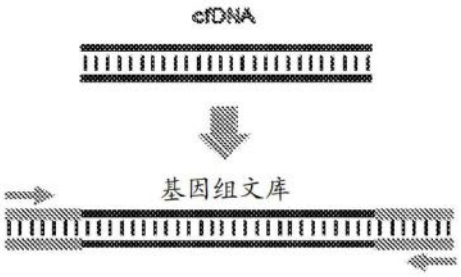


图11A

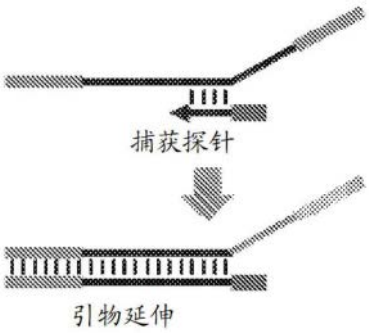


图11B

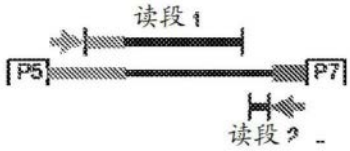


图11C

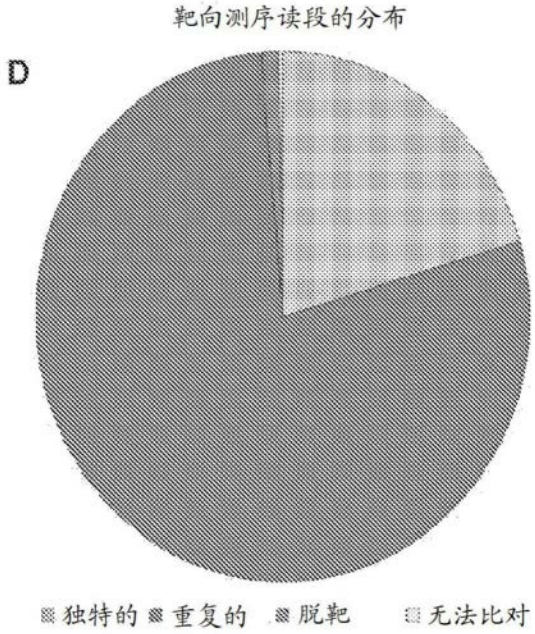


图11D

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACGAGCTTANNNACGTATGCCA	9	TGCAGGACCAGAGAATTCGAATA CACCCTGTCGNNNACGTATGCCA	249	TGCAGGACCAGAGAATTCGAATA CAACGTCAACNNNACGTATGCCA	489
TGCAGGACCAGAGAATTCGAATA CATTGCTCACNNNACGTATGCCA	10	TGCAGGACCAGAGAATTCGAATA CATATCAATGNNNACGTATGCCA	250	TGCAGGACCAGAGAATTCGAATA CAGTGTCTAGNNNACGTATGCCA	490
TGCAGGACCAGAGAATTCGAATA CATAATACACNNNACGTATGCCA	11	TGCAGGACCAGAGAATTCGAATA CACTGCAGATNNNACGTATGCCA	251	TGCAGGACCAGAGAATTCGAATA CAGCGCCAGTNNNACGTATGCCA	491
TGCAGGACCAGAGAATTCGAATA CATCAGCATGNNNACGTATGCCA	12	TGCAGGACCAGAGAATTCGAATA CAATCGGATCNNNACGTATGCCA	252	TGCAGGACCAGAGAATTCGAATA CAGCTCTGAANNNACGTATGCCA	492
TGCAGGACCAGAGAATTCGAATA CAACTGTAGCNNNACGTATGCCA	13	TGCAGGACCAGAGAATTCGAATA CACTGTTCCANNNACGTATGCCA	253	TGCAGGACCAGAGAATTCGAATA CAAGACTTGCNNNACGTATGCCA	493
TGCAGGACCAGAGAATTCGAATA CAATTATGCANNNACGTATGCCA	14	TGCAGGACCAGAGAATTCGAATA CATCACATTTNNNACGTATGCCA	254	TGCAGGACCAGAGAATTCGAATA CAGATGGTCTNNNACGTATGCCA	494
TGCAGGACCAGAGAATTCGAATA CATGACCTTCNNNACGTATGCCA	15	TGCAGGACCAGAGAATTCGAATA CAGCGTGGCTNNNACGTATGCCA	255	TGCAGGACCAGAGAATTCGAATA CATTGTGAATNNNACGTATGCCA	495
TGCAGGACCAGAGAATTCGAATA CAAAAATCCTNNNACGTATGCCA	16	TGCAGGACCAGAGAATTCGAATA CACGGAGTAANNNACGTATGCCA	256	TGCAGGACCAGAGAATTCGAATA CACAGCGCGTNNNACGTATGCCA	496
TGCAGGACCAGAGAATTCGAATA CAGGTTCCGGNNNACGTATGCCA	17	TGCAGGACCAGAGAATTCGAATA CAGTGTCCGGNNNACGTATGCCA	257	TGCAGGACCAGAGAATTCGAATA CATGCCAAGTNNNACGTATGCCA	497
TGCAGGACCAGAGAATTCGAATA CAACGTGCATNNNACGTATGCCA	18	TGCAGGACCAGAGAATTCGAATA CATATTGTAGNNNACGTATGCCA	258	TGCAGGACCAGAGAATTCGAATA CACGTCGTTTNNNACGTATGCCA	498
TGCAGGACCAGAGAATTCGAATA CACGCCCCATNNNACGTATGCCA	19	TGCAGGACCAGAGAATTCGAATA CATAGTATTGNNNACGTATGCCA	259	TGCAGGACCAGAGAATTCGAATA CACCAACGGCNNNACGTATGCCA	499
TGCAGGACCAGAGAATTCGAATA CAGTAAGCCTNNNACGTATGCCA	20	TGCAGGACCAGAGAATTCGAATA CAAGCGCTTANNNACGTATGCCA	260	TGCAGGACCAGAGAATTCGAATA CACAGTTATANNNACGTATGCCA	500
TGCAGGACCAGAGAATTCGAATA CAAGTAATAGNNNACGTATGCCA	21	TGCAGGACCAGAGAATTCGAATA CATGCAGGTTNNNACGTATGCCA	261	TGCAGGACCAGAGAATTCGAATA CACGAAGGCGNNNACGTATGCCA	501
TGCAGGACCAGAGAATTCGAATA CAAAGTCCCANNNACGTATGCCA	22	TGCAGGACCAGAGAATTCGAATA CACCTCCGGTNNNACGTATGCCA	262	TGCAGGACCAGAGAATTCGAATA CAATGGCTACNNNACGTATGCCA	502
TGCAGGACCAGAGAATTCGAATA CAAGTGCATCNNNACGTATGCCA	23	TGCAGGACCAGAGAATTCGAATA CAAGACGGATNNNACGTATGCCA	263	TGCAGGACCAGAGAATTCGAATA CATCGCATGANNNACGTATGCCA	503
TGCAGGACCAGAGAATTCGAATA CAGACATATTNNNACGTATGCCA	24	TGCAGGACCAGAGAATTCGAATA CATCTGTCTGNNNACGTATGCCA	264	TGCAGGACCAGAGAATTCGAATA CAATATCCTTNNNACGTATGCCA	504
TGCAGGACCAGAGAATTCGAATA CAGTCCACAANNNACGTATGCCA	25	TGCAGGACCAGAGAATTCGAATA CATTCACCGTNNNACGTATGCCA	265	TGCAGGACCAGAGAATTCGAATA CATGAAGCAGNNNACGTATGCCA	505
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TGCAGGACCAGAGAATTCGAATA CAATCATGATNNNACGTATGCCA	31	TGCAGGACCAGAGAATTCGAATA CACTAATAACNNNACGTATGCCA	271	TGCAGGACCAGAGAATTCGAATA CAAAACCTATNNNACGTATGCCA	511
TGCAGGACCAGAGAATTCGAATA CATGACGGTTNNNACGTATGCCA	32	TGCAGGACCAGAGAATTCGAATA CAACGGACAANNNACGTATGCCA	272	TGCAGGACCAGAGAATTCGAATA CACTGATTTTNNNACGTATGCCA	512
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TGCAGGACCAGAGAATTCGAATA CAGTTACCCTNNNACGTATGCCA	34	TGCAGGACCAGAGAATTCGAATA CAGGACAACANNNACGTATGCCA	274	TGCAGGACCAGAGAATTCGAATA CAACTGCGCGNNNACGTATGCCA	514
TGCAGGACCAGAGAATTCGAATA CACTTAACGGNNNACGTATGCCA	35	TGCAGGACCAGAGAATTCGAATA CAGAAAGTTANNNACGTATGCCA	275	TGCAGGACCAGAGAATTCGAATA CAGAACGACANNNACGTATGCCA	515
TGCAGGACCAGAGAATTCGAATA CACGCTCCTGNNNACGTATGCCA	36	TGCAGGACCAGAGAATTCGAATA CAAACACAGGNNNACGTATGCCA	276	TGCAGGACCAGAGAATTCGAATA CATATATTGGNNNACGTATGCCA	516
TGCAGGACCAGAGAATTCGAATA CATCTCGGTTNNNACGTATGCCA	37	TGCAGGACCAGAGAATTCGAATA CACCAGAATCNNNACGTATGCCA	277	TGCAGGACCAGAGAATTCGAATA CATAGATGCCNNNACGTATGCCA	517
TGCAGGACCAGAGAATTCGAATA CAGCTCGAGCNNNACGTATGCCA	38	TGCAGGACCAGAGAATTCGAATA CATTCACCACNNNACGTATGCCA	278	TGCAGGACCAGAGAATTCGAATA CAGCAAGTAGNNNACGTATGCCA	518
TGCAGGACCAGAGAATTCGAATA CACGCTTCGCNNNACGTATGCCA	39	TGCAGGACCAGAGAATTCGAATA CATCGAGAGANNNACGTATGCCA	279	TGCAGGACCAGAGAATTCGAATA CAAACGACCTNNNACGTATGCCA	519
TGCAGGACCAGAGAATTCGAATA CAATCCAGACNNNACGTATGCCA	40	TGCAGGACCAGAGAATTCGAATA CACGATGTCANNNACGTATGCCA	280	TGCAGGACCAGAGAATTCGAATA CAGTACAGTCNNNACGTATGCCA	520
TGCAGGACCAGAGAATTCGAATA CATAGCACTGNNNACGTATGCCA	41	TGCAGGACCAGAGAATTCGAATA CACGGCAGGANNNACGTATGCCA	281	TGCAGGACCAGAGAATTCGAATA CATATGCGGTNNNACGTATGCCA	521

图12A

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACTGGCTTTNNNACGTATGCCA	42	TGCAGGACCAGAGAATTCGAATA CAAGAACCAGNNNACGTATGCCA	282	TGCAGGACCAGAGAATTCGAATA CAATAATAGGNNNACGTATGCCA	522
TGCAGGACCAGAGAATTCGAATA CAGCAAATGGNNNACGTATGCCA	43	TGCAGGACCAGAGAATTCGAATA CAGATTTTGANNNACGTATGCCA	283	TGCAGGACCAGAGAATTCGAATA CAGTTACTAANNNACGTATGCCA	523
TGCAGGACCAGAGAATTCGAATA CAGGATGACANNNACGTATGCCA	44	TGCAGGACCAGAGAATTCGAATA CAAACACGTCNNNACGTATGCCA	284	TGCAGGACCAGAGAATTCGAATA CACCCTTGTANNNACGTATGCCA	524
TGCAGGACCAGAGAATTCGAATA CAGCCCCACTNNNACGTATGCCA	45	TGCAGGACCAGAGAATTCGAATA CAACCTCTACNNNACGTATGCCA	285	TGCAGGACCAGAGAATTCGAATA CAACATTTCTNNNACGTATGCCA	525
TGCAGGACCAGAGAATTCGAATA CACTAGCCGGNNNACGTATGCCA	46	TGCAGGACCAGAGAATTCGAATA CAGGCGTTTANNNACGTATGCCA	286	TGCAGGACCAGAGAATTCGAATA CACCGACTTTNNNACGTATGCCA	526
TGCAGGACCAGAGAATTCGAATA CACCCTCCTCNNNACGTATGCCA	47	TGCAGGACCAGAGAATTCGAATA CACCCGAAGCNNNACGTATGCCA	287	TGCAGGACCAGAGAATTCGAATA CATATGAACTNNNACGTATGCCA	527
TGCAGGACCAGAGAATTCGAATA CATGTAGTGCNNNACGTATGCCA	48	TGCAGGACCAGAGAATTCGAATA CATACCTACCNNNACGTATGCCA	288	TGCAGGACCAGAGAATTCGAATA CATTCTTTTCNNNACGTATGCCA	528
TGCAGGACCAGAGAATTCGAATA CAGAATGTGGNNNACGTATGCCA	49	TGCAGGACCAGAGAATTCGAATA CATTTACGCCNNNACGTATGCCA	289	TGCAGGACCAGAGAATTCGAATA CAATAGGTTTNNNACGTATGCCA	529
TGCAGGACCAGAGAATTCGAATA CAAATGATCTNNNACGTATGCCA	50	TGCAGGACCAGAGAATTCGAATA CAAGGTATGGNNNACGTATGCCA	290	TGCAGGACCAGAGAATTCGAATA CACGACGTTANNNACGTATGCCA	530
TGCAGGACCAGAGAATTCGAATA CACACTAACGNNNACGTATGCCA	51	TGCAGGACCAGAGAATTCGAATA CAACTACAATNNNACGTATGCCA	291	TGCAGGACCAGAGAATTCGAATA CAAGCATAGGNNNACGTATGCCA	531
TGCAGGACCAGAGAATTCGAATA CACGTCGGACNNNACGTATGCCA	52	TGCAGGACCAGAGAATTCGAATA CACTCCTCAANNNACGTATGCCA	292	TGCAGGACCAGAGAATTCGAATA CACTGCATGTNNNACGTATGCCA	532
TGCAGGACCAGAGAATTCGAATA CAGCAACTTGNNNACGTATGCCA	53	TGCAGGACCAGAGAATTCGAATA CAGATACAAANNNACGTATGCCA	293	TGCAGGACCAGAGAATTCGAATA CACGACGCCANNNACGTATGCCA	533
TGCAGGACCAGAGAATTCGAATA CACGGTGGAGNNNACGTATGCCA	54	TGCAGGACCAGAGAATTCGAATA CACCAACACANNNACGTATGCCA	294	TGCAGGACCAGAGAATTCGAATA CAAACGCCCGNNNACGTATGCCA	534
TGCAGGACCAGAGAATTCGAATA CAGTAACCGTNNNACGTATGCCA	55	TGCAGGACCAGAGAATTCGAATA CAACCCATTCNNNACGTATGCCA	295	TGCAGGACCAGAGAATTCGAATA CACTCTCGATNNNACGTATGCCA	535
TGCAGGACCAGAGAATTCGAATA CATAGTTTTCNNNACGTATGCCA	56	TGCAGGACCAGAGAATTCGAATA CATCTAAGCGNNNACGTATGCCA	296	TGCAGGACCAGAGAATTCGAATA CACCCTGACCNNNACGTATGCCA	536
TGCAGGACCAGAGAATTCGAATA CACTGTCGTTNNNACGTATGCCA	57	TGCAGGACCAGAGAATTCGAATA CACTTAAGGCNNNACGTATGCCA	297	TGCAGGACCAGAGAATTCGAATA CAGTTGTAATNNNACGTATGCCA	537
TGCAGGACCAGAGAATTCGAATA CATTCGAGGTNNNACGTATGCCA	58	TGCAGGACCAGAGAATTCGAATA CACGAATCCANNNACGTATGCCA	298	TGCAGGACCAGAGAATTCGAATA CAAAAAGACTNNNACGTATGCCA	538
TGCAGGACCAGAGAATTCGAATA CACCTCCACGNNNACGTATGCCA	59	TGCAGGACCAGAGAATTCGAATA CACAACTAATNNNACGTATGCCA	299	TGCAGGACCAGAGAATTCGAATA CATCCTAGCTNNNACGTATGCCA	539
TGCAGGACCAGAGAATTCGAATA CAGAGACTAGNNNACGTATGCCA	60	TGCAGGACCAGAGAATTCGAATA CATCACACCTNNNACGTATGCCA	300	TGCAGGACCAGAGAATTCGAATA CAACCAAAGGNNNACGTATGCCA	540
TGCAGGACCAGAGAATTCGAATA CATGAACTATNNNACGTATGCCA	61	TGCAGGACCAGAGAATTCGAATA CAGACCGTCGNNNACGTATGCCA	301	TGCAGGACCAGAGAATTCGAATA CAACGAGTTCNNNACGTATGCCA	541
TGCAGGACCAGAGAATTCGAATA CAGTTGATTANNNACGTATGCCA	62	TGCAGGACCAGAGAATTCGAATA CACTTTAAGANNNACGTATGCCA	302	TGCAGGACCAGAGAATTCGAATA CACTATGGTGNNNACGTATGCCA	542
TGCAGGACCAGAGAATTCGAATA CATCCACTCANNNACGTATGCCA	63	TGCAGGACCAGAGAATTCGAATA CATGTGATTANNNACGTATGCCA	303	TGCAGGACCAGAGAATTCGAATA CACCACCGTCNNNACGTATGCCA	543
TGCAGGACCAGAGAATTCGAATA CAGTGACTGTNNNACGTATGCCA	64	TGCAGGACCAGAGAATTCGAATA CAACCCAATGNNNACGTATGCCA	304	TGCAGGACCAGAGAATTCGAATA CAGAATCGCTNNNACGTATGCCA	544
TGCAGGACCAGAGAATTCGAATA CATTACGGCANNNACGTATGCCA	65	TGCAGGACCAGAGAATTCGAATA CAACGTGTACNNNACGTATGCCA	305	TGCAGGACCAGAGAATTCGAATA CAAGTGTTATNNNACGTATGCCA	545
TGCAGGACCAGAGAATTCGAATA CACACCTCCGNNNACGTATGCCA	66	TGCAGGACCAGAGAATTCGAATA CAATGAAATGNNNACGTATGCCA	306	TGCAGGACCAGAGAATTCGAATA CAACGCGTCGNNNACGTATGCCA	546
TGCAGGACCAGAGAATTCGAATA CAAAGAAGAANNNACGTATGCCA	67	TGCAGGACCAGAGAATTCGAATA CATCCTCGTANNNACGTATGCCA	307	TGCAGGACCAGAGAATTCGAATA CACTCGTGTTNNNACGTATGCCA	547
TGCAGGACCAGAGAATTCGAATA CAGAACCTGTNNNACGTATGCCA	68	TGCAGGACCAGAGAATTCGAATA CAGTAACAGGNNNACGTATGCCA	308	TGCAGGACCAGAGAATTCGAATA CATTGTAGATNNNACGTATGCCA	548
TGCAGGACCAGAGAATTCGAATA CAGAATAACANNNCTAGCGTTAC	69	TGCAGGACCAGAGAATTCGAATA CAACTCGGTANNNCTAGCGTTAC	309	TGCAGGACCAGAGAATTCGAATA CAGCCGCAGTNNNCTAGCGTTAC	549
TGCAGGACCAGAGAATTCGAATA CAGCCTCGTCNNNCTAGCGTTAC	70	TGCAGGACCAGAGAATTCGAATA CAACGCTTAGNNNCTAGCGTTAC	310	TGCAGGACCAGAGAATTCGAATA CAAGTGACGANNNCTAGCGTTAC	550
TGCAGGACCAGAGAATTCGAATA CACCCGCACTNNNCTAGCGTTAC	71	TGCAGGACCAGAGAATTCGAATA CATCAAGCTGNNNCTAGCGTTAC	311	TGCAGGACCAGAGAATTCGAATA CAATACCTCCNNNCTAGCGTTAC	551
TGCAGGACCAGAGAATTCGAATA CACCACGATANNNCTAGCGTTAC	72	TGCAGGACCAGAGAATTCGAATA CATAGCTAATNNNCTAGCGTTAC	312	TGCAGGACCAGAGAATTCGAATA CACTTTTTGANNNCTAGCGTTAC	552
TGCAGGACCAGAGAATTCGAATA CACGGTACATNNNCTAGCGTTAC	73	TGCAGGACCAGAGAATTCGAATA CACGGCATTANNNCTAGCGTTAC	313	TGCAGGACCAGAGAATTCGAATA CAATATCATGNNNCTAGCGTTAC	553
TGCAGGACCAGAGAATTCGAATA CACCATATCCNNNCTAGCGTTAC	74	TGCAGGACCAGAGAATTCGAATA CAAATGATGANNNCTAGCGTTAC	314	TGCAGGACCAGAGAATTCGAATA CATACATATGNNNCTAGCGTTAC	554

图12B

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACATACGGTNNNCTAGCGTTAC	75	TGCAGGACCAGAGAATTCGAATA CATCGCGATANNNCTAGCGTTAC	315	TGCAGGACCAGAGAATTCGAATA CAACTTTTGTNNNCTAGCGTTAC	555
TGCAGGACCAGAGAATTCGAATA CAAATAGCTTNNNCTAGCGTTAC	76	TGCAGGACCAGAGAATTCGAATA CACACAGGTTNNNCTAGCGTTAC	316	TGCAGGACCAGAGAATTCGAATA CATAATGTACNNNCTAGCGTTAC	556
TGCAGGACCAGAGAATTCGAATA CACCAGGTATNNNCTAGCGTTAC	77	TGCAGGACCAGAGAATTCGAATA CAACGGTGCCNNNCTAGCGTTAC	317	TGCAGGACCAGAGAATTCGAATA CAAACGACAGNNNCTAGCGTTAC	557
TGCAGGACCAGAGAATTCGAATA CACAACCTGANNNCTAGCGTTAC	78	TGCAGGACCAGAGAATTCGAATA CAGTTACAGCNNNCTAGCGTTAC	318	TGCAGGACCAGAGAATTCGAATA CAGCTCCTATNNNCTAGCGTTAC	558
TGCAGGACCAGAGAATTCGAATA CATGATGGTCNNNCTAGCGTTAC	79	TGCAGGACCAGAGAATTCGAATA CATGCGATGTNNNCTAGCGTTAC	319	TGCAGGACCAGAGAATTCGAATA CACCGAAACTNNNCTAGCGTTAC	559
TGCAGGACCAGAGAATTCGAATA CAGGAGCCGANNNCTAGCGTTAC	80	TGCAGGACCAGAGAATTCGAATA CAATGGTGCTNNNCTAGCGTTAC	320	TGCAGGACCAGAGAATTCGAATA CAGCTAGGAANNNCTAGCGTTAC	560
TGCAGGACCAGAGAATTCGAATA CAATGCGGCCNNNCTAGCGTTAC	81	TGCAGGACCAGAGAATTCGAATA CAACCCCAGGNNNCTAGCGTTAC	321	TGCAGGACCAGAGAATTCGAATA CAGCTTCCGCNNNCTAGCGTTAC	561
TGCAGGACCAGAGAATTCGAATA CATGCTGTAGNNNCTAGCGTTAC	82	TGCAGGACCAGAGAATTCGAATA CAGCAGACGGNNNCTAGCGTTAC	322	TGCAGGACCAGAGAATTCGAATA CAACAGCATCNNNCTAGCGTTAC	562
TGCAGGACCAGAGAATTCGAATA CAGCATTGACNNNCTAGCGTTAC	83	TGCAGGACCACAGAATTCGAATA CACTGGCAGCNNNCTAGCGTTAC	323	TGCAGGACCAGAGAATTCGAATA CAACGAGAGTNNNCTAGCGTTAC	563
TGCAGGACCAGAGAATTCGAATA CATTTGTACTNNNCTAGCGTTAC	84	TGCAGGACCAGAGAATTCGAATA CAAGAGAGTCNNNCTAGCGTTAC	324	TGCAGGACCAGAGAATTCGAATA CAATCATATGNNNCTAGCGTTAC	564
TGCAGGACCAGAGAATTCGAATA CACATATGGCNNNCTAGCGTTAC	85	TGCAGGACCAGAGAATTCGAATA CACGTTTTATNNNCTAGCGTTAC	325	TGCAGGACCAGAGAATTCGAATA CATGAGATTTNNNCTAGCGTTAC	565
TGCAGGACCAGAGAATTCGAATA CAGCATGAAGNNNCTAGCGTTAC	86	TGCAGGACCAGAGAATTCGAATA CAAGAGGTCANNNCTAGCGTTAC	326	TGCAGGACCAGAGAATTCGAATA CAGCCGGCCGNNNCTAGCGTTAC	566
TGCAGGACCAGAGAATTCGAATA CACAGGAAACNNNCTAGCGTTAC	87	TGCAGGACCAGAGAATTCGAATA CATTCTCTCCNNNCTAGCGTTAC	327	TGCAGGACCAGAGAATTCGAATA CAAGGCGCAGNNNCTAGCGTTAC	567
TGCAGGACCAGAGAATTCGAATA CACCTAAGACNNNCTAGCGTTAC	88	TGCAGGACCAGAGAATTCGAATA CACGTGTCTTNNNCTAGCGTTAC	328	TGCAGGACCAGAGAATTCGAATA CAGTACACACNNNCTAGCGTTAC	568
TGCAGGACCAGAGAATTCGAATA CAACCTAGGTNNNCTAGCGTTAC	89	TGCAGGACCAGAGAATTCGAATA CACTCAGCAANNNCTAGCGTTAC	329	TGCAGGACCAGAGAATTCGAATA CAAGATTTCANNNCTAGCGTTAC	569
TGCAGGACCAGAGAATTCGAATA CACCATTGTCNNNCTAGCGTTAC	90	TGCAGGACCAGAGAATTCGAATA CATCTTATGTNNNCTAGCGTTAC	330	TGCAGGACCAGAGAATTCGAATA CATGCATCTCNNNCTAGCGTTAC	570
TGCAGGACCAGAGAATTCGAATA CATCGGTTTCNNNCTAGCGTTAC	91	TGCAGGACCAGAGAATTCGAATA CATCGGCACGNNNCTAGCGTTAC	331	TGCAGGACCAGAGAATTCGAATA CACTCAGAGTNNNCTAGCGTTAC	571
TGCAGGACCAGAGAATTCGAATA CACACCTGTTNNNCTAGCGTTAC	92	TGCAGGACCAGAGAATTCGAATA CACGTTTCTGNNNCTAGCGTTAC	332	TGCAGGACCAGAGAATTCGAATA CAACTCTGTCNNNCTAGCGTTAC	572
TGCAGGACCAGAGAATTCGAATA CAAGAGAGAGNNNCTAGCGTTAC	93	TGCAGGACCAGAGAATTCGAATA CAATGTGAGGNNNCTAGCGTTAC	333	TGCAGGACCAGAGAATTCGAATA CATTATCCGCNNNCTAGCGTTAC	573
TGCAGGACCAGAGAATTCGAATA CAATGGCCCGNNNCTAGCGTTAC	94	TGCAGGACCAGAGAATTCGAATA CAAGAAACATNNNCTAGCGTTAC	334	TGCAGGACCAGAGAATTCGAATA CAGCCCTTGCNNNCTAGCGTTAC	574
TGCAGGACCAGAGAATTCGAATA CATAGCGTGTNNNCTAGCGTTAC	95	TGCAGGACCAGAGAATTCGAATA CAGAGAGAAGNNNCTAGCGTTAC	335	TGCAGGACCAGAGAATTCGAATA CAAACTTCTTNNNCTAGCGTTAC	575
TGCAGGACCAGAGAATTCGAATA CAGAAGACACNNNCTAGCGTTAC	96	TGCAGGACCAGAGAATTCGAATA CACTTCAGGANNNCTAGCGTTAC	336	TGCAGGACCAGAGAATTCGAATA CATTGTAGGCNNNCTAGCGTTAC	576
TGCAGGACCAGAGAATTCGAATA CATCATTTGTNNNCTAGCGTTAC	97	TGCAGGACCAGAGAATTCGAATA CATCCCTCGGNNNCTAGCGTTAC	337	TGCAGGACCAGAGAATTCGAATA CATGACCCAANNNCTAGCGTTAC	577
TGCAGGACCAGAGAATTCGAATA CATCGAACACNNNCTAGCGTTAC	98	TGCAGGACCAGAGAATTCGAATA CACCTTCCTTNNNCTAGCGTTAC	338	TGCAGGACCAGAGAATTCGAATA CACCTCTGTANNNCTAGCGTTAC	578
TGCAGGACCAGAGAATTCGAATA CAAGCTTACGNNNCTAGCGTTAC	99	TGCAGGACCAGAGAATTCGAATA CATAGTTATGNNNCTAGCGTTAC	339	TGCAGGACCAGAGAATTCGAATA CAAGCCACTANNNCTAGCGTTAC	579
TGCAGGACCAGAGAATTCGAATA CACTCGGTTTNNNCTAGCGTTAC	100	TGCAGGACCAGAGAATTCGAATA CAGCATAGAGNNNCTAGCGTTAC	340	TGCAGGACCAGAGAATTCGAATA CATGTATGATNNNCTAGCGTTAC	580
TGCAGGACCAGAGAATTCGAATA CAAATCGTTANNNCTAGCGTTAC	101	TGCAGGACCAGAGAATTCGAATA CATAGCTCCTNNNCTAGCGTTAC	341	TGCAGGACCAGAGAATTCGAATA CACAGGTCGCNNNCTAGCGTTAC	581
TGCAGGACCAGAGAATTCGAATA CATAACAGTTNNNCTAGCGTTAC	102	TGCAGGACCAGAGAATTCGAATA CAACCACGTANNNCTAGCGTTAC	342	TGCAGGACCAGAGAATTCGAATA CATTTTTTTTNNNCTAGCGTTAC	582
TGCAGGACCAGAGAATTCGAATA CAATCCTGTCNNNCTAGCGTTAC	103	TGCAGGACCAGAGAATTCGAATA CACATCGTCTNNNCTAGCGTTAC	343	TGCAGGACCAGAGAATTCGAATA CATTTGCGGANNNCTAGCGTTAC	583
TGCAGGACCAGAGAATTCGAATA CAGTAATGTTNNNCTAGCGTTAC	104	TGCAGGACCAGAGAATTCGAATA CAAGAGATTANNNCTAGCGTTAC	344	TGCAGGACCAGAGAATTCGAATA CAAGCCTGTANNNCTAGCGTTAC	584
TGCAGGACCAGAGAATTCGAATA CATTGCGCGGNNNCTAGCGTTAC	105	TGCAGGACCAGAGAATTCGAATA CAATCAAAGANNNCTAGCGTTAC	345	TGCAGGACCAGAGAATTCGAATA CAGCGGCACTNNNCTAGCGTTAC	585
TGCAGGACCAGAGAATTCGAATA CAGTCAGGAANNNCTAGCGTTAC	106	TGCAGGACCAGAGAATTCGAATA CAGGAGTACANNNCTAGCGTTAC	346	TGCAGGACCAGAGAATTCGAATA CATGTTGAGCNNNCTAGCGTTAC	586
TGCAGGACCAGAGAATTCGAATA CAGTTAAAAGNNNCTAGCGTTAC	107	TGCAGGACCAGAGAATTCGAATA CAATAGCAGGNNNCTAGCGTTAC	347	TGCAGGACCAGAGAATTCGAATA CAAAAAGTTGNNNCTAGCGTTAC	587

图12C

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATGTCATAANNNCTAGCGTTAC	108	TGCAGGACCAGAGAATTCGAATA CATCTAATTCNNNCTAGCGTTAC	348	TGCAGGACCAGAGAATTCGAATA CACGGTGCCANNNCTAGCGTTAC	588
TGCAGGACCAGAGAATTCGAATA CAACTTGAATNNNCTAGCGTTAC	109	TGCAGGACCAGAGAATTCGAATA CAGTTCCCGCNNNCTAGCGTTAC	349	TGCAGGACCAGAGAATTCGAATA CACAGCGGTCNNNCTAGCGTTAC	589
TGCAGGACCAGAGAATTCGAATA CATGTGGCATNNNCTAGCGTTAC	110	TGCAGGACCAGAGAATTCGAATA CATAGATTTGNNNCTAGCGTTAC	350	TGCAGGACCAGAGAATTCGAATA CAAGCTAACCNNNCTAGCGTTAC	590
TGCAGGACCAGAGAATTCGAATA CATCTACACCNNNCTAGCGTTAC	111	TGCAGGACCAGAGAATTCGAATA CACGGCAGAGNNNCTAGCGTTAC	351	TGCAGGACCAGAGAATTCGAATA CAACGGCGTCNNNCTAGCGTTAC	591
TGCAGGACCAGAGAATTCGAATA CATCATGCCTNNNCTAGCGTTAC	112	TGCAGGACCAGAGAATTCGAATA CACCTCGTGCNNNCTAGCGTTAC	352	TGCAGGACCAGAGAATTCGAATA CATAGTTCAANNNCTAGCGTTAC	592
TGCAGGACCAGAGAATTCGAATA CATCTAGCCTNNNCTAGCGTTAC	113	TGCAGGACCAGAGAATTCGAATA CACCCTTGATNNNCTAGCGTTAC	353	TGCAGGACCAGAGAATTCGAATA CAATGTAGCCNNNCTAGCGTTAC	593
TGCAGGACCAGAGAATTCGAATA CAATAAAGCANNNCTAGCGTTAC	114	TGCAGGACCAGAGAATTCGAATA CACGTCACGGNNNCTAGCGTTAC	354	TGCAGGACCAGAGAATTCGAATA CAAGAAGCACNNNCTAGCGTTAC	594
TGCAGGACCAGAGAATTCGAATA CATGCATAATNNNCTAGCGTTAC	115	TGCAGGACCAGAGAATTCGAATA CAGTTTGGCANNNCTAGCGTTAC	355	TGCAGGACCAGAGAATTCGAATA CAGAAGCGCGNNNCTAGCGTTAC	595
TGCAGGACCAGAGAATTCGAATA CACATGACGTNNNCTAGCGTTAC	116	TGCAGGACCAGAGAATTCGAATA CATGCTCTGTNNNCTAGCGTTAC	356	TGCAGGACCAGAGAATTCGAATA CACGGTATACNNNCTAGCGTTAC	596
TGCAGGACCAGAGAATTCGAATA CACTTATCATNNNCTAGCGTTAC	117	TGCAGGACCAGAGAATTCGAATA CATCAGTATANNNCTAGCGTTAC	357	TGCAGGACCAGAGAATTCGAATA CATAACATACNNNCTAGCGTTAC	597
TGCAGGACCAGAGAATTCGAATA CACGGCCTGANNNCTAGCGTTAC	118	TGCAGGACCAGAGAATTCGAATA CACCCAAGTANNNCTAGCGTTAC	358	TGCAGGACCAGAGAATTCGAATA CACTGCTATCNNNCTAGCGTTAC	598
TGCAGGACCAGAGAATTCGAATA CACGTCAATGNNNCTAGCGTTAC	119	TGCAGGACCAGAGAATTCGAATA CAAAGCTAAANNNCTAGCGTTAC	359	TGCAGGACCAGAGAATTCGAATA CACGGCAACCNNNCTAGCGTTAC	599
TGCAGGACCAGAGAATTCGAATA CAGTTATACTNNNCTAGCGTTAC	120	TGCAGGACCAGAGAATTCGAATA CAAGATCCACNNNCTAGCGTTAC	360	TGCAGGACCAGAGAATTCGAATA CACAAAAACANNNCTAGCGTTAC	600
TGCAGGACCAGAGAATTCGAATA CAGGAGGTATNNNCTAGCGTTAC	121	TGCAGGACCAGAGAATTCGAATA CAGCATCGGCNNNCTAGCGTTAC	361	TGCAGGACCAGAGAATTCGAATA CACGTTAGCANNNCTAGCGTTAC	601
TGCAGGACCAGAGAATTCGAATA CAATTGTTCTNNNCTAGCGTTAC	122	TGCAGGACCAGAGAATTCGAATA CACTCTGGAANNNCTAGCGTTAC	362	TGCAGGACCAGAGAATTCGAATA CACCCTAATCNNNCTAGCGTTAC	602
TGCAGGACCAGAGAATTCGAATA CAAACTCCAGNNNCTAGCGTTAC	123	TGCAGGACCAGAGAATTCGAATA CAAGTCTGACNNNCTAGCGTTAC	363	TGCAGGACCAGAGAATTCGAATA CATGTGGCCGNNNCTAGCGTTAC	603
TGCAGGACCAGAGAATTCGAATA CACGAGGTCCNNNCTAGCGTTAC	124	TGCAGGACCAGAGAATTCGAATA CAGAGGCCGANNNCTAGCGTTAC	364	TGCAGGACCAGAGAATTCGAATA CATCTAGAGCNNNCTAGCGTTAC	604
TGCAGGACCAGAGAATTCGAATA CACGCGACCANNNCTAGCGTTAC	125	TGCAGGACCAGAGAATTCGAATA CATGGTGGAANNNCTAGCGTTAC	365	TGCAGGACCAGAGAATTCGAATA CATACGCATGNNNCTAGCGTTAC	605
TGCAGGACCAGAGAATTCGAATA CATGCCGCCTNNNCTAGCGTTAC	126	TGCAGGACCAGAGAATTCGAATA CACGGTGTTANNNCTAGCGTTAC	366	TGCAGGACCAGAGAATTCGAATA CATTGCCCCGNNNCTAGCGTTAC	606
TGCAGGACCAGAGAATTCGAATA CAGTTACGACNNNCTAGCGTTAC	127	TGCAGGACCAGAGAATTCGAATA CATCGCGCAGNNNCTAGCGTTAC	367	TGCAGGACCAGAGAATTCGAATA CATGGTTCCTNNNCTAGCGTTAC	607
TGCAGGACCAGAGAATTCGAATA CATTATCATCNNNCTAGCGTTAC	128	TGCAGGACCAGAGAATTCGAATA CAGCTGTGTANNNCTAGCGTTAC	368	TGCAGGACCAGAGAATTCGAATA CAAACGGTGANNNCTAGCGTTAC	608
TGCAGGACCAGAGAATTCGAATA CACCTTCTCTNNNGATCGACATG	129	TGCAGGACCAGAGAATTCGAATA CAACGTGCGCNNNGATCGACATG	369	TGCAGGACCAGAGAATTCGAATA CAGGCTATACNNNGATCGACATG	609
TGCAGGACCAGAGAATTCGAATA CAAACAGGTGNNNGATCGACATG	130	TGCAGGACCAGAGAATTCGAATA CAATCAGCCANNNGATCGACATG	370	TGCAGGACCAGAGAATTCGAATA CAATTGGTTANNNGATCGACATG	610
TGCAGGACCAGAGAATTCGAATA CAACTTGTCCNNNGATCGACATG	131	TGCAGGACCAGAGAATTCGAATA CAGATACTTANNNGATCGACATG	371	TGCAGGACCAGAGAATTCGAATA CACAGGATGANNNGATCGACATG	611
TGCAGGACCAGAGAATTCGAATA CATTGGTAATNNNGATCGACATG	132	TGCAGGACCAGAGAATTCGAATA CAATTTCGCCNNNGATCGACATG	372	TGCAGGACCAGAGAATTCGAATA CACGTTATCCNNNGATCGACATG	612
TGCAGGACCAGAGAATTCGAATA CAGGACTCGCNNNGATCGACATG	133	TGCAGGACCAGAGAATTCGAATA CACTTAAAGTNNNGATCGACATG	373	TGCAGGACCAGAGAATTCGAATA CAGTTCAATANNNGATCGACATG	613
TGCAGGACCAGAGAATTCGAATA CATGCGTCAANNNGATCGACATG	134	TGCAGGACCAGAGAATTCGAATA CATATGCCCTNNNGATCGACATG	374	TGCAGGACCAGAGAATTCGAATA CACAAAATCTNNNGATCGACATG	614
TGCAGGACCAGAGAATTCGAATA CACAGAATAANNNGATCGACATG	135	TGCAGGACCAGAGAATTCGAATA CAACTTGACGNNNGATCGACATG	375	TGCAGGACCAGAGAATTCGAATA CACTGCAAACNNNGATCGACATG	615
TGCAGGACCAGAGAATTCGAATA CATCCGAGGCNNNGATCGACATG	136	TGCAGGACCAGAGAATTCGAATA CAAGGAACCANNNGATCGACATG	376	TGCAGGACCAGAGAATTCGAATA CAGGTGCCCANNNGATCGACATG	616
TGCAGGACCAGAGAATTCGAATA CAATTTCTTGNNNGATCGACATG	137	TGCAGGACCAGAGAATTCGAATA CATGAGCGAANNNGATCGACATG	377	TGCAGGACCAGAGAATTCGAATA CACGATAACCNNNGATCGACATG	617
TGCAGGACCAGAGAATTCGAATA CAACTTGTAANNNGATCGACATG	138	TGCAGGACCAGAGAATTCGAATA CATGCTGTGANNNGATCGACATG	378	TGCAGGACCAGAGAATTCGAATA CATTATGACANNNGATCGACATG	618
TGCAGGACCAGAGAATTCGAATA CACACGGTGCNNNGATCGACATG	139	TGCAGGACCAGAGAATTCGAATA CAGGTTCGTANNNGATCGACATG	379	TGCAGGACCAGAGAATTCGAATA CAACCTTCACNNNGATCGACATG	619
TGCAGGACCAGAGAATTCGAATA CAAACTCGGTNNNGATCGACATG	140	TGCAGGACCAGAGAATTCGAATA CAACAAACAANNNGATCGACATG	380	TGCAGGACCAGAGAATTCGAATA CATCTTCTCCNNNGATCGACATG	620

图12D

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGCCTATTCNNNGATCGACATG	141	TGCAGGACCAGAGAATTCGAATA CAAGCTAGAGNNNGATCGACATG	381	TGCAGGACCAGAGAATTCGAATA CACCCCAGCTNNNGATCGACATG	621
TGCAGGACCAGAGAATTCGAATA CACCGCTAAANNNGATCGACATG	142	TGCAGGACCAGAGAATTCGAATA CATTAAATATNNNGATCGACATG	382	TGCAGGACCAGAGAATTCGAATA CACTAGTGTGNNNGATCGACATG	622
TGCAGGACCAGAGAATTCGAATA CAGTGAGATGNNNGATCGACATG	143	TGCAGGACCAGAGAATTCGAATA CAAGGAGTCANNNGATCGACATG	383	TGCAGGACCAGAGAATTCGAATA CAGTTCTAAANNNGATCGACATG	623
TGCAGGACCAGAGAATTCGAATA CATCTCTCAGNNNGATCGACATG	144	TGCAGGACCAGAGAATTCGAATA CACGCACAGCNNNGATCGACATG	384	TGCAGGACCAGAGAATTCGAATA CAGCGTTTTCNNNGATCGACATG	624
TGCAGGACCAGAGAATTCGAATA CATCTCTAGCNNNGATCGACATG	145	TGCAGGACCAGAGAATTCGAATA CAGCGGACAGNNNGATCGACATG	385	TGCAGGACCAGAGAATTCGAATA CAGTCTGCCCNNNGATCGACATG	625
TGCAGGACCAGAGAATTCGAATA CACAAGCGCCNNNGATCGACATG	146	TGCAGGACCAGAGAATTCGAATA CACGCTCGTCNNNGATCGACATG	386	TGCAGGACCAGAGAATTCGAATA CAACAGAAATNNNGATCGACATG	626
TGCAGGACCAGAGAATTCGAATA CAGGCAGTAANNNGATCGACATG	147	TGCAGGACCAGAGAATTCGAATA CATCTGATGGNNNGATCGACATG	387	TGCAGGACCAGAGAATTCGAATA CATTGCTATTNNNGATCGACATG	627
TGCAGGACCAGAGAATTCGAATA CATTGGCTGANNNGATCGACATG	148	TGCAGGACCAGAGAATTCGAATA CAGGCTAGAANNNGATCGACATG	388	TGCAGGACCAGAGAATTCGAATA CACCCTGTGCNNNGATCGACATG	628
TGCAGGACCAGAGAATTCGAATA CAACAGCGAANNNGATCGACATG	149	TGCAGGACCAGAGAATTCGAATA CAATGAGGCANNNGATCGACATG	389	TGCAGGACCAGAGAATTCGAATA CAGCAGTCCGNNNGATCGACATG	629
TGCAGGACCAGAGAATTCGAATA CAAAGTTTCANNNGATCGACATG	150	TGCAGGACCAGAGAATTCGAATA CACACCCGTCNNNGATCGACATG	390	TGCAGGACCAGAGAATTCGAATA CAGTAACCCANNNGATCGACATG	630
TGCAGGACCAGAGAATTCGAATA CACGCTCTATNNNGATCGACATG	151	TGCAGGACCAGAGAATTCGAATA CATCATCGGANNNGATCGACATG	391	TGCAGGACCAGAGAATTCGAATA CAACATTGTANNNGATCGACATG	631
TGCAGGACCAGAGAATTCGAATA CATAGGAGTGNNNGATCGACATG	152	TGCAGGACCAGAGAATTCGAATA CAGGCAAGCGNNNGATCGACATG	392	TGCAGGACCAGAGAATTCGAATA CAAAACCGTCNNNGATCGACATG	632
TGCAGGACCAGAGAATTCGAATA CATCAGCACANNNGATCGACATG	153	TGCAGGACCAGAGAATTCGAATA CACAGTCGATNNNGATCGACATG	393	TGCAGGACCAGAGAATTCGAATA CAATTCTGCCNNNGATCGACATG	633
TGCAGGACCAGAGAATTCGAATA CACGAACTACNNNGATCGACATG	154	TGCAGGACCAGAGAATTCGAATA CATGCTACTCNNNGATCGACATG	394	TGCAGGACCAGAGAATTCGAATA CATCTAGGCANNNGATCGACATG	634
TGCAGGACCAGAGAATTCGAATA CATACTAAACNNNGATCGACATG	155	TGCAGGACCAGAGAATTCGAATA CATCCATACCNNNGATCGACATG	395	TGCAGGACCAGAGAATTCGAATA CAGGTCTACANNNGATCGACATG	635
TGCAGGACCAGAGAATTCGAATA CAGGTACAAGNNNGATCGACATG	156	TGCAGGACCAGAGAATTCGAATA CAACCGCGACNNNGATCGACATG	396	TGCAGGACCAGAGAATTCGAATA CAGGTGAGCGNNNGATCGACATG	636
TGCAGGACCAGAGAATTCGAATA CAACAGGCTTNNNGATCGACATG	157	TGCAGGACCAGAGAATTCGAATA CAGGCAAAGTNNNGATCGACATG	397	TGCAGGACCAGAGAATTCGAATA CATGTCTTTANNNGATCGACATG	637
TGCAGGACCAGAGAATTCGAATA CAGAAACCCTNNNGATCGACATG	158	TGCAGGACCAGAGAATTCGAATA CAGGATCCCGNNNGATCGACATG	398	TGCAGGACCAGAGAATTCGAATA CATGGCTTGANNNGATCGACATG	638
TGCAGGACCAGAGAATTCGAATA CATCCGCATTNNNGATCGACATG	159	TGCAGGACCAGAGAATTCGAATA CACCTCTCTTNNNGATCGACATG	399	TGCAGGACCAGAGAATTCGAATA CAATTACGCGNNNGATCGACATG	639
TGCAGGACCAGAGAATTCGAATA CACAATCTGGNNNGATCGACATG	160	TGCAGGACCAGAGAATTCGAATA CATCGTCGCCNNNGATCGACATG	400	TGCAGGACCAGAGAATTCGAATA CATGGCTCTTNNNGATCGACATG	640
TGCAGGACCAGAGAATTCGAATA CAACCTTACCNNNGATCGACATG	161	TGCAGGACCAGAGAATTCGAATA CACCTATGTCNNNGATCGACATG	401	TGCAGGACCAGAGAATTCGAATA CACACTCACTNNNGATCGACATG	641
TGCAGGACCAGAGAATTCGAATA CAGCGGTCTGNNNGATCGACATG	162	TGCAGGACCAGAGAATTCGAATA CAGGATGCTTNNNGATCGACATG	402	TGCAGGACCAGAGAATTCGAATA CACTGCAGGCNNNGATCGACATG	642
TGCAGGACCAGAGAATTCGAATA CAAATCACGCNNNGATCGACATG	163	TGCAGGACCAGAGAATTCGAATA CAATTGAGAANNNGATCGACATG	403	TGCAGGACCAGAGAATTCGAATA CACCCAATCTNNNGATCGACATG	643
TGCAGGACCAGAGAATTCGAATA CAAATAGTAGNNNGATCGACATG	164	TGCAGGACCAGAGAATTCGAATA CAGTGTTGTGNNNGATCGACATG	404	TGCAGGACCAGAGAATTCGAATA CAACGTAACCNNNGATCGACATG	644
TGCAGGACCAGAGAATTCGAATA CAGGCATCTANNNGATCGACATG	165	TGCAGGACCAGAGAATTCGAATA CAAAGCAATANNNGATCGACATG	405	TGCAGGACCAGAGAATTCGAATA CAACCGTCCCNNNGATCGACATG	645
TGCAGGACCAGAGAATTCGAATA CAAGCGCCTGNNNGATCGACATG	166	TGCAGGACCAGAGAATTCGAATA CATTAGCGCANNNGATCGACATG	406	TGCAGGACCAGAGAATTCGAATA CATTCGCGAANNNGATCGACATG	646
TGCAGGACCAGAGAATTCGAATA CAGACCCGGTNNNGATCGACATG	167	TGCAGGACCAGAGAATTCGAATA CAAACGGATGNNNGATCGACATG	407	TGCAGGACCAGAGAATTCGAATA CACGCACAATNNNGATCGACATG	647
TGCAGGACCAGAGAATTCGAATA CACGGTAAAGNNNGATCGACATG	168	TGCAGGACCAGAGAATTCGAATA CAGCATGGAANNNGATCGACATG	408	TGCAGGACCAGAGAATTCGAATA CACAATCTCCNNNGATCGACATG	648
TGCAGGACCAGAGAATTCGAATA CAAGGATGCANNNGATCGACATG	169	TGCAGGACCAGAGAATTCGAATA CATCTCATATNNNGATCGACATG	409	TGCAGGACCAGAGAATTCGAATA CATCAGAGTCNNNGATCGACATG	649
TGCAGGACCAGAGAATTCGAATA CATTCTGGAGNNNGATCGACATG	170	TGCAGGACCAGAGAATTCGAATA CACTGCGCCTNNNGATCGACATG	410	TGCAGGACCAGAGAATTCGAATA CAAATCGTGCNNNGATCGACATG	650
TGCAGGACCAGAGAATTCGAATA CAGCTCAAACNNNGATCGACATG	171	TGCAGGACCAGAGAATTCGAATA CAGATTCGCANNNGATCGACATG	411	TGCAGGACCAGAGAATTCGAATA CACTAGCATGNNNGATCGACATG	651
TGCAGGACCAGAGAATTCGAATA CATAAGTTACNNNGATCGACATG	172	TGCAGGACCAGAGAATTCGAATA CAATCTATCTNNNGATCGACATG	412	TGCAGGACCAGAGAATTCGAATA CAGATTAACTNNNGATCGACATG	652
TGCAGGACCAGAGAATTCGAATA CACAACCCTTNNNGATCGACATG	173	TGCAGGACCAGAGAATTCGAATA CAGTCACCCCNNNGATCGACATG	413	TGCAGGACCAGAGAATTCGAATA CAGGCTACGCNNNGATCGACATG	653

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACCTTCCGGNNNGATCGACATG	174	TGCAGGACCAGAGAATTCGAATA CACGTTGTGANNNGATCGACATG	414	TGCAGGACCAGAGAATTCGAATA CAATACGAGGNNNGATCGACATG	654
TGCAGGACCAGAGAATTCGAATA CAGTGAGAGTNNNGATCGACATG	175	TGCAGGACCAGAGAATTCGAATA CAGCTCTGCCNNNGATCGACATG	415	TGCAGGACCAGAGAATTCGAATA CAAAATGTCTNNNGATCGACATG	655
TGCAGGACCAGAGAATTCGAATA CAGCGTCCAGNNNGATCGACATG	176	TGCAGGACCAGAGAATTCGAATA CACATCGATGNNNGATCGACATG	416	TGCAGGACCAGAGAATTCGAATA CAGCGCATCGNNNGATCGACATG	656
TGCAGGACCAGAGAATTCGAATA CATTTATTCGNNNGATCGACATG	177	TGCAGGACCAGAGAATTCGAATA CAAGTCGCCGNNNGATCGACATG	417	TGCAGGACCAGAGAATTCGAATA CACTCCGGTGNNNGATCGACATG	657
TGCAGGACCAGAGAATTCGAATA CAGTAATAAGNNNGATCGACATG	178	TGCAGGACCAGAGAATTCGAATA CAGATAGCGANNNGATCGACATG	418	TGCAGGACCAGAGAATTCGAATA CAGATAAGGCNNNGATCGACATG	658
TGCAGGACCAGAGAATTCGAATA CATACAAGCCNNNGATCGACATG	179	TGCAGGACCAGAGAATTCGAATA CATCTTTGGCNNNGATCGACATG	419	TGCAGGACCAGAGAATTCGAATA CAGCACATCANNNGATCGACATG	659
TGCAGGACCAGAGAATTCGAATA CAAAGCCGAANNNGATCGACATG	180	TGCAGGACCAGAGAATTCGAATA CATCTCATCGNNNGATCGACATG	420	TGCAGGACCAGAGAATTCGAATA CATCCTATGCNNNGATCGACATG	660
TGCAGGACCAGAGAATTCGAATA CAATACTTTCNNNGATCGACATG	181	TGCAGGACCAGAGAATTCGAATA CATGAGCGCCNNNGATCGACATG	421	TGCAGGACCAGAGAATTCGAATA CACGCATCCCNNNGATCGACATG	661
TGCAGGACCAGAGAATTCGAATA CACTGGATCANNNGATCGACATG	182	TGCAGGACCAGAGAATTCGAATA CAAGTCTCGANNNGATCGACATG	422	TGCAGGACCAGAGAATTCGAATA CAACCGGTCGNNNGATCGACATG	662
TGCAGGACCAGAGAATTCGAATA CAAACGCCTANNNGATCGACATG	183	TGCAGGACCAGAGAATTCGAATA CAAAGGTATANNNGATCGACATG	423	TGCAGGACCAGAGAATTCGAATA CACACGATGTNNNGATCGACATG	663
TGCAGGACCAGAGAATTCGAATA CAGTCGAGAANNNGATCGACATG	184	TGCAGGACCAGAGAATTCGAATA CAGGTGTCGCNNNGATCGACATG	424	TGCAGGACCAGAGAATTCGAATA CAAACTCGCANNNGATCGACATG	664
TGCAGGACCAGAGAATTCGAATA CATAATTCTCNNNGATCGACATG	185	TGCAGGACCAGAGAATTCGAATA CATCACATCCNNNGATCGACATG	425	TGCAGGACCAGAGAATTCGAATA CACCCCTTCCNNNGATCGACATG	665
TGCAGGACCAGAGAATTCGAATA CATAACCCTCNNNGATCGACATG	186	TGCAGGACCAGAGAATTCGAATA CAGCATACACNNNGATCGACATG	426	TGCAGGACCAGAGAATTCGAATA CATCTTCGTGNNNGATCGACATG	666
TGCAGGACCAGAGAATTCGAATA CAGCGCTTGGNNNGATCGACATG	187	TGCAGGACCAGAGAATTCGAATA CATCCAACAGNNNGATCGACATG	427	TGCAGGACCAGAGAATTCGAATA CATATTTAAANNNGATCGACATG	667
TGCAGGACCAGAGAATTCGAATA CACGGACACCNNNGATCGACATG	188	TGCAGGACCAGAGAATTCGAATA CATCTGCCTANNNGATCGACATG	428	TGCAGGACCAGAGAATTCGAATA CATTAATGCANNNGATCGACATG	668
TGCAGGACCAGAGAATTCGAATA CATGGAAGTGNNNTGCATCAGGT	189	TGCAGGACCAGAGAATTCGAATA CACACACCGGNNNTGCATCAGGT	429	TGCAGGACCAGAGAATTCGAATA CACTTTGGTCNNNTGCATCAGGT	669
TGCAGGACCAGAGAATTCGAATA CAAAGTCTATNNNTGCATCAGGT	190	TGCAGGACCAGAGAATTCGAATA CAGACCTCCCNNNTGCATCAGGT	430	TGCAGGACCAGAGAATTCGAATA CATACGAAGGNNNTGCATCAGGT	670
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TGCAGGACCAGAGAATTCGAATA CATTCTCCTCNNNTGCATCAGGT	192	TGCAGGACCAGAGAATTCGAATA CATCTCCGGCNNNTGCATCAGGT	432	TGCAGGACCAGAGAATTCGAATA CAGTTTATCTNNNTGCATCAGGT	672
TGCAGGACCAGAGAATTCGAATA CACCAGCCCTNNNTGCATCAGGT	193	TGCAGGACCAGAGAATTCGAATA CACCAGCGTGNNNTGCATCAGGT	433	TGCAGGACCAGAGAATTCGAATA CATTTCGAAANNNTGCATCAGGT	673
TGCAGGACCAGAGAATTCGAATA CAAACAAAACNNNTGCATCAGGT	194	TGCAGGACCAGAGAATTCGAATA CAAAATATAANNNTGCATCAGGT	434	TGCAGGACCAGAGAATTCGAATA CACAGATCACNNNTGCATCAGGT	674
TGCAGGACCAGAGAATTCGAATA CACGCTCACCNNNTGCATCAGGT	195	TGCAGGACCAGAGAATTCGAATA CAGCAATTTANNNTGCATCAGGT	435	TGCAGGACCAGAGAATTCGAATA CATTGGAAGGNNNTGCATCAGGT	675
TGCAGGACCAGAGAATTCGAATA CATGGTGATCNNNTGCATCAGGT	196	TGCAGGACCAGAGAATTCGAATA CAACTCAGTGNNNTGCATCAGGT	436	TGCAGGACCAGAGAATTCGAATA CAGTGCGGCTNNNTGCATCAGGT	676
TGCAGGACCAGAGAATTCGAATA CAGTTGCTAGNNNTGCATCAGGT	197	TGCAGGACCAGAGAATTCGAATA CAAGAGGCATNNNTGCATCAGGT	437	TGCAGGACCAGAGAATTCGAATA CATGAAGGCANNNTGCATCAGGT	677
TGCAGGACCAGAGAATTCGAATA CATCACCCTANNNTGCATCAGGT	198	TGCAGGACCAGAGAATTCGAATA CATAGGCTTGNNNTGCATCAGGT	438	TGCAGGACCAGAGAATTCGAATA CAAAAAGTACNNNTGCATCAGGT	678
TGCAGGACCAGAGAATTCGAATA CAGACTCTGANNNTGCATCAGGT	199	TGCAGGACCAGAGAATTCGAATA CACACACAGTNNNTGCATCAGGT	439	TGCAGGACCAGAGAATTCGAATA CAGATGGAACNNNTGCATCAGGT	679
TGCAGGACCAGAGAATTCGAATA CACGTATGACNNNTGCATCAGGT	200	TGCAGGACCAGAGAATTCGAATA CATGATAGAANNNTGCATCAGGT	440	TGCAGGACCAGAGAATTCGAATA CAGCCTCGAGNNNTGCATCAGGT	680
TGCAGGACCAGAGAATTCGAATA CATGCACCGGNNNTGCATCAGGT	201	TGCAGGACCAGAGAATTCGAATA CAGACAACGANNNTGCATCAGGT	441	TGCAGGACCAGAGAATTCGAATA CAAAATAAATNNNTGCATCAGGT	681
TGCAGGACCAGAGAATTCGAATA CAACTGATGCNNNTGCATCAGGT	202	TGCAGGACCAGAGAATTCGAATA CACTGCCTCGNNNTGCATCAGGT	442	TGCAGGACCAGAGAATTCGAATA CATTCCCCCCNNNTGCATCAGGT	682
TGCAGGACCAGAGAATTCGAATA CATACGTTCCNNNTGCATCAGGT	203	TGCAGGACCAGAGAATTCGAATA CAGTTTCCCANNNTGCATCAGGT	443	TGCAGGACCAGAGAATTCGAATA CATTCTTCTTNNNTGCATCAGGT	683
TGCAGGACCAGAGAATTCGAATA CAGGGCCGCGNNNTGCATCAGGT	204	TGCAGGACCAGAGAATTCGAATA CATTCAATAGNNNTGCATCAGGT	444	TGCAGGACCAGAGAATTCGAATA CATTGTGGCANNNTGCATCAGGT	684
TGCAGGACCAGAGAATTCGAATA CAATCTTTGTNNNTGCATCAGGT	205	TGCAGGACCAGAGAATTCGAATA CATAGCCATGNNNTGCATCAGGT	445	TGCAGGACCAGAGAATTCGAATA CATCCCATGTNNNTGCATCAGGT	685
TGCAGGACCAGAGAATTCGAATA CATTGTACTTNNNTGCATCAGGT	206	TGCAGGACCAGAGAATTCGAATA CAGTTGTTAANNNTGCATCAGGT	446	TGCAGGACCAGAGAATTCGAATA CAGTGTTGACNNNTGCATCAGGT	686

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATGTTAATGNNNTGCATCAGGT	207	TGCAGGACCAGAGAATTCGAATA CACTTGCACTNNNTGCATCAGGT	447	TGCAGGACCAGAGAATTCGAATA CATCGCCTATNNNTGCATCAGGT	687
TGCAGGACCAGAGAATTCGAATA CAAACATTGTNNNTGCATCAGGT	208	TGCAGGACCAGAGAATTCGAATA CATTAGAGCCNNNTGCATCAGGT	448	TGCAGGACCAGAGAATTCGAATA CACGCTGACGNNNTGCATCAGGT	688
TGCAGGACCAGAGAATTCGAATA CACGCCCGAANNNTGCATCAGGT	209	TGCAGGACCAGAGAATTCGAATA CAGCCCCTACNNNTGCATCAGGT	449	TGCAGGACCAGAGAATTCGAATA CATGGTGGTTNNNTGCATCAGGT	689
TGCAGGACCAGAGAATTCGAATA CACAGCGCACNNNTGCATCAGGT	210	TGCAGGACCAGAGAATTCGAATA CAAATGGACGNNNTGCATCAGGT	450	TGCAGGACCAGAGAATTCGAATA CACTATCTTANNNTGCATCAGGT	690
TGCAGGACCAGAGAATTCGAATA CACGAGTATCNNNTGCATCAGGT	211	TGCAGGACCAGAGAATTCGAATA CAAGACCTGTNNNTGCATCAGGT	451	TGCAGGACCAGAGAATTCGAATA CAATAACCTANNNTGCATCAGGT	691
TGCAGGACCAGAGAATTCGAATA CAATGGTGGANNNTGCATCAGGT	212	TGCAGGACCAGAGAATTCGAATA CACTTACATTNNNTGCATCAGGT	452	TGCAGGACCAGAGAATTCGAATA CAAGAGTGTGNNNTGCATCAGGT	692
TGCAGGACCAGAGAATTCGAATA CATCACACTCNNNTGCATCAGGT	213	TGCAGGACCAGAGAATTCGAATA CATAAGAAACNNNTGCATCAGGT	453	TGCAGGACCAGAGAATTCGAATA CAAATGGCGANNNTGCATCAGGT	693
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TGCAGGACCAGAGAATTCGAATA CAGAGTTTTANNNTGCATCAGGT	215	TGCAGGACCAGAGAATTCGAATA CATCTAGGTGNNNTGCATCAGGT	455	TGCAGGACCAGAGAATTCGAATA CATGCCCCCANNNTGCATCAGGT	695
TGCAGGACCAGAGAATTCGAATA CAGGCCTTTTNNNTGCATCAGGT	216	TGCAGGACCAGAGAATTCGAATA CAGTGTGTTCNNNTGCATCAGGT	456	TGCAGGACCAGAGAATTCGAATA CACGAGCTCGNNNTGCATCAGGT	696
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TGCAGGACCAGAGAATTCGAATA CAGAAGTATANNNTGCATCAGGT	220	TGCAGGACCAGAGAATTCGAATA CAAGGCGCGANNNTGCATCAGGT	460	TGCAGGACCAGAGAATTCGAATA CAGATCCTGANNNTGCATCAGGT	700
TGCAGGACCAGAGAATTCGAATA CAGAATCACCNNNTGCATCAGGT	221	TGCAGGACCAGAGAATTCGAATA CAGAGCTCTANNNTGCATCAGGT	461	TGCAGGACCAGAGAATTCGAATA CAAGAAGTATNNNTGCATCAGGT	701
TGCAGGACCAGAGAATTCGAATA CACTTACCGTNNNTGCATCAGGT	222	TGCAGGACCAGAGAATTCGAATA CATCATAATGNNNTGCATCAGGT	462	TGCAGGACCAGAGAATTCGAATA CAAACCCACANNNTGCATCAGGT	702
TGCAGGACCAGAGAATTCGAATA CATCTTTACANNNTGCATCAGGT	223	TGCAGGACCAGAGAATTCGAATA CAGGATGGTANNNTGCATCAGGT	463	TGCAGCACCAGAGAATTCGAATA CATGCCGAATNNNTGCATCAGGT	703
TGCAGGACCAGAGAATTCGAATA CACGAAGTGANNNTGCATCAGGT	224	TGCAGGACCAGAGAATTCGAATA CATAGCCTTCNNNTGCATCAGGT	464	TGCAGGACCAGAGAATTCGAATA CAATCAGAGGNNNTGCATCAGGT	704
TGCAGGACCAGAGAATTCGAATA CACTTGTGGANNNTGCATCAGGT	225	TGCAGGACCAGAGAATTCGAATA CAATCCCCGCNNNTGCATCAGGT	465	TGCAGGACCAGAGAATTCGAATA CAGTCATATANNNTGCATCAGGT	705
TGCAGGACCAGAGAATTCGAATA CAGTTCTCTGNNNTGCATCAGGT	226	TGCAGGACCAGAGAATTCGAATA CAGATTGCTGNNNTGCATCAGGT	466	TGCAGGACCAGAGAATTCGAATA CAACCCACCCNNNTGCATCAGGT	706
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TGCAGGACCAGAGAATTCGAATA CAAAATGCTTNNNTGCATCAGGT	228	TGCAGGACCAGAGAATTCGAATA CACGGAACGGNNNTGCATCAGGT	468	TGCAGGACCAGAGAATTCGAATA CATGCTGAACNNNTGCATCAGGT	708
TGCAGGACCAGAGAATTCGAATA CAATCGCGATNNNTGCATCAGGT	229	TGCAGGACCAGAGAATTCGAATA CAGCTCTTTGNNNTGCATCAGGT	469	TGCAGGACCAGAGAATTCGAATA CAGCAGCATTNNNTGCATCAGGT	709
TGCAGGACCAGAGAATTCGAATA CAGGCTCGTGNNNTGCATCAGGT	230	TGCAGGACCAGAGAATTCGAATA CAGTAATCGCNNNTGCATCAGGT	470	TGCAGGACCAGAGAATTCGAATA CAGGCGATGGNNNTGCATCAGGT	710
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TGCAGGACCAGAGAATTCGAATA CACAAATTTGNNNTGCATCAGGT	232	TGCAGGACCAGAGAATTCGAATA CACACACACANNNTGCATCAGGT	472	TGCAGGACCAGAGAATTCGAATA CATGGAGGCGNNNTGCATCAGGT	712
TGCAGGACCAGAGAATTCGAATA CATTTTTTCCNNNTGCATCAGGT	233	TGCAGGACCAGAGAATTCGAATA CATAAATAAANNNTGCATCAGGT	473	TGCAGGACCAGAGAATTCGAATA CAGTATTACANNNTGCATCAGGT	713
TGCAGGACCAGAGAATTCGAATA CATTTAACGANNNTGCATCAGGT	234	TGCAGGACCAGAGAATTCGAATA CAAACGCATCNNNTGCATCAGGT	474	TGCAGGACCAGAGAATTCGAATA CACGACAATCNNNTGCATCAGGT	714
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TGCAGGACCAGAGAATTCGAATA CAATTGATTGNNNTGCATCAGGT	237	TGCAGGACCAGAGAATTCGAATA CATAAGCCTGNNNTGCATCAGGT	477	TGCAGGACCAGAGAATTCGAATA CACGAAGACANNNTGCATCAGGT	717
TGCAGGACCAGAGAATTCGAATA CATGCATAGCNNNTGCATCAGGT	238	TGCAGGACCAGAGAATTCGAATA CATAGCAGAGNNNTGCATCAGGT	478	TGCAGGACCAGAGAATTCGAATA CACCAATGACNNNTGCATCAGGT	718
TGCAGGACCAGAGAATTCGAATA CAGACAGATGNNNTGCATCAGGT	239	TGCAGGACCAGAGAATTCGAATA CACTTGGAACNNNTGCATCAGGT	479	TGCAGGACCAGAGAATTCGAATA CAAGCCTTCTNNNTGCATCAGGT	719

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
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TGCAGGACCAGAGAATTCGAATA CATGCGATACNNNTGCATCAGGT	241	TGCAGGACCAGAGAATTCGAATA CACTATCTATNNNTGCATCAGGT	481	TGCAGGACCAGAGAATTCGAATA CACCTTATGCNNNTGCATCAGGT	721
TGCAGGACCAGAGAATTCGAATA CAACACTGCANNNTGCATCAGGT	242	TGCAGGACCAGAGAATTCGAATA CACAATTTAGNNNTGCATCAGGT	482	TGCAGGACCAGAGAATTCGAATA CATTAATGACNNNTGCATCAGGT	722
TGCAGGACCAGAGAATTCGAATA CAGTCACTCTNNNTGCATCAGGT	243	TGCAGGACCAGAGAATTCGAATA CACTAAACGCNNNTGCATCAGGT	483	TGCAGGACCAGAGAATTCGAATA CACTACCTTGNNNTGCATCAGGT	723
TGCAGGACCAGAGAATTCGAATA CATTGTATTCNNNTGCATCAGGT	244	TGCAGGACCAGAGAATTCGAATA CATAGTAGAANNNTGCATCAGGT	484	TGCAGGACCAGAGAATTCGAATA CAAGGATCTCNNNTGCATCAGGT	724
TGCAGGACCAGAGAATTCGAATA CAAACCTAGCNNNTGCATCAGGT	245	TGCAGGACCAGAGAATTCGAATA CAGCAAAGTGNNNTGCATCAGGT	485	TGCAGGACCAGAGAATTCGAATA CAAAGATCAANNNTGCATCAGGT	725
TGCAGGACCAGAGAATTCGAATA CAGCCGGATCNNNTGCATCAGGT	246	TGCAGGACCAGAGAATTCGAATA CACAAGTTATNNNTGCATCAGGT	486	TGCAGGACCAGAGAATTCGAATA CAGAATGAGCNNNTGCATCAGGT	726
TGCAGGACCAGAGAATTCGAATA CAAGGATCCTNNNTGCATCAGGT	247	TGCAGGACCAGAGAATTCGAATA CACAACTGACNNNTGCATCAGGT	487	TGCAGGACCAGAGAATTCGAATA CAACTAGATTNNNTGCATCAGGT	727
TGCAGGACCAGAGAATTCGAATA CATACTGGACNNNTGCATCAGGT	248	TGCAGGACCAGAGAATTCGAATA CATTCGTCGTNNNTGCATCAGGT	488	TGCAGGACCAGAGAATTCGAATA CATTTTCCGGNNNTGCATCAGGT	728

图12H

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATATGCGCANNNACGTATGCCA	729	TGCAGGACCAGAGAATTCGAATA CAGCGATTACNNNACGTATGCCA	969	TGCAGGACCAGAGAATTCGAATA CACAATGACCNNNACGTATGCCA	1209
TGCAGGACCAGAGAATTCGAATA CAGTTCACCTNNNACGTATGCCA	730	TGCAGGACCAGAGAATTCGAATA CATAGTCCTCNNNACGTATGCCA	970	TGCAGGACCAGAGAATTCGAATA CAGCTACGTANNNACGTATGCCA	1210
TGCAGGACCAGAGAATTCGAATA CATCCTACACNNNACGTATGCCA	731	TGCAGGACCAGAGAATTCGAATA CAGTTATAACNNNACGTATGCCA	971	TGCAGGACCAGAGAATTCGAATA CAGCCAGCACNNNACGTATGCCA	1211
TGCAGGACCAGAGAATTCGAATA CACTACTCTGNNNACGTATGCCA	732	TGCAGGACCAGAGAATTCGAATA CATATCTTCANNNACGTATGCCA	972	TGCAGGACCAGAGAATTCGAATA CACGATCCGGNNNACGTATGCCA	1212
TGCAGGACCAGAGAATTCGAATA CACCTTCCCCNNNACGTATGCCA	733	TGCAGGACCAGAGAATTCGAATA CAACGTTCGANNNACGTATGCCA	973	TGCAGGACCAGAGAATTCGAATA CATTGGACACNNNACGTATGCCA	1213
TGCAGGACCAGAGAATTCGAATA CAGAAGATCGNNNACGTATGCCA	734	TGCAGGACCAGAGAATTCGAATA CAACTCGTGANNNACGTATGCCA	974	TGCAGGACCAGAGAATTCGAATA CAACAATGCCNNNACGTATGCCA	1214
TGCAGGACCAGAGAATTCGAATA CACTCCGCTGNNNACGTATGCCA	735	TGCAGGACCAGAGAATTCGAATA CAGGACTACTNNNACGTATGCCA	975	TGCAGGACCAGAGAATTCGAATA CACCTTTATANNNACGTATGCCA	1215
TGCAGGACCAGAGAATTCGAATA CATATGTCCCNNNACGTATGCCA	736	TGCAGGACCAGAGAATTCGAATA CATCTGTACCNNNACGTATGCCA	976	TGCAGGACCAGAGAATTCGAATA CAGTGGCTGCNNNACGTATGCCA	1216
TGCAGGACCAGAGAATTCGAATA CATATTTGCTNNNACGTATGCCA	737	TGCAGGACCAGAGAATTCGAATA CACCCTAACTNNNACGTATGCCA	977	TGCAGGACCAGAGAATTCGAATA CAATCTCCGTNNNACGTATGCCA	1217
TGCAGGACCAGAGAATTCGAATA CAGTCCAGGCNNNACGTATGCCA	738	TGCAGGACCAGAGAATTCGAATA CATTGGAGAGNNNACGTATGCCA	978	TGCAGGACCAGAGAATTCGAATA CAATGGCCATNNNACGTATGCCA	1218
TGCAGGACCAGAGAATTCGAATA CAAAGATGGCNNNACGTATGCCA	739	TGCAGGACCAGAGAATTCGAATA CAGAATCAAANNNACGTATGCCA	979	TGCAGGACCAGAGAATTCGAATA CATTTGATAGNNNACGTATGCCA	1219
TGCAGGACCAGAGAATTCGAATA CAGTCCCGAGNNNACGTATGCCA	740	TGCAGGACCAGAGAATTCGAATA CAGTTTCGTCNNNACGTATGCCA	980	TGCAGGACCAGAGAATTCGAATA CAGTCCCGGANNNACGTATGCCA	1220
TGCAGGACCAGAGAATTCGAATA CAAGGTTTCGNNNACGTATGCCA	741	TGCAGGACCAGAGAATTCGAATA CACTACACAGNNNACGTATGCCA	981	TGCAGGACCAGAGAATTCGAATA CAGGCTTCAANNNACGTATGCCA	1221
TGCAGGACCAGAGAATTCGAATA CATGCAAAGGNNNACGTATGCCA	742	TGCAGGACCAGAGAATTCGAATA CAAGTCAGTCNNNACGTATGCCA	982	TGCAGGACCAGAGAATTCGAATA CACCTTTTTTNNNACGTATGCCA	1222
TGCAGGACCAGAGAATTCGAATA CAAGGTGTAGNNNACGTATGCCA	743	TGCAGGACCAGAGAATTCGAATA CACAACGAGANNNACGTATGCCA	983	TGCAGGACCAGAGAATTCGAATA CAACGCCCGANNNACGTATGCCA	1223
TGCAGGACCAGAGAATTCGAATA CACACGAGTTNNNACGTATGCCA	744	TGCAGGACCAGAGAATTCGAATA CATAGGCTCANNNACGTATGCCA	984	TGCAGGACCAGAGAATTCGAATA CACCCCTAGCNNNACGTATGCCA	1224
TGCAGGACCAGAGAATTCGAATA CACACCGCCTNNNACGTATGCCA	745	TGCAGGACCAGAGAATTCGAATA CAGGCCCATGNNNACGTATGCCA	985	TGCAGGACCAGAGAATTCGAATA CACGGAGGCANNNACGTATGCCA	1225
TGCAGGACCAGAGAATTCGAATA CAAAGCTACCNNNACGTATGCCA	746	TGCAGGACCAGAGAATTCGAATA CAGGCAGTCCNNNACGTATGCCA	986	TGCAGGACCAGAGAATTCGAATA CACTATGAATNNNACGTATGCCA	1226
TGCAGGACCAGAGAATTCGAATA CAGAACCGAANNNACGTATGCCA	747	TGCAGGACCAGAGAATTCGAATA CATCGATTGGNNNACGTATGCCA	987	TGCAGGACCAGAGAATTCGAATA CAGACCGCGTNNNACGTATGCCA	1227
TGCAGGACCAGAGAATTCGAATA CAAGTACTGCNNNACGTATGCCA	748	TGCAGGACCAGAGAATTCGAATA CATAGACAGCNNNACGTATGCCA	988	TGCAGGACCAGAGAATTCGAATA CATACTAGTANNNACGTATGCCA	1228
TGCAGGACCAGAGAATTCGAATA CAAACAATTCNNNACGTATGCCA	749	TGCAGGACCAGAGAATTCGAATA CAACTAAGTTNNNACGTATGCCA	989	TGCAGGACCAGAGAATTCGAATA CAACCAGTGTNNNACGTATGCCA	1229
TGCAGGACCAGAGAATTCGAATA CAGTATTAACNNNACGTATGCCA	750	TGCAGGACCAGAGAATTCGAATA CAATGTTCGGNNNACGTATGCCA	990	TGCAGGACCAGAGAATTCGAATA CAGATGCCTANNNACGTATGCCA	1230
TGCAGGACCAGAGAATTCGAATA CATGATTATGNNNACGTATGCCA	751	TGCAGGACCAGAGAATTCGAATA CAAGCCCAATNNNACGTATGCCA	991	TGCAGGACCAGAGAATTCGAATA CACCATATTTNNNACGTATGCCA	1231
TGCAGGACCAGAGAATTCGAATA CAGCAAACCTNNNACGTATGCCA	752	TGCAGGACCAGAGAATTCGAATA CAGTGAGTTCNNNACGTATGCCA	992	TGCAGGACCAGAGAATTCGAATA CAAAACCACCNNNACGTATGCCA	1232
TGCAGGACCAGAGAATTCGAATA CAGAATCTTANNNACGTATGCCA	753	TGCAGGACCAGAGAATTCGAATA CAGTGCTAACNNNACGTATGCCA	993	TGCAGGACCAGAGAATTCGAATA CAGCACGAAANNNACGTATGCCA	1233
TGCAGGACCAGAGAATTCGAATA CAGAGGACGCNNNACGTATGCCA	754	TGCAGGACCAGAGAATTCGAATA CAGCCACCGANNNACGTATGCCA	994	TGCAGGACCAGAGAATTCGAATA CAACGACAGANNNACGTATGCCA	1234
TGCAGGACCAGAGAATTCGAATA CAAGCCAAAGNNNACGTATGCCA	755	TGCAGGACCAGAGAATTCGAATA CAAGTCCGATNNNACGTATGCCA	995	TGCAGGACCAGAGAATTCGAATA CAATACCATANNNACGTATGCCA	1235
TGCAGGACCAGAGAATTCGAATA CAGGACGCTCNNNACGTATGCCA	756	TGCAGGACCAGAGAATTCGAATA CAGTTAAATCNNNACGTATGCCA	996	TGCAGGACCAGAGAATTCGAATA CACCAGTTCTNNNACGTATGCCA	1236
TGCAGGACCAGAGAATTCGAATA CAGCTGCCCTNNNACGTATGCCA	757	TGCAGGACCAGAGAATTCGAATA CAACTGACTGNNNACGTATGCCA	997	TGCAGGACCAGAGAATTCGAATA CATTGCTGGANNNACGTATGCCA	1237
TGCAGGACCAGAGAATTCGAATA CACCCTTTTCNNNACGTATGCCA	758	TGCAGGACCAGAGAATTCGAATA CACTTCATGCNNNACGTATGCCA	998	TGCAGGACCAGAGAATTCGAATA CAGCCCATTTNNNACGTATGCCA	1238
TGCAGGACCAGAGAATTCGAATA CATCGCAGATNNNACGTATGCCA	759	TGCAGGACCAGAGAATTCGAATA CAACCAGCATNNNACGTATGCCA	999	TGCAGGACCAGAGAATTCGAATA CAAACAGCTCNNNACGTATGCCA	1239
TGCAGGACCAGAGAATTCGAATA CAATCGCATGNNNACGTATGCCA	760	TGCAGGACCAGAGAATTCGAATA CAGGCGTCCANNNACGTATGCCA	1000	TGCAGGACCAGAGAATTCGAATA CACTGTTCTGNNNACGTATGCCA	1240

图13A

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAGATGGCANNNACGTATGCCA	761	TGCAGGACCAGAGAATTCGAATA CAAACAACCCNNNACGTATGCCA	1001	TGCAGGACCAGAGAATTCGAATA CATGGAATAANNNACGTATGCCA	1241
TGCAGGACCAGAGAATTCGAATA CATCATCGCTNNNACGTATGCCA	762	TGCAGGACCAGAGAATTCGAATA CAGGTCTTAGNNNACGTATGCCA	1002	TGCAGGACCAGAGAATTCGAATA CATTCCGTTCNNNACGTATGCCA	1242
TGCAGGACCAGAGAATTCGAATA CACGTGTTCTNNNACGTATGCCA	763	TGCAGGACCAGAGAATTCGAATA CAGCCCGGATNNNACGTATGCCA	1003	TGCAGGACCAGAGAATTCGAATA CACACGCAATNNNACGTATGCCA	1243
TGCAGGACCAGAGAATTCGAATA CAGGTTATTANNNACGTATGCCA	764	TGCAGGACCAGAGAATTCGAATA CAATCCCGAANNNACGTATGCCA	1004	TGCAGGACCAGAGAATTCGAATA CAGCTTATCCNNNACGTATGCCA	1244
TGCAGGACCAGAGAATTCGAATA CAAGAGTTAANNNACGTATGCCA	765	TGCAGGACCAGAGAATTCGAATA CATTTACTCANNNACGTATGCCA	1005	TGCAGGACCAGAGAATTCGAATA CAGGCATAGANNNACGTATGCCA	1245
TGCAGGACCAGAGAATTCGAATA CATGAAATTCNNNACGTATGCCA	766	TGCAGGACCAGAGAATTCGAATA CATCCACCGCNNNACGTATGCCA	1006	TGCAGGACCAGAGAATTCGAATA CAAGCGCCGTNNNACGTATGCCA	1246
TGCAGGACCAGAGAATTCGAATA CACTTACCTGNNNACGTATGCCA	767	TGCAGGACCAGAGAATTCGAATA CACCAGATTGNNNACGTATGCCA	1007	TGCAGGACCAGAGAATTCGAATA CACAAATTCANNNACGTATGCCA	1247
TGCAGGACCAGAGAATTCGAATA CAAACTCGTGNNNACGTATGCCA	768	TGCAGGACCAGAGAATTCGAATA CACATGGTCANNNACGTATGCCA	1008	TGCAGGACCAGAGAATTCGAATA CATAATGCATNNNACGTATGCCA	1248
TGCAGGACCAGAGAATTCGAATA CAGGACACGGNNNACGTATGCCA	769	TGCAGGACCAGAGAATTCGAATA CACCATTTCGNNNACGTATGCCA	1009	TGCAGGACCAGAGAATTCGAATA CAACTCGTCTNNNACGTATGCCA	1249
TGCAGGACCAGAGAATTCGAATA CATCTCGCGCNNNACGTATGCCA	770	TGCAGGACCAGAGAATTCGAATA CATGTCGCGGNNNACGTATGCCA	1010	TGCAGGACCAGAGAATTCGAATA CAAAATTGTGNNNACGTATGCCA	1250
TGCAGGACCAGAGAATTCGAATA CACTTCCAGTNNNACGTATGCCA	771	TGCAGGACCAGAGAATTCGAATA CAAACAATAGNNNACGTATGCCA	1011	TGCAGGACCAGAGAATTCGAATA CATGAGAGGTNNNACGTATGCCA	1251
TGCAGGACCAGAGAATTCGAATA CAATAGTTACNNNACGTATGCCA	772	TGCAGGACCAGAGAATTCGAATA CATTCGACGANNNACGTATGCCA	1012	TGCAGGACCAGAGAATTCGAATA CAGCCATACANNNACGTATGCCA	1252
TGCAGGACCAGAGAATTCGAATA CACGACTTGANNNACGTATGCCA	773	TGCAGGACCAGAGAATTCGAATA CACCTTGAGANNNACGTATGCCA	1013	TGCAGGACCAGAGAATTCGAATA CAGTCCTTCANNNACGTATGCCA	1253
TGCAGGACCAGAGAATTCGAATA CATGCTTTATNNNACGTATGCCA	774	TGCAGGACCAGAGAATTCGAATA CAACGCTCTTNNNACGTATGCCA	1014	TGCAGGACCAGAGAATTCGAATA CAGTGCGGAGNNNACGTATGCCA	1254
TGCAGGACCAGAGAATTCGAATA CAGCCACTTTNNNACGTATGCCA	775	TGCAGGACCAGAGAATTCGAATA CACACGAAGANNNACGTATGCCA	1015	TGCAGGACCAGAGAATTCGAATA CATTTAGACANNNACGTATGCCA	1255
TGCAGGACCAGAGAATTCGAATA CATATCGGACNNNACGTATGCCA	776	TGCAGGACCAGAGAATTCGAATA CAGGCCACACNNNACGTATGCCA	1016	TGCAGGACCAGAGAATTCGAATA CACACCCGCTNNNACGTATGCCA	1256
TGCAGGACCAGAGAATTCGAATA CAATTCCATTNNNACGTATGCCA	777	TGCAGGACCAGAGAATTCGAATA CATCTGTGAGNNNACGTATGCCA	1017	TGCAGGACCAGAGAATTCGAATA CAATTCTAGANNNACGTATGCCA	1257
TGCAGGACCAGAGAATTCGAATA CAAATGCTGCNNNACGTATGCCA	778	TGCAGGACCAGAGAATTCGAATA CAAAAGCCAGNNNACGTATGCCA	1018	TGCAGGACCAGAGAATTCGAATA CACGGACCAGNNNACGTATGCCA	1258
TGCAGGACCAGAGAATTCGAATA CAACGCGATTNNNACGTATGCCA	779	TGCAGGACCAGAGAATTCGAATA CACCAGTTGANNNACGTATGCCA	1019	TGCAGGACCAGAGAATTCGAATA CACGACCGCANNNACGTATGCCA	1259
TGCAGGACCAGAGAATTCGAATA CATAGCTAGCNNNACGTATGCCA	780	TGCAGGACCAGAGAATTCGAATA CACTTGTAGGNNNACGTATGCCA	1020	TGCAGGACCAGAGAATTCGAATA CACATATAGTNNNACGTATGCCA	1260
TGCAGGACCAGAGAATTCGAATA CAGCAACGTTNNNACGTATGCCA	781	TGCAGGACCAGAGAATTCGAATA CAATATGCATNNNACGTATGCCA	1021	TGCAGGACCAGAGAATTCGAATA CATGTGATATNNNACGTATGCCA	1261
TGCAGGACCAGAGAATTCGAATA CACGTCCTATNNNACGTATGCCA	782	TGCAGGACCAGAGAATTCGAATA CACCAGGCGTNNNACGTATGCCA	1022	TGCAGGACCAGAGAATTCGAATA CAATCCTAAANNNACGTATGCCA	1262
TGCAGGACCAGAGAATTCGAATA CAGCCACACGNNNACGTATGCCA	783	TGCAGGACCAGAGAATTCGAATA CAATGTTTAGNNNACGTATGCCA	1023	TGCAGGACCAGAGAATTCGAATA CATGATGAGGNNNACGTATGCCA	1263
TGCAGGACCAGAGAATTCGAATA CAGGCTTCCCNNNACGTATGCCA	784	TGCAGGACCAGAGAATTCGAATA CACTGTCCGCNNNACGTATGCCA	1024	TGCAGGACCAGAGAATTCGAATA CAGCTCGACGNNNACGTATGCCA	1264
TGCAGGACCAGAGAATTCGAATA CAGTTGACACNNNACGTATGCCA	785	TGCAGGACCAGAGAATTCGAATA CATTTTACCANNNACGTATGCCA	1025	TGCAGGACCAGAGAATTCGAATA CATTAGCTAANNNACGTATGCCA	1265
TGCAGGACCAGAGAATTCGAATA CAGCATCTTCNNNACGTATGCCA	786	TGCAGGACCAGAGAATTCGAATA CATGCCCTGCNNNACGTATGCCA	1026	TGCAGGACCAGAGAATTCGAATA CATGCTTTTANNNACGTATGCCA	1266
TGCAGGACCAGAGAATTCGAATA CAACAATTGTNNNACGTATGCCA	787	TGCAGGACCAGAGAATTCGAATA CACCTTTGACNNNACGTATGCCA	1027	TGCAGGACCAGAGAATTCGAATA CAATCACAGCNNNACGTATGCCA	1267
TGCAGGACCAGAGAATTCGAATA CAGATCCCCCNNNACGTATGCCA	788	TGCAGGACCAGAGAATTCGAATA CAATTATTTTNNNACGTATGCCA	1028	TGCAGGACCAGAGAATTCGAATA CAAATCTCGGNNNACGTATGCCA	1268
TGCAGGACCAGAGAATTCGAATA CAGCCCAGTGNNNCTAGCGTTAC	789	TGCAGGACCAGAGAATTCGAATA CAGTGTGGAANNNCTAGCGTTAC	1029	TGCAGGACCAGAGAATTCGAATA CAACACTGGTNNNCTAGCGTTAC	1269
TGCAGGACCAGAGAATTCGAATA CAGCGGTGCTNNNCTAGCGTTAC	790	TGCAGGACCAGAGAATTCGAATA CAACTCGTAGNNNCTAGCGTTAC	1030	TGCAGGACCAGAGAATTCGAATA CATTTGTTTGNNNCTAGCGTTAC	1270
TGCAGGACCAGAGAATTCGAATA CATACGTGCANNNCTAGCGTTAC	791	TGCAGGACCAGAGAATTCGAATA CATCGCGTCCNNNCTAGCGTTAC	1031	TGCAGGACCAGAGAATTCGAATA CACGACACGCNNNCTAGCGTTAC	1271
TGCAGGACCAGAGAATTCGAATA CACACCCACCNNNCTAGCGTTAC	792	TGCAGGACCAGAGAATTCGAATA CAGCCTAATGNNNCTAGCGTTAC	1032	TGCAGGACCAGAGAATTCGAATA CACGCGAGAGNNNCTAGCGTTAC	1272

图13B

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACACAGAAGNNNCTAGCGTTAC	793	TGCAGGACCAGAGAATTCGAATA CAGCGTGTTANNNCTAGCGTTAC	1033	TGCAGGACCAGAGAATTCGAATA CATAAGTAGANNNCTAGCGTTAC	1273
TGCAGGACCAGAGAATTCGAATA CACGCTAACANNNCTAGCGTTAC	794	TGCAGGACCAGAGAATTCGAATA CACGAGAAACNNNCTAGCGTTAC	1034	TGCAGGACCAGAGAATTCGAATA CAAAGACGTGNNNCTAGCGTTAC	1274
TGCAGGACCAGAGAATTCGAATA CAGACCTATGNNNCTAGCGTTAC	795	TGCAGGACCAGAGAATTCGAATA CAATGCTCAGNNNCTAGCGTTAC	1035	TGCAGGACCAGAGAATTCGAATA CACGGAACAANNNCTAGCGTTAC	1275
TGCAGGACCAGAGAATTCGAATA CAAAAAGGAANNNCTAGCGTTAC	796	TGCAGGACCAGAGAATTCGAATA CAGTCAGCTANNNCTAGCGTTAC	1036	TGCAGGACCAGAGAATTCGAATA CACTGTCGAANNNCTAGCGTTAC	1276
TGCAGGACCAGAGAATTCGAATA CAACAGAGGTNNNCTAGCGTTAC	797	TGCAGGACCAGAGAATTCGAATA CAGGTAGCGGNNNCTAGCGTTAC	1037	TGCAGGACCAGAGAATTCGAATA CAAGCCTACANNNCTAGCGTTAC	1277
TGCAGGACCAGAGAATTCGAATA CACGTAGCATNNNCTAGCGTTAC	798	TGCAGGACCAGAGAATTCGAATA CACCTGGTCCNNNCTAGCGTTAC	1038	TGCAGGACCAGAGAATTCGAATA CACCAATTGGNNNCTAGCGTTAC	1278
TGCAGGACCAGAGAATTCGAATA CATCCCCAGCNNNCTAGCGTTAC	799	TGCAGGACCAGAGAATTCGAATA CACAGCACCGNNNCTAGCGTTAC	1039	TGCAGGACCAGAGAATTCGAATA CAGAGTCTACNNNCTAGCGTTAC	1279
TGCAGGACCAGAGAATTCGAATA CAGTACCTGANNNCTAGCGTTAC	800	TGCAGGACCAGAGAATTCGAATA CACATTGTGGNNNCTAGCGTTAC	1040	TGCAGGACCAGAGAATTCGAATA CAAATGTTACNNNCTAGCGTTAC	1280
TGCAGGACCAGAGAATTCGAATA CAAGAGAGGAANNNCTAGCGTTAC	801	TGCAGGACCAGAGAATTCGAATA CAAGGAACTGNNNCTAGCGTTAC	1041	TGCAGGACCAGAGAATTCGAATA CAAGTGGCAANNNCTAGCGTTAC	1281
TGCAGGACCAGAGAATTCGAATA CAGTAACTCGNNNCTAGCGTTAC	802	TGCAGGACCAGAGAATTCGAATA CAGTTATTAGNNNCTAGCGTTAC	1042	TGCAGGACCAGAGAATTCGAATA CAGGTTAACCNNNCTAGCGTTAC	1282
TGCAGGACCAGAGAATTCGAATA CAGGTACATCNNNCTAGCGTTAC	803	TGCAGGACCAGAGAATTCGAATA CAAATGTTCTNNNCTAGCGTTAC	1043	TGCAGGACCAGAGAATTCGAATA CATTGTGGTGNNNCTAGCGTTAC	1283
TGCAGGACCAGAGAATTCGAATA CAGTTAACCGNNNCTAGCGTTAC	804	TGCAGGACCAGAGAATTCGAATA CAGACAATCCNNNCTAGCGTTAC	1044	TGCAGGACCAGAGAATTCGAATA CAAAATGGCGNNNCTAGCGTTAC	1284
TGCAGGACCAGAGAATTCGAATA CAAACGAGTGNNNCTAGCGTTAC	805	TGCAGGACCAGAGAATTCGAATA CAATCTAGATNNNCTAGCGTTAC	1045	TGCAGGACCAGAGAATTCGAATA CACTGTAGGTNNNCTAGCGTTAC	1285
TGCAGGACCAGAGAATTCGAATA CATCTCACTGNNNCTAGCGTTAC	806	TGCAGGACCAGAGAATTCGAATA CAGCGACGTCNNNCTAGCGTTAC	1046	TGCAGGACCAGAGAATTCGAATA CACTAAGCGTNNNCTAGCGTTAC	1286
TGCAGGACCAGAGAATTCGAATA CATACGAGCTNNNCTAGCGTTAC	807	TGCAGGACCAGAGAATTCGAATA CACACCCCGTNNNCTAGCGTTAC	1047	TGCAGGACCAGAGAATTCGAATA CAGTTTATGANNNCTAGCGTTAC	1287
TGCAGGACCAGAGAATTCGAATA CACAGATACCNNNCTAGCGTTAC	808	TGCAGGACCAGAGAATTCGAATA CACGCCTCGTNNNCTAGCGTTAC	1048	TGCAGGACCAGAGAATTCGAATA CAACGACTGTNNNCTAGCGTTAC	1288
TGCAGGACCAGAGAATTCGAATA CATACATTTCNNNCTAGCGTTAC	809	TGCAGGACCAGAGAATTCGAATA CACTGACACANNNCTAGCGTTAC	1049	TGCAGGACCAGAGAATTCGAATA CACCTAGTAGNNNCTAGCGTTAC	1289
TGCAGGACCAGAGAATTCGAATA CAGTGTAAGGNNNCTAGCGTTAC	810	TGCAGGACCAGAGAATTCGAATA CATGCTTTGCNNNCTAGCGTTAC	1050	TGCAGGACCAGAGAATTCGAATA CAGGTTCTGANNNCTAGCGTTAC	1290
TGCAGGACCAGAGAATTCGAATA CAGGTTGAAGNNNCTAGCGTTAC	811	TGCAGGACCAGAGAATTCGAATA CAACTGTCTCNNNCTAGCGTTAC	1051	TGCAGGACCAGAGAATTCGAATA CATACATCCCNNNCTAGCGTTAC	1291
TGCAGGACCAGAGAATTCGAATA CACGTCCCTGNNNCTAGCGTTAC	812	TGCAGGACCAGAGAATTCGAATA CATATTGTCTNNNCTAGCGTTAC	1052	TGCAGGACCAGAGAATTCGAATA CACTCGGAATNNNCTAGCGTTAC	1292
TGCAGGACCAGAGAATTCGAATA CAAATCCCTCNNNCTAGCGTTAC	813	TGCAGGACCAGAGAATTCGAATA CAATTTGACANNNCTAGCGTTAC	1053	TGCAGGACCAGAGAATTCGAATA CATCAGTTGGNNNCTAGCGTTAC	1293
TGCAGGACCAGAGAATTCGAATA CATGCCCCACNNNCTAGCGTTAC	814	TGCAGGACCAGAGAATTCGAATA CACGCACACGNNNCTAGCGTTAC	1054	TGCAGGACCAGAGAATTCGAATA CAAGTGCCTANNNCTAGCGTTAC	1294
TGCAGGACCAGAGAATTCGAATA CAGTATTATGNNNCTAGCGTTAC	815	TGCAGGACCAGAGAATTCGAATA CACCGCGAACNNNCTAGCGTTAC	1055	TGCAGGACCAGAGAATTCGAATA CAGTATGTATNNNCTAGCGTTAC	1295
TGCAGGACCAGAGAATTCGAATA CATTGATTGANNNCTAGCGTTAC	816	TGCAGGACCAGAGAATTCGAATA CATTAGGCGTNNNCTAGCGTTAC	1056	TGCAGGACCAGAGAATTCGAATA CAGCAGCAGGNNNCTAGCGTTAC	1296
TGCAGGACCAGAGAATTCGAATA CATGCGACGCNNNCTAGCGTTAC	817	TGCAGGACCAGAGAATTCGAATA CATCGGAGCCNNNCTAGCGTTAC	1057	TGCAGGACCAGAGAATTCGAATA CAGCAGGTCCNNNCTAGCGTTAC	1297
TGCAGGACCAGAGAATTCGAATA CAGTGGTTCANNNCTAGCGTTAC	818	TGCAGGACCAGAGAATTCGAATA CAGTCTACAGNNNCTAGCGTTAC	1058	TGCAGGACCAGAGAATTCGAATA CATGTAGGCTNNNCTAGCGTTAC	1298
TGCAGGACCAGAGAATTCGAATA CAGCCGGCTANNNCTAGCGTTAC	819	TGCAGGACCAGAGAATTCGAATA CACCGCGTCTNNNCTAGCGTTAC	1059	TGCAGGACCAGAGAATTCGAATA CATAACGACCNNNCTAGCGTTAC	1299
TGCAGGACCAGAGAATTCGAATA CACCTTGCGCNNNCTAGCGTTAC	820	TGCAGGACCAGAGAATTCGAATA CATTAAACTGNNNCTAGCGTTAC	1060	TGCAGGACCAGAGAATTCGAATA CACGATCGGCNNNCTAGCGTTAC	1300
TGCAGGACCAGAGAATTCGAATA CAGGTAAGTGNNNCTAGCGTTAC	821	TGCAGGACCAGAGAATTCGAATA CAATAAGAACNNNCTAGCGTTAC	1061	TGCAGGACCAGAGAATTCGAATA CAGGCCAAGGNNNCTAGCGTTAC	1301
TGCAGGACCAGAGAATTCGAATA CAGTGTCCAANNNCTAGCGTTAC	822	TGCAGGACCAGAGAATTCGAATA CAATCATGCGNNNCTAGCGTTAC	1062	TGCAGGACCAGAGAATTCGAATA CAGACATAAANNNCTAGCGTTAC	1302
TGCAGGACCAGAGAATTCGAATA CATGCACTGANNNCTAGCGTTAC	823	TGCAGGACCAGAGAATTCGAATA CACCAACTAGNNNCTAGCGTTAC	1063	TGCAGGACCAGAGAATTCGAATA CACGCACATANNNCTAGCGTTAC	1303
TGCAGGACCAGAGAATTCGAATA CAGAAACTTTNNNCTAGCGTTAC	824	TGCAGGACCAGAGAATTCGAATA CACTCGAGTANNNCTAGCGTTAC	1064	TGCAGGACCAGAGAATTCGAATA CAGCCTAGGCNNNCTAGCGTTAC	1304

图13C

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATGTGTAGCNNNCTAGCGTTAC	825	TGCAGGACCAGAGAATTCGAATA CACTTTGCCANNNCTAGCGTTAC	1065	TGCAGGACCAGAGAATTCGAATA CATCCGCAAANNNCTAGCGTTAC	1305
TGCAGGACCAGAGAATTCGAATA CATCTACCTGNNNCTAGCGTTAC	826	TGCAGGACCAGAGAATTCGAATA CAAATTCTGANNNCTAGCGTTAC	1066	TGCAGGACCAGAGAATTCGAATA CACTTATAGANNNCTAGCGTTAC	1306
TGCAGGACCAGAGAATTCGAATA CATCTCTTAANNNCTAGCGTTAC	827	TGCAGGACCAGAGAATTCGAATA CAGATCGCATNNNCTAGCGTTAC	1067	TGCAGGACCAGAGAATTCGAATA CACGGCGGAANNNCTAGCGTTAC	1307
TGCAGGACCAGAGAATTCGAATA CAATCGAATTNNNCTAGCGTTAC	828	TGCAGGACCAGAGAATTCGAATA CATGTGTTGGNNNCTAGCGTTAC	1068	TGCAGGACCAGAGAATTCGAATA CAGTAGCACTNNNCTAGCGTTAC	1308
TGCAGGACCAGAGAATTCGAATA CATTTTTGGTNNNCTAGCGTTAC	829	TGCAGGACCAGAGAATTCGAATA CAGTAACATTNNNCTAGCGTTAC	1069	TGCAGGACCAGAGAATTCGAATA CAGCTGTCAANNNCTAGCGTTAC	1309
TGCAGGACCAGAGAATTCGAATA CATCAGTCCTNNNCTAGCGTTAC	830	TGCAGGACCAGAGAATTCGAATA CAACGCATCANNNCTAGCGTTAC	1070	TGCAGGACCAGAGAATTCGAATA CAGTGCCAGCNNNCTAGCGTTAC	1310
TGCAGGACCAGAGAATTCGAATA CAGTGCACATNNNCTAGCGTTAC	831	TGCAGGACCAGAGAATTCGAATA CATAGGAAGCNNNCTAGCGTTAC	1071	TGCAGGACCAGAGAATTCGAATA CATTCATATCNNNCTAGCGTTAC	1311
TGCAGGACCAGAGAATTCGAATA CAGTAGAAGCNNNCTAGCGTTAC	832	TGCAGGACCAGAGAATTCGAATA CAGCAATGTCNNNCTAGCGTTAC	1072	TGCAGGACCAGAGAATTCGAATA CACCCATGCCNNNCTAGCGTTAC	1312
TGCAGGACCAGAGAATTCGAATA CACAGCATTGNNNCTAGCGTTAC	833	TGCAGGACCAGAGAATTCGAATA CAGCCGGCATNNNCTAGCGTTAC	1073	TGCAGGACCAGAGAATTCGAATA CATTAGTTGANNNCTAGCGTTAC	1313
TGCAGGACCAGAGAATTCGAATA CAGGCCTAGGNNNCTAGCGTTAC	834	TGCAGGACCAGAGAATTCGAATA CACTGAGGCCNNNCTAGCGTTAC	1074	TGCAGGACCAGAGAATTCGAATA CAATCAGAAANNNCTAGCGTTAC	1314
TGCAGGACCAGAGAATTCGAATA CACAGTTTGCNNNCTAGCGTTAC	835	TGCAGGACCAGAGAATTCGAATA CACTGCTGCCNNNCTAGCGTTAC	1075	TGCAGGACCAGAGAATTCGAATA CATTAGAACTNNNCTAGCGTTAC	1315
TGCAGGACCAGAGAATTCGAATA CATCCCAAGANNNCTAGCGTTAC	836	TGCAGGACCAGAGAATTCGAATA CAGTGGCGGANNNCTAGCGTTAC	1076	TGCAGGACCAGAGAATTCGAATA CAGTGCTATGNNNCTAGCGTTAC	1316
TGCAGGACCAGAGAATTCGAATA CATTAGGACCNNNCTAGCGTTAC	837	TGCAGGACCAGAGAATTCGAATA CAAGGCTACTNNNCTAGCGTTAC	1077	TGCAGGACCAGAGAATTCGAATA CATTGGATCGNNNCTAGCGTTAC	1317
TGCAGGACCAGAGAATTCGAATA CAACAATTTGNNNCTAGCGTTAC	838	TGCAGGACCAGAGAATTCGAATA CAACTTTGTTNNNCTAGCGTTAC	1078	TGCAGGACCAGAGAATTCGAATA CACAAGAATANNNCTAGCGTTAC	1318
TGCAGGACCAGAGAATTCGAATA CATGCTCGAANNNCTAGCGTTAC	839	TGCAGGACCAGAGAATTCGAATA CAGCCATATGNNNCTAGCGTTAC	1079	TGCAGGACCAGAGAATTCGAATA CAAGCACCATNNNCTAGCGTTAC	1319
TGCAGGACCAGAGAATTCGAATA CAGGCGGTAGNNNCTAGCGTTAC	840	TGCAGGACCAGAGAATTCGAATA CAAGCCTGGCNNNCTAGCGTTAC	1080	TGCAGGACCAGAGAATTCGAATA CAACTAGACCNNNCTAGCGTTAC	1320
TGCAGGACCAGAGAATTCGAATA CAAATTAACCNNNCTAGCGTTAC	841	TGCAGGACCAGAGAATTCGAATA CAACGTGTGTNNNCTAGCGTTAC	1081	TGCAGGACCAGAGAATTCGAATA CAATCATTAGNNNCTAGCGTTAC	1321
TGCAGGACCAGAGAATTCGAATA CACGACACCGNNNCTAGCGTTAC	842	TGCAGGACCAGAGAATTCGAATA CATTTTCATGNNNCTAGCGTTAC	1082	TGCAGGACCAGAGAATTCGAATA CAAGAACCTCNNNCTAGCGTTAC	1322
TGCAGGACCAGAGAATTCGAATA CAGTGAGGATNNNCTAGCGTTAC	843	TGCAGGACCAGAGAATTCGAATA CAGCTGCGACNNNCTAGCGTTAC	1083	TGCAGGACCAGAGAATTCGAATA CAGATTTTCTNNNCTAGCGTTAC	1323
TGCAGGACCAGAGAATTCGAATA CAAAATTAAANNNCTAGCGTTAC	844	TGCAGGACCAGAGAATTCGAATA CACAAAATAGNNNCTAGCGTTAC	1084	TGCAGGACCAGAGAATTCGAATA CAAGTACGGANNNCTAGCGTTAC	1324
TGCAGGACCAGAGAATTCGAATA CACATGCCAANNNCTAGCGTTAC	845	TGCAGGACCAGAGAATTCGAATA CACTAAACTANNNCTAGCGTTAC	1085	TGCAGGACCAGAGAATTCGAATA CACGCCTAAANNNCTAGCGTTAC	1325
TGCAGGACCAGAGAATTCGAATA CACCATCAGANNNCTAGCGTTAC	846	TGCAGGACCAGAGAATTCGAATA CAAAATGATGNNNCTAGCGTTAC	1086	TGCAGGACCAGAGAATTCGAATA CAAGTTGGTCNNNCTAGCGTTAC	1326
TGCAGGACCAGAGAATTCGAATA CAATATAAAANNNCTAGCGTTAC	847	TGCAGGACCAGAGAATTCGAATA CACTTGCTTGNNNCTAGCGTTAC	1087	TGCAGGACCAGAGAATTCGAATA CATGCGCACGNNNCTAGCGTTAC	1327
TGCAGGACCAGAGAATTCGAATA CAGCCTCCGTNNNCTAGCGTTAC	848	TGCAGGACCAGAGAATTCGAATA CAGATAGGCANNNCTAGCGTTAC	1088	TGCAGGACCAGAGAATTCGAATA CATTGGTACGNNNCTAGCGTTAC	1328
TGCAGGACCAGAGAATTCGAATA CATCCAATCCNNNGATCGACATG	849	TGCAGGACCAGAGAATTCGAATA CACAGATTATNNNGATCGACATG	1089	TGCAGGACCAGAGAATTCGAATA CAATGAGATANNNGATCGACATG	1329
TGCAGGACCAGAGAATTCGAATA CAAAATGCCCNNNGATCGACATG	850	TGCAGGACCAGAGAATTCGAATA CAGTTACGGTNNNGATCGACATG	1090	TGCAGGACCAGAGAATTCGAATA CAATCGGTACNNNGATCGACATG	1330
TGCAGGACCAGAGAATTCGAATA CAACTGTCGANNNGATCGACATG	851	TGCAGGACCAGAGAATTCGAATA CAACAGTTGCNNNGATCGACATG	1091	TGCAGGACCAGAGAATTCGAATA CATGTCGTTCNNNGATCGACATG	1331
TGCAGGACCAGAGAATTCGAATA CAGCTGTTGANNNGATCGACATG	852	TGCAGGACCAGAGAATTCGAATA CAAACTGCACNNNGATCGACATG	1092	TGCAGGACCAGAGAATTCGAATA CATGTGTATANNNGATCGACATG	1332
TGCAGGACCAGAGAATTCGAATA CAGGTAACCTNNNGATCGACATG	853	TGCAGGACCAGAGAATTCGAATA CAAGAATATGNNNGATCGACATG	1093	TGCAGGACCAGAGAATTCGAATA CAGTGGATCTNNNGATCGACATG	1333
TGCAGGACCAGAGAATTCGAATA CACTTTTCCCNNNGATCGACATG	854	TGCAGGACCAGAGAATTCGAATA CATCGTCCTANNNGATCGACATG	1094	TGCAGGACCAGAGAATTCGAATA CATGTTCAATNNNGATCGACATG	1334
TGCAGGACCAGAGAATTCGAATA CAGAGAGCCGNNNGATCGACATG	855	TGCAGGACCAGAGAATTCGAATA CACAGAATCCNNNGATCGACATG	1095	TGCAGGACCAGAGAATTCGAATA CACGCGTGTGNNNGATCGACATG	1335
TGCAGGACCAGAGAATTCGAATA CACAGACAGANNNGATCGACATG	856	TGCAGGACCAGAGAATTCGAATA CACTTGACAGNNNGATCGACATG	1096	TGCAGGACCAGAGAATTCGAATA CACTCCTCGGNNNGATCGACATG	1336

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATATATGACNNNGATCGACATG	857	TGCAGGACCAGAGAATTCGAATA CACTGGTAGTNNNGATCGACATG	1097	TGCAGGACCAGAGAATTCGAATA CAGACTAATTNNNGATCGACATG	1337
TGCAGGACCAGAGAATTCGAATA CAGTCCGACGNNNGATCGACATG	858	TGCAGGACCAGAGAATTCGAATA CACGGATCTANNNGATCGACATG	1098	TGCAGGACCAGAGAATTCGAATA CACAATAAGANNNGATCGACATG	1338
TGCAGGACCAGAGAATTCGAATA CAACTGCATGNNNGATCGACATG	859	TGCAGGACCAGAGAATTCGAATA CAAAAAAGAGNNNGATCGACATG	1099	TGCAGGACCAGAGAATTCGAATA CATTTACCGCNNNGATCGACATG	1339
TGCAGGACCAGAGAATTCGAATA CATACCTAAANNNGATCGACATG	860	TGCAGGACCAGAGAATTCGAATA CAGGAGACATNNNGATCGACATG	1100	TGCAGGACCAGAGAATTCGAATA CAGTGTATTANNNGATCGACATG	1340
TGCAGGACCAGAGAATTCGAATA CAACCAGATCNNNGATCGACATG	861	TGCAGGACCAGAGAATTCGAATA CATCCGGAGCNNNGATCGACATG	1101	TGCAGGACCAGAGAATTCGAATA CAAGATGTAANNNGATCGACATG	1341
TGCAGGACCAGAGAATTCGAATA CAGGCAAATGNNNGATCGACATG	862	TGCAGGACCAGAGAATTCGAATA CATGTTATTCNNNGATCGACATG	1102	TGCAGGACCAGAGAATTCGAATA CATTATTCGTNNNGATCGACATG	1342
TGCAGGACCAGAGAATTCGAATA CAGAACGTCTNNNGATCGACATG	863	TGCAGGACCAGAGAATTCGAATA CAGCGAGACGNNNGATCGACATG	1103	TGCAGGACCAGAGAATTCGAATA CAAGTCACACNNNGATCGACATG	1343
TGCAGGACCAGAGAATTCGAATA CACCACCAAANNNGATCGACATG	864	TGCAGGACCAGAGAATTCGAATA CATTATCGAANNNGATCGACATG	1104	TGCAGGACCAGAGAATTCGAATA CACTGACAACNNNGATCGACATG	1344
TGCAGGACCAGAGAATTCGAATA CATTTTCCAANNNGATCGACATG	865	TGCAGGACCAGAGAATTCGAATA CAGTGCCAATNNNGATCGACATG	1105	TGCAGGACCAGAGAATTCGAATA CAACGCCGGTNNNGATCGACATG	1345
TGCAGGACCAGAGAATTCGAATA CAGTTAGTTANNNGATCGACATG	866	TGCAGGACCAGAGAATTCGAATA CAGCTAAAAANNNGATCGACATG	1106	TGCAGGACCAGAGAATTCGAATA CAGGTGACCCNNNGATCGACATG	1346
TGCAGGACCAGAGAATTCGAATA CATCAGCTCTNNNGATCGACATG	867	TGCAGGACCAGAGAATTCGAATA CAATCCAATANNNGATCGACATG	1107	TGCAGGACCAGAGAATTCGAATA CACCTTAGCTNNNGATCGACATG	1347
TGCAGGACCAGAGAATTCGAATA CATGCGGAGGNNNGATCGACATG	868	TGCAGGACCAGAGAATTCGAATA CATTCAAGGCNNNGATCGACATG	1108	TGCAGGACCAGAGAATTCGAATA CACTCGCTATNNNGATCGACATG	1348
TGCAGGACCAGAGAATTCGAATA CATCTGCAAGNNNGATCGACATG	869	TGCAGGACCAGAGAATTCGAATA CATTATTAAANNNGATCGACATG	1109	TGCAGGACCAGAGAATTCGAATA CAAGCCTAGTNNNGATCGACATG	1349
TGCAGGACCAGAGAATTCGAATA CATCTAACCCNNNGATCGACATG	870	TGCAGGACCAGAGAATTCGAATA CAAACTCTAANNNGATCGACATG	1110	TGCAGGACCAGAGAATTCGAATA CAGAGAGTTGNNNGATCGACATG	1350
TGCAGGACCAGAGAATTCGAATA CACGTAGGAANNNGATCGACATG	871	TGCAGGACCAGAGAATTCGAATA CAGACTCCAANNNGATCGACATG	1111	TGCAGGACCAGAGAATTCGAATA CATAAGAGGCNNNGATCGACATG	1351
TGCAGGACCAGAGAATTCGAATA CACAAGACTCNNNGATCGACATG	872	TGCAGGACCAGAGAATTCGAATA CACAGCCTCCNNNGATCGACATG	1112	TGCAGGACCAGAGAATTCGAATA CAGTTAATACNNNGATCGACATG	1352
TGCAGGACCAGAGAATTCGAATA CATTCCGTGTNNNGATCGACATG	873	TGCAGGACCAGAGAATTCGAATA CAGAGTCACTNNNGATCGACATG	1113	TGCAGGACCAGAGAATTCGAATA CAGGTCCGCANNNGATCGACATG	1353
TGCAGGACCAGAGAATTCGAATA CAGTGAACGANNNGATCGACATG	874	TGCAGGACCAGAGAATTCGAATA CAAGAACTGGNNNGATCGACATG	1114	TGCAGGACCAGAGAATTCGAATA CATAAGCATTNNNGATCGACATG	1354
TGCAGGACCAGAGAATTCGAATA CAGCTAAACCNNNGATCGACATG	875	TGCAGGACCAGAGAATTCGAATA CAGCGTATTGNNNGATCGACATG	1115	TGCAGGACCAGAGAATTCGAATA CAGTACGCATNNNGATCGACATG	1355
TGCAGGACCAGAGAATTCGAATA CACAATTTTCNNNGATCGACATG	876	TGCAGGACCAGAGAATTCGAATA CACTTAAATGNNNGATCGACATG	1116	TGCAGGACCAGAGAATTCGAATA CAAACGAACGNNNGATCGACATG	1356
TGCAGGACCAGAGAATTCGAATA CATGAGGAACNNNGATCGACATG	877	TGCAGGACCAGAGAATTCGAATA CATTAGCCTCNNNGATCGACATG	1117	TGCAGGACCAGAGAATTCGAATA CAGTAGGTTCNNNGATCGACATG	1357
TGCAGGACCAGAGAATTCGAATA CAGTAATCTANNNGATCGACATG	878	TGCAGGACCAGAGAATTCGAATA CAACCAGAGANNNGATCGACATG	1118	TGCAGGACCAGAGAATTCGAATA CACTTTTTCNNNGATCGACATG	1358
TGCAGGACCAGAGAATTCGAATA CATATCTCCGNNNGATCGACATG	879	TGCAGGACCAGAGAATTCGAATA CATCAGCCAANNNGATCGACATG	1119	TGCAGGACCAGAGAATTCGAATA CAATGACCCANNNGATCGACATG	1359
TGCAGGACCAGAGAATTCGAATA CAGCTACGGCNNNGATCGACATG	880	TGCAGGACCAGAGAATTCGAATA CACCGAATACNNNGATCGACATG	1120	TGCAGGACCAGAGAATTCGAATA CAATCAGTTANNNGATCGACATG	1360
TGCAGGACCAGAGAATTCGAATA CAATATCTGANNNGATCGACATG	881	TGCAGGACCAGAGAATTCGAATA CAGCGGCAAGNNNGATCGACATG	1121	TGCAGGACCAGAGAATTCGAATA CATAGTAAAGNNNGATCGACATG	1361
TGCAGGACCAGAGAATTCGAATA CATACTTAGANNNGATCGACATG	882	TGCAGGACCAGAGAATTCGAATA CATAAATCGTNNNGATCGACATG	1122	TGCAGGACCAGAGAATTCGAATA CACCCGATGGNNNGATCGACATG	1362
TGCAGGACCAGAGAATTCGAATA CATCATTTTGNNNGATCGACATG	883	TGCAGGACCAGAGAATTCGAATA CAAAGCTTCGNNNGATCGACATG	1123	TGCAGGACCAGAGAATTCGAATA CACACAGCATNNNGATCGACATG	1363
TGCAGGACCAGAGAATTCGAATA CAGCGTGGAGNNNGATCGACATG	884	TGCAGGACCAGAGAATTCGAATA CAATGCATATNNNGATCGACATG	1124	TGCAGGACCAGAGAATTCGAATA CACAGGTACTNNNGATCGACATG	1364
TGCAGGACCAGAGAATTCGAATA CATAAGACGGNNNGATCGACATG	885	TGCAGGACCAGAGAATTCGAATA CATCTCTCCTNNNGATCGACATG	1125	TGCAGGACCAGAGAATTCGAATA CACATAACCGNNNGATCGACATG	1365
TGCAGGACCAGAGAATTCGAATA CAAGGCCTTANNNGATCGACATG	886	TGCAGGACCAGAGAATTCGAATA CATAGTGGTCNNNGATCGACATG	1126	TGCAGGACCAGAGAATTCGAATA CAGTACTGGTNNNGATCGACATG	1366
TGCAGGACCAGAGAATTCGAATA CACATCTCACNNNGATCGACATG	887	TGCAGGACCAGAGAATTCGAATA CAGAAAGCTCNNNGATCGACATG	1127	TGCAGGACCAGAGAATTCGAATA CAGCAAGTCTNNNGATCGACATG	1367
TGCAGGACCAGAGAATTCGAATA CATGCGATCANNNGATCGACATG	888	TGCAGGACCAGAGAATTCGAATA CATGACTATANNNGATCGACATG	1128	TGCAGGACCAGAGAATTCGAATA CACGTGCTCCNNNGATCGACATG	1368

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACGGAGGACNNNGATCGACATG	889	TGCAGGACCAGAGAATTCGAATA CACATGACTGNNNGATCGACATG	1129	TGCAGGACCAGAGAATTCGAATA CACACTACCTNNNGATCGACATG	1369
TGCAGGACCAGAGAATTCGAATA CAACTAATTGNNNGATCGACATG	890	TGCAGGACCAGAGAATTCGAATA CACCAAAGTCNNNGATCGACATG	1130	TGCAGGACCAGAGAATTCGAATA CAGTGTATATNNNGATCGACATG	1370
TGCAGGACCAGAGAATTCGAATA CATGCCTAGANNNGATCGACATG	891	TGCAGGACCAGAGAATTCGAATA CACGCATTTCNNNGATCGACATG	1131	TGCAGGACCAGAGAATTCGAATA CAATGACGCTNNNGATCGACATG	1371
TGCAGGACCAGAGAATTCGAATA CACTATCCGTNNNGATCGACATG	892	TGCAGGACCAGAGAATTCGAATA CAACCCGGTGNNNGATCGACATG	1132	TGCAGGACCAGAGAATTCGAATA CAAGGCACTTNNNGATCGACATG	1372
TGCAGGACCAGAGAATTCGAATA CATGCCAGGCNNNGATCGACATG	893	TGCAGGACCAGAGAATTCGAATA CACTTGCGTTNNNGATCGACATG	1133	TGCAGGACCAGAGAATTCGAATA CAGGCAGGCANNNGATCGACATG	1373
TGCAGGACCAGAGAATTCGAATA CAGCGGAGCANNNGATCGACATG	894	TGCAGGACCAGAGAATTCGAATA CATTATGCAANNNGATCGACATG	1134	TGCAGGACCAGAGAATTCGAATA CACTATGTTTNNNGATCGACATG	1374
TGCAGGACCAGAGAATTCGAATA CAAGACCCATNNNGATCGACATG	895	TGCAGGACCAGAGAATTCGAATA CATATTTGAGNNNGATCGACATG	1135	TGCAGGACCAGAGAATTCGAATA CATAAATATTNNNGATCGACATG	1375
TGCAGGACCAGAGAATTCGAATA CATTGACCTCNNNGATCGACATG	896	TGCAGGACCAGAGAATTCGAATA CATGTTCGCTNNNGATCGACATG	1136	TGCAGGACCAGAGAATTCGAATA CAGACACCATNNNGATCGACATG	1376
TGCAGGACCAGAGAATTCGAATA CACTTGCTCANNNGATCGACATG	897	TGCAGGACCAGAGAATTCGAATA CATAGCATCGNNNGATCGACATG	1137	TGCAGGACCAGAGAATTCGAATA CATAGATACTNNNGATCGACATG	1377
TGCAGGACCAGAGAATTCGAATA CAATGCTGCANNNGATCGACATG	898	TGCAGGACCAGAGAATTCGAATA CATTCAGAGCNNNGATCGACATG	1138	TGCAGGACCAGAGAATTCGAATA CATACCCTGTNNNGATCGACATG	1378
TGCAGGACCAGAGAATTCGAATA CAAACGGACANNNGATCGACATG	899	TGCAGGACCAGAGAATTCGAATA CAAACGCAGANNNGATCGACATG	1139	TGCAGGACCAGAGAATTCGAATA CAGTCGCCGANNNGATCGACATG	1379
TGCAGGACCAGAGAATTCGAATA CAGCGATCATNNNGATCGACATG	900	TGCAGGACCAGAGAATTCGAATA CATATGGCGTNNNGATCGACATG	1140	TGCAGGACCAGAGAATTCGAATA CACCTCTTAGNNNGATCGACATG	1380
TGCAGGACCAGAGAATTCGAATA CATGAGACAGNNNGATCGACATG	901	TGCAGGACCAGAGAATTCGAATA CAAGCCTATGNNNGATCGACATG	1141	TGCAGGACCAGAGAATTCGAATA CATAAGATTCNNNGATCGACATG	1381
TGCAGGACCAGAGAATTCGAATA CAGCCACTGGNNNGATCGACATG	902	TGCAGGACCAGAGAATTCGAATA CACACTCTACNNNGATCGACATG	1142	TGCAGGACCAGAGAATTCGAATA CACGCGTACGNNNGATCGACATG	1382
TGCAGGACCAGAGAATTCGAATA CAGGTTTGACNNNGATCGACATG	903	TGCAGGACCAGAGAATTCGAATA CAAAACTGAANNNGATCGACATG	1143	TGCAGGACCAGAGAATTCGAATA CACTGACCAANNNGATCGACATG	1383
TGCAGGACCAGAGAATTCGAATA CAAACTTGGCNNNGATCGACATG	904	TGCAGGACCAGAGAATTCGAATA CACTTCCGCGNNNGATCGACATG	1144	TGCAGGACCAGAGAATTCGAATA CAAAGACCGANNNGATCGACATG	1384
TGCAGGACCAGAGAATTCGAATA CAACCTAATANNNGATCGACATG	905	TGCAGGACCAGAGAATTCGAATA CAACGTCGGCNNNGATCGACATG	1145	TGCAGGACCAGAGAATTCGAATA CAAATGATTCNNNGATCGACATG	1385
TGCAGGACCAGAGAATTCGAATA CAGCACAGAANNNGATCGACATG	906	TGCAGGACCAGAGAATTCGAATA CAGTACCCAANNNGATCGACATG	1146	TGCAGGACCAGAGAATTCGAATA CACCCCCCAANNNGATCGACATG	1386
TGCAGGACCAGAGAATTCGAATA CATGTGTCAGNNNGATCGACATG	907	TGCAGGACCAGAGAATTCGAATA CAACCGCATANNNGATCGACATG	1147	TGCAGGACCAGAGAATTCGAATA CAGCCTGAATNNNGATCGACATG	1387
TGCAGGACCAGAGAATTCGAATA CAAGTAACAANNNGATCGACATG	908	TGCAGGACCAGAGAATTCGAATA CAAACCACCTNNNGATCGACATG	1148	TGCAGGACCAGAGAATTCGAATA CATCGGTAGTNNNGATCGACATG	1388
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TGCAGGACCAGAGAATTCGAATA CAGAACTCGTNNNTGCATCAGGT	911	TGCAGGACCAGAGAATTCGAATA CAGCTAGGTTNNNTGCATCAGGT	1151	TGCAGGACCAGAGAATTCGAATA CATAGAGACGNNNTGCATCAGGT	1391
TGCAGGACCAGAGAATTCGAATA CAGCAGGCGANNNTGCATCAGGT	912	TGCAGGACCAGAGAATTCGAATA CATTTGACTTNNNTGCATCAGGT	1152	TGCAGGACCAGAGAATTCGAATA CAGCGGATGGNNNTGCATCAGGT	1392
TGCAGGACCAGAGAATTCGAATA CAGGCTCTCCNNNTGCATCAGGT	913	TGCAGGACCAGAGAATTCGAATA CACAAACATTNNNTGCATCAGGT	1153	TGCAGGACCAGAGAATTCGAATA CACTCACCATNNNTGCATCAGGT	1393
TGCAGGACCAGAGAATTCGAATA CAAATACATCNNNTGCATCAGGT	914	TGCAGGACCAGAGAATTCGAATA CATTGCAATANNNTGCATCAGGT	1154	TGCAGGACCAGAGAATTCGAATA CAATGGTAAANNNTGCATCAGGT	1394
TGCAGGACCAGAGAATTCGAATA CAAGGTCAACNNNTGCATCAGGT	915	TGCAGGACCAGAGAATTCGAATA CAACAAGGCANNNTGCATCAGGT	1155	TGCAGGACCAGAGAATTCGAATA CATATCAACANNNTGCATCAGGT	1395
TGCAGGACCAGAGAATTCGAATA CATGAGCCGCNNNTGCATCAGGT	916	TGCAGGACCAGAGAATTCGAATA CAGGTGCTGCNNNTGCATCAGGT	1156	TGCAGGACCAGAGAATTCGAATA CAAAAGTCAANNNTGCATCAGGT	1396
TGCAGGACCAGAGAATTCGAATA CATTAGTTTCNNNTGCATCAGGT	917	TGCAGGACCAGAGAATTCGAATA CAAGGTCGTTNNNTGCATCAGGT	1157	TGCAGGACCAGAGAATTCGAATA CACAAAGGCANNNTGCATCAGGT	1397
TGCAGGACCAGAGAATTCGAATA CAGTCGTAGTNNNTGCATCAGGT	918	TGCAGGACCAGAGAATTCGAATA CACAACGGAANNNTGCATCAGGT	1158	TGCAGGACCAGAGAATTCGAATA CACGATGACTNNNTGCATCAGGT	1398
TGCAGGACCAGAGAATTCGAATA CAAAAGGATTNNNTGCATCAGGT	919	TGCAGGACCAGAGAATTCGAATA CAGATCGAACNNNTGCATCAGGT	1159	TGCAGGACCAGAGAATTCGAATA CACGATTGTGNNNTGCATCAGGT	1399
TGCAGGACCAGAGAATTCGAATA CATTTTTAGCNNNTGCATCAGGT	920	TGCAGGACCAGAGAATTCGAATA CAGGAAGACTNNNTGCATCAGGT	1160	TGCAGGACCAGAGAATTCGAATA CATTATGTTGNNNTGCATCAGGT	1400

图13F

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAATAACTCANNNTGCATCAGGT	921	TGCAGGACCAGAGAATTCGAATA CAGGTAAATANNNTGCATCAGGT	1161	TGCAGGACCAGAGAATTCGAATA CAGTATTGATNNNTGCATCAGGT	1401
TGCAGGACCAGAGAATTCGAATA CATTTTAACCNNNTGCATCAGGT	922	TGCAGGACCAGAGAATTCGAATA CAGGTAGAACNNNTGCATCAGGT	1162	TGCAGGACCAGAGAATTCGAATA CAAGGAGGTTNNNTGCATCAGGT	1402
TGCAGGACCAGAGAATTCGAATA CAGTGCCGACNNNTGCATCAGGT	923	TGCAGGACCAGAGAATTCGAATA CAATATGAGANNNTGCATCAGGT	1163	TGCAGGACCAGAGAATTCGAATA CAACTGCCCCNNNTGCATCAGGT	1403
TGCAGGACCAGAGAATTCGAATA CAGAATAGATNNNTGCATCAGGT	924	TGCAGGACCAGAGAATTCGAATA CATGGAAATANNNTGCATCAGGT	1164	TGCAGGACCAGAGAATTCGAATA CAAAATCTCANNNTGCATCAGGT	1404
TGCAGGACCAGAGAATTCGAATA CAGCTGAGCCNNNTGCATCAGGT	925	TGCAGGACCAGAGAATTCGAATA CATAACCAATNNNTGCATCAGGT	1165	TGCAGGACCAGAGAATTCGAATA CACCATGTGANNNTGCATCAGGT	1405
TGCAGGACCAGAGAATTCGAATA CAACAGGCAANNNTGCATCAGGT	926	TGCAGGACCAGAGAATTCGAATA CAGTCTGATGNNNTGCATCAGGT	1166	TGCAGGACCAGAGAATTCGAATA CACCCCTTTTNNNTGCATCAGGT	1406
TGCAGGACCAGAGAATTCGAATA CAGACCGCACNNNTGCATCAGGT	927	TGCAGGACCAGAGAATTCGAATA CATTTATGAGNNNTGCATCAGGT	1167	TGCAGGACCAGAGAATTCGAATA CAGCTAGCGCNNNTGCATCAGGT	1407
TGCAGGACCAGAGAATTCGAATA CACTTATTCANNNTGCATCAGGT	928	TGCAGGACCAGAGAATTCGAATA CAATGATTTGNNNTGCATCAGGT	1168	TGCAGGACCAGAGAATTCGAATA CAAACACCGTNNNTGCATCAGGT	1408
TGCAGGACCAGAGAATTCGAATA CAGTGTGCTANNNTGCATCAGGT	929	TGCAGGACCAGAGAATTCGAATA CACTCATCGTNNNTGCATCAGGT	1169	TGCAGGACCAGAGAATTCGAATA CACTGAGATCNNNTGCATCAGGT	1409
TGCAGGACCAGAGAATTCGAATA CAATTTAGTGNNNTGCATCAGGT	930	TGCAGGACCAGAGAATTCGAATA CACTCCATACNNNTGCATCAGGT	1170	TGCAGGACCAGAGAATTCGAATA CAAATGGGTCNNNTGCATCAGGT	1410
TGCAGGACCAGAGAATTCGAATA CATCGGAGAANNNTGCATCAGGT	931	TGCAGGACCAGAGAATTCGAATA CAGCTAGCATNNNTGCATCAGGT	1171	TGCAGGACCAGAGAATTCGAATA CAATTGCCAGNNNTGCATCAGGT	1411
TGCAGGACCAGAGAATTCGAATA CACGCCGAACNNNTGCATCAGGT	932	TGCAGGACCAGAGAATTCGAATA CAAATCATCANNNTGCATCAGGT	1172	TGCAGGACCAGAGAATTCGAATA CATTAATTCCNNNTGCATCAGGT	1412
TGCAGGACCAGAGAATTCGAATA CAGCTTCGCCNNNTGCATCAGGT	933	TGCAGGACCAGAGAATTCGAATA CACGTCTCATNNNTGCATCAGGT	1173	TGCAGGACCAGAGAATTCGAATA CAAGCATATTNNNTGCATCAGGT	1413
TGCAGGACCAGAGAATTCGAATA CAACAATCATNNNTGCATCAGGT	934	TGCAGGACCAGAGAATTCGAATA CAACTCGTTCNNNTGCATCAGGT	1174	TGCAGGACCAGAGAATTCGAATA CACCCATTACNNNTGCATCAGGT	1414
TGCAGGACCAGAGAATTCGAATA CATGATCGCANNNTGCATCAGGT	935	TGCAGGACCAGAGAATTCGAATA CAAGTTCTGGNNNTGCATCAGGT	1175	TGCAGGACCAGAGAATTCGAATA CACTCGTTTGNNNTGCATCAGGT	1415
TGCAGGACCAGAGAATTCGAATA CACACAGTACNNNTGCATCAGGT	936	TGCAGGACCAGAGAATTCGAATA CAACTAGTATNNNTGCATCAGGT	1176	TGCAGGACCAGAGAATTCGAATA CAGGTATCGTNNNTGCATCAGGT	1416
TGCAGGACCAGAGAATTCGAATA CAGTCAAGTCNNNTGCATCAGGT	937	TGCAGGACCAGAGAATTCGAATA CAATTGCGCANNNTGCATCAGGT	1177	TGCAGGACCAGAGAATTCGAATA CAGTACCCTTNNNTGCATCAGGT	1417
TGCAGGACCAGAGAATTCGAATA CAGCTCCCACNNNTGCATCAGGT	938	TGCAGGACCAGAGAATTCGAATA CACGAGCGCTNNNTGCATCAGGT	1178	TGCAGGACCAGAGAATTCGAATA CACAACTTTTNNNTGCATCAGGT	1418
TGCAGGACCAGAGAATTCGAATA CATTACTTGTNNNTGCATCAGGT	939	TGCAGGACCAGAGAATTCGAATA CAACGACCATNNNTGCATCAGGT	1179	TGCAGGACCAGAGAATTCGAATA CAGAACTTGCNNNTGCATCAGGT	1419
TGCAGGACCAGAGAATTCGAATA CATAATGTGTNNNTGCATCAGGT	940	TGCAGGACCAGAGAATTCGAATA CATAAGTGAANNNTGCATCAGGT	1180	TGCAGGACCAGAGAATTCGAATA CATATTATGGNNNTGCATCAGGT	1420
TGCAGGACCAGAGAATTCGAATA CATACCATTTNNNTGCATCAGGT	941	TGCAGGACCAGAGAATTCGAATA CATCTCGCCGNNNTGCATCAGGT	1181	TGCAGGACCAGAGAATTCGAATA CAGCCCGCGGNNNTGCATCAGGT	1421
TGCAGGACCAGAGAATTCGAATA CAGTCCGTAANNNTGCATCAGGT	942	TGCAGGACCAGAGAATTCGAATA CAAATACTGTNNNTGCATCAGGT	1182	TGCAGGACCAGAGAATTCGAATA CAGCAAAAGCNNNTGCATCAGGT	1422
TGCAGGACCAGAGAATTCGAATA CAAGCGGTAANNNTGCATCAGGT	943	TGCAGGACCAGAGAATTCGAATA CATATGTTCTNNNTGCATCAGGT	1183	TGCAGGACCAGAGAATTCGAATA CAGATACGCTNNNTGCATCAGGT	1423
TGCAGGACCAGAGAATTCGAATA CAGGAAACTGNNNTGCATCAGGT	944	TGCAGGACCAGAGAATTCGAATA CACCAGCGGTNNNTGCATCAGGT	1184	TGCAGGACCAGAGAATTCGAATA CACAGTATCGNNNTGCATCAGGT	1424
TGCAGGACCAGAGAATTCGAATA CAGGCCACGTNNNTGCATCAGGT	945	TGCAGGACCAGAGAATTCGAATA CACGGTTGATNNNTGCATCAGGT	1185	TGCAGGACCAGAGAATTCGAATA CACTCACTGTNNNTGCATCAGGT	1425
TGCAGGACCAGAGAATTCGAATA CATCATTGAANNNTGCATCAGGT	946	TGCAGGACCAGAGAATTCGAATA CACGCTGCAGNNNTGCATCAGGT	1186	TGCAGGACCAGAGAATTCGAATA CACCGTCAGGNNNTGCATCAGGT	1426
TGCAGGACCAGAGAATTCGAATA CAGCGTCAATNNNTGCATCAGGT	947	TGCAGGACCAGAGAATTCGAATA CAGTCTAAATNNNTGCATCAGGT	1187	TGCAGGACCAGAGAATTCGAATA CAGCTTCTGTNNNTGCATCAGGT	1427
TGCAGGACCAGAGAATTCGAATA CACGGAAGCGNNNTGCATCAGGT	948	TGCAGGACCAGAGAATTCGAATA CAGTAATTACNNNTGCATCAGGT	1188	TGCAGGACCAGAGAATTCGAATA CATTATATTTNNNTGCATCAGGT	1428
TGCAGGACCAGAGAATTCGAATA CAGTTCGAACNNNTGCATCAGGT	949	TGCAGGACCAGAGAATTCGAATA CATTCCGGTTNNNTGCATCAGGT	1189	TGCAGGACCAGAGAATTCGAATA CAGGTTJACGNNNTGCATCAGGT	1429
TGCAGGACCAGAGAATTCGAATA CAGGCCCCTTNNNTGCATCAGGT	950	TGCAGGACCAGAGAATTCGAATA CAGAGCGTGGNNNTGCATCAGGT	1190	TGCAGGACCAGAGAATTCGAATA CAGGACGATANNNTGCATCAGGT	1430
TGCAGGACCAGAGAATTCGAATA CAATGGCTCANNNTGCATCAGGT	951	TGCAGGACCAGAGAATTCGAATA CAATTTACTCNNNTGCATCAGGT	1191	TGCAGGACCAGAGAATTCGAATA CAAGTCAGGANNNTGCATCAGGT	1431
TGCAGGACCAGAGAATTCGAATA CATTGACGGTNNNTGCATCAGGT	952	TGCAGGACCAGAGAATTCGAATA CACAACACTGNNNTGCATCAGGT	1192	TGCAGGACCAGAGAATTCGAATA CACTACGAACNNNTGCATCAGGT	1432

图13G

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATGGACGTTNNNTGCATCAGGT	953	TGCAGGACCAGAGAATTCGAATA CACCGCGGCGNNNTGCATCAGGT	1193	TGCAGGACCAGAGAATTCGAATA CAAGCCATGTNNNTGCATCAGGT	1433
TGCAGGACCAGAGAATTCGAATA CATGACAGTCNNNTGCATCAGGT	954	TGCAGGACCAGAGAATTCGAATA CACTAAGCTGNNNTGCATCAGGT	1194	TGCAGGACCAGAGAATTCGAATA CATTCCAGTGNNNTGCATCAGGT	1434
TGCAGGACCAGAGAATTCGAATA CACTACCTGTNNNTGCATCAGGT	955	TGCAGGACCAGAGAATTCGAATA CAATTCAAGTNNNTGCATCAGGT	1195	TGCAGGACCAGAGAATTCGAATA CAACCCTGTTNNNTGCATCAGGT	1435
TGCAGGACCAGAGAATTCGAATA CAAGGTCCCGNNNTGCATCAGGT	956	TGCAGGACCAGAGAATTCGAATA CAATTGGCGTNNNTGCATCAGGT	1196	TGCAGGACCAGAGAATTCGAATA CACCCTTTCTNNNTGCATCAGGT	1436
TGCAGGACCAGAGAATTCGAATA CATTCATCTANNNTGCATCAGGT	957	TGCAGGACCAGAGAATTCGAATA CATGATTTGANNNTGCATCAGGT	1197	TGCAGGACCAGAGAATTCGAATA CAATGTTGATNNNTGCATCAGGT	1437
TGCAGGACCAGAGAATTCGAATA CAGATAAAGTNNNTGCATCAGGT	958	TGCAGGACCAGAGAATTCGAATA CAACTGCCGGNNNTGCATCAGGT	1198	TGCAGGACCAGAGAATTCGAATA CACACTGGCGNNNTGCATCAGGT	1438
TGCAGGACCAGAGAATTCGAATA CACACGGAAANNNTGCATCAGGT	959	TGCAGGACCAGAGAATTCGAATA CATTAATCCTNNNTGCATCAGGT	1199	TGCAGGACCAGAGAATTCGAATA CATTCGGTAGNNNTGCATCAGGT	1439
TGCAGGACCAGAGAATTCGAATA CATGTGAGGANNNTGCATCAGGT	960	TGCAGGACCAGAGAATTCGAATA CACTACGCTTNNNTGCATCAGGT	1200	TGCAGGACCAGAGAATTCGAATA CAACCCTGCCNNNTGCATCAGGT	1440
TGCAGGACCAGAGAATTCGAATA CACGTGATCANNNTGCATCAGGT	961	TGCAGGACCAGAGAATTCGAATA CATAGCTATANNNTGCATCAGGT	1201	TGCAGGACCAGAGAATTCGAATA CAGTACCTAGNNNTGCATCAGGT	1441
TGCAGGACCAGAGAATTCGAATA CATGCGTTGANNNTGCATCAGGT	962	TGCAGGACCAGAGAATTCGAATA CATGCACTCTNNNTGCATCAGGT	1202	TGCAGGACCAGAGAATTCGAATA CACGATAATTNNNTGCATCAGGT	1442
TGCAGGACCAGAGAATTCGAATA CATCGCTCCGNNNTGCATCAGGT	963	TGCAGGACCAGAGAATTCGAATA CAGTGCTCCCNNNTGCATCAGGT	1203	TGCAGGACCAGAGAATTCGAATA CAGCCAACCGNNNTGCATCAGGT	1443
TGCAGGACCAGAGAATTCGAATA CACCAGTCAANNNTGCATCAGGT	964	TGCAGGACCAGAGAATTCGAATA CAGCCACCAGNNNTGCATCAGGT	1204	TGCAGGACCAGAGAATTCGAATA CATAACATCANNNTGCATCAGGT	1444
TGCAGGACCAGAGAATTCGAATA CACACATTCCNNNTGCATCAGGT	965	TGCAGGACCAGAGAATTCGAATA CATTATGTGANNNTGCATCAGGT	1205	TGCAGGACCAGAGAATTCGAATA CAGCAAGAACNNNTGCATCAGGT	1445
TGCAGGACCAGAGAATTCGAATA CAGGTATATTNNNTGCATCAGGT	966	TGCAGGACCAGAGAATTCGAATA CAATACTCCCNNNTGCATCAGGT	1206	TGCAGGACCAGAGAATTCGAATA CAACGTGATCNNNTGCATCAGGT	1446
TGCAGGACCAGAGAATTCGAATA CATAAGATGANNNTGCATCAGGT	967	TGCAGGACCAGAGAATTCGAATA CAACTATGGCNNNTGCATCAGGT	1207	TGCAGGACCAGAGAATTCGAATA CACGTTCCTANNNTGCATCAGGT	1447
TGCAGGACCAGAGAATTCGAATA CATTAAAATTNNNTGCATCAGGT	968	TGCAGGACCAGAGAATTCGAATA CAACGGCCTGNNNTGCATCAGGT	1208	TGCAGGACCAGAGAATTCGAATA CAATGCCAGTNNNTGCATCAGGT	1448

图13H

池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACAGGCTCGNNNACGTATGCCA	1449	TGCAGGACCAGAGAATTCGAATA CAACTACCAGNNNACGTATGCCA	1689	TGCAGGACCAGAGAATTCGAATA CAGAACGCCCNNNACGTATGCCA	1929
TGCAGGACCAGAGAATTCGAATA CATTGAAGCCNNNACGTATGCCA	1450	TGCAGGACCAGAGAATTCGAATA CATTATTGAGNNNACGTATGCCA	1690	TGCAGGACCAGAGAATTCGAATA CAACCAATGCNNNACGTATGCCA	1930
TGCAGGACCAGAGAATTCGAATA CACACAGAGANNNACGTATGCCA	1451	TGCAGGACCAGAGAATTCGAATA CAACTGTGTGNNNACGTATGCCA	1691	TGCAGGACCAGAGAATTCGAATA CAGACCGATTNNNACGTATGCCA	1931
TGCAGGACCAGAGAATTCGAATA CAGGACTCCGNNNACGTATGCCA	1452	TGCAGGACCAGAGAATTCGAATA CATTGATCGGNNNACGTATGCCA	1692	TGCAGGACCAGAGAATTCGAATA CAATGTTATGNNNACGTATGCCA	1932
TGCAGGACCAGAGAATTCGAATA CATTGGTTAANNNACGTATGCCA	1453	TGCAGGACCAGAGAATTCGAATA CATTCTCGGTNNNACGTATGCCA	1693	TGCAGGACCAGAGAATTCGAATA CAGGAAGAAGNNNACGTATGCCA	1933
TGCAGGACCAGAGAATTCGAATA CATACTAACANNNACGTATGCCA	1454	TGCAGGACCAGAGAATTCGAATA CACCAGTTAGNNNACGTATGCCA	1694	TGCAGGACCAGAGAATTCGAATA CAGTTATACANNNACGTATGCCA	1934
TGCAGGACCAGAGAATTCGAATA CAGTCCAATGNNNACGTATGCCA	1455	TGCAGGACCAGAGAATTCGAATA CAAGAACAATNNNACGTATGCCA	1695	TGCAGGACCAGAGAATTCGAATA CACCTCCTAANNNACGTATGCCA	1935
TGCAGGACCAGAGAATTCGAATA CAAGGCACGGNNNACGTATGCCA	1456	TGCAGGACCAGAGAATTCGAATA CATCCGAAGTNNNACGTATGCCA	1696	TGCAGGACCAGAGAATTCGAATA CATAAACATCNNNACGTATGCCA	1936
TGCAGGACCAGAGAATTCGAATA CAATCATGTANNNACGTATGCCA	1457	TGCAGGACCAGAGAATTCGAATA CATCGGCTCCNNNACGTATGCCA	1697	TGCAGGACCAGAGAATTCGAATA CACGGCGGTTNNNACGTATGCCA	1937
TGCAGGACCAGAGAATTCGAATA CAAAAAGGTTNNNACGTATGCCA	1458	TGCAGGACCAGAGAATTCGAATA CACAGTCCCCNNNACGTATGCCA	1698	TGCAGGACCAGAGAATTCGAATA CATTAACAACNNNACGTATGCCA	1938
TGCAGGACCAGAGAATTCGAATA CAAGGCACCCNNNACGTATGCCA	1459	TGCAGGACCAGAGAATTCGAATA CAGTCAACTGNNNACGTATGCCA	1699	TGCAGGACCAGAGAATTCGAATA CATGGCCATANNNACGTATGCCA	1939
TGCAGGACCAGAGAATTCGAATA CATTGAAAGANNNACGTATGCCA	1460	TGCAGGACCAGAGAATTCGAATA CAGGCGGCTTNNNACGTATGCCA	1700	TGCAGGACCAGAGAATTCGAATA CAGAGTGATGNNNACGTATGCCA	1940
TGCAGGACCAGAGAATTCGAATA CACTCGACTTNNNACGTATGCCA	1461	TGCAGGACCAGAGAATTCGAATA CAATGCGCTANNNACGTATGCCA	1701	TGCAGGACCAGAGAATTCGAATA CACTAATGCGNNNACGTATGCCA	1941
TGCAGGACCAGAGAATTCGAATA CAGCGAATTCNNNACGTATGCCA	1462	TGCAGGACCAGAGAATTCGAATA CAGCTCCGGANNNACGTATGCCA	1702	TGCAGGACCAGAGAATTCGAATA CAAGGTTAAANNNACGTATGCCA	1942
TGCAGGACCAGAGAATTCGAATA CACCCCCGCGNNNACGTATGCCA	1463	TGCAGGACCAGAGAATTCGAATA CATGCTGGCGNNNACGTATGCCA	1703	TGCAGGACCAGAGAATTCGAATA CAACAGTACCNNNACGTATGCCA	1943
TGCAGGACCAGAGAATTCGAATA CAGATAAGCGNNNACGTATGCCA	1464	TGCAGGACCAGAGAATTCGAATA CACTAACGTGNNNACGTATGCCA	1704	TGCAGGACCAGAGAATTCGAATA CAATGTGATTNNNACGTATGCCA	1944
TGCAGGACCAGAGAATTCGAATA CAGAACGATGNNNACGTATGCCA	1465	TGCAGGACCAGAGAATTCGAATA CAGAATACAANNNACGTATGCCA	1705	TGCAGGACCAGAGAATTCGAATA CAGCTGCCGANNNACGTATGCCA	1945
TGCAGGACCAGAGAATTCGAATA CAAATATTATNNNACGTATGCCA	1466	TGCAGGACCAGAGAATTCGAATA CAATGACAAANNNACGTATGCCA	1706	TGCAGGACCAGAGAATTCGAATA CACTTTTTAGNNNACGTATGCCA	1946
TGCAGGACCAGAGAATTCGAATA CATAAGCTATNNNACGTATGCCA	1467	TGCAGGACCAGAGAATTCGAATA CAACGGCTCGNNNACGTATGCCA	1707	TGCAGGACCAGAGAATTCGAATA CATCCCAAAGNNNACGTATGCCA	1947
TGCAGGACCAGAGAATTCGAATA CAACTCGGCGNNNACGTATGCCA	1468	TGCAGGACCAGAGAATTCGAATA CAACAGATAANNNACGTATGCCA	1708	TGCAGGACCAGAGAATTCGAATA CAGACACTACNNNACGTATGCCA	1948
TGCAGGACCAGAGAATTCGAATA CACGACTGCGNNNACGTATGCCA	1469	TGCAGGACCAGAGAATTCGAATA CATGTAGCCANNNACGTATGCCA	1709	TGCAGGACCAGAGAATTCGAATA CAATACCGACNNNACGTATGCCA	1949
TGCAGGACCAGAGAATTCGAATA CATCCGACTTNNNACGTATGCCA	1470	TGCAGGACCAGAGAATTCGAATA CACTTCTGCANNNACGTATGCCA	1710	TGCAGGACCAGAGAATTCGAATA CAGTTGAAAANNNACGTATGCCA	1950
TGCAGGACCAGAGAATTCGAATA CAGGAGGAGGNNNACGTATGCCA	1471	TGCAGGACCAGAGAATTCGAATA CATTACCTTANNNACGTATGCCA	1711	TGCAGGACCAGAGAATTCGAATA CAATTTCCTANNNACGTATGCCA	1951
TGCAGGACCAGAGAATTCGAATA CACAGGCAGGNNNACGTATGCCA	1472	TGCAGGACCAGAGAATTCGAATA CATCAATTCTNNNACGTATGCCA	1712	TGCAGGACCAGAGAATTCGAATA CAACGTTCAGNNNACGTATGCCA	1952
TGCAGGACCAGAGAATTCGAATA CAATCTCATTNNNACGTATGCCA	1473	TGCAGGACCAGAGAATTCGAATA CAAGGTTCGTNNNACGTATGCCA	1713	TGCAGGACCAGAGAATTCGAATA CAAATACGAANNNACGTATGCCA	1953
TGCAGGACCAGAGAATTCGAATA CAAGGCGATANNNACGTATGCCA	1474	TGCAGGACCAGAGAATTCGAATA CAATTTTAAANNNACGTATGCCA	1714	TGCAGGACCAGAGAATTCGAATA CACCAACTGANNNACGTATGCCA	1954
TGCAGGACCAGAGAATTCGAATA CACCTAGATGNNNACGTATGCCA	1475	TGCAGGACCAGAGAATTCGAATA CATTGCAGACNNNACGTATGCCA	1715	TGCAGGACCAGAGAATTCGAATA CAATCCGTCTNNNACGTATGCCA	1955
TGCAGGACCAGAGAATTCGAATA CACCTACCATNNNACGTATGCCA	1476	TGCAGGACCAGAGAATTCGAATA CACCCCACTGNNNACGTATGCCA	1716	TGCAGGACCAGAGAATTCGAATA CACGTCCGCTNNNACGTATGCCA	1956

图14A

池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAACGTCCANNNACGTATGCCA	1477	TGCAGGACCAGAGAATTCGAATA CACTTCCTGANNNACGTATGCCA	1717	TGCAGGACCAGAGAATTCGAATA CATATACACANNNACGTATGCCA	1957
TGCAGGACCAGAGAATTCGAATA CAGCACTTAGNNNACGTATGCCA	1478	TGCAGGACCAGAGAATTCGAATA CAAGAACTCCNNNACGTATGCCA	1718	TGCAGGACCAGAGAATTCGAATA CACTCTATATNNNACGTATGCCA	1958
TGCAGGACCAGAGAATTCGAATA CAGATCGGAANNNACGTATGCCA	1479	TGCAGGACCAGAGAATTCGAATA CACTGTAAGCNNNACGTATGCCA	1719	TGCAGGACCAGAGAATTCGAATA CACTCACAGANNNACGTATGCCA	1959
TGCAGGACCAGAGAATTCGAATA CACGCCATAANNNACGTATGCCA	1480	TGCAGGACCAGAGAATTCGAATA CAAGTCGATCNNNACGTATGCCA	1720	TGCAGGACCAGAGAATTCGAATA CAGCCGGTGTNNNACGTATGCCA	1960
TGCAGGACCAGAGAATTCGAATA CATTAAGTTGNNNACGTATGCCA	1481	TGCAGGACCAGAGAATTCGAATA CAGTAATAGANNNACGTATGCCA	1721	TGCAGGACCAGAGAATTCGAATA CATACGTCAGNNNACGTATGCCA	1961
TGCAGGACCAGAGAATTCGAATA CAGCCAGCTGNNNACGTATGCCA	1482	TGCAGGACCAGAGAATTCGAATA CACGGAGCTCNNNACGTATGCCA	1722	TGCAGGACCAGAGAATTCGAATA CATCTGCTCANNNACGTATGCCA	1962
TGCAGGACCAGAGAATTCGAATA CAAAACGGCTNNNACGTATGCCA	1483	TGCAGGACCAGAGAATTCGAATA CATTGTCTTANNNACGTATGCCA	1723	TGCAGGACCAGAGAATTCGAATA CAACGTATATNNNACGTATGCCA	1963
TGCAGGACCAGAGAATTCGAATA CAGTATTTCTNNNACGTATGCCA	1484	TGCAGGACCAGAGAATTCGAATA CATTTTCGTANNNACGTATGCCA	1724	TGCAGGACCAGAGAATTCGAATA CACGAGCCACNNNACGTATGCCA	1964
TGCAGGACCAGAGAATTCGAATA CAGGTCTCCCNNNACGTATGCCA	1485	TGCAGGACCAGAGAATTCGAATA CAAACGGAACNNNACGTATGCCA	1725	TGCAGGACCAGAGAATTCGAATA CATCGCTCTANNNACGTATGCCA	1965
TGCAGGACCAGAGAATTCGAATA CACAAGTCTGNNNACGTATGCCA	1486	TGCAGGACCAGAGAATTCGAATA CAACCACGGCNNNACGTATGCCA	1726	TGCAGGACCAGAGAATTCGAATA CACGGAAGATNNNACGTATGCCA	1966
TGCAGGACCAGAGAATTCGAATA CAGAGCACAANNNACGTATGCCA	1487	TGCAGGACCAGAGAATTCGAATA CAGAGTATTTNNNACGTATGCCA	1727	TGCAGGACCAGAGAATTCGAATA CATTAGCGGTNNNACGTATGCCA	1967
TGCAGGACCAGAGAATTCGAATA CATCAAACCGNNNACGTATGCCA	1488	TGCAGGACCAGAGAATTCGAATA CACCCGCCTANNNACGTATGCCA	1728	TGCAGGACCAGAGAATTCGAATA CATGAGCTCANNNACGTATGCCA	1968
TGCAGGACCAGAGAATTCGAATA CATTCCGCTANNNACGTATGCCA	1489	TGCAGGACCAGAGAATTCGAATA CAAGTATGCCNNNACGTATGCCA	1729	TGCAGGACCAGAGAATTCGAATA CATACACGTGNNNACGTATGCCA	1969
TGCAGGACCAGAGAATTCGAATA CAATTGCACGNNNACGTATGCCA	1490	TGCAGGACCAGAGAATTCGAATA CATAGCAGCTNNNACGTATGCCA	1730	TGCAGGACCAGAGAATTCGAATA CATAGTGTATNNNACGTATGCCA	1970
TGCAGGACCAGAGAATTCGAATA CAATACCTAANNNACGTATGCCA	1491	TGCAGGACCAGAGAATTCGAATA CACGCGTGACNNNACGTATGCCA	1731	TGCAGGACCAGAGAATTCGAATA CACATTAGGCNNNACGTATGCCA	1971
TGCAGGACCAGAGAATTCGAATA CAGGACCGGANNNACGTATGCCA	1492	TGCAGGACCAGAGAATTCGAATA CAAAATACGANNNACGTATGCCA	1732	TGCAGGACCAGAGAATTCGAATA CAACACCACANNNACGTATGCCA	1972
TGCAGGACCAGAGAATTCGAATA CATGTCCCGCNNNACGTATGCCA	1493	TGCAGGACCAGAGAATTCGAATA CACTAGATATNNNACGTATGCCA	1733	TGCAGGACCAGAGAATTCGAATA CAGTGCGTCGNNNACGTATGCCA	1973
TGCAGGACCAGAGAATTCGAATA CAGCCCCAGANNNACGTATGCCA	1494	TGCAGGACCAGAGAATTCGAATA CAATGTTGGCNNNACGTATGCCA	1734	TGCAGGACCAGAGAATTCGAATA CATATGTTCNNNACGTATGCCA	1974
TGCAGGACCAGAGAATTCGAATA CACAAGCCCGNNNACGTATGCCA	1495	TGCAGGACCAGAGAATTCGAATA CACTACGCAANNNACGTATGCCA	1735	TGCAGGACCAGAGAATTCGAATA CAGTGGTCGCNNNACGTATGCCA	1975
TGCAGGACCAGAGAATTCGAATA CAGCCATTGANNNACGTATGCCA	1496	TGCAGGACCAGAGAATTCGAATA CATTTCTGTANNNACGTATGCCA	1736	TGCAGGACCAGAGAATTCGAATA CACTGGACCGNNNACGTATGCCA	1976
TGCAGGACCAGAGAATTCGAATA CATGAACACCNNNACGTATGCCA	1497	TGCAGGACCAGAGAATTCGAATA CACCTCCCTCNNNACGTATGCCA	1737	TGCAGGACCAGAGAATTCGAATA CAGGCGTGTCNNNACGTATGCCA	1977
TGCAGGACCAGAGAATTCGAATA CAGAATCCGTNNNACGTATGCCA	1498	TGCAGGACCAGAGAATTCGAATA CAGACTTGACNNNACGTATGCCA	1738	TGCAGGACCAGAGAATTCGAATA CAAGTCTAATNNNACGTATGCCA	1978
TGCAGGACCAGAGAATTCGAATA CATTAATCGANNNACGTATGCCA	1499	TGCAGGACCAGAGAATTCGAATA CAGTCATCGANNNACGTATGCCA	1739	TGCAGGACCAGAGAATTCGAATA CACTCATGCTNNNACGTATGCCA	1979
TGCAGGACCAGAGAATTCGAATA CACGCCACTCNNNACGTATGCCA	1500	TGCAGGACCAGAGAATTCGAATA CAATCTAGTANNNACGTATGCCA	1740	TGCAGGACCAGAGAATTCGAATA CAAGTTCTCCNNNACGTATGCCA	1980
TGCAGGACCAGAGAATTCGAATA CACCCTTAGTNNNACGTATGCCA	1501	TGCAGGACCAGAGAATTCGAATA CACGAAGATGNNNACGTATGCCA	1741	TGCAGGACCAGAGAATTCGAATA CAGTGAAGGTNNNACGTATGCCA	1981
TGCAGGACCAGAGAATTCGAATA CATTTCCTGGNNNACGTATGCCA	1502	TGCAGGACCAGAGAATTCGAATA CAATTTGCAANNNACGTATGCCA	1742	TGCAGGACCAGAGAATTCGAATA CAGTTTTAAGNNNACGTATGCCA	1982
TGCAGGACCAGAGAATTCGAATA CATTCAACGGNNNACGTATGCCA	1503	TGCAGGACCAGAGAATTCGAATA CAGACCGGCTNNNACGTATGCCA	1743	TGCAGGACCAGAGAATTCGAATA CAAAAGCAATNNNACGTATGCCA	1983
TGCAGGACCAGAGAATTCGAATA CATTGAGGAGNNNACGTATGCCA	1504	TGCAGGACCAGAGAATTCGAATA CACTTGTCACNNNACGTATGCCA	1744	TGCAGGACCAGAGAATTCGAATA CATGAAGCGANNNACGTATGCCA	1984
TGCAGGACCAGAGAATTCGAATA CATTCACGCTNNNACGTATGCCA	1505	TGCAGGACCAGAGAATTCGAATA CACTCGTAAGNNNACGTATGCCA	1745	TGCAGGACCAGAGAATTCGAATA CAGTAGTGCTNNNACGTATGCCA	1985

图14B

池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATCGCGGTGNNNACGTATGCCA	1506	TGCAGGACCAGAGAATTCGAATA CAGCCTTACTNNNNACGTATGCCA	1746	TGCAGGACCAGAGAATTCGAATA CAACTATGTANNNACGTATGCCA	1986
TGCAGGACCAGAGAATTCGAATA CAAATTCCGGNNNACGTATGCCA	1507	TGCAGGACCAGAGAATTCGAATA CAGCATGTGTNNNACGTATGCCA	1747	TGCAGGACCAGAGAATTCGAATA CAGAAGTTCCNNNACGTATGCCA	1987
TGCAGGACCAGAGAATTCGAATA CACGTCATGANNNACGTATGCCA	1508	TGCAGGACCAGAGAATTCGAATA CACTACTGTCNNNACGTATGCCA	1748	TGCAGGACCAGAGAATTCGAATA CACGGTGCTGNNNACGTATGCCA	1988
TGCAGGACCAGAGAATTCGAATA CACGTTTATTNNNCTAGCGTTAC	1509	TGCAGGACCAGAGAATTCGAATA CAATCTAACANNNCTAGCGTTAC	1749	TGCAGGACCAGAGAATTCGAATA CATGCAAATTNNNCTAGCGTTAC	1989
TGCAGGACCAGAGAATTCGAATA CACTGCACGGNNNCTAGCGTTAC	1510	TGCAGGACCAGAGAATTCGAATA CAACGATTCGNNNCTAGCGTTAC	1750	TGCAGGACCAGAGAATTCGAATA CAACTTGTGGNNNCTAGCGTTAC	1990
TGCAGGACCAGAGAATTCGAATA CAACCTTGTCNNNCTAGCGTTAC	1511	TGCAGGACCAGAGAATTCGAATA CAAAACCTTANNNCTAGCGTTAC	1751	TGCAGGACCAGAGAATTCGAATA CATCGCTGCCNNNCTAGCGTTAC	1991
TGCAGGACCAGAGAATTCGAATA CATCCACCCGNNNCTAGCGTTAC	1512	TGCAGGACCAGAGAATTCGAATA CACGTAAAAANNNCTAGCGTTAC	1752	TGCAGGACCAGAGAATTCGAATA CATCCGTTCTNNNCTAGCGTTAC	1992
TGCAGGACCAGAGAATTCGAATA CAAAGGCCGGNNNCTAGCGTTAC	1513	TGCAGGACCAGAGAATTCGAATA CATCTGAGACNNNCTAGCGTTAC	1753	TGCAGGACCAGAGAATTCGAATA CACGGTACTANNNCTAGCGTTAC	1993
TGCAGGACCAGAGAATTCGAATA CAGGCAATAGNNNCTAGCGTTAC	1514	TGCAGGACCAGAGAATTCGAATA CATGGCGATTNNNCTAGCGTTAC	1754	TGCAGGACCAGAGAATTCGAATA CAAGATATCTNNNCTAGCGTTAC	1994
TGCAGGACCAGAGAATTCGAATA CACGCTAGCGNNNCTAGCGTTAC	1515	TGCAGGACCAGAGAATTCGAATA CACATCTTGCNNNCTAGCGTTAC	1755	TGCAGGACCAGAGAATTCGAATA CACTCAAGTGNNNCTAGCGTTAC	1995
TGCAGGACCAGAGAATTCGAATA CATGTTCTATNNNCTAGCGTTAC	1516	TGCAGGACCAGAGAATTCGAATA CATCTTTCGGNNNCTAGCGTTAC	1756	TGCAGGACCAGAGAATTCGAATA CAACCTCCTANNNCTAGCGTTAC	1996
TGCAGGACCAGAGAATTCGAATA CATTAATATANNNCTAGCGTTAC	1517	TGCAGGACCAGAGAATTCGAATA CAGCGAACAANNNCTAGCGTTAC	1757	TGCAGGACCAGAGAATTCGAATA CAAGCAATTTNNNCTAGCGTTAC	1997
TGCAGGACCAGAGAATTCGAATA CAATATGGTTNNNCTAGCGTTAC	1518	TGCAGGACCAGAGAATTCGAATA CAGAGTAGACNNNCTAGCGTTAC	1758	TGCAGGACCAGAGAATTCGAATA CAGCCCCGAANNNCTAGCGTTAC	1998
TGCAGGACCAGAGAATTCGAATA CAGCTGGTTANNNCTAGCGTTAC	1519	TGCAGGACCAGAGAATTCGAATA CACTCATGGANNNCTAGCGTTAC	1759	TGCAGGACCAGAGAATTCGAATA CACCAAATCGNNNCTAGCGTTAC	1999
TGCAGGACCAGAGAATTCGAATA CAAGACTGAGNNNCTAGCGTTAC	1520	TGCAGGACCAGAGAATTCGAATA CATTCCCGGCNNNCTAGCGTTAC	1760	TGCAGGACCAGAGAATTCGAATA CAGATCGGTTNNNCTAGCGTTAC	2000
TGCAGGACCAGAGAATTCGAATA CAGACTTGCANNNCTAGCGTTAC	1521	TGCAGGACCAGAGAATTCGAATA CATGGCCTAANNNCTAGCGTTAC	1761	TGCAGGACCAGAGAATTCGAATA CAACCCCTGCNNNCTAGCGTTAC	2001
TGCAGGACCAGAGAATTCGAATA CAGTCTATCCNNNCTAGCGTTAC	1522	TGCAGGACCAGAGAATTCGAATA CAAGCGCAAANNNCTAGCGTTAC	1762	TGCAGGACCAGAGAATTCGAATA CAACCCACTTNNNCTAGCGTTAC	2002
TGCAGGACCAGAGAATTCGAATA CAAGCTATCGNNNCTAGCGTTAC	1523	TGCAGGACCAGAGAATTCGAATA CAATAGAAACNNNCTAGCGTTAC	1763	TGCAGGACCAGAGAATTCGAATA CAAGACCTTGNNNCTAGCGTTAC	2003
TGCAGGACCAGAGAATTCGAATA CAGGCGAACGNNNCTAGCGTTAC	1524	TGCAGGACCAGAGAATTCGAATA CATCGGCTGGNNNCTAGCGTTAC	1764	TGCAGGACCAGAGAATTCGAATA CACCTTGATCNNNCTAGCGTTAC	2004
TGCAGGACCAGAGAATTCGAATA CAACGAATGGNNNCTAGCGTTAC	1525	TGCAGGACCAGAGAATTCGAATA CAGTGCTCGGNNNCTAGCGTTAC	1765	TGCAGGACCAGAGAATTCGAATA CAAAGTATTCNNNCTAGCGTTAC	2005
TGCAGGACCAGAGAATTCGAATA CATCATGCTCNNNCTAGCGTTAC	1526	TGCAGGACCAGAGAATTCGAATA CAAATGCCACNNNCTAGCGTTAC	1766	TGCAGGACCAGAGAATTCGAATA CACATCCAAGNNNCTAGCGTTAC	2006
TGCAGGACCAGAGAATTCGAATA CATTGCTTATNNNCTAGCGTTAC	1527	TGCAGGACCAGAGAATTCGAATA CAATCACGTGNNNCTAGCGTTAC	1767	TGCAGGACCAGAGAATTCGAATA CACACAAGTCNNNCTAGCGTTAC	2007
TGCAGGACCAGAGAATTCGAATA CAAAGCCAGANNNCTAGCGTTAC	1528	TGCAGGACCAGAGAATTCGAATA CATCACGACANNNCTAGCGTTAC	1768	TGCAGGACCAGAGAATTCGAATA CATAAAATGGNNNCTAGCGTTAC	2008
TGCAGGACCAGAGAATTCGAATA CAGCAGCTCGNNNCTAGCGTTAC	1529	TGCAGGACCAGAGAATTCGAATA CATGTTACGGNNNCTAGCGTTAC	1769	TGCAGGACCAGAGAATTCGAATA CAATCTACAANNNCTAGCGTTAC	2009
TGCAGGACCAGAGAATTCGAATA CACCGAGTCGNNNCTAGCGTTAC	1530	TGCAGGACCAGAGAATTCGAATA CATTACCGCTNNNCTAGCGTTAC	1770	TGCAGGACCAGAGAATTCGAATA CAGCGAGAATNNNCTAGCGTTAC	2010
TGCAGGACCAGAGAATTCGAATA CAAACAGACGNNNCTAGCGTTAC	1531	TGCAGGACCAGAGAATTCGAATA CACCCTTTAGNNNCTAGCGTTAC	1771	TGCAGGACCAGAGAATTCGAATA CAGTAGCCATNNNCTAGCGTTAC	2011
TGCAGGACCAGAGAATTCGAATA CACCCAAACANNNCTAGCGTTAC	1532	TGCAGGACCAGAGAATTCGAATA CAGTCTTGAGNNNCTAGCGTTAC	1772	TGCAGGACCAGAGAATTCGAATA CAAAGGCAGTNNNCTAGCGTTAC	2012
TGCAGGACCAGAGAATTCGAATA CAAAGGCGATNNNCTAGCGTTAC	1533	TGCAGGACCAGAGAATTCGAATA CACTTTGACCNNNCTAGCGTTAC	1773	TGCAGGACCAGAGAATTCGAATA CAGTAGACTCNNNCTAGCGTTAC	2013
TGCAGGACCAGAGAATTCGAATA CACCTTAAAANNNCTAGCGTTAC	1534	TGCAGGACCAGAGAATTCGAATA CACTTCTCAGNNNCTAGCGTTAC	1774	TGCAGGACCAGAGAATTCGAATA CAGGTATGCTNNNCTAGCGTTAC	2014

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACATACCTCNNNCTAGCGTTAC	1535	TGCAGGACCAGAGAATTCGAATA CATGTTGCAGNNNCTAGCGTTAC	1775	TGCAGGACCAGAGAATTCGAATA CAGGTTTTAANNNCTAGCGTTAC	2015
TGCAGGACCAGAGAATTCGAATA CAGCCAATCANNNCTAGCGTTAC	1536	TGCAGGACCAGAGAATTCGAATA CAAACCCAACNNNCTAGCGTTAC	1776	TGCAGGACCAGAGAATTCGAATA CAACAGAAGCNNNCTAGCGTTAC	2016
TGCAGGACCAGAGAATTCGAATA CACTTAGGCANNNCTAGCGTTAC	1537	TGCAGGACCAGAGAATTCGAATA CATAAGCACCNNNCTAGCGTTAC	1777	TGCAGGACCAGAGAATTCGAATA CACAGCACGCNNNCTAGCGTTAC	2017
TGCAGGACCAGAGAATTCGAATA CACGCACCAGNNNCTAGCGTTAC	1538	TGCAGGACCAGAGAATTCGAATA CAGATGTAAANNNCTAGCGTTAC	1778	TGCAGGACCAGAGAATTCGAATA CAACCGTAACNNNCTAGCGTTAC	2018
TGCAGGACCAGAGAATTCGAATA CATTCCCGTANNNCTAGCGTTAC	1539	TGCAGGACCAGAGAATTCGAATA CAGTTATGCGNNNCTAGCGTTAC	1779	TGCAGGACCAGAGAATTCGAATA CAGGAAGCCGNNNCTAGCGTTAC	2019
TGCAGGACCAGAGAATTCGAATA CATTCAGAATNNNCTAGCGTTAC	1540	TGCAGGACCAGAGAATTCGAATA CAGCGCGGAANNNCTAGCGTTAC	1780	TGCAGGACCAGAGAATTCGAATA CAGAGGATCANNNCTAGCGTTAC	2020
TGCAGGACCAGAGAATTCGAATA CAGGCATTACNNNCTAGCGTTAC	1541	TGCAGGACCAGAGAATTCGAATA CAAGATTTGTNNNCTAGCGTTAC	1781	TGCAGGACCAGAGAATTCGAATA CACGGTTCGGNNNCTAGCGTTAC	2021
TGCAGGACCAGAGAATTCGAATA CAAACCAAAANNNCTAGCGTTAC	1542	TGCAGGACCAGAGAATTCGAATA CACACAGCTANNNCTAGCGTTAC	1782	TGCAGGACCAGAGAATTCGAATA CAATCCACAGNNNCTAGCGTTAC	2022
TGCAGGACCAGAGAATTCGAATA CAACGCTGTANNNCTAGCGTTAC	1543	TGCAGGACCAGAGAATTCGAATA CAACGGCAGGNNNCTAGCGTTAC	1783	TGCAGGACCAGAGAATTCGAATA CAGAGACCCCNNNCTAGCGTTAC	2023
TGCAGGACCAGAGAATTCGAATA CAACGATCTGNNNCTAGCGTTAC	1544	TGCAGGACCAGAGAATTCGAATA CATACGGAAGNNNCTAGCGTTAC	1784	TGCAGGACCAGAGAATTCGAATA CACTCCGGAGNNNCTAGCGTTAC	2024
TGCAGGACCAGAGAATTCGAATA CAGCATGAGANNNCTAGCGTTAC	1545	TGCAGGACCAGAGAATTCGAATA CACTCGATGANNNCTAGCGTTAC	1785	TGCAGGACCAGAGAATTCGAATA CATCGCCTCGNNNCTAGCGTTAC	2025
TGCAGGACCAGAGAATTCGAATA CAGTAAGTCCNNNCTAGCGTTAC	1546	TGCAGGACCAGAGAATTCGAATA CATCCCCCCTNNNCTAGCGTTAC	1786	TGCAGGACCAGAGAATTCGAATA CATCATTCCGNNNCTAGCGTTAC	2026
TGCAGGACCAGAGAATTCGAATA CAAAGCGAGTNNNCTAGCGTTAC	1547	TGCAGGACCAGAGAATTCGAATA CACCATCTACNNNCTAGCGTTAC	1787	TGCAGGACCAGAGAATTCGAATA CAGAACTACCNNNCTAGCGTTAC	2027
TGCAGGACCAGAGAATTCGAATA CAAGATCTGCNNNCTAGCGTTAC	1548	TGCAGGACCAGAGAATTCGAATA CAAAGCAGGTNNNCTAGCGTTAC	1788	TGCAGGACCAGAGAATTCGAATA CATAATTTTTNNNCTAGCGTTAC	2028
TGCAGGACCAGAGAATTCGAATA CACCCGTCACNNNCTAGCGTTAC	1549	TGCAGGACCAGAGAATTCGAATA CAAAGTCAAANNNCTAGCGTTAC	1789	TGCAGGACCAGAGAATTCGAATA CAGATTGTGCNNNCTAGCGTTAC	2029
TGCAGGACCAGAGAATTCGAATA CATCCTCGCGNNNCTAGCGTTAC	1550	TGCAGGACCAGAGAATTCGAATA CAATTCGACGNNNCTAGCGTTAC	1790	TGCAGGACCAGAGAATTCGAATA CATGGCGCACNNNCTAGCGTTAC	2030
TGCAGGACCAGAGAATTCGAATA CACATGTCGANNNCTAGCGTTAC	1551	TGCAGGACCAGAGAATTCGAATA CAACCAGCCGNNNCTAGCGTTAC	1791	TGCAGGACCAGAGAATTCGAATA CAAAATCAGANNNCTAGCGTTAC	2031
TGCAGGACCAGAGAATTCGAATA CAAACGGTTCNNNCTAGCGTTAC	1552	TGCAGGACCAGAGAATTCGAATA CATAGTCGGTNNNCTAGCGTTAC	1792	TGCAGGACCAGAGAATTCGAATA CAAGGCTATCNNNCTAGCGTTAC	2032
TGCAGGACCAGAGAATTCGAATA CACCCCAATTNNNCTAGCGTTAC	1553	TGCAGGACCAGAGAATTCGAATA CATGCGCATANNNCTAGCGTTAC	1793	TGCAGGACCAGAGAATTCGAATA CATCTTGTGCNNNCTAGCGTTAC	2033
TGCAGGACCAGAGAATTCGAATA CAACCGTTCTNNNCTAGCGTTAC	1554	TGCAGGACCAGAGAATTCGAATA CATAGAACCCNNNCTAGCGTTAC	1794	TGCAGGACCAGAGAATTCGAATA CACCATTCCANNNCTAGCGTTAC	2034
TGCAGGACCAGAGAATTCGAATA CAACTCTAAANNNCTAGCGTTAC	1555	TGCAGGACCAGAGAATTCGAATA CAGGTTTGTGNNNCTAGCGTTAC	1795	TGCAGGACCAGAGAATTCGAATA CATAGATTACNNNCTAGCGTTAC	2035
TGCAGGACCAGAGAATTCGAATA CAATGAGCTCNNNCTAGCGTTAC	1556	TGCAGGACCAGAGAATTCGAATA CAAAGTTTGTNNNCTAGCGTTAC	1796	TGCAGGACCAGAGAATTCGAATA CAGTTTGCTCNNNCTAGCGTTAC	2036
TGCAGGACCAGAGAATTCGAATA CATCTAAGGCNNNCTAGCGTTAC	1557	TGCAGGACCAGAGAATTCGAATA CATTAGCGACNNNCTAGCGTTAC	1797	TGCAGGACCAGAGAATTCGAATA CATCTTCGGTNNNCTAGCGTTAC	2037
TGCAGGACCAGAGAATTCGAATA CACAATAGCCNNNCTAGCGTTAC	1558	TGCAGGACCAGAGAATTCGAATA CAGATATATCNNNCTAGCGTTAC	1798	TGCAGGACCAGAGAATTCGAATA CAAGTAGTCCNNNCTAGCGTTAC	2038
TGCAGGACCAGAGAATTCGAATA CATCTTGCGTNNNCTAGCGTTAC	1559	TGCAGGACCAGAGAATTCGAATA CAAACTGTGCNNNCTAGCGTTAC	1799	TGCAGGACCAGAGAATTCGAATA CACGGTGTATNNNCTAGCGTTAC	2039
TGCAGGACCAGAGAATTCGAATA CACAAGAGCANNNCTAGCGTTAC	1560	TGCAGGACCAGAGAATTCGAATA CACGAATGGANNNCTAGCGTTAC	1800	TGCAGGACCAGAGAATTCGAATA CACTGTTTGCNNNCTAGCGTTAC	2040
TGCAGGACCAGAGAATTCGAATA CAGCTTGGATNNNCTAGCGTTAC	1561	TGCAGGACCAGAGAATTCGAATA CACTTCGTTGNNNCTAGCGTTAC	1801	TGCAGGACCAGAGAATTCGAATA CAAACGTTGCNNNCTAGCGTTAC	2041
TGCAGGACCAGAGAATTCGAATA CACTAAATACNNNCTAGCGTTAC	1562	TGCAGGACCAGAGAATTCGAATA CATCGTGGTANNNCTAGCGTTAC	1802	TGCAGGACCAGAGAATTCGAATA CAATAAATGGNNNCTAGCGTTAC	2042
TGCAGGACCAGAGAATTCGAATA CACCTAAAATNNNCTAGCGTTAC	1563	TGCAGGACCAGAGAATTCGAATA CAGCAAAATANNNCTAGCGTTAC	1803	TGCAGGACCAGAGAATTCGAATA CAACGCGTGCNNNCTAGCGTTAC	2043

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGAACCTCANNNCTAGCGTTAC	1564	TGCAGGACCAGAGAATTCGAATA CAAGACTAAANNNCTAGCGTTAC	1804	TGCAGGACCAGAGAATTCGAATA CACGTTGGTANNNCTAGCGTTAC	2044
TGCAGGACCAGAGAATTCGAATA CAGAGGCCTCNNNCTAGCGTTAC	1565	TGCAGGACCAGAGAATTCGAATA CATGCGAGTTNNNCTAGCGTTAC	1805	TGCAGGACCAGAGAATTCGAATA CAAGGCGTAANNNCTAGCGTTAC	2045
TGCAGGACCAGAGAATTCGAATA CAAGGTGATGNNNCTAGCGTTAC	1566	TGCAGGACCAGAGAATTCGAATA CAGTTCTGAGNNNCTAGCGTTAC	1806	TGCAGGACCAGAGAATTCGAATA CATGCCTATCNNNCTAGCGTTAC	2046
TGCAGGACCAGAGAATTCGAATA CAACGCGTTANNNCTAGCGTTAC	1567	TGCAGGACCAGAGAATTCGAATA CATCGGCGTGNNNCTAGCGTTAC	1807	TGCAGGACCAGAGAATTCGAATA CAAAAGCTCCNNNCTAGCGTTAC	2047
TGCAGGACCAGAGAATTCGAATA CAGGTGGCTCNNNCTAGCGTTAC	1568	TGCAGGACCAGAGAATTCGAATA CAGATCCGGCNNNCTAGCGTTAC	1808	TGCAGGACCAGAGAATTCGAATA CAAGGACGATNNNCTAGCGTTAC	2048
TGCAGGACCAGAGAATTCGAATA CAGAGATCAGNNNGATCGACATG	1569	TGCAGGACCAGAGAATTCGAATA CAGTGTATGCNNNGATCGACATG	1809	TGCAGGACCAGAGAATTCGAATA CACTTGAAGCNNNGATCGACATG	2049
TGCAGGACCAGAGAATTCGAATA CATACGTGTGNNNGATCGACATG	1570	TGCAGGACCAGAGAATTCGAATA CAAGTATTTGNNNGATCGACATG	1810	TGCAGGACCAGAGAATTCGAATA CATGCCCTCGNNNGATCGACATG	2050
TGCAGGACCAGAGAATTCGAATA CAAGTTATCANNNGATCGACATG	1571	TGCAGGACCAGAGAATTCGAATA CAAGTAAAACNNNGATCGACATG	1811	TGCAGGACCAGAGAATTCGAATA CAAGCGAAACNNNGATCGACATG	2051
TGCAGGACCAGAGAATTCGAATA CACAGTGATCNNNGATCGACATG	1572	TGCAGGACCAGAGAATTCGAATA CAAGCCACCGNNNGATCGACATG	1812	TGCAGGACCAGAGAATTCGAATA CATAGAGTGGNNNGATCGACATG	2052
TGCAGGACCAGAGAATTCGAATA CATACGCGGCNNNGATCGACATG	1573	TGCAGGACCAGAGAATTCGAATA CAAAGTGTCCNNNGATCGACATG	1813	TGCAGGACCAGAGAATTCGAATA CAAGCAGCAANNNGATCGACATG	2053
TGCAGGACCAGAGAATTCGAATA CAGTGTGTACNNNGATCGACATG	1574	TGCAGGACCAGAGAATTCGAATA CACTATTTGTNNNGATCGACATG	1814	TGCAGGACCAGAGAATTCGAATA CACCTATTATNNNGATCGACATG	2054
TGCAGGACCAGAGAATTCGAATA CAGTGTTTAANNNGATCGACATG	1575	TGCAGGACCAGAGAATTCGAATA CAGTGTATCGNNNGATCGACATG	1815	TGCAGGACCAGAGAATTCGAATA CAGCGACGAGNNNGATCGACATG	2055
TGCAGGACCAGAGAATTCGAATA CAGCTCTACTNNNGATCGACATG	1576	TGCAGGACCAGAGAATTCGAATA CAATAGTATCNNNGATCGACATG	1816	TGCAGGACCAGAGAATTCGAATA CAACGATTTANNNGATCGACATG	2056
TGCAGGACCAGAGAATTCGAATA CATTGTGCTCNNNGATCGACATG	1577	TGCAGGACCAGAGAATTCGAATA CACCGCTGAGNNNGATCGACATG	1817	TGCAGGACCAGAGAATTCGAATA CAAATTGTTGNNNGATCGACATG	2057
TGCAGGACCAGAGAATTCGAATA CATATAAGCTNNNGATCGACATG	1578	TGCAGGACCAGAGAATTCGAATA CATTATTTTANNNGATCGACATG	1818	TGCAGGACCAGAGAATTCGAATA CACATTAAGTNNNGATCGACATG	2058
TGCAGGACCAGAGAATTCGAATA CAAGAACGACNNNGATCGACATG	1579	TGCAGGACCAGAGAATTCGAATA CAACAAGACGNNNGATCGACAIG	1819	TGCAGGACCAGAGAATTCGAATA CAGACGGAGCNNNGATCGACATG	2059
TGCAGGACCAGAGAATTCGAATA CATACGATATNNNGATCGACATG	1580	TGCAGGACCAGAGAATTCGAATA CATAAGTATCNNNGATCGACATG	1820	TGCAGGACCAGAGAATTCGAATA CACCGATAGTNNNGATCGACATG	2060
TGCAGGACCAGAGAATTCGAATA CATAAACCTANNNGATCGACATG	1581	TGCAGGACCAGAGAATTCGAATA CAGGCACACCNNNGATCGACATG	1821	TGCAGGACCAGAGAATTCGAATA CAAGTATTGTNNNGATCGACATG	2061
TGCAGGACCAGAGAATTCGAATA CATAACGTTANNNGATCGACATG	1582	TGCAGGACCAGAGAATTCGAATA CAGTACCTCTNNNGATCGACATG	1822	TGCAGGACCAGAGAATTCGAATA CATTTCGGCTNNNGATCGACATG	2062
TGCAGGACCAGAGAATTCGAATA CAGCACGTGCNNNGATCGACATG	1583	TGCAGGACCAGAGAATTCGAATA CACTGTGATGNNNGATCGACATG	1823	TGCAGGACCAGAGAATTCGAATA CAGTAGACAGNNNGATCGACATG	2063
TGCAGGACCAGAGAATTCGAATA CACCCTCGACNNNGATCGACATG	1584	TGCAGGACCAGAGAATTCGAATA CAACAAGGACNNNGATCGACATG	1824	TGCAGGACCAGAGAATTCGAATA CAACGAAGTGNNNGATCGACATG	2064
TGCAGGACCAGAGAATTCGAATA CATTGCATCCNNNGATCGACATG	1585	TGCAGGACCAGAGAATTCGAATA CAAGAGGCTANNNGATCGACAIG	1825	TGCAGGACCAGAGAATTCGAATA CACGTCTTTGNNNGATCGACATG	2065
TGCAGGACCAGAGAATTCGAATA CATCAACTGGNNNGATCGACATG	1586	TGCAGGACCAGAGAATTCGAATA CAATTGAGTTNNNGATCGACATG	1826	TGCAGGACCAGAGAATTCGAATA CAACACAGGANNNGATCGACATG	2066
TGCAGGACCAGAGAATTCGAATA CAATTGCCCTNNNGATCGACATG	1587	TGCAGGACCAGAGAATTCGAATA CACGTTCTCANNNGATCGACATG	1827	TGCAGGACCAGAGAATTCGAATA CAGGTCACTANNNGATCGACATG	2067
TGCAGGACCAGAGAATTCGAATA CATACATGTANNNGATCGACATG	1588	TGCAGGACCAGAGAATTCGAATA CAGGTAGCTTNNNGATCGACATG	1828	TGCAGGACCAGAGAATTCGAATA CAGAACGAACNNNGATCGACATG	2068
TGCAGGACCAGAGAATTCGAATA CAGACTTGGTNNNGATCGACATG	1589	TGCAGGACCAGAGAATTCGAATA CATCCTTGTGNNNGATCGACATG	1829	TGCAGGACCAGAGAATTCGAATA CACCTAACTCNNNGATCGACATG	2069
TGCAGGACCAGAGAATTCGAATA CAGTCCCATTNNNGATCGACATG	1590	TGCAGGACCAGAGAATTCGAATA CAGCCGACACNNNGATCGACATG	1830	TGCAGGACCAGAGAATTCGAATA CAAAGACTTTNNNGATCGACATG	2070
TGCAGGACCAGAGAATTCGAATA CAAGATGGTGNNNGATCGACATG	1591	TGCAGGACCAGAGAATTCGAATA CAACTAGAGGNNNGATCGACATG	1831	TGCAGGACCAGAGAATTCGAATA CAGGACATCTNNNGATCGACATG	2071
TGCAGGACCAGAGAATTCGAATA CAGACACAGANNNGATCGACATG	1592	TGCAGGACCAGAGAATTCGAATA CAACAGTCGTNNNGATCGACATG	1832	TGCAGGACCAGAGAATTCGAATA CAGGCGTAAANNNGATCGACATG	2072

图14E

池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACGCGTTTTNNNGATCGACATG	1593	TGCAGGACCAGAGAATTCGAATA CACGAGGCGANNNGATCGACATG	1833	TGCAGGACCAGAGAATTCGAATA CAGTACCAGTNNNGATCGACATG	2073
TGCAGGACCAGAGAATTCGAATA CACCCAGAGCNNNGATCGACATG	1594	TGCAGGACCAGAGAATTCGAATA CAACCGAAAGNNNGATCGACATG	1834	TGCAGGACCAGAGAATTCGAATA CAGAATTTACNNNGATCGACATG	2074
TGCAGGACCAGAGAATTCGAATA CACGCAGCTGNNNGATCGACATG	1595	TGCAGGACCAGAGAATTCGAATA CAGTTTGAGCNNNGATCGACATG	1835	TGCAGGACCAGAGAATTCGAATA CAAACACCCANNNGATCGACATG	2075
TGCAGGACCAGAGAATTCGAATA CACTTTGGCTNNNGATCGACATG	1596	TGCAGGACCAGAGAATTCGAATA CAGTATGCGTNNNGATCGACATG	1836	TGCAGGACCAGAGAATTCGAATA CAAGTTATTGNNNGATCGACATG	2076
TGCAGGACCAGAGAATTCGAATA CAGTTGATCGNNNGATCGACATG	1597	TGCAGGACCAGAGAATTCGAATA CAATGTAACTNNNGATCGACATG	1837	TGCAGGACCAGAGAATTCGAATA CACTTCTTTTNNNGATCGACATG	2077
TGCAGGACCAGAGAATTCGAATA CAGTGAAGTGNNNGATCGACATG	1598	TGCAGGACCAGAGAATTCGAATA CAAGACGTAGNNNGATCGACATG	1838	TGCAGGACCAGAGAATTCGAATA CAGAGCTCCGNNNGATCGACATG	2078
TGCAGGACCAGAGAATTCGAATA CACACGTTGANNNGATCGACATG	1599	TGCAGGACCAGAGAATTCGAATA CATTGGCGCGNNNGATCGACATG	1839	TGCAGGACCAGAGAATTCGAATA CAGAACCCCGNNNGATCGACATG	2079
TGCAGGACCAGAGAATTCGAATA CACAATCCAGNNNGATCGACATG	1600	TGCAGGACCAGAGAATTCGAATA CAGGACTCATNNNGATCGACATG	1840	TGCAGGACCAGAGAATTCGAATA CAATTGTGATNNNGATCGACATG	2080
TGCAGGACCAGAGAATTCGAATA CAGCGCAGAGNNNGATCGACATG	1601	TGCAGGACCAGAGAATTCGAATA CAGTCCGGTGNNNGATCGACATG	1841	TGCAGGACCAGAGAATTCGAATA CAAGTTCTTTNNNGATCGACATG	2081
TGCAGGACCAGAGAATTCGAATA CACTCTGATCNNNGATCGACATG	1602	TGCAGGACCAGAGAATTCGAATA CAGCAAGCCCNNNGATCGACATG	1842	TGCAGGACCAGAGAATTCGAATA CAGCACGGTCNNNGATCGACATG	2082
TGCAGGACCAGAGAATTCGAATA CATATGCCAGNNNGATCGACATG	1603	TGCAGGACCAGAGAATTCGAATA CAAGCATGGANNNGATCGACATG	1843	TGCAGGACCAGAGAATTCGAATA CAGTATCCCTNNNGATCGACATG	2083
TGCAGGACCAGAGAATTCGAATA CAGTTGGTCANNNGATCGACATG	1604	TGCAGGACCAGAGAATTCGAATA CAAGCAGCCCNNNGATCGACATG	1844	TGCAGGACCAGAGAATTCGAATA CAGCAAGTGANNNGATCGACATG	2084
TGCAGGACCAGAGAATTCGAATA CACCTCTCGGNNNGATCGACATG	1605	TGCAGGACCAGAGAATTCGAATA CAATCTCTATNNNGATCGACATG	1845	TGCAGGACCAGAGAATTCGAATA CATAAGATAGNNNGATCGACATG	2085
TGCAGGACCAGAGAATTCGAATA CATGGTACACNNNGATCGACATG	1606	TGCAGGACCAGAGAATTCGAATA CATAATGCCGNNNGATCGACATG	1846	TGCAGGACCAGAGAATTCGAATA CAGCAATCTGNNNGATCGACATG	2086
TGCAGGACCAGAGAATTCGAATA CACCTCGGCTNNNGATCGACATG	1607	TGCAGGACCAGAGAATTCGAATA CACAGGCGGANNNGATCGACATG	1847	TGCAGGACCAGAGAATTCGAATA CACTGCCAGGNNNGATCGACATG	2087
TGCAGGACCAGAGAATTCGAATA CAGCGACGGANNNGATCGACATG	1608	TGCAGGACCAGAGAATTCGAATA CAGCGAATGANNNGATCGACATG	1848	TGCAGGACCAGAGAATTCGAATA CAGGTTTATANNNGATCGACATG	2088
TGCAGGACCAGAGAATTCGAATA CACCCTGATTNNNGATCGACATG	1609	TGCAGGACCAGAGAATTCGAATA CAAGCGTACTNNNGATCGACATG	1849	TGCAGGACCAGAGAATTCGAATA CAAACTTGCGNNNGATCGACATG	2089
TGCAGGACCAGAGAATTCGAATA CAATTCTCTANNNGATCGACATG	1610	TGCAGGACCAGAGAATTCGAATA CACCCAGGCANNNGATCGACATG	1850	TGCAGGACCAGAGAATTCGAATA CACCAACGCGNNNGATCGACATG	2090
TGCAGGACCAGAGAATTCGAATA CACTGTCAAGNNNGATCGACATG	1611	TGCAGGACCAGAGAATTCGAATA CAGGCCTGTGNNNGATCGACATG	1851	TGCAGGACCAGAGAATTCGAATA CATGGAAGACNNNGATCGACATG	2091
TGCAGGACCAGAGAATTCGAATA CAATTACCGGNNNGATCGACATG	1612	TGCAGGACCAGAGAATTCGAATA CACCTAGGCGNNNGATCGACATG	1852	TGCAGGACCAGAGAATTCGAATA CAATTGAAGANNNGATCGACATG	2092
TGCAGGACCAGAGAATTCGAATA CATAATATCGNNNGATCGACATG	1613	TGCAGGACCAGAGAATTCGAATA CACCGTTTTGNNNGATCGACATG	1853	TGCAGGACCAGAGAATTCGAATA CATTTTCACANNNGATCGACATG	2093
TGCAGGACCAGAGAATTCGAATA CAATAGACTTNNNGATCGACATG	1614	TGCAGGACCAGAGAATTCGAATA CAGACGCACCNNNGATCGACATG	1854	TGCAGGACCAGAGAATTCGAATA CAACGAACTCNNNGATCGACATG	2094
TGCAGGACCAGAGAATTCGAATA CACCTGATAGNNNGATCGACATG	1615	TGCAGGACCAGAGAATTCGAATA CAACTTATGANNNGATCGACATG	1855	TGCAGGACCAGAGAATTCGAATA CAAGGCCGTCNNNGATCGACATG	2095
TGCAGGACCAGAGAATTCGAATA CAGCCGCACANNNGATCGACATG	1616	TGCAGGACCAGAGAATTCGAATA CAAGATCAAANNNGATCGACATG	1856	TGCAGGACCAGAGAATTCGAATA CATTGGAGCTNNNGATCGACATG	2096
TGCAGGACCAGAGAATTCGAATA CACGAATATTNNNGATCGACATG	1617	TGCAGGACCAGAGAATTCGAATA CATACTTCCGNNNGATCGACATG	1857	TGCAGGACCAGAGAATTCGAATA CAACAGACAGNNNGATCGACATG	2097
TGCAGGACCAGAGAATTCGAATA CAGTCAATCGNNNGATCGACATG	1618	TGCAGGACCAGAGAATTCGAATA CACGTTAGACNNNGATCGACATG	1858	TGCAGGACCAGAGAATTCGAATA CAATCGTCAGNNNGATCGACATG	2098
TGCAGGACCAGAGAATTCGAATA CATCAGCCCCNNNGATCGACATG	1619	TGCAGGACCAGAGAATTCGAATA CAGGAGTTAGNNNGATCGACATG	1859	TGCAGGACCAGAGAATTCGAATA CATTATGTCTNNNGATCGACATG	2099
TGCAGGACCAGAGAATTCGAATA CAGGAGTTCTNNNGATCGACATG	1620	TGCAGGACCAGAGAATTCGAATA CAGACCTCTTNNNGATCGACATG	1860	TGCAGGACCAGAGAATTCGAATA CAGTCACGATNNNGATCGACATG	2100
TGCAGGACCAGAGAATTCGAATA CAGTCAATCCNNNGATCGACATG	1621	TGCAGGACCAGAGAATTCGAATA CAGCCCGCAANNNGATCGACATG	1861	TGCAGGACCAGAGAATTCGAATA CACATTCTGCNNNGATCGACATG	2101

图14F

池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAACGATTATNNNGATCGACATG	1622	TGCAGGACCAGAGAATTCGAATA CAGAACCCATNNNGATCGACATG	1862	TGCAGGACCAGAGAATTCGAATA CAGAAAAACTNNNGATCGACATG	2102
TGCAGGNCCAGAGAATTCGAATA CACAATCCGANNNGATCGACATG	1623	TGCAGGACCAGAGAATTCGAATA CACCACTGCCNNNGATCGACATG	1863	TGCAGGACCAGAGAATTCGAATA CATCGTCGTTNNNGATCGACATG	2103
TGCAGGACCAGAGAATTCGAATA CAGGCAATGANNNGATCGACATG	1624	TGCAGGACCAGAGAATTCGAATA CACTAATTTCNNNGATCGACATG	1864	TGCAGGACCAGAGAATTCGAATA CAATTGTGGCNNNGATCGACATG	2104
TGCAGGACCAGAGAATTCGAATA CACTGTCAGANNNGATCGACATG	1625	TGCAGGACCAGAGAATTCGAATA CACGGTCCAGNNNGATCGACATG	1865	TGCAGGACCAGAGAATTCGAATA CAACTGGACTNNNGATCGACATG	2105
TGCAGGACCAGAGAATTCGAATA CACAGACCTANNNGATCGACATG	1626	TGCAGGACCAGAGAATTCGAATA CATTTCGCACNNNGATCGACATG	1866	TGCAGGACCAGAGAATTCGAATA CACGTTGTTCNNNGATCGACATG	2106
TGCAGGACCAGAGAATTCGAATA CAGATCATCGNNNGATCGACATG	1627	TGCAGGACCAGAGAATTCGAATA CAGGATAAGCNNNGATCGACATG	1867	TGCAGGACCAGAGAATTCGAATA CACAAGACCTNNNGATCGACATG	2107
TGCAGGACCAGAGAATTCGAATA CAGAACGAGTNNNGATCGACATG	1628	TGCAGGACCAGAGAATTCGAATA CACTCGCAGGNNNGATCGACATG	1868	TGCAGGACCAGAGAATTCGAATA CATACCCCCGNNNGATCGACATG	2108
TGCAGGACCAGAGAATTCGAATA CATCGGTGATNNNTGCATCAGGT	1629	TGCAGGACCAGAGAATTCGAATA CAACTGAAAANNNTGCATCAGGT	1869	TGCAGGACCAGAGAATTCGAATA CACCTACCGCNNNTGCATCAGGT	2109
TGCAGGACCAGAGAATTCGAATA CAATTGCAATNNNTGCATCAGGT	1630	TGCAGGACCAGAGAATTCGAATA CAAGTCTTTTNNNTGCATCAGGT	1870	TGCAGGACCAGAGAATTCGAATA CAAGACAGTGNNNTGCATCAGGT	2110
TGCAGGACCAGAGAATTCGAATA CATTAACGATNNNTGCATCAGGT	1631	TGCAGGACCAGAGAATTCGAATA CAGGTGTTACNNNTGCATCAGGT	1871	TGCAGGACCAGAGAATTCGAATA CAGTCCTATCNNNTGCATCAGGT	2111
TGCAGGACCAGAGAATTCGAATA CATGTACGTGNNNTGCATCAGGT	1632	TGCAGGACCAGAGAATTCGAATA CATATCCGCTNNNTGCATCAGGT	1872	TGCAGGACCAGAGAATTCGAATA CAGGCGCTCTNNNTGCATCAGGT	2112
TGCAGGACCAGAGAATTCGAATA CAGCGTGTGCNNNTGCATCAGGT	1633	TGCAGGACCAGAGAATTCGAATA CAGCGTGAGGNNNTGCATCAGGT	1873	TGCAGGACCAGAGAATTCGAATA CATTGATTCTNNNTGCATCAGGT	2113
TGCAGGACCAGAGAATTCGAATA CACCATATAANNNTGCATCAGGT	1634	TGCAGGACCAGAGAATTCGAATA CAGCCGTTCCNNNTGCATCAGGT	1874	TGCAGGACCAGACAATTCGAATA CAATAATGTCNNNTGCATCAGGT	2114
TGCAGGACCAGAGAATTCGAATA CAAAATTGAGNNNTGCATCAGGT	1635	TGCAGGACCAGAGAATTCGAATA CATTACCCCANNNTGCATCAGGT	1875	TGCAGGACCAGAGAATTCGAATA CAGAGTTAAANNNTGCATCAGGT	2115
TGCAGGACCAGAGAATTCGAATA CAGTATCACGNNNTGCATCAGGT	1636	TGCAGGACCAGAGAATTCGAATA CAGACCCCTCNNNTGCATCAGGT	1876	TGCAGGACCAGAGAATTCGAATA CACGACACATNNNTGCATCAGGT	2116
TGCAGGACCAGAGAATTCGAATA CACCTTAGGANNNTGCATCAGGT	1637	TGCAGGACCAGAGAATTCGAATA CATATGGAGGNNNTGCATCAGGT	1877	TGCAGGACCAGAGAATTCGAATA CATTGGCCGGNNNTGCATCAGGT	2117
TGCAGGACCAGAGAATTCGAATA CATAAAAAGCNNNTGCATCAGGT	1638	TGCAGGACCAGAGAATTCGAATA CAGACGGTCCNNNTGCATCAGGT	1878	TGCAGGACCAGAGAATTCGAATA CAGAACTTTANNNTGCATCAGGT	2118
TGCAGGACCAGAGAATTCGAATA CATGCATCCTNNNTGCATCAGGT	1639	TGCAGGACCAGAGAATTCGAATA CACTACGACANNNTGCATCAGGT	1879	TGCAGGACCAGAGAATTCGAATA CACCAAAACCNNNTGCATCAGGT	2119
TGCAGGACCAGAGAATTCGAATA CACAGCCTGGNNNTGCATCAGGT	1640	TGCAGGACCAGAGAATTCGAATA CATGACTACGNNNTGCATCAGGT	1880	TGCAGGACCAGAGAATTCGAATA CAATACCAGCNNNTGCATCAGGT	2120
TGCAGGACCAGAGAATTCGAATA CACACACTAGNNNTGCATCAGGT	1641	TGCAGGACCAGAGAATTCGAATA CAGGACGTTTNNNTGCATCAGGT	1881	TGCAGGACCAGAGAATTCGAATA CAAGTAGAATNNNTGCATCAGGT	2121
TGCAGGACCAGAGAATTCGAATA CACGTATCCTNNNTGCATCAGGT	1642	TGCAGGACCAGAGAATTCGAATA CAAAGCCTCANNNTGCATCAGGT	1882	TGCAGGACCAGAGAATTCGAATA CAGTACTACGNNNTGCATCAGGT	2122
TGCAGGACCAGAGAATTCGAATA CATGGCTTAGNNNTGCATCAGGT	1643	TGCAGGACCAGAGAATTCGAATA CACTTTAAAGNNNTGCATCAGGT	1883	TGCAGGACCAGAGAATTCGAATA CATTCATGAANNNTGCATCAGGT	2123
TGCAGGACCAGAGAATTCGAATA CACTGTCATCNNNTGCATCAGGT	1644	TGCAGGACCAGAGAATTCGAATA CATTTGATTCNNNTGCATCAGGT	1884	TGCAGGACCAGAGAATTCGAATA CACCTAAGGTNNNTGCATCAGGT	2124
TGCAGGACCAGAGAATTCGAATA CATCCAGAACNNNTGCATCAGGT	1645	TGCAGGACCAGAGAATTCGAATA CACTGTATTTNNNTGCATCAGGT	1885	TGCAGGACCAGAGAATTCGAATA CAACAAAGGCNNNTGCATCAGGT	2125
TGCAGGACCAGAGAATTCGAATA CACGAGTACTNNNTGCATCAGGT	1646	TGCAGGACCAGAGAATTCGAATA CATTAATTGGNNNTGCATCAGGT	1886	TGCAGGACCAGAGAATTCGAATA CAGAGGCAGCNNNTGCATCAGGT	2126
TGCAGGACCAGAGAATTCGAATA CAGATCGAGANNNTGCATCAGGT	1647	TGCAGGACCAGAGAATTCGAATA CACAGAGTTCNNNTGCATCAGGT	1887	TGCAGGACCAGAGAATTCGAATA CACTACTCGTNNNTGCATCAGGT	2127
TGCAGGACCAGAGAATTCGAATA CAAGAATAACNNNTGCATCAGGT	1648	TGCAGGACCAGAGAATTCGAATA CAGCATCTAGNNNTGCATCAGGT	1888	TGCAGGACCAGAGAATTCGAATA CAGGTAGTGANNNTGCATCAGGT	2128
TGCAGGACCAGAGAATTCGAATA CAGCGCACCANNNTGCATCAGGT	1649	TGCAGGACCAGAGAATTCGAATA CATTGTCTATNNNTGCATCAGGT	1889	TGCAGGACCAGAGAATTCGAATA CACCACCACCNNNTGCATCAGGT	2129
TGCAGGACCAGAGAATTCGAATA CACAGCAACTNNNTGCATCAGGT	1650	TGCAGGACCAGAGAATTCGAATA CACATCCTGTNNNTGCATCAGGT	1890	TGCAGGACCAGAGAATTCGAATA CATGTGTGACNNNTGCATCAGGT	2130

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGTGCCATANNNTGCATCAGGT	1651	TGCAGGACCAGAGAATTCGAATA CACATTCAAANNNTGCATCAGGT	1891	TGCAGGACCAGAGAATTCGAATA CACACCCTGCNNNTGCATCAGGT	2131
TGCAGGACCAGAGAATTCGAATA CAATCTATTCNNNTGCATCAGGT	1652	TGCAGGACCAGAGAATTCGAATA CAAAAGCCTCNNNTGCATCAGGT	1892	TGCAGGACCAGAGAATTCGAATA CATCGCCATTNNNTGCATCAGGT	2132
TGCAGGACCAGAGAATTCGAATA CAAGTATGTTNNNTGCATCAGGT	1653	TGCAGGACCAGAGAATTCGAATA CATGATCAATNNNTGCATCAGGT	1893	TGCAGGACCAGAGAATTCGAATA CAACTTCGCTNNNTGCATCAGGT	2133
TGCAGGACCAGAGAATTCGAATA CAGGTTCTTCNNNTGCATCAGGT	1654	TGCAGGACCAGAGAATTCGAATA CAATATGATCNNNTGCATCAGGT	1894	TGCAGGACCAGAGAATTCGAATA CATTGCTTTANNNTGCATCAGGT	2134
TGCAGGACCAGAGAATTCGAATA CATAGTGGCTNNNTGCATCAGGT	1655	TGCAGGACCAGAGAATTCGAATA CAGGACCGAGNNNTGCATCAGGT	1895	TGCAGGACCAGAGAATTCGAATA CAGCACGAGGNNNTGCATCAGGT	2135
TGCAGGACCAGAGAATTCGAATA CACGAACTTCNNNTGCATCAGGT	1656	TGCAGGACCAGAGAATTCGAATA CACCCCTAATNNNTGCATCAGGT	1896	TGCAGGACCAGAGAATTCGAATA CACGAATGTCNNNTGCATCAGGT	2136
TGCAGGACCAGAGAATTCGAATA CAAGTTCAATNNNTGCATCAGGT	1657	TGCAGGACCAGAGAATTCGAATA CACTCAAAGCNNNTGCATCAGGT	1897	TGCAGGACCAGAGAATTCGAATA CATGGCTAGTNNNTGCATCAGGT	2137
TGCAGGACCAGAGAATTCGAATA CATTGTTCGCNNNTGCATCAGGT	1658	TGCAGGACCAGAGAATTCGAATA CACTTCGTACNNNTGCATCAGGT	1898	TGCAGGACCAGAGAATTCGAATA CAGTGTTATANNNTGCATCAGGT	2138
TGCAGGACCAGAGAATTCGAATA CAGTCATGCANNNTGCATCAGGT	1659	TGCAGGACCAGAGAATTCGAATA CAATTGGCCANNNTGCATCAGGT	1899	TGCAGGACCAGAGAATTCGAATA CATTCCTTCCNNNTGCATCAGGT	2139
TGCAGGACCAGAGAATTCGAATA CACTGTAATANNNTGCATCAGGT	1660	TGCAGGACCAGAGAATTCGAATA CACGAAGGTANNNTGCATCAGGT	1900	TGCAGGACCAGAGAATTCGAATA CATCAACTAANNNTGCATCAGGT	2140
TGCAGGACCAGAGAATTCGAATA CATTCGGCCCNNNTGCATCAGGT	1661	TGCAGGACCAGAGAATTCGAATA CAGGCCTTGGNNNTGCATCAGGT	1901	TGCAGGACCAGAGAATTCGAATA CATTTACAAGNNNTGCATCAGGT	2141
TGCAGGACCAGAGAATTCGAATA CATCTCTCTCNNNTGCATCAGGT	1662	TGCAGGACCAGAGAATTCGAATA CAACAATATCNNNTGCATCAGGT	1902	TGCAGGACCAGAGAATTCGAATA CATCCTGCCGNNNTGCATCAGGT	2142
TGCAGGACCAGAGAATTCGAATA CACTTCGCGCNNNTGCATCAGGT	1663	TGCAGGACCAGAGAATTCGAATA CATCACAACGNNNTGCATCAGGT	1903	TGCAGGACCAGAGAATTCGAATA CATCGGCTAANNNTGCATCAGGT	2143
TGCAGGACCAGAGAATTCGAATA CAACAGATTTNNNTGCATCAGGT	1664	TGCAGGACCAGAGAATTCGAATA CAACTGTACGNNNTGCATCAGGT	1904	TGCAGGACCAGAGAATTCGAATA CAAGGAGCATNNNTGCATCAGGT	2144
TGCAGGACCAGAGAATTCGAATA CACAGACAAGNNNTGCATCAGGT	1665	TGCAGGACCAGAGAATTCGAATA CATCTCAATTNNNTGCATCAGGT	1905	TGCAGGACCAGAGAATTCGAATA CAGGAATACGNNNTGCATCAGGT	2145
TGCAGGACCAGAGAATTCGAATA CACAGCTACANNNTGCATCAGGT	1666	TGCAGGACCAGAGAATTCGAATA CAAGGCTCTANNNTGCATCAGGT	1906	TGCAGGACCAGAGAATTCGAATA CATGAGACGANNNTGCATCAGGT	2146
TGCAGGACCAGAGAATTCGAATA CAGACCGAGGNNNTGCATCAGGT	1667	TGCAGGACCAGAGAATTCGAATA CACCTTACCANNNTGCATCAGGT	1907	TGCAGGACCAGAGAATTCGAATA CACCACCAGGNNNTGCATCAGGT	2147
TGCAGGACCAGAGAATTCGAATA CACCTATAAANNNTGCATCAGGT	1668	TGCAGGACCAGAGAATTCGAATA CAGATTCCTCNNNTGCATCAGGT	1908	TGCAGGACCAGAGAATTCGAATA CAAGCTCATGNNNTGCATCAGGT	2148
TGCAGGACCAGAGAATTCGAATA CACCTAACCTNNNTGCATCAGGT	1669	TGCAGGACCAGAGAATTCGAATA CATGCCTGTTNNNTGCATCAGGT	1909	TGCAGGACCAGAGAATTCGAATA CATATACCGGNNNTGCATCAGGT	2149
TGCAGGACCAGAGAATTCGAATA CATTTAGCGGNNNTGCATCAGGT	1670	TGCAGGACCAGAGAATTCGAATA CATCACCAAGNNNTGCATCAGGT	1910	TGCAGGACCAGAGAATTCGAATA CAGATGCCATNNNTGCATCAGGT	2150
TGCAGGACCAGAGAATTCGAATA CATAAACCATNNNTGCATCAGGT	1671	TGCAGGACCAGAGAATTCGAATA CACTTCCGGCNNNTGCATCAGGT	1911	TGCAGGACCAGAGAATTCGAATA CATTGAGCTGNNNTGCATCAGGT	2151
TGCAGGACCAGAGAATTCGAATA CAGCTAACTGNNNTGCATCAGGT	1672	TGCAGGACCAGAGAATTCGAATA CAAAACGCAGNNNTGCATCAGGT	1912	TGCAGGACCAGAGAATTCGAATA CATAAATGGANNNTGCATCAGGT	2152
TGCAGGACCAGAGAATTCGAATA CAGTACAGAGNNNTGCATCAGGT	1673	TGCAGGACCAGAGAATTCGAATA CACGCATTCTNNNTGCATCAGGT	1913	TGCAGGACCAGAGAATTCGAATA CAACATGAAANNNTGCATCAGGT	2153
TGCAGGACCAGAGAATTCGAATA CACCGGACCANNNTGCATCAGGT	1674	TGCAGGACCAGAGAATTCGAATA CACGCCTATTNNNTGCATCAGGT	1914	TGCAGGACCAGAGAATTCGAATA CACTCGGAGCNNNTGCATCAGGT	2154
TGCAGGACCAGAGAATTCGAATA CACCTCTAGTNNNTGCATCAGGT	1675	TGCAGGACCAGAGAATTCGAATA CATCATCATTNNNTGCATCAGGT	1915	TGCAGGACCAGAGAATTCGAATA CAGTTTCGTGNNNTGCATCAGGT	2155
TGCAGGACCAGAGAATTCGAATA CAGCCCCTGTNNNTGCATCAGGT	1676	TGCAGGACCAGAGAATTCGAATA CAAATTCAGTNNNTGCATCAGGT	1916	TGCAGGACCAGAGAATTCGAATA CACAACATGCNNNTGCATCAGGT	2156
TGCAGGACCAGAGAATTCGAATA CACGGACTGCNNNTGCATCAGGT	1677	TGCAGGACCAGAGAATTCGAATA CAATTCTCGCNNNTGCATCAGGT	1917	TGCAGGACCAGAGAATTCGAATA CATGGTGCGCNNNTGCATCAGGT	2157
TGCAGGACCAGAGAATTCGAATA CACCCTCTGGNNNTGCATCAGGT	1678	TGCAGGACCAGAGAATTCGAATA CAATAGAGTANNNTGCATCAGGT	1918	TGCAGGACCAGAGAATTCGAATA CATACGGAGANNNTGCATCAGGT	2158
TGCAGGACCAGAGAATTCGAATA CAACCAAGTCNNNTGCATCAGGT	1679	TGCAGGACCAGAGAATTCGAATA CAGAGCGGACNNNTGCATCAGGT	1919	TGCAGGACCAGAGAATTCGAATA CAGGCGTGGANNNTGCATCAGGT	2159

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGCGTGGTCNNNTGCATCAGGT	1680	TGCAGGACCAGAGAATTCGAATA CAACTTTTACNNNTGCATCAGGT	1920	TGCAGGACCAGAGAATTCGAATA CATCTAACGGNNNTGCATCAGGT	2160
TGCAGGACCAGAGAATTCGAATA CACCGACGCANNNTGCATCAGGT	1681	TGCAGGACCAGAGAATTCGAATA CAAGTCAAAANNNTGCATCAGGT	1921	TGCAGGACCAGAGAATTCGAATA CATATAGCATNNNTGCATCAGGT	2161
TGCAGGACCAGAGAATTCGAATA CATTACCGGANNNTGCATCAGGT	1682	TGCAGGACCAGAGAATTCGAATA CATCTAGACGNNNTGCATCAGGT	1922	TGCAGGACCAGAGAATTCGAATA CACGCTCCGTNNNTGCATCAGGT	2162
TGCAGGACCAGAGAATTCGAATA CATCTTTGCGNNNTGCATCAGGT	1683	TGCAGGACCAGAGAATTCGAATA CACAAATGTTNNNTGCATCAGGT	1923	TGCAGGACCAGAGAATTCGAATA CAATACATGTNNNTGCATCAGGT	2163
TGCAGGACCAGAGAATTCGAATA CACACAATTANNNTGCATCAGGT	1684	TGCAGGACCAGAGAATTCGAATA CATGGCTTTCNNNTGCATCAGGT	1924	TGCAGGACCAGAGAATTCGAATA CAGGCTCGCANNNTGCATCAGGT	2164
TGCAGGACCAGAGAATTCGAATA CACCTACATCNNNTGCATCAGGT	1685	TGCAGGACCAGAGAATTCGAATA CARGGCTGTTNNNTGCATCAGGT	1925	TGCAGGACCAGAGAATTCGAATA CAGTTTAGTANNNTGCATCAGGT	2165
TGCAGGACCAGAGAATTCGAATA CAATTACTGANNNTGCATCAGGT	1686	TGCAGGACCAGAGAATTCGAATA CAAACTATTGNNNTGCATCAGGT	1926	TGCAGGACCAGAGAATTCGAATA CACTGAAATTNNNTGCATCAGGT	2166
TGCAGGACCAGAGAATTCGAATA CATTTTTCGANNNTGCATCAGGT	1687	TGCAGGACCAGAGAATTCGAATA CAATGTATTGNNNTGCATCAGGT	1927	TGCAGGACCAGAGAATTCGAATA CAAACACCTGNNNTGCATCAGGT	2167
TGCAGGACCAGAGAATTCGAATA CAAGGTGCTTNNNTGCATCAGGT	1688	TGCAGGACCAGAGAATTCGAATA CACGTCGGCANNNTGCATCAGGT	1928	TGCAGGACCAGAGAATTCGAATA CAGGAAAACCNNNTGCATCAGGT	2168

图14I

池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG CTTCTCANNNACGTATGCCA	2169	TGCAGGACCAGAGAATTCGAATACAA TACGTATNNNACGTATGCCA	2409	TGCAGGACCAGAGAATTCGAATACAT TGAGAAANNNACGTATGCCA	2649
TGCAGGACCAGAGAATTCGAATACAA TGCTACGNNNACGTATGCCA	2170	TGCAGGACCAGAGAATTCGAATACAA ACTAGCCNNNACGTATGCCA	2410	TGCAGGACCAGAGAATTCGAATACAA ATATCCANNNACGTATGCCA	2650
TGCAGGACCAGAGAATTCGAATACAT ACTCTCGNNNACGTATGCCA	2171	TGCAGGACCAGAGAATTCGAATACAC GGATTACNNNACGTATGCCA	2411	TGCAGGACCAGAGAATTCGAATACAA TGGACCTNNNACGTATGCCA	2651
TGCAGGACCAGAGAATTCGAATACAC GCTCGCANNNACGTATGCCA	2172	TGCAGGACCAGAGAATTCGAATACAG GACGCCTNNNACGTATGCCA	2412	TGCAGGACCAGAGAATTCGAATACAG GCATACTNNNACGTATGCCA	2652
TGCAGGACCAGAGAATTCGAATACAA CGGTTACNNNACGTATGCCA	2173	TGCAGGACCAGAGAATTCGAATACAC GTTAAATNNNACGTATGCCA	2413	TGCAGGACCAGAGAATTCGAATACAC TAAAAAGNNNACGTATGCCA	2653
TGCAGGACCAGAGAATTCGAATACAT AGCACACNNNACGTATGCCA	2174	TGCAGGACCAGAGAATTCGAATACAG GCTAGTTNNNACGTATGCCA	2414	TGCAGGACCAGAGAATTCGAATACAA TACATACNNNACGTATGCCA	2654
TGCAGGACCAGAGAATTCGAATACAC GTCTCTANNNACGTATGCCA	2175	TGCAGGACCAGAGAATTCGAATACAT CAGAAGGNNNACGTATGCCA	2415	TGCAGGACCAGAGAATTCGAATACAT ATGGCCANNNACGTATGCCA	2655
TGCAGGACCAGAGAATTCGAATACAG CTCCGCTNNNACGTATGCCA	2176	TGCAGGACCAGAGAATTCGAATACAA CCAACTGNNNACGTATGCCA	2416	TGCAGGACCAGAGAATTCGAATACAA TGATGCCNNNACGTATGCCA	2656
TGCAGGACCAGAGAATTCGAATACAG TGGCACCNNNACGTATGCCA	2177	TGCAGGACCAGAGAATTCGAATACAT CGACAACNNNACGTATGCCA	2417	TGCAGGACCAGAGAATTCGAATACAA GGTAGGTNNNACGTATGCCA	2657
TGCAGGACCAGAGAATTCGAATACAG CACTATGNNNACGTATGCCA	2178	TGCAGGACCAGAGAATTCGAATACAG TCGTACANNNACGTATGCCA	2418	TGCAGGACCAGAGAATTCGAATACAT CCCTAGTNNNACGTATGCCA	2658
TGCAGGACCAGAGAATTCGAATACAA ATAACGANNNACGTATGCCA	2179	TGCAGGACCAGAGAATTCGAATACAG CCAGAGGNNNACGTATGCCA	2419	TGCAGGACCAGAGAATTCGAATACAG TATTTGANNNACGTATGCCA	2659
TGCAGGACCAGAGAATTCGAATACAG GTATAGGNNNACGTATGCCA	2180	TGCAGGACCAGAGAATTCGAATACAC ATAGTATNNNACGTATGCCA	2420	TGCAGGACCAGAGAATTCGAATACAA GTGAATANNNACGTATGCCA	2660
TGCAGGACCAGAGAATTCGAATACAA GAACCCTNNNACGTATGCCA	2181	TGCAGGACCAGAGAATTCGAATACAT AAATGTCNNNACGTATGCCA	2421	TGCAGGACCAGAGAATTCGAATACAA ATCGCACNNNACGTATGCCA	2661
TGCAGGACCAGAGAATTCGAATACAG CCGCGTANNNACGTATGCCA	2182	TGCAGGACCAGAGAATTCGAATACAG CGTCGGTNNNACGTATGCCA	2422	TGCAGGACCAGAGAATTCGAATACAG TCCCCCANNNACGTATGCCA	2662
TGCAGGACCAGAGAATTCGAATACAT TCCCTGANNNACGTATGCCA	2183	TGCAGGACCAGAGAATTCGAATACAT TTGAACANNNACGTATGCCA	2423	TGCAGGACCAGAGAATTCGAATACAG CCCACTCNNNACGTATGCCA	2663
TGCAGGACCAGAGAATTCGAATACAA TGGCATCNNNACGTATGCCA	2184	TGCAGGACCAGAGAATTCGAATACAT AACTATGNNNACGTATGCCA	2424	TGCAGGACCAGAGAATTCGAATACAG AGATATANNNACGTATGCCA	2664
TGCAGGACCAGAGAATTCGAATACAA AGGATCGNNNACGTATGCCA	2185	TGCAGGACCAGAGAATTCGAATACAT CAGATGCNNNACGTATGCCA	2425	TGCAGGACCAGAGAATTCGAATACAG CACTACANNNACGTATGCCA	2665
TGCAGGACCAGAGAATTCGAATACAG TGCATCANNNACGTATGCCA	2186	TGCAGGACCAGAGAATTCGAATACAC TCAACAGNNNACGTATGCCA	2426	TGCAGGACCAGAGAATTCGAATACAA CTTTGCCNNNACGTATGCCA	2666
TGCAGGACCAGAGAATTCGAATACAG TCGTCTTNNNACGTATGCCA	2187	TGCAGGACCAGAGAATTCGAATACAA TAAAGTGNNNACGTATGCCA	2427	TGCAGGACCAGAGAATTCGAATACAC TGAGGCCNNNACGTATGCCA	2667
TGCAGGACCAGAGAATTCGAATACAC TTGAGGTNNNACGTATGCCA	2188	TGCAGGACCAGAGAATTCGAATACAA GAGCAGTNNNACGTATGCCA	2428	TGCAGGACCAGAGAATTCGAATACAA AGTAGGCNNNACGTATGCCA	2668
TGCAGGACCAGAGAATTCGAATACAT ACATCAANNNACGTATGCCA	2189	TGCAGGACCAGAGAATTCGAATACAT ATGTCTTNNNACGTATGCCA	2429	TGCAGCACCAGAGAATTCGAATACAG CTTCTACNNNACGTATGCCA	2669
TGCAGGACCAGAGAATTCGAATACAC CGAACCGNNNACGTATGCCA	2190	TGCAGGACCAGAGAATTCGAATACAG CAGAGATNNNACGTATGCCA	2430	TGCAGGACCAGAGAATTCGAATACAT GGAGGATNNNACGTATGCCA	2670
TGCAGGACCAGAGAATTCGAATACAC CCACACCNNNACGTATGCCA	2191	TGCAGGACCAGAGAATTCGAATACAT CTCACCANNNACGTATGCCA	2431	TGCAGGACCAGAGAATTCGAATACAG CTAACCANNNACGTATGCCA	2671
TGCAGGACCAGAGAATTCGAATACAA CGTAAAANNNACGTATGCCA	2192	TGCAGGACCAGAGAATTCGAATACAC CCCTTGGNNNACGTATGCCA	2432	TGCAGGACCAGAGAATTCGAATACAA CCCTTACNNNACGTATGCCA	2672
TGCAGGACCAGAGAATTCGAATACAG TAGAGTGNNNACGTATGCCA	2193	TGCAGGACCAGAGAATTCGAATACAC AGTGGCCNNNACGTATGCCA	2433	TGCAGGACCAGAGAATTCGAATACAG TCTTCTGNNNACGTATGCCA	2673
TGCAGGACCAGAGAATTCGAATACAC CACATAGNNNACGTATGCCA	2194	TGCAGGACCAGAGAATTCGAATACAC TGATCGANNNACGTATGCCA	2434	TGCAGGACCAGAGAATTCGAATACAC GGAGCCTNNNACGTATGCCA	2674
TGCAGGACCAGAGAATTCGAATACAT CTGTGCTNNNACGTATGCCA	2195	TGCAGGACCAGAGAATTCGAATACAT GGTACGTNNNACGTATGCCA	2435	TGCAGGACCAGAGAATTCGAATACAC CTGATGANNNACGTATGCCA	2675
TGCAGGACCAGAGAATTCGAATACAT AGTACATNNNACGTATGCCA	2196	TGCAGGACCAGAGAATTCGAATACAG TACGGCCNNNACGTATGCCA	2436	TGCAGGACCAGAGAATTCGAATACAT CGATACGNNNACGTATGCCA	2676
TGCAGGACCAGAGAATTCGAATACAC CGGACACNNNACGTATGCCA	2197	TGCAGGACCAGAGAATTCGAATACAC CATGCGGNNNACGTATGCCA	2437	TGCAGGACCAGAGAATTCGAATACAA AGAATGTNNNACGTATGCCA	2677
TGCAGGACCAGAGAATTCGAATACAG TAAGCTCNNNACGTATGCCA	2198	TGCAGGACCAGAGAATTCGAATACAC AAGTAGGNNNACGTATGCCA	2438	TGCAGGACCAGAGAATTCGAATACAT GCGCTCCNNNACGTATGCCA	2678
TGCAGGACCAGAGAATTCGAATACAA CTTGGTGNNNACGTATGCCA	2199	TGCAGGACCAGAGAATTCGAATACAC ATCAAATNNNACGTATGCCA	2439	TGCAGGACCAGAGAATTCGAATACAA AGTCATTNNNACGTATGCCA	2679
TGCAGGACCAGAGAATTCGAATACAC GACCTGGNNNACGTATGCCA	2200	TGCAGGACCAGAGAATTCGAATACAG ACTGGTTNNNACGTATGCCA	2440	TGCAGCACCAGAGAATTCGAATACAT GTAATGTNNNACGTATGCCA	2680

图15A

池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT GAGGATGNNNACGTATGCCA	2201	TGCAGGACCAGAGAATTCGAATACAG CAAATTTNNNACGTATGCCA	2441	TGCAGGACCAGAGAATTCGAATACAA TCTACCCNNNACGTATGCCA	2681
TGCAGGACCAGAGAATTCGAATACAC TCGTGCCNNNACGTATGCCA	2202	TGCAGGACCAGAGAATTCGAATACAT TAGTGTANNNACGTATGCCA	2442	TGCAGGACCAGAGAATTCGAATACAT GCCACAANNNACGTATGCCA	2682
TGCAGGACCAGAGAATTCGAATACAT TGCTCGTNNNACGTATGCCA	2203	TGCAGGACCAGAGAATTCGAATACAG ATGAAATNNNACGTATGCCA	2443	TGCAGGACCAGAGAATTCGAATACAG AGTGTTCNNNACGTATGCCA	2683
TGCAGGACCAGAGAATTCGAATACAA CACTGACNNNACGTATGCCA	2204	TGCAGGACCAGAGAATTCGAATACAT TGCCGAANNNACGTATGCCA	2444	TGCAGGACCAGAGAATTCGAATACAA ACAGCCTNNNACGTATGCCA	2684
TGCAGGACCAGAGAATTCGAATACAG TTGGTACNNNACGTATGCCA	2205	TGCAGGACCAGAGAATTCGAATACAT CCTCCTTNNNACGTATGCCA	2445	TGCAGGACCAGAGAATTCGAATACAG GACGACGNNNACGTATGCCA	2685
TGCAGGACCAGAGAATTCGAATACAT TCAGTCCNNNACGTATGCCA	2206	TGCAGGACCAGAGAATTCGAATACAC CCCATTANNNACGTATGCCA	2446	TGCAGGACCAGAGAATTCGAATACAA TTCCGGANNNACGTATGCCA	2686
TGCAGGACCAGAGAATTCGAATACAG TAACAAANNNACGTATGCCA	2207	TGCAGGACCAGAGAATTCGAATACAG TTTGTTTNNNACGTATGCCA	2447	TGCAGGACCAGAGAATTCGAATACAG GTCTCAANNNACGTATGCCA	2687
TGCAGGACCAGAGAATTCGAATACAC AACTGGTNNNACGTATGCCA	2208	TGCAGGACCAGAGAATTCGAATACAT ATCCCGTNNNACGTATGCCA	2448	TGCAGGACCAGAGAATTCGAATACAC ACCATGANNNACGTATGCCA	2688
TGCAGGACCAGAGAATTCGAATACAT GGATACCNNNACGTATGCCA	2209	TGCAGGACCAGAGAATTCGAATACAT TCGGTGANNNACGTATGCCA	2449	TGCAGGACCAGAGAATTCGAATACAC AAACGGANNNACGTATGCCA	2689
TGCAGGACCAGAGAATTCGAATACAA TGCACCANNNACGTATGCCA	2210	TGCAGGACCAGAGAATTCGAATACAC GTAAGGANNNACGTATGCCA	2450	TGCAGGACCAGAGAATTCGAATACAA GAGCGTANNNACGTATGCCA	2690
TGCAGGACCAGAGAATTCGAATACAA CTCCTTGNNNACGTATGCCA	2211	TGCAGGACCAGAGAATTCGAATACAC TTTCTTTNNNACGTATGCCA	2451	TGCAGGACCAGAGAATTCGAATACAC CCCTGACNNNACGTATGCCA	2691
TGCAGGACCAGAGAATTCGAATACAA ATAGTTCNNNACGTATGCCA	2212	TGCAGGACCAGAGAATTCGAATACAG ACTTTTTNNNACGTATGCCA	2452	TGCAGGACCAGAGAATTCGAATACAC CAAGTTGNNNACGTATGCCA	2692
TGCAGGACCAGAGAATTCGAATACAT GAGAGCANNNACGTATGCCA	2213	TGCAGGACCAGAGAATTCGAATACAG GTTAAGGNNNACGTATGCCA	2453	TGCAGGACCAGAGAATTCGAATACAT GTGTAATNNNACGTATGCCA	2693
TGCAGGACCAGAGAATTCGAATACAT CACCCCGNNNACGTATGCCA	2214	TGCAGGACCAGAGAATTCGAATACAA TCACGGTNNNACGTATGCCA	2454	TGCAGGACCAGAGAATTCGAATACAA TTTGTGANNNACGTATGCCA	2694
TGCAGGACCAGAGAATTCGAATACAT AATGGAANNNACGTATGCCA	2215	TGCAGGACCAGAGAATTCGAATACAC ATTTAGANNNACGTATGCCA	2455	TGCAGGACCAGAGAATTCGAATACAG TAGCGTTNNNACGTATGCCA	2695
TGCAGGACCAGAGAATTCGAATACAT CCAAATANNNACGTATGCCA	2216	TGCAGGACCAGAGAATTCGAATACAC ACGGCANNNACGTATGCCA	2456	TGCAGGACCAGAGAATTCGAATACAC ACGTGATNNNACGTATGCCA	2696
TGCAGGACCAGAGAATTCGAATACAG AGGCTCCNNNACGTATGCCA	2217	TGCAGGACCAGAGAATTCGAATACAC TGAATCGNNNACGTATGCCA	2457	TGCAGGACCAGAGAATTCGAATACAA ACAGCGANNNACGTATGCCA	2697
TGCAGGACCAGAGAATTCGAATACAT CCGCGTCNNNACGTATGCCA	2218	TGCAGGACCAGAGAATTCGAATACAT TGTGTAANNNACGTATGCCA	2458	TGCAGGACCAGAGAATTCGAATACAA AATGCGGNNNACGTATGCCA	2698
TGCAGGACCAGAGAATTCGAATACAG CATTGCANNNACGTATGCCA	2219	TGCAGGACCAGAGAATTCGAATACAC CGCGTGANNNACGTATGCCA	2459	TGCAGGACCAGAGAATTCGAATACAT ACCAAGCNNNACGTATGCCA	2699
TGCAGGACCAGAGAATTCGAATACAC CCCTTAANNNACGTATGCCA	2220	TGCAGGACCAGAGAATTCGAATACAA ACCAAGGNNNACGTATGCCA	2460	TGCAGGACCAGAGAATTCGAATACAC GACCCTCNNNACGTATGCCA	2700
TGCAGGACCAGAGAATTCGAATACAG ACCGCCANNNACGTATGCCA	2221	TGCAGGACCAGAGAATTCGAATACAT CGTTTGCNNNACGTATGCCA	2461	TGCAGGACCAGAGAATTCGAATACAA CACCCTTNNNACGTATGCCA	2701
TGCAGGACCAGAGAATTCGAATACAG ATCTGACNNNACGTATGCCA	2222	TGCAGGACCAGAGAATTCGAATACAC TATTCGCNNNACGTATGCCA	2462	TGCAGGACCAGAGAATTCGAATACAC TGTCGCCNNNACGTATGCCA	2702
TGCAGGACCAGAGAATTCGAATACAG CATGTTGNNNACGTATGCCA	2223	TGCAGGACCAGAGAATTCGAATACAA ACAGATANNNACGTATGCCA	2463	TGCAGGACCAGAGAATTCGAATACAA GCCGCCANNNACGTATGCCA	2703
TGCAGGACCAGAGAATTCGAATACAT AGCACGTNNNACGTATGCCA	2224	TGCAGGACCAGAGAATTCGAATACAC TATTATCNNNACGTATGCCA	2464	TGCAGGACCAGAGAATTCGAATACAT GTACAATNNNACGTATGCCA	2704
TGCAGGACCAGAGAATTCGAATACAG GTCCAATNNNACGTATGCCA	2225	TGCAGGACCAGAGAATTCGAATACAT CCCAATCNNNACGTATGCCA	2465	TGCAGGACCAGAGAATTCGAATACAG ATCTACGNNNACGTATGCCA	2705
TGCAGGACCAGAGAATTCGAATACAA CCCTCTANNNACGTATGCCA	2226	TGCAGGACCAGAGAATTCGAATACAC TAAAGTTNNNACGTATGCCA	2466	TGCAGGACCAGAGAATTCGAATACAC CAGTCTTNNNACGTATGCCA	2706
TGCAGGACCAGAGAATTCGAATACAT TACGACGNNNACGTATGCCA	2227	TGCAGGACCAGAGAATTCGAATACAA GCTAATTNNNACGTATGCCA	2467	TGCAGGACCAGAGAATTCGAATACAG CTGCAATNNNACGTATGCCA	2707
TGCAGGACCAGAGAATTCGAATACAC ATATCGGNNNACGTATGCCA	2228	TGCAGGACCAGAGAATTCGAATACAT TGTTATCNNNACGTATGCCA	2468	TGCAGGACCAGAGAATTCGAATACAG AAGAGTCNNNACGTATGCCA	2708
TGCAGGACCAGAGAATTCGAATACAG CGATATCNNNCTAGCGTTAC	2229	TGCAGGACCAGAGAATTCGAATACAT AGTACGCNNNCTAGCGTTAC	2469	TGCAGGACCAGAGAATTCGAATACAA CAACTCGNNNCTAGCGTTAC	2709
TGCAGGACCAGAGAATTCGAATACAT ACGAGGANNNCTAGCGTTAC	2230	TGCAGGACCAGAGAATTCGAATACAC AGGCTATNNNCTAGCGTTAC	2470	TGCAGGACCAGAGAATTCGAATACAT GCGCAATNNNCTAGCGTTAC	2710
TGCAGGACCAGAGAATTCGAATACAT CTTACATNNNCTAGCGTTAC	2231	TGCAGGACCAGAGAATTCGAATACAC ATTAGTANNNCTAGCGTTAC	2471	TGCAGGACCAGAGAATTCGAATACAT AAGAACANNNCTAGCGTTAC	2711
TGCAGGACCAGAGAATTCGAATACAG CGTCTCCNNNCTAGCGTTAC	2232	TGCAGGACCAGAGAATTCGAATACAC CTCTAACNNNCTAGCGTTAC	2472	TGCAGGACCAGAGAATTCGAATACAC GCTTGCCNNNCTAGCGTTAC	2712

图15B

池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACATAATCCGGNNNCTAGCGTTAC	2233	TGCAGGACCAGAGAATTCGAATACATAGTGTCGNNNCTAGCGTTAC	2473	TGCAGGACCAGAGAATTCGAATACATTACACGGNNNCTAGCGTTAC	2713
TGCAGGACCAGAGAATTCGAATACACAGCATACNNNCTAGCGTTAC	2234	TGCAGGACCAGAGAATTCGAATACACGCAGAGGNNNCTAGCGTTAC	2474	TGCAGGACCAGAGAATTCGAATACACTCCACCGNNNCTAGCGTTAC	2714
TGCAGGACCAGAGAATTCGAATACAGTTCTCCANNNCTAGCGTTAC	2235	TGCAGGACCAGAGAATTCGAATACAGCGGTTCGNNNCTAGCGTTAC	2475	TGCAGGACCAGAGAATTCGAATACACGACCCAGNNNCTAGCGTTAC	2715
TGCAGGACCAGAGAATTCGAATACAAGTTCCTCNNNCTAGCGTTAC	2236	TGCAGGACCAGAGAATTCGAATACACCAGAGTTNNNCTAGCGTTAC	2476	TGCAGGACCAGAGAATTCGAATACACGGTCAGCNNNCTAGCGTTAC	2716
TGCAGGACCAGAGAATTCGAATACAAAATCGAANNNCTAGCGTTAC	2237	TGCAGGACCAGAGAATTCGAATACATGATGAAANNNCTAGCGTTAC	2477	TGCAGGACCAGAGAATTCGAATACACACTATCCNNNCTAGCGTTAC	2717
TGCAGGACCAGAGAATTCGAATACAPGATTATCNNNCTAGCGTTAC	2238	TGCAGGACCAGAGAATTCGAATACAGGTGAATGNNNCTAGCGTTAC	2478	TGCAGGACCAGAGAATTCGAATACACTAGTCTCNNNCTAGCGTTAC	2718
TGCAGGACCAGAGAATTCGAATACAGTTTCACCNNNCTAGCGTTAC	2239	TGCAGGACCAGAGAATTCGAATACAGTATGTGCNNNCTAGCGTTAC	2479	TGCAGGACCAGAGAATTCGAATACATACCTTCGNNNCTAGCGTTAC	2719
TGCAGGACCAGAGAATTCGAATACAATTACATGNNNCTAGCGTTAC	2240	TGCAGGACCAGAGAATTCGAATACAAATACTACNNNCTAGCGTTAC	2480	TGCAGGACCAGAGAATTCGAATACAAACCAGAGNNNCTAGCGTTAC	2720
TGCAGGACCAGAGAATTCGAATACAACCATCCTNNNCTAGCGTTAC	2241	TGCAGGACCAGAGAATTCGAATACATTCGGATGNNNCTAGCGTTAC	2481	TGCAGGACCAGAGAATTCGAATACATGACTCGANNNCTAGCGTTAC	2721
TGCAGGACCAGAGAATTCGAATACACAGACTACNNNCTAGCGTTAC	2242	TGCAGGACCAGAGAATTCGAATACATACATTAGNNNCTAGCGTTAC	2482	TGCAGGACCAGAGAATTCGAATACAACCCAGATNNNCTAGCGTTAC	2722
TGCAGGACCAGAGAATTCGAATACACATTGGTGNNNCTAGCGTTAC	2243	TGCAGGACCAGAGAATTCGAATACATGGCCCGANNNCTAGCGTTAC	2483	TGCAGGACCAGAGAATTCGAATACATGCGCTTTNNNCTAGCGTTAC	2723
TGCAGGACCAGAGAATTCGAATACAGAGACCTTNNNCTAGCGTTAC	2244	TGCAGGACCAGAGAATTCGAATACAGTTGAGTCNNNCTAGCGTTAC	2484	TGCAGGACCAGAGAATTCGAATACAGGAGGACCNNNCTAGCGTTAC	2724
TGCAGGACCAGAGAATTCGAATACATCAGGCCGNNNCTAGCGTTAC	2245	TGCAGGACCAGAGAATTCGAATACAGTTAGCACNNNCTAGCGTTAC	2485	TGCAGGACCAGAGAATTCGAATACATCGTCCATNNNCTAGCGTTAC	2725
TGCAGGACCAGAGAATTCGAATACACAACACACNNNCTAGCGTTAC	2246	TGCAGGACCAGAGAATTCGAATACAAGTTCCCTNNNCTAGCGTTAC	2486	TGCAGGACCAGAGAATTCGAATACACGACCTCCNNNCTAGCGTTAC	2726
TGCAGGACCAGAGAATTCGAATACACGACGTCGNNNCTAGCGTTAC	2247	TGCAGGACCAGAGAATTCGAATACACATGGAGANNNCTAGCGTTAC	2487	TGCAGGACCAGAGAATTCGAATACAAGATTCCGNNNCTAGCGTTAC	2727
TGCAGGACCAGAGAATTCGAATACATAGACTATNNNCTAGCGTTAC	2248	TGCAGGACCAGAGAATTCGAATACAAATCGTCGNNNCTAGCGTTAC	2488	TGCAGGACCAGAGAATTCGAATACAACTCGAACNNNCTAGCGTTAC	2728
TGCAGGACCAGAGAATTCGAATACACCGAGAAANNNCTAGCGTTAC	2249	TGCAGGACCAGAGAATTCGAATACAACTCGCAANNNCTAGCGTTAC	2489	TGCAGGACCAGAGAATTCGAATACAAGACGATGNNNCTAGCGTTAC	2729
TGCAGGACCAGAGAATTCGAATACATTCCATATNNNCTAGCGTTAC	2250	TGCAGGACCAGAGAATTCGAATACATCAGCCTTNNNCTAGCGTTAC	2490	TGCAGGACCAGAGAATTCGAATACAGAACTTATNNNCTAGCGTTAC	2730
TGCAGGACCAGAGAATTCGAATACAGCCATGATNNNCTAGCGTTAC	2251	TGCAGGACCAGAGAATTCGAATACATTGCCTCANNNCTAGCGTTAC	2491	TGCAGGACCAGAGAATTCGAATACAACCAGCGCNNNCTAGCGTTAC	2731
TGCAGGACCAGAGAATTCGAATACAGGCGACGANNNCTAGCGTTAC	2252	TGCAGGACCAGAGAATTCGAATACAGGACCCACNNNCTAGCGTTAC	2492	TGCAGGACCAGAGAATTCGAATACATACCTCTGNNNCTAGCGTTAC	2732
TGCAGGACCAGAGAATTCGAATACACCCAGTAANNNCTAGCGTTAC	2253	TGCAGGACCAGAGAATTCGAATACATTCTCCAGNNNCTAGCGTTAC	2493	TGCAGGACCAGAGAATTCGAATACACGGAGCGANNNCTAGCGTTAC	2733
TGCAGGACCAGAGAATTCGAATACACTCAAACGNNNCTAGCGTTAC	2254	TGCAGGACCAGAGAATTCGAATACAGTCCTCGCNNNCTAGCGTTAC	2494	TGCAGGACCAGAGAATTCGAATACAACCGGAAANNNCTAGCGTTAC	2734
TGCAGGACCAGAGAATTCGAATACACAGATCTGNNNCTAGCGTTAC	2255	TGCAGGACCAGAGAATTCGAATACAAATAGTCTNNNCTAGCGTTAC	2495	TGCAGGACCAGAGAATTCGAATACAGGATCGCCNNNCTAGCGTTAC	2735
TGCAGGACCAGAGAATTCGAATACAAGAAAATCNNNCTAGCGTTAC	2256	TGCAGGACCAGAGAATTCGAATACAGCTGGATTNNNCTAGCGTTAC	2496	TGCAGGACCAGAGAATTCGAATACAATCAGCACNNNCTAGCGTTAC	2736
TGCAGGACCAGAGAATTCGAATACAATCTTTCANNNCTAGCGTTAC	2257	TGCAGGACCAGAGAATTCGAATACATTCGTCACNNNCTAGCGTTAC	2497	TGCAGGACCAGAGAATTCGAATACAAACTCTCCNNNCTAGCGTTAC	2737
TGCAGGACCAGAGAATTCGAATACACCCATCTANNNCTAGCGTTAC	2258	TGCAGGACCAGAGAATTCGAATACAATTATGACNNNCTAGCGTTAC	2498	TGCAGGACCAGAGAATTCGAATACATATGAGTTNNNCTAGCGTTAC	2738
TGCAGGACCAGAGAATTCGAATACACTAAGGTCNNNCTAGCGTTAC	2259	TGCAGGACCAGAGAATTCGAATACATTTTAGAGNNNCTAGCGTTAC	2499	TGCAGGACCAGAGAATTCGAATACAAGGCGTCCNNNCTAGCGTTAC	2739
TGCAGGACCAGAGAATTCGAATACACACCGACGNNNCTAGCGTTAC	2260	TGCAGGACCAGAGAATTCGAATACAGATATACTNNNCTAGCGTTAC	2500	TGCAGGACCAGAGAATTCGAATACAAGAATTAGNNNCTAGCGTTAC	2740
TGCAGGACCAGAGAATTCGAATACAGTTTAGATNNNCTAGCGTTAC	2261	TGCAGGACCAGAGAATTCGAATACACCTACCCGNNNCTAGCGTTAC	2501	TGCAGGACCAGAGAATTCGAATACAGATTTAGTNNNCTAGCGTTAC	2741
TGCAGGACCAGAGAATTCGAATACATCCCCTCCNNNCTAGCGTTAC	2262	TGCAGGACCAGAGAATTCGAATACAAACCTTTTNNNCTAGCGTTAC	2502	TGCAGGACCAGAGAATTCGAATACATATTTCTGNNNCTAGCGTTAC	2742
TGCAGGACCAGAGAATTCGAATACATTAATCAGNNNCTAGCGTTAC	2263	TGCAGGACCAGAGAATTCGAATACAATGTGTATNNNCTAGCGTTAC	2503	TGCAGGACCAGAGAATTCGAATACAGCTGTACANNNCTAGCGTTAC	2743
TGCAGGACCAGAGAATTCGAATACACATTCGAGNNNCTAGCGTTAC	2264	TGCAGGACCAGAGAATTCGAATACATCCCACGCNNNCTAGCGTTAC	2504	TGCAGGACCAGAGAATTCGAATACAGCTTACGANNNCTAGCGTTAC	2744

图15C

池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA ACCGTGTNNNCTAGCGTTAC	2265	TGCAGGACCAGAGAATTCGAATACAC GCCTCTGNNNCTAGCGTTAC	2505	TGCAGGACCAGAGAATTCGAATACAC CCACGGANNNCTAGCGTTAC	2745
TGCAGGACCAGAGAATTCGAATACAC CCAATTCNNNCTAGCGTTAC	2266	TGCAGGACCAGAGAATTCGAATACAC TATAACANNNCTAGCGTTAC	2506	TGCAGGACCAGAGAATTCGAATACAT GGATCTGNNNCTAGCGTTAC	2746
TGCAGGACCAGAGAATTCGAATACAT TGGTGGTNNNCTAGCGTTAC	2267	TGCAGGACCAGAGAATTCGAATACAG ACTGACTNNNCTAGCGTTAC	2507	TGCAGGACCAGAGAATTCGAATACAT CCACGAANNNCTAGCGTTAC	2747
TGCAGGACCAGAGAATTCGAATACAT GCTTAGGNNNCTAGCGTTAC	2268	TGCAGGACCAGAGAATTCGAATACAC TGGCCAGNNNCTAGCGTTAC	2508	TGCAGGACCAGAGAATTCGAATACAT CAAGACCNNNCTAGCGTTAC	2748
TGCAGGACCAGAGAATTCGAATACAA CACCCCCNNNCTAGCGTTAC	2269	TGCAGGACCAGAGAATTCGAATACAA AGCCAAGNNNCTAGCGTTAC	2509	TGCAGGACCAGAGAATTCGAATACAG GCAGACGNNNCTAGCGTTAC	2749
TGCAGGACCAGAGAATTCGAATACAC CATTGAGNNNCTAGCGTTAC	2270	TGCAGGACCAGAGAATTCGAATACAC GCTTTTGNNNCTAGCGTTAC	2510	TGCAGGACCAGAGAATTCGAATACAT TTTTACGNNNCTAGCGTTAC	2750
TGCAGGACCAGAGAATTCGAATACAA GTTAAACNNNCTAGCGTTAC	2271	TGCAGGACCAGAGAATTCGAATACAT TTCCCTCNNNCTAGCGTTAC	2511	TGCAGGACCAGAGAATTCGAATACAG CGTTTGANNNCTAGCGTTAC	2751
TGCAGGACCAGAGAATTCGAATACAT ATAGTACNNNCTAGCGTTAC	2272	TGCAGGACCAGAGAATTCGAATACAC TTACTCGNNNCTAGCGTTAC	2512	TGCAGGACCAGAGAATTCGAATACAA GGTACTCNNNCTAGCGTTAC	2752
TGCAGGACCAGAGAATTCGAATACAC AGTGTACNNNCTAGCGTTAC	2273	TGCAGGACCAGAGAATTCGAATACAA TCGAGTCNNNCTAGCGTTAC	2513	TGCAGGACCAGAGAATTCGAATACAT TCTGTTANNNCTAGCGTTAC	2753
TGCAGGACCAGAGAATTCGAATACAG CGTCTTTNNNCTAGCGTTAC	2274	TGCAGGACCAGAGAATTCGAATACAT TGTACGGNNNCTAGCGTTAC	2514	TGCAGGACCAGAGAATTCGAATACAC CGATGTANNNCTAGCGTTAC	2754
TGCAGGACCAGAGAATTCGAATACAT GACTCAGNNNCTAGCGTTAC	2275	TGCAGGACCAGAGAATTCGAATACAC ACCATTCNNNCTAGCGTTAC	2515	TGCAGGACCAGAGAATTCGAATACAG TCGGTTANNNCTAGCGTTAC	2755
TGCAGGACCAGAGAATTCGAATACAA CTTAGTANNNCTAGCGTTAC	2276	TGCAGGACCAGAGAATTCGAATACAC CCTGTTTNNNGTAGCGTTAC	2516	TGCAGGACCAGAGAATTCGAATACAC GAACCCGNNNCTAGCGTTAC	2756
TGCAGGACCAGAGAATTCGAATACAA AACATGANNNCTAGCGTTAC	2277	TGCAGGACCAGAGAATTCGAATACAT GCATTAANNNCTAGCGTTAC	2517	TGCAGGACCAGAGAATTCGAATACAT TCGACTCNNNCTAGCGTTAC	2757
TGCAGGACCAGAGAATTCGAATACAG TTAGGCTNNNCTAGCGTTAC	2278	TGCAGGACCAGAGAATTCGAATACAC GTAGCGCNNNCTAGCGTTAC	2518	TGCAGGACCAGAGAATTCGAATACAT TCAGCCTNNNCTAGCGTTAC	2758
TGCAGGACCAGAGAATTCGAATACAT CCGCAGGNNNCTAGCGTTAC	2279	TGCAGGACCAGAGAATTCGAATACAG TCTCCTANNNCTAGCGTTAC	2519	TGCAGGACCAGAGAATTCGAATACAC ACTTGAGNNNCTAGCGTTAC	2759
TGCAGGACCAGAGAATTCGAATACAA GTACATTNNNCTAGCGTTAC	2280	TGCAGGACCAGAGAATTCGAATACAT GCGCCGANNNCTAGCGTTAC	2520	TGCAGGACCAGAGAATTCGAATACAT CACGCGGNNNCTAGCGTTAC	2760
TGCAGGACCAGAGAATTCGAATACAG GTCGTATNNNCTAGCGTTAC	2281	TGCAGGACCAGAGAATTCGAATACAC AATGATTNNNCTAGCGTTAC	2521	TGCAGGACCAGAGAATTCGAATACAC ACTGTAGNNNCTAGCGTTAC	2761
TGCAGGACCAGAGAATTCGAATACAA GACGACANNNCTAGCGTTAC	2282	TGCAGGACCAGAGAATTCGAATACAA GCGAGGCNNNCTAGCGTTAC	2522	TGCAGGACCAGAGAATTCGAATACAA CCAAGCTNNNCTAGCGTTAC	2762
TGCAGGACCAGAGAATTCGAATACAA AGTTCTANNNCTAGCGTTAC	2283	TGCAGGACCAGAGAATTCGAATACAT TGAATACNNNCTAGCGTTAC	2523	TGCAGGACCAGAGAATTCGAATACAA CTGCAACNNNCTAGCGTTAC	2763
TGCAGGACCAGAGAATTCGAATACAA CCGAACTNNNCTAGCGTTAC	2284	TGCAGGACCAGAGAATTCGAATACAA CCGCCAGNNNCTAGCGTTAC	2524	TGCAGGACCAGAGAATTCGAATACAT AACGGTCNNNCTAGCGTTAC	2764
TGCAGGACCAGAGAATTCGAATACAG GCAATTCNNNCTAGCGTTAC	2285	TGCAGGACCAGAGAATTCGAATACAG GCGACAGNNNCTAGCGTTAC	2525	TGCAGGACCAGAGAATTCGAATACAA GTTTGTANNNCTAGCGTTAC	2765
TGCAGGACCAGAGAATTCGAATACAG TCACACANNNCTAGCGTTAC	2286	TGCAGGACCAGAGAATTCGAATACAA TATCCAANNNCTAGCGTTAC	2526	TGCAGGACCAGAGAATTCGAATACAC ACGTTTCNNNCTAGCGTTAC	2766
TGCAGGACCAGAGAATTCGAATACAC GGAAATGNNNCTAGCGTTAC	2287	TGCAGGACCAGAGAATTCGAATACAA TGTTGTANNNCTAGCGTTAC	2527	TGCAGGACCAGAGAATTCGAATACAT TAAAACCNNNCTAGCGTTAC	2767
TGCAGGACCAGAGAATTCGAATACAC TGTCTACNNNCTAGCGTTAC	2288	TGCAGGACCAGAGAATTCGAATACAG ATTGTTANNNCTAGCGTTAC	2528	TGCAGGACCAGAGAATTCGAATACAT TCGTAGCNNNCTAGCGTTAC	2768
TGCAGGACCAGAGAATTCGAATACAG AGCCAGGNNNGATCGACATG	2289	TGCAGGACCAGAGAATTCGAATACAG TCCACGGNNNGATCGACATG	2529	TGCAGGACCAGAGAATTCGAATACAT GCGTAGTNNNGATCGACATG	2769
TGCAGGACCAGAGAATTCGAATACAC ACTCCTANNNGATCGACATG	2290	TGCAGGACCAGAGAATTCGAATACAT GACTGACNNNGATCGACATG	2530	TGCAGGACCAGAGAATTCGAATACAG CTTTGCTNNNGATCGACATG	2770
TGCAGGACCAGAGAATTCGAATACAC TTTCCCTNNNGATCGACATG	2291	TGCAGGACCAGAGAATTCGAATACAT GATTTAGNNNGATCGACATG	2531	TGCAGGACCAGAGAATTCGAATACAG TAAATAGNNNGATCGACATG	2771
TGCAGGACCAGAGAATTCGAATACAC TGAGCTANNNGATCGACATG	2292	TGCAGGACCAGAGAATTCGAATACAA CATACTANNNGATCGACATG	2532	TGCAGGACCAGAGAATTCGAATACAC GCTGTCCNNNGATCGACATG	2772
TGCAGGACCAGAGAATTCGAATACAG TCTGACANNNGATCGACATG	2293	TGCAGGACCAGAGAATTCGAATACAA GCATCCANNNGATCGACATG	2533	TGCAGGACCAGAGAATTCGAATACAC TTAGAGCNNNGATCGACATG	2773
TGCAGGACCAGAGAATTCGAATACAC TGACGCGNNNGATCGACATG	2294	TGCAGGACCAGAGAATTCGAATACAA CGGCAAANNNGATCGACATG	2534	TGCAGGACCAGAGAATTCGAATACAG GACATAGNNNGATCGACATG	2774
TGCAGGACCAGAGAATTCGAATACAG TGATGGANNNGATCGACATG	2295	TGCAGGACCAGAGAATTCGAATACAC TTTGCTGNNNGATCGACATG	2535	TGCAGGACCAGAGAATTCGAATACAT CTACAGGNNNGATCGACATG	2775
TGCAGGACCAGAGAATTCGAATACAG AATTCTANNNGATCGACATG	2296	TGCAGGACCAGAGAATTCGAATACAT TAACTAGNNNGATCGACATG	2536	TGCAGGACCAGAGAATTCGAATACAC AAACTCGNNNGATCGACATG	2776

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池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC GTGCATANNNGATCGACATG	2297	TGCAGGACCAGAGAATTCGAATACAC GTACTGANNNGATCGACATG	2537	TGCAGGACCAGAGAATTCGAATACAG CTATTCCNNNGATCGACATG	2777
TGCAGGACCAGAGAATTCGAATACAT GGCGTGCNNNGATCGACATG	2298	TGCAGGACCAGAGAATTCGAATACAT AGTATCANNNGATCGACATG	2538	TGCAGGACCAGAGAATTCGAATACAG TCCAGTANNNGATCGACATG	2778
TGCAGGACCAGAGAATTCGAATACAC CAGTGCGNNNGATCGACATG	2299	TGCAGGACCAGAGAATTCGAATACAC CTGACAANNNGATCGACATG	2539	TGCAGGACCAGAGAATTCGAATACAG GCGAGACNNNGATCGACATG	2779
TGCAGGACCAGAGAATTCGAATACAT GCCCCTGNNNGATCGACATG	2300	TGCAGGACCAGAGAATTCGAATACAC GTGGCCANNNGATCGACATG	2540	TGCAGGACCAGAGAATTCGAATACAT TTCATACNNNGATCGACATG	2780
TGCAGGACCAGAGAATTCGAATACAT CCGTCGCNNNGATCGACATG	2301	TGCAGGACCAGAGAATTCGAATACAG CGTATACNNNGATCGACATG	2541	TGCAGGACCAGAGAATTCGAATACAC AGCTGTANNNGATCGACATG	2781
TGCAGGACCAGAGAATTCGAATACAC TCCTCCGNNNGATCGACATG	2302	TGCAGGACCAGAGAATTCGAATACAC CGCTGCANNNGATCGACATG	2542	TGCAGGACCAGAGAATTCGAATACAA CTGCTCTNNNGATCGACATG	2782
TGCAGGACCAGAGAATTCGAATACAG CTCCATTNNNGATCGACATG	2303	TGCAGGACCAGAGAATTCGAATACAA CCGTTAGNNNGATCGACATG	2543	TGCAGGACCAGAGAATTCGAATACAA AAGTTCTNNNGATCGACATG	2783
TGCAGGACCAGAGAATTCGAATACAG ACTCCTTNNNGATCGACATG	2304	TGCAGGACCAGAGAATTCGAATACAT GTACTTTNNNGATCGACATG	2544	TGCAGGACCAGAGAATTCGAATACAG AATCGAGNNNGATCGACATG	2784
TGCAGGACCAGAGAATTCGAATACAT GTAACTANNNGATCGACATG	2305	TGCAGGACCAGAGAATTCGAATACAC ATTATGANNNGATCGACATG	2545	TGCAGCACCAGAGAATTCGAATACAC TCCCGCANNNGATCGACATG	2785
TGCAGGACCAGAGAATTCGAATACAA GAGTCTCNNNGATCGACATG	2306	TGCAGGACCAGAGAATTCGAATACAC AGACCCGNNNGATCGACATG	2546	TGCAGGACCAGAGAATTCGAATACAG AAAACTANNNGATCGACATG	2786
TGCAGGACCAGAGAATTCGAATACAC TTTCTAANNNGATCGACATG	2307	TGCAGGACCAGAGAATTCGAATACAT AGCACCANNNGATCGACATG	2547	TGCAGGACCAGAGAATTCGAATACAA CCCTAAGNNNGATCGACATG	2787
TGCAGGACCAGAGAATTCGAATACAC GAGACCCNNNGATCGACATG	2308	TGCAGGACCAGAGAATTCGAATACAT GGAGTGANNNGATCGACATG	2548	TGCAGGACCAGAGAATTCGAATACAG GTCATACNNNGATCGACATG	2788
TGCAGGACCAGAGAATTCGAATACAT TTTAGTCNNNGATCGACATG	2309	TGCAGGACCAGAGAATTCGAATACAG GACGTGGNNNGATCGACATG	2549	TGCAGGACCAGAGAATTCGAATACAT GGTTGTGNNNGATCGACATG	2789
TGCAGGACCAGAGAATTCGAATACAA TGTGCTGNNNGATCGACATG	2310	TGCAGGACCAGAGAATTCGAATACAC CTTACACNNNGATCGACATG	2550	TGCAGGACCAGAGAATTCGAATACAA AGTTCCGNNNGATCGACATG	2790
TGCAGGACCAGAGAATTCGAATACAC CCAGGTGNNNGATCGACATG	2311	TGCAGGACCAGAGAATTCGAATACAT GGCAGCCNNNGATCGACATG	2551	TGCAGGACCAGAGAATTCGAATACAA TCAATGTNNNGATCGACATG	2791
TGCAGGACCAGAGAATTCGAATACAG AACCAAGNNNGATCGACATG	2312	TGCAGGACCAGAGAATTCGAATACAC CTTACTGNNNGATCGACATG	2552	TGCAGGACCAGAGAATTCGAATACAC ATTGATANNNGATCGACATG	2792
TGCAGGACCAGAGAATTCGAATACAC CTGAGGCNNNGATCGACATG	2313	TGCAGGACCAGAGAATTCGAATACAT TACTCTANNNGATCGACATG	2553	TGCAGGACCAGAGAATTCGAATACAG GAGGAAANNNGATCGACATG	2793
TGCAGGACCAGAGAATTCGAATACAA TAAGCGGNNNGATCGACATG	2314	TGCAGGACCAGAGAATTCGAATACAC CGCCTACNNNGATCGACATG	2554	TGCAGGACCAGAGAATTCGAATACAC ATTTTACNNNGATCGACATG	2794
TGCAGGACCAGAGAATTCGAATACAT TTGTCATNNNGATCGACATG	2315	TGCAGGACCAGAGAATTCGAATACAC CTTAGAGNNNGATCGACATG	2555	TGCAGGACCAGAGAATTCGAATACAG AACTTCGNNNGATCGACATG	2795
TGCAGGACCAGAGAATTCGAATACAA GCGTTTGNNNGATCGACATG	2316	TGCAGGACCAGAGAATTCGAATACAT TCTATGTNNNGATCGACATG	2556	TGCAGGACCAGAGAATTCGAATACAC GTCACCCNNNGATCGACATG	2796
TGCAGGACCAGAGAATTCGAATACAG CTATTTTNNNGATCGACATG	2317	TGCAGGACCAGAGAATTCGAATACAT TTTACACNNNGATCGACATG	2557	TGCAGGACCAGAGAATTCGAATACAA CGTTAATNNNGATCGACATG	2797
TGCAGGACCAGAGAATTCGAATACAT GACACCANNNGATCGACATG	2318	TGCAGGACCAGAGAATTCGAATACAT TGTTTTGNNNGATCGACATG	2558	TGCAGGACCAGAGAATTCGAATACAG GTGTGTTNNNGATCGACATG	2798
TGCAGGACCAGAGAATTCGAATACAC GCTCAAANNNGATCGACATG	2319	TGCAGGACCAGAGAATTCGAATACAC AAAGACGNNNGATCGACATG	2559	TGCAGGACCAGAGAATTCGAATACAG AAATAGTNNNGATCGACATG	2799
TGCAGGACCAGAGAATTCGAATACAG CGCATTANNNGATCGACATG	2320	TGCAGGACCAGAGAATTCGAATACAA CCTCCGCNNNGATCGACATG	2560	TGCAGGACCAGAGAATTCGAATACAG TCTATTTNNNGATCGACATG	2800
TGCAGGACCAGAGAATTCGAATACAT GTAAATGNNNGATCGACATG	2321	TGCAGGACCAGAGAATTCGAATACAG TTAACATNNNGATCGACATG	2561	TGCAGGACCAGAGAATTCGAATACAT AGTAGCCNNNGATCGACATG	2801
TGCAGGACCAGAGAATTCGAATACAA GCACTACNNNGATCGACATG	2322	TGCAGGACCAGAGAATTCGAATACAC GATGCGCNNNGATCGACATG	2562	TGCAGGACCAGAGAATTCGAATACAG TACAAAANNNGATCGACATG	2802
TGCAGGACCAGAGAATTCGAATACAG ATTCAGCNNNGATCGACATG	2323	TGCAGGACCAGAGAATTCGAATACAC CTCGAAANNNGATCGACATG	2563	TGCAGGACCAGAGAATTCGAATACAA GAGTACGNNNGATCGACATG	2803
TGCAGGACCAGAGAATTCGAATACAC TGCTCCGNNNGATCGACATG	2324	TGCAGGACCAGAGAATTCGAATACAA TGTCGACNNNGATCGACATG	2564	TGCAGGACCAGAGAATTCGAATACAT AGACTTANNNGATCGACATG	2804
TGCAGGACCAGAGAATTCGAATACAG CACGATTNNNGATCGACATG	2325	TGCAGGACCAGAGAATTCGAATACAT AACAGCCNNNGATCGACATG	2565	TGCAGGACCAGAGAATTCGAATACAC GAGCAAANNNGATCGACATG	2805
TGCAGGACCAGAGAATTCGAATACAA TGTCATANNNGATCGACATG	2326	TGCAGGACCAGAGAATTCGAATACAG CGCAGTCNNNGATCGACATG	2566	TGCAGGACCAGAGAATTCGAATACAA GCGTCGCNNNGATCGACATG	2806
TGCAGGACCAGAGAATTCGAATACAA CAGGACANNNGATCGACATG	2327	TGCAGGACCAGAGAATTCGAATACAA TCATAACNNNGATCGACATG	2567	TGCAGGACCAGAGAATTCGAATACAG CTGGTCGNNNGATCGACATG	2807
TGCAGGACCAGAGAATTCGAATACAC CGTAAGTNNNGATCGACATG	2328	TGCAGGACCAGAGAATTCGAATACAA AGGTCTCNNNGATCGACATG	2568	TGCAGGACCAGAGAATTCGAATACAA GTCCACANNNGATCGACATG	2808

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池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA AAGAATCNNNGATCGACATG	2329	TGCAGGACCAGAGAATTCGAATACAG AAATACANNNGATCGACATG	2569	TGCAGGACCAGAGAATTCGAATACAT CCCTTAGNNNGATCGACATG	2809
TGCAGGACCAGAGAATTCGAATACAC AAGCCTANNNGATCGACATG	2330	TGCAGGACCAGAGAATTCGAATACAA CGTACTGNNNGATCGACATG	2570	TGCAGGACCAGAGAATTCGAATACAC CGGATGCNNNGATCGACATG	2810
TGCAGGACCAGAGAATTCGAATACAC TAACTAANNNGATCGACATG	2331	TGCAGGACCAGAGAATTCGAATACAA TTAAGTCNNNGATCGACATG	2571	TGCAGGACCAGAGAATTCGAATACAT CTATATCNNNGATCGACATG	2811
TGCAGGACCAGAGAATTCGAATACAC GCGTAATNNNGATCGACATG	2332	TGCAGGACCAGAGAATTCGAATACAC GTGAAAGNNNGATCGACATG	2572	TGCAGGACCAGAGAATTCGAATACAA GACCCTANNNGATCGACATG	2812
TGCAGGACCAGAGAATTCGAATACAG AGGTCTTNNNGATCGACATG	2333	TGCAGGACCAGAGAATTCGAATACAG GTTAATTNNNGATCGACATG	2573	TGCAGGACCAGAGAATTCGAATACAG GCTGGTCNNNGATCGACATG	2813
TGCAGGACCAGAGAATTCGAATACAA GCCGCTGNNNGATCGACATG	2334	TGCAGGACCAGAGAATTCGAATACAT GACACGTNNNGATCGACATG	2574	TGCAGGACCAGAGAATTCGAATACAG ACGATGANNNGATCGACATG	2814
TGCAGGACCAGAGAATTCGAATACAG GTCAACANNNGATCGACATG	2335	TGCAGGACCAGAGAATTCGAATACAC CCAGTGGNNNGATCGACATG	2575	TGCAGGACCAGAGAATTCGAATACAG CCCATAANNNGATCGACATG	2815
TGCAGGACCAGAGAATTCGAATACAA TCAGGAGNNNGATCGACATG	2336	TGCAGGACCAGAGAATTCGAATACAT CCAAGGTNNNGATCGACATG	2576	TGCAGGACCAGAGAATTCGAATACAA GTTTCATNNNGATCGACATG	2816
TGCAGGACCAGAGAATTCGAATACAC GCCAGAGNNNGATCGACATG	2337	TGCAGGACCAGAGAATTCGAATACAT GAGTATTNNNGATCGACATG	2577	TGCAGGACCAGAGAATTCGAATACAT CGACTTCNNNGATCGACATG	2817
TGCAGGACCAGAGAATTCGAATACAG AGGTGGCNNNGATCGACATG	2338	TGCAGGACCAGAGAATTCGAATACAT GTACGGTNNNGATCGACATG	2578	TGCAGGACCAGAGAATTCGAATACAC GCTACTTNNNGATCGACATG	2818
TGCAGGACCAGAGAATTCGAATACAG CCAAGCCNNNGATCGACATG	2339	TGCAGGACCAGAGAATTCGAATACAC GCGTCAGNNNGATCGACATG	2579	TGCAGGACCAGAGAATTCGAATACAC GAAAACGNNNGATCGACATG	2819
TGCAGGACCAGAGAATTCGAATACAC TGGTGGCNNNGATCGACATG	2340	TGCAGGACCAGAGAATTCGAATACAC GGATGTTNNNGATCGACATG	2580	TGCAGGACCAGAGAATTCGAATACAT TATGGCGNNNGATCGACATG	2820
TGCAGGACCAGAGAATTCGAATACAC GTATGTGNNNGATCGACATG	2341	TGCAGGACCAGAGAATTCGAATACAG ACAAGGTNNNGATCGACATG	2581	TGCAGGACCAGAGAATTCGAATACAG CTATTAANNNGATCGACATG	2821
TGCAGGACCAGAGAATTCGAATACAT GCGTTTCNNNGATCGACATG	2342	TGCAGGACCAGAGAATTCGAATACAA TTAAAAANNNGATCGACATG	2582	TGCAGGACCAGAGAATTCGAATACAG GCCCGCGNNNGATCGACATG	2822
TGCAGGACCAGAGAATTCGAATACAT AAATTTANNNGATCGACATG	2343	TGCAGGACCAGAGAATTCGAATACAA CGACCCGNNNGATCGACATG	2583	TGCAGGACCAGAGAATTCGAATACAG ACGCTGCNNNGATCGACATG	2823
TGCAGGACCAGAGAATTCGAATACAT CGGACATNNNGATCGACATG	2344	TGCAGGACCAGAGAATTCGAATACAT CAAACTANNNGATCGACATG	2584	TGCAGGACCAGAGAATTCGAATACAA CGAGCCCNNNGATCGACATG	2824
TGCAGGACCAGAGAATTCGAATACAT AAACACTNNNGATCGACATG	2345	TGCAGGACCAGAGAATTCGAATACAC ACGCCGANNNGATCGACATG	2585	TGCAGGACCAGAGAATTCGAATACAT TCATCGCNNNGATCGACATG	2825
TGCAGGACCAGAGAATTCGAATACAT TAGGCCANNNGATCGACATG	2346	TGCAGGACCAGAGAATTCGAATACAC GATCAGTNNNGATCGACATG	2586	TGCAGGACCAGAGAATTCGAATACAC ATAAAAGNNNGATCGACATG	2826
TGCAGGACCAGAGAATTCGAATACAA GCCCTCCNNNGATCGACATG	2347	TGCAGGACCAGAGAATTCGAATACAC ACTTTGCNNNGATCGACATG	2587	TGCAGGACCAGAGAATTCGAATACAC TCGCGCTNNNGATCGACATG	2827
TGCAGGACCAGAGAATTCGAATACAC GGAAAACNNNGATCGACATG	2348	TGCAGGACCAGAGAATTCGAATACAT CCTGATCNNNGATCGACATG	2588	TGCAGGACCAGAGAATTCGAATACAG ACATGTCNNNGATCGACATG	2828
TGCAGGACCAGAGAATTCGAATACAG GCCGGTTNNNTGCATCAGGT	2349	TGCAGGACCAGAGAATTCGAATACAG AACTCCANNNTGCATCAGGT	2589	TGCAGGACCAGAGAATTCGAATACAC TCACCGCNNNTGCATCAGGT	2829
TGCAGGACCAGAGAATTCGAATACAT AGGCTACNNNTGCATCAGGT	2350	TGCAGGACCAGAGAATTCGAATACAG GTCAATCNNNTGCATCAGGT	2590	TGCAGGACCAGAGAATTCGAATACAC ACGTCTTNNNTGCATCAGGT	2830
TGCAGGACCAGAGAATTCGAATACAC CACTTGTNNNTGCATCAGGT	2351	TGCAGGACCAGAGAATTCGAATACAT ATGCAGCNNNTGCATCAGGT	2591	TGCAGGACCAGAGAATTCGAATACAA CTGCGTANNNTGCATCAGGT	2831
TGCAGGACCAGAGAATTCGAATACAG ATAGAGCNNNTGCATCAGGT	2352	TGCAGGACCAGAGAATTCGAATACAG CACCTCCNNNTGCATCAGGT	2592	TGCAGGACCAGAGAATTCGAATACAT AAATTATNNNTGCATCAGGT	2832
TGCAGGACCAGAGAATTCGAATACAA GTCCAGTNNNTGCATCAGGT	2353	TGCAGGACCAGAGAATTCGAATACAT CAAGTGCNNNTGCATCAGGT	2593	TGCAGGACCAGAGAATTCGAATACAT AGTCTAANNNTGCATCAGGT	2833
TGCAGGACCAGAGAATTCGAATACAG TCATCAGNNNTGCATCAGGT	2354	TGCAGGACCAGAGAATTCGAATACAT TGCCGTTNNNTGCATCAGGT	2594	TGCAGGACCAGAGAATTCGAATACAC AAACTATNNNTGCATCAGGT	2834
TGCAGGACCAGAGAATTCGAATACAT TTCGGAGNNNTGCATCAGGT	2355	TGCAGGACCAGAGAATTCGAATACAG TGGAGTANNNTGCATCAGGT	2595	TGCAGGACCAGAGAATTCGAATACAT CACTGTCNNNTGCATCAGGT	2835
TGCAGGACCAGAGAATTCGAATACAC TCAGGATNNNTGCATCAGGT	2356	TGCAGGACCAGAGAATTCGAATACAG CCTCACCNNNTGCATCAGGT	2596	TGCAGGACCAGAGAATTCGAATACAA ACAAATGNNNTGCATCAGGT	2836
TGCAGGACCAGAGAATTCGAATACAC CTATCCANNNTGCATCAGGT	2357	TGCAGGACCAGAGAATTCGAATACAA CACACCANNNTGCATCAGGT	2597	TGCAGGACCAGAGAATTCGAATACAT TTTCTTCNNNTGCATCAGGT	2837
TGCAGGACCAGAGAATTCGAATACAC AATGCTGNNNTGCATCAGGT	2358	TGCAGGACCAGAGAATTCGAATACAA CCCCATTNNNTGCATCAGGT	2598	TGCAGGACCAGAGAATTCGAATACAC TTCAGTCNNNTGCATCAGGT	2838
TGCAGGACCAGAGAATTCGAATACAC GGTGAAANNNTGCATCAGGT	2359	TGCAGGACCAGAGAATTCGAATACAA TAGTCTANNNTGCATCAGGT	2599	TGCAGGACCAGAGAATTCGAATACAA GGTCTGTNNNTGCATCAGGT	2839
TGCAGGACCAGAGAATTCGAATACAG TTGCAACNNNTGCATCAGGT	2360	TGCAGGACCAGAGAATTCGAATACAG AATGTCCNNNTGCATCAGGT	2600	TGCAGGACCAGAGAATTCGAATACAG CAAACAGNNNTGCATCAGGT	2840

图15F

池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG AGAGCTANNNTGCATCAGGT	2361	TGCAGGACCAGAGAATTCGAATACAC TAGATCGNNNTGCATCAGGT	2601	TGCAGGACCAGAGAATTCGAATACAC CGAGAGGNNNTGCATCAGGT	2841
TGCAGGACCAGAGAATTCGAATACAG CCTAACANNNTGCATCAGGT	2362	TGCAGGACCAGAGAATTCGAATACAG GCAACCCNNNTGCATCAGGT	2602	TGCAGGACCAGAGAATTCGAATACAA TATTGCANNNTGCATCAGGT	2842
TGCAGGACCAGAGAATTCGAATACAC TGAGACTNNNTGCATCAGGT	2363	TGCAGGACCAGAGAATTCGAATACAG GAGAGAANNNTGCATCAGGT	2603	TGCAGGACCAGAGAATTCGAATACAT CTCTGGTNNNTGCATCAGGT	2843
TGCAGGACCAGAGAATTCGAATACAA GGTTGCANNNTGCATCAGGT	2364	TGCAGGACCAGAGAATTCGAATACAG TTGTCCTNNNTGCATCAGGT	2604	TGCAGGACCAGAGAATTCGAATACAA TTGGAGGNNNTGCATCAGGT	2844
TGCAGGACCAGAGAATTCGAATACAG GAAGCTANNNTGCATCAGGT	2365	TGCAGGACCAGAGAATTCGAATACAT GGCATACNNNTGCATCAGGT	2605	TGCAGGACCAGAGAATTCGAATACAC ATCATTTNNNTGCATCAGGT	2845
TGCAGGACCAGAGAATTCGAATACAC CCTGTATNNNTGCATCAGGT	2366	TGCAGGACCAGAGAATTCGAATACAG AGGCAATNNNTGCATCAGGT	2606	TGCAGGACCAGAGAATTCGAATACAG AGGTGATNNNTGCATCAGGT	2846
TGCAGGACCAGAGAATTCGAATACAT AGCCTCTNNNTGCATCAGGT	2367	TGCAGGACCAGAGAATTCGAATACAT CTCACGTNNNTGCATCAGGT	2607	TGCAGGACCAGAGAATTCGAATACAC CCCGTCANNNTGCATCAGGT	2847
TGCAGGACCAGAGAATTCGAATACAA GGTACCTNNNTGCATCAGGT	2368	TGCAGGACCAGAGAATTCGAATACAC TGCGGCANNNTGCATCAGGT	2608	TGCAGGACCAGAGAATTCGAATACAG ACAGGTANNNTGCATCAGGT	2848
TGCAGGACCAGAGAATTCGAATACAT GTTATCTNNNTGCATCAGGT	2369	TGCAGGACCAGAGAATTCGAATACAC TTAATGANNNTGCATCAGGT	2609	TGCAGGACCAGAGAATTCGAATACAG CGTTAGANNNTGCATCAGGT	2849
TGCAGGACCAGAGAATTCGAATACAG ACTTACGNNNTGCATCAGGT	2370	TGCAGGACCAGAGAATTCGAATACAA ACTCACGNNNTGCATCAGGT	2610	TGCAGGACCAGAGAATTCGAATACAC CTTCTAGNNNTGCATCAGGT	2850
TGCAGGACCAGAGAATTCGAATACAA GTTCCACNNNTGCATCAGGT	2371	TGCAGGACCAGAGAATTCGAATACAA GCAGTGANNNTGCATCAGGT	2611	TGCAGGACCAGAGAATTCGAATACAA GGCTTGTNNNTGCATCAGGT	2851
TGCAGGACCAGAGAATTCGAATACAC CTTCTGANNNTGCATCAGGT	2372	TGCAGGACCAGAGAATTCGAATACAT AATACTGNNNTGCATCAGGT	2612	TGCAGGACCAGAGAATTCGAATACAT GGAGTTCNNNTGCATCAGGT	2852
TGCAGGACCAGAGAATTCGAATACAC GACACTANNNTGCATCAGGT	2373	TGCAGGACCAGAGAATTCGAATACAA AAGTCCCNNNTGCATCAGGT	2613	TGCAGGACCAGAGAATTCGAATACAC CACCGAGNNNTGCATCAGGT	2853
TGCAGGACCAGAGAATTCGAATACAC TGTGAGTNNNTGCATCAGGT	2374	TGCAGGACCAGAGAATTCGAATACAG CTGGAAANNNTGCATCAGGT	2614	TGCAGGACCAGAGAATTCGAATACAG GAATGCANNNTGCATCAGGT	2854
TGCAGGACCAGAGAATTCGAATACAA GAGACACNNNTGCATCAGGT	2375	TGCAGGACCAGAGAATTCGAATACAA AGAGGAGNNNTGCATCAGGT	2615	TGCAGGACCAGAGAATTCGAATACAA CATTACANNNTGCATCAGGT	2855
TGCAGGACCAGAGAATTCGAATACAT AATTGTGNNNTGCATCAGGT	2376	TGCAGGACCAGAGAATTCGAATACAG TGGAAGTNNNTGCATCAGGT	2616	TGCAGGACCAGAGAATTCGAATACAA GTCTCTCNNNTGCATCAGGT	2856
TGCAGGACCAGAGAATTCGAATACAG TAATTTGNNNTGCATCAGGT	2377	TGCAGGACCAGAGAATTCGAATACAC GCGGACTNNNTGCATCAGGT	2617	TGCAGGACCAGAGAATTCGAATACAT AGTGCCANNNTGCATCAGGT	2857
TGCAGGACCAGAGAATTCGAATACAG ATACTATNNNTGCATCAGGT	2378	TGCAGGACCAGAGAATTCGAATACAT ACTTGTTNNNTGCATCAGGT	2618	TGCAGGACCAGAGAATTCGAATACAG CAATGCTNNNTGCATCAGGT	2858
TGCAGGACCAGAGAATTCGAATACAA GTGGATGNNNTGCATCAGGT	2379	TGCAGGACCAGAGAATTCGAATACAA ACTGACCNNNTGCATCAGGT	2619	TGCAGGACCAGAGAATTCGAATACAG TTGAATTNNNTGCATCAGGT	2859
TGCAGGACCAGAGAATTCGAATACAT TATAGACNNNTGCATCAGGT	2380	TGCAGGACCAGAGAATTCGAATACAT GCTGGTANNNTGCATCAGGT	2620	TGCAGGACCAGAGAATTCGAATACAC CACTTCANNNTGCATCAGGT	2860
TGCAGGACCAGAGAATTCGAATACAG AGTTTCGNNNTGCATCAGGT	2381	TGCAGGACCAGAGAATTCGAATACAA TATTTTTNNNTGCATCAGGT	2621	TGCAGGACCAGAGAATTCGAATACAT CCATTCGNNNTGCATCAGGT	2861
TGCAGGACCAGAGAATTCGAATACAC AGAGATGNNNTGCATCAGGT	2382	TGCAGGACCAGAGAATTCGAATACAT CCCCATANNNTGCATCAGGT	2622	TGCAGGACCAGAGAATTCGAATACAC ACTCTCANNNTGCATCAGGT	2862
TGCAGGACCAGAGAATTCGAATACAG ACTCAACNNNTGCATCAGGT	2383	TGCAGGACCAGAGAATTCGAATACAC AAGTTGCNNNTGCATCAGGT	2623	TGCAGGACCAGAGAATTCGAATACAG ACCTGATNNNTGCATCAGGT	2863
TGCAGGACCAGAGAATTCGAATACAT TCGCTGTNNNTGCATCAGGT	2384	TGCAGGACCAGAGAATTCGAATACAT GAACCGTNNNTGCATCAGGT	2624	TGCAGGACCAGAGAATTCGAATACAA GAGCTCTNNNTGCATCAGGT	2864
TGCAGGACCAGAGAATTCGAATACAC GTCCGAGNNNTGCATCAGGT	2385	TGCAGGACCAGAGAATTCGAATACAC GCATTGANNNTGCATCAGGT	2625	TGCAGGACCAGAGAATTCGAATACAC TGGATTGNNNTGCATCAGGT	2865
TGCAGGACCAGAGAATTCGAATACAG CATGCATNNNTGCATCAGGT	2386	TGCAGGACCAGAGAATTCGAATACAC GGCGTTGNNNTGCATCAGGT	2626	TGCAGGACCAGAGAATTCGAATACAT GCTATCCNNNTGCATCAGGT	2866
TGCAGGACCAGAGAATTCGAATACAA AAGTGCGNNNTGCATCAGGT	2387	TGCAGGACCAGAGAATTCGAATACAC CCGCCCGNNNTGCATCAGGT	2627	TGCAGGACCAGAGAATTCGAATACAG ACGTTGTNNNTGCATCAGGT	2867
TGCAGGACCAGAGAATTCGAATACAG AAAGCACNNNTGCATCAGGT	2388	TGCAGGACCAGAGAATTCGAATACAC AAGCTACNNNTGCATCAGGT	2628	TGCAGGACCAGAGAATTCGAATACAA TTCATCTNNNTGCATCAGGT	2868
TGCAGGACCAGAGAATTCGAATACAG GCTGCTGNNNTGCATCAGGT	2389	TGCAGGACCAGAGAATTCGAATACAC GGTTCAANNNTGCATCAGGT	2629	TGCAGGACCAGAGAATTCGAATACAC GATTCAGNNNTGCATCAGGT	2869
TGCAGGACCAGAGAATTCGAATACAG CGGAAGCNNNTGCATCAGGT	2390	TGCAGGACCAGAGAATTCGAATACAC AACGTTGNNNTGCATCAGGT	2630	TGCAGGACCAGAGAATTCGAATACAT GGTGCATNNNTGCATCAGGT	2870
TGCAGGACCAGAGAATTCGAATACAA TCACATANNNTGCATCAGGT	2391	TGCAGGACCAGAGAATTCGAATACAG TACTAGCNNNTGCATCAGGT	2631	TGCAGGACCAGAGAATTCGAATACAT GTGTTTNNNTGCATCAGGT	2871
TGCAGGACCAGAGAATTCGAATACAA GTCTCTGNNNTGCATCAGGT	2392	TGCAGGACCAGAGAATTCGAATACAT GAGTGTCNNNTGCATCAGGT	2632	TGCAGGACCAGAGAATTCGAATACAT GGCATCANNNTGCATCAGGT	2872

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池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC GCCCCCGNNNTGCATCAGGT	2393	TGCAGGACCAGAGAATTCGAATACAC AAACAGGNNNTGCATCAGGT	2633	TGCAGGACCAGAGAATTCGAATACAT AAGCTGCNNNTGCATCAGGT	2873
TGCAGGACCAGAGAATTCGAATACAT TTAATCCNNNTGCATCAGGT	2394	TGCAGGACCAGAGAATTCGAATACAG CATGCTANNNTGCATCAGGT	2634	TGCAGGACCAGAGAATTCGAATACAA CGGACTTNNNTGCATCAGGT	2874
TGCAGGACCAGAGAATTCGAATACAC CGTCGGANNNTGCATCAGGT	2395	TGCAGGACCAGAGAATTCGAATACAG ATTCACGNNNTGCATCAGGT	2635	TGCAGGACCAGAGAATTCGAATACAT GAATTACNNNTGCATCAGGT	2875
TGCAGGACCAGAGAATTCGAATACAT GAGAAATNNNTGCATCAGGT	2396	TGCAGGACCAGAGAATTCGAATACAG TAGATCCNNNTGCATCAGGT	2636	TGCAGGACCAGAGAATTCGAATACAA ACAGAGCNNNTGCATCAGGT	2876
TGCAGGACCAGAGAATTCGAATACAC GTTATAANNNTGCATCAGGT	2397	TGCAGGACCAGAGAATTCGAATACAC GCCAACGNNNTGCATCAGGT	2637	TGCAGGACCAGAGAATTCGAATACAC ATGTTCCNNNTGCATCAGGT	2877
TGCAGGACCAGAGAATTCGAATACAT CTAAAACNNNTGCATCAGGT	2398	TGCAGGACCAGAGAATTCGAATACAG AGCATAGNNNTGCATCAGGT	2638	TGCAGGACCAGAGAATTCGAATACAT CGTCTACNNNTGCATCAGGT	2878
TGCAGGACCAGAGAATTCGAATACAA CACTCGANNNTGCATCAGGT	2399	TGCAGGACCAGAGAATTCGAATACAG GTGTCATNNNTGCATCAGGT	2639	TGCAGGACCAGAGAATTCGAATACAG TAGAGACNNNTGCATCAGGT	2879
TGCAGGACCAGAGAATTCGAATACAG CATCGTANNNTGCATCAGGT	2400	TGCAGGACCAGAGAATTCGAATACAT CTTCGACNNNTGCATCAGGT	2640	TGCAGGACCAGAGAATTCGAATACAT ATAGTGTNNNTGCATCAGGT	2880
TGCAGGACCAGAGAATTCGAATACAG TAAGACGNNNTGCATCAGGT	2401	TGCAGGACCAGAGAATTCGAATACAG ATCAGCTNNNTGCATCAGGT	2641	TGCAGGACCAGAGAATTCGAATACAG GAGAGTTNNNTGCATCAGGT	2881
TGCAGGACCAGAGAATTCGAATACAA AAGCCCTNNNTGCATCAGGT	2402	TGCAGGACCAGAGAATTCGAATACAT CGACCTTNNNTGCATCAGGT	2642	TGCAGGACCAGAGAATTCGAATACAT ACATTCTNNNTGCATCAGGT	2882
TGCAGGACCAGAGAATTCGAATACAC CATGGTANNNTGCATCAGGT	2403	TGCAGGACCAGAGAATTCGAATACAA GCCCACGNNNTGCATCAGGT	2643	TGCAGGACCAGAGAATTCGAATACAC ACAATGCNNNTGCATCAGGT	2883
TGCAGGACCAGAGAATTCGAATACAC GAAATAANNNTGCATCAGGT	2404	TGCAGGACCAGAGAATTCGAATACAG AGATCTCNNNTGCATCAGGT	2644	TGCAGGACCAGAGAATTCGAATACAG ATATTACNNNTGCATCAGGT	2884
TGCAGGACCAGAGAATTCGAATACAG ATCAAAANNNTGCATCAGGT	2405	TGCAGGACCAGAGAATTCGAATACAT CTTTAACNNNTGCATCAGGT	2645	TGCAGGACCAGAGAATTCGAATACAC GGCTTTTNNNTGCATCAGGT	2885
TGCAGGACCAGAGAATTCGAATACAA GTGCCGCNNNTGCATCAGGT	2406	TGCAGGACCAGAGAATTCGAATACAT CCCTAACNNNTGCATCAGGT	2646	TGCAGGACCAGAGAATTCGAATACAG CTGCTGGNNNTGCATCAGGT	2886
TGCAGGACCAGAGAATTCGAATACAC CCTGGCTNNNTGCATCAGGT	2407	TGCAGGACCAGAGAATTCGAATACAA CTCGACANNNTGCATCAGGT	2647	TGCAGGACCAGAGAATTCGAATACAA AGGCGCGNNNTGCATCAGGT	2887
TGCAGGACCAGAGAATTCGAATACAC AAGTTCGNNNTGCATCAGGT	2408	TGCAGGACCAGAGAATTCGAATACAT GAGAGACNNNTGCATCAGGT	2648	TGCAGGACCAGAGAATTCGAATACAA CGGTGAANNNTGCATCAGGT	2888

图15H

池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC CACGGACNNNACGTATGCCA	2889	TGCAGGACCAGAGAATTCGAATACAC ATGCGTANNNACGTATGCCA	3129	TGCAGGACCAGAGAATTCGAATACAG TGTGATCNNNACGTATGCCA	3369
TGCAGGACCAGAGAATTCGAATACAA ATCCTCCNNNACGTATGCCA	2890	TGCAGGACCAGAGAATTCGAATACAT CGTGCGGNNNACGTATGCCA	3130	TGCAGGACCAGAGAATTCGAATACAA AAGCGCANNNACGTATGCCA	3370
TGCAGGACCAGAGAATTCGAATACAG TGGCCGTNNNACGTATGCCA	2891	TGCAGGACCAGAGAATTCGAATACAG TAGTGGANNNACGTATGCCA	3131	TGCAGGACCAGAGAATTCGAATACAT CGTGGATNNNACGTATGCCA	3371
TGCAGGACCAGAGAATTCGAATACAA GAGTAGCNNNACGTATGCCA	2892	TGCAGGACCAGAGAATTCGAATACAG TTGTTGGNNNACGTATGCCA	3132	TGCAGGACCAGAGAATTCGAATACAT CACCGAANNNACGTATGCCA	3372
TGCAGGACCAGAGAATTCGAATACAT CCTGCGCNNNACGTATGCCA	2893	TGCAGGACCAGAGAATTCGAATACAA GAGCTTCNNNACGTATGCCA	3133	TGCAGGACCAGAGAATTCGAATACAG CCGTTGGNNNACGTATGCCA	3373
TGCAGGACCAGAGAATTCGAATACAT TCTCGTGNNNACGTATGCCA	2894	TGCAGGACCAGAGAATTCGAATACAG TACTGTGNNNACGTATGCCA	3134	TGCAGGACCAGAGAATTCGAATACAA CACGGTTNNNACGTATGCCA	3374
TGCAGGACCAGAGAATTCGAATACAT GGTATGCNNNACGTATGCCA	2895	TGCAGGACCAGAGAATTCGAATACAA GCAACCTNNNACGTATGCCA	3135	TGCAGGACCAGAGAATTCGAATACAG CTCACGGNNNACGTATGCCA	3375
TGCAGGACCAGAGAATTCGAATACAA TCACTCCNNNACGTATGCCA	2896	TGCAGGACCAGAGAATTCGAATACAG CCCTGCTNNNACGTATGCCA	3136	TGCAGGACCAGAGAATTCGAATACAC AATCGCANNNACGTATGCCA	3376
TGCAGGACCAGAGAATTCGAATACAA ACAAGGCNNNACGTATGCCA	2897	TGCAGGACCAGAGAATTCGAATACAC TCTCGCGNNNACGTATGCCA	3137	TGCAGGACCAGAGAATTCGAATACAT AATATATNNNACGTATGCCA	3377
TGCAGGACCAGAGAATTCGAATACAC CGTCTTANNNACGTATGCCA	2898	TGCAGGACCAGAGAATTCGAATACAC TACTTGCNNNACGTATGCCA	3138	TGCAGGACCAGAGAATTCGAATACAC ATTACCCNNNACGTATGCCA	3378
TGCAGGACCAGAGAATTCGAATACAA AAAATTANNNACGTATGCCA	2899	TGCAGGACCAGAGAATTCGAATACAA TAATGAGNNNACGTATGCCA	3139	TGCAGGACCAGAGAATTCGAATACAG ACTACTGNNNACGTATGCCA	3379
TGCAGGACCAGAGAATTCGAATACAA CACAGAGNNNACGTATGCCA	2900	TGCAGGACCAGAGAATTCGAATACAC CGTAGTANNNACGTATGCCA	3140	TGCAGGACCAGAGAATTCGAATACAG TGCACGCNNNACGTATGCCA	3380
TGCAGGACCAGAGAATTCGAATACAG GTGCGCTNNNACGTATGCCA	2901	TGCAGGACCAGAGAATTCGAATACAA GCAACAGNNNACGTATGCCA	3141	TGCAGGACCAGAGAATTCGAATACAG GCTATTGNNNACGTATGCCA	3381
TGCAGGACCAGAGAATTCGAATACAC GTGACGCNNNACGTATGCCA	2902	TGCAGGACCAGAGAATTCGAATACAC TGTGTCTNNNACGTATGCCA	3142	TGCAGGACCAGAGAATTCGAATACAG GTGGTGGNNNACGTATGCCA	3382
TGCAGGACCAGAGAATTCGAATACAG ACCCCCTNNNACGTATGCCA	2903	TGCAGGACCAGAGAATTCGAATACAT CCAAACGNNNACGTATGCCA	3143	TGCAGGACCAGAGAATTCGAATACAT GCGTACANNNACGTATGCCA	3383
TGCAGGACCAGAGAATTCGAATACAA CATTTGANNNACGTATGCCA	2904	TGCAGGACCAGAGAATTCGAATACAT GTCAAGCNNNACGTATGCCA	3144	TGCAGGACCAGAGAATTCGAATACAA TTCTTCANNNACGTATGCCA	3384
TGCAGGACCAGAGAATTCGAATACAG GTGGCAGNNNACGTATGCCA	2905	TGCAGGACCAGAGAATTCGAATACAA GTGTCACNNNACGTATGCCA	3145	TGCAGGACCAGAGAATTCGAATACAT CTGGTCTNNNACGTATGCCA	3385
TGCAGGACCAGAGAATTCGAATACAG AGGCCAGNNNACGTATGCCA	2906	TGCAGGACCAGAGAATTCGAATACAC CTCAAGANNNACGTATGCCA	3146	TGCAGGACCAGAGAATTCGAATACAG CGAGCCTNNNACGTATGCCA	3386
TGCAGGACCAGAGAATTCGAATACAA CTGAGTNNNACGTATGCCA	2907	TGCAGGACCAGAGAATTCGAATACAG TGAAAGCNNNACGTATGCCA	3147	TGCAGGACCAGAGAATTCGAATACAA GCCGTGCNNNACGTATGCCA	3387
TGCAGGACCAGAGAATTCGAATACAC CAAAAGGNNNACGTATGCCA	2908	TGCAGGACCAGAGAATTCGAATACAT TGCGCCCNNNACGTATGCCA	3148	TGCAGGACCAGAGAATTCGAATACAG ATAACCCNNNACGTATGCCA	3388
TGCAGGACCAGAGAATTCGAATACAA AGCAACGNNNACGTATGCCA	2909	TGCAGGACCAGAGAATTCGAATACAG TATTGCGNNNACGTATGCCA	3149	TGCAGGACCAGAGAATTCGAATACAC GGAACCCNNNACGTATGCCA	3389
TGCAGGACCAGAGAATTCGAATACAC GCTTTGTNNNACGTATGCCA	2910	TGCAGGACCAGAGAATTCGAATACAA CAAATAGNNNACGTATGCCA	3150	TGCAGGACCAGAGAATTCGAATACAG TCCAGCGNNNACGTATGCCA	3390
TGCAGGACCAGAGAATTCGAATACAT GGATGCTNNNACGTATGCCA	2911	TGCAGGACCAGAGAATTCGAATACAC TACGCGGNNNACGTATGCCA	3151	TGCAGGACCAGAGAATTCGAATACAC GTGAGCCNNNACGTATGCCA	3391
TGCAGGACCAGAGAATTCGAATACAT CAATGGCNNNACGTATGCCA	2912	TGCAGGACCAGAGAATTCGAATACAT GTATACANNNACGTATGCCA	3152	TGCAGGACCAGAGAATTCGAATACAT CGGCCAGNNNACGTATGCCA	3392
TGCAGGACCAGAGAATTCGAATACAA ACTACTANNNACGTATGCCA	2913	TGCAGGACCAGAGAATTCGAATACAA GACCTACNNNACGTATGCCA	3153	TGCAGGACCAGAGAATTCGAATACAC CGCCAAGNNNACGTATGCCA	3393
TGCAGGACCAGAGAATTCGAATACAT TGCGATGNNNACGTATGCCA	2914	TGCAGGACCAGAGAATTCGAATACAT TCCCATGNNNACGTATGCCA	3154	TGCAGGACCAGAGAATTCGAATACAG GCTGTTANNNACGTATGCCA	3394
TGCAGGACCAGAGAATTCGAATACAG AGATACGNNNACGTATGCCA	2915	TGCAGGACCAGAGAATTCGAATACAT AGCCCTTNNNACGTATGCCA	3155	TGCAGGACCAGAGAATTCGAATACAT GAAAATGNNNACGTATGCCA	3395
TGCAGGACCAGAGAATTCGAATACAT CCTTTTTNNNACGTATGCCA	2916	TGCAGGACCAGAGAATTCGAATACAG GTTCACANNNACGTATGCCA	3156	TGCAGGACCAGAGAATTCGAATACAC TTCTATANNNACGTATGCCA	3396
TGCAGGACCAGAGAATTCGAATACAG TTAGCGTNNNACGTATGCCA	2917	TGCAGGACCAGAGAATTCGAATACAG ACGTTTGNNNACGTATGCCA	3157	TGCAGGACCAGAGAATTCGAATACAT CCCCGCANNNACGTATGCCA	3397
TGCAGGACCAGAGAATTCGAATACAG CGGCGCCNNNACGTATGCCA	2918	TGCAGGACCAGAGAATTCGAATACAT GTTGATANNNACGTATGCCA	3158	TGCAGGACCAGAGAATTCGAATACAT GTCTACCNNNACGTATGCCA	3398
TGCAGGACCAGAGAATTCGAATACAA TGCTCTCNNNACGTATGCCA	2919	TGCAGGACCAGAGAATTCGAATACAA GTATTACNNNACGTATGCCA	3159	TGCAGGACCAGAGAATTCGAATACAT GTAGTTANNNACGTATGCCA	3399
TGCAGGACCAGAGAATTCGAATACAT TATCTACNNNACGTATGCCA	2920	TGCAGGACCAGAGAATTCGAATACAG AGAACACNNNACGTATGCCA	3160	TGCAGGACCAGAGAATTCGAATACAT GGTTTAANNNACGTATGCCA	3400
TGCAGGACCAGAGAATTCGAATACAT TCTATTGNNNACGTATGCCA	2921	TGCAGGACCAGAGAATTCGAATACAC CTAAATANNNACGTATGCCA	3161	TGCAGGACCAGAGAATTCGAATACAG AGACGGCNNNACGTATGCCA	3401

图16A

池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC CAGTACANNNACGTATGCCA	2922	TGCAGGACCAGAGAATTCGAATACAA TTTCACTNNNACGTATGCCA	3162	TGCAGGACCAGAGAATTCGAATACAC GTCGAGCNNNACGTATGCCA	3402
TGCAGGACCAGAGAATTCGAATACAA CAGAATANNNACGTATGCCA	2923	TGCAGGACCAGAGAATTCGAATACAG TCAACGTNNNACGTATGCCA	3163	TGCAGGACCAGAGAATTCGAATACAC AACAGTCNNNACGTATGCCA	3403
TGCAGGACCAGAGAATTCGAATACAG TATATACNNNACGTATGCCA	2924	TGCAGGACCAGAGAATTCGAATACAG CGTGCTGNNNACGTATGCCA	3164	TGCAGGACCAGAGAATTCGAATACAT GTTGCGANNNACGTATGCCA	3404
TGCAGGACCAGAGAATTCGAATACAT ATTAACGNNNACGTATGCCA	2925	TGCAGGACCAGAGAATTCGAATACAA AACCCACNNNACGTATGCCA	3165	TGCAGGACCAGAGAATTCGAATACAC GTATTTTNNNACGTATGCCA	3405
TGCAGGACCAGAGAATTCGAATACAG GTTAGAGNNNACGTATGCCA	2926	TGCAGGACCAGAGAATTCGAATACAC CCCTGTGNNNACGTATGCCA	3166	TGCAGGACCAGAGAATTCGAATACAG TACGTCANNNACGTATGCCA	3406
TGCAGGACCAGAGAATTCGAATACAC TAGGATCNNNACGTATGCCA	2927	TGCAGGACCAGAGAATTCGAATACAA GTAGCCTNNNACGTATGCCA	3167	TGCAGGACCAGAGAATTCGAATACAC CTAGCGGNNNACGTATGCCA	3407
TGCAGGACCAGAGAATTCGAATACAG ACTAGGANNNACGTATGCCA	2928	TGCAGGACCAGAGAATTCGAATACAA TCCATGGNNNACGTATGCCA	3168	TGCAGGACCAGAGAATTCGAATACAA GAGCCGGNNNACGTATGCCA	3408
TGCAGGACCAGAGAATTCGAATACAA GTTATCTNNNACGTATGCCA	2929	TGCAGGACCAGAGAATTCGAATACAC GCATCTTNNNACGTATGCCA	3169	TGCAGGACCAGAGAATTCGAATACAG GCGCCCGNNNACGTATGCCA	3409
TGCAGGACCAGAGAATTCGAATACAG ACGTCCGNNNACGTATGCCA	2930	TGCAGGACCAGAGAATTCGAATACAA GAATCCCNNNACGTATGCCA	3170	TGCAGGACCAGAGAATTCGAATACAC AGCATGTNNNACGTATGCCA	3410
TGCAGGACCAGAGAATTCGAATACAA TGGAAATNNNACGTATGCCA	2931	TGCAGGACCAGAGAATTCGAATACAC GTTGTGTNNNACGTATGCCA	3171	TGCAGGACCAGAGAATTCGAATACAA GCTTAATNNNACGTATGCCA	3411
TGCAGGACCAGAGAATTCGAATACAT GTTCAGGNNNACGTATGCCA	2932	TGCAGGACCAGAGAATTCGAATACAG AAACCAGNNNACGTATGCCA	3172	TGCAGGACCAGAGAATTCGAATACAC TCACCCGNNNACGTATGCCA	3412
TGCAGGACCAGAGAATTCGAATACAT GCAATCGNNNACGTATGCCA	2933	TGCAGGACCAGAGAATTCGAATACAG GATACTCNNNACGTATGCCA	3173	TGCAGGACCAGAGAATTCGAATACAT CGGACGCNNNACGTATGCCA	3413
TGCAGGACCAGAGAATTCGAATACAT TATGGATNNNACGTATGCCA	2934	TGCAGGACCAGAGAATTCGAATACAA GGCCGAGNNNACGTATGCCA	3174	TGCAGGACCAGAGAATTCGAATACAA ACTGCGTNNNACGTATGCCA	3414
TGCAGGACCAGAGAATTCGAATACAA CATCGTGNNNACGTATGCCA	2935	TGCAGGACCAGAGAATTCGAATACAC ACTGTTCNNNACGTATGCCA	3175	TGCAGGACCAGAGAATTCGAATACAG CCTCCTGNNNACGTATGCCA	3415
TGCAGGACCAGAGAATTCGAATACAA AAGTAGTNNNACGTATGCCA	2936	TGCAGGACCAGAGAATTCGAATACAG TGGAGGCNNNACGTATGCCA	3176	TGCAGGACCAGAGAATTCGAATACAT AGTTAACNNNACGTATGCCA	3416
TGCAGGACCAGAGAATTCGAATACAT AATAACCNNNACGTATGCCA	2937	TGCAGGACCAGAGAATTCGAATACAA GTATCGCNNNACGTATGCCA	3177	TGCAGGACCAGAGAATTCGAATACAG GACTTCANNNACGTATGCCA	3417
TGCAGGACCAGAGAATTCGAATACAA TTCTCATNNNACGTATGCCA	2938	TGCAGGACCAGAGAATTCGAATACAT CGAGATCNNNACGTATGCCA	3178	TGCAGGACCAGAGAATTCGAATACAG CCGCATGNNNACGTATGCCA	3418
TGCAGGACCAGAGAATTCGAATACAA CATCCCTNNNACGTATGCCA	2939	TGCAGGACCAGAGAATTCGAATACAC GGTAGTTNNNACGTATGCCA	3179	TGCAGGACCAGAGAATTCGAATACAT GGAGTAGNNNACGTATGCCA	3419
TGCAGGACCAGAGAATTCGAATACAT GAAAGTANNNACGTATGCCA	2940	TGCAGGACCAGAGAATTCGAATACAC CGTATCTNNNACGTATGCCA	3180	TGCAGGACCAGAGAATTCGAATACAC TGTTATTNNNACGTATGCCA	3420
TGCAGGACCAGAGAATTCGAATACAG ACATTATNNNACGTATGCCA	2941	TGCAGGACCAGAGAATTCGAATACAA ACGCACTNNNACGTATGCCA	3181	TGCAGGACCAGAGAATTCGAATACAA AGAGCACNNNACGTATGCCA	3421
TGCAGGACCAGAGAATTCGAATACAG GATACGANNNACGTATGCCA	2942	TGCAGGACCAGAGAATTCGAATACAC CGATTGANNNACGTATGCCA	3182	TGCAGGACCAGAGAATTCGAATACAC GTCGAATNNNACGTATGCCA	3422
TGCAGGACCAGAGAATTCGAATACAG TACATATNNNACGTATGCCA	2943	TGCAGGACCAGAGAATTCGAATACAG CTCTAAGNNNACGTATGCCA	3183	TGCAGGACCAGAGAATTCGAATACAC TCGTGAANNNACGTATGCCA	3423
TGCAGGACCAGAGAATTCGAATACAT CATAGCGNNNACGTATGCCA	2944	TGCAGGACCAGAGAATTCGAATACAG GTGAGTANNNACGTATGCCA	3184	TGCAGGACCAGAGAATTCGAATACAG ATGGCAANNNACGTATGCCA	3424
TGCAGGACCAGAGAATTCGAATACAC TTGAACGNNNACGTATGCCA	2945	TGCAGGACCAGAGAATTCGAATACAG CCTATGANNNACGTATGCCA	3185	TGCAGGACCAGAGAATTCGAATACAT AGGTGGANNNACGTATGCCA	3425
TGCAGGACCAGAGAATTCGAATACAC TTCCCAANNNACGTATGCCA	2946	TGCAGGACCAGAGAATTCGAATACAA CGGAGCGNNNACGTATGCCA	3186	TGCAGGACCAGAGAATTCGAATACAG ATGACTCNNNACGTATGCCA	3426
TGCAGGACCAGAGAATTCGAATACAA GAGCCCCNNNACGTATGCCA	2947	TGCAGGACCAGAGAATTCGAATACAC TGTGACANNNACGTATGCCA	3187	TGCAGGACCAGAGAATTCGAATACAG CTCTGTTNNNACGTATGCCA	3427
TGCAGGACCAGAGAATTCGAATACAA TAATCACNNNACGTATGCCA	2948	TGCAGGACCAGAGAATTCGAATACAC GTCCGTCNNNACGTATGCCA	3188	TGCAGGACCAGAGAATTCGAATACAA CGCAACTNNNACGTATGCCA	3428
TGCAGGACCAGAGAATTCGAATACAG ACGACAANNNCTAGCGTTAC	2949	TGCAGGACCAGAGAATTCGAATACAA TCGTGACNNNCTAGCGTTAC	3189	TGCAGGACCAGAGAATTCGAATACAC GAATGCTNNNCTAGCGTTAC	3429
TGCAGGACCAGAGAATTCGAATACAC GAATTATNNNCTAGCGTTAC	2950	TGCAGGACCAGAGAATTCGAATACAC CATGTCTNNNCTAGCGTTAC	3190	TGCAGGACCAGAGAATTCGAATACAA GCCAATCNNNCTAGCGTTAC	3430
TGCAGGACCAGAGAATTCGAATACAC GCGCTGANNNCTAGCGTTAC	2951	TGCAGGACCAGAGAATTCGAATACAC CTTTTGGNNNCTAGCGTTAC	3191	TGCAGGACCAGAGAATTCGAATACAG CAGTTTGNNNCTAGCGTTAC	3431
TGCAGGACCAGAGAATTCGAATACAT CAATTAGNNNCTAGCGTTAC	2952	TGCAGGACCAGAGAATTCGAATACAC GCGTCGANNNCTAGCGTTAC	3192	TGCAGGACCAGAGAATTCGAATACAC GCAATGTNNNCTAGCGTTAC	3432
TGCAGGACCAGAGAATTCGAATACAA TGAGCAGNNNCTAGCGTTAC	2953	TGCAGGACCAGAGAATTCGAATACAG CCCCCATNNNCTAGCGTTAC	3193	TGCAGGACCAGAGAATTCGAATACAT GCAGTGTNNNCTAGCGTTAC	3433
TGCAGGACCAGAGAATTCGAATACAT GACTTAANNNCTAGCGTTAC	2954	TGCAGGACCAGAGAATTCGAATACAG TCTTTCGNNNCTAGCGTTAC	3194	TGCAGGACCAGAGAATTCGAATACAA GTCCATGNNNCTAGCGTTAC	3434

图16B

池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT GAGAATANNNCTAGCGTTAC	2955	TGCAGGACCAGAGAATTCGAATACAA TCCACGANNNCTAGCGTTAC	3195	TGCAGGACCAGAGAATTCGAATACAC TATTCATNNNCTAGCGTTAC	3435
TGCAGGACCAGAGAATTCGAATACAC TTTTTCTNNNCTAGCGTTAC	2956	TGCAGGACCAGAGAATTCGAATACAT ATGCATANNNCTAGCGTTAC	3196	TGCAGGACCAGAGAATTCGAATACAG TCGTTCTNNNCTAGCGTTAC	3436
TGCAGGACCAGAGAATTCGAATACAG TCGCAATNNNCTAGCGTTAC	2957	TGCAGGACCAGAGAATTCGAATACAG AGAAATTNNNCTAGCGTTAC	3197	TGCAGGACCAGAGAATTCGAATACAC GTTGTAGNNNCTAGCGTTAC	3437
TGCAGGACCAGAGAATTCGAATACAA TCCATCCNNNCTAGCGTTAC	2958	TGCAGGACCAGAGAATTCGAATACAC CTCAATCNNNCTAGCGTTAC	3198	TGCAGGACCAGAGAATTCGAATACAG ACAGCGGNNNCTAGCGTTAC	3438
TGCAGGACCAGAGAATTCGAATACAA GATATGANNNCTAGCGTTAC	2959	TGCAGGACCAGAGAATTCGAATACAC AAAACAANNNCTAGCGTTAC	3199	TGCAGGACCAGAGAATTCGAATACAT ACACCCTNNNCTAGCGTTAC	3439
TGCAGGACCAGAGAATTCGAATACAT AGCTACGNNNCTAGCGTTAC	2960	TGCAGGACCAGAGAATTCGAATACAG TGATGTCNNNCTAGCGTTAC	3200	TGCAGGACCAGAGAATTCGAATACAC GTTAAGCNNNCTAGCGTTAC	3440
TGCAGGACCAGAGAATTCGAATACAT TACAGGCNNNCTAGCGTTAC	2961	TGCAGGACCAGAGAATTCGAATACAT GCCGTAANNNCTAGCGTTAC	3201	TGCAGGACCAGAGAATTCGAATACAA TCGCCTTNNNCTAGCGTTAC	3441
TGCAGGACCAGAGAATTCGAATACAG ACTACACNNNCTAGCGTTAC	2962	TGCAGGACCAGAGAATTCGAATACAA GCTCTAGNNNCTAGCGTTAC	3202	TGCAGGACCAGAGAATTCGAATACAG CTATGCANNNCTAGCGTTAC	3442
TGCAGGACCAGAGAATTCGAATACAA TTTTAGGNNNCTAGCGTTAC	2963	TGCAGGACCAGAGAATTCGAATACAG GCGTGCTNNNCTAGCGTTAC	3203	TGCAGGACCAGAGAATTCGAATACAA CGCACGCNNNCTAGCGTTAC	3443
TGCAGGACCAGAGAATTCGAATACAT TTTCAGTNNNCTAGCGTTAC	2964	TGCAGGACCAGAGAATTCGAATACAG ACGTCATNNNCTAGCGTTAC	3204	TGCAGGACCAGAGAATTCGAATACAC GTCACAANNNCTAGCGTTAC	3444
TGCAGGACCAGAGAATTCGAATACAG CAGAACANNNCTAGCGTTAC	2965	TGCAGGACCAGAGAATTCGAATACAT GTATTAGNNNCTAGCGTTAC	3205	TGCAGGACCAGAGAATTCGAATACAC GCGATCGNNNCTAGCGTTAC	3445
TGCAGGACCAGAGAATTCGAATACAC GAGTAGANNNCTAGCGTTAC	2966	TGCAGGACCAGAGAATTCGAATACAA TGATTACNNNCTAGCGTTAC	3206	TGCAGGACCAGAGAATTCGAATACAG TTAGACCNNNCTAGCGTTAC	3446
TGCAGGACCAGAGAATTCGAATACAG TCGGAGGNNNCTAGCGTTAC	2967	TGCAGGACCAGAGAATTCGAATACAA GTCCGAANNNCTAGCGTTAC	3207	TGCAGGACCAGAGAATTCGAATACAT CGCGAGCNNNCTAGCGTTAC	3447
TGCAGGACCAGAGAATTCGAATACAA TGTACTANNNCTAGCGTTAC	2968	TGCAGGACCAGAGAATTCGAATACAT TCTTCCCNNNCTAGCGTTAC	3208	TGCAGGACCAGAGAATTCGAATACAT GTAAACTNNNCTAGCGTTAC	3448
TGCAGGACCAGAGAATTCGAATACAT ACTCCGTNNNCTAGCGTTAC	2969	TGCAGGACCAGAGAATTCGAATACAT CTCCTAGNNNCTAGCGTTAC	3209	TGCAGGACCAGAGAATTCGAATACAT GCCATAGNNNCTAGCGTTAC	3449
TGCAGGACCAGAGAATTCGAATACAC ACATTGGNNNCTAGCGTTAC	2970	TGCAGGACCAGAGAATTCGAATACAG ACTTATANNNCTAGCGTTAC	3210	TGCAGGACCAGAGAATTCGAATACAT AATTACGNNNCTAGCGTTAC	3450
TGCAGGACCAGAGAATTCGAATACAT TAGCAATNNNCTAGCGTTAC	2971	TGCAGGACCAGAGAATTCGAATACAC GAGTGAANNNCTAGCGTTAC	3211	TGCAGGACCAGAGAATTCGAATACAC CCGCGCCNNNCTAGCGTTAC	3451
TGCAGGACCAGAGAATTCGAATACAT CCAACGANNNCTAGCGTTAC	2972	TGCAGGACCAGAGAATTCGAATACAT ATAAATTNNNCTAGCGTTAC	3212	TGCAGGACCAGAGAATTCGAATACAC AATATCANNNCTAGCGTTAC	3452
TGCAGGACCAGAGAATTCGAATACAT TGATCCCNNNCTAGCGTTAC	2973	TGCAGGACCAGAGAATTCGAATACAG CGGTGAGNNNCTAGCGTTAC	3213	TGCAGGACCAGAGAATTCGAATACAA TTAAGGANNNCTAGCGTTAC	3453
TGCAGGACCAGAGAATTCGAATACAT ATTAATANNNCTAGCGTTAC	2974	TGCAGGACCAGAGAATTCGAATACAA GTCCCTTNNNCTAGCGTTAC	3214	TGCAGGACCAGAGAATTCGAATACAA TATACACNNNCTAGCGTTAC	3454
TGCAGGACCAGAGAATTCGAATACAT AAGTTTGNNNCTAGCGTTAC	2975	TGCAGGACCAGAGAATTCGAATACAA GACTTATNNNCTAGCGTTAC	3215	TGCAGGACCAGAGAATTCGAATACAT ATTGACANNNCTAGCGTTAC	3455
TGCAGGACCAGAGAATTCGAATACAG GCCGCGCNNNCTAGCGTTAC	2976	TGCAGGACCAGAGAATTCGAATACAT GGCACTANNNCTAGCGTTAC	3216	TGCAGGACCAGAGAATTCGAATACAA CGAAAATNNNCTAGCGTTAC	3456
TGCAGGACCAGAGAATTCGAATACAT CACACGANNNCTAGCGTTAC	2977	TGCAGGACCAGAGAATTCGAATACAA TTCCTATNNNCTAGCGTTAC	3217	TGCAGGACCAGAGAATTCGAATACAG TAGGACANNNCTAGCGTTAC	3457
TGCAGGACCAGAGAATTCGAATACAG AGTCGTTNNNCTAGCGTTAC	2978	TGCAGGACCAGAGAATTCGAATACAC TGATATANNNCTAGCGTTAC	3218	TGCAGGACCAGAGAATTCGAATACAC CCCCAGTNNNCTAGCGTTAC	3458
TGCAGGACCAGAGAATTCGAATACAA GAGCCTTNNNCTAGCGTTAC	2979	TGCAGGACCAGAGAATTCGAATACAC AAGCACTNNNCTAGCGTTAC	3219	TGCAGGACCAGAGAATTCGAATACAC CTACGTTNNNCTAGCGTTAC	3459
TGCAGGACCAGAGAATTCGAATACAC CTTGCTANNNCTAGCGTTAC	2980	TGCAGGACCAGAGAATTCGAATACAG CGCATGCNNNCTAGCGTTAC	3220	TGCAGGACCAGAGAATTCGAATACAT GGTGAGANNNCTAGCGTTAC	3460
TGCAGGACCAGAGAATTCGAATACAA TCATAGTNNNCTAGCGTTAC	2981	TGCAGGACCAGAGAATTCGAATACAT TCTCAATNNNCTAGCGTTAC	3221	TGCAGGACCAGAGAATTCGAATACAC TAGCACANNNCTAGCGTTAC	3461
TGCAGGACCAGAGAATTCGAATACAT AGCAATTNNNCTAGCGTTAC	2982	TGCAGGACCAGAGAATTCGAATACAT CGCCACCNNNCTAGCGTTAC	3222	TGCAGGACCAGAGAATTCGAATACAT CATGTAANNNCTAGCGTTAC	3462
TGCAGGACCAGAGAATTCGAATACAC AATTGTANNNCTAGCGTTAC	2983	TGCAGGACCAGAGAATTCGAATACAG GACGGACNNNCTAGCGTTAC	3223	TGCAGGACCAGAGAATTCGAATACAG GACGAATNNNCTAGCGTTAC	3463
TGCAGGACCAGAGAATTCGAATACAT TCGGCAANNNCTAGCGTTAC	2984	TGCAGGACCAGAGAATTCGAATACAC GAACAGANNNCTAGCGTTAC	3224	TGCAGGACCAGAGAATTCGAATACAG GATGGCGNNNCTAGCGTTAC	3464
TGCAGGACCAGAGAATTCGAATACAC GTAGTCTNNNCTAGCGTTAC	2985	TGCAGGACCAGAGAATTCGAATACAT ATCTCGCNNNCTAGCGTTAC	3225	TGCAGGACCAGAGAATTCGAATACAT CCCAGTTNNNCTAGCGTTAC	3465
TGCAGGACCAGAGAATTCGAATACAC TAGGCTANNNCTAGCGTTAC	2986	TGCAGGACCAGAGAATTCGAATACAT GCATCAGNNNCTAGCGTTAC	3226	TGCAGGACCAGAGAATTCGAATACAC GAGACAANNNCTAGCGTTAC	3466
TGCAGGACCAGAGAATTCGAATACAA ATCAATCNNNCTAGCGTTAC	2987	TGCAGGACCAGAGAATTCGAATACAC CTAAAGCNNNCTAGCGTTAC	3227	TGCAGGACCAGAGAATTCGAATACAC AATACCGNNNCTAGCGTTAC	3467

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池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG CCCTCGTNNNCTAGCGTTAC	2988	TGCAGGACCAGAGAATTCGAATACAT TTGACAANNNCTAGCGTTAC	3228	TGCAGGACCAGAGAATTCGAATACAT TTATGTCNNNCTAGCGTTAC	3468
TGCAGGACCAGAGAATTCGAATACAA GGTTGAGNNNCTAGCGTTAC	2989	TGCAGGACCAGAGAATTCGAATACAC CCGCCATNNNCTAGCGTTAC	3229	TGCAGGACCAGAGAATTCGAATACAT GGTAACGNNNCTAGCGTTAC	3469
TGCAGGACCAGAGAATTCGAATACAC AGCCAGCNNNCTAGCGTTAC	2990	TGCAGGACCAGAGAATTCGAATACAT TGCATAANNNCTAGCGTTAC	3230	TGCAGGACCAGAGAATTCGAATACAA GCCCATANNNCTAGCGTTAC	3470
TGCAGGACCAGAGAATTCGAATACAA CIAATGTNNNCTAGCGTTAC	2991	TGCAGGACCAGAGAATTCGAATACAA CAGAGCANNNCTAGCGTTAC	3231	TGCAGGACCAGAGAATTCGAATACAA TCCTCCANNNCTAGCGTTAC	3471
TGCAGGACCAGAGAATTCGAATACAG GTAAGACNNNCTAGCGTTAC	2992	TGCAGGACCAGAGAATTCGAATACAG GTACGTTNNNCTAGCGTTAC	3232	TGCAGGACCAGAGAATTCGAATACAT TTTTGACNNNCTAGCGTTAC	3472
TGCAGGACCAGAGAATTCGAATACAC TCGCGAGNNNCTAGCGTTAC	2993	TGCAGGACCAGAGAATTCGAATACAG ATGCACTNNNCTAGCGTTAC	3233	TGCAGGACCAGAGAATTCGAATACAA TAGCCTGNNNCTAGCGTTAC	3473
TGCAGGACCAGAGAATTCGAATACAC TGCCGCTNNNCTAGCGTTAC	2994	TGCAGGACCAGAGAATTCGAATACAA TCTAAACNNNCTAGCGTTAC	3234	TGCAGGACCAGAGAATTCGAATACAG GAGTCTTNNNCTAGCGTTAC	3474
TGCAGGACCAGAGAATTCGAATACAA CTGCGGCNNNCTAGCGTTAC	2995	TGCAGGACCAGAGAATTCGAATACAA CGAGAACNNNCTAGCGTTAC	3235	TGCAGGACCAGAGAATTCGAATACAA CCCCACCNNNCTAGCGTTAC	3475
TGCAGGACCAGAGAATTCGAATACAC CICTACANNNCTAGCGTTAC	2996	TGCAGGACCAGAGAATTCGAATACAC CGCAAGCNNNCTAGCGTTAC	3236	TGCAGGACCAGAGAATTCGAATACAC GCGGCATNNNCTAGCGTTAC	3476
TGCAGGACCAGAGAATTCGAATACAT GGCCACGNNNCTAGCGTTAC	2997	TGCAGGACCAGAGAATTCGAATACAA CGACAAGNNNCTAGCGTTAC	3237	TGCAGGACCAGAGAATTCGAATACAT CCAGACANNNCTAGCGTTAC	3477
TGCAGGACCAGAGAATTCGAATACAA CGCAATCNNNCTAGCGTTAC	2998	TGCAGGACCAGAGAATTCGAATACAC GCCGATGNNNCTAGCGTTAC	3238	TGCAGGACCAGAGAATTCGAATACAA AATGCAANNNCTAGCGTTAC	3478
TGCAGGACCAGAGAATTCGAATACAG GTTTGCANNNCTAGCGTTAC	2999	TGCAGGACCAGAGAATTCGAATACAA ATCCAGCNNNCTAGCGTTAC	3239	TGCAGGACCAGAGAATTCGAATACAA ATTCGCGNNNCTAGCGTTAC	3479
TGCAGGACCAGAGAATTCGAATACAG GTTAGGANNNCTAGCGTTAC	3000	TGCAGGACCAGAGAATTCGAATACAA TTAATGCNNNCTAGCGTTAC	3240	TGCAGGACCAGAGAATTCGAATACAG TGTCCTTNNNCTAGCGTTAC	3480
TGCAGGACCAGAGAATTCGAATACAT CCTCGGCNNNCTAGCGTTAC	3001	TGCAGGACCAGAGAATTCGAATACAG CGCTTCCNNNCTAGCGTTAC	3241	TGCAGGACCAGAGAATTCGAATACAC ATGTAATNNNCTAGCGTTAC	3481
TGCAGGACCAGAGAATTCGAATACAA AACACGGNNNCTAGCGTTAC	3002	TGCAGGACCAGAGAATTCGAATACAT ACAATTGNNNCTAGCGTTAC	3242	TGCAGGACCAGAGAATTCGAATACAA CGCATACNNNCTAGCGTTAC	3482
TGCAGGACCAGAGAATTCGAATACAG AAAATCANNNCTAGCGTTAC	3003	TGCAGGACCAGAGAATTCGAATACAG TGGAACANNNCTAGCGTTAC	3243	TGCAGGACCAGAGAATTCGAATACAA TGCCCCCNNNCTAGCGTTAC	3483
TGCAGGACCAGAGAATTCGAATACAC GTATCTCNNNCTAGCGTTAC	3004	TGCAGGACCAGAGAATTCGAATACAC TCTGTGTNNNCTAGCGTTAC	3244	TGCAGGACCAGAGAATTCGAATACAC TCCCCAGNNNCTAGCGTTAC	3484
TGCAGGACCAGAGAATTCGAATACAC GGCCACANNNCTAGCGTTAC	3005	TGCAGGACCAGAGAATTCGAATACAT GCAGTACNNNCTAGCGTTAC	3245	TGCAGGACCAGAGAATTCGAATACAT CTACTTANNNCTAGCGTTAC	3485
TGCAGGACCAGAGAATTCGAATACAT CATTCATNNNCTAGCGTTAC	3006	TGCAGGACCAGAGAATTCGAATACAG ACAACTCNNNCTAGCGTTAC	3246	TGCAGGACCAGAGAATTCGAATACAT ACCGGTANNNCTAGCGTTAC	3486
TGCAGGACCAGAGAATTCGAATACAA TAGATGANNNCTAGCGTTAC	3007	TGCAGGACCAGAGAATTCGAATACAC GAGAGGCNNNCTAGCGTTAC	3247	TGCAGGACCAGAGAATTCGAATACAA ACCTATANNNCTAGCGTTAC	3487
TGCAGGACCAGAGAATTCGAATACAG CACTGCGNNNCTAGCGTTAC	3008	TGCAGGACCAGAGAATTCGAATACAC TAAATGTNNNCTAGCGTTAC	3248	TGCAGGACCAGAGAATTCGAATACAG CGACTGCNNNCTAGCGTTAC	3488
TGCAGGACCAGAGAATTCGAATACAA CTCCCTANNNGATCGACATG	3009	TGCAGGACCAGAGAATTCGAATACAG GCTCACGNNNGATCGACATG	3249	TGCAGGACCAGAGAATTCGAATACAC GAGTCTANNNGATCGACATG	3489
TGCAGGACCAGAGAATTCGAATACAA CAAAACANNNGATCGACATG	3010	TGCAGGACCAGAGAATTCGAATACAA CGTTTCCNNNGATCGACATG	3250	TGCAGGACCAGAGAATTCGAATACAT ATGAAAGNNNGATCGACATG	3490
TGCAGGACCAGAGAATTCGAATACAT ATGTACANNNGATCGACATG	3011	TGCAGGACCAGAGAATTCGAATACAT GCCAGTANNNGATCGACATG	3251	TGCAGGACCAGAGAATTCGAATACAA CTGGCCGNNNGATCGACATG	3491
TGCAGGACCAGAGAATTCGAATACAT CGGTCTTNNNGATCGACATG	3012	TGCAGGACCAGAGAATTCGAATACAG TAAGTGGNNNGATCGACATG	3252	TGCAGGACCAGAGAATTCGAATACAC AACCATGNNNGATCGACATG	3492
TGCAGGACCAGAGAATTCGAATACAT CCATATTNNNGATCGACATG	3013	TGCAGGACCAGAGAATTCGAATACAC ACCTACTNNNGATCGACATG	3253	TGCAGGACCAGAGAATTCGAATACAA AGGTAGCNNNGATCGACATG	3493
TGCAGGACCAGAGAATTCGAATACAA TGACTCGNNNGATCGACATG	3014	TGCAGGACCAGAGAATTCGAATACAG ATTTGATNNNGATCGACATG	3254	TGCAGGACCAGAGAATTCGAATACAT TCTCAGCNNNGATCGACATG	3494
TGCAGGACCAGAGAATTCGAATACAT AATCTCTNNNGATCGACATG	3015	TGCAGGACCAGAGAATTCGAATACAA ACTACATNNNGATCGACATG	3255	TGCAGGACCAGAGAATTCGAATACAT TCAGGTGNNNGATCGACATG	3495
TGCAGGACCAGAGAATTCGAATACAG AATACTTNNNGATCGACATG	3016	TGCAGGACCAGAGAATTCGAATACAG CCTTGAANNNGATCGACATG	3256	TGCAGGACCAGAGAATTCGAATACAC CAATCCTNNNGATCGACATG	3496
TGCAGGACCAGAGAATTCGAATACAC CACTAGANNNGATCGACATG	3017	TGCAGGACCAGAGAATTCGAATACAT AATATTANNNGATCGACATG	3257	TGCAGGACCAGAGAATTCGAATACAG ACAGTTCNNNGATCGACATG	3497
TGCAGGACCAGAGAATTCGAATACAT TTGGACGNNNGATCGACATG	3018	TGCAGGACCAGAGAATTCGAATACAG GTTTAATNNNGATCGACATG	3258	TGCAGGACCAGAGAATTCGAATACAA TCTTTACNNNGATCGACATG	3498
TGCAGGACCAGAGAATTCGAATACAG AAGTCCTNNNGATCGACATG	3019	TGCAGGACCAGAGAATTCGAATACAC CCACCGTNNNGATCGACATG	3259	TGCAGGACCAGAGAATTCGAATACAG CAATATTNNNGATCGACATG	3499
TGCAGGACCAGAGAATTCGAATACAC CTATGCTNNNGATCGACATG	3020	TGCAGGACCAGAGAATTCGAATACAC TACTTCGNNNGATCGACATG	3260	TGCAGGACCAGAGAATTCGAATACAG TCTCCATNNNGATCGACATG	3500

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池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT CGATGTGNNNGATCGACATG	3021	TGCAGGACCAGAGAATTCGAATACAA TGCGTCANNNGATCGACATG	3261	TGCAGGACCAGAGAATTCGAATACAC AACAATTNNNGATCGACATG	3501
TGCAGGACCAGAGAATTCGAATACAT GTACACGNNNGATCGACATG	3022	TGCAGGACCAGAGAATTCGAATACAA ACATGTTNNNGATCGACATG	3262	TGCAGGACCAGAGAATTCGAATACAT CGTAGACNNNGATCGACATG	3502
TGCAGGACCAGAGAATTCGAATACAT CTTTAGTNNNGATCGACATG	3023	TGCAGGACCAGAGAATTCGAATACAC CTGTTTGNNNGATCGACATG	3263	TGCAGGACCAGAGAATTCGAATACAG TAGATAANNNGATCGACATG	3503
TGCAGGACCAGAGAATTCGAATACAC GTAGGCCNNNGATCGACATG	3024	TGCAGGACCAGAGAATTCGAATACAC ACAAGCTNNNGATCGACATG	3264	TGCAGGACCAGAGAATTCGAATACAA CATATACNNNGATCGACATG	3504
TGCAGGACCAGAGAATTCGAATACAA CCTTTATNNNGATCGACATG	3025	TGCAGGACCAGAGAATTCGAATACAG ATAAGATNNNGATCGACATG	3265	TGCAGGACCAGAGAATTCGAATACAC ACGACGCNNNGATCGACATG	3505
TGCAGGACCAGAGAATTCGAATACAC GTCTATCNNNGATCGACATG	3026	TGCAGGACCAGAGAATTCGAATACAA GACCTCANNNGATCGACATG	3266	TGCAGGACCAGAGAATTCGAATACAC ACAAAAANNNGATCGACATG	3506
TGCAGGACCAGAGAATTCGAATACAG TAGAAATNNNGATCGACATG	3027	TGCAGGACCAGAGAATTCGAATACAC TCCAAGANNNGATCGACATG	3267	TGCAGGACCAGAGAATTCGAATACAC GTACCGCNNNGATCGACATG	3507
TGCAGGACCAGAGAATTCGAATACAC GTACCAANNNGATCGACATG	3028	TGCAGGACCAGAGAATTCGAATACAG GTATTCGNNNGATCGACATG	3268	TGCAGGACCAGAGAATTCGAATACAC CACAATGNNNGATCGACATG	3508
TGCAGGACCAGAGAATTCGAATACAC ACCACCCNNNGATCGACATG	3029	TGCAGGACCAGAGAATTCGAATACAA CTCGGATNNNGATCGACATG	3269	TGCAGGACCAGAGAATTCGAATACAC GCTCTGCNNNGATCGACATG	3509
TGCAGGACCAGAGAATTCGAATACAT GCGGCGTNNNGATCGACATG	3030	TGCAGGACCAGAGAATTCGAATACAT ATATCGANNNGATCGACATG	3270	TGCAGGACCAGAGAATTCGAATACAG TCAAGCTNNNGATCGACATG	3510
TGCAGGACCAGAGAATTCGAATACAG CCCCCCGNNNGATCGACATG	3031	TGCAGGACCAGAGAATTCGAATACAA TCCACTCNNNGATCGACATG	3271	TGCAGGACCAGAGAATTCGAATACAA CTCTTCGNNNGATCGACATG	3511
TGCAGGACCAGAGAATTCGAATACAT AGTAAGANNNGATCGACATG	3032	TGCAGGACCAGAGAATTCGAATACAG AACTGGANNNGATCGACATG	3272	TGCAGGACCAGAGAATTCGAATACAA ACACGGANNNGATCGACATG	3512
TGCAGGACCAGAGAATTCGAATACAT CTGAATANNNGATCGACATG	3033	TGCAGGACCAGAGAATTCGAATACAG ATCAGAGNNNGATCGACATG	3273	TGCAGGACCAGAGAATTCGAATACAA CCGCGCANNNGATCGACATG	3513
TGCAGGACCAGAGAATTCGAATACAC TAATACANNNGATCGACATG	3034	TGCAGGACCAGAGAATTCGAATACAT TGAACTANNNGATCGACATG	3274	TGCAGGACCAGAGAATTCGAATACAC ACCTTGTNNNGATCGACATG	3514
TGCAGGACCAGAGAATTCGAATACAA TGTCACGNNNGATCGACATG	3035	TGCAGGACCAGAGAATTCGAATACAG CCAGCCANNNGATCGACATG	3275	TGCAGGACCAGAGAATTCGAATACAT TATGCGGNNNGATCGACATG	3515
TGCAGGACCAGAGAATTCGAATACAA ACAGAATNNNGATCGACATG	3036	TGCAGGACCAGAGAATTCGAATACAT TTACTGTNNNGATCGACATG	3276	TGCAGGACCAGAGAATTCGAATACAG ACTCTTCNNNGATCGACATG	3516
TGCAGGACCAGAGAATTCGAATACAG CCCAGGTNNNGATCGACATG	3037	TGCAGGACCAGAGAATTCGAATACAT GTCAGGTNNNGATCGACATG	3277	TGCAGGACCAGAGAATTCGAATACAG AGTCTTGNNNGATCGACATG	3517
TGCAGGACCAGAGAATTCGAATACAG CTCATGANNNGATCGACATG	3038	TGCAGGACCAGAGAATTCGAATACAC AGCGTTANNNGATCGACATG	3278	TGCAGGACCAGAGAATTCGAATACAT AGAATCTNNNGATCGACATG	3518
TGCAGGACCAGAGAATTCGAATACAC CGGTCGANNNGATCGACATG	3039	TGCAGGACCAGAGAATTCGAATACAT GTGATCGNNNGATCGACATG	3279	TGCAGGACCAGAGAATTCGAATACAC GACCACGNNNGATCGACATG	3519
TGCAGGACCAGAGAATTCGAATACAC AATTCCCNNNGATCGACATG	3040	TGCAGGACCAGAGAATTCGAATACAG CTCGTAANNNGATCGACATG	3280	TGCAGGACCAGAGAATTCGAATACAT GGATTCGNNNGATCGACATG	3520
TGCAGGACCAGAGAATTCGAATACAC CAGGCCANNNGATCGACATG	3041	TGCAGGACCAGAGAATTCGAATACAA TTCTACTNNNGATCGACATG	3281	TGCAGGACCAGAGAATTCGAATACAC GACTAGTNNNGATCGACATG	3521
TGCAGGACCAGAGAATTCGAATACAC CTGCGGANNNGATCGACATG	3042	TGCAGGACCAGAGAATTCGAATACAG ATCAGTCNNNGATCGACATG	3282	TGCAGGACCAGAGAATTCGAATACAC CCAAAACNNNGATCGACATG	3522
TGCAGGACCAGAGAATTCGAATACAG CTAAAGGNNNGATCGACATG	3043	TGCAGGACCAGAGAATTCGAATACAG GATTATTNNNGATCGACATG	3283	TGCAGGACCAGAGAATTCGAATACAT GACCCCCNNNGATCGACATG	3523
TGCAGGACCAGAGAATTCGAATACAT TTAAGGTNNNGATCGACATG	3044	TGCAGGACCAGAGAATTCGAATACAC CATTCGTNNNGATCGACATG	3284	TGCAGGACCAGAGAATTCGAATACAG CATTAGCNNNGATCGACATG	3524
TGCAGGACCAGAGAATTCGAATACAA AACGTAANNNGATCGACATG	3045	TGCAGGACCAGAGAATTCGAATACAG TACATGCNNNGATCGACATG	3285	TGCAGGACCAGAGAATTCGAATACAG CCAGATTNNNGATCGACATG	3525
TGCAGGACCAGAGAATTCGAATACAA ATTTGGTNNNGATCGACATG	3046	TGCAGGACCAGAGAATTCGAATACAC GTCGCAGNNNGATCGACATG	3286	TGCAGGACCAGAGAATTCGAATACAA CAACTATNNNGATCGACATG	3526
TGCAGGACCAGAGAATTCGAATACAA CGTTAGCNNNGATCGACATG	3047	TGCAGGACCAGAGAATTCGAATACAT ATTTGTCNNNGATCGACATG	3287	TGCAGGACCAGAGAATTCGAATACAG TAGGTCTNNNGATCGACATG	3527
TGCAGGACCAGAGAATTCGAATACAA AGTTTTGNNNGATCGACATG	3048	TGCAGGACCAGAGAATTCGAATACAA CAGTCCANNNGATCGACATG	3288	TGCAGGACCAGAGAATTCGAATACAA ATAAGGTNNNGATCGACATG	3528
TGCAGGACCAGAGAATTCGAATACAA GCGTTCANNNGATCGACATG	3049	TGCAGGACCAGAGAATTCGAATACAG CGATTGTNNNGATCGACATG	3289	TGCAGGACCAGAGAATTCGAATACAA AGAGAAANNNGATCGACATG	3529
TGCAGGACCAGAGAATTCGAATACAG GACTTGTNNNGATCGACATG	3050	TGCAGGACCAGAGAATTCGAATACAC CTGGAATNNNGATCGACATG	3290	TGCAGGACCAGAGAATTCGAATACAT TTTGTGTNNNGATCGACATG	3530
TGCAGGACCAGAGAATTCGAATACAC GTCAGATNNNGATCGACATG	3051	TGCAGGACCAGAGAATTCGAATACAA CGAGCAANNNGATCGACATG	3291	TGCAGGACCAGAGAATTCGAATACAA GGCGTTTNNNGATCGACATG	3531
TGCAGGACCAGAGAATTCGAATACAC CAGAAGANNNGATCGACATG	3052	TGCAGGACCAGAGAATTCGAATACAA CACCAACNNNGATCGACATG	3292	TGCAGGACCAGAGAATTCGAATACAA AAAGCTANNNGATCGACATG	3532
TGCAGGACCAGAGAATTCGAATACAG CGATCTANNNGATCGACATG	3053	TGCAGGACCAGAGAATTCGAATACAT TTAGTCTNNNGATCGACATG	3293	TGCAGGACCAGAGAATTCGAATACAA CCGGATTNNNGATCGACATG	3533

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池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA TCACCGANNNGATCGACATG	3054	TGCAGGACCAGAGAATTCGAATACAT GTAGCTGNNNGATCGACATG	3294	TGCAGGACCAGAGAATTCGAATACAC TCAAATANNNGATCGACATG	3534
TGCAGGACCAGAGAATTCGAATACAA CACTAATNNNGATCGACATG	3055	TGCAGGACCAGAGAATTCGAATACAG GCTTACANNNGATCGACATG	3295	TGCAGGACCAGAGAATTCGAATACAC GAGAACANNNGATCGACATG	3535
TGCAGGACCAGAGAATTCGAATACAA TATGAAGNNNGATCGACATG	3056	TGCAGGACCAGAGAATTCGAATACAC GACCAGCNNNGATCGACATG	3296	TGCAGGACCAGAGAATTCGAATACAC CCAGGACNNNGATCGACATG	3536
TGCAGGACCAGAGAATTCGAATACAA GTAAGCGNNNGATCGACATG	3057	TGCAGGACCAGAGAATTCGAATACAG CCAAAAGNNNGATCGACATG	3297	TGCAGGACCAGAGAATTCGAATACAC CAGCTCCNNNGATCGACATG	3537
TGCAGGACCAGAGAATTCGAATACAG ACGCTATNNNGATCGACATG	3058	TGCAGGACCAGAGAATTCGAATACAC GAGGTAANNNGATCGACATG	3298	TGCAGGACCAGAGAATTCGAATACAT ATACATGNNNGATCGACATG	3538
TGCAGGACCAGAGAATTCGAATACAT GACATCGNNNGATCGACATG	3059	TGCAGGACCAGAGAATTCGAATACAC AGTCATGNNNGATCGACATG	3299	TGCAGGACCAGAGAATTCGAATACAT ATAGTTGNNNGATCGACATG	3539
TGCAGGACCAGAGAATTCGAATACAG CAGAAACNNNGATCGACATG	3060	TGCAGGACCAGAGAATTCGAATACAT GACCACANNNGATCGACATG	3300	TGCAGGACCAGAGAATTCGAATACAC ATAGTTANNNGATCGACATG	3540
TGCAGGACCAGAGAATTCGAATACAT TTTTGCANNNGATCGACATG	3061	TGCAGGACCAGAGAATTCGAATACAG GAACACANNNGATCGACATG	3301	TGCAGGACCAGAGAATTCGAATACAT TCATTACNNNGATCGACATG	3541
TGCAGGACCAGAGAATTCGAATACAC TACCCGCNNNGATCGACATG	3062	TGCAGGACCAGAGAATTCGAATACAT AGTAATCNNNGATCGACATG	3302	TGCAGGACCAGAGAATTCGAATACAT GCTACCTNNNGATCGACATG	3542
TGCAGGACCAGAGAATTCGAATACAA TAATGCTNNNGATCGACATG	3063	TGCAGGACCAGAGAATTCGAATACAC CGACGGTNNNGATCGACATG	3303	TGCAGGACCAGAGAATTCGAATACAG TAGCTTGNNNGATCGACATG	3543
TGCAGGACCAGAGAATTCGAATACAA AGCAGTGNNNGATCGACATG	3064	TGCAGGACCAGAGAATTCGAATACAT TGCCTTGNNNGATCGACATG	3304	TGCAGGACCAGAGAATTCGAATACAC CGGATATNNNGATCGACATG	3544
TGCAGGACCAGAGAATTCGAATACAA CACGTCANNNGATCGACATG	3065	TGCAGGACCAGAGAATTCGAATACAG AGCGGCANNNGATCGACATG	3305	TGCAGGACCAGAGAATTCGAATACAC AGCCGCANNNGATCGACATG	3545
TGCAGGACCAGAGAATTCGAATACAG TAATACTNNNGATCGACATG	3066	TGCAGGACCAGAGAATTCGAATACAG GCCTGCANNNGATCGACATG	3306	TGCAGGACCAGAGAATTCGAATACAG ATCCTCTNNNGATCGACATG	3546
TGCAGGACCAGAGAATTCGAATACAA ACAAACANNNGATCGACATG	3067	TGCAGGACCAGAGAATTCGAATACAT CGTCAAGNNNGATCGACATG	3307	TGCAGGACCAGAGAATTCGAATACAA GTACCCANNNGATCGACATG	3547
TGCAGGACCAGAGAATTCGAATACAT ACATGGCNNNGATCGACATG	3068	TGCAGGACCAGAGAATTCGAATACAG GACGGCANNNGATCGACATG	3308	TGCAGGACCAGAGAATTCGAATACAA CGGAGTANNNGATCGACATG	3548
TGCAGGACCAGAGAATTCGAATACAC GTGTCAANNNTGCATCAGGT	3069	TGCAGGACCAGAGAATTCGAATACAG CATGCCGNNNTGCATCAGGT	3309	TGCAGGACCAGAGAATTCGAATACAG TAAAAGTNNNTGCATCAGGT	3549
TGCAGGACCAGAGAATTCGAATACAC TTTAACTNNNTGCATCAGGT	3070	TGCAGGACCAGAGAATTCGAATACAC GTCTAAGNNNTGCATCAGGT	3310	TGCAGGACCAGAGAATTCGAATACAT AGGTGTCNNNTGCATCAGGT	3550
TGCAGGACCAGAGAATTCGAATACAG TAAGGTGNNNTGCATCAGGT	3071	TGCAGGACCAGAGAATTCGAATACAG CGTGATTNNNTGCATCAGGT	3311	TGCAGGACCAGAGAATTCGAATACAT AGACCGTNNNTGCATCAGGT	3551
TGCAGGACCAGAGAATTCGAATACAG AATAGCGNNNTGCATCAGGT	3072	TGCAGGACCAGAGAATTCGAATACAT TAGTCCCNNNTGCATCAGGT	3312	TGCAGGACCAGAGAATTCGAATACAG CTCGTTTNNNTGCATCAGGT	3552
TGCAGGACCAGAGAATTCGAATACAT AATTAATNNNTGCATCAGGT	3073	TGCAGGACCAGAGAATTCGAATACAT GGCATTGNNNTGCATCAGGT	3313	TGCAGGACCAGAGAATTCGAATACAA AATCTTGNNNTGCATCAGGT	3553
TGCAGGACCAGAGAATTCGAATACAC TCTTGTGNNNTGCATCAGGT	3074	TGCAGGACCAGAGAATTCGAATACAG ACGGTGGNNNTGCATCAGGT	3314	TGCAGGACCAGAGAATTCGAATACAG ACCAACTNNNTGCATCAGGT	3554
TGCAGGACCAGAGAATTCGAATACAT GCGCGTGNNNTGCATCAGGT	3075	TGCAGGACCAGAGAATTCGAATACAG CGCTTTTNNNTGCATCAGGT	3315	TGCAGGACCAGAGAATTCGAATACAT CACCTACNNNTGCATCAGGT	3555
TGCAGGACCAGAGAATTCGAATACAG ACGAAACNNNTGCATCAGGT	3076	TGCAGGACCAGAGAATTCGAATACAC GTGGACCNNNTGCATCAGGT	3316	TGCAGGACCAGAGAATTCGAATACAG TTAATTGNNNTGCATCAGGT	3556
TGCAGGACCAGAGAATTCGAATACAC GTTTAGGNNNTGCATCAGGT	3077	TGCAGGACCAGAGAATTCGAATACAA TGTCTTTNNNTGCATCAGGT	3317	TGCAGGACCAGAGAATTCGAATACAG CAATTATNNNTGCATCAGGT	3557
TGCAGGACCAGAGAATTCGAATACAG TAGCCTANNNTGCATCAGGT	3078	TGCAGGACCAGAGAATTCGAATACAT GAAAGCGNNNTGCATCAGGT	3318	TGCAGGACCAGAGAATTCGAATACAA ACGAGACNNNTGCATCAGGT	3558
TGCAGGACCAGAGAATTCGAATACAA TTCCCTGNNNTGCATCAGGT	3079	TGCAGGACCAGAGAATTCGAATACAC CGTGCGANNNTGCATCAGGT	3319	TGCAGGACCAGAGAATTCGAATACAA TCGGCATNNNTGCATCAGGT	3559
TGCAGGACCAGAGAATTCGAATACAA ACGAAATNNNTGCATCAGGT	3080	TGCAGGACCAGAGAATTCGAATACAT ACAACATNNNTGCATCAGGT	3320	TGCAGGACCAGAGAATTCGAATACAC CACACGGNNNTGCATCAGGT	3560
TGCAGGACCAGAGAATTCGAATACAA ACCCCCCNNNTGCATCAGGT	3081	TGCAGGACCAGAGAATTCGAATACAA TTACTCTNNNTGCATCAGGT	3321	TGCAGGACCAGAGAATTCGAATACAG GCCAGGANNNTGCATCAGGT	3561
TGCAGGACCAGAGAATTCGAATACAC TATGATANNNTGCATCAGGT	3082	TGCAGGACCAGAGAATTCGAATACAG TTCCCTANNNTGCATCAGGT	3322	TGCAGGACCAGAGAATTCGAATACAG AGGAGTTNNNTGCATCAGGT	3562
TGCAGGACCAGAGAATTCGAATACAT ACATGATNNNTGCATCAGGT	3083	TGCAGGACCAGAGAATTCGAATACAC ACACGGCNNNTGCATCAGGT	3323	TGCAGGACCAGAGAATTCGAATACAC CACCGCTNNNTGCATCAGGT	3563
TGCAGGACCAGAGAATTCGAATACAT GTACATANNNTGCATCAGGT	3084	TGCAGGACCAGAGAATTCGAATACAT ACAATTCNNNTGCATCAGGT	3324	TGCAGGACCAGAGAATTCGAATACAA CGATGAGNNNTGCATCAGGT	3564
TGCAGGACCAGAGAATTCGAATACAT ACGAAAANNNTGCATCAGGT	3085	TGCAGGACCAGAGAATTCGAATACAG TTGAAGGNNNTGCATCAGGT	3325	TGCAGGACCAGAGAATTCGAATACAT TAGCATANNNTGCATCAGGT	3565
TGCAGGACCAGAGAATTCGAATACAC ATAACATNNNTGCATCAGGT	3086	TGCAGGACCAGAGAATTCGAATACAC TTAACTTNNNTGCATCAGGT	3326	TGCAGGACCAGAGAATTCGAATACAA GTCCCAANNNTGCATCAGGT	3566

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池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG GAGAATCNNNTGCATCAGGT	3087	TGCAGGACCAGAGAATTCGAATACAA CTTACCCNNNTGCATCAGGT	3327	TGCAGGACCAGAGAATTCGAATACAA GCCTCTTNNNTGCATCAGGT	3567
TGCAGGACCAGAGAATTCGAATACAT CTTGTCGNNNTGCATCAGGT	3088	TGCAGGACCAGAGAATTCGAATACAG AGTTCGTNNNTGCATCAGGT	3328	TGCAGGACCAGAGAATTCGAATACAT CACCATCNNNTGCATCAGGT	3568
TGCAGGACCAGAGAATTCGAATACAT AAGCGCTNNNTGCATCAGGT	3089	TGCAGGACCAGAGAATTCGAATACAT TTCCAATNNNTGCATCAGGT	3329	TGCAGGACCAGAGAATTCGAATACAC TCATCACNNNTGCATCAGGT	3569
TGCAGGACCAGAGAATTCGAATACAT TCTAGAANNNTGCATCAGGT	3090	TGCAGGACCAGAGAATTCGAATACAA TAAGTTCNNNTGCATCAGGT	3330	TGCAGGACCAGAGAATTCGAATACAA CGGCGAGNNNTGCATCAGGT	3570
TGCAGGACCAGAGAATTCGAATACAT TGCTTGCNNNTGCATCAGGT	3091	TGCAGGACCAGAGAATTCGAATACAA ATGTACTNNNTGCATCAGGT	3331	TGCAGGACCAGAGAATTCGAATACAC TCGGACGNNNTGCATCAGGT	3571
TGCAGGACCAGAGAATTCGAATACAC AGCGTATNNNTGCATCAGGT	3092	TGCAGGACCAGAGAATTCGAATACAG TCCAAGTNNNTGCATCAGGT	3332	TGCAGGACCAGAGAATTCGAATACAT ACGGCATNNNTGCATCAGGT	3572
TGCAGGACCAGAGAATTCGAATACAA AGCAGCTNNNTGCATCAGGT	3093	TGCAGGACCAGAGAATTCGAATACAT CGACCAANNNTGCATCAGGT	3333	TGCAGGACCAGAGAATTCGAATACAT TTAGTAGNNNTGCATCAGGT	3573
TGCAGGACCAGAGAATTCGAATACAC ATGCCTTNNNTGCATCAGGT	3094	TGCAGGACCAGAGAATTCGAATACAC TCGATAGNNNTGCATCAGGT	3334	TGCAGGACCAGAGAATTCGAATACAA GGAAGAGNNNTGCATCAGGT	3574
TGCAGGACCAGAGAATTCGAATACAC GCGGTGTNNNTGCATCAGGT	3095	TGCAGGACCAGAGAATTCGAATACAA CTTCCCANNNTGCATCAGGT	3335	TGCAGGACCAGAGAATTCGAATACAC CGCGCAANNNTGCATCAGGT	3575
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TGCAGGACCAGAGAATTCGAATACAA GTTACGCNNNTGCATCAGGT	3097	TGCAGGACCAGAGAATTCGAATACAC ATTGCGANNNTGCATCAGGT	3337	TGCAGGACCAGAGAATTCGAATACAA TACACTANNNTGCATCAGGT	3577
TGCAGGACCAGAGAATTCGAATACAG CTAAGCTNNNTGCATCAGGT	3098	TGCAGGACCAGAGAATTCGAATACAC AGCACATNNNTGCATCAGGT	3338	TGCAGGACCAGAGAATTCGAATACAC CACGCCTNNNTGCATCAGGT	3578
TGCAGGACCAGAGAATTCGAATACAT CGCAGTANNNTGCATCAGGT	3099	TGCAGGACCAGAGAATTCGAATACAC CCGGCAANNNTGCATCAGGT	3339	TGCAGGACCAGAGAATTCGAATACAT GAAGTGGNNNTGCATCAGGT	3579
TGCAGGACCAGAGAATTCGAATACAC AGATCGTNNNTGCATCAGGT	3100	TGCAGGACCAGAGAATTCGAATACAA CAGATGGNNNTGCATCAGGT	3340	TGCAGGACCAGAGAATTCGAATACAG AGTTGTCNNNTGCATCAGGT	3580
TGCAGGACCAGAGAATTCGAATACAC GAAAAATNNNTGCATCAGGT	3101	TGCAGGACCAGAGAATTCGAATACAT GCGTATGNNNTGCATCAGGT	3341	TGCAGGACCAGAGAATTCGAATACAC CCGGCTTNNNTGCATCAGGT	3581
TGCAGGACCAGAGAATTCGAATACAG CCAGACCNNNTGCATCAGGT	3102	TGCAGGACCAGAGAATTCGAATACAA CAGGAGTNNNTGCATCAGGT	3342	TGCAGGACCAGAGAATTCGAATACAC AGATAGGNNNTGCATCAGGT	3582
TGCAGGACCAGAGAATTCGAATACAG CTGCACGNNNTGCATCAGGT	3103	TGCAGGACCAGAGAATTCGAATACAC ATCCATCNNNTGCATCAGGT	3343	TGCAGGACCAGAGAATTCGAATACAA AGTCCGTNNNTGCATCAGGT	3583
TGCAGGACCAGAGAATTCGAATACAC TGGAACTNNNTGCATCAGGT	3104	TGCAGGACCAGAGAATTCGAATACAC TACGCCCNNNTGCATCAGGT	3344	TGCAGGACCAGAGAATTCGAATACAA ATCAGAANNNTGCATCAGGT	3584
TGCAGGACCAGAGAATTCGAATACAA TAGCAAANNNTGCATCAGGT	3105	TGCAGGACCAGAGAATTCGAATACAG ACCTACANNNTGCATCAGGT	3345	TGCAGGACCAGAGAATTCGAATACAC ACTCAGANNNTGCATCAGGT	3585
TGCAGGACCAGAGAATTCGAATACAG AGCTATCNNNTGCATCAGGT	3106	TGCAGGACCAGAGAATTCGAATACAT CCCACCGNNNTGCATCAGGT	3346	TGCAGGACCAGAGAATTCGAATACAT TATTCCANNNTGCATCAGGT	3586
TGCAGGACCAGAGAATTCGAATACAA GGTATCCNNNTGCATCAGGT	3107	TGCAGGACCAGAGAATTCGAATACAC ATTCGCTNNNTGCATCAGGT	3347	TGCAGGACCAGAGAATTCGAATACAA AGTAACANNNTGCATCAGGT	3587
TGCAGGACCAGAGAATTCGAATACAT TGGAGTCNNNTGCATCAGGT	3108	TGCAGGACCAGAGAATTCGAATACAG ATCTGGTNNNTGCATCAGGT	3348	TGCAGGACCAGAGAATTCGAATACAT TGTGCCTNNNTGCATCAGGT	3588
TGCAGGACCAGAGAATTCGAATACAC GGCTTCCNNNTGCATCAGGT	3109	TGCAGGACCAGAGAATTCGAATACAT ATCGTTTNNNTGCATCAGGT	3349	TGCAGGACCAGAGAATTCGAATACAA AGAGTCGNNNTGCATCAGGT	3589
TGCAGGACCAGAGAATTCGAATACAT CAGGTTGNNNTGCATCAGGT	3110	TGCAGGACCAGAGAATTCGAATACAG GATTCTGNNNTGCATCAGGT	3350	TGCAGGACCAGAGAATTCGAATACAA GCTGTTGNNNTGCATCAGGT	3590
TGCAGGACCAGAGAATTCGAATACAC GGCGCGCNNNTGCATCAGGT	3111	TGCAGGACCAGAGAATTCGAATACAC CGCATCCNNNTGCATCAGGT	3351	TGCAGGACCAGAGAATTCGAATACAA TATTGACNNNTGCATCAGGT	3591
TGCAGGACCAGAGAATTCGAATACAA TGTGTCGNNNTGCATCAGGT	3112	TGCAGGACCAGAGAATTCGAATACAG ACTAAAANNNTGCATCAGGT	3352	TGCAGGACCAGAGAATTCGAATACAA AATATTTNNNTGCATCAGGT	3592
TGCAGGACCAGAGAATTCGAATACAC TTTGGAGNNNTGCATCAGGT	3113	TGCAGGACCAGAGAATTCGAATACAC TGGATGTNNNTGCATCAGGT	3353	TGCAGGACCAGAGAATTCGAATACAC TCAAGACNNNTGCATCAGGT	3593
TGCAGGACCAGAGAATTCGAATACAC GCCCACTNNNTGCATCAGGT	3114	TGCAGGACCAGAGAATTCGAATACAC CGTTTACNNNTGCATCAGGT	3354	TGCAGGACCAGAGAATTCGAATACAA GACGAACNNNTGCATCAGGT	3594
TGCAGGACCAGAGAATTCGAATACAA ACACTGCNNNTGCATCAGGT	3115	TGCAGGACCAGAGAATTCGAATACAA ATTATCGNNNTGCATCAGGT	3355	TGCAGGACCAGAGAATTCGAATACAA GGCAGGCNNNTGCATCAGGT	3595
TGCAGGACCAGAGAATTCGAATACAG CGCCGTANNNTGCATCAGGT	3116	TGCAGGACCAGAGAATTCGAATACAC ACTCGAANNNTGCATCAGGT	3356	TGCAGGACCAGAGAATTCGAATACAA CTTATAGNNNTGCATCAGGT	3596
TGCAGGACCAGAGAATTCGAATACAG TAGCATCNNNTGCATCAGGT	3117	TGCAGGACCAGAGAATTCGAATACAG AACGTTCNNNTGCATCAGGT	3357	TGCAGGACCAGAGAATTCGAATACAC TACTAAANNNTGCATCAGGT	3597
TGCAGGACCAGAGAATTCGAATACAT GCAGCATNNNTGCATCAGGT	3118	TGCAGGACCAGAGAATTCGAATACAA CCCGCAGNNNTGCATCAGGT	3358	TGCAGGACCAGAGAATTCGAATACAT TTAGAGTNNNTGCATCAGGT	3598
TGCAGGACCAGAGAATTCGAATACAT GCAGACTNNNTGCATCAGGT	3119	TGCAGGACCAGAGAATTCGAATACAG TCTCTGTNNNTGCATCAGGT	3359	TGCAGGACCAGAGAATTCGAATACAC TGCTTCANNNTGCATCAGGT	3599

图16G

池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA AGATGCGNNNTGCATCAGGT	3120	TGCAGGACCAGAGAATTCGAATACAA TTGATCANNNTGCATCAGGT	3360	TGCAGGACCAGAGAATTCGAATACAA GGTTCTGNNNTGCATCAGGT	3600
TGCAGGACCAGAGAATTCGAATACAA ACATATCNNNTGCATCAGGT	3121	TGCAGGACCAGAGAATTCGAATACAA AGTTTACNNNTGCATCAGGT	3361	TGCAGGACCAGAGAATTCGAATACAA GTAGGTGNNNTGCATCAGGT	3601
TGCAGGACCAGAGAATTCGAATACAT GGAACGANNNTGCATCAGGT	3122	TGCAGGACCAGAGAATTCGAATACAT GTTGTAANNNTGCATCAGGT	3362	TGCAGGACCAGAGAATTCGAATACAC CCGATAANNNTGCATCAGGT	3602
TGCAGGACCAGAGAATTCGAATACAT GCTCTTGNNNTGCATCAGGT	3123	TGCAGGACCAGAGAATTCGAATACAC TCTCAACNNNTGCATCAGGT	3363	TGCAGGACCAGAGAATTCGAATACAC AGAGTGANNNTGCATCAGGT	3603
TGCAGGACCAGAGAATTCGAATACAA CTCCTGTNNNTGCATCAGGT	3124	TGCAGGACCAGAGAATTCGAATACAA ACGGCCCNNNTGCATCAGGT	3364	TGCAGGACCAGAGAATTCGAATACAG TTCGCTTNNNTGCATCAGGT	3604
TGCAGGACCAGAGAATTCGAATACAA AACGTGGNNNTGCATCAGGT	3125	TGCAGGACCAGAGAATTCGAATACAA ATGGTAANNNTGCATCAGGT	3365	TGCAGGACCAGAGAATTCGAATACAG TTATCAANNNTGCATCAGGT	3605
TGCAGGACCAGAGAATTCGAATACAT GTCCCTANNNTGCATCAGGT	3126	TGCAGGACCAGAGAATTCGAATACAT ACAACCGNNNTGCATCAGGT	3366	TGCAGGACCAGAGAATTCGAATACAA GATGCTCNNNTGCATCAGGT	3606
TGCAGGACCAGAGAATTCGAATACAA ATCGCTGNNNTGCATCAGGT	3127	TGCAGGACCAGAGAATTCGAATACAA TACGGTCNNNTGCATCAGGT	3367	TGCAGGACCAGAGAATTCGAATACAA ACGTAAANNNTGCATCAGGT	3607
TGCAGGACCAGAGAATTCGAATACAG AAGCATGNNNTGCATCAGGT	3128	TGCAGGACCAGAGAATTCGAATACAT GCGCTGGNNNTGCATCAGGT	3368	TGCAGGACCAGAGAATTCGAATACAG CATTTCCNNNTGCATCAGGT	3608

图16H

池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT GATTCAANNNACGTATGCCA	3609	TGCAGGACCAGAGAATTCGAATACAA TTTCCCGNNNACGTATGCCA	3849	TGCAGGACCAGAGAATTCGAATACAA CGAGACANNNACGTATGCCA	4089
TGCAGGACCAGAGAATTCGAATACAA CAAGTAANNNACGTATGCCA	3610	TGCAGGACCAGAGAATTCGAATACAA TCCCAGANNNACGTATGCCA	3850	TGCAGGACCAGAGAATTCGAATACAC GCTAATGNNNACGTATGCCA	4090
TGCAGGACCAGAGAATTCGAATACAA TGACCGTNNNACGTATGCCA	3611	TGCAGGACCAGAGAATTCGAATACAC GCAGACGNNNACGTATGCCA	3851	TGCAGGACCAGAGAATTCGAATACAT ACGTCGANNNACGTATGCCA	4091
TGCAGGACCAGAGAATTCGAATACAA TCTCGTCNNNACGTATGCCA	3612	TGCAGGACCAGAGAATTCGAATACAC GATACGTNNNACGTATGCCA	3852	TGCAGGACCAGAGAATTCGAATACAA TTCGTGGNNNACGTATGCCA	4092
TGCAGGACCAGAGAATTCGAATACAG GCAACAANNNACGTATGCCA	3613	TGCAGGACCAGAGAATTCGAATACAT CCTGCTANNNACGTATGCCA	3853	TGCAGGACCAGAGAATTCGAATACAG TAGAGGTNNNACGTATGCCA	4093
TGCAGGACCAGAGAATTCGAATACAA GGCGCCTNNNACGTATGCCA	3614	TGCAGGACCAGAGAATTCGAATACAA ATTACACNNNACGTATGCCA	3854	TGCAGGACCAGAGAATTCGAATACAG GCGGTTCNNNACGTATGCCA	4094
TGCAGGACCAGAGAATTCGAATACAT GCTTACCNNNACGTATGCCA	3615	TGCAGGACCAGAGAATTCGAATACAT TTCCGACNNNACGTATGCCA	3855	TGCAGGACCAGAGAATTCGAATACAA TAGGCTCNNNACGTATGCCA	4095
TGCAGGACCAGAGAATTCGAATACAC GCACGACNNNACGTATGCCA	3616	TGCAGGACCAGAGAATTCGAATACAC TCCCCCTNNNACGTATGCCA	3856	TGCAGGACCAGAGAATTCGAATACAT CCAATTTNNNACGTATGCCA	4096
TGCAGGACCAGAGAATTCGAATACAG AGGCTTTNNNACGTATGCCA	3617	TGCAGGACCAGAGAATTCGAATACAA CAATTCANNNACGTATGCCA	3857	TGCAGGACCAGAGAATTCGAATACAC TGCCGAGNNNACGTATGCCA	4097
TGCAGGACCAGAGAATTCGAATACAC ATTCATTNNNACGTATGCCA	3618	TGCAGGACCAGAGAATTCGAATACAA GCAGCGGNNNACGTATGCCA	3858	TGCAGGACCAGAGAATTCGAATACAC TGTAGTGNNNACGTATGCCA	4098
TGCAGGACCAGAGAATTCGAATACAC AATCATANNNACGTATGCCA	3619	TGCAGGACCAGAGAATTCGAATACAA TCCGATGNNNACGTATGCCA	3859	TGCAGGACCAGAGAATTCGAATACAA ACGGTCTNNNACGTATGCCA	4099
TGCAGGACCAGAGAATTCGAATACAC TACGATGNNNACGTATGCCA	3620	TGCAGGACCAGAGAATTCGAATACAT ACGCACANNNACGTATGCCA	3860	TGCAGGACCAGAGAATTCGAATACAC AGGCGTCNNNACGTATGCCA	4100
TGCAGGACCAGAGAATTCGAATACAG AGGTACANNNACGTATGCCA	3621	TGCAGGACCAGAGAATTCGAATACAC CACCATTNNNACGTATGCCA	3861	TGCAGGACCAGAGAATTCGAATACAC TTGCCTANNNACGTATGCCA	4101
TGCAGGACCAGAGAATTCGAATACAC TCGTCTANNNACGTATGCCA	3622	TGCAGGACCAGAGAATTCGAATACAA AAGGTCGNNNACGTATGCCA	3862	TGCAGGACCAGAGAATTCGAATACAC TTCCGTANNNACGTATGCCA	4102
TGCAGGACCAGAGAATTCGAATACAA GAAGGAGNNNACGTATGCCA	3623	TGCAGGACCAGAGAATTCGAATACAG CAGTGTTNNNACGTATGCCA	3863	TGCAGGACCAGAGAATTCGAATACAC AGACGTTNNNACGTATGCCA	4103
TGCAGGACCAGAGAATTCGAATACAG TGACATCNNNACGTATGCCA	3624	TGCAGGACCAGAGAATTCGAATACAT CGAACTGNNNACGTATGCCA	3864	TGCAGGACCAGAGAATTCGAATACAA GGAACGTNNNACGTATGCCA	4104
TGCAGGACCAGAGAATTCGAATACAG CGGTGGANNNACGTATGCCA	3625	TGCAGGACCAGAGAATTCGAATACAT TCGCTACNNNACGTATGCCA	3865	TGCAGGACCAGAGAATTCGAATACAT TGCGTAGNNNACGTATGCCA	4105
TGCAGGACCAGAGAATTCGAATACAC ACAAATTNNNACGTATGCCA	3626	TGCAGGACCAGAGAATTCGAATACAT ATTCATCNNNACGTATGCCA	3866	TGCAGGACCAGAGAATTCGAATACAG CCCGATGNNNACGTATGCCA	4106
TGCAGGACCAGAGAATTCGAATACAC CGTGCAGNNNACGTATGCCA	3627	TGCAGGACCAGAGAATTCGAATACAA AACTACTNNNACGTATGCCA	3867	TGCAGGACCAGAGAATTCGAATACAA ACGTCTGNNNACGTATGCCA	4107
TGCAGGACCAGAGAATTCGAATACAA AATTACCNNNACGTATGCCA	3628	TGCAGGACCAGAGAATTCGAATACAG CCCGTAGNNNACGTATGCCA	3868	TGCAGGACCAGAGAATTCGAATACAC TCTACACNNNACGTATGCCA	4108
TGCAGGACCAGAGAATTCGAATACAG CAGACAANNNACGTATGCCA	3629	TGCAGGACCAGAGAATTCGAATACAA GTCGTTGNNNACGTATGCCA	3869	TGCAGGACCAGAGAATTCGAATACAA CGCGGTCNNNACGTATGCCA	4109
TGCAGGACCAGAGAATTCGAATACAT TCTAAGANNNACGTATGCCA	3630	TGCAGGACCAGAGAATTCGAATACAT GACAGCTNNNACGTATGCCA	3870	TGCAGGACCAGAGAATTCGAATACAC ATCCAGANNNACGTATGCCA	4110
TGCAGGACCAGAGAATTCGAATACAC ATTGAGCNNNACGTATGCCA	3631	TGCAGGACCAGAGAATTCGAATACAT CAGCGATNNNACGTATGCCA	3871	TGCAGGACCAGAGAATTCGAATACAA AGTCGAGNNNACGTATGCCA	4111
TGCAGGACCAGAGAATTCGAATACAA TGAGAGCNNNACGTATGCCA	3632	TGCAGGACCAGAGAATTCGAATACAG AGTAAATNNNACGTATGCCA	3872	TGCAGGACCAGAGAATTCGAATACAG GCAGCCTNNNACGTATGCCA	4112
TGCAGGACCAGAGAATTCGAATACAT TTCCCGANNNACGTATGCCA	3633	TGCAGGACCAGAGAATTCGAATACAG CTGCCTCNNNACGTATGCCA	3873	TGCAGGACCAGAGAATTCGAATACAT TATACAGNNNACGTATGCCA	4113
TGCAGGACCAGAGAATTCGAATACAT TGCGAACNNNACGTATGCCA	3634	TGCAGGACCAGAGAATTCGAATACAC TTGACGANNNACGTATGCCA	3874	TGCAGGACCAGAGAATTCGAATACAC CCGTCGTNNNACGTATGCCA	4114
TGCAGGACCAGAGAATTCGAATACAT GCAGATGNNNACGTATGCCA	3635	TGCAGGACCAGAGAATTCGAATACAC CTCTTTCNNNACGTATGCCA	3875	TGCAGGACCAGAGAATTCGAATACAT AATTTAANNNACGTATGCCA	4115
TGCAGGACCAGAGAATTCGAATACAC CAACCCCNNNACGTATGCCA	3636	TGCAGGACCAGAGAATTCGAATACAA CACAAGGNNNACGTATGCCA	3876	TGCAGGACCAGAGAATTCGAATACAT TCATCATNNNACGTATGCCA	4116
TGCAGGACCAGAGAATTCGAATACAG ACAATGGNNNACGTATGCCA	3637	TGCAGGACCAGAGAATTCGAATACAT CTCCAGTNNNACGTATGCCA	3877	TGCAGGACCAGAGAATTCGAATACAC ATGTATANNNACGTATGCCA	4117
TGCAGGACCAGAGAATTCGAATACAC AGAGCCCNNNACGTATGCCA	3638	TGCAGGACCAGAGAATTCGAATACAT ATTGGTANNNACGTATGCCA	3878	TGCAGGACCAGAGAATTCGAATACAG TAGTTATNNNACGTATGCCA	4118
TGCAGGACCAGAGAATTCGAATACAA AGAATACNNNACGTATGCCA	3639	TGCAGGACCAGAGAATTCGAATACAG CTTCATCNNNACGTATGCCA	3879	TGCAGGACCAGAGAATTCGAATACAT GTATCGGNNNACGTATGCCA	4119
TGCAGGACCAGAGAATTCGAATACAA GGTAAATNNNACGTATGCCA	3640	TGCAGGACCAGAGAATTCGAATACAT TCGTTTANNNACGTATGCCA	3880	TGCAGGACCAGAGAATTCGAATACAA GAGGTTGNNNACGTATGCCA	4120

图17A

池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG CCCCAAGNNNACGTATGCCA	3641	TGCAGGACCAGAGAATTCGAATACAT ACGTGACNNNACGTATGCCA	3881	TGCAGGACCAGAGAATTCGAATACAG CACAAGANNNACGTATGCCA	4121
TGCAGGACCAGAGAATTCGAATACAC TGCTTGTNNNACGTATGCCA	3642	TGCAGGACCAGAGAATTCGAATACAT GTTGGTGNNNACGTATGCCA	3882	TGCAGGACCAGAGAATTCGAATACAA ACCCGGCNNNACGTATGCCA	4122
TGCAGGACCAGAGAATTCGAATACAA CACGGCCNNNACGTATGCCA	3643	TGCAGGACCAGAGAATTCGAATACAC ATCACAGNNNACGTATGCCA	3883	TGCAGGACCAGAGAATTCGAATACAT GTGGCTANNNACGTATGCCA	4123
TGCAGGACCAGAGAATTCGAATACAA CGACCTANNNACGTATGCCA	3644	TGCAGGACCAGAGAATTCGAATACAA ACGGCGGNNNACGTATGCCA	3884	TGCAGGACCAGAGAATTCGAATACAG TAGCTCANNNACGTATGCCA	4124
TGCAGGACCAGAGAATTCGAATACAA TTAGAAGNNNACGTATGCCA	3645	TGCAGGACCAGAGAATTCGAATACAA ATGTGAANNNACGTATGCCA	3885	TGCAGGACCAGAGAATTCGAATACAG GCTGGCTNNNACGTATGCCA	4125
TGCAGGACCAGAGAATTCGAATACAG CCGTACGNNNACGTATGCCA	3646	TGCAGGACCAGAGAATTCGAATACAG TAGCCGCNNNACGTATGCCA	3886	TGCAGGACCAGAGAATTCGAATACAT ACAGCTGNNNACGTATGCCA	4126
TGCAGGACCAGAGAATTCGAATACAC AGAAAGCNNNACGTATGCCA	3647	TGCAGGACCAGAGAATTCGAATACAT GTGAATTNNNACGTATGCCA	3887	TGCAGGACCAGAGAATTCGAATACAC TTGTGTCNNNACGTATGCCA	4127
TGCAGGACCAGAGAATTCGAATACAC CACCTTANNNACGTATGCCA	3648	TGCAGGACCAGAGAATTCGAATACAC GGTAAGANNNACGTATGCCA	3888	TGCAGGACCAGAGAATTCGAATACAA GCATCGTNNNACGTATGCCA	4128
TGCAGGACCAGAGAATTCGAATACAA AGGATTANNNACGTATGCCA	3649	TGCAGGACCAGAGAATTCGAATACAT CTGGTGANNNACGTATGCCA	3889	TGCAGGACCAGAGAATTCGAATACAA ATAAAGCNNNACGTATGCCA	4129
TGCAGGACCAGAGAATTCGAATACAA GCAAATANNNACGTATGCCA	3650	TGCAGGACCAGAGAATTCGAATACAG TCCGTTTNNNACGTATGCCA	3890	TGCAGGACCAGAGAATTCGAATACAC TATGGGANNNACGTATGCCA	4130
TGCAGGACCAGAGAATTCGAATACAC ACTTCGTNNNACGTATGCCA	3651	TGCAGGACCAGAGAATTCGAATACAC CGTCGAGNNNACGTATGCCA	3891	TGCAGGACCAGAGAATTCGAATACAC CGCCCGCNNNACGTATGCCA	4131
TGCAGGACCAGAGAATTCGAATACAA TTCGTCCNNNACGTATGCCA	3652	TGCAGGACCAGAGAATTCGAATACAT CGATCCTNNNACGTATGCCA	3892	TGCAGGACCAGAGAATTCGAATACAT CGTTTCGNNNACGTATGCCA	4132
TGCAGGACCAGAGAATTCGAATACAT TCTTGGCNNNACGTATGCCA	3653	TGCAGGACCAGAGAATTCGAATACAT TTGCGTCNNNACGTATGCCA	3893	TGCAGGACCAGAGAATTCGAATACAC CTAGCAANNNACGTATGCCA	4133
TGCAGGACCAGAGAATTCGAATACAT TGGCTCTNNNACGTATGCCA	3654	TGCAGGACCAGAGAATTCGAATACAC TCGGCTCNNNACGTATGCCA	3894	TGCAGGACCAGAGAATTCGAATACAT GAACATTNNNACGTATGCCA	4134
TGCAGGACCAGAGAATTCGAATACAG GAGACTANNNACGTATGCCA	3655	TGCAGGACCAGAGAATTCGAATACAT CCACGCCNNNACGTATGCCA	3895	TGCAGGACCAGAGAATTCGAATACAT GTAACATNNNACGTATGCCA	4135
TGCAGGACCAGAGAATTCGAATACAA ATACTTGNNNACGTATGCCA	3656	TGCAGGACCAGAGAATTCGAATACAA CGTGCCGNNNACGTATGCCA	3896	TGCAGGACCAGAGAATTCGAATACAG TCGGAAANNNACGTATGCCA	4136
TGCAGGACCAGAGAATTCGAATACAG CTGTTAGNNNACGTATGCCA	3657	TGCAGGACCAGAGAATTCGAATACAT GTGGTACNNNACGTATGCCA	3897	TGCAGGACCAGAGAATTCGAATACAG TTGGCCGNNNACGTATGCCA	4137
TGCAGGACCAGAGAATTCGAATACAA CAACCTGNNNACGTATGCCA	3658	TGCAGGACCAGAGAATTCGAATACAA GCCGAAANNNACGTATGCCA	3898	TGCAGGACCAGAGAATTCGAATACAG CGATAGANNNACGTATGCCA	4138
TGCAGGACCAGAGAATTCGAATACAT CGTGCCCNNNACGTATGCCA	3659	TGCAGGACCAGAGAATTCGAATACAC TCCTAACNNNACGTATGCCA	3899	TGCAGGACCAGAGAATTCGAATACAT TAACGTANNNACGTATGCCA	4139
TGCAGGACCAGAGAATTCGAATACAG ACTCTCTNNNACGTATGCCA	3660	TGCAGGACCAGAGAATTCGAATACAG AAGGCGCNNNACGTATGCCA	3900	TGCAGGACCAGAGAATTCGAATACAC CTTATATNNNACGTATGCCA	4140
TGCAGGACCAGAGAATTCGAATACAT ATAACACNNNACGTATGCCA	3661	TGCAGGACCAGAGAATTCGAATACAC GTTCACTNNNACGTATGCCA	3901	TGCAGGACCAGAGAATTCGAATACAA AACAGATNNNACGTATGCCA	4141
TGCAGGACCAGAGAATTCGAATACAT GAGCCTANNNACGTATGCCA	3662	TGCAGGACCAGAGAATTCGAATACAG AGATGTGNNNACGTATGCCA	3902	TGCAGGACCAGAGAATTCGAATACAT ACCCATGNNNACGTATGCCA	4142
TGCAGGACCAGAGAATTCGAATACAC AGACGAANNNACGTATGCCA	3663	TGCAGGACCAGAGAATTCGAATACAG CTCACTTNNNACGTATGCCA	3903	TGCAGGACCAGAGAATTCGAATACAA AAAGAGANNNACGTATGCCA	4143
TGCAGGACCAGAGAATTCGAATACAC GGAATGANNNACGTATGCCA	3664	TGCAGGACCAGAGAATTCGAATACAC GAAGCTTNNNACGTATGCCA	3904	TGCAGGACCAGAGAATTCGAATACAC GTTCGAANNNACGTATGCCA	4144
TGCAGGACCAGAGAATTCGAATACAG GTGATGANNNACGTATGCCA	3665	TGCAGGACCAGAGAATTCGAATACAT ACTCGAGNNNACGTATGCCA	3905	TGCAGGACCAGAGAATTCGAATACAA TGGATCCNNNACGTATGCCA	4145
TGCAGGACCAGAGAATTCGAATACAC ACCTCTANNNACGTATGCCA	3666	TGCAGGACCAGAGAATTCGAATACAT TCTTGTANNNACGTATGCCA	3906	TGCAGGACCAGAGAATTCGAATACAG CTCGATANNNACGTATGCCA	4146
TGCAGGACCAGAGAATTCGAATACAA CTGGTACNNNACGTATGCCA	3667	TGCAGGACCAGAGAATTCGAATACAG AAGAAGGNNNACGTATGCCA	3907	TGCAGGACCAGAGAATTCGAATACAT GTAACCGNNNACGTATGCCA	4147
TGCAGGACCAGAGAATTCGAATACAG CAAATCCNNNACGTATGCCA	3668	TGCAGGACCAGAGAATTCGAATACAA GCCACGCNNNACGTATGCCA	3908	TGCAGGACCAGAGAATTCGAATACAA TCTACTTNNNACGTATGCCA	4148
TGCAGGACCAGAGAATTCGAATACAA ATATAAANNNCTAGCGTTAC	3669	TGCAGGACCAGAGAATTCGAATACAC TATACGGNNNCTAGCGTTAC	3909	TGCAGGACCAGAGAATTCGAATACAG ATCGTACNNNCTAGCGTTAC	4149
TGCAGGACCAGAGAATTCGAATACAT GGTTATANNNCTAGCGTTAC	3670	TGCAGGACCAGAGAATTCGAATACAA GATCTTANNNCTAGCGTTAC	3910	TGCAGGACCAGAGAATTCGAATACAT GAACGTCNNNCTAGCGTTAC	4150
TGCAGGACCAGAGAATTCGAATACAA CCCGCTCNNNCTAGCGTTAC	3671	TGCAGGACCAGAGAATTCGAATACAA CAACCCANNNCTAGCGTTAC	3911	TGCAGGACCAGAGAATTCGAATACAT CCAACTCNNNCTAGCGTTAC	4151
TGCAGGACCAGAGAATTCGAATACAT GCGAAAGNNNCTAGCGTTAC	3672	TGCAGGACCAGAGAATTCGAATACAT GCTAACGNNNCTAGCGTTAC	3912	TGCAGGACCAGAGAATTCGAATACAG CGGAGGTNNNCTAGCGTTAC	4152
TGCAGGACCAGAGAATTCGAATACAC GTCTGCCNNNCTAGCGTTAC	3673	TGCAGGACCAGAGAATTCGAATACAT GTAGTCGNNNCTAGCGTTAC	3913	TGCAGGACCAGAGAATTCGAATACAT GCCCATTNNNCTAGCGTTAC	4153

图17B

池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA GTTGTATNNNCTAGCGTTAC	3674	TGCAGGACCAGAGAATTCGAATACAA TGGTCGTNNNCTAGCGTTAC	3914	TGCAGGACCAGAGAATTCGAATACAA CGATCACNNNCTAGCGTTAC	4154
TGCAGGACCAGAGAATTCGAATACAG GCTACTANNNCTAGCGTTAC	3675	TGCAGGACCAGAGAATTCGAATACAA GTAGGACNNNCTAGCGTTAC	3915	TGCAGGACCAGAGAATTCGAATACAT AAGGTAANNNCTAGCGTTAC	4155
TGCAGGACCAGAGAATTCGAATACAA CATCATANNNCTAGCGTTAC	3676	TGCAGGACCAGAGAATTCGAATACAA AAAAAAANNNCTAGCGTTAC	3916	TGCAGGACCAGAGAATTCGAATACAA CCTACGANNNCTAGCGTTAC	4156
TGCAGGACCAGAGAATTCGAATACAA TTCCAGGNNNCTAGCGTTAC	3677	TGCAGGACCAGAGAATTCGAATACAA GTTCATANNNCTAGCGTTAC	3917	TGCAGGACCAGAGAATTCGAATACAC ACACCAANNNCTAGCGTTAC	4157
TGCAGGACCAGAGAATTCGAATACAT TTTGITGNNNCTAGCGTTAC	3678	TGCAGGACCAGAGAATTCGAATACAG AAGGTCANNNCTAGCGTTAC	3918	TGCAGGACCAGAGAATTCGAATACAT GGTCGGCNNNCTAGCGTTAC	4158
TGCAGGACCAGAGAATTCGAATACAA GTGGACANNNCTAGCGTTAC	3679	TGCAGGACCAGAGAATTCGAATACAT GAATGCCNNNCTAGCGTTAC	3919	TGCAGGACCAGAGAATTCGAATACAT TATCTGTNNNCTAGCGTTAC	4159
TGCAGGACCAGAGAATTCGAATACAG AGAGGTTNNNCTAGCGTTAC	3680	TGCAGGACCAGAGAATTCGAATACAA CACCCGGNNNCTAGCGTTAC	3920	TGCAGGACCAGAGAATTCGAATACAT CGAGCCGNNNCTAGCGTTAC	4160
TGCAGGACCAGAGAATTCGAATACAC TTCCCGGNNNCTAGCGTTAC	3681	TGCAGGACCAGAGAATTCGAATACAC TAAGGCANNNCTAGCGTTAC	3921	TGCAGGACCAGAGAATTCGAATACAT ACCGATGNNNCTAGCGTTAC	4161
TGCAGGACCAGAGAATTCGAATACAA CCTCCATNNNCTAGCGTTAC	3682	TGCAGGACCAGAGAATTCGAATACAA CCCCTATNNNCTAGCGTTAC	3922	TGCAGGACCAGAGAATTCGAATACAG AACGGATNNNCTAGCGTTAC	4162
TGCAGGACCAGAGAATTCGAATACAC AAGAGGTNNNCTAGCGTTAC	3683	TGCAGGACCAGAGAATTCGAATACAA GATAGATNNNCTAGCGTTAC	3923	TGCAGGACCAGAGAATTCGAATACAT TGTTCTANNNCTAGCGTTAC	4163
TGCAGGACCAGAGAATTCGAATACAG AAAGTCGNNNCTAGCGTTAC	3684	TGCAGGACCAGAGAATTCGAATACAG GAGTGATNNNCTAGCGTTAC	3924	TGCAGGACCAGAGAATTCGAATACAG GTCGTCGNNNCTAGCGTTAC	4164
TGCAGGACCAGAGAATTCGAATACAC GCGAAAANNNCTAGCGTTAC	3685	TGCAGGACCAGAGAATTCGAATACAA TAGAGGCNNNCTAGCGTTAC	3925	TGCAGGACCAGAGAATTCGAATACAA TGCTTCCNNNCTAGCGTTAC	4165
TGCAGGACCAGAGAATTCGAATACAC CTGGCAGNNNCTAGCGTTAC	3686	TGCAGGACCAGAGAATTCGAATACAC CCCGCGCNNNCTAGCGTTAC	3926	TGCAGGACCAGAGAATTCGAATACAT CAGGACTNNNCTAGCGTTAC	4166
TGCAGGACCAGAGAATTCGAATACAA GCAGATGNNNCTAGCGTTAC	3687	TGCAGGACCAGAGAATTCGAATACAC CATACTCNNNCTAGCGTTAC	3927	TGCAGGACCAGAGAATTCGAATACAA AGACATANNNCTAGCGTTAC	4167
TGCAGGACCAGAGAATTCGAATACAA GAGGCCGNNNCTAGCGTTAC	3688	TGCAGGACCAGAGAATTCGAATACAT GATTCCCNNNCTAGCGTTAC	3928	TGCAGGACCAGAGAATTCGAATACAC CATCGTTNNNCTAGCGTTAC	4168
TGCAGGACCAGAGAATTCGAATACAC GTGCGTGNNNCTAGCGTTAC	3689	TGCAGGACCAGAGAATTCGAATACAA GAACGGTNNNCTAGCGTTAC	3929	TGCAGGACCAGAGAATTCGAATACAT AACACCGNNNCTAGCGTTAC	4169
TGCAGGACCAGAGAATTCGAATACAT GGTACGANNNCTAGCGTTAC	3690	TGCAGGACCAGAGAATTCGAATACAG CTTCAAGNNNCTAGCGTTAC	3930	TGCAGGACCAGAGAATTCGAATACAC CTCCTCCNNNCTAGCGTTAC	4170
TGCAGGACCAGAGAATTCGAATACAC GCGCCAANNNCTAGCGTTAC	3691	TGCAGGACCAGAGAATTCGAATACAA AATATCCNNNCTAGCGTTAC	3931	TGCAGGACCAGAGAATTCGAATACAT CGGACTANNNCTAGCGTTAC	4171
TGCAGGACCAGAGAATTCGAATACAT GAGCACTNNNCTAGCGTTAC	3692	TGCAGGACCAGAGAATTCGAATACAC GTCCCCANNNCTAGCGTTAC	3932	TGCAGGACCAGAGAATTCGAATACAG GCAAACANNNCTAGCGTTAC	4172
TGCAGGACCAGAGAATTCGAATACAT CATCGTCNNNCTAGCGTTAC	3693	TGCAGGACCAGAGAATTCGAATACAA CTAATCANNNCTAGCGTTAC	3933	TGCAGGACCAGAGAATTCGAATACAG GAAACACNNNCTAGCGTTAC	4173
TGCAGGACCAGAGAATTCGAATACAA GCCAAGANNNCTAGCGTTAC	3694	TGCAGGACCAGAGAATTCGAATACAT GACGCCGNNNCTAGCGTTAC	3934	TGCAGGACCAGAGAATTCGAATACAT ACACTCCNNNCTAGCGTTAC	4174
TGCAGGACCAGAGAATTCGAATACAC GAGGACGNNNCTAGCGTTAC	3695	TGCAGGACCAGAGAATTCGAATACAG CGTGCCANNNCTAGCGTTAC	3935	TGCAGGACCAGAGAATTCGAATACAC GGACCTGNNNCTAGCGTTAC	4175
TGCAGGACCAGAGAATTCGAATACAT GTGACTGNNNCTAGCGTTAC	3696	TGCAGGACCAGAGAATTCGAATACAA AATTGGANNNCTAGCGTTAC	3936	TGCAGGACCAGAGAATTCGAATACAA TCCTGAGNNNCTAGCGTTAC	4176
TGCAGGACCAGAGAATTCGAATACAA CCTTCAGNNNCTAGCGTTAC	3697	TGCAGGACCAGAGAATTCGAATACAT GTTCACCNNNCTAGCGTTAC	3937	TGCAGGACCAGAGAATTCGAATACAC CCGTCTGNNNCTAGCGTTAC	4177
TGCAGGACCAGAGAATTCGAATACAG TTAAGTTNNNCTAGCGTTAC	3698	TGCAGGACCAGAGAATTCGAATACAA TCCGCAANNNCTAGCGTTAC	3938	TGCAGGACCAGAGAATTCGAATACAG GCTCAATNNNCTAGCGTTAC	4178
TGCAGGACCAGAGAATTCGAATACAA CCCAGGCNNNCTAGCGTTAC	3699	TGCAGGACCAGAGAATTCGAATACAT CAGATTANNNCTAGCGTTAC	3939	TGCAGGACCAGAGAATTCGAATACAG TGCTTGANNNCTAGCGTTAC	4179
TGCAGGACCAGAGAATTCGAATACAC CGATGATNNNCTAGCGTTAC	3700	TGCAGGACCAGAGAATTCGAATACAC GCTAAGTNNNCTAGCGTTAC	3940	TGCAGGACCAGAGAATTCGAATACAA TTAACTGNNNCTAGCGTTAC	4180
TGCAGGACCAGAGAATTCGAATACAG ATCTCGANNNCTAGCGTTAC	3701	TGCAGGACCAGAGAATTCGAATACAC ACACCTTNNNCTAGCGTTAC	3941	TGCAGGACCAGAGAATTCGAATACAT CCAGATGNNNCTAGCGTTAC	4181
TGCAGGACCAGAGAATTCGAATACAG GAGATGTNNNCTAGCGTTAC	3702	TGCAGGACCAGAGAATTCGAATACAA AGCCTGTNNNCTAGCGTTAC	3942	TGCAGGACCAGAGAATTCGAATACAC CGCGCGGNNNCTAGCGTTAC	4182
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TGCAGGACCAGAGAATTCGAATACAA CTCAGCANNNCTAGCGTTAC	3704	TGCAGGACCAGAGAATTCGAATACAT GTCGCTTNNNCTAGCGTTAC	3944	TGCAGGACCAGAGAATTCGAATACAG GTTGGTTNNNCTAGCGTTAC	4184
TGCAGGACCAGAGAATTCGAATACAA GATAGGCNNNCTAGCGTTAC	3705	TGCAGGACCAGAGAATTCGAATACAG AAATTTCNNNCTAGCGTTAC	3945	TGCAGGACCAGAGAATTCGAATACAG GCAGATANNNCTAGCGTTAC	4185
TGCAGGACCAGAGAATTCGAATACAC GAATTGCNNNCTAGCGTTAC	3706	TGCAGGACCAGAGAATTCGAATACAT ACGGTGTNNNCTAGCGTTAC	3946	TGCAGGACCAGAGAATTCGAATACAA TGCAACCNNNCTAGCGTTAC	4186

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT ACCAGGTNNNCTAGCGTTAC	3707	TGCAGGACCAGAGAATTCGAATACAC CGACCAGNNNCTAGCGTTAC	3947	TGCAGGACCAGAGAATTCGAATACAG CGCGCCGNNNCTAGCGTTAC	4187
TGCAGGACCAGAGAATTCGAATACAT ATACTCTNNNCTAGCGTTAC	3708	TGCAGGACCAGAGAATTCGAATACAT GATAAAGNNNCTAGCGTTAC	3948	TGCAGGACCAGAGAATTCGAATACAC AAAGTGGNNNCTAGCGTTAC	4188
TGCAGGACCAGAGAATTCGAATACAA GCTTCTCNNNCTAGCGTTAC	3709	TGCAGGACCAGAGAATTCGAATACAT ATGGCTGNNNCTAGCGTTAC	3949	TGCAGGACCAGAGAATTCGAATACAT AAAAGCANNNCTAGCGTTAC	4189
TGCAGGACCAGAGAATTCGAATACAA CCTGAGTNNNCTAGCGTTAC	3710	TGCAGGACCAGAGAATTCGAATACAC CCCTCCTNNNCTAGCGTTAC	3950	TGCAGGACCAGAGAATTCGAATACAA TCTGTGGNNNCTAGCGTTAC	4190
TGCAGGACCAGAGAATTCGAATACAC ATAGATTNNNCTAGCGTTAC	3711	TGCAGGACCAGAGAATTCGAATACAT CTTACCGNNNCTAGCGTTAC	3951	TGCAGGACCAGAGAATTCGAATACAC GTATATANNNCTAGCGTTAC	4191
TGCAGGACCAGAGAATTCGAATACAA GCGGAATNNNCTAGCGTTAC	3712	TGCAGGACCAGAGAATTCGAATACAG CAATCGTNNNCTAGCGTTAC	3952	TGCAGGACCAGAGAATTCGAATACAG GTATTGCNNNCTAGCGTTAC	4192
TGCAGGACCAGAGAATTCGAATACAG GCATGCCNNNCTAGCGTTAC	3713	TGCAGGACCAGAGAATTCGAATACAC TAGCGCGNNNCTAGCGTTAC	3953	TGCAGGACCAGAGAATTCGAATACAT ACAAACTNNNCTAGCGTTAC	4193
TGCAGGACCAGAGAATTCGAATACAG ATATCCGNNNCTAGCGTTAC	3714	TGCAGGACCAGAGAATTCGAATACAT ACTCTGCNNNCTAGCGTTAC	3954	TGCAGGACCAGAGAATTCGAATACAC TCTTAATNNNCTAGCGTTAC	4194
TGCAGGACCAGAGAATTCGAATACAG CTCAGCGNNNCTAGCGTTAC	3715	TGCAGGACCAGAGAATTCGAATACAA TGGCAGANNNCTAGCGTTAC	3955	TGCAGGACCAGAGAATTCGAATACAG GTCTGATNNNCTAGCGTTAC	4195
TGCAGGACCAGAGAATTCGAATACAC TTCAAGGNNNCTAGCGTTAC	3716	TGCAGGACCAGAGAATTCGAATACAC GAGGTTTNNNCTAGCGTTAC	3956	TGCAGGACCAGAGAATTCGAATACAT CAGGAAGNNNCTAGCGTTAC	4196
TGCAGGACCAGAGAATTCGAATACAT CAGTAATNNNCTAGCGTTAC	3717	TGCAGGACCAGAGAATTCGAATACAC CAGCTAANNNCTAGCGTTAC	3957	TGCAGGACCAGAGAATTCGAATACAC ACGCTTTNNNCTAGCGTTAC	4197
TGCAGGACCAGAGAATTCGAATACAC GGGCCAANNNCTAGCGTTAC	3718	TGCAGGACCAGAGAATTCGAATACAT GTGCCGGNNNCTAGCGTTAC	3958	TGCAGGACCAGAGAATTCGAATACAG GCGGCAANNNCTAGCGTTAC	4198
TGCAGGACCAGAGAATTCGAATACAA TGATCATNNNCTAGCGTTAC	3719	TGCAGGACCAGAGAATTCGAATACAT GCCGTTTNNNCTAGCGTTAC	3959	TGCAGGACCAGAGAATTCGAATACAG AAGTTGGNNNCTAGCGTTAC	4199
TGCAGGACCAGAGAATTCGAATACAG GCGCGTTNNNCTAGCGTTAC	3720	TGCAGGACCAGAGAATTCGAATACAC TCCGTGCNNNCTAGCGTTAC	3960	TGCAGGACCAGAGAATTCGAATACAG CAGGTGGNNNCTAGCGTTAC	4200
TGCAGGACCAGAGAATTCGAATACAA GTCCGCGNNNCTAGCGTTAC	3721	TGCAGGACCAGAGAATTCGAATACAG CACAATCNNNCTAGCGTTAC	3961	TGCAGGACCAGAGAATTCGAATACAT GTAATCANNNCTAGCGTTAC	4201
TGCAGGACCAGAGAATTCGAATACAC ACTGGTANNNCTAGCGTTAC	3722	TGCAGGACCAGAGAATTCGAATACAC ATCGTGANNNCTAGCGTTAC	3962	TGCAGGACCAGAGAATTCGAATACAG TCAACCANNNCTAGCGTTAC	4202
TGCAGGACCAGAGAATTCGAATACAC TAAGACCNNNCTAGCGTTAC	3723	TGCAGGACCAGAGAATTCGAATACAC AAGGTTCNNNCTAGCGTTAC	3963	TGCAGGACCAGAGAATTCGAATACAG AGCAACANNNCTAGCGTTAC	4203
TGCAGGACCAGAGAATTCGAATACAA CGCTACANNNCTAGCGTTAC	3724	TGCAGGACCAGAGAATTCGAATACAG AAAGGTCNNNCTAGCGTTAC	3964	TGCAGGACCAGAGAATTCGAATACAA CCGTCGGNNNCTAGCGTTAC	4204
TGCAGGACCAGAGAATTCGAATACAA GCAAAAANNNCTAGCGTTAC	3725	TGCAGGACCAGAGAATTCGAATACAA GAAGGTCNNNCTAGCGTTAC	3965	TGCAGGACCAGAGAATTCGAATACAT AGCGGCCNNNCTAGCGTTAC	4205
TGCAGGACCAGAGAATTCGAATACAC GAGTGCCNNNCTAGCGTTAC	3726	TGCAGGACCAGAGAATTCGAATACAC CATGCTTNNNCTAGCGTTAC	3966	TGCAGGACCAGAGAATTCGAATACAG AAGCAGTNNNCTAGCGTTAC	4206
TGCAGGACCAGAGAATTCGAATACAA ACCGGAANNNCTAGCGTTAC	3727	TGCAGGACCAGAGAATTCGAATACAT TCAACTNNNCTAGCGTTAC	3967	TGCAGGACCAGAGAATTCGAATACAT TGGTATANNNCTAGCGTTAC	4207
TGCAGGACCAGAGAATTCGAATACAA AAAGCATNNNCTAGCGTTAC	3728	TGCAGGACCAGAGAATTCGAATACAT CTGGCAANNNCTAGCGTTAC	3968	TGCAGGACCAGAGAATTCGAATACAG AAGTGTGNNNCTAGCGTTAC	4208
TGCAGGACCAGAGAATTCGAATACAC CCCCGGCNNNGATCGACATG	3729	TGCAGGACCAGAGAATTCGAATACAG ITTACAANNNGATCGACATG	3969	TGCAGGACCAGAGAATTCGAATACAC TGCTTTGNNNGATCGACATG	4209
TGCAGGACCAGAGAATTCGAATACAT TGGTTGGNNNGATCGACATG	3730	TGCAGGACCAGAGAATTCGAATACAA CCCACAANNNGATCGACATG	3970	TGCAGGACCAGAGAATTCGAATACAG TTCCGCCNNNGATCGACATG	4210
TGCAGGACCAGAGAATTCGAATACAT CCACGTTNNNGATCGACATG	3731	TGCAGGACCAGAGAATTCGAATACAG GCTCATANNNGATCGACATG	3971	TGCAGGACCAGAGAATTCGAATACAC GACTATCNNNGATCGACATG	4211
TGCAGGACCAGAGAATTCGAATACAA TGAAGTANNNGATCGACATG	3732	TGCAGGACCAGAGAATTCGAATACAA GCATTGCNNNGATCGACATG	3972	TGCAGGACCAGAGAATTCGAATACAC TGTAGCANNNGATCGACATG	4212
TGCAGGACCAGAGAATTCGAATACAA CAATAAGNNNGATCGACATG	3733	TGCAGGACCAGAGAATTCGAATACAA ACCCGATNNNGATCGACATG	3973	TGCAGGACCAGAGAATTCGAATACAC GCGGTCANNNGATCGACATG	4213
TGCAGGACCAGAGAATTCGAATACAC ATGTTTTNNNGATCGACATG	3734	TGCAGGACCAGAGAATTCGAATACAT GACCAACNNNGATCGACATG	3974	TGCAGGACCAGAGAATTCGAATACAT CCATGAGNNNGATCGACATG	4214
TGCAGGACCAGAGAATTCGAATACAT CCGGTCCNNNGATCGACATG	3735	TGCAGGACCAGAGAATTCGAATACAG CCGAGGANNNGATCGACATG	3975	TGCAGGACCAGAGAATTCGAATACAG GCTCCCTNNNGATCGACATG	4215
TGCAGGACCAGAGAATTCGAATACAG TTACGTGNNNGATCGACATG	3736	TGCAGGACCAGAGAATTCGAATACAA ATATGGANNNGATCGACATG	3976	TGCAGGACCAGAGAATTCGAATACAA GCCTAACNNNGATCGACATG	4216
TGCAGGACCAGAGAATTCGAATACAG GTCCTGGNNNGATCGACATG	3737	TGCAGGACCAGAGAATTCGAATACAT TTCGGTCNNNGATCGACATG	3977	TGCAGGACCAGAGAATTCGAATACAC GAGGAATNNNGATCGACATG	4217
TGCAGGACCAGAGAATTCGAATACAC TGTACAGNNNGATCGACATG	3738	TGCAGGACCAGAGAATTCGAATACAT TAGGTTANNNGATCGACATG	3978	TGCAGGACCAGAGAATTCGAATACAC CCGAGCANNNGATCGACATG	4218
TGCAGGACCAGAGAATTCGAATACAC ATAAGTTNNNGATCGACATG	3739	TGCAGGACCAGAGAATTCGAATACAA ACGGGTTNNNGATCGACATG	3979	TGCAGGACCAGAGAATTCGAATACAT ACAATACNNNGATCGACATG	4219

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA AATCCTANNNGATCGACATG	3740	TGCAGGACCAGAGAATTCGAATACAA GGTAAGCNNNGATCGACATG	3980	TGCAGGACCAGAGAATTCGAATACAT AACATGTNNNGATCGACATG	4220
TGCAGGACCAGAGAATTCGAATACAC ATCATGGNNNGATCGACATG	3741	TGCAGGACCAGAGAATTCGAATACAA ATTGACTNNNGATCGACATG	3981	TGCAGGACCAGAGAATTCGAATACAG TTGCGGCNNNGATCGACATG	4221
TGCAGGACCAGAGAATTCGAATACAT TCACTGCNNNGATCGACATG	3742	TGCAGGACCAGAGAATTCGAATACAT ACTGTAANNNGATCGACATG	3982	TGCAGGACCAGAGAATTCGAATACAA TCTGCAGNNNGATCGACATG	4222
TGCAGGACCAGAGAATTCGAATACAT TGCCGCCNNNGATCGACATG	3743	TGCAGGACCAGAGAATTCGAATACAT TCTCTGGNNNGATCGACATG	3983	TGCAGGACCAGAGAATTCGAATACAG GTTAGTCNNNGATCGACATG	4223
TGCAGGACCAGAGAATTCGAATACAT GTCCTGTNNNGATCGACATG	3744	TGCAGGACCAGAGAATTCGAATACAA GAAGAAANNNGATCGACATG	3984	TGCAGGACCAGAGAATTCGAATACAC TTAAGATNNNGATCGACATG	4224
TGCAGGACCAGAGAATTCGAATACAG GCGGTCTNNNGATCGACATG	3745	TGCAGGACCAGAGAATTCGAATACAA AATGAACNNNGATCGACATG	3985	TGCAGGACCAGAGAATTCGAATACAC TCCTACANNNGATCGACATG	4225
TGCAGGACCAGAGAATTCGAATACAA CCCACGGNNNGATCGACATG	3746	TGCAGGACCAGAGAATTCGAATACAA ACACACCNNNGATCGACATG	3986	TGCAGGACCAGAGAATTCGAATACAG CTCAGTANNNGATCGACATG	4226
TGCAGGACCAGAGAATTCGAATACAT CCTTTAANNNGATCGACATG	3747	TGCAGGACCAGAGAATTCGAATACAT AAATGCTNNNGATCGACATG	3987	TGCAGGACCAGAGAATTCGAATACAG GTACTACNNNGATCGACATG	4227
TGCAGGACCAGAGAATTCGAATACAT TACAAGTNNNGATCGACATG	3748	TGCAGGACCAGAGAATTCGAATACAA CCGGTTANNNGATCGACATG	3988	TGCAGGACCAGAGAATTCGAATACAT AGTATGTNNNGATCGACATG	4228
TGCAGGACCAGAGAATTCGAATACAT CGAGGAANNNGATCGACATG	3749	TGCAGGACCAGAGAATTCGAATACAC CGGCGTANNNGATCGACATG	3989	TGCAGGACCAGAGAATTCGAATACAA AGCATCCNNNGATCGACATG	4229
TGCAGGACCAGAGAATTCGAATACAG ACACTCANNNGATCGACATG	3750	TGCAGGACCAGAGAATTCGAATACAC GTAGACTNNNGATCGACATG	3990	TGCAGGACCAGAGAATTCGAATACAA CTAAAAGNNNGATCGACATG	4230
TGCAGGACCAGAGAATTCGAATACAA GTCTAGGNNNGATCGACATG	3751	TGCAGGACCAGAGAATTCGAATACAG GAAGTCANNNGATCGACATG	3991	TGCAGGACCAGAGAATTCGAATACAA CTTTAAGNNNGATCGACATG	4231
TGCAGGACCAGAGAATTCGAATACAA TCTTACTNNNGATCGACATG	3752	TGCAGGACCAGAGAATTCGAATACAA GAATTGANNNGATCGACATG	3992	TGCAGGACCAGAGAATTCGAATACAA CGAATAANNNGATCGACATG	4232
TGCAGGACCAGAGAATTCGAATACAA AAGAGAANNNGATCGACATG	3753	TGCAGGACCAGAGAATTCGAATACAA CCCCTTANNNGATCGACATG	3993	TGCAGGACCAGAGAATTCGAATACAT AGCGTCANNNGATCGACATG	4233
TGCAGGACCAGAGAATTCGAATACAA CAGCAGANNNGATCGACATG	3754	TGCAGGACCAGAGAATTCGAATACAT ACAGACCNNNGATCGACATG	3994	TGCAGGACCAGAGAATTCGAATACAA TCATCCCNNNGATCGACATG	4234
TGCAGGACCAGAGAATTCGAATACAT GAGTACCNNNGATCGACATG	3755	TGCAGGACCAGAGAATTCGAATACAA TTAGACTNNNGATCGACATG	3995	TGCAGGACCAGAGAATTCGAATACAA AAACAACNNNGATCGACATG	4235
TGCAGGACCAGAGAATTCGAATACAG ACTGTCANNNGATCGACATG	3756	TGCAGGACCAGAGAATTCGAATACAC ACTAGACNNNGATCGACATG	3996	TGCAGGACCAGAGAATTCGAATACAC TATCAGGNNNGATCGACATG	4236
TGCAGGACCAGAGAATTCGAATACAT CGAGGCCNNNGATCGACATG	3757	TGCAGGACCAGAGAATTCGAATACAG CCCTAAANNNGATCGACATG	3997	TGCAGGACCAGAGAATTCGAATACAT ACTGTCCNNNGATCGACATG	4237
TGCAGGACCAGAGAATTCGAATACAG TCCATAGNNNGATCGACATG	3758	TGCAGGACCAGAGAATTCGAATACAA GAGTGGTNNNGATCGACATG	3998	TGCAGGACCAGAGAATTCGAATACAA GGACACANNNGATCGACATG	4238
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TGCAGGACCAGAGAATTCGAATACAA CACACTGNNNGATCGACATG	3760	TGCAGGACCAGAGAATTCGAATACAA GCATCACNNNGATCGACATG	4000	TGCAGGACCAGAGAATTCGAATACAC TTGTACCNNNGATCGACATG	4240
TGCAGGACCAGAGAATTCGAATACAA GGTGACANNNGATCGACATG	3761	TGCAGGACCAGAGAATTCGAATACAA ATTGGAANNNGATCGACATG	4001	TGCAGGACCAGAGAATTCGAATACAG GATGCGGNNNGATCGACATG	4241
TGCAGGACCAGAGAATTCGAATACAA AACAATGNNNGATCGACATG	3762	TGCAGGACCAGAGAATTCGAATACAC TAGCCCCNNNGATCGACATG	4002	TGCAGGACCAGAGAATTCGAATACAC TGATTGGNNNGATCGACATG	4242
TGCAGGACCAGAGAATTCGAATACAG ATTTGTANNNGATCGACATG	3763	TGCAGGACCAGAGAATTCGAATACAT CTTGCTGNNNGATCGACATG	4003	TGCAGGACCAGAGAATTCGAATACAG CAACTCANNNGATCGACATG	4243
TGCAGGACCAGAGAATTCGAATACAC CCCCGATNNNGATCGACATG	3764	TGCAGGACCAGAGAATTCGAATACAC CGTCCTGNNNGATCGACATG	4004	TGCAGGACCAGAGAATTCGAATACAT ACCTCACNNNGATCGACATG	4244
TGCAGGACCAGAGAATTCGAATACAA GGAGCGCNNNGATCGACATG	3765	TGCAGGACCAGAGAATTCGAATACAC CTAACGANNNGATCGACATG	4005	TGCAGGACCAGAGAATTCGAATACAT GCACCCCNNNGATCGACATG	4245
TGCAGGACCAGAGAATTCGAATACAC CCTGGAGNNNGATCGACATG	3766	TGCAGGACCAGAGAATTCGAATACAA AAATAGCNNNGATCGACATG	4006	TGCAGGACCAGAGAATTCGAATACAG TTCCTACNNNGATCGACATG	4246
TGCAGGACCAGAGAATTCGAATACAC GCACTCCNNNGATCGACATG	3767	TGCAGGACCAGAGAATTCGAATACAA AGCACTCNNNGATCGACATG	4007	TGCAGGACCAGAGAATTCGAATACAT ACTGTTTNNNGATCGACATG	4247
TGCAGGACCAGAGAATTCGAATACAG AAGTCAGNNNGATCGACATG	3768	TGCAGGACCAGAGAATTCGAATACAG TTCAACGNNNGATCGACATG	4008	TGCAGGACCAGAGAATTCGAATACAC TTCATATNNNGATCGACATG	4248
TGCAGGACCAGAGAATTCGAATACAG GCGTCGTNNNGATCGACATG	3769	TGCAGGACCAGAGAATTCGAATACAC GTCTGTTNNNGATCGACATG	4009	TGCAGGACCAGAGAATTCGAATACAT CTGCTGTNNNGATCGACATG	4249
TGCAGGACCAGAGAATTCGAATACAC ATTGTCCNNNGATCGACATG	3770	TGCAGGACCAGAGAATTCGAATACAG CACGGCTNNNGATCGACATG	4010	TGCAGGACCAGAGAATTCGAATACAT GGTATTANNNGATCGACATG	4250
TGCAGGACCAGAGAATTCGAATACAT AGTAACTNNNGATCGACATG	3771	TGCAGGACCAGAGAATTCGAATACAA GCCAAACNNNGATCGACATG	4011	TGCAGGACCAGAGAATTCGAATACAA GAATGTANNNGATCGACATG	4251
TGCAGGACCAGAGAATTCGAATACAT AGATGTTHNNGATCGACATG	3772	TGCAGGACCAGAGAATTCGAATACAC ATAAACTNNNGATCGACATG	4012	TGCAGGACCAGAGAATTCGAATACAG GCGAGCANNNGATCGACATG	4252

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA ATGAGCGNNNGATCGACATG	3773	TGCAGGACCAGAGAATTCGAATACAT CGTAAGCNNNGATCGACATG	4013	TGCAGGACCAGAGAATTCGAATACAG CCACAATNNNGATCGACATG	4253
TGCAGGACCAGAGAATTCGAATACAA CTTGCGANNNGATCGACATG	3774	TGCAGGACCAGAGAATTCGAATACAG AGCTTGTNNNGATCGACATG	4014	TGCAGGACCAGAGAATTCGAATACAT ATTCTCANNNGATCGACATG	4254
TGCAGGACCAGAGAATTCGAATACAG GCGTACCNNNGATCGACATG	3775	TGCAGGACCAGAGAATTCGAATACAG TTTTGTTNNNGATCGACATG	4015	TGCAGGACCAGAGAATTCGAATACAA AGACCTCNNNGATCGACATG	4255
TGCAGGACCAGAGAATTCGAATACAG GTCACATNNNGATCGACATG	3776	TGCAGGACCAGAGAATTCGAATACAT GAGTAGGNNNGATCGACATG	4016	TGCAGGACCAGAGAATTCGAATACAC ACATAATNNNGATCGACATG	4256
TGCAGGACCAGAGAATTCGAATACAC ACTTAAANNNGATCGACATG	3777	TGCAGGACCAGAGAATTCGAATACAT GAGTCTGNNNGATCGACATG	4017	TGCAGGACCAGAGAATTCGAATACAA CCCTGAANNNGATCGACATG	4257
TGCAGGACCAGAGAATTCGAATACAT TTACCTANNNGATCGACATG	3778	TGCAGGACCAGAGAATTCGAATACAA GAAGCTGNNNGATCGACATG	4018	TGCAGGACCAGAGAATTCGAATACAG TAGACCTNNNGATCGACATG	4258
TGCAGGACCAGAGAATTCGAATACAA GTTTGGCNNNGATCGACATG	3779	TGCAGGACCAGAGAATTCGAATACAT AGAAGCGNNNGATCGACATG	4019	TGCAGGACCAGAGAATTCGAATACAC CCTACCGNNNGATCGACATG	4259
TGCAGGACCAGAGAATTCGAATACAG AGACATGNNNGATCGACATG	3780	TGCAGGACCAGAGAATTCGAATACAG CTTATGGNNNGATCGACATG	4020	TGCAGGACCAGAGAATTCGAATACAT ATCCCACNNNGATCGACATG	4260
TGCAGGACCAGAGAATTCGAATACAG AGGCATANNNGATCGACATG	3781	TGCAGGACCAGAGAATTCGAATACAG GCATATCNNNGATCGACATG	4021	TGCAGGACCAGAGAATTCGAATACAA GTCATTANNNGATCGACATG	4261
TGCAGGACCAGAGAATTCGAATACAC CTGCTCGNNNGATCGACATG	3782	TGCAGGACCAGAGAATTCGAATACAT CCGCTTANNNGATCGACATG	4022	TGCAGGACCAGAGAATTCGAATACAG GAACAACNNNGATCGACATG	4262
TGCAGGACCAGAGAATTCGAATACAT TGCTAGGNNNGATCGACATG	3783	TGCAGGACCAGAGAATTCGAATACAT TTATAGGNNNGATCGACATG	4023	TGCAGGACCAGAGAATTCGAATACAA TCTCTGCNNNGATCGACATG	4263
TGCAGGACCAGAGAATTCGAATACAT CCCCGACNNNGATCGACATG	3784	TGCAGGACCAGAGAATTCGAATACAA TGCTTAANNNGATCGACATG	4024	TGCAGGACCAGAGAATTCGAATACAC TGTACCTNNNGATCGACATG	4264
TGCAGGACCAGAGAATTCGAATACAC ACGAATCNNNGATCGACATG	3785	TGCAGGACCAGAGAATTCGAATACAT GACGTACNNNGATCGACATG	4025	TGCAGGACCAGAGAATTCGAATACAG ATCCAGTNNNGATCGACATG	4265
TGCAGGACCAGAGAATTCGAATACAG CGTCGCANNNGATCGACATG	3786	TGCAGGACCAGAGAATTCGAATACAA GAGAAAANNNGATCGACATG	4026	TGCAGGACCAGAGAATTCGAATACAT AAGTTCANNNGATCGACATG	4266
TGCAGGACCAGAGAATTCGAATACAA ATCCAATNNNGATCGACATG	3787	TGCAGGACCAGAGAATTCGAATACAT GTCTCGTNNNGATCGACATG	4027	TGCAGGACCAGAGAATTCGAATACAC CGTTAGANNNGATCGACATG	4267
TGCAGGACCAGAGAATTCGAATACAC GCGAACCNNNGATCGACATG	3788	TGCAGGACCAGAGAATTCGAATACAC GTTATGGNNNGATCGACATG	4028	TGCAGGACCAGAGAATTCGAATACAA AGAGACCNNNGATCGACATG	4268
TGCAGGACCAGAGAATTCGAATACAT ATGATCANNNTGCATCAGGT	3789	TGCAGGACCAGAGAATTCGAATACAT ATTGAGTNNNTGCATCAGGT	4029	TGCAGGACCAGAGAATTCGAATACAC GCCCTACNNNTGCATCAGGT	4269
TGCAGGACCAGAGAATTCGAATACAT TGGCACANNNTGCATCAGGT	3790	TGCAGGACCAGAGAATTCGAATACAA ATAGAGTNNNTGCATCAGGT	4030	TGCAGGACCAGAGAATTCGAATACAG ACGGCCTNNNTGCATCAGGT	4270
TGCAGGACCAGAGAATTCGAATACAC TACACCTNNNTGCATCAGGT	3791	TGCAGGACCAGAGAATTCGAATACAC AGACATCNNNTGCATCAGGT	4031	TGCAGGACCAGAGAATTCGAATACAC GCGGAGANNNTGCATCAGGT	4271
TGCAGGACCAGAGAATTCGAATACAT TAGAGTTNNNTGCATCAGGT	3792	TGCAGGACCAGAGAATTCGAATACAG AAGCCAANNNTGCATCAGGT	4032	TGCAGGACCAGAGAATTCGAATACAG CGATAAGNNNTGCATCAGGT	4272
TGCAGGACCAGAGAATTCGAATACAG GTGTTGTNNNTGCATCAGGT	3793	TGCAGGACCAGAGAATTCGAATACAC AGTCCAANNNTGCATCAGGT	4033	TGCAGGACCAGAGAATTCGAATACAA CGCTAGTNNNTGCATCAGGT	4273
TGCAGGACCAGAGAATTCGAATACAC CAGACGCNNNTGCATCAGGT	3794	TGCAGGACCAGAGAATTCGAATACAT TCCGACTNNNTGCATCAGGT	4034	TGCAGGACCAGAGAATTCGAATACAT TTGAATGNNNTGCATCAGGT	4274
TGCAGGACCAGAGAATTCGAATACAT GTTGGCANNNTGCATCAGGT	3795	TGCAGGACCAGAGAATTCGAATACAA CAGTATTNNNTGCATCAGGT	4035	TGCAGGACCAGAGAATTCGAATACAT ATTAAATNNNTGCATCAGGT	4275
TGCAGGACCAGAGAATTCGAATACAT CTTCCTCNNNTGCATCAGGT	3796	TGCAGGACCAGAGAATTCGAATACAG AGAATATNNNTGCATCAGGT	4036	TGCAGGACCAGAGAATTCGAATACAC GTGTTGANNNTGCATCAGGT	4276
TGCAGGACCAGAGAATTCGAATACAC AAGATAANNNTGCATCAGGT	3797	TGCAGGACCAGAGAATTCGAATACAA GTAAGGCNNNTGCATCAGGT	4037	TGCAGGACCAGAGAATTCGAATACAA AGCTTATNNNTGCATCAGGT	4277
TGCAGGACCAGAGAATTCGAATACAT ACTAGCGNNNTGCATCAGGT	3798	TGCAGGACCAGAGAATTCGAATACAA GCGTATCNNNTGCATCAGGT	4038	TGCAGGACCAGAGAATTCGAATACAC CCCGACTNNNTGCATCAGGT	4278
TGCAGGACCAGAGAATTCGAATACAG ACACAAGNNNTGCATCAGGT	3799	TGCAGGACCAGAGAATTCGAATACAT ACGGTTGNNNTGCATCAGGT	4039	TGCAGGACCAGAGAATTCGAATACAG TCGTCAANNNTGCATCAGGT	4279
TGCAGGACCAGAGAATTCGAATACAG TTACCTCNNNTGCATCAGGT	3800	TGCAGGACCAGAGAATTCGAATACAA AGGAAGGNNNTGCATCAGGT	4040	TGCAGGACCAGAGAATTCGAATACAT ACATCGGNNNTGCATCAGGT	4280
TGCAGGACCAGAGAATTCGAATACAT CTACCACNNNTGCATCAGGT	3801	TGCAGGACCAGAGAATTCGAATACAC ATTGGACNNNTGCATCAGGT	4041	TGCAGGACCAGAGAATTCGAATACAG ACTTTCCNNNTGCATCAGGT	4281
TGCAGGACCAGAGAATTCGAATACAT AGTCGTGNNNTGCATCAGGT	3802	TGCAGGACCAGAGAATTCGAATACAT AAGGCTCNNNTGCATCAGGT	4042	TGCAGGACCAGAGAATTCGAATACAT GCCCTATNNNTGCATCAGGT	4282
TGCAGGACCAGAGAATTCGAATACAA ATGCAGGNNNTGCATCAGGT	3803	TGCAGGACCAGAGAATTCGAATACAC GAAGCGGNNNTGCATCAGGT	4043	TGCAGGACCAGAGAATTCGAATACAT GACGGAANNNTGCATCAGGT	4283
TGCAGGACCAGAGAATTCGAATACAC ATGGACTNNNTGCATCAGGT	3804	TGCAGGACCAGAGAATTCGAATACAG ACGATTCNNNTGCATCAGGT	4044	TGCAGGACCAGAGAATTCGAATACAG CTGCCAGNNNTGCATCAGGT	4284
TGCAGGACCAGAGAATTCGAATACAT TGCGAGTNNNTGCATCAGGT	3805	TGCAGGACCAGAGAATTCGAATACAG TCGATACNNNTGCATCAGGT	4045	TGCAGGACCAGAGAATTCGAATACAT CATATAGNNNTGCATCAGGT	4285

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT TGCAAGCNNNTGCATCAGGT	3806	TGCAGGACCAGAGAATTCGAATACAC ATCAATANNNTGCATCAGGT	4046	TGCAGGACCAGAGAATTCGAATACAT GTGCGATNNNTGCATCAGGT	4286
TGCAGGACCAGAGAATTCGAATACAC CTCGGAGNNNTGCATCAGGT	3807	TGCAGGACCAGAGAATTCGAATACAC ACACATGNNNTGCATCAGGT	4047	TGCAGGACCAGAGAATTCGAATACAC ACGATCANNNTGCATCAGGT	4287
TGCAGGACCAGAGAATTCGAATACAT AACATTGNNNTGCATCAGGT	3808	TGCAGGACCAGAGAATTCGAATACAG CAGCGAGNNNTGCATCAGGT	4048	TGCAGGACCAGAGAATTCGAATACAG ACTGCCGNNNTGCATCAGGT	4288
TGCAGGACCAGAGAATTCGAATACAG AGGTTAGNNNTGCATCAGGT	3809	TGCAGGACCAGAGAATTCGAATACAT ACGGCTANNNTGCATCAGGT	4049	TGCAGGACCAGAGAATTCGAATACAG TGGTCATNNNTGCATCAGGT	4289
TGCAGGACCAGAGAATTCGAATACAA GAAACTANNNTGCATCAGGT	3810	TGCAGGACCAGAGAATTCGAATACAC AGCAGAANNNTGCATCAGGT	4050	TGCAGGACCAGAGAATTCGAATACAT GTGAGCTNNNTGCATCAGGT	4290
TGCAGGACCAGAGAATTCGAATACAT CCACCTANNNTGCATCAGGT	3811	TGCAGGACCAGAGAATTCGAATACAA AGATTAGNNNTGCATCAGGT	4051	TGCAGGACCAGAGAATTCGAATACAA ACCGTCANNNTGCATCAGGT	4291
TGCAGGACCAGAGAATTCGAATACAT CCTTCCTNNNTGCATCAGGT	3812	TGCAGGACCAGAGAATTCGAATACAG CAAAGACNNNTGCATCAGGT	4052	TGCAGGACCAGAGAATTCGAATACAA TTACAGTNNNTGCATCAGGT	4292
TGCAGGACCAGAGAATTCGAATACAA ACTCCGANNNTGCATCAGGT	3813	TGCAGGACCAGAGAATTCGAATACAA TAAACAGNNNTGCATCAGGT	4053	TGCAGGACCAGAGAATTCGAATACAG CAATAAANNNTGCATCAGGT	4293
TGCAGGACCAGAGAATTCGAATACAA ATTAGCTNNNTGCATCAGGT	3814	TGCAGGACCAGAGAATTCGAATACAT TCCAAAANNNTGCATCAGGT	4054	TGCAGGACCAGAGAATTCGAATACAA GCTTAGCNNNTGCATCAGGT	4294
TGCAGGACCAGAGAATTCGAATACAA TAGTAAGNNNTGCATCAGGT	3815	TGCAGGACCAGAGAATTCGAATACAT GGTATCGNNNTGCATCAGGT	4055	TGCAGGACCAGAGAATTCGAATACAT CATTGCCNNNTGCATCAGGT	4295
TGCAGGACCAGAGAATTCGAATACAG TTGTACTNNNTGCATCAGGT	3816	TGCAGGACCAGAGAATTCGAATACAA ACACTTANNNTGCATCAGGT	4056	TGCAGGACCAGAGAATTCGAATACAC ACTATAANNNTGCATCAGGT	4296
TGCAGGACCAGAGAATTCGAATACAC GCAATTGNNNTGCATCAGGT	3817	TGCAGGACCAGAGAATTCGAATACAA CCGTGGCNNNTGCATCAGGT	4057	TGCAGGACCAGAGAATTCGAATACAC TGCGTCCNNNTGCATCAGGT	4297
TGCAGGACCAGAGAATTCGAATACAG GAGGCGTNNNTGCATCAGGT	3818	TGCAGGACCAGAGAATTCGAATACAA GTCTAGCNNNTGCATCAGGT	4058	TGCAGGACCAGAGAATTCGAATACAC GATGAGANNNTGCATCAGGT	4298
TGCAGGACCAGAGAATTCGAATACAG TAACTGCNNNTGCATCAGGT	3819	TGCAGGACCAGAGAATTCGAATACAA GACTCCANNNTGCATCAGGT	4059	TGCAGGACCAGAGAATTCGAATACAT AGAAGGCNNNTGCATCAGGT	4299
TGCAGGACCAGAGAATTCGAATACAT GTCAACGNNNTGCATCAGGT	3820	TGCAGGACCAGAGAATTCGAATACAC CAGGATTNNNTGCATCAGGT	4060	TGCAGGACCAGAGAATTCGAATACAA TACACCGNNNTGCATCAGGT	4300
TGCAGGACCAGAGAATTCGAATACAC GATTTTTNNNTGCATCAGGT	3821	TGCAGGACCAGAGAATTCGAATACAA GAATGATNNNTGCATCAGGT	4061	TGCAGGACCAGAGAATTCGAATACAT CCAGCAANNNTGCATCAGGT	4301
TGCAGGACCAGAGAATTCGAATACAC CGTATTCNNNTGCATCAGGT	3822	TGCAGGACCAGAGAATTCGAATACAA CGACATCNNNTGCATCAGGT	4062	TGCAGGACCAGAGAATTCGAATACAG TGTTCCTNNNTGCATCAGGT	4302
TGCAGGACCAGAGAATTCGAATACAG CCGCGATNNNTGCATCAGGT	3823	TGCAGGACCAGAGAATTCGAATACAG TAAAAACNNNTGCATCAGGT	4063	TGCAGGACCAGAGAATTCGAATACAG AAACGTGNNNTGCATCAGGT	4303
TGCAGGACCAGAGAATTCGAATACAG GCCCTAGNNNTGCATCAGGT	3824	TGCAGGACCAGAGAATTCGAATACAA TTAACACNNNTGCATCAGGT	4064	TGCAGGACCAGAGAATTCGAATACAC CCTCTAANNNTGCATCAGGT	4304
TGCAGGACCAGAGAATTCGAATACAA ACAGGCANNNTGCATCAGGT	3825	TGCAGGACCAGAGAATTCGAATACAA CAAATTCNNNTGCATCAGGT	4065	TGCAGGACCAGAGAATTCGAATACAA CCGAGCCNNNTGCATCAGGT	4305
TGCAGGACCAGAGAATTCGAATACAA CCTATGGNNNTGCATCAGGT	3826	TGCAGGACCAGAGAATTCGAATACAC GTCCATTNNNTGCATCAGGT	4066	TGCAGGACCAGAGAATTCGAATACAG CGCCCTTNNNTGCATCAGGT	4306
TGCAGGACCAGAGAATTCGAATACAT GTGTCGANNNTGCATCAGGT	3827	TGCAGGACCAGAGAATTCGAATACAA GAAATCANNNTGCATCAGGT	4067	TGCAGGACCAGAGAATTCGAATACAA AATAGACNNNTGCATCAGGT	4307
TGCAGGACCAGAGAATTCGAATACAG TGGATTCNNNTGCATCAGGT	3828	TGCAGGACCAGAGAATTCGAATACAA AATCACTNNNTGCATCAGGT	4068	TGCAGGACCAGAGAATTCGAATACAT GACACTGNNNTGCATCAGGT	4308
TGCAGGACCAGAGAATTCGAATACAT CGGACCGNNNTGCATCAGGT	3829	TGCAGGACCAGAGAATTCGAATACAC TCCACGCNNNTGCATCAGGT	4069	TGCAGGACCAGAGAATTCGAATACAA GCGCGAGNNNTGCATCAGGT	4309
TGCAGGACCAGAGAATTCGAATACAA AACATAGNNNTGCATCAGGT	3830	TGCAGGACCAGAGAATTCGAATACAG AATAATGNNNTGCATCAGGT	4070	TGCAGGACCAGAGAATTCGAATACAG CAGAAGTNNNTGCATCAGGT	4310
TGCAGGACCAGAGAATTCGAATACAA GAAGCGTNNNTGCATCAGGT	3831	TGCAGGACCAGAGAATTCGAATACAT GTGACCANNNTGCATCAGGT	4071	TGCAGGACCAGAGAATTCGAATACAG GCTGATTNNNTGCATCAGGT	4311
TGCAGGACCAGAGAATTCGAATACAC CCTCACGNNNTGCATCAGGT	3832	TGCAGGACCAGAGAATTCGAATACAT CGATTAANNNTGCATCAGGT	4072	TGCAGGACCAGAGAATTCGAATACAG TAGAATANNNTGCATCAGGT	4312
TGCAGGACCAGAGAATTCGAATACAA ACTGTCGNNNTGCATCAGGT	3833	TGCAGGACCAGAGAATTCGAATACAC GCCAAATNNNTGCATCAGGT	4073	TGCAGGACCAGAGAATTCGAATACAC CATCGAANNNTGCATCAGGT	4313
TGCAGGACCAGAGAATTCGAATACAT CTTGGAGNNNTGCATCAGGT	3834	TGCAGGACCAGAGAATTCGAATACAC TTGTAAANNNTGCATCAGGT	4074	TGCAGGACCAGAGAATTCGAATACAT TGCCTACNNNTGCATCAGGT	4314
TGCAGGACCAGAGAATTCGAATACAG TGAAATANNNTGCATCAGGT	3835	TGCAGGACCAGAGAATTCGAATACAA ATTAGAGNNNTGCATCAGGT	4075	TGCAGGACCAGAGAATTCGAATACAA CTCCCATNNNTGCATCAGGT	4315
TGCAGGACCAGAGAATTCGAATACAT GCTTCTGNNNTGCATCAGGT	3836	TGCAGGACCAGAGAATTCGAATACAT AGCTTGGNNNTGCATCAGGT	4076	TGCAGGACCAGAGAATTCGAATACAG TTTCCACNNNTGCATCAGGT	4316
TGCAGGACCAGAGAATTCGAATACAT GACTTCCNNNTGCATCAGGT	3837	TGCAGGACCAGAGAATTCGAATACAA TAGGAGCNNNTGCATCAGGT	4077	TGCAGGACCAGAGAATTCGAATACAG ATATTGTNNNTGCATCAGGT	4317
TGCAGGACCAGAGAATTCGAATACAC CCGGATGNNNTGCATCAGGT	3838	TGCAGGACCAGAGAATTCGAATACAT TATACTCNNNTGCATCAGGT	4078	TGCAGGACCAGAGAATTCGAATACAA CTGAGGANNNTGCATCAGGT	4318

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG AGGACATNNNTGCATCAGGT	3839	TGCAGGACCAGAGAATTCGAATACAT TGTTGCCNNNTGCATCAGGT	4079	TGCAGGACCAGAGAATTCGAATACAG TAGTCTGNNNTGCATCAGGT	4319
TGCAGGACCAGAGAATTCGAATACAC AGGTATCNNNTGCATCAGGT	3840	TGCAGGACCAGAGAATTCGAATACAT TCCGAGANNNTGCATCAGGT	4080	TGCAGGACCAGAGAATTCGAATACAT GTAAATCNNNTGCATCAGGT	4320
TGCAGGACCAGAGAATTCGAATACAG TAGTATTNNNTGCATCAGGT	3841	TGCAGGACCAGAGAATTCGAATACAA TCCCATCNNNTGCATCAGGT	4081	TGCAGGACCAGAGAATTCGAATACAG CATATGCNNNTGCATCAGGT	4321
TGCAGGACCAGAGAATTCGAATACAA AGGAGGANNNTGCATCAGGT	3842	TGCAGGACCAGAGAATTCGAATACAT TTGCCACNNNTGCATCAGGT	4082	TGCAGGACCAGAGAATTCGAATACAA TTCGTAANNNTGCATCAGGT	4322
TGCAGGACCAGAGAATTCGAATACAA AGAGCCANNNTGCATCAGGT	3843	TGCAGGACCAGAGAATTCGAATACAG TGAGCGGNNNTGCATCAGGT	4083	TGCAGGACCAGAGAATTCGAATACAA ATCCACGNNNTGCATCAGGT	4323
TGCAGGACCAGAGAATTCGAATACAG TCTCTCANNNTGCATCAGGT	3844	TGCAGGACCAGAGAATTCGAATACAT CGCATCTNNNTGCATCAGGT	4084	TGCAGGACCAGAGAATTCGAATACAG CGCCGCGNNNTGCATCAGGT	4324
TGCAGGACCAGAGAATTCGAATACAA CGGTGTTNNNTGCATCAGGT	3845	TGCAGGACCAGAGAATTCGAATACAT CTGCAGANNNTGCATCAGGT	4085	TGCAGGACCAGAGAATTCGAATACAG GCTCGACNNNTGCATCAGGT	4325
TGCAGGACCAGAGAATTCGAATACAC GTACGATNNNTGCATCAGGT	3846	TGCAGGACCAGAGAATTCGAATACAG CCCAAGCNNNTGCATCAGGT	4086	TGCAGGACCAGAGAATTCGAATACAA CCCCGAGNNNTGCATCAGGT	4326
TGCAGGACCAGAGAATTCGAATACAG AGGTGTANNNTGCATCAGGT	3847	TGCAGGACCAGAGAATTCGAATACAT TTCTCGGNNNTGCATCAGGT	4087	TGCAGGACCAGAGAATTCGAATACAA GTCACCANNNTGCATCAGGT	4327
TGCAGGACCAGAGAATTCGAATACAC ACCACAANNNTGCATCAGGT	3848	TGCAGGACCAGAGAATTCGAATACAG GCCTACGNNNTGCATCAGGT	4088	TGCAGGACCAGAGAATTCGAATACAA AAATTCCNNNTGCATCAGGT	4328

图17H

池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGCCCTCTGNNNACGTATGCCA	4329	TGCAGGACCAGAGAATTCGAATA CATGTTGTCCNNNACGTATGCCA	4569	TGCAGGACCAGAGAATTCGAATA CATGAAACAANNNACGTATGCCA	4809
TGCAGGACCAGAGAATTCGAATA CAGCAAAGGTNNNACGTATGCCA	4330	TGCAGGACCAGAGAATTCGAATA CATAACCAGCNNNACGTATGCCA	4570	TGCAGGACCAGAGAATTCGAATA CACCGTTGCCNNNACGTATGCCA	4810
TGCAGGACCAGAGAATTCGAATA CATTTCTATGNNNACGTATGCCA	4331	TGCAGGACCAGAGAATTCGAATA CATGCGCGACNNNACGTATGCCA	4571	TGCAGGACCAGAGAATTCGAATA CAGCATTGGTNNNACGTATGCCA	4811
TGCAGGACCAGAGAATTCGAATA CACGTGCAATNNNACGTATGCCA	4332	TGCAGGACCAGAGAATTCGAATA CAATCGTCTCNNNACGTATGCCA	4572	TGCAGGACCAGAGAATTCGAATA CATAGGCCATNNNACGTATGCCA	4812
TGCAGGACCAGAGAATTCGAATA CAGTTTAGGCNNNACGTATGCCA	4333	TGCAGGACCAGAGAATTCGAATA CATCCGCACCNNNACGTATGCCA	4573	TGCAGGACCAGAGAATTCGAATA CAACTCCTCANNNACGTATGCCA	4813
TGCAGGACCAGAGAATTCGAATA CAAAAATGACNNNACGTATGCCA	4334	TGCAGGACCAGAGAATTCGAATA CATTACTGAANNNACGTATGCCA	4574	TGCAGGACCAGAGAATTCGAATA CACTAGGCGCNNNACGTATGCCA	4814
TGCAGGACCAGAGAATTCGAATA CAGTACTAGGNNNACGTATGCCA	4335	TGCAGGACCAGAGAATTCGAATA CAAGGTCCGCNNNACGTATGCCA	4575	TGCAGGACCAGAGAATTCGAATA CAAGTTTAGTNNNACGTATGCCA	4815
TGCAGGACCAGAGAATTCGAATA CACACCCAGGNNNACGTATGCCA	4336	TGCAGGACCAGAGAATTCGAATA CAGTGCCCTCNNNACGTATGCCA	4576	TGCAGGACCAGAGAATTCGAATA CATTGATACANNNACGTATGCCA	4816
TGCAGGACCAGAGAATTCGAATA CAGCCGCCTTNNNACGTATGCCA	4337	TGCAGGACCAGAGAATTCGAATA CAGCGTAGCCNNNACGTATGCCA	4577	TGCAGGACCAGAGAATTCGAATA CAACAATTACNNNACGTATGCCA	4817
TGCAGGACCAGAGAATTCGAATA CACAACGTCANNNACGTATGCCA	4338	TGCAGGACCAGAGAATTCGAATA CATAGCCAACNNNACGTATGCCA	4578	TGCAGGACCAGAGAATTCGAATA CAATACCGGTNNNACGTATGCCA	4818
TGCAGGACCAGAGAATTCGAATA CATCTCAAGGNNNACGTATGCCA	4339	TGCAGGACCAGAGAATTCGAATA CAATATACCANNNACGTATGCCA	4579	TGCAGGACCAGAGAATTCGAATA CATGAAGCCTNNNACGTATGCCA	4819
TGCAGGACCAGAGAATTCGAATA CATCATAAACNNNACGTATGCCA	4340	TGCAGGACCAGAGAATTCGAATA CATAAAATCCNNNACGTATGCCA	4580	TGCAGGACCAGAGAATTCGAATA CATTACCTGCNNNACGTATGCCA	4820
TGCAGGACCAGAGAATTCGAATA CATCCTCCCCNNNACGTATGCCA	4341	TGCAGGACCAGAGAATTCGAATA CAGATGGTGANNNACGTATGCCA	4581	TGCAGGACCAGAGAATTCGAATA CATATCAGATNNNACGTATGCCA	4821
TGCAGGACCAGAGAATTCGAATA CAAGTAACCCNNNACGTATGCCA	4342	TGCAGGACCAGAGAATTCGAATA CAGAACGTAGNNNACGTATGCCA	4582	TGCAGGACCAGAGAATTCGAATA CAGAAGAATTNNNACGTATGCCA	4822
TGCAGGACCAGAGAATTCGAATA CAGTGACAAGNNNACGTATGCCA	4343	TGCAGGACCAGAGAATTCGAATA CAATATTAATNNNACGTATGCCA	4583	TGCAGGACCAGAGAATTCGAATA CAGATCACGTNNNACGTATGCCA	4823
TGCAGGACCAGAGAATTCGAATA CAGCAATACCNNNACGTATGCCA	4344	TGCAGGACCAGAGAATTCGAATA CATACTGAATNNNACGTATGCCA	4584	TGCAGGACCAGAGAATTCGAATA CAAGGTAGACNNNACGTATGCCA	4824
TGCAGGACCAGAGAATTCGAATA CAAATACGTTNNNACGTATGCCA	4345	TGCAGGACCAGAGAATTCGAATA CAGTCCGAGCNNNACGTATGCCA	4585	TGCAGGACCAGAGAATTCGAATA CATTGACCGANNNACGTATGCCA	4825
TGCAGGACCAGAGAATTCGAATA CACCATGTAGNNNACGTATGCCA	4346	TGCAGGACCAGAGAATTCGAATA CACCTGGTAANNNACGTATGCCA	4586	TGCAGGACCAGAGAATTCGAATA CACCACTGTTNNNACGTATGCCA	4826
TGCAGGACCAGAGAATTCGAATA CACCCAACGGNNNACGTATGCCA	4347	TGCAGGACCAGAGAATTCGAATA CACCCTAGAANNNACGTATGCCA	4587	TGCAGGACCAGAGAATTCGAATA CAGTCAGAAGNNNACGTATGCCA	4827
TGCAGGACCAGAGAATTCGAATA CAGCGGTTGCNNNACGTATGCCA	4348	TGCAGGACCAGAGAATTCGAATA CATTAAAGTCNNNACGTATGCCA	4588	TGCAGGACCAGAGAATTCGAATA CACCGACCTCNNNACGTATGCCA	4828
TGCAGGACCAGAGAATTCGAATA CAGTGATCTGNNNACGTATGCCA	4349	TGCAGGACCAGAGAATTCGAATA CAACGTGGCCNNNACGTATGCCA	4589	TGCAGGACCAGAGAATTCGAATA CAATTAGTGTNNNACGTATGCCA	4829
TGCAGGACCAGAGAATTCGAATA CATAAGCCGTNNNACGTATGCCA	4350	TGCAGGACCAGAGAATTCGAATA CAGCTATCCTNNNACGTATGCCA	4590	TGCAGGACCAGAGAATTCGAATA CAGCATACCANNNACGTATGCCA	4830
TGCAGGACCAGAGAATTCGAATA CATGTTTGTCNNNACGTATGCCA	4351	TGCAGGACCAGAGAATTCGAATA CAAGCGTTGTNNNACGTATGCCA	4591	TGCAGGACCAGAGAATTCGAATA CAAGTTTTTCNNNACGTATGCCA	4831
TGCAGGACCAGAGAATTCGAATA CAACGAGCGGNNNACGTATGCCA	4352	TGCAGGACCAGAGAATTCGAATA CACTTCGCTANNNACGTATGCCA	4592	TGCAGGACCAGAGAATTCGAATA CATTCGCGTTNNNACGTATGCCA	4832
TGCAGGACCAGAGAATTCGAATA CATAGATCGCNNNACGTATGCCA	4353	TGCAGGACCAGAGAATTCGAATA CACATTTTTGNNNACGTATGCCA	4593	TGCAGGACCAGAGAATTCGAATA CATGGAGCCCNNNACGTATGCCA	4833
TGCAGGACCAGAGAATTCGAATA CATGATACGCNNNACGTATGCCA	4354	TGCAGGACCAGAGAATTCGAATA CAAACTTCGGNNNACGTATGCCA	4594	TGCAGGACCAGAGAATTCGAATA CACGTGGCACNNNACGTATGCCA	4834
TGCAGGACCAGAGAATTCGAATA CATAGTTACANNNACGTATGCCA	4355	TGCAGGACCAGAGAATTCGAATA CATACCGTGANNNACGTATGCCA	4595	TGCAGGACCAGAGAATTCGAATA CATCTTACTANNNACGTATGCCA	4835
TGCAGGACCAGAGAATTCGAATA CACTTGGTGANNNACGTATGCCA	4356	TGCAGGACCAGAGAATTCGAATA CAAGCTTTTTNNNACGTATGCCA	4596	TGCAGGACCAGAGAATTCGAATA CAATCCGGTANNNACGTATGCCA	4836
TGCAGGACCAGAGAATTCGAATA CATTAATCTCNNNACGTATGCCA	4357	TGCAGGACCAGAGAATTCGAATA CATGTTCTCGNNNACGTATGCCA	4597	TGCAGGACCAGAGAATTCGAATA CAGACACCTANNNACGTATGCCA	4837
TGCAGGACCAGAGAATTCGAATA CATTAGACGCNNNACGTATGCCA	4358	TGCAGGACCAGAGAATTCGAATA CAAATCGGCTNNNACGTATGCCA	4598	TGCAGGACCAGAGAATTCGAATA CATCCGTCTANNNACGTATGCCA	4838
TGCAGGACCAGAGAATTCGAATA CAACACCAGTNNNACGTATGCCA	4359	TGCAGGACCAGAGAATTCGAATA CATGAACCACNNNACGTATGCCA	4599	TGCAGGACCAGAGAATTCGAATA CAAGATTACTNNNACGTATGCCA	4839
TGCAGGACCAGAGAATTCGAATA CAACCAGGAANNNACGTATGCCA	4360	TGCAGGACCAGAGAATTCGAATA CAATTTCATCNNNACGTATGCCA	4600	TGCAGGACCAGAGAATTCGAATA CAAGATTGAANNNACGTATGCCA	4840
TGCAGGACCAGAGAATTCGAATA CAATGCATGCNNNACGTATGCCA	4361	TGCAGGACCAGAGAATTCGAATA CACAGTCACANNNACGTATGCCA	4601	TGCAGGACCAGAGAATTCGAATA CATTTAAAGCNNNACGTATGCCA	4841

图18A

池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATACACATANNNACGTATGCCA	4362	TGCAGGACCAGAGAATTCGAATA CACCCATAGANNNACGTATGCCA	4602	TGCAGGACCAGAGAATTCGAATA CAGAATTGCCNNNACGTATGCCA	4842
TGCAGGACCAGAGAATTCGAATA CATCTTTCAANNNACGTATGCCA	4363	TGCAGGACCAGAGAATTCGAATA CACAGAATGGNNNACGTATGCCA	4603	TGCAGGACCAGAGAATTCGAATA CATTACGTCCNNNACGTATGCCA	4843
TGCAGGACCAGAGAATTCGAATA CACTATCAAANNNACGTATGCCA	4364	TGCAGGACCAGAGAATTCGAATA CAGTATGAAANNNACGTATGCCA	4604	TGCAGGACCAGAGAATTCGAATA CAATGAGGACNNNACGTATGCCA	4844
TGCAGGACCAGAGAATTCGAATA CATTACCAAANNNACGTATGCCA	4365	TGCAGGACCAGAGAATTCGAATA CAGTTIAAGTNNNACGTATGCCA	4605	TGCAGGACCAGAGAATTCGAATA CAATTGTTAGNNNACGTATGCCA	4845
TGCAGGACCAGAGAATTCGAATA CACCGGCGATNNNACGTATGCCA	4366	TGCAGGACCAGAGAATTCGAATA CAGCGTTATGNNNACGTATGCCA	4606	TGCAGGACCAGAGAATTCGAATA CAGCTTGTAGNNNACGTATGCCA	4846
TGCAGGACCAGAGAATTCGAATA CAGTTGTATANNNACGTATGCCA	4367	TGCAGGACCAGAGAATTCGAATA CATCCGTTACNNNACGTATGCCA	4607	TGCAGGACCAGAGAATTCGAATA CATTGCTTCGNNNACGTATGCCA	4847
TGCAGGACCAGAGAATTCGAATA CAATACGGCTNNNACGTATGCCA	4368	TGCAGGACCAGAGAATTCGAATA CACGARAACCTNNNACGTATGCCA	4608	TGCAGGACCAGAGAATTCGAATA CAAAAGGCTGNNNACGTATGCCA	4848
TGCAGGACCAGAGAATTCGAATA CATGGCAACTNNNACGTATGCCA	4369	TGCAGGACCAGAGAATTCGAATA CACGGCCATGNNNACGTATGCCA	4609	TGCAGGACCAGAGAATTCGAATA CACTTACGAGNNNACGTATGCCA	4849
TGCAGGACCAGAGAATTCGAATA CAGATTTCAANNNACGTATGCCA	4370	TGCAGGACCAGAGAATTCGAATA CACGAAAAGCNNNACGTATGCCA	4610	TGCAGGACCAGAGAATTCGAATA CAATCTATAGNNNACGTATGCCA	4850
TGCAGGACCAGAGAATTCGAATA CAGTATCTTTNNNACGTATGCCA	4371	TGCAGGACCAGAGAATTCGAATA CAAGGTTGTCNNNACGTATGCCA	4611	TGCAGGACCAGAGAATTCGAATA CAGGTACACTNNNACGTATGCCA	4851
TGCAGGACCAGAGAATTCGAATA CAGCAACAGANNNACGTATGCCA	4372	TGCAGGACCAGAGAATTCGAATA CAACGAAGGTNNNACGTATGCCA	4612	TGCAGGACCAGAGAATTCGAATA CACCGCCTCANNNACGTATGCCA	4852
TGCAGGACCAGAGAATTCGAATA CAGCGTTCAANNNACGTATGCCA	4373	TGCAGGACCAGAGAATTCGAATA CATCCCCCGANNNACGTATGCCA	4613	TGCAGGACCAGAGAATTCGAATA CACAGGACGGNNNACGTATGCCA	4853
TGCAGGACCAGAGAATTCGAATA CAGTATTCGGNNNACGTATGCCA	4374	TGCAGGACCAGAGAATTCGAATA CAAGCGATCTNNNACGTATGCCA	4614	TGCAGGACCAGAGAATTCGAATA CAATCATGGCNNNACGTATGCCA	4854
TGCAGGACCAGAGAATTCGAATA CATCCTATATNNNACGTATGCCA	4375	TGCAGGACCAGAGAATTCGAATA CACTATAATGNNNACGTATGCCA	4615	TGCAGGACCAGAGAATTCGAATA CATATAGGTTNNNACGTATGCCA	4855
TGCAGGACCAGAGAATTCGAATA CAAGTCGTACNNNACGTATGCCA	4376	TGCAGGACCAGAGAATTCGAATA CATTCGTCTGNNNACGTATGCCA	4616	TGCAGGACCAGAGAATTCGAATA CAGATTTAACNNNACGTATGCCA	4856
TGCAGGACCAGAGAATTCGAATA CACCTAGACANNNACGTATGCCA	4377	TGCAGGACCAGAGAATTCGAATA CAGCGCCTTCNNNACGTATGCCA	4617	TGCAGGACCAGAGAATTCGAATA CAATGGAACGNNNACGTATGCCA	4857
TGCAGGACCAGAGAATTCGAATA CAATTGGTCGNNNACGTATGCCA	4378	TGCAGGACCAGAGAATTCGAATA CACGCAATCANNNACGTATGCCA	4618	TGCAGGACCAGAGAATTCGAATA CAGCTTTCACNNNACGTATGCCA	4858
TGCAGGACCAGAGAATTCGAATA CAGGTCACGCNNNACGTATGCCA	4379	TGCAGGACCAGAGAATTCGAATA CAGTCGGTCGNNNACGTATGCCA	4619	TGCAGGACCAGAGAATTCGAATA CAGTCCGTGGNNNACGTATGCCA	4859
TGCAGGACCAGAGAATTCGAATA CACACCAAACNNNACGTATGCCA	4380	TGCAGGACCAGAGAATTCGAATA CATAGCAGGANNNACGTATGCCA	4620	TGCAGGACCAGAGAATTCGAATA CATACTCCCANNNACGTATGCCA	4860
TGCAGGACCAGAGAATTCGAATA CAGAATTCATNNNACGTATGCCA	4381	TGCAGGACCAGAGAATTCGAATA CAGATGGAGTNNNACGTATGCCA	4621	TGCAGGACCAGAGAATTCGAATA CAGCCCGTCTNNNACGTATGCCA	4861
TGCAGGACCAGAGAATTCGAATA CATTCGCACTNNNACGTATGCCA	4382	TGCAGGACCAGAGAATTCGAATA CAAAGCACCTNNNACGTATGCCA	4622	TGCAGGACCAGAGAATTCGAATA CAGTCACTGANNNACGTATGCCA	4862
TGCAGGACCAGAGAATTCGAATA CACCGTTAAGNNNACGTATGCCA	4383	TGCAGGACCAGAGAATTCGAATA CAAGCGGCCTNNNACGTATGCCA	4623	TGCAGGACCAGAGAATTCGAATA CAAGCCGAGGNNNACGTATGCCA	4863
TGCAGGACCAGAGAATTCGAATA CACGCCTGCTNNNACGTATGCCA	4384	TGCAGGACCAGAGAATTCGAATA CACGTTTGCTNNNACGTATGCCA	4624	TGCAGGACCAGAGAATTCGAATA CAGCTATATANNNACGTATGCCA	4864
TGCAGGACCAGAGAATTCGAATA CAAAAACAGTNNNACGTATGCCA	4385	TGCAGGACCAGAGAATTCGAATA CACCTGCATTNNNACGTATGCCA	4625	TGCAGGACCAGAGAATTCGAATA CATCTCTCGANNNACGTATGCCA	4865
TGCAGGACCAGAGAATTCGAATA CAGAGATTTTNNNACGTATGCCA	4386	TGCAGGACCAGAGAATTCGAATA CAATTGAATCNNNACGTATGCCA	4626	TGCAGGACCAGAGAATTCGAATA CAACAATAGANNNACGTATGCCA	4866
TGCAGGACCAGAGAATTCGAATA CAACCAGTTGNNNACGTATGCCA	4387	TGCAGGACCAGAGAATTCGAATA CATCCGTGCCNNNACGTATGCCA	4627	TGCAGGACCAGAGAATTCGAATA CAGAGAGCATNNNACGTATGCCA	4867
TGCAGGACCAGAGAATTCGAATA CAAGTTCGCANNNACGTATGCCA	4388	TGCAGGACCAGAGAATTCGAATA CATCTCAGGANNNACGTATGCCA	4628	TGCAGGACCAGAGAATTCGAATA CACGATATGCNNNACGTATGCCA	4868
TGCAGGACCAGAGAATTCGAATA CAGATGACCTNNNCTAGCGTTAC	4389	TGCAGGACCAGAGAATTCGAATA CAAAGCCGTTNNNCTAGCGTTAC	4629	TGCAGGACCAGAGAATTCGAATA CACTTCCTCTNNNCTAGCGTTAC	4869
TGCAGGACCAGAGAATTCGAATA CACACGTATGNNNCTAGCGTTAC	4390	TGCAGGACCAGAGAATTCGAATA CACACCCTCGNNNCTAGCGTTAC	4630	TGCAGGACCAGAGAATTCGAATA CAAACAGTTTNNNCTAGCGTTAC	4870
TGCAGGACCAGAGAATTCGAATA CATGTCGGCGNNNCTAGCGTTAC	4391	TGCAGGACCAGAGAATTCGAATA CAGCTAGTTGNNNCTAGCGTTAC	4631	TGCAGGACCAGAGAATTCGAATA CATGTGGACTNNNCTAGCGTTAC	4871
TGCAGGACCAGAGAATTCGAATA CAGACCAAAGNNNCTAGCGTTAC	4392	TGCAGGACCAGAGAATTCGAATA CACCGTTACTNNNCTAGCGTTAC	4632	TGCAGGACCAGAGAATTCGAATA CACCTCGCACNNNCTAGCGTTAC	4872
TGCAGGACCAGAGAATTCGAATA CACTGCTACTNNNCTAGCGTTAC	4393	TGCAGGACCAGAGAATTCGAATA CATAAGCGTCNNNCTAGCGTTAC	4633	TGCAGGACCAGAGAATTCGAATA CACGGTTTCTNNNCTAGCGTTAC	4873
TGCAGGACCAGAGAATTCGAATA CACTCCAACTNNNCTAGCGTTAC	4394	TGCAGGACCAGAGAATTCGAATA CAGGTAAACGNNNCTAGCGTTAC	4634	TGCAGGACCAGAGAATTCGAATA CAACGTCGATNNNCTAGCGTTAC	4874

图18B

池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACAATCCCTNNNCTAGCGTTAC	4395	TGCAGGACCAGAGAATTCGAATA CAGAACCAGANNNCTAGCGTTAC	4635	TGCAGGACCAGAGAATTCGAATA CATTGGCTTCNNNCTAGCGTTAC	4875
TGCAGGACCAGAGAATTCGAATA CATCGTGCAANNNCTAGCGTTAC	4396	TGCAGGACCAGAGAATTCGAATA CAGGACTGTTNNNCTAGCGTTAC	4636	TGCAGGACCAGAGAATTCGAATA CAATGGACGANNNCTAGCGTTAC	4876
TGCAGGACCAGAGAATTCGAATA CAAAGCCATCNNNCTAGCGTTAC	4397	TGCAGGACCAGAGAATTCGAATA CAATCGTGTGNNNCTAGCGTTAC	4637	TGCAGGACCAGAGAATTCGAATA CATGCAAGAGNNNCTAGCGTTAC	4877
TGCAGGACCAGAGAATTCGAATA CAATGAACTTNNNCTAGCGTTAC	4398	TGCAGGACCAGAGAATTCGAATA CAGTCACGGCNNNCTAGCGTTAC	4638	TGCAGGACCAGAGAATTCGAATA CAGAAATATGNNNCTAGCGTTAC	4878
TGCAGGACCAGAGAATTCGAATA CATGGCCGGTNNNCTAGCGTTAC	4399	TGCAGGACCAGAGAATTCGAATA CATCTCGTACNNNCTAGCGTTAC	4639	TGCAGGACCAGAGAATTCGAATA CAACACATATNNNCTAGCGTTAC	4879
TGCAGGACCAGAGAATTCGAATA CATGCCACGGNNNCTAGCGTTAC	4400	TGCAGGACCAGAGAATTCGAATA CAAGTCGCGCNNNCTAGCGTTAC	4640	TGCAGGACCAGAGAATTCGAATA CAGTACGACTNNNCTAGCGTTAC	4880
TGCAGGACCAGAGAATTCGAATA CAGTCTTCGTNNNCTAGCGTTAC	4401	TGCAGGACCAGAGAATTCGAATA CACATAGTCGNNNCTAGCGTTAC	4641	TGCAGGACCAGAGAATTCGAATA CACGCCGCGGNNNCTAGCGTTAC	4881
TGCAGGACCAGAGAATTCGAATA CAAACGTAGGNNNCTAGCGTTAC	4402	TGCAGGACCAGAGAATTCGAATA CACATGTACGNNNCTAGCGTTAC	4642	TGCAGGACCAGAGAATTCGAATA CATAGTGCACNNNCTAGCGTTAC	4882
TGCAGGACCAGAGAATTCGAATA CAATGGAGCANNNCTAGCGTTAC	4403	TGCAGGACCAGAGAATTCGAATA CAGCGTATCANNNCTAGCGTTAC	4643	TGCAGGACCAGAGAATTCGAATA CATCAATGCGNNNCTAGCGTTAC	4883
TGCAGGACCAGAGAATTCGAATA CATGACGGCCNNNCTAGCGTTAC	4404	TGCAGGACCAGAGAATTCGAATA CACAATTCTTNNNCTAGCGTTAC	4644	TGCAGGACCAGAGAATTCGAATA CAATGTAAGANNNCTAGCGTTAC	4884
TGCAGGACCAGAGAATTCGAATA CACTTAGGACNNNCTAGCGTTAC	4405	TGCAGGACCAGAGAATTCGAATA CAACTCTATTNNNCTAGCGTTAC	4645	TGCAGGACCAGAGAATTCGAATA CATATGTTAGNNNCTAGCGTTAC	4885
TGCAGGACCAGAGAATTCGAATA CAGACAGAGTNNNCTAGCGTTAC	4406	TGCAGGACCAGAGAATTCGAATA CATCATCCCANNNCTAGCGTTAC	4646	TGCAGGACCAGAGAATTCGAATA CATCAAATCANNNCTAGCGTTAC	4886
TGCAGGACCAGAGAATTCGAATA CAAAGTCGTCNNNCTAGCGTTAC	4407	TGCAGGACCAGAGAATTCGAATA CAGGCTTGGCNNNCTAGCGTTAC	4647	TGCAGGACCAGAGAATTCGAATA CACACTTAGGNNNCTAGCGTTAC	4887
TGCAGGACCAGAGAATTCGAATA CATACAAAAGNNNCTAGCGTTAC	4408	TGCAGGACCAGAGAATTCGAATA CAGTTCCTTGNNNCTAGCGTTAC	4648	TGCAGGACCAGAGAATTCGAATA CATAGGATAANNNCTAGCGTTAC	4888
TGCAGGACCAGAGAATTCGAATA CATCTCCTGANNNCTAGCGTTAC	4409	TGCAGGACCAGAGAATTCGAATA CAATGAGAATNNNCTAGCGTTAC	4649	TGCAGGACCAGAGAATTCGAATA CAATCCCGTTNNNCTAGCGTTAC	4889
TGCAGGACCAGAGAATTCGAATA CAAGCTGGTTNNNCTAGCGTTAC	4410	TGCAGGACCAGAGAATTCGAATA CACTGTATCCNNNCTAGCGTTAC	4650	TGCAGGACCAGAGAATTCGAATA CAACAATCCGNNNCTAGCGTTAC	4890
TGCAGGACCAGAGAATTCGAATA CAAATCAAGANNNCTAGCGTTAC	4411	TGCAGGACCAGAGAATTCGAATA CATACGCCCCNNNCTAGCGTTAC	4651	TGCAGGACCAGAGAATTCGAATA CACTATTAAGNNNCTAGCGTTAC	4891
TGCAGGACCAGAGAATTCGAATA CAACCACAACNNNCTAGCGTTAC	4412	TGCAGGACCAGAGAATTCGAATA CATGGCCGACNNNCTAGCGTTAC	4652	TGCAGGACCAGAGAATTCGAATA CAGCGTATGTNNNCTAGCGTTAC	4892
TGCAGGACCAGAGAATTCGAATA CAGCTATAATNNNCTAGCGTTAC	4413	TGCAGGACCAGAGAATTCGAATA CACCGCTGCTNNNCTAGCGTTAC	4653	TGCAGGACCAGAGAATTCGAATA CAATTGGTATNNNCTAGCGTTAC	4893
TGCAGGACCAGAGAATTCGAATA CAGGACCGCTNNNCTAGCGTTAC	4414	TGCAGGACCAGAGAATTCGAATA CAGGTAGCCCNNNCTAGCGTTAC	4654	TGCAGGACCAGAGAATTCGAATA CATTTCTGCGNNNCTAGCGTTAC	4894
TGCAGGACCAGAGAATTCGAATA CAGTCCCTATNNNCTAGCGTTAC	4415	TGCAGGACCAGAGAATTCGAATA CATGACGTTGNNNCTAGCGTTAC	4655	TGCAGGACCAGAGAATTCGAATA CAGAATCCCANNNCTAGCGTTAC	4895
TGCAGGACCAGAGAATTCGAATA CATTGCTGAGNNNCTAGCGTTAC	4416	TGCAGGACCAGAGAATTCGAATA CACCCACTATNNNCTAGCGTTAC	4656	TGCAGGACCAGAGAATTCGAATA CACTTTCACGNNNCTAGCGTTAC	4896
TGCAGGACCAGAGAATTCGAATA CATTGGCGTTNNNCTAGCGTTAC	4417	TGCAGGACCAGAGAATTCGAATA CAAAGTGTAANNNCTAGCGTTAC	4657	TGCAGGACCAGAGAATTCGAATA CACGGATCATNNNCTAGCGTTAC	4897
TGCAGGACCAGAGAATTCGAATA CAATCATTTCNNNCTAGCGTTAC	4418	TGCAGGACCAGAGAATTCGAATA CAGGAGTATGNNNCTAGCGTTAC	4658	TGCAGGACCAGAGAATTCGAATA CAACAGTGCTNNNCTAGCGTTAC	4898
TGCAGGACCAGAGAATTCGAATA CAGATGTATTNNNCTAGCGTTAC	4419	TGCAGGACCAGAGAATTCGAATA CAAGTGATAANNNCTAGCGTTAC	4659	TGCAGGACCAGAGAATTCGAATA CACTTAGTCCNNNCTAGCGTTAC	4899
TGCAGGACCAGAGAATTCGAATA CAGATCATATNNNCTAGCGTTAC	4420	TGCAGGACCAGAGAATTCGAATA CATAATTCGANNNCTAGCGTTAC	4660	TGCAGGACCAGAGAATTCGAATA CAAGTGCCCGNNNCTAGCGTTAC	4900
TGCAGGACCAGAGAATTCGAATA CACCCCGCTANNNCTAGCGTTAC	4421	TGCAGGACCAGAGAATTCGAATA CAAGCTTTGGNNNCTAGCGTTAC	4661	TGCAGGACCAGAGAATTCGAATA CATGAAATCTNNNCTAGCGTTAC	4901
TGCAGGACCAGAGAATTCGAATA CAAAAATCGANNNCTAGCGTTAC	4422	TGCAGGACCAGAGAATTCGAATA CAACATGTCGNNNCTAGCGTTAC	4662	TGCAGGACCAGAGAATTCGAATA CATCAGTTAANNNCTAGCGTTAC	4902
TGCAGGACCAGAGAATTCGAATA CAATGTACATNNNCTAGCGTTAC	4423	TGCAGGACCAGAGAATTCGAATA CATCAGCGCGNNNCTAGCGTTAC	4663	TGCAGGACCAGAGAATTCGAATA CAAACCCTGANNNCTAGCGTTAC	4903
TGCAGGACCAGAGAATTCGAATA CAGCCATCTTNNNCTAGCGTTAC	4424	TGCAGGACCAGAGAATTCGAATA CAGCCCGGTANNNCTAGCGTTAC	4664	TGCAGGACCAGAGAATTCGAATA CATCATGATANNNCTAGCGTTAC	4904
TGCAGGACCAGAGAATTCGAATA CAAATGCTCGNNNCTAGCGTTAC	4425	TGCAGGACCAGAGAATTCGAATA CACCATTCACNNNCTAGCGTTAC	4665	TGCAGGACCAGAGAATTCGAATA CAAAGCCTTGNNNCTAGCGTTAC	4905
TGCAGGACCAGAGAATTCGAATA CACACGTCGGNNNCTAGCGTTAC	4426	TGCAGGACCAGAGAATTCGAATA CATTCCCCTTNNNCTAGCGTTAC	4666	TGCAGGACCAGAGAATTCGAATA CAAGCATACCNNNCTAGCGTTAC	4906
TGCAGGACCAGAGAATTCGAATA CACTATGCGANNNCTAGCGTTAC	4427	TGCAGGACCAGAGAATTCGAATA CAACCCTCCGNNNCTAGCGTTAC	4667	TGCAGGACCAGAGAATTCGAATA CAGGCATTTGNNNCTAGCGTTAC	4907

图18C

池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGTCTGGTANNNCTAGCGTTAC	4428	TGCAGGACCAGAGAATTCGAATA CACACCTTACNNNCTAGCGTTAC	4668	TGCAGGACCAGAGAATTCGAATA CAGCGAGTCCNNNCTAGCGTTAC	4908
TGCAGGACCAGAGAATTCGAATA CAGTCAGTGTNNNCTAGCGTTAC	4429	TGCAGGACCAGAGAATTCGAATA CAGGAGTTGANNNCTAGCGTTAC	4669	TGCAGGACCAGAGAATTCGAATA CATTTTGAGANNNCTAGCGTTAC	4909
TGCAGGACCAGAGAATTCGAATA CAGTCCAGTTNNNCTAGCGTTAC	4430	TGCAGGACCAGAGAATTCGAATA CAGACAAGACNNNCTAGCGTTAC	4670	TGCAGGACCAGAGAATTCGAATA CAATCCTTATNNNCTAGCGTTAC	4910
TGCAGGACCAGAGAATTCGAATA CAGATGAAGCNNNCTAGCGTTAC	4431	TGCAGGACCAGAGAATTCGAATA CAGTCTACGANNNCTAGCGTTAC	4671	TGCAGGACCAGAGAATTCGAATA CATCGAAAAAANNNCTAGCGTTAC	4911
TGCAGGACCAGAGAATTCGAATA CAAAACCATTNNNCTAGCGTTAC	4432	TGCAGGACCAGAGAATTCGAATA CATCGCTCATNNNCTAGCGTTAC	4672	TGCAGGACCAGAGAATTCGAATA CAGCTCCGTCNNNCTAGCGTTAC	4912
TGCAGGACCAGAGAATTCGAATA CACCTGCGCTNNNCTAGCGTTAC	4433	TGCAGGACCAGAGAATTCGAATA CACCAAGCCGNNNCTAGCGTTAC	4673	TGCAGGACCAGAGAATTCGAATA CACCAGTTTCNNNCTAGCGTTAC	4913
TGCAGGACCAGAGAATTCGAATA CACACCCGAGNNNCTAGCGTTAC	4434	TGCAGGACCAGAGAATTCGAATA CACCCTCGGTNNNCTAGCGTTAC	4674	TGCAGGACCAGAGAATTCGAATA CACTTGGCTTNNNCTAGCGTTAC	4914
TGCAGGACCAGAGAATTCGAATA CATACTACAANNNCTAGCGTTAC	4435	TGCAGGACCAGAGAATTCGAATA CAAACTAGTTNNNCTAGCGTTAC	4675	TGCAGGACCAGAGAATTCGAATA CACCGCCATCNNNCTAGCGTTAC	4915
TGCAGGACCAGAGAATTCGAATA CATAACCGACNNNCTAGCGTTAC	4436	TGCAGGACCAGAGAATTCGAATA CAGAGTGAGTNNNCTAGCGTTAC	4676	TGCAGGACCAGAGAATTCGAATA CAGATCGATCNNNCTAGCGTTAC	4916
TGCAGGACCAGAGAATTCGAATA CATCTATAGANNNCTAGCGTTAC	4437	TGCAGGACCAGAGAATTCGAATA CACAATACTANNNCTAGCGTTAC	4677	TGCAGGACCAGAGAATTCGAATA CAACGCGGCTNNNCTAGCGTTAC	4917
TGCAGGACCAGAGAATTCGAATA CAGGTGAGGCNNNCTAGCGTTAC	4438	TGCAGGACCAGAGAATTCGAATA CACCTTTGGTNNNCTAGCGTTAC	4678	TGCAGGACCAGAGAATTCGAATA CATCTCGAGANNNCTAGCGTTAC	4918
TGCAGGACCAGAGAATTCGAATA CACATACTCCNNNCTAGCGTTAC	4439	TGCAGGACCAGAGAATTCGAATA CATTCACACCNNNCTAGCGTTAC	4679	TGCAGGACCAGAGAATTCGAATA CAATTGGCACNNNCTAGCGTTAC	4919
TGCAGGACCAGAGAATTCGAATA CATAAGAGTANNNCTAGCGTTAC	4440	TGCAGGACCAGAGAATTCGAATA CAGTTATCCCNNNCTAGCGTTAC	4680	TGCAGGACCAGAGAATTCGAATA CACGCCGAGTNNNCTAGCGTTAC	4920
TGCAGGACCAGAGAATTCGAATA CAGTGTGAGANNNCTAGCGTTAC	4441	TGCAGGACCAGAGAATTCGAATA CAAAACTTGTNNNCTAGCGTTAC	4681	TGCAGGACCAGAGAATTCGAATA CACTTCAGCTNNNCTAGCGTTAC	4921
TGCAGGACCAGAGAATTCGAATA CATTCCCGATNNNCTAGCGTTAC	4442	TGCAGGACCAGAGAATTCGAATA CACAACCCAANNNCTAGCGTTAC	4682	TGCAGGACCAGAGAATTCGAATA CAAAATAAGCNNNCTAGCGTTAC	4922
TGCAGGACCAGAGAATTCGAATA CAAGTACGAGNNNCTAGCGTTAC	4443	TGCAGGACCAGAGAATTCGAATA CAGTTCACGANNNCTAGCGTTAC	4683	TGCAGGACCAGAGAATTCGAATA CAGCCTAAGTNNNCTAGCGTTAC	4923
TGCAGGACCAGAGAATTCGAATA CAGGTGAACANNNCTAGCGTTAC	4444	TGCAGGACCAGAGAATTCGAATA CACGTCTACTNNNCTAGCGTTAC	4684	TGCAGGACCAGAGAATTCGAATA CAGATGTTCGNNNCTAGCGTTAC	4924
TGCAGGACCAGAGAATTCGAATA CACACTAGCANNNCTAGCGTTAC	4445	TGCAGGACCAGAGAATTCGAATA CATCAACAGCNNNCTAGCGTTAC	4685	TGCAGGACCAGAGAATTCGAATA CAAACGAGGTNNNCTAGCGTTAC	4925
TGCAGGACCAGAGAATTCGAATA CAAGCAGAACNNNCTAGCGTTAC	4446	TGCAGGACCAGAGAATTCGAATA CATTGAGTCGNNNCTAGCGTTAC	4686	TGCAGGACCAGAGAATTCGAATA CAATAGACAANNNCTAGCGTTAC	4926
TGCAGGACCAGAGAATTCGAATA CATTTTAAAANNNCTAGCGTTAC	4447	TGCAGGACCAGAGAATTCGAATA CAGCATCTGANNNCTAGCGTTAC	4687	TGCAGGACCAGAGAATTCGAATA CATATTTGGANNNCTAGCGTTAC	4927
TGCAGGACCAGAGAATTCGAATA CACTTCGAGANNNCTAGCGTTAC	4448	TGCAGGACCAGAGAATTCGAATA CATGGCAGTTNNNCTAGCGTTAC	4688	TGCAGGACCAGAGAATTCGAATA CATCCGTGTTNNNCTAGCGTTAC	4928
TGCAGGACCAGAGAATTCGAATA CATGCAATGCNNNGATCGACATG	4449	TGCAGGACCAGAGAATTCGAATA CAGATCTCTCNNNGATCGACATG	4689	TGCAGGACCAGAGAATTCGAATA CATCCTCGATNNNGATCGACATG	4929
TGCAGGACCAGAGAATTCGAATA CAGACGCCACNNNGATCGACATG	4450	TGCAGGACCAGAGAATTCGAATA CAGAGCGCGANNNGATCGACATG	4690	TGCAGGACCAGAGAATTCGAATA CATTTGGAGCNNNGATCGACATG	4930
TGCAGGACCAGAGAATTCGAATA CAGTTTTTCANNNGATCGACATG	4451	TGCAGGACCAGAGAATTCGAATA CACTCTCTAGNNNGATCGACATG	4691	TGCAGGACCAGAGAATTCGAATA CACTTCCACANNNGATCGACATG	4931
TGCAGGACCAGAGAATTCGAATA CAGTTTTATCNNNGATCGACATG	4452	TGCAGGACCAGAGAATTCGAATA CACGTGGCGTNNNGATCGACATG	4692	TGCAGGACCAGAGAATTCGAATA CAAATTTGCANNNGATCGACATG	4932
TGCAGGACCAGAGAATTCGAATA CAACACCGGCNNNGATCGACATG	4453	TGCAGGACCAGAGAATTCGAATA CAAGCTAGTCNNNGATCGACATG	4693	TGCAGGACCAGAGAATTCGAATA CAAATCTGATNNNGATCGACATG	4933
TGCAGGACCAGAGAATTCGAATA CACGCTTTACNNNGATCGACATG	4454	TGCAGGACCAGAGAATTCGAATA CAGCTATGTGNNNGATCGACATG	4694	TGCAGGACCAGAGAATTCGAATA CATCCACTTGNNNGATCGACATG	4934
TGCAGGACCAGAGAATTCGAATA CAGTAAATGANNNGATCGACATG	4455	TGCAGGACCAGAGAATTCGAATA CATCTGCTTGNNNGATCGACATG	4695	TGCAGGACCAGAGAATTCGAATA CATGGTTAGCNNNGATCGACATG	4935
TGCAGGACCAGAGAATTCGAATA CATTTGAAGTNNNGATCGACATG	4456	TGCAGGACCAGAGAATTCGAATA CAGTACGCTANNNGATCGACATG	4696	TGCAGGACCAGAGAATTCGAATA CACTGTAACGNNNGATCGACATG	4936
TGCAGGACCAGAGAATTCGAATA CACACCACTTNNNGATCGACATG	4457	TGCAGGACCAGAGAATTCGAATA CAGACCCGTGNNNGATCGACATG	4697	TGCAGGACCAGAGAATTCGAATA CATATTAGTGNNNGATCGACATG	4937
TGCAGGACCAGAGAATTCGAATA CATGTAAGAANNNGATCGACATG	4458	TGCAGGACCAGAGAATTCGAATA CAGTCATGACNNNGATCGACATG	4698	TGCAGGACCAGAGAATTCGAATA CATGCACATGNNNGATCGACATG	4938
TGCAGGACCAGAGAATTCGAATA CACGCTGAATNNNGATCGACATG	4459	TGCAGGACCAGAGAATTCGAATA CACGCTAGATNNNGATCGACATG	4699	TGCAGGACCAGAGAATTCGAATA CAACCTTCGTNNNGATCGACATG	4939
TGCAGGACCAGAGAATTCGAATA CACTTATTGTNNNGATCGACATG	4460	TGCAGGACCAGAGAATTCGAATA CAGTAATGAANNNGATCGACATG	4700	TGCAGGACCAGAGAATTCGAATA CAGCGTGCACNNNGATCGACATG	4940

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池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
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TGCAGGACCAGAGAATTCGAATA CAACCGGCTGNNNGATCGACATG	4462	TGCAGGACCAGAGAATTCGAATA CACACGTACANNNGATCGACATG	4702	TGCAGGACCAGAGAATTCGAATA CATTGTAAACNNNGATCGACATG	4942
TGCAGGACCAGAGAATTCGAATA CACAAAATTCNNNGATCGACATG	4463	TGCAGGACCAGAGAATTCGAATA CATGACTAATNNNGATCGACATG	4703	TGCAGGACCAGAGAATTCGAATA CAAACGCAAGNNNGATCGACATG	4943
TGCAGGACCAGAGAATTCGAATA CAACTAAAGANNNGATCGACATG	4464	TGCAGGACCAGAGAATTCGAATA CACTACCGCCNNNGATCGACATG	4704	TGCAGGACCAGAGAATTCGAATA CAGTAATCATNNNGATCGACATG	4944
TGCAGGACCAGAGAATTCGAATA CATAGTCTCCNNNGATCGACATG	4465	TGCAGGACCAGAGAATTCGAATA CAGGCACTTANNNGATCGACATG	4705	TGCAGGACCAGAGAATTCGAATA CAGTCTGCTTNNNGATCGACATG	4945
TGCAGGACCAGACAATTCGAATA CACTAACACANNNGATCGACATG	4466	TGCAGGACCAGAGAATTCGAATA CATCCTTAGCNNNGATCGACATG	4706	TGCAGGACCAGAGAATTCGAATA CAGATGGTTCNNNGATCGACATG	4946
TGCAGGACCAGAGAATTCGAATA CATGCACGCGNNNGATCGACATG	4467	TGCAGGACCAGAGAATTCGAATA CAGCTATAGCNNNGATCGACATG	4707	TGCAGGACCAGAGAATTCGAATA CACTTGGCAANNNGATCGACATG	4947
TGCAGGACCAGAGAATTCGAATA CAACTGGAAGNNNGATCGACATG	4468	TGCAGGACCAGAGAATTCGAATA CAAATGAACANNNGATCGACATG	4708	TGCAGGACCAGAGAATTCGAATA CATACCGAACNNNGATCGACATG	4948
TGCAGGACCAGAGAATTCGAATA CAGCAATCCANNNGATCGACATG	4469	TGCAGGACCAGAGAATTCGAATA CAGTAGTAAANNNGATCGACATG	4709	TGCAGGACCAGAGAATTCGAATA CAGTGAGTGANNNGATCGACATG	4949
TGCAGGACCAGAGAATTCGAATA CAAATCCTAANNNGATCGACATG	4470	TGCAGGACCAGAGAATTCGAATA CATAGTTCGGNNNGATCGACATG	4710	TGCAGGACCAGAGAATTCGAATA CACAGGTGAANNNGATCGACATG	4950
TGCAGGACCAGAGAATTCGAATA CAAAGCGGTANNNGATCGACATG	4471	TGCAGGACCAGAGAATTCGAATA CAGTTGTGACNNNGATCGACATG	4711	TGCAGGACCAGAGAATTCGAATA CAAGGTCAGANNNGATCGACATG	4951
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TGCAGGACCAGAGAATTCGAATA CATCACGCTTNNNGATCGACATG	4474	TGCAGGACCAGAGAATTCGAATA CATTGGCGTANNNGATCGACATG	4714	TGCAGGACCAGAGAATTCGAATA CAGAGTGTCTNNNGATCGACATG	4954
TGCAGGACCAGAGAATTCGAATA CATTAGGTGCNNNGATCGACATG	4475	TGCAGGACCAGAGAATTCGAATA CAATTATCCTNNNGATCGACATG	4715	TGCAGGACCAGAGAATTCGAATA CAAAACATCTNNNGATCGACATG	4955
TGCAGGACCAGAGAATTCGAATA CATCCGACGGNNNGATCGACATG	4476	TGCAGGACCAGAGAATTCGAATA CACTTTGAAANNNGATCGACATG	4716	TGCAGGACCAGAGAATTCGAATA CATAAAGCTTNNNGATCGACATG	4956
TGCAGGACCAGAGAATTCGAATA CAAAAGCAGCNNNGATCGACATG	4477	TGCAGGACCAGAGAATTCGAATA CACTAGTACGNNNGATCGACATG	4717	TGCAGGACCAGAGAATTCGAATA CATTAGTGCGNNNGATCGACATG	4957
TGCAGGACCAGAGAATTCGAATA CAGTGCCGGTNNNGATCGACATG	4478	TGCAGGACCAGAGAATTCGAATA CATCCCACATNNNGATCGACATG	4718	TGCAGGACCAGAGAATTCGAATA CAGTTCGCCCNNNGATCGACATG	4958
TGCAGGACCAGAGAATTCGAATA CAACGATATTNNNGATCGACATG	4479	TGCAGGACCAGAGAATTCGAATA CAGTATCGACNNNGATCGACATG	4719	TGCAGGACCAGAGAATTCGAATA CAGTGACCTANNNGATCGACATG	4959
TGCAGGACCAGAGAATTCGAATA CAACAACAGGNNNGATCGACATG	4480	TGCAGGACCAGAGAATTCGAATA CAGGCCTCAGNNNGATCGACATG	4720	TGCAGGACCAGAGAATTCGAATA CAGGACAATGNNNGATCGACATG	4960
TGCAGGACCAGAGAATTCGAATA CACTCCGAAANNNGATCGACATG	4481	TGCAGGACCAGAGAATTCGAATA CACGGCTTAANNNGATCGACATG	4721	TGCAGGACCAGAGAATTCGAATA CATATAGGAANNNGATCGACATG	4961
TGCAGGACCAGAGAATTCGAATA CATCAAGCCANNNGATCGACATG	4482	TGCAGGACCAGAGAATTCGAATA CACATAGCACNNNGATCGACATG	4722	TGCAGGACCAGAGAATTCGAATA CACTAGCGGCNNNGATCGACATG	4962
TGCAGGACCAGAGAATTCGAATA CACATTAACANNNGATCGACATG	4483	TGCAGGACCAGAGAATTCGAATA CACCACTTTGNNNGATCGACATG	4723	TGCAGGACCAGAGAATTCGAATA CAGCGTTTAGNNNGATCGACATG	4963
TGCAGGACCAGAGAATTCGAATA CAAACACGAGNNNGATCGACATG	4484	TGCAGGACCAGAGAATTCGAATA CATGTGATGCNNNGATCGACATG	4724	TGCAGGACCAGAGAATTCGAATA CAGTATGTCGNNNGATCGACATG	4964
TGCAGGACCAGAGAATTCGAATA CATCCATCACNNNGATCGACATG	4485	TGCAGGACCAGAGAATTCGAATA CAATCGCTAGNNNGATCGACATG	4725	TGCAGGACCAGAGAATTCGAATA CACATGTGACNNNGATCGACATG	4965
TGCAGGACCAGAGAATTCGAATA CAGTCGCACGNNNGATCGACATG	4486	TGCAGGACCAGAGAATTCGAATA CAGAATTAGANNNGATCGACATG	4726	TGCAGGACCAGAGAATTCGAATA CAATCAAAAGNNNGATCGACATG	4966
TGCAGGACCAGAGAATTCGAATA CATGGCACGCNNNGATCGACATG	4487	TGCAGGACCAGAGAATTCGAATA CAGCGGTCGTNNNGATCGACATG	4727	TGCAGGACCAGAGAATTCGAATA CAATAAACTCNNNGATCGACATG	4967
TGCAGGACCAGAGAATTCGAATA CATTTCAGAANNNGATCGACATG	4488	TGCAGGACCAGAGAATTCGAATA CAAATTGCATNNNGATCGACATG	4728	TGCAGGACCAGAGAATTCGAATA CACCGGATCGNNNGATCGACATG	4968
TGCAGGACCAGAGAATTCGAATA CATACGTCTCNNNGATCGACATG	4489	TGCAGGACCAGAGAATTCGAATA CATGGAACCTNNNGATCGACATG	4729	TGCAGGACCAGAGAATTCGAATA CACCGGCTAGNNNGATCGACATG	4969
TGCAGGACCAGAGAATTCGAATA CACCGATCTTNNNGATCGACATG	4490	TGCAGGACCAGAGAATTCGAATA CAAGCGCATTNNNGATCGACATG	4730	TGCAGGACCAGAGAATTCGAATA CACTGTGGTANNNGATCGACATG	4970
TGCAGGACCAGAGAATTCGAATA CAATTAAGCTNNNGATCGACATG	4491	TGCAGGACCAGAGAATTCGAATA CATTCCCTCTNNNGATCGACATG	4731	TGCAGGACCAGAGAATTCGAATA CAGAACGTGANNNGATCGACATG	4971
TGCAGGACCAGAGAATTCGAATA CAAACTTCCCNNNGATCGACATG	4492	TGCAGGACCAGAGAATTCGAATA CAATTGTCGGNNNGATCGACATG	4732	TGCAGGACCAGAGAATTCGAATA CACGGCTGACNNNGATCGACATG	4972
TGCAGGACCAGAGAATTCGAATA CAGTCGCTTTNNNGATCGACATG	4493	TGCAGGACCAGAGAATTCGAATA CATAATGCGCNNNGATCGACATG	4733	TGCAGGACCAGAGAATTCGAATA CAGGCATCATNNNGATCGACATG	4973

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池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGCCAGTATNNNGATCGACATG	4494	TGCAGGACCAGAGAATTCGAATA CAACGCATTGNNNGATCGACATG	4734	TGCAGGACCAGAGAATTCGAATA CACCGCAGGTNNNGATCGACATG	4974
TGCAGGACCAGAGAATTCGAATA CAGAGAAAAANNNGATCGACATG	4495	TGCAGGACCAGAGAATTCGAATA CATGTCGGTANNNGATCGACATG	4735	TGCAGGACCAGAGAATTCGAATA CATCCTACTGNNNGATCGACATG	4975
TGCAGGACCAGAGAATTCGAATA CAATAGCCCANNNGATCGACATG	4496	TGCAGGACCAGAGAATTCGAATA CATTTTCAACNNNGATCGACATG	4736	TGCAGGACCAGAGAATTCGAATA CATCCCGACCNNNGATCGACATG	4976
TGCAGGACCAGAGAATTCGAATA CACACGTCCCNNNGATCGACATG	4497	TGCAGGACCAGAGAATTCGAATA CATAAGTACTNNNGATCGACATG	4737	TGCAGGACCAGAGAATTCGAATA CATGTAGGTCNNNGATCGACATG	4977
TGCAGGACCAGAGAATTCGAATA CAAAGTTATCNNNGATCGACATG	4498	TGCAGGACCAGAGAATTCGAATA CAAATTAGTCNNNGATCGACATG	4738	TGCAGGACCAGAGAATTCGAATA CACGGCGCTANNNGATCGACATG	4978
TGCAGGACCAGAGAATTCGAATA CACTTTTCGGNNNGATCGACATG	4499	TGCAGGACCAGAGAATTCGAATA CAGGAAATATNNNGATCGACATG	4739	TGCAGGACCAGAGAATTCGAATA CACCTATTTANNNGATCGACATG	4979
TGCAGGACCAGAGAATTCGAATA CAGAATGGTGNNNGATCGACATG	4500	TGCAGGACCAGAGAATTCGAATA CATTTTTTAANNNGATCGACATG	4740	TGCAGGACCAGAGAATTCGAATA CAGAACAAGCNNNGATCGACATG	4980
TGCAGGACCAGAGAATTCGAATA CAGGACGTAANNNGATCGACATG	4501	TGCAGGACCAGAGAATTCGAATA CACACGTAACNNNGATCGACATG	4741	TGCAGGACCAGAGAATTCGAATA CATCCCATTGNNNGATCGACATG	4981
TGCAGGACCAGAGAATTCGAATA CACCCGAACGNNNGATCGACATG	4502	TGCAGGACCAGAGAATTCGAATA CAGTTTCCGTNNNGATCGACATG	4742	TGCAGGACCAGAGAATTCGAATA CATACTGTGGNNNGATCGACATG	4982
TGCAGGACCAGAGAATTCGAATA CATCCGTATCNNNGATCGACATG	4503	TGCAGGACCAGAGAATTCGAATA CAAGTATCTANNNGATCGACATG	4743	TGCAGGACCAGAGAATTCGAATA CAGCGCTTAANNNGATCGACATG	4983
TGCAGGACCAGAGAATTCGAATA CATTTCGTTANNNGATCGACATG	4504	TGCAGGACCAGAGAATTCGAATA CATCTAGTGGNNNGATCGACATG	4744	TGCAGGACCAGAGAATTCGAATA CAGCCTCCCANNNGATCGACATG	4984
TGCAGGACCAGAGAATTCGAATA CATGCTACAGNNNGATCGACATG	4505	TGCAGGACCAGAGAATTCGAATA CAGAGTACAGNNNGATCGACATG	4745	TGCAGGACCAGAGAATTCGAATA CACACGATACNNNGATCGACATG	4985
TGCAGGACCAGAGAATTCGAATA CAGTTACTTTNNNGATCGACATG	4506	TGCAGGACCAGAGAATTCGAATA CAACTCCAGANNNGATCGACATG	4746	TGCAGGACCAGAGAATTCGAATA CAGTGTCAACNNNGATCGACATG	4986
TGCAGGACCAGAGAATTCGAATA CAAATGCCTGNNNGATCGACATG	4507	TGCAGGACCAGAGAATTCGAATA CAAAACACAANNNGATCGACATG	4747	TGCAGGACCAGAGAATTCGAATA CATACGCCGGNNNGATCGACATG	4987
TGCAGGACCAGAGAATTCGAATA CACCAGGCACNNNGATCGACATG	4508	TGCAGGACCAGAGAATTCGAATA CAGCCGCAACNNNGATCGACATG	4748	TGCAGGACCAGAGAATTCGAATA CAAATCCGACNNNGATCGACATG	4988
TGCAGGACCAGAGAATTCGAATA CATGGCGACCNNNTGCATCAGGT	4509	TGCAGGACCAGAGAATTCGAATA CAGATCTTAANNNTGCATCAGGT	4749	TGCAGGACCAGAGAATTCGAATA CAGCCGCCGGNNNTGCATCAGGT	4989
TGCAGGACCAGAGAATTCGAATA CAAAGAGGCTNNNTGCATCAGGT	4510	TGCAGGACCAGAGAATTCGAATA CACTAGAGTCNNNTGCATCAGGT	4750	TGCAGGACCAGAGAATTCGAATA CACCTGCCGTNNNTGCATCAGGT	4990
TGCAGGACCAGAGAATTCGAATA CATTACCCACNNNTGCATCAGGT	4511	TGCAGGACCAGAGAATTCGAATA CAGCATTCTCNNNTGCATCAGGT	4751	TGCAGGACCAGAGAATTCGAATA CACGTTACCTNNNTGCATCAGGT	4991
TGCAGGACCAGAGAATTCGAATA CATGCGGATTNNNTGCATCAGGT	4512	TGCAGGACCAGAGAATTCGAATA CAGCAGCCACNNNTGCATCAGGT	4752	TGCAGGACCAGAGAATTCGAATA CACGATTAGCNNNTGCATCAGGT	4992
TGCAGGACCAGAGAATTCGAATA CACAGGTTGTNNNTGCATCAGGT	4513	TGCAGGACCAGAGAATTCGAATA CAAGCTGCGCNNNTGCATCAGGT	4753	TGCAGGACCAGAGAATTCGAATA CAAACCTAATNNNTGCATCAGGT	4993
TGCAGGACCAGAGAATTCGAATA CAAACATAGANNNTGCATCAGGT	4514	TGCAGGACCAGAGAATTCGAATA CACCCGCTACNNNTGCATCAGGT	4754	TGCAGGACCAGAGAATTCGAATA CAATCGGCTANNNTGCATCAGGT	4994
TGCAGGACCAGAGAATTCGAATA CAGAAATGATNNNTGCATCAGGT	4515	TGCAGGACCAGAGAATTCGAATA CACAAGGCAANNNTGCATCAGGT	4755	TGCAGGACCAGAGAATTCGAATA CAGGAACCCCNNNTGCATCAGGT	4995
TGCAGGACCAGAGAATTCGAATA CATGTGCTGANNNTGCATCAGGT	4516	TGCAGGACCAGAGAATTCGAATA CAGATGTTATNNNTGCATCAGGT	4756	TGCAGGACCAGAGAATTCGAATA CATCACACAGNNNTGCATCAGGT	4996
TGCAGGACCAGAGAATTCGAATA CAAGGCAGATNNNTGCATCAGGT	4517	TGCAGGACCAGAGAATTCGAATA CACGGTATTGNNNTGCATCAGGT	4757	TGCAGGACCAGAGAATTCGAATA CACTATTGAANNNTGCATCAGGT	4997
TGCAGGACCAGAGAATTCGAATA CATAGGTTATNNNTGCATCAGGT	4518	TGCAGGACCAGAGAATTCGAATA CAGTATTTAGNNNTGCATCAGGT	4758	TGCAGGACCAGAGAATTCGAATA CACGCGATATNNNTGCATCAGGT	4998
TGCAGGACCAGAGAATTCGAATA CATTTTTGTGNNNTGCATCAGGT	4519	TGCAGGACCAGAGAATTCGAATA CAGGATCAGANNNTGCATCAGGT	4759	TGCAGGACCAGAGAATTCGAATA CACTTATGTTNNNTGCATCAGGT	4999
TGCAGGACCAGAGAATTCGAATA CAAAACAAGTNNNTGCATCAGGT	4520	TGCAGGACCAGAGAATTCGAATA CAATCGAAAANNNTGCATCAGGT	4760	TGCAGGACCAGAGAATTCGAATA CAATTTGGTANNNTGCATCAGGT	5000
TGCAGGACCAGAGAATTCGAATA CACGTGGTTANNNTGCATCAGGT	4521	TGCAGGACCAGAGAATTCGAATA CAGCCATTTCNNNTGCATCAGGT	4761	TGCAGGACCAGAGAATTCGAATA CAAGGCAACANNNTGCATCAGGT	5001
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TGCAGGACCAGAGAATTCGAATA CATCTAGTCCNNNTGCATCAGGT	4524	TGCAGGACCAGAGAATTCGAATA CAACCCTATCNNNTGCATCAGGT	4764	TGCAGGACCAGAGAATTCGAATA CACGTGTAACNNNTGCATCAGGT	5004
TGCAGGACCAGAGAATTCGAATA CAAACAAGATNNNTGCATCAGGT	4525	TGCAGGACCAGAGAATTCGAATA CAAAAAGCCGNNNTGCATCAGGT	4765	TGCAGGACCAGAGAATTCGAATA CACAGATCCANNNTGCATCAGGT	5005
TGCAGGACCAGAGAATTCGAATA CATAATGAAGNNNTGCATCAGGT	4526	TGCAGGACCAGAGAATTCGAATA CAGAGTGCGGNNNTGCATCAGGT	4766	TGCAGGACCAGAGAATTCGAATA CACCAGCACGNNNTGCATCAGGT	5006

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池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
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TGCAGGACCAGAGAATTCGAATA CATTGCACGANNNTGCATCAGGT	4528	TGCAGGACCAGAGAATTCGAATA CACAGATGAGNNNTGCATCAGGT	4768	TGCAGGACCAGAGAATTCGAATA CAGTCGAATCNNNTGCATCAGGT	5008
TGCAGGACCAGAGAATTCGAATA CAACTACTAANNNTGCATCAGGT	4529	TGCAGGACCAGAGAATTCGAATA CACAGCTTAGNNNTGCATCAGGT	4769	TGCAGGACCAGAGAATTCGAATA CATCCATAAANNNTGCATCAGGT	5009
TGCAGGACCAGAGAATTCGAATA CAACTCATAANNNTGCATCAGGT	4530	TGCAGGACCAGAGAATTCGAATA CAACTTCTTANNNTGCATCAGGT	4770	TGCAGGACCAGAGAATTCGAATA CAGTCCCACCNNNTGCATCAGGT	5010
TGCAGGACCAGAGAATTCGAATA CAAGGACTGANNNTGCATCAGGT	4531	TGCAGGACCAGAGAATTCGAATA CACAACAGAGNNNTGCATCAGGT	4771	TGCAGGACCAGAGAATTCGAATA CATGGTTGACNNNTGCATCAGGT	5011
TGCAGGACCAGAGAATTCGAATA CACACATCCTNNNTGCATCAGGT	4532	TGCAGGACCAGAGAATTCGAATA CACGTAGATCNNNTGCATCAGGT	4772	TGCAGGACCAGAGAATTCGAATA CAAGACAACGNNNTGCATCAGGT	5012
TGCAGGACCAGAGAATTCGAATA CAATAGCGAGNNNTGCATCAGGT	4533	TGCAGGACCAGAGAATTCGAATA CACCTCCCGANNNTGCATCAGGT	4773	TGCAGGACCAGAGAATTCGAATA CAATATTCAGNNNTGCATCAGGT	5013
TGCAGGACCAGAGAATTCGAATA CAAGGAAGTCNNNTGCATCAGGT	4534	TGCAGGACCAGAGAATTCGAATA CAGACTTTGGNNNTGCATCAGGT	4774	TGCAGGACCAGAGAATTCGAATA CAGAGGAACTNNNTGCATCAGGT	5014
TGCAGGACCAGAGAATTCGAATA CAGAAGCCTTNNNTGCATCAGGT	4535	TGCAGGACCAGAGAATTCGAATA CAGAACATCCNNNTGCATCAGGT	4775	TGCAGGACCAGAGAATTCGAATA CAGAAGAACCNNNTGCATCAGGT	5015
TGCAGGACCAGAGAATTCGAATA CACCCCCTTCNNNTGCATCAGGT	4536	TGCAGGACCAGAGAATTCGAATA CACAGCATCANNNTGCATCAGGT	4776	TGCAGGACCAGAGAATTCGAATA CAGCAACAAGNNNTGCATCAGGT	5016
TGCAGGACCAGAGAATTCGAATA CAAGAAACCGNNNTGCATCAGGT	4537	TGCAGGACCAGAGAATTCGAATA CACTTCTGACNNNTGCATCAGGT	4777	TGCAGGACCAGAGAATTCGAATA CACTAAACCGNNNTGCATCAGGT	5017
TGCAGGACCAGAGAATTCGAATA CAGACATCTGNNNTGCATCAGGT	4538	TGCAGGACCAGAGAATTCGAATA CATCCCGTTANNNTGCATCAGGT	4778	TGCAGGACCAGAGAATTCGAATA CAGGAGGTCGNNNTGCATCAGGT	5018
TGCAGGACCAGAGAATTCGAATA CAACGCCCTCNNNTGCATCAGGT	4539	TGCAGGACCAGAGAATTCGAATA CATTTCCATANNNTGCATCAGGT	4779	TGCAGGACCAGAGAATTCGAATA CACGCGCGTANNNTGCATCAGGT	5019
TGCAGGACCAGAGAATTCGAATA CAGTCACCGGNNNTGCATCAGGT	4540	TGCAGGACCAGAGAATTCGAATA CACGTGCGACNNNTGCATCAGGT	4780	TGCAGGACCAGAGAATTCGAATA CACCGAGTGCNNNTGCATCAGGT	5020
TGCAGGACCAGAGAATTCGAATA CAAGAGCGATNNNTGCATCAGGT	4541	TGCAGGACCAGAGAATTCGAATA CAACGCTGGCNNNTGCATCAGGT	4781	TGCAGGACCAGAGAATTCGAATA CAGTTCAAGCNNNTGCATCAGGT	5021
TGCAGGACCAGAGAATTCGAATA CAATGGCTTGNNNTGCATCAGGT	4542	TGCAGGACCAGAGAATTCGAATA CAGAGATTCCNNNTGCATCAGGT	4782	TGCAGGACCAGAGAATTCGAATA CACAGCCCGANNNTGCATCAGGT	5022
TGCAGGACCAGAGAATTCGAATA CACCTGCAAANNNTGCATCAGGT	4543	TGCAGGACCAGAGAATTCGAATA CAGAGGACTANNNTGCATCAGGT	4783	TGCAGGACCAGAGAATTCGAATA CACCTTGACTNNNTGCATCAGGT	5023
TGCAGGACCAGAGAATTCGAATA CAGTCGAACTNNNTGCATCAGGT	4544	TGCAGGACCAGAGAATTCGAATA CATTGATTAGNNNTGCATCAGGT	4784	TGCAGGACCAGAGAATTCGAATA CAGACGCAAANNNTGCATCAGGT	5024
TGCAGGACCAGAGAATTCGAATA CATGTGGAGANNNTGCATCAGGT	4545	TGCAGGACCAGAGAATTCGAATA CACATGCATGNNNTGCATCAGGT	4785	TGCAGGACCAGAGAATTCGAATA CATGATCCTCNNNTGCATCAGGT	5025
TGCAGGACCAGAGAATTCGAATA CAAACGTGCTNNNTGCATCAGGT	4546	TGCAGGACCAGAGAATTCGAATA CATTGACCCTNNNTGCATCAGGT	4786	TGCAGGACCAGAGAATTCGAATA CAAGAAATTGNNNTGCATCAGGT	5026
TGCAGGACCAGAGAATTCGAATA CAAAGATTGANNNTGCATCAGGT	4547	TGCAGGACCAGAGAATTCGAATA CAGGCCACTGNNNTGCATCAGGT	4787	TGCAGGACCAGAGAATTCGAATA CAGTGTGGCCNNNTGCATCAGGT	5027
TGCAGGACCAGAGAATTCGAATA CAACGTTATANNNTGCATCAGGT	4548	TGCAGGACCAGAGAATTCGAATA CATTCCTCTCNNNTGCATCAGGT	4788	TGCAGGACCAGAGAATTCGAATA CACATGTAGCNNNTGCATCAGGT	5028
TGCAGGACCAGAGAATTCGAATA CACCGCATAANNNTGCATCAGGT	4549	TGCAGGACCAGAGAATTCGAATA CAGCATTCAGNNNTGCATCAGGT	4789	TGCAGGACCAGAGAATTCGAATA CATAGCCCCCNNNTGCATCAGGT	5029
TGCAGGACCAGAGAATTCGAATA CACGATTTCCNNNTGCATCAGGT	4550	TGCAGGACCAGAGAATTCGAATA CAGTAACTTANNNTGCATCAGGT	4790	TGCAGGACCAGAGAATTCGAATA CAGTCTTGCTNNNTGCATCAGGT	5030
TGCAGGACCAGAGAATTCGAATA CAGTAAAACANNNTGCATCAGGT	4551	TGCAGGACCAGAGAATTCGAATA CAACTATGATNNNTGCATCAGGT	4791	TGCAGGACCAGAGAATTCGAATA CATGTAAGCCNNNTGCATCAGGT	5031
TGCAGGACCAGAGAATTCGAATA CAGGTGGTCCNNNTGCATCAGGT	4552	TGCAGGACCAGAGAATTCGAATA CAACTAAGAANNNTGCATCAGGT	4792	TGCAGGACCAGAGAATTCGAATA CAACAGAGACNNNTGCATCAGGT	5032
TGCAGGACCAGAGAATTCGAATA CAATGTCGTGNNNTGCATCAGGT	4553	TGCAGGACCAGAGAATTCGAATA CATAGGTTTANNNTGCATCAGGT	4793	TGCAGGACCAGAGAATTCGAATA CAAGTTCAGCNNNTGCATCAGGT	5033
TGCAGGACCAGAGAATTCGAATA CACGTAATATNNNTGCATCAGGT	4554	TGCAGGACCAGAGAATTCGAATA CACCTCGTCGNNNTGCATCAGGT	4794	TGCAGGACCAGAGAATTCGAATA CACCTGCTTANNNTGCATCAGGT	5034
TGCAGGACCAGAGAATTCGAATA CAACTCGCTTNNNTGCATCAGGT	4555	TGCAGGACCAGAGAATTCGAATA CAGGCTAGCCNNNTGCATCAGGT	4795	TGCAGGACCAGAGAATTCGAATA CAACACCTCTNNNTGCATCAGGT	5035
TGCAGGACCAGAGAATTCGAATA CACCATACGANNNTGCATCAGGT	4556	TGCAGGACCAGAGAATTCGAATA CAGGTTGTACNNNTGCATCAGGT	4796	TGCAGGACCAGAGAATTCGAATA CATATTGAACNNNTGCATCAGGT	5036
TGCAGGACCAGAGAATTCGAATA CACGGACAAANNNTGCATCAGGT	4557	TGCAGGACCAGAGAATTCGAATA CATAAAGCGGNNNTGCATCAGGT	4797	TGCAGGACCAGAGAATTCGAATA CAGATTGGTCNNNTGCATCAGGT	5037
TGCAGGACCAGAGAATTCGAATA CACGCTGTTTNNNTGCATCAGGT	4558	TGCAGGACCAGAGAATTCGAATA CAAATCTTTCNNNTGCATCAGGT	4798	TGCAGGACCAGAGAATTCGAATA CAAAAGAAAGNNNTGCATCAGGT	5038
TGCAGGACCAGAGAATTCGAATA CACTCCCATANNNTGCATCAGGT	4559	TGCAGGACCAGAGAATTCGAATA CACCAAGGAANNNTGCATCAGGT	4799	TGCAGGACCAGAGAATTCGAATA CATAAAAATANNNTGCATCAGGT	5039

图18G

池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGGCTTGCGNNNTGCATCAGGT	4560	TGCAGGACCAGAGAATTCGAATA CAACAAAAGTNNNTGCATCAGGT	4800	TGCAGGACCAGAGAATTCGAATA CATGTCCAGANNNTGCATCAGGT	5040
TGCAGGACCAGAGAATTCGAATA CAAAATTTCGNNNTGCATCAGGT	4561	TGCAGGACCAGAGAATTCGAATA CAGGCCCCGGNNNTGCATCAGGT	4801	TGCAGGACCAGAGAATTCGAATA CATTTGAGGCNNNTGCATCAGGT	5041
TGCAGGACCAGAGAATTCGAATA CATACCTAGGNNNTGCATCAGGT	4562	TGCAGGACCAGAGAATTCGAATA CAAACATGCCNNNTGCATCAGGT	4802	TGCAGGACCAGAGAATTCGAATA CACCATCCTANNNTGCATCAGGT	5042
TGCAGGACCAGAGAATTCGAATA CACACGCACGNNNTGCATCAGGT	4563	TGCAGGACCAGAGAATTCGAATA CATCGGAGTTNNNTGCATCAGGT	4803	TGCAGGACCAGAGAATTCGAATA CACTCCAGAANNNTGCATCAGGT	5043
TGCAGGACCAGAGAATTCGAATA CACATTGCAGNNNTGCATCAGGT	4564	TGCAGGACCAGAGAATTCGAATA CATAGCGGAANNNTGCATCAGGT	4804	TGCAGGACCAGAGAATTCGAATA CACAGATGGANNNTGCATCAGGT	5044
TGCAGGACCAGAGAATTCGAATA CAGCATTAATNNNTGCATCAGGT	4565	TGCAGGACCAGAGAATTCGAATA CAGTCTACTCNNNTGCATCAGGT	4805	TGCAGGACCAGAGAATTCGAATA CATAATCCCCNNNTGCATCAGGT	5045
TGCAGGACCAGAGAATTCGAATA CAAGACGCCCNNNTGCATCAGGT	4566	TGCAGGACCAGAGAATTCGAATA CATTTGACCCNNNTGCATCAGGT	4806	TGCAGGACCAGAGAATTCGAATA CAAGGCGCTCNNNTGCATCAGGT	5046
TGCAGGACCAGAGAATTCGAATA CACACACGATNNNTGCATCAGGT	4567	TGCAGGACCAGAGAATTCGAATA CAAAGGAGAGNNNTGCATCAGGT	4807	TGCAGGACCAGAGAATTCGAATA CAATTGTCAANNNTGCATCAGGT	5047
TGCAGGACCAGAGAATTCGAATA CATGATTGTANNNTGCATCAGGT	4568	TGCAGGACCAGAGAATTCGAATA CATTTCGCCANNNTGCATCAGGT	4808	TGCAGGACCAGAGAATTCGAATA CACGCGTTAANNNTGCATCAGGT	5048

图18H

池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATTGATGCGNNNACGTATGCCA	5049	TGCAGGACCAGAGAATTCGAATA CATAACTAACNNNACGTATGCCA	5289	TGCAGGACCAGAGAATTCGAATA CAGTTGCGCGNNNACGTATGCCA	5529
TGCAGGACCAGAGAATTCGAATA CACCCTACGCNNNACGTATGCCA	5050	TGCAGGACCAGAGAATTCGAATA CAAAACTCGCNNNACGTATGCCA	5290	TGCAGGACCAGAGAATTCGAATA CAGGAACATGNNNACGTATGCCA	5530
TGCAGGACCAGAGAATTCGAATA CAGCGGCGAANNNACGTATGCCA	5051	TGCAGGACCAGAGAATTCGAATA CATGAGTTGCNNNACGTATGCCA	5291	TGCAGGACCAGAGAATTCGAATA CACGGTAACTNNNACGTATGCCA	5531
TGCAGGACCAGAGAATTCGAATA CATAGCCGCGNNNACGTATGCCA	5052	TGCAGGACCAGAGAATTCGAATA CAACAACAAANNNACGTATGCCA	5292	TGCAGGACCAGAGAATTCGAATA CAATGTGTGCNNNACGTATGCCA	5532
TGCAGGACCAGAGAATTCGAATA CAGAAGCGATNNNACGTATGCCA	5053	TGCAGGACCAGAGAATTCGAATA CAGCCCTACCNNNACGTATGCCA	5293	TGCAGGACCAGAGAATTCGAATA CACGAGTTGTNNNACGTATGCCA	5533
TGCAGGACCAGAGAATTCGAATA CAGACAGTGANNNACGTATGCCA	5054	TGCAGGACCAGAGAATTCGAATA CAGTTGAGAGNNNACGTATGCCA	5294	TGCAGGACCAGAGAATTCGAATA CATGAACTCGNNNACGTATGCCA	5534
TGCAGGACCAGAGAATTCGAATA CACTTTATCANNNACGTATGCCA	5055	TGCAGGACCAGAGAATTCGAATA CACAGTGACTNNNACGTATGCCA	5295	TGCAGGACCAGAGAATTCGAATA CAACATCGCANNNACGTATGCCA	5535
TGCAGGACCAGAGAATTCGAATA CACAGGAAGTNNNACGTATGCCA	5056	TGCAGGACCAGAGAATTCGAATA CATGAAGACGNNNACGTATGCCA	5296	TGCAGGACCAGAGAATTCGAATA CAGAATTGTTNNNACGTATGCCA	5536
TGCAGGACCAGAGAATTCGAATA CAGTATTGGCNNNACGTATGCCA	5057	TGCAGGACCAGAGAATTCGAATA CACCCTATGTNNNACGTATGCCA	5297	TGCAGGACCAGAGAATTCGAATA CAAAACACTTNNNACGTATGCCA	5537
TGCAGGACCAGAGAATTCGAATA CATCAGCCGGNNNACGTATGCCA	5058	TGCAGGACCAGAGAATTCGAATA CATGGTTTGGNNNACGTATGCCA	5298	TGCAGGACCAGAGAATTCGAATA CATGTTTGCCNNNACGTATGCCA	5538
TGCAGGACCAGAGAATTCGAATA CAAGCAGGATNNNACGTATGCCA	5059	TGCAGGACCAGAGAATTCGAATA CAGCACTCGGNNNACGTATGCCA	5299	TGCAGGACCAGAGAATTCGAATA CACGCGTGCANNNACGTATGCCA	5539
TGCAGGACCAGAGAATTCGAATA CAGTTAGTGCNNNACGTATGCCA	5060	TGCAGGACCAGAGAATTCGAATA CAAAAGAGTTNNNACGTATGCCA	5300	TGCAGGACCAGAGAATTCGAATA CAGTAATGCCNNNACGTATGCCA	5540
TGCAGGACCAGAGAATTCGAATA CAATTGTAGTNNNACGTATGCCA	5061	TGCAGGACCAGAGAATTCGAATA CAGTTCGTGANNNACGTATGCCA	5301	TGCAGGACCAGAGAATTCGAATA CAGTTCAGACNNNACGTATGCCA	5541
TGCAGGACCAGAGAATTCGAATA CAAGCACGTTNNNACGTATGCCA	5062	TGCAGGACCAGAGAATTCGAATA CATCCCCACGNNNACGTATGCCA	5302	TGCAGGACCAGAGAATTCGAATA CATAATCAGTNNNACGTATGCCA	5542
TGCAGGACCAGAGAATTCGAATA CACCCCGGTTNNNACGTATGCCA	5063	TGCAGGACCAGAGAATTCGAATA CAAAATTCTGNNNACGTATGCCA	5303	TGCAGGACCAGAGAATTCGAATA CATTCCCAACNNNACGTATGCCA	5543
TGCAGGACCAGAGAATTCGAATA CAATATCTCTNNNACGTATGCCA	5064	TGCAGGACCAGAGAATTCGAATA CATCCACAGANNNACGTATGCCA	5304	TGCAGGACCAGAGAATTCGAATA CACTAGTAGCNNNACGTATGCCA	5544
TGCAGGACCAGAGAATTCGAATA CAATCTTCATNNNACGTATGCCA	5065	TGCAGGACCAGAGAATTCGAATA CAAGAGTTTTNNNACGTATGCCA	5305	TGCAGGACCAGAGAATTCGAATA CATTAATACGNNNACGTATGCCA	5545
TGCAGGACCAGAGAATTCGAATA CAGGTACTCANNNACGTATGCCA	5066	TGCAGGACCAGAGAATTCGAATA CATGGAGCGGNNNACGTATGCCA	5306	TGCAGGACCAGAGAATTCGAATA CATACAGAGGNNNACGTATGCCA	5546
TGCAGGACCAGAGAATTCGAATA CACCACCTATNNNACGTATGCCA	5067	TGCAGGACCAGAGAATTCGAATA CACTTTAATCNNNACGTATGCCA	5307	TGCAGGACCAGAGAATTCGAATA CACGGCACCANNNACGTATGCCA	5547
TGCAGGACCAGAGAATTCGAATA CAATAATAAANNNACGTATGCCA	5068	TGCAGGACCAGAGAATTCGAATA CAACGTCAGTNNNACGTATGCCA	5308	TGCAGGACCAGAGAATTCGAATA CATCTCCCAANNNACGTATGCCA	5548
TGCAGGACCAGAGAATTCGAATA CAACATAATCNNNACGTATGCCA	5069	TGCAGGACCAGAGAATTCGAATA CATGGAGCTTNNNACGTATGCCA	5309	TGCAGGACCAGAGAATTCGAATA CAGTACTGCANNNACGTATGCCA	5549
TGCAGGACCAGAGAATTCGAATA CACCTTCGTANNNACGTATGCCA	5070	TGCAGGACCAGAGAATTCGAATA CAGCACACCGNNNACGTATGCCA	5310	TGCAGGACCAGAGAATTCGAATA CAGTAGTACCNNNACGTATGCCA	5550
TGCAGGACCAGAGAATTCGAATA CAGGATCTTGNNNACGTATGCCA	5071	TGCAGGACCAGAGAATTCGAATA CATTTGCTGCNNNACGTATGCCA	5311	TGCAGGACCAGAGAATTCGAATA CATAACCGTGNNNACGTATGCCA	5551
TGCAGGACCAGAGAATTCGAATA CAGAGGCGGTNNNACGTATGCCA	5072	TGCAGGACCAGAGAATTCGAATA CACAGCGAAANNNACGTATGCCA	5312	TGCAGGACCAGAGAATTCGAATA CACGGATAGANNNACGTATGCCA	5552
TGCAGGACCAGAGAATTCGAATA CACTCAAAATNNNACGTATGCCA	5073	TGCAGGACCAGAGAATTCGAATA CAACGATTGCNNNACGTATGCCA	5313	TGCAGGACCAGAGAATTCGAATA CAGGAATAGCNNNACGTATGCCA	5553
TGCAGGACCAGAGAATTCGAATA CACAACTGCANNNACGTATGCCA	5074	TGCAGGACCAGAGAATTCGAATA CATAGCGTTGNNNACGTATGCCA	5314	TGCAGGACCAGAGAATTCGAATA CAGGAGTCAANNNACGTATGCCA	5554
TGCAGGACCAGAGAATTCGAATA CACGGTTCCCNNNACGTATGCCA	5075	TGCAGGACCAGAGAATTCGAATA CAACGCTGCGNNNACGTATGCCA	5315	TGCAGGACCAGAGAATTCGAATA CAATTAGCTANNNACGTATGCCA	5555
TGCAGGACCAGAGAATTCGAATA CAGTGGTAGANNNACGTATGCCA	5076	TGCAGGACCAGAGAATTCGAATA CAGTTTATTGNNNACGTATGCCA	5316	TGCAGGACCAGAGAATTCGAATA CAAGACATTTNNNACGTATGCCA	5556
TGCAGGACCAGAGAATTCGAATA CATCTGAGTGNNNACGTATGCCA	5077	TGCAGGACCAGAGAATTCGAATA CAGCGAAAATGNNNACGTATGCCA	5317	TGCAGGACCAGAGAATTCGAATA CATCTACGCTNNNACGTATGCCA	5557
TGCAGGACCAGAGAATTCGAATA CACAGCCTTTNNNACGTATGCCA	5078	TGCAGGACCAGAGAATTCGAATA CATTTATTGCNNNACGTATGCCA	5318	TGCAGGACCAGAGAATTCGAATA CATGCCTTCANNNACGTATGCCA	5558
TGCAGGACCAGAGAATTCGAATA CAGTGTGTTGNNNACGTATGCCA	5079	TGCAGGACCAGAGAATTCGAATA CATCCAGCGGNNNACGTATGCCA	5319	TGCAGGACCAGAGAATTCGAATA CAAGATCACCNNNACGTATGCCA	5559
TGCAGGACCAGAGAATTCGAATA CAATTGTAACNNNACGTATGCCA	5080	TGCAGGACCAGAGAATTCGAATA CACGCATGCGNNNACGTATGCCA	5320	TGCAGGACCAGAGAATTCGAATA CAATCCTTTANNNACGTATGCCA	5560
TGCAGGACCAGAGAATTCGAATA CAAAGTTCATNNNACGTATGCCA	5081	TGCAGGACCAGAGAATTCGAATA CAATGCTGGTNNNACGTATGCCA	5321	TGCAGGACCAGAGAATTCGAATA CAGTAGTTCGNNNACGTATGCCA	5561

图19A

池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAAGTCGCTNNNACGTATGCCA	5082	TGCAGGACCAGAGAATTCGAATA CAAATGGCCTNNNACGTATGCCA	5322	TGCAGGACCAGAGAATTCGAATA CAGGCCCGGCNNNACGTATGCCA	5562
TGCAGGACCAGAGAATTCGAATA CAATATCAGTNNNACGTATGCCA	5083	TGCAGGACCAGAGAATTCGAATA CAGGTTTAGCNNNACGTATGCCA	5323	TGCAGGACCAGAGAATTCGAATA CAAGGCCAGGNNNACGTATGCCA	5563
TGCAGGACCAGAGAATTCGAATA CATTCTCGGANNNACGTATGCCA	5084	TGCAGGACCAGAGAATTCGAATA CATTCCCAGTNNNACGTATGCCA	5324	TGCAGGACCAGAGAATTCGAATA CATTGTCAGGNNNACGTATGCCA	5564
TGCAGGACCAGAGAATTCGAATA CATCTTGAAANNNACGTATGCCA	5085	TGCAGGACCAGAGAATTCGAATA CAAGCGATGANNNACGTATGCCA	5325	TGCAGGACCAGAGAATTCGAATA CAAAATCTGTNNNACGTATGCCA	5565
TGCAGGACCAGAGAATTCGAATA CATTACCGAGNNNACGTATGCCA	5086	TGCAGGACCAGAGAATTCGAATA CACCGGTCAGNNNACGTATGCCA	5326	TGCAGGACCAGAGAATTCGAATA CAATAAAAATNNNACGTATGCCA	5566
TGCAGGACCAGAGAATTCGAATA CAACTTAGATNNNACGTATGCCA	5087	TGCAGGACCAGAGAATTCGAATA CAAGTATACTNNNACGTATGCCA	5327	TGCAGGACCAGAGAATTCGAATA CATGTCACAGNNNACGTATGCCA	5567
TGCAGGACCAGAGAATTCGAATA CACATCGGTANNNACGTATGCCA	5088	TGCAGGACCAGAGAATTCGAATA CAGACTGAGANNNACGTATGCCA	5328	TGCAGGACCAGAGAATTCGAATA CATCTCATGCNNNACGTATGCCA	5568
TGCAGGACCAGAGAATTCGAATA CACCAGCGCANNNACGTATGCCA	5089	TGCAGGACCAGAGAATTCGAATA CATCACGTTCNNNACGTATGCCA	5329	TGCAGGACCAGAGAATTCGAATA CAGAACGCTTNNNACGTATGCCA	5569
TGCAGGACCAGAGAATTCGAATA CATATCGATANNNACGTATGCCA	5090	TGCAGGACCAGAGAATTCGAATA CACTCACTACNNNACGTATGCCA	5330	TGCAGGACCAGAGAATTCGAATA CATCTCAGCTNNNACGTATGCCA	5570
TGCAGGACCAGAGAATTCGAATA CAAGACTCTGNNNACGTATGCCA	5091	TGCAGGACCAGAGAATTCGAATA CAGAAGAGAGNNNACGTATGCCA	5331	TGCAGGACCAGAGAATTCGAATA CAGATGCGAANNNACGTATGCCA	5571
TGCAGGACCAGAGAATTCGAATA CAAGAGCACANNNACGTATGCCA	5092	TGCAGGACCAGAGAATTCGAATA CACCCTGCACNNNACGTATGCCA	5332	TGCAGGACCAGAGAATTCGAATA CACTCTATCGNNNACGTATGCCA	5572
TGCAGGACCAGAGAATTCGAATA CATACCGTAGNNNACGTATGCCA	5093	TGCAGGACCAGAGAATTCGAATA CAGCAACGAANNNACGTATGCCA	5333	TGCAGGACCAGAGAATTCGAATA CAGACGGTAANNNACGTATGCCA	5573
TGCAGGACCAGAGAATTCGAATA CAGAAGGTGTNNNACGTATGCCA	5094	TGCAGGACCAGAGAATTCGAATA CAGCTACCTTNNNACGTATGCCA	5334	TGCAGGACCAGAGAATTCGAATA CATATATTTTNNNACGTATGCCA	5574
TGCAGGACCAGAGAATTCGAATA CATTGGACCANNNACGTATGCCA	5095	TGCAGGACCAGAGAATTCGAATA CAACACCTTCNNNACGTATGCCA	5335	TGCAGGACCAGAGAATTCGAATA CATGCATTCCNNNACGTATGCCA	5575
TGCAGGACCAGAGAATTCGAATA CAGCAATCACNNNACGTATGCCA	5096	TGCAGGACCAGAGAATTCGAATA CACTGTTAAANNNACGTATGCCA	5336	TGCAGGACCAGAGAATTCGAATA CATATATCTCNNNACGTATGCCA	5576
TGCAGGACCAGAGAATTCGAATA CATTGAGCGTNNNACGTATGCCA	5097	TGCAGGACCAGAGAATTCGAATA CAATCTCGGANNNACGTATGCCA	5337	TGCAGGACCAGAGAATTCGAATA CACCGGCTGANNNACGTATGCCA	5577
TGCAGGACCAGAGAATTCGAATA CACAAGTGTCNNNACGTATGCCA	5098	TGCAGGACCAGAGAATTCGAATA CAATGTTGCGNNNACGTATGCCA	5338	TGCAGGACCAGAGAATTCGAATA CAGAATCAGGNNNACGTATGCCA	5578
TGCAGGACCAGAGAATTCGAATA CAGTCTAATANNNACGTATGCCA	5099	TGCAGGACCAGAGAATTCGAATA CAGCACATGTNNNACGTATGCCA	5339	TGCAGGACCAGAGAATTCGAATA CATCCTAGAGNNNACGTATGCCA	5579
TGCAGGACCAGAGAATTCGAATA CAAAGAAATCNNNACGTATGCCA	5100	TGCAGGACCAGAGAATTCGAATA CAAATCCGGTNNNACGTATGCCA	5340	TGCAGGACCAGAGAATTCGAATA CACCGTGTGGNNNACGTATGCCA	5580
TGCAGGACCAGAGAATTCGAATA CAGCTAGATCNNNACGTATGCCA	5101	TGCAGGACCAGAGAATTCGAATA CACTATTTACNNNACGTATGCCA	5341	TGCAGGACCAGAGAATTCGAATA CATAGTTTCTNNNACGTATGCCA	5581
TGCAGGACCAGAGAATTCGAATA CAGATAAGTANNNACGTATGCCA	5102	TGCAGGACCAGAGAATTCGAATA CACGTGCCAGNNNACGTATGCCA	5342	TGCAGGACCAGAGAATTCGAATA CAGATAACGGNNNACGTATGCCA	5582
TGCAGGACCAGAGAATTCGAATA CAGGTTCAGTNNNACGTATGCCA	5103	TGCAGGACCAGAGAATTCGAATA CACCGGTAGCNNNACGTATGCCA	5343	TGCAGGACCAGAGAATTCGAATA CACTCGTAGTNNNACGTATGCCA	5583
TGCAGGACCAGAGAATTCGAATA CAAGCTGACTNNNACGTATGCCA	5104	TGCAGGACCAGAGAATTCGAATA CAACATATGTNNNACGTATGCCA	5344	TGCAGGACCAGAGAATTCGAATA CAGCACTTTCNNNACGTATGCCA	5584
TGCAGGACCAGAGAATTCGAATA CATGCGCCAGNNNACGTATGCCA	5105	TGCAGGACCAGAGAATTCGAATA CATGGTGGCCNNNACGTATGCCA	5345	TGCAGGACCAGAGAATTCGAATA CAGTTCTCGTNNNACGTATGCCA	5585
TGCAGGACCAGAGAATTCGAATA CATGTCAGTGNNNACGTATGCCA	5106	TGCAGGACCAGAGAATTCGAATA CACAACTCAGNNNACGTATGCCA	5346	TGCAGGACCAGAGAATTCGAATA CACTTACGTCNNNACGTATGCCA	5586
TGCAGGACCAGAGAATTCGAATA CAGAATCGTCNNNACGTATGCCA	5107	TGCAGGACCAGAGAATTCGAATA CACCAATTTTNNNACGTATGCCA	5347	TGCAGGACCAGAGAATTCGAATA CACAGAAGACNNNACGTATGCCA	5587
TGCAGGACCAGAGAATTCGAATA CACCCCATGCNNNACGTATGCCA	5108	TGCAGGACCAGAGAATTCGAATA CAAACTGAGGNNNACGTATGCCA	5348	TGCAGGACCAGAGAATTCGAATA CATAAGTCTANNNACGTATGCCA	5588
TGCAGGACCAGAGAATTCGAATA CACATTAGCGNNNCTAGCGTTAC	5109	TGCAGGACCAGAGAATTCGAATA CAACGTAGTCNNNCTAGCGTTAC	5349	TGCAGGACCAGAGAATTCGAATA CACATACTAANNNCTAGCGTTAC	5589
TGCAGGACCAGAGAATTCGAATA CAATCCACCTNNNCTAGCGTTAC	5110	TGCAGGACCAGAGAATTCGAATA CAGCATGGCCNNNCTAGCGTTAC	5350	TGCAGGACCAGAGAATTCGAATA CACCGAATCANNNCTAGCGTTAC	5590
TGCAGGACCAGAGAATTCGAATA CAACATGCGTNNNCTAGCGTTAC	5111	TGCAGGACCAGAGAATTCGAATA CAAGTCAGAGNNNCTAGCGTTAC	5351	TGCAGGACCAGAGAATTCGAATA CACTATTTTGNNNCTAGCGTTAC	5591
TGCAGGACCAGAGAATTCGAATA CAGCTTTACCNNNCTAGCGTTAC	5112	TGCAGGACCAGAGAATTCGAATA CATGAATACTNNNCTAGCGTTAC	5352	TGCAGGACCAGAGAATTCGAATA CACCCGACAGNNNCTAGCGTTAC	5592
TGCAGGACCAGAGAATTCGAATA CAAACCTCCTNNNCTAGCGTTAC	5113	TGCAGGACCAGAGAATTCGAATA CAGTATGAGGNNNCTAGCGTTAC	5353	TGCAGGACCAGAGAATTCGAATA CAACTTCGAGNNNCTAGCGTTAC	5593
TGCAGGACCAGAGAATTCGAATA CACTTTATGTNNNCTAGCGTTAC	5114	TGCAGGACCAGAGAATTCGAATA CAGACTTGTGNNNCTAGCGTTAC	5354	TGCAGGACCAGAGAATTCGAATA CATGATGCTGNNNCTAGCGTTAC	5594

图19B

池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACTCGCCTGNNNCTAGCGTTAC	5115	TGCAGGACCAGAGAATTCGAATA CAAATTAAGGNNNCTAGCGTTAC	5355	TGCAGGACCAGAGAATTCGAATA CAGCGCAGGANNNCTAGCGTTAC	5595
TGCAGGACCAGAGAATTCGAATA CAATGATGTTNNNCTAGCGTTAC	5116	TGCAGGACCAGAGAATTCGAATA CACGGTTGTANNNCTAGCGTTAC	5356	TGCAGGACCAGAGAATTCGAATA CATTCACAAANNNCTAGCGTTAC	5596
TGCAGGACCAGAGAATTCGAATA CAGAGTTGGANNNCTAGCGTTAC	5117	TGCAGGACCAGAGAATTCGAATA CACCTGTCCGNNNCTAGCGTTAC	5357	TGCAGGACCAGAGAATTCGAATA CAATGCACTGNNNCTAGCGTTAC	5597
TGCAGGACCAGAGAATTCGAATA CAACAACCACNNNCTAGCGTTAC	5118	TGCAGGACCAGAGAATTCGAATA CAGTGACGCCNNNCTAGCGTTAC	5358	TGCAGGACCAGAGAATTCGAATA CAGTTGCCGGNNNCTAGCGTTAC	5598
TGCAGGACCAGAGAATTCGAATA CATACCGCAANNNCTAGCGTTAC	5119	TGCAGGACCAGAGAATTCGAATA CAGTGTTGCANNNCTAGCGTTAC	5359	TGCAGGACCAGAGAATTCGAATA CAATTTTCCANNNCTAGCGTTAC	5599
TGCAGGACCAGAGAATTCGAATA CAGGTTAAAANNNCTAGCGTTAC	5120	TGCAGGACCAGAGAATTCGAATA CACCCGATTTNNNCTAGCGTTAC	5360	TGCAGGACCAGAGAATTCGAATA CACCAGCAGCNNNCTAGCGTTAC	5600
TGCAGGACCAGAGAATTCGAATA CACGGAAAGTNNNCTAGCGTTAC	5121	TGCAGGACCAGAGAATTCGAATA CATTTCCGTGNNNCTAGCGTTAC	5361	TGCAGGACCAGAGAATTCGAATA CACGGACAGGNNNCTAGCGTTAC	5601
TGCAGGACCAGAGAATTCGAATA CAGTGGTCCGNNNCTAGCGTTAC	5122	TGCAGGACCAGAGAATTCGAATA CAAAGGTCCTNNNCTAGCGTTAC	5362	TGCAGGACCAGAGAATTCGAATA CATCTGCGTTNNNCTAGCGTTAC	5602
TGCAGGACCAGAGAATTCGAATA CAGGTGTCCGNNNCTAGCGTTAC	5123	TGCAGGACCAGAGAATTCGAATA CAGAGCCAAANNNCTAGCGTTAC	5363	TGCAGGACCAGAGAATTCGAATA CATTTGCTATNNNCTAGCGTTAC	5603
TGCAGGACCAGAGAATTCGAATA CATCGCACTTNNNCTAGCGTTAC	5124	TGCAGGACCAGAGAATTCGAATA CACCGTTCAANNNCTAGCGTTAC	5364	TGCAGGACCAGAGAATTCGAATA CATTTCCTTTNNNCTAGCGTTAC	5604
TGCAGGACCAGAGAATTCGAATA CATTCGGTCTNNNCTAGCGTTAC	5125	TGCAGGACCAGAGAATTCGAATA CAGCGCGGTTNNNCTAGCGTTAC	5365	TGCAGGACCAGAGAATTCGAATA CACGAGACTTNNNCTAGCGTTAC	5605
TGCAGGACCAGAGAATTCGAATA CAACGAGGATNNNCTAGCGTTAC	5126	TGCAGGACCAGAGAATTCGAATA CACTTCTAGCNNNCTAGCGTTAC	5366	TGCAGGACCAGAGAATTCGAATA CAAACTAGAANNNCTAGCGTTAC	5606
TGCAGGACCAGAGAATTCGAATA CAGTAGATGGNNNCTAGCGTTAC	5127	TGCAGGACCAGAGAATTCGAATA CAGTGTAAAANNNCTAGCGTTAC	5367	TGCAGGACCAGAGAATTCGAATA CACCTCGATTNNNCTAGCGTTAC	5607
TGCAGGACCAGAGAATTCGAATA CACCACACTTNNNCTAGCGTTAC	5128	TGCAGGACCAGAGAATTCGAATA CAACTATGCGNNNCTAGCGTTAC	5368	TGCAGGACCAGAGAATTCGAATA CAGTGAAGACNNNCTAGCGTTAC	5608
TGCAGGACCAGAGAATTCGAATA CAGTTTGCGANNNCTAGCGTTAC	5129	TGCAGGACCAGAGAATTCGAATA CACGCCAGACNNNCTAGCGTTAC	5369	TGCAGGACCAGAGAATTCGAATA CAACGTTACGNNNCTAGCGTTAC	5609
TGCAGGACCAGAGAATTCGAATA CAACGGTATCNNNCTAGCGTTAC	5130	TGCAGGACCAGAGAATTCGAATA CAATCAGTGCNNNCTAGCGTTAC	5370	TGCAGGACCAGAGAATTCGAATA CACGTCCTGCNNNCTAGCGTTAC	5610
TGCAGGACCAGAGAATTCGAATA CAATGATAGANNNCTAGCGTTAC	5131	TGCAGGACCAGAGAATTCGAATA CAGTTCTACCNNNCTAGCGTTAC	5371	TGCAGGACCAGAGAATTCGAATA CAACTCCTACNNNCTAGCGTTAC	5611
TGCAGGACCAGAGAATTCGAATA CACAATAACTNNNCTAGCGTTAC	5132	TGCAGGACCAGAGAATTCGAATA CACACCATAGNNNCTAGCGTTAC	5372	TGCAGGACCAGAGAATTCGAATA CAGTTAGGTCNNNCTAGCGTTAC	5612
TGCAGGACCAGAGAATTCGAATA CAGATCCTAGNNNCTAGCGTTAC	5133	TGCAGGACCAGAGAATTCGAATA CACAAAGATANNNCTAGCGTTAC	5373	TGCAGGACCAGAGAATTCGAATA CACTCATGAGNNNCTAGCGTTAC	5613
TGCAGGACCAGAGAATTCGAATA CAATTACCCCNNNCTAGCGTTAC	5134	TGCAGGACCAGAGAATTCGAATA CACAAGGCTTNNNCTAGCGTTAC	5374	TGCAGGACCAGAGAATTCGAATA CATATTTACCNNNCTAGCGTTAC	5614
TGCAGGACCAGAGAATTCGAATA CACTGTGCGGNNNCTAGCGTTAC	5135	TGCAGGACCAGAGAATTCGAATA CAGTCGTTAGNNNCTAGCGTTAC	5375	TGCAGGACCAGAGAATTCGAATA CACCTTCATGNNNCTAGCGTTAC	5615
TGCAGGACCAGAGAATTCGAATA CATATGTGTANNNCTAGCGTTAC	5136	TGCAGGACCAGAGAATTCGAATA CAAACGTTCGNNNCTAGCGTTAC	5376	TGCAGGACCAGAGAATTCGAATA CAGGACTAGANNNCTAGCGTTAC	5616
TGCAGGACCAGAGAATTCGAATA CAGCTCCTTANNNCTAGCGTTAC	5137	TGCAGGACCAGAGAATTCGAATA CAATGGCTGTNNNCTAGCGTTAC	5377	TGCAGGACCAGAGAATTCGAATA CAGTGGCAAANNNCTAGCGTTAC	5617
TGCAGGACCAGAGAATTCGAATA CAAAAAGCGCNNNCTAGCGTTAC	5138	TGCAGGACCAGAGAATTCGAATA CAATTCTATCNNNCTAGCGTTAC	5378	TGCAGGACCAGAGAATTCGAATA CAAATAAACGNNNCTAGCGTTAC	5618
TGCAGGACCAGAGAATTCGAATA CATGGTATATNNNCTAGCGTTAC	5139	TGCAGGACCAGAGAATTCGAATA CAGGTAGCAANNNCTAGCGTTAC	5379	TGCAGGACCAGAGAATTCGAATA CAGTATACCGNNNCTAGCGTTAC	5619
TGCAGGACCAGAGAATTCGAATA CACATCACGANNNCTAGCGTTAC	5140	TGCAGGACCAGAGAATTCGAATA CATGGTGACTNNNCTAGCGTTAC	5380	TGCAGGACCAGAGAATTCGAATA CACCAAATTANNNCTAGCGTTAC	5620
TGCAGGACCAGAGAATTCGAATA CACTCATTCGNNNCTAGCGTTAC	5141	TGCAGGACCAGAGAATTCGAATA CATCCTAATTNNNCTAGCGTTAC	5381	TGCAGGACCAGAGAATTCGAATA CATTCTTTAGNNNCTAGCGTTAC	5621
TGCAGGACCAGAGAATTCGAATA CAGGCGCATCNNNCTAGCGTTAC	5142	TGCAGGACCAGAGAATTCGAATA CAGCCCGGCGNNNCTAGCGTTAC	5382	TGCAGGACCAGAGAATTCGAATA CATGTTCGTCNNNCTAGCGTTAC	5622
TGCAGGACCAGAGAATTCGAATA CAAAAGATTGNNNCTAGCGTTAC	5143	TGCAGGACCAGAGAATTCGAATA CACCCGCAAGNNNCTAGCGTTAC	5383	TGCAGGACCAGAGAATTCGAATA CACGGGCTCTNNNCTAGCGTTAC	5623
TGCAGGACCAGAGAATTCGAATA CATGAAAGATNNNCTAGCGTTAC	5144	TGCAGGACCAGAGAATTCGAATA CATCCCTGGCNNNCTAGCGTTAC	5384	TGCAGGACCAGAGAATTCGAATA CACGAGTGTTNNNCTAGCGTTAC	5624
TGCAGGACCAGAGAATTCGAATA CACAGGGTTANNNCTAGCGTTAC	5145	TGCAGGACCAGAGAATTCGAATA CAGATCCCTTNNNCTAGCGTTAC	5385	TGCAGGACCAGAGAATTCGAATA CAGCGGTATTNNNCTAGCGTTAC	5625
TGCAGGACCAGAGAATTCGAATA CACGAATTCGNNNCTAGCGTTAC	5146	TGCAGGACCAGAGAATTCGAATA CATAGATGAANNNCTAGCGTTAC	5386	TGCAGGACCAGAGAATTCGAATA CAAAGTCTCGNNNCTAGCGTTAC	5626
TGCAGGACCAGAGAATTCGAATA CATAACCACGNNNCTAGCGTTAC	5147	TGCAGGACCAGAGAATTCGAATA CAAGGCAAGTNNNCTAGCGTTAC	5387	TGCAGGACCAGAGAATTCGAATA CAGTAGCAAGNNNCTAGCGTTAC	5627

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAGCAGGTANNNCTAGCGTTAC	5148	TGCAGGACCAGAGAATTCGAATA CATAATCTGANNNCTAGCGTTAC	5388	TGCAGGACCAGAGAATTCGAATA CACGGAGAGCNNNCTAGCGTTAC	5628
TGCAGGACCAGAGAATTCGAATA CACACAAGGANNNCTAGCGTTAC	5149	TGCAGGACCAGAGAATTCGAATA CAGGCCAAAANNNCTAGCGTTAC	5389	TGCAGGACCAGAGAATTCGAATA CAGCTTTTGCNNNCTAGCGTTAC	5629
TGCAGGACCAGAGAATTCGAATA CAACTAGCCANNNCTAGCGTTAC	5150	TGCAGGACCAGAGAATTCGAATA CAAAGCGTCTNNNCTAGCGTTAC	5390	TGCAGGACCAGAGAATTCGAATA CATATGTAGTNNNCTAGCGTTAC	5630
TGCAGGACCAGAGAATTCGAATA CACACGTGGCNNNCTAGCGTTAC	5151	TGCAGGACCAGAGAATTCGAATA CACATGGCCGNNNCTAGCGTTAC	5391	TGCAGGACCAGAGAATTCGAATA CAATCTCTCGNNNCTAGCGTTAC	5631
TGCAGGACCAGAGAATTCGAATA CACCAGTCGGNNNCTAGCGTTAC	5152	TGCAGGACCAGAGAATTCGAATA CAGGAAGATCNNNCTAGCGTTAC	5392	TGCAGGACCAGAGAATTCGAATA CAGTGTTTCCNNNCTAGCGTTAC	5632
TGCAGGACCAGAGAATTCGAATA CACACCCCTGNNNCTAGCGTTAC	5153	TGCAGGACCAGAGAATTCGAATA CATCAGCTAGNNNCTAGCGTTAC	5393	TGCAGGACCAGAGAATTCGAATA CACGTAGTACNNNCTAGCGTTAC	5633
TGCAGGACCAGAGAATTCGAATA CACAATACATNNNCTAGCGTTAC	5154	TGCAGGACCAGAGAATTCGAATA CACTGCTAAGNNNCTAGCGTTAC	5394	TGCAGGACCAGAGAATTCGAATA CAGCGGAAATNNNCTAGCGTTAC	5634
TGCAGGACCAGAGAATTCGAATA CACTGCATAGNNNCTAGCGTTAC	5155	TGCAGGACCAGAGAATTCGAATA CACACTTGGANNNCTAGCGTTAC	5395	TGCAGGACCAGAGAATTCGAATA CATAATTCAGNNNCTAGCGTTAC	5635
TGCAGGACCAGAGAATTCGAATA CACTGAAAAANNNCTAGCGTTAC	5156	TGCAGGACCAGAGAATTCGAATA CACTCGAATGNNNCTAGCGTTAC	5396	TGCAGGACCAGAGAATTCGAATA CACGCGCGGCNNNCTAGCGTTAC	5636
TGCAGGACCAGAGAATTCGAATA CAGTCCATTCNNNCTAGCGTTAC	5157	TGCAGGACCAGAGAATTCGAATA CACGCTTAAGNNNCTAGCGTTAC	5397	TGCAGGACCAGAGAATTCGAATA CACGAAGAGTNNNCTAGCGTTAC	5637
TGCAGGACCAGAGAATTCGAATA CATTAGTGGCNNNCTAGCGTTAC	5158	TGCAGGACCAGAGAATTCGAATA CAATATTGTGNNNCTAGCGTTAC	5398	TGCAGGACCAGAGAATTCGAATA CAAGCGTGTTNNNCTAGCGTTAC	5638
TGCAGGACCAGAGAATTCGAATA CAACTGGCATNNNCTAGCGTTAC	5159	TGCAGGACCAGAGAATTCGAATA CATTTCACGCNNNCTAGCGTTAC	5399	TGCAGGACCAGAGAATTCGAATA CACGAAAGCANNNCTAGCGTTAC	5639
TGCAGGACCAGAGAATTCGAATA CAATGGTTGCNNNCTAGCGTTAC	5160	TGCAGGACCAGAGAATTCGAATA CATTCCATCGNNNCTAGCGTTAC	5400	TGCAGGACCAGAGAATTCGAATA CAGTCTACGTNNNCTAGCGTTAC	5640
TGCAGGACCAGAGAATTCGAATA CATGGCTCCCNNNCTAGCGTTAC	5161	TGCAGGACCAGAGAATTCGAATA CAAATGACCCNNNCTAGCGTTAC	5401	TGCAGGACCAGAGAATTCGAATA CACATGCGGCNNNCTAGCGTTAC	5641
TGCAGGACCAGAGAATTCGAATA CAGATTTTCCNNNCTAGCGTTAC	5162	TGCAGGACCAGAGAATTCGAATA CAATCAGTCGNNNCTAGCGTTAC	5402	TGCAGGACCAGAGAATTCGAATA CATGACCGGCNNNCTAGCGTTAC	5642
TGCAGGACCAGAGAATTCGAATA CAGCCTACAANNNCTAGCGTTAC	5163	TGCAGGACCAGAGAATTCGAATA CACTCTGAAGNNNCTAGCGTTAC	5403	TGCAGGACCAGAGAATTCGAATA CAACTTTAGANNNCTAGCGTTAC	5643
TGCAGGACCAGAGAATTCGAATA CAGGATTCACNNNCTAGCGTTAC	5164	TGCAGGACCAGAGAATTCGAATA CAAAAGTGATNNNCTAGCGTTAC	5404	TGCAGGACCAGAGAATTCGAATA CAAGCTCCCGNNNCTAGCGTTAC	5644
TGCAGGACCAGAGAATTCGAATA CAATTCGCAGNNNCTAGCGTTAC	5165	TGCAGGACCAGAGAATTCGAATA CATCAACCTCNNNCTAGCGTTAC	5405	TGCAGGACCAGAGAATTCGAATA CAAGACATCCNNNCTAGCGTTAC	5645
TGCAGGACCAGAGAATTCGAATA CACGGCTACGNNNCTAGCGTTAC	5166	TGCAGGACCAGAGAATTCGAATA CAGCTAATGCNNNCTAGCGTTAC	5406	TGCAGGACCAGAGAATTCGAATA CACTCAATGGNNNCTAGCGTTAC	5646
TGCAGGACCAGAGAATTCGAATA CAATCCTAGGNNNCTAGCGTTAC	5167	TGCAGGACCAGAGAATTCGAATA CATATTGGCGNNNCTAGCGTTAC	5407	TGCAGGACCAGAGAATTCGAATA CATATTCCGCNNNCTAGCGTTAC	5647
TGCAGGACCAGAGAATTCGAATA CATCGTACCTNNNCTAGCGTTAC	5168	TGCAGGACCAGAGAATTCGAATA CATACTATCTNNNCTAGCGTTAC	5408	TGCAGGACCAGAGAATTCGAATA CATTCACCTGNNNCTAGCGTTAC	5648
TGCAGGACCAGAGAATTCGAATA CACATCTAAANNNGATCGACATG	5169	TGCAGGACCAGAGAATTCGAATA CAGACTCGGCNNNGATCGACATG	5409	TGCAGGACCAGAGAATTCGAATA CACTCTGTACNNNGATCGACATG	5649
TGCAGGACCAGAGAATTCGAATA CAAGTGAACGNNNGATCGACATG	5170	TGCAGGACCAGAGAATTCGAATA CAGCTGTATGNNNGATCGACATG	5410	TGCAGGACCAGAGAATTCGAATA CATTGATTTCNNNGATCGACATG	5650
TGCAGGACCAGAGAATTCGAATA CACTGAACTGNNNGATCGACATG	5171	TGCAGGACCAGAGAATTCGAATA CAAAATTGCTNNNGATCGACATG	5411	TGCAGGACCAGAGAATTCGAATA CAGCACATACNNNGATCGACATG	5651
TGCAGGACCAGAGAATTCGAATA CAGATACGAGNNNGATCGACATG	5172	TGCAGGACCAGAGAATTCGAATA CAACATGTTANNNGATCGACATG	5412	TGCAGGACCAGAGAATTCGAATA CAGCTTGTGANNNGATCGACATG	5652
TGCAGGACCAGAGAATTCGAATA CATTTCCTAANNNGATCGACATG	5173	TGCAGGACCAGAGAATTCGAATA CAAGATGGACNNNGATCGACATG	5413	TGCAGGACCAGAGAATTCGAATA CATACGGTACNNNGATCGACATG	5653
TGCAGGACCAGAGAATTCGAATA CATAGTCTTTNNNGATCGACATG	5174	TGCAGGACCAGAGAATTCGAATA CATGTCTCCANNNGATCGACATG	5414	TGCAGGACCAGAGAATTCGAATA CACACGGTCGNNNGATCGACATG	5654
TGCAGGACCAGAGAATTCGAATA CAAGTTGCCANNNGATCGACATG	5175	TGCAGGACCAGAGAATTCGAATA CATTGGCTAGNNNGATCGACATG	5415	TGCAGGACCAGAGAATTCGAATA CACCAAGGTTNNNGATCGACATG	5655
TGCAGGACCAGAGAATTCGAATA CAAGCGACAANNNGATCGACATG	5176	TGCAGGACCAGAGAATTCGAATA CATAATTTCCNNNGATCGACATG	5416	TGCAGGACCAGAGAATTCGAATA CAGTTCGGCGNNNGATCGACATG	5656
TGCAGGACCAGAGAATTCGAATA CAGGATAAATNNNGATCGACATG	5177	TGCAGGACCAGAGAATTCGAATA CAGTGTTAATNNNGATCGACATG	5417	TGCAGGACCAGAGAATTCGAATA CAACGCAGCCNNNGATCGACATG	5657
TGCAGGACCAGAGAATTCGAATA CATTTGAAACNNNGATCGACATG	5178	TGCAGGACCAGAGAATTCGAATA CATGAGCAAGNNNGATCGACATG	5418	TGCAGGACCAGAGAATTCGAATA CACCCCGAGANNNGATCGACATG	5658
TGCAGGACCAGAGAATTCGAATA CAGAGGATACNNNGATCGACATG	5179	TGCAGGACCAGAGAATTCGAATA CACGCCCCTANNNGATCGACATG	5419	TGCAGGACCAGAGAATTCGAATA CACTCCATGTNNNGATCGACATG	5659
TGCAGGACCAGAGAATTCGAATA CAACTGGATCNNNGATCGACATG	5180	TGCAGGACCAGAGAATTCGAATA CAGTCACAGTNNNGATCGACATG	5420	TGCAGGACCAGAGAATTCGAATA CATTTGCACCNNNGATCGACATG	5660

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAAATGGATNNNGATCGACATG	5181	TGCAGGACCAGAGAATTCGAATA CAGTTGGTGTNNNGATCGACATG	5421	TGCAGGACCAGAGAATTCGAATA CAATTACAACNNNGATCGACATG	5661
TGCAGGACCAGAGAATTCGAATA CACGCATGATNNNGATCGACATG	5182	TGCAGGACCAGAGAATTCGAATA CACTTATTACNNNGATCGACATG	5422	TGCAGGACCAGAGAATTCGAATA CATGCCCACCNNNGATCGACATG	5662
TGCAGGACCAGAGAATTCGAATA CATACGAATTNNNGATCGACATG	5183	TGCAGGACCAGAGAATTCGAATA CACTCGCAAANNNGATCGACATG	5423	TGCAGGACCAGAGAATTCGAATA CAGATTGGAGNNNGATCGACATG	5663
TGCAGGACCAGAGAATTCGAATA CAGGAAAGCTNNNGATCGACATG	5184	TGCAGGACCAGAGAATTCGAATA CACTAGGTGTNNNGATCGACATG	5424	TGCAGGACCAGAGAATTCGAATA CATCATACCCNNNGATCGACATG	5664
TGCAGGACCAGAGAATTCGAATA CACCAACAACNNNGATCGACATG	5185	TGCAGGACCAGAGAATTCGAATA CACAACATATNNNGATCGACATG	5425	TGCAGGACCAGAGAATTCGAATA CAGGTGGATANNNGATCGACATG	5665
TGCAGGACCAGAGAATTCGAATA CAACGGGACCNNNGATCGACATG	5186	TGCAGGACCAGAGAATTCGAATA CAACCGATACNNNGATCGACATG	5426	TGCAGGACCAGAGAATTCGAATA CAGACATTCGNNNGATCGACATG	5666
TGCAGGACCAGAGAATTCGAATA CAGGAGTCCCNNNGATCGACATG	5187	TGCAGGACCAGAGAATTCGAATA CACCGACTGGNNNGATCGACATG	5427	TGCAGGACCAGAGAATTCGAATA CAATCTGCGANNNGATCGACATG	5667
TGCAGGACCAGAGAATTCGAATA CACCACGCAGNNNGATCGACATG	5188	TGCAGGACCAGAGAATTCGAATA CACAACGCATNNNGATCGACATG	5428	TGCAGGACCAGAGAATTCGAATA CAGGCACCCANNNGATCGACATG	5668
TGCAGGACCAGAGAATTCGAATA CAACTCGCCCNNNGATCGACATG	5189	TGCAGGACCAGAGAATTCGAATA CATTTTAATTNNNGATCGACATG	5429	TGCAGGACCAGAGAATTCGAATA CAAATGTTTGNNNGATCGACATG	5669
TGCAGGACCAGAGAATTCGAATA CACTGAAGAGNNNGATCGACATG	5190	TGCAGGACCAGAGAATTCGAATA CAAGTGTATTNNNGATCGACATG	5430	TGCAGGACCAGAGAATTCGAATA CAACCTGGTANNNGATCGACATG	5670
TGCAGGACCAGAGAATTCGAATA CAGGAGCACGNNNGATCGACATG	5191	TGCAGGACCAGAGAATTCGAATA CAACTTCAGGNNNGATCGACATG	5431	TGCAGGACCAGAGAATTCGAATA CAACTGAGAGNNNGATCGACATG	5671
TGCAGGACCAGAGAATTCGAATA CAGGAGCGACNNNGATCGACATG	5192	TGCAGGACCAGAGAATTCGAATA CAAAGCCGCCNNNGATCGACATG	5432	TGCAGGACCAGAGAATTCGAATA CAGAATTAAGNNNGATCGACATG	5672
TGCAGGACCAGAGAATTCGAATA CAGGAACCTTNNNGATCGACATG	5193	TGCAGGACCAGAGAATTCGAATA CACCACGGTGNNNGATCGACATG	5433	TGCAGGACCAGAGAATTCGAATA CAATTACGGCNNNGATCGACATG	5673
TGCAGGACCAGAGAATTCGAATA CAGCCCTGTCNNNGATCGACATG	5194	TGCAGGACCAGAGAATTCGAATA CAGGCTCTTTNNNGATCGACATG	5434	TGCAGGACCAGAGAATTCGAATA CACAGTCTAGNNNGATCGACATG	5674
TGCAGGACCAGAGAATTCGAATA CAAGTAATCTNNNGATCGACATG	5195	TGCAGGACCAGAGAATTCGAATA CACTTAGCCTNNNGATCGACATG	5435	TGCAGGACCAGAGAATTCGAATA CAATCCCTTGNNNGATCGACATG	5675
TGCAGGACCAGAGAATTCGAATA CACGCTCGAGNNNGATCGACATG	5196	TGCAGGACCAGAGAATTCGAATA CAATTAGCATNNNGATCGACATG	5436	TGCAGGACCAGAGAATTCGAATA CATGTCCACTNNNGATCGACATG	5676
TGCAGGACCAGAGAATTCGAATA CAGTCATGGTNNNGATCGACATG	5197	TGCAGGACCAGAGAATTCGAATA CAGCAGCTTANNNGATCGACATG	5437	TGCAGGACCAGAGAATTCGAATA CAGGTACGCCNNNGATCGACATG	5677
TGCAGGACCAGAGAATTCGAATA CAGATTCCAGNNNGATCGACATG	5198	TGCAGGACCAGAGAATTCGAATA CAACATACGCNNNGATCGACATG	5438	TGCAGGACCAGAGAATTCGAATA CATGAGCAGANNNGATCGACATG	5678
TGCAGGACCAGAGAATTCGAATA CACTATTACTNNNGATCGACATG	5199	TGCAGGACCAGAGAATTCGAATA CAGTCGAAAGNNNGATCGACATG	5439	TGCAGGACCAGAGAATTCGAATA CAGATCCGTANNNGATCGACATG	5679
TGCAGGACCAGAGAATTCGAATA CAAGGTCTACNNNGATCGACATG	5200	TGCAGGACCAGAGAATTCGAATA CATTCTAGTTNNNGATCGACATG	5440	TGCAGGACCAGAGAATTCGAATA CATCACTAAANNNGATCGACATG	5680
TGCAGGACCAGAGAATTCGAATA CACCTGTAGANNNGATCGACATG	5201	TGCAGGACCAGAGAATTCGAATA CACACGCTCCNNNGATCGACATG	5441	TGCAGGACCAGAGAATTCGAATA CAAATAGATGNNNGATCGACATG	5681
TGCAGGACCAGAGAATTCGAATA CATCCTGTCANNNGATCGACATG	5202	TGCAGGACCAGAGAATTCGAATA CACCGAGGTCNNNGATCGACATG	5442	TGCAGGACCAGAGAATTCGAATA CATCGCGCTCNNNGATCGACATG	5682
TGCAGGACCAGAGAATTCGAATA CACCCTGCGTNNNGATCGACATG	5203	TGCAGGACCAGAGAATTCGAATA CACATTCAGGNNNGATCGACATG	5443	TGCAGGACCAGAGAATTCGAATA CAACCGACGCNNNGATCGACATG	5683
TGCAGGACCAGAGAATTCGAATA CAACAATGAANNNGATCGACATG	5204	TGCAGGACCAGAGAATTCGAATA CATCCATAGGNNNGATCGACATG	5444	TGCAGGACCAGAGAATTCGAATA CACACGGACCNNNGATCGACATG	5684
TGCAGGACCAGAGAATTCGAATA CAGGTGGAGCNNNGATCGACATG	5205	TGCAGGACCAGAGAATTCGAATA CATTACTCATNNNGATCGACATG	5445	TGCAGGACCAGAGAATTCGAATA CAATATCGATNNNGATCGACATG	5685
TGCAGGACCAGAGAATTCGAATA CAGGATAGACNNNGATCGACATG	5206	TGCAGGACCAGAGAATTCGAATA CAATCTGATANNNGATCGACATG	5446	TGCAGGACCAGAGAATTCGAATA CATACCACGANNNGATCGACATG	5686
TGCAGGACCAGAGAATTCGAATA CAGAGTGCCCNNNGATCGACATG	5207	TGCAGGACCAGAGAATTCGAATA CAGTCCACTTNNNGATCGACATG	5447	TGCAGGACCAGAGAATTCGAATA CAAAGAACGCNNNGATCGACATG	5687
TGCAGGACCAGAGAATTCGAATA CAAAACGGTGNNNGATCGACATG	5208	TGCAGGACCAGAGAATTCGAATA CACAGGAACANNNGATCGACATG	5448	TGCAGGACCAGAGAATTCGAATA CAAGTACCTGNNNGATCGACATG	5688
TGCAGGACCAGAGAATTCGAATA CAAATAGCAANNNGATCGACATG	5209	TGCAGGACCAGAGAATTCGAATA CACTAGCTTCNNNGATCGACATG	5449	TGCAGGACCAGAGAATTCGAATA CAGTTTTAGANNNGATCGACATG	5689
TGCAGGACCAGAGAATTCGAATA CATCAATTGANNNGATCGACATG	5210	TGCAGGACCAGAGAATTCGAATA CATTTGGCGANNNGATCGACATG	5450	TGCAGGACCAGAGAATTCGAATA CAGGATTTTANNNGATCGACATG	5690
TGCAGGACCAGAGAATTCGAATA CAAGCAATGGNNNGATCGACATG	5211	TGCAGGACCAGAGAATTCGAATA CACCGGAAGGNNNGATCGACATG	5451	TGCAGGACCAGAGAATTCGAATA CATAGTATACNNNGATCGACATG	5691
TGCAGGACCAGAGAATTCGAATA CAGTAGTGAGNNNGATCGACATG	5212	TGCAGGACCAGAGAATTCGAATA CATCCCAACTNNNGATCGACATG	5452	TGCAGGACCAGAGAATTCGAATA CACGTATGGTNNNGATCGACATG	5692
TGCAGGACCAGAGAATTCGAATA CACACTGCGGNNNGATCGACATG	5213	TGCAGGACCAGAGAATTCGAATA CATTCACGGANNNGATCGACATG	5453	TGCAGGACCAGAGAATTCGAATA CATCCCGGCTNNNGATCGACATG	5693

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAACCGCTCCNNNGATCGACATG	5214	TGCAGGACCAGAGAATTCGAATA CAATTTTACCNNNGATCGACATG	5454	TGCAGGACCAGAGAATTCGAATA CAGCGCTCTCNNNGATCGACATG	5694
TGCAGGACCAGAGAATTCGAATA CACTAGGTTGNNNGATCGACATG	5215	TGCAGGACCAGAGAATTCGAATA CATGGAGTCTNNNGATCGACATG	5455	TGCAGGACCAGAGAATTCGAATA CACATTCCCANNNGATCGACATG	5695
TGCAGGACCAGAGAATTCGAATA CATAAAATAANNNGATCGACATG	5216	TGCAGGACCAGAGAATTCGAATA CACGACGACCNNNGATCGACATG	5456	TGCAGGACCAGAGAATTCGAATA CATCGCCCCANNNGATCGACATG	5696
TGCAGGACCAGAGAATTCGAATA CAGTCACGTANNNGATCGACATG	5217	TGCAGGACCAGAGAATTCGAATA CATCCCATACNNNGATCGACATG	5457	TGCAGGACCAGAGAATTCGAATA CATGCATTGGNNNGATCGACATG	5697
TGCAGGACCAGAGAATTCGAATA CAGGTTCGATNNNGATCGACATG	5218	TGCAGGACCAGAGAATTCGAATA CAGCCCTTATNNNGATCGACATG	5458	TGCAGGACCAGAGAATTCGAATA CAATCAGATTNNNGATCGACATG	5698
TGCAGGACCAGAGAATTCGAATA CACAATGGAGNNNGATCGACATG	5219	TGCAGGACCAGAGAATTCGAATA CAGTCCCGCTNNNGATCGACATG	5459	TGCAGGACCAGAGAATTCGAATA CACTTTTATGNNNGATCGACATG	5699
TGCAGGACCAGAGAATTCGAATA CACCGAGGGTNNNGATCGACATG	5220	TGCAGGACCAGAGAATTCGAATA CAGGGCCCTTNNNGATCGACATG	5460	TGCAGGACCAGAGAATTCGAATA CAAAAGTCGGNNNGATCGACATG	5700
TGCAGGACCAGAGAATTCGAATA CACAAACGAGNNNGATCGACATG	5221	TGCAGGACCAGAGAATTCGAATA CATCAGCTTCNNNGATCGACATG	5461	TGCAGGACCAGAGAATTCGAATA CAACGAGTGANNNGATCGACATG	5701
TGCAGGACCAGAGAATTCGAATA CAGATATGTTNNNGATCGACATG	5222	TGCAGGACCAGAGAATTCGAATA CAGGCTCGGTNNNGATCGACATG	5462	TGCAGGACCAGAGAATTCGAATA CAGAAATTAGNNNGATCGACATG	5702
TGCAGGACCAGAGAATTCGAATA CAGTTCTGTCNNNGATCGACATG	5223	TGCAGGACCAGAGAATTCGAATA CAAAGTTCGCNNNGATCGACATG	5463	TGCAGGACCAGAGAATTCGAATA CAATTATCTCNNNGATCGACATG	5703
TGCAGGACCAGAGAATTCGAATA CATCTTTTCTNNNGATCGACATG	5224	TGCAGGACCAGAGAATTCGAATA CAAACGCCGCNNNGATCGACATG	5464	TGCAGGACCAGAGAATTCGAATA CAGCTCGGCANNNGATCGACATG	5704
TGCAGGACCAGAGAATTCGAATA CAAAAGACATNNNGATCGACATG	5225	TGCAGGACCAGAGAATTCGAATA CATTACTATCNNNGATCGACATG	5465	TGCAGGACCAGAGAATTCGAATA CAGTTAGAGGNNNGATCGACATG	5705
TGCAGGACCAGAGAATTCGAATA CAACCCATGANNNGATCGACATG	5226	TGCAGGACCAGAGAATTCGAATA CATTCAAGATNNNGATCGACATG	5466	TGCAGGACCAGAGAATTCGAATA CAACCAGCTANNNGATCGACATG	5706
TGCAGGACCAGAGAATTCGAATA CATCCTCACANNNGATCGACATG	5227	TGCAGGACCAGAGAATTCGAATA CACTCAGTTCNNNGATCGACATG	5467	TGCAGGACCAGAGAATTCGAATA CAGGAGTGCGNNNGATCGACATG	5707
TGCAGGACCAGAGAATTCGAATA CATTGAGGTCNNNGATCGACATG	5228	TGCAGGACCAGAGAATTCGAATA CAAAGAATTGNNNGATCGACATG	5468	TGCAGGACCAGAGAATTCGAATA CATCGATATANNNGATCGACATG	5708
TGCAGGACCAGAGAATTCGAATA CAGCGTACTANNNTGCATCAGGT	5229	TGCAGGACCAGAGAATTCGAATA CAGACTACCANNNTGCATCAGGT	5469	TGCAGGACCAGAGAATTCGAATA CAGCGGTAGCNNNTGCATCAGGT	5709
TGCAGGACCAGAGAATTCGAATA CAAGGTTAGCNNNTGCATCAGGT	5230	TGCAGGACCAGAGAATTCGAATA CACACGCTAANNNTGCATCAGGT	5470	TGCAGGACCAGAGAATTCGAATA CACTGATTAANNNTGCATCAGGT	5710
TGCAGGACCAGAGAATTCGAATA CACTCCACATNNNTGCATCAGGT	5231	TGCAGGACCAGAGAATTCGAATA CAAGTCATATNNNTGCATCAGGT	5471	TGCAGGACCAGAGAATTCGAATA CACACTTCACNNNTGCATCAGGT	5711
TGCAGGACCAGAGAATTCGAATA CACGATCTAGNNNTGCATCAGGT	5232	TGCAGGACCAGAGAATTCGAATA CATCTAGGACNNNTGCATCAGGT	5472	TGCAGGACCAGAGAATTCGAATA CATAGGCGTTNNNTGCATCAGGT	5712
TGCAGGACCAGAGAATTCGAATA CATCGATAATNNNTGCATCAGGT	5233	TGCAGGACCAGAGAATTCGAATA CAAGAACTTTNNNTGCATCAGGT	5473	TGCAGGACCAGAGAATTCGAATA CAATATGTCANNNTGCATCAGGT	5713
TGCAGGACCAGAGAATTCGAATA CACCACGAGCNNNTGCATCAGGT	5234	TGCAGGACCAGAGAATTCGAATA CAACCACTGANNNTGCATCAGGT	5474	TGCAGGACCAGAGAATTCGAATA CAGTCGATTGNNNTGCATCAGGT	5714
TGCAGGACCAGAGAATTCGAATA CAGTGGAATGNNNTGCATCAGGT	5235	TGCAGGACCAGAGAATTCGAATA CAACACGATCNNNTGCATCAGGT	5475	TGCAGGACCAGAGAATTCGAATA CAATAGAGCGNNNTGCATCAGGT	5715
TGCAGGACCAGAGAATTCGAATA CAAAAAATGCNNNTGCATCAGGT	5236	TGCAGGACCAGAGAATTCGAATA CAGTTACCAGNNNTGCATCAGGT	5476	TGCAGGACCAGAGAATTCGAATA CAGACTAAGGNNNTGCATCAGGT	5716
TGCAGGACCAGAGAATTCGAATA CAGACTAGTCNNNTGCATCAGGT	5237	TGCAGGACCAGAGAATTCGAATA CACGCTACCCNNNTGCATCAGGT	5477	TGCAGGACCAGAGAATTCGAATA CACCTACCTANNNTGCATCAGGT	5717
TGCAGGACCAGAGAATTCGAATA CACGTAGAAGNNNTGCATCAGGT	5238	TGCAGGACCAGAGAATTCGAATA CAAGAGGTACNNNTGCATCAGGT	5478	TGCAGGACCAGAGAATTCGAATA CATAGGAGACNNNTGCATCAGGT	5718
TGCAGGACCAGAGAATTCGAATA CAGTGTGAAGNNNTGCATCAGGT	5239	TGCAGGACCAGAGAATTCGAATA CAAATCTCTTNNNTGCATCAGGT	5479	TGCAGGACCAGAGAATTCGAATA CACCGTCATTNNNTGCATCAGGT	5719
TGCAGGACCAGAGAATTCGAATA CAAAGTACTTNNNTGCATCAGGT	5240	TGCAGGACCAGAGAATTCGAATA CAATATTTAANNNTGCATCAGGT	5480	TGCAGGACCAGAGAATTCGAATA CAGTGTTCAGNNNTGCATCAGGT	5720
TGCAGGACCAGAGAATTCGAATA CACGAACGTTNNNTGCATCAGGT	5241	TGCAGGACCAGAGAATTCGAATA CATATCGAATNNNTGCATCAGGT	5481	TGCAGGACCAGAGAATTCGAATA CAAGCGGTTTNNNTGCATCAGGT	5721
TGCAGGACCAGAGAATTCGAATA CAATTGCTGGNNNTGCATCAGGT	5242	TGCAGGACCAGAGAATTCGAATA CAGCTAAATTNNNTGCATCAGGT	5482	TGCAGGACCAGAGAATTCGAATA CAAACTCTTTNNNTGCATCAGGT	5722
TGCAGGACCAGAGAATTCGAATA CATGTGTGTGNNNTGCATCAGGT	5243	TGCAGGACCAGAGAATTCGAATA CATTTCAGCCNNNTGCATCAGGT	5483	TGCAGGACCAGAGAATTCGAATA CATAACGTATNNNTGCATCAGGT	5723
TGCAGGACCAGAGAATTCGAATA CAACATCTTTNNNTGCATCAGGT	5244	TGCAGGACCAGAGAATTCGAATA CAGTTCACAGNNNTGCATCAGGT	5484	TGCAGGACCAGAGAATTCGAATA CAAAGGACTGNNNTGCATCAGGT	5724
TGCAGGACCAGAGAATTCGAATA CACGATGCTANNNTGCATCAGGT	5245	TGCAGGACCAGAGAATTCGAATA CAGCATTCCTNNNTGCATCAGGT	5485	TGCAGGACCAGAGAATTCGAATA CAAGGAGAAGNNNTGCATCAGGT	5725
TGCAGGACCAGAGAATTCGAATA CATAGTCCAGNNNTGCATCAGGT	5246	TGCAGGACCAGAGAATTCGAATA CATTACACCCNNNTGCATCAGGT	5486	TGCAGGACCAGAGAATTCGAATA CATCGAACGTNNNTGCATCAGGT	5726

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACAGTAATTNNNTGCATCAGGT	5247	TGCAGGACCAGAGAATTCGAATA CATATTTTATNNNTGCATCAGGT	5487	TGCAGGACCAGAGAATTCGAATA CACGGACATTNNNTGCATCAGGT	5727
TGCAGGACCAGAGAATTCGAATA CAAAGGTGGTNNNTGCATCAGGT	5248	TGCAGGACCAGAGAATTCGAATA CATGTCCGCCNNNTGCATCAGGT	5488	TGCAGGACCAGAGAATTCGAATA CATTCCGCATNNNTGCATCAGGT	5728
TGCAGGACCAGAGAATTCGAATA CACGGTGGTCNNNTGCATCAGGT	5249	TGCAGGACCAGAGAATTCGAATA CAAAACCCGTNNNTGCATCAGGT	5489	TGCAGGACCAGAGAATTCGAATA CACGCGGCTANNNTGCATCAGGT	5729
TGCAGGACCAGAGAATTCGAATA CAGTGGTTGTNNNTGCATCAGGT	5250	TGCAGGACCAGAGAATTCGAATA CAGTACCGATNNNTGCATCAGGT	5490	TGCAGGACCAGAGAATTCGAATA CAGTTTCTGCNNNTGCATCAGGT	5730
TGCAGGACCAGAGAATTCGAATA CATGTATTCTNNNTGCATCAGGT	5251	TGCAGGACCAGAGAATTCGAATA CACGCGTTCCNNNTGCATCAGGT	5491	TGCAGGACCAGAGAATTCGAATA CAAGACAGCANNNTGCATCAGGT	5731
TGCAGGACCAGAGAATTCGAATA CATAAGTCGCNNNTGCATCAGGT	5252	TGCAGGACCAGAGAATTCGAATA CACTCCAATCNNNTGCATCAGGT	5492	TGCAGGACCAGAGAATTCGAATA CAGACCCTCCNNNTGCATCAGGT	5732
TGCAGGACCAGAGAATTCGAATA CATAGGAGCANNNTGCATCAGGT	5253	TGCAGGACCAGAGAATTCGAATA CACCGCAGACNNNTGCATCAGGT	5493	TGCAGGACCAGAGAATTCGAATA CATACTCGCTNNNTGCATCAGGT	5733
TGCAGGACCAGAGAATTCGAATA CACATAAATCNNNTGCATCAGGT	5254	TGCAGGACCAGAGAATTCGAATA CACGCTTAGANNNTGCATCAGGT	5494	TGCAGGACCAGAGAATTCGAATA CATTCGTATTNNNTGCATCAGGT	5734
TGCAGGACCAGAGAATTCGAATA CAAGCTGTACNNNTGCATCAGGT	5255	TGCAGGACCAGAGAATTCGAATA CAGAAAAGCCNNNTGCATCAGGT	5495	TGCAGGACCAGAGAATTCGAATA CATACTTAGNNNTGCATCAGGT	5735
TGCAGGACCAGAGAATTCGAATA CATTGCGCTTNNNTGCATCAGGT	5256	TGCAGGACCAGAGAATTCGAATA CACTCATCCANNNTGCATCAGGT	5496	TGCAGGACCAGAGAATTCGAATA CAGACTACGTNNNTGCATCAGGT	5736
TGCAGGACCAGAGAATTCGAATA CAAGGCGTGGNNNTGCATCAGGT	5257	TGCAGGACCAGAGAATTCGAATA CAAAGAGTATNNNTGCATCAGGT	5497	TGCAGGACCAGAGAATTCGAATA CAACGAGTCTNNNTGCATCAGGT	5737
TGCAGGACCAGAGAATTCGAATA CAGTCTAGGTNNNTGCATCAGGT	5258	TGCAGGACCAGAGAATTCGAATA CAAATTGTCANNNTGCATCAGGT	5498	TGCAGGACCAGAGAATTCGAATA CAGATCGTTGNNNTGCATCAGGT	5738
TGCAGGACCAGAGAATTCGAATA CATCCGTAAGNNNTGCATCAGGT	5259	TGCAGGACCAGAGAATTCGAATA CAATAATACCNNNTGCATCAGGT	5499	TGCAGGACCAGAGAATTCGAATA CAGATGGACANNNTGCATCAGGT	5739
TGCAGGACCAGAGAATTCGAATA CATATCGGCANNNTGCATCAGGT	5260	TGCAGGACCAGAGAATTCGAATA CAAATTTTGGNNNTGCATCAGGT	5500	TGCAGGACCAGAGAATTCGAATA CATCGTAGTGNNNTGCATCAGGT	5740
TGCAGGACCAGAGAATTCGAATA CAATCATCGGNNNTGCATCAGGT	5261	TGCAGGACCAGAGAATTCGAATA CAGCACAGTTNNNTGCATCAGGT	5501	TGCAGGACCAGAGAATTCGAATA CACCACATCTNNNTGCATCAGGT	5741
TGCAGGACCAGAGAATTCGAATA CAACGTCTGANNNTGCATCAGGT	5262	TGCAGGACCAGAGAATTCGAATA CATTAAACCANNNTGCATCAGGT	5502	TGCAGGACCAGAGAATTCGAATA CAGTGCTACANNNTGCATCAGGT	5742
TGCAGGACCAGAGAATTCGAATA CAACGGTACTNNNTGCATCAGGT	5263	TGCAGGACCAGAGAATTCGAATA CAATGGAGACNNNTGCATCAGGT	5503	TGCAGGACCAGAGAATTCGAATA CATTCTTCAANNNTGCATCAGGT	5743
TGCAGGACCAGAGAATTCGAATA CATGCAAGGANNNTGCATCAGGT	5264	TGCAGGACCAGAGAATTCGAATA CAAAAGACGCNNNTGCATCAGGT	5504	TGCAGGACCAGAGAATTCGAATA CATTACAGTANNNTGCATCAGGT	5744
TGCAGGACCAGAGAATTCGAATA CAAGACTCACNNNTGCATCAGGT	5265	TGCAGGACCAGAGAATTCGAATA CAATCCGAACNNNTGCATCAGGT	5505	TGCAGGACCAGAGAATTCGAATA CAAGACGCGGNNNTGCATCAGGT	5745
TGCAGGACCAGAGAATTCGAATA CACAATCAGCNNNTGCATCAGGT	5266	TGCAGGACCAGAGAATTCGAATA CAGTTAGGAGNNNTGCATCAGGT	5506	TGCAGGACCAGAGAATTCGAATA CAGGAGCTCCNNNTGCATCAGGT	5746
TGCAGGACCAGAGAATTCGAATA CATGGCTGTANNNTGCATCAGGT	5267	TGCAGGACCAGAGAATTCGAATA CATGGCCAGCNNNTGCATCAGGT	5507	TGCAGGACCAGAGAATTCGAATA CAATTAACCANNNTGCATCAGGT	5747
TGCAGGACCAGAGAATTCGAATA CAGTTTACCCNNNTGCATCAGGT	5268	TGCAGGACCAGAGAATTCGAATA CAATGTGCACNNNTGCATCAGGT	5508	TGCAGGACCAGAGAATTCGAATA CAATCGAGCTNNNTGCATCAGGT	5748
TGCAGGACCAGAGAATTCGAATA CACGTCAGTANNNTGCATCAGGT	5269	TGCAGGACCAGAGAATTCGAATA CAGTACAACCNNNTGCATCAGGT	5509	TGCAGGACCAGAGAATTCGAATA CAGGAAACGTNNNTGCATCAGGT	5749
TGCAGGACCAGAGAATTCGAATA CACGACGGAGNNNTGCATCAGGT	5270	TGCAGGACCAGAGAATTCGAATA CAGTGGCGAGNNNTGCATCAGGT	5510	TGCAGGACCAGAGAATTCGAATA CATGAAGAGCNNNTGCATCAGGT	5750
TGCAGGACCAGAGAATTCGAATA CAATATGCGCNNNTGCATCAGGT	5271	TGCAGGACCAGAGAATTCGAATA CAAGCTCTCTNNNTGCATCAGGT	5511	TGCAGGACCAGAGAATTCGAATA CAATCCGGATNNNTGCATCAGGT	5751
TGCAGGACCAGAGAATTCGAATA CAGCTGGCCANNNTGCATCAGGT	5272	TGCAGGACCAGAGAATTCGAATA CAACCTCTTGNNNTGCATCAGGT	5512	TGCAGGACCAGAGAATTCGAATA CAGTTGTCTCNNNTGCATCAGGT	5752
TGCAGGACCAGAGAATTCGAATA CACGCGTCTCNNNTGCATCAGGT	5273	TGCAGGACCAGAGAATTCGAATA CATCAGCGTANNNTGCATCAGGT	5513	TGCAGGACCAGAGAATTCGAATA CATGGATAGGNNNTGCATCAGGT	5753
TGCAGGACCAGAGAATTCGAATA CAATAAGTGANNNTGCATCAGGT	5274	TGCAGGACCAGAGAATTCGAATA CATCAGACGTNNNTGCATCAGGT	5514	TGCAGGACCAGAGAATTCGAATA CAAAACCAGGNNNTGCATCAGGT	5754
TGCAGGACCAGAGAATTCGAATA CAGACAGTCTNNNTGCATCAGGT	5275	TGCAGGACCAGAGAATTCGAATA CATATAGATCNNNTGCATCAGGT	5515	TGCAGGACCAGAGAATTCGAATA CACGGCGACTNNNTGCATCAGGT	5755
TGCAGGACCAGAGAATTCGAATA CAGCAAGGTANNNTGCATCAGGT	5276	TGCAGGACCAGAGAATTCGAATA CAACCCGCCTNNNTGCATCAGGT	5516	TGCAGGACCAGAGAATTCGAATA CATTATCGCCNNNTGCATCAGGT	5756
TGCAGGACCAGAGAATTCGAATA CACACGAACTNNNTGCATCAGGT	5277	TGCAGGACCAGAGAATTCGAATA CAGCAGGATANNNTGCATCAGGT	5517	TGCAGGACCAGAGAATTCGAATA CAAGCCACATNNNTGCATCAGGT	5757
TGCAGGACCAGAGAATTCGAATA CATACACTGGNNNTGCATCAGGT	5278	TGCAGGACCAGAGAATTCGAATA CAAGAATGCGNNNTGCATCAGGT	5518	TGCAGGACCAGAGAATTCGAATA CATGCTCATCNNNTGCATCAGGT	5758
TGCAGGACCAGAGAATTCGAATA CAATTTCGTTNNNTGCATCAGGT	5279	TGCAGGACCAGAGAATTCGAATA CAACAAGTGGNNNTGCATCAGGT	5519	TGCAGGACCAGAGAATTCGAATA CAGCTGGAGGNNNTGCATCAGGT	5759

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATCTGCGCCNNNTGCATCAGGT	5280	TGCAGGACCAGAGAATTCGAATA CAGTCCGGCANNNTGCATCAGGT	5520	TGCAGGACCAGAGAATTCGAATA CAAAAGATGTNNNTGCATCAGGT	5760
TGCAGGACCAGAGAATTCGAATA CACGAGCTATNNNTGCATCAGGT	5281	TGCAGGACCAGAGAATTCGAATA CAGCCCTGAGNNNTGCATCAGGT	5521	TGCAGGACCAGAGAATTCGAATA CATCAGAAAANNNTGCATCAGGT	5761
TGCAGGACCAGAGAATTCGAATA CAACGCCATANNNTGCATCAGGT	5282	TGCAGGACCAGAGAATTCGAATA CAAACTATGTNNNTGCATCAGGT	5522	TGCAGGACCAGAGAATTCGAATA CAGTCCTGAANNNTGCATCAGGT	5762
TGCAGGACCAGAGAATTCGAATA CATCCTCTGANNNTGCATCAGGT	5283	TGCAGGACCAGAGAATTCGAATA CATCTGATCCNNNTGCATCAGGT	5523	TGCAGGACCAGAGAATTCGAATA CAGCTAGGCCNNNTGCATCAGGT	5763
TGCAGGACCAGAGAATTCGAATA CAAATTCTAGNNNTGCATCAGGT	5284	TGCAGGACCAGAGAATTCGAATA CATAATAGAGNNNTGCATCAGGT	5524	TGCAGGACCAGAGAATTCGAATA CACTCCTGTANNNTGCATCAGGT	5764
TGCAGGACCAGAGAATTCGAATA CACCTCAGCCNNNTGCATCAGGT	5285	TGCAGGACCAGAGAATTCGAATA CAGGCCGTTGNNNTGCATCAGGT	5525	TGCAGGACCAGAGAATTCGAATA CATTGATCAANNNTGCATCAGGT	5765
TGCAGGACCAGAGAATTCGAATA CAACCCCGGANNNTGCATCAGGT	5286	TGCAGGACCAGAGAATTCGAATA CACAACAAGGNNNTGCATCAGGT	5526	TGCAGGACCAGAGAATTCGAATA CACTGTTCGTNNNTGCATCAGGT	5766
TGCAGGACCAGAGAATTCGAATA CAGTGATAGGNNNTGCATCAGGT	5287	TGCAGGACCAGAGAATTCGAATA CACCCTGAAANNNTGCATCAGGT	5527	TGCAGGACCAGAGAATTCGAATA CATCTTATCANNNTGCATCAGGT	5767
TGCAGGACCAGAGAATTCGAATA CATTGAATTGNNNTGCATCAGGT	5288	TGCAGGACCAGAGAATTCGAATA CACTGCTGTTNNNTGCATCAGGT	5528	TGCAGGACCAGAGAATTCGAATA CATACTGGCANNNTGCATCAGGT	5768

图19H

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC GCGACGTNNNACGTATGCCA	5769	TGCAGGACCAGAGAATTCGAATACAC TCTGCTANNNACGTATGCCA	6009	TGCAGGACCAGAGAATTCGAATACAT GTACGCANNNACGTATGCCA	6249
TGCAGGACCAGAGAATTCGAATACAC CGATCAANNNACGTATGCCA	5770	TGCAGGACCAGAGAATTCGAATACAT TACATGANNNACGTATGCCA	6010	TGCAGGACCAGAGAATTCGAATACAG ATGTGTCNNNACGTATGCCA	6250
TGCAGGACCAGAGAATTCGAATACAG GCAATCTNNNACGTATGCCA	5771	TGCAGGACCAGAGAATTCGAATACAC GAGGATANNNACGTATGCCA	6011	TGCAGGACCAGAGAATTCGAATACAC TAGACTGNNNACGTATGCCA	6251
TGCAGGACCAGAGAATTCGAATACAC TAGGAGANNNACGTATGCCA	5772	TGCAGGACCAGAGAATTCGAATACAC GACATGTNNNACGTATGCCA	6012	TGCAGGACCAGAGAATTCGAATACAG ATCGTGTNNNACGTATGCCA	6252
TGCAGGACCAGAGAATTCGAATACAT TGATAACNNNACGTATGCCA	5773	TGCAGGACCAGAGAATTCGAATACAC CTTGAAGNNNACGTATGCCA	6013	TGCAGGACCAGAGAATTCGAATACAT TATCTCANNNACGTATGCCA	6253
TGCAGGACCAGAGAATTCGAATACAG AGTACTCNNNACGTATGCCA	5774	TGCAGGACCAGAGAATTCGAATACAC AACGATCNNNACGTATGCCA	6014	TGCAGGACCAGAGAATTCGAATACAA ACCCTAGNNNACGTATGCCA	6254
TGCAGGACCAGAGAATTCGAATACAA TGCCGCGNNNACGTATGCCA	5775	TGCAGGACCAGAGAATTCGAATACAG ACTAGAGNNNACGTATGCCA	6015	TGCAGGACCAGAGAATTCGAATACAT ATCATAGNNNACGTATGCCA	6255
TGCAGGACCAGAGAATTCGAATACAA AATAGCANNNACGTATGCCA	5776	TGCAGGACCAGAGAATTCGAATACAC TGCAGTANNNACGTATGCCA	6016	TGCAGGACCAGAGAATTCGAATACAC GTTCGTTNNNACGTATGCCA	6256
TGCAGGACCAGAGAATTCGAATACAA TCAGACCNNNACGTATGCCA	5777	TGCAGGACCAGAGAATTCGAATACAA TGTGACCNNNACGTATGCCA	6017	TGCAGGACCAGAGAATTCGAATACAA TACAAAGNNNACGTATGCCA	6257
TGCAGGACCAGAGAATTCGAATACAG GTGCGTCNNNACGTATGCCA	5778	TGCAGGACCAGAGAATTCGAATACAA CGAATTTNNNACGTATGCCA	6018	TGCAGGACCAGAGAATTCGAATACAG TCCTCATNNNACGTATGCCA	6258
TGCAGGACCAGAGAATTCGAATACAT GTTTCCCNNNACGTATGCCA	5779	TGCAGGACCAGAGAATTCGAATACAA TTGTTTCNNNACGTATGCCA	6019	TGCAGGACCAGAGAATTCGAATACAA GTAGCAGNNNACGTATGCCA	6259
TGCAGGACCAGAGAATTCGAATACAA AATTCCANNNACGTATGCCA	5780	TGCAGGACCAGAGAATTCGAATACAC GCCGTGANNNACGTATGCCA	6020	TGCAGGACCAGAGAATTCGAATACAG AAAACATNNNACGTATGCCA	6260
TGCAGGACCAGAGAATTCGAATACAA ATGTGCCNNNACGTATGCCA	5781	TGCAGGACCAGAGAATTCGAATACAC ACTCAAGNNNACGTATGCCA	6021	TGCAGGACCAGAGAATTCGAATACAT TCGCCTANNNACGTATGCCA	6261
TGCAGGACCAGAGAATTCGAATACAC ACATGACNNNACGTATGCCA	5782	TGCAGGACCAGAGAATTCGAATACAA GCAATCCNNNACGTATGCCA	6022	TGCAGGACCAGAGAATTCGAATACAA GAGTTGGNNNACGTATGCCA	6262
TGCAGGACCAGAGAATTCGAATACAG ACCTGGCNNNACGTATGCCA	5783	TGCAGGACCAGAGAATTCGAATACAT CCATTATNNNACGTATGCCA	6023	TGCAGGACCAGAGAATTCGAATACAC AATATTGNNNACGTATGCCA	6263
TGCAGGACCAGAGAATTCGAATACAC CAAAATTNNNACGTATGCCA	5784	TGCAGGACCAGAGAATTCGAATACAA ATTGCTANNNACGTATGCCA	6024	TGCAGGACCAGAGAATTCGAATACAA AACCTCGNNNACGTATGCCA	6264
TGCAGGACCAGAGAATTCGAATACAA TTGTCCCNNNACGTATGCCA	5785	TGCAGGACCAGAGAATTCGAATACAC GATCCAANNNACGTATGCCA	6025	TGCAGGACCAGAGAATTCGAATACAA GTTAATCNNNACGTATGCCA	6265
TGCAGGACCAGAGAATTCGAATACAC GTCGACGNNNACGTATGCCA	5786	TGCAGGACCAGAGAATTCGAATACAC TCGGTGGNNNACGTATGCCA	6026	TGCAGGACCAGAGAATTCGAATACAG ACTCTAGNNNACGTATGCCA	6266
TGCAGGACCAGAGAATTCGAATACAC CCGCTCANNNACGTATGCCA	5787	TGCAGGACCAGAGAATTCGAATACAG AGATTAANNNACGTATGCCA	6027	TGCAGGACCAGAGAATTCGAATACAA GGAAAAANNNACGTATGCCA	6267
TGCAGGACCAGAGAATTCGAATACAA TGGACTCNNNACGTATGCCA	5788	TGCAGGACCAGAGAATTCGAATACAA TCAGGCTNNNACGTATGCCA	6028	TGCAGGACCAGAGAATTCGAATACAT GACTAGCNNNACGTATGCCA	6268
TGCAGGACCAGAGAATTCGAATACAT TGTAACANNNACGTATGCCA	5789	TGCAGGACCAGAGAATTCGAATACAG CGGCCCGNNNACGTATGCCA	6029	TGCAGGACCAGAGAATTCGAATACAC ATCGTAGNNNACGTATGCCA	6269
TGCAGGACCAGAGAATTCGAATACAG TTTACTTNNNACGTATGCCA	5790	TGCAGGACCAGAGAATTCGAATACAT TTAAATANNNACGTATGCCA	6030	TGCAGGACCAGAGAATTCGAATACAA GGTGTTCNNNACGTATGCCA	6270
TGCAGGACCAGAGAATTCGAATACAT GGATAAANNNACGTATGCCA	5791	TGCAGGACCAGAGAATTCGAATACAC ATGGCGCNNNACGTATGCCA	6031	TGCAGGACCAGAGAATTCGAATACAG CCATTAGNNNACGTATGCCA	6271
TGCAGGACCAGAGAATTCGAATACAA TCCTTCGNNNACGTATGCCA	5792	TGCAGGACCAGAGAATTCGAATACAT CGGTTAGNNNACGTATGCCA	6032	TGCAGGACCAGAGAATTCGAATACAC GTTCTGTNNNACGTATGCCA	6272
TGCAGGACCAGAGAATTCGAATACAC GCATACANNNACGTATGCCA	5793	TGCAGGACCAGAGAATTCGAATACAC GCCTGGANNNACGTATGCCA	6033	TGCAGGACCAGAGAATTCGAATACAT CCGCCTGNNNACGTATGCCA	6273
TGCAGGACCAGAGAATTCGAATACAA CACCGATNNNACGTATGCCA	5794	TGCAGGACCAGAGAATTCGAATACAT TCCTGTGNNNACGTATGCCA	6034	TGCAGGACCAGAGAATTCGAATACAC CTACACTNNNACGTATGCCA	6274
TGCAGGACCAGAGAATTCGAATACAA TTGCTCCNNNACGTATGCCA	5795	TGCAGGACCAGAGAATTCGAATACAG GCGCCTANNNACGTATGCCA	6035	TGCAGGACCAGAGAATTCGAATACAA GAAGATTNNNACGTATGCCA	6275
TGCAGGACCAGAGAATTCGAATACAA TCTTCTANNNACGTATGCCA	5796	TGCAGGACCAGAGAATTCGAATACAC CCGGCGGNNNACGTATGCCA	6036	TGCAGGACCAGAGAATTCGAATACAA GTCCTTCNNNACGTATGCCA	6276
TGCAGGACCAGAGAATTCGAATACAT CGAAATTNNNACGTATGCCA	5797	TGCAGGACCAGAGAATTCGAATACAA TTCGGCANNNACGTATGCCA	6037	TGCAGGACCAGAGAATTCGAATACAG CATTATANNNACGTATGCCA	6277
TGCAGGACCAGAGAATTCGAATACAC AAGTCACNNNACGTATGCCA	5798	TGCAGGACCAGAGAATTCGAATACAC AAATGAANNNACGTATGCCA	6038	TGCAGGACCAGAGAATTCGAATACAG TGGCATTNNNACGTATGCCA	6278
TGCAGGACCAGAGAATTCGAATACAT GACCCGGNNNACGTATGCCA	5799	TGCAGGACCAGAGAATTCGAATACAT AGGATGGNNNACGTATGCCA	6039	TGCAGGACCAGAGAATTCGAATACAA ACGTCACNNNACGTATGCCA	6279
TGCAGGACCAGAGAATTCGAATACAA GCTGCCGNNNACGTATGCCA	5800	TGCAGGACCAGAGAATTCGAATACAT TGGACGTNNNACGTATGCCA	6040	TGCAGGACCAGAGAATTCGAATACAG TTAACTANNNACGTATGCCA	6280

图20A

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT CACTCGTNNNACGTATGCCA	5801	TGCAGGACCAGAGAATTCGAATACAT CGTGAGTNNNACGTATGCCA	6041	TGCAGGACCAGAGAATTCGAATACAT AAAGATGNNNACGTATGCCA	6281
TGCAGGACCAGAGAATTCGAATACAG TTACCGANNNACGTATGCCA	5802	TGCAGGACCAGAGAATTCGAATACAG GAACTTCNNNACGTATGCCA	6042	TGCAGGACCAGAGAATTCGAATACAA ATTTCCTNNNACGTATGCCA	6282
TGCAGGACCAGAGAATTCGAATACAC TTAGATANNNACGTATGCCA	5803	TGCAGGACCAGAGAATTCGAATACAA TGTGCCANNNACGTATGCCA	6043	TGCAGGACCAGAGAATTCGAATACAC GGCAAAANNNACGTATGCCA	6283
TGCAGGACCAGAGAATTCGAATACAA GGCTAGANNNACGTATGCCA	5804	TGCAGGACCAGAGAATTCGAATACAC CGGTGCANNNACGTATGCCA	6044	TGCAGGACCAGAGAATTCGAATACAT CGCACAANNNACGTATGCCA	6284
TGCAGGACCAGAGAATTCGAATACAT CACAGGTNNNACGTATGCCA	5805	TGCAGGACCAGAGAATTCGAATACAC TATTGCCNNNACGTATGCCA	6045	TGCAGGACCAGAGAATTCGAATACAA GGTCGCCNNNACGTATGCCA	6285
TGCAGGACCAGAGAATTCGAATACAG ATATTTGNNNACGTATGCCA	5806	TGCAGGACCAGAGAATTCGAATACAT TAAGGCCNNNACGTATGCCA	6046	TGCAGGACCAGAGAATTCGAATACAG GATTCGTNNNACGTATGCCA	6286
TGCAGGACCAGAGAATTCGAATACAT TGTGTTTNNNACGTATGCCA	5807	TGCAGGACCAGAGAATTCGAATACAT GTTAAACNNNACGTATGCCA	6047	TGCAGGACCAGAGAATTCGAATACAA GCATCTGNNNACGTATGCCA	6287
TGCAGGACCAGAGAATTCGAATACAG AAAAAAGNNNACGTATGCCA	5808	TGCAGGACCAGAGAATTCGAATACAC TTGGTTCNNNACGTATGCCA	6048	TGCAGGACCAGAGAATTCGAATACAC CCACAAANNNACGTATGCCA	6288
TGCAGGACCAGAGAATTCGAATACAG GCATGTTNNNACGTATGCCA	5809	TGCAGGACCAGAGAATTCGAATACAG GTAATTTNNNACGTATGCCA	6049	TGCAGGACCAGAGAATTCGAATACAA GTTATACNNNACGTATGCCA	6289
TGCAGGACCAGAGAATTCGAATACAG GCTTTTCNNNACGTATGCCA	5810	TGCAGGACCAGAGAATTCGAATACAA TTATCAGNNNACGTATGCCA	6050	TGCAGGACCAGAGAATTCGAATACAT CTATCATNNNACGTATGCCA	6290
TGCAGGACCAGAGAATTCGAATACAA CTAATACNNNACGTATGCCA	5811	TGCAGGACCAGAGAATTCGAATACAT GCGTTCTNNNACGTATGCCA	6051	TGCAGGACCAGAGAATTCGAATACAC GGCTCTCNNNACGTATGCCA	6291
TGCAGGACCAGAGAATTCGAATACAG TAGCCCGNNNACGTATGCCA	5812	TGCAGGACCAGAGAATTCGAATACAT GATCCAGNNNACGTATGCCA	6052	TGCAGGACCAGAGAATTCGAATACAG TGATTATNNNACGTATGCCA	6292
TGCAGGACCAGAGAATTCGAATACAT AACGTCGNNNACGTATGCCA	5813	TGCAGGACCAGAGAATTCGAATACAC AGTTCAGNNNACGTATGCCA	6053	TGCAGGACCAGAGAATTCGAATACAT AGACTCGNNNACGTATGCCA	6293
TGCAGGACCAGAGAATTCGAATACAT TTCAAGANNNACGTATGCCA	5814	TGCAGGACCAGAGAATTCGAATACAT GCGACATNNNACGTATGCCA	6054	TGCAGGACCAGAGAATTCGAATACAA ACGTTTANNNACGTATGCCA	6294
TGCAGGACCAGAGAATTCGAATACAC ACAAGAGNNNACGTATGCCA	5815	TGCAGGACCAGAGAATTCGAATACAA GCAGTAGNNNACGTATGCCA	6055	TGCAGGACCAGAGAATTCGAATACAA AGTAAGTNNNACGTATGCCA	6295
TGCAGGACCAGAGAATTCGAATACAC CCGTTTANNNACGTATGCCA	5816	TGCAGGACCAGAGAATTCGAATACAT TAGTGATNNNACGTATGCCA	6056	TGCAGGACCAGAGAATTCGAATACAA TGTTAACNNNACGTATGCCA	6296
TGCAGGACCAGAGAATTCGAATACAG TTAAGAANNNACGTATGCCA	5817	TGCAGGACCAGAGAATTCGAATACAC ACATTAANNNACGTATGCCA	6057	TGCAGGACCAGAGAATTCGAATACAT AATCACANNNACGTATGCCA	6297
TGCAGGACCAGAGAATTCGAATACAG AACCTACNNNACGTATGCCA	5818	TGCAGGACCAGAGAATTCGAATACAA GGTGCCCNNNACGTATGCCA	6058	TGCAGGACCAGAGAATTCGAATACAC ATGCTTCNNNACGTATGCCA	6298
TGCAGGACCAGAGAATTCGAATACAA GCGACTTNNNACGTATGCCA	5819	TGCAGGACCAGAGAATTCGAATACAA CCTGGCGNNNACGTATGCCA	6059	TGCAGGACCAGAGAATTCGAATACAA GCATTATNNNACGTATGCCA	6299
TGCAGGACCAGAGAATTCGAATACAC GCACTAANNNACGTATGCCA	5820	TGCAGGACCAGAGAATTCGAATACAC GGCGATCNNNACGTATGCCA	6060	TGCAGGACCAGAGAATTCGAATACAA GGCATAGNNNACGTATGCCA	6300
TGCAGGACCAGAGAATTCGAATACAG GTGTTCANNNACGTATGCCA	5821	TGCAGGACCAGAGAATTCGAATACAT AGACCTGNNNACGTATGCCA	6061	TGCAGGACCAGAGAATTCGAATACAC ATACGCANNNACGTATGCCA	6301
TGCAGGACCAGAGAATTCGAATACAC TTTTCAANNNACGTATGCCA	5822	TGCAGGACCAGAGAATTCGAATACAA GACTACCNNNACGTATGCCA	6062	TGCAGGACCAGAGAATTCGAATACAA GACCCGCNNNACGTATGCCA	6302
TGCAGGACCAGAGAATTCGAATACAG ATTCATANNNACGTATGCCA	5823	TGCAGGACCAGAGAATTCGAATACAC TTAGACGNNNACGTATGCCA	6063	TGCAGGACCAGAGAATTCGAATACAT TCCCTAGNNNACGTATGCCA	6303
TGCAGGACCAGAGAATTCGAATACAT TGACGACNNNACGTATGCCA	5824	TGCAGGACCAGAGAATTCGAATACAC GGCGGCCNNNACGTATGCCA	6064	TGCAGGACCAGAGAATTCGAATACAA GTGTGCTNNNACGTATGCCA	6304
TGCAGGACCAGAGAATTCGAATACAC CTTGTACNNNACGTATGCCA	5825	TGCAGGACCAGAGAATTCGAATACAG CCGATATNNNACGTATGCCA	6065	TGCAGGACCAGAGAATTCGAATACAC CTGTACTNNNACGTATGCCA	6305
TGCAGGACCAGAGAATTCGAATACAG GTGCGGANNNACGTATGCCA	5826	TGCAGGACCAGAGAATTCGAATACAC CCGGCCCNNNACGTATGCCA	6066	TGCAGGACCAGAGAATTCGAATACAC ACACCCCNNNACGTATGCCA	6306
TGCAGGACCAGAGAATTCGAATACAT CATGAATNNNACGTATGCCA	5827	TGCAGGACCAGAGAATTCGAATACAC CTCGCTGNNNACGTATGCCA	6067	TGCAGGACCAGAGAATTCGAATACAT TTGGTGGNNNACGTATGCCA	6307
TGCAGGACCAGAGAATTCGAATACAG CGAAAGTNNNACGTATGCCA	5828	TGCAGGACCAGAGAATTCGAATACAC AGCCATANNNACGTATGCCA	6068	TGCAGGACCAGAGAATTCGAATACAG TTAGCCANNNACGTATGCCA	6308
TGCAGGACCAGAGAATTCGAATACAA AAATAATNNNCTAGCGTTAC	5829	TGCAGGACCAGAGAATTCGAATACAA ATGGAGCNNNCTAGCGTTAC	6069	TGCAGGACCAGAGAATTCGAATACAA CGACACTNNNCTAGCGTTAC	6309
TGCAGGACCAGAGAATTCGAATACAT TCGTGTCNNNCTAGCGTTAC	5830	TGCAGGACCAGAGAATTCGAATACAT CACAGACNNNCTAGCGTTAC	6070	TGCAGGACCAGAGAATTCGAATACAG CATGACTNNNCTAGCGTTAC	6310
TGCAGGACCAGAGAATTCGAATACAT CGTCTTGNNNCTAGCGTTAC	5831	TGCAGGACCAGAGAATTCGAATACAT CCGTCCGNNNCTAGCGTTAC	6071	TGCAGGACCAGAGAATTCGAATACAT AGTTGTANNNCTAGCGTTAC	6311
TGCAGGACCAGAGAATTCGAATACAG ACTGTGTNNNCTAGCGTTAC	5832	TGCAGGACCAGAGAATTCGAATACAG AATGGACNNNCTAGCGTTAC	6072	TGCAGGACCAGAGAATTCGAATACAC CTGTTCANNNCTAGCGTTAC	6312
TGCAGGACCAGAGAATTCGAATACAC CATTGGANNNCTAGCGTTAC	5833	TGCAGGACCAGAGAATTCGAATACAG TGCTCAANNNCTAGCGTTAC	6073	TGCAGGACCAGAGAATTCGAATACAC TGAGTCANNNCTAGCGTTAC	6313

图20B

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC ACAGCGCNNNCTAGCGTTAC	5834	TGCAGGACCAGAGAATTCGAATACAT GTTCGGANNNCTAGCGTTAC	6074	TGCAGGACCAGAGAATTCGAATACAT CATCTTANNNCTAGCGTTAC	6314
TGCAGGACCAGAGAATTCGAATACAA CCCCGTCNNNCTAGCGTTAC	5835	TGCAGGACCAGAGAATTCGAATACAC TGCGTGGNNNCTAGCGTTAC	6075	TGCAGGACCAGAGAATTCGAATACAC ACATTTTNNNCTAGCGTTAC	6315
TGCAGGACCAGAGAATTCGAATACAT CACCTTGNNNCTAGCGTTAC	5836	TGCAGGACCAGAGAATTCGAATACAA CCGTCAANNNCTAGCGTTAC	6076	TGCAGGACCAGAGAATTCGAATACAG CCACATANNNCTAGCGTTAC	6316
TGCAGGACCAGAGAATTCGAATACAA GTACCACNNNCTAGCGTTAC	5837	TGCAGGACCAGAGAATTCGAATACAG GTAACGANNNCTAGCGTTAC	6077	TGCAGGACCAGAGAATTCGAATACAT AAACAGANNNCTAGCGTTAC	6317
TGCAGGACCAGAGAATTCGAATACAA CAAATGANNNCTAGCGTTAC	5838	TGCAGGACCAGAGAATTCGAATACAA TCCGAGTNNNCTAGCGTTAC	6078	TGCAGGACCAGAGAATTCGAATACAG GTACCATNNNCTAGCGTTAC	6318
TGCAGGACCAGAGAATTCGAATACAA TTGTTGANNNCTAGCGTTAC	5839	TGCAGGACCAGAGAATTCGAATACAA CCAACCANNNCTAGCGTTAC	6079	TGCAGGACCAGAGAATTCGAATACAA GAAAAAGNNNCTAGCGTTAC	6319
TGCAGGACCAGAGAATTCGAATACAA CGGAAACNNNCTAGCGTTAC	5840	TGCAGGACCAGAGAATTCGAATACAC AGTATATNNNCTAGCGTTAC	6080	TGCAGGACCAGAGAATTCGAATACAG CTCTCATNNNCTAGCGTTAC	6320
TGCAGGACCAGAGAATTCGAATACAG AGAACGTNNNCTAGCGTTAC	5841	TGCAGGACCAGAGAATTCGAATACAT CCGATAGNNNCTAGCGTTAC	6081	TGCAGGACCAGAGAATTCGAATACAA GGCACAANNNCTAGCGTTAC	6321
TGCAGGACCAGAGAATTCGAATACAT ACCATGGNNNCTAGCGTTAC	5842	TGCAGGACCAGAGAATTCGAATACAT TAGTATGNNNCTAGCGTTAC	6082	TGCAGGACCAGAGAATTCGAATACAG CGATGAANNNCTAGCGTTAC	6322
TGCAGGACCAGAGAATTCGAATACAC AAAACGGNNNCTAGCGTTAC	5843	TGCAGGACCAGAGAATTCGAATACAA CATTCAANNNCTAGCGTTAC	6083	TGCAGGACCAGAGAATTCGAATACAT CACTTATNNNCTAGCGTTAC	6323
TGCAGGACCAGAGAATTCGAATACAT AGTGAGGNNNCTAGCGTTAC	5844	TGCAGGACCAGAGAATTCGAATACAG TACTGACNNNCTAGCGTTAC	6084	TGCAGGACCAGAGAATTCGAATACAT AGGCCGCNNNCTAGCGTTAC	6324
TGCAGGACCAGAGAATTCGAATACAC GTGATACNNNCTAGCGTTAC	5845	TGCAGGACCAGAGAATTCGAATACAC CTCATTGNNNCTAGCGTTAC	6085	TGCAGGACCAGAGAATTCGAATACAA TTTAAATNNNCTAGCGTTAC	6325
TGCAGGACCAGAGAATTCGAATACAG TGCCCCTNNNCTAGCGTTAC	5846	TGCAGGACCAGAGAATTCGAATACAA TGGCACTNNNCTAGCGTTAC	6086	TGCAGGACCAGAGAATTCGAATACAT CTGTTTANNNCTAGCGTTAC	6326
TGCAGGACCAGAGAATTCGAATACAG GACAGTANNNCTAGCGTTAC	5847	TGCAGGACCAGAGAATTCGAATACAC CCCACGTNNNCTAGCGTTAC	6087	TGCAGGACCAGAGAATTCGAATACAA GTTGAAANNNCTAGCGTTAC	6327
TGCAGGACCAGAGAATTCGAATACAC TAGTATANNNCTAGCGTTAC	5848	TGCAGGACCAGAGAATTCGAATACAC AAACCTGNNNCTAGCGTTAC	6088	TGCAGGACCAGAGAATTCGAATACAA TATGACTNNNCTAGCGTTAC	6328
TGCAGGACCAGAGAATTCGAATACAG AACCTTGNNNCTAGCGTTAC	5849	TGCAGGACCAGAGAATTCGAATACAC GGCCAGTNNNCTAGCGTTAC	6089	TGCAGGACCAGAGAATTCGAATACAG AAGACTGNNNCTAGCGTTAC	6329
TGCAGGACCAGAGAATTCGAATACAC TGTTTATNNNCTAGCGTTAC	5850	TGCAGGACCAGAGAATTCGAATACAG ACAACCTNNNCTAGCGTTAC	6090	TGCAGGACCAGAGAATTCGAATACAG TGCGTGCNNNCTAGCGTTAC	6330
TGCAGGACCAGAGAATTCGAATACAA ATAGGATNNNCTAGCGTTAC	5851	TGCAGGACCAGAGAATTCGAATACAT GGCACATNNNCTAGCGTTAC	6091	TGCAGGACCAGAGAATTCGAATACAA TGTCCGANNNCTAGCGTTAC	6331
TGCAGGACCAGAGAATTCGAATACAC GTCAAGTNNNCTAGCGTTAC	5852	TGCAGGACCAGAGAATTCGAATACAC CAAGTACNNNCTAGCGTTAC	6092	TGCAGGACCAGAGAATTCGAATACAT GTTATAGNNNCTAGCGTTAC	6332
TGCAGGACCAGAGAATTCGAATACAG CTGTTTCNNNCTAGCGTTAC	5853	TGCAGGACCAGAGAATTCGAATACAC ACGACCGNNNCTAGCGTTAC	6093	TGCAGGACCAGAGAATTCGAATACAT GTCGTAGNNNCTAGCGTTAC	6333
TGCAGGACCAGAGAATTCGAATACAA CCGTGCGNNNCTAGCGTTAC	5854	TGCAGGACCAGAGAATTCGAATACAC CGTGATANNNCTAGCGTTAC	6094	TGCAGGACCAGAGAATTCGAATACAG ACGCTTANNNCTAGCGTTAC	6334
TGCAGGACCAGAGAATTCGAATACAC AGCTGCGNNNCTAGCGTTAC	5855	TGCAGGACCAGAGAATTCGAATACAC ATTGCCTNNNCTAGCGTTAC	6095	TGCAGGACCAGAGAATTCGAATACAG AATTACTNNNCTAGCGTTAC	6335
TGCAGGACCAGAGAATTCGAATACAT CCTTACGNNNCTAGCGTTAC	5856	TGCAGGACCAGAGAATTCGAATACAT GTTGTTTNNNCTAGCGTTAC	6096	TGCAGGACCAGAGAATTCGAATACAT CGACCCCNNNCTAGCGTTAC	6336
TGCAGGACCAGAGAATTCGAATACAA ACGAAGCNNNCTAGCGTTAC	5857	TGCAGGACCAGAGAATTCGAATACAT GTTTTTGNNNCTAGCGTTAC	6097	TGCAGGACCAGAGAATTCGAATACAG CCTCCACNNNCTAGCGTTAC	6337
TGCAGGACCAGAGAATTCGAATACAG AAGTTTTNNNCTAGCGTTAC	5858	TGCAGGACCAGAGAATTCGAATACAG CTCCTCGNNNCTAGCGTTAC	6098	TGCAGGACCAGAGAATTCGAATACAC TGTATAANNNCTAGCGTTAC	6338
TGCAGGACCAGAGAATTCGAATACAG CCGTTAANNNCTAGCGTTAC	5859	TGCAGGACCAGAGAATTCGAATACAC CACCTGCNNNCTAGCGTTAC	6099	TGCAGGACCAGAGAATTCGAATACAT TCGAGTGNNNCTAGCGTTAC	6339
TGCAGGACCAGAGAATTCGAATACAT GTGCCAANNNCTAGCGTTAC	5860	TGCAGGACCAGAGAATTCGAATACAG AGCGGTGNNNCTAGCGTTAC	6100	TGCAGGACCAGAGAATTCGAATACAT AAGTGCCNNNCTAGCGTTAC	6340
TGCAGGACCAGAGAATTCGAATACAG CAAAACGNNNCTAGCGTTAC	5861	TGCAGGACCAGAGAATTCGAATACAA ACAACGGNNNCTAGCGTTAC	6101	TGCAGGACCAGAGAATTCGAATACAC AGATAAANNNCTAGCGTTAC	6341
TGCAGGACCAGAGAATTCGAATACAC GTAAGAGNNNCTAGCGTTAC	5862	TGCAGGACCAGAGAATTCGAATACAA ITGCTTTNNNCTAGCGTTAC	6102	TGCAGGACCAGAGAATTCGAATACAC GAATCACNNNCTAGCGTTAC	6342
TGCAGGACCAGAGAATTCGAATACAT GACGTCANNNCTAGCGTTAC	5863	TGCAGGACCAGAGAATTCGAATACAC CAGAGAANNNCTAGCGTTAC	6103	TGCAGGACCAGAGAATTCGAATACAG AGCTTACNNNCTAGCGTTAC	6343
TGCAGGACCAGAGAATTCGAATACAC TCCCTAANNNCTAGCGTTAC	5864	TGCAGGACCAGAGAATTCGAATACAG ATACCTGNNNCTAGCGTTAC	6104	TGCAGGACCAGAGAATTCGAATACAT CATCTGCNNNCTAGCGTTAC	6344
TGCAGGACCAGAGAATTCGAATACAT ATTCAGANNNCTAGCGTTAC	5865	TGCAGGACCAGAGAATTCGAATACAA CTTATTCNNNCTAGCGTTAC	6105	TGCAGGACCAGAGAATTCGAATACAC CACGTGGNNNCTAGCGTTAC	6345
TGCAGGACCAGAGAATTCGAATACAC TAGCAACNNNCTAGCGTTAC	5866	TGCAGGACCAGAGAATTCGAATACAA GTTGTTANNNCTAGCGTTAC	6106	TGCAGGACCAGAGAATTCGAATACAC GTGTATGNNNCTAGCGTTAC	6346

图20C

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG AATGCCTNNNCTAGCGTTAC	5867	TGCAGGACCAGAGAATTCGAATACAA TCACTGCNNNCTAGCGTTAC	6107	TGCAGGACCAGAGAATTCGAATACAC TCTCCGCNNNCTAGCGTTAC	6347
TGCAGGACCAGAGAATTCGAATACAG ACTTCTCNNNCTAGCGTTAC	5868	TGCAGGACCAGAGAATTCGAATACAA GCAAACGNNNCTAGCGTTAC	6108	TGCAGGACCAGAGAATTCGAATACAC AAGAGTGNNNCTAGCGTTAC	6348
TGCAGGACCAGAGAATTCGAATACAT AATTAGCNNNCTAGCGTTAC	5869	TGCAGGACCAGAGAATTCGAATACAA GACTATTNNNCTAGCGTTAC	6109	TGCAGGACCAGAGAATTCGAATACAT AGCTCTCNNNCTAGCGTTAC	6349
TGCAGGACCAGAGAATTCGAATACAC GTGTGGCNNNCTAGCGTTAC	5870	TGCAGGACCAGAGAATTCGAATACAC TGAAACCNNNCTAGCGTTAC	6110	TGCAGGACCAGAGAATTCGAATACAG TGGCAGCNNNCTAGCGTTAC	6350
TGCAGGACCAGAGAATTCGAATACAG ACTCGATNNNCTAGCGTTAC	5871	TGCAGGACCAGAGAATTCGAATACAA GGAAAGGNNNCTAGCGTTAC	6111	TGCAGGACCAGAGAATTCGAATACAT GCATCGANNNCTAGCGTTAC	6351
TGCAGGACCAGAGAATTCGAATACAG CGATCGCNNNCTAGCGTTAC	5872	TGCAGGACCAGAGAATTCGAATACAC CCTAGTTNNNCTAGCGTTAC	6112	TGCAGGACCAGAGAATTCGAATACAC GGTCCGANNNCTAGCGTTAC	6352
TGCAGGACCAGAGAATTCGAATACAA CTCTACCNNNCTAGCGTTAC	5873	TGCAGGACCAGAGAATTCGAATACAC AAACCACNNNCTAGCGTTAC	6113	TGCAGGACCAGAGAATTCGAATACAA AGCCACTNNNCTAGCGTTAC	6353
TGCAGGACCAGAGAATTCGAATACAG GAAGGCCNNNCTAGCGTTAC	5874	TGCAGGACCAGAGAATTCGAATACAT TGTAGTANNNCTAGCGTTAC	6114	TGCAGGACCAGAGAATTCGAATACAG ATCTTTNNNCTAGCGTTAC	6354
TGCAGGACCAGAGAATTCGAATACAC ATATTAGNNNCTAGCGTTAC	5875	TGCAGGACCAGAGAATTCGAATACAG TACAGCTNNNCTAGCGTTAC	6115	TGCAGGACCAGAGAATTCGAATACAG GCTCTAANNNCTAGCGTTAC	6355
TGCAGGACCAGAGAATTCGAATACAC GGTGACCNNNCTAGCGTTAC	5876	TGCAGGACCAGAGAATTCGAATACAA GTGTACCNNNCTAGCGTTAC	6116	TGCAGGACCAGAGAATTCGAATACAT CTATGTTNNNCTAGCGTTAC	6356
TGCAGGACCAGAGAATTCGAATACAG TGCATGTNNNCTAGCGTTAC	5877	TGCAGGACCAGAGAATTCGAATACAT TTTATGCNNNCTAGCGTTAC	6117	TGCAGGACCAGAGAATTCGAATACAA CCGCGTGNNNCTAGCGTTAC	6357
TGCAGGACCAGAGAATTCGAATACAT AAGTGTTNNNCTAGCGTTAC	5878	TGCAGGACCAGAGAATTCGAATACAA ATCCGTGNNNCTAGCGTTAC	6118	TGCAGGACCAGAGAATTCGAATACAG TACTCCTNNNCTAGCGTTAC	6358
TGCAGGACCAGAGAATTCGAATACAA CCTTATTNNNCTAGCGTTAC	5879	TGCAGGACCAGAGAATTCGAATACAC GATCTGANNNCTAGCGTTAC	6119	TGCAGGACCAGAGAATTCGAATACAG GAGCCCTNNNCTAGCGTTAC	6359
TGCAGGACCAGAGAATTCGAATACAA CTCCACTNNNCTAGCGTTAC	5880	TGCAGGACCAGAGAATTCGAATACAG ATAGATANNNCTAGCGTTAC	6120	TGCAGGACCAGAGAATTCGAATACAT ATCGAGCNNNCTAGCGTTAC	6360
TGCAGGACCAGAGAATTCGAATACAC CAAATATNNNCTAGCGTTAC	5881	TGCAGGACCAGAGAATTCGAATACAG AGTCCTANNNCTAGCGTTAC	6121	TGCAGGACCAGAGAATTCGAATACAC CGTTGAANNNCTAGCGTTAC	6361
TGCAGGACCAGAGAATTCGAATACAC AAGATGGNNNCTAGCGTTAC	5882	TGCAGGACCAGAGAATTCGAATACAC ATGTGGTNNNCTAGCGTTAC	6122	TGCAGGACCAGAGAATTCGAATACAC GAAGAACNNNCTAGCGTTAC	6362
TGCAGGACCAGAGAATTCGAATACAC CCAAGGCNNNCTAGCGTTAC	5883	TGCAGGACCAGAGAATTCGAATACAG ATCGCGCNNNCTAGCGTTAC	6123	TGCAGGACCAGAGAATTCGAATACAA GTGATCCNNNCTAGCGTTAC	6363
TGCAGGACCAGAGAATTCGAATACAT AAGCGGANNNCTAGCGTTAC	5884	TGCAGGACCAGAGAATTCGAATACAA CCACATGNNNCTAGCGTTAC	6124	TGCAGGACCAGAGAATTCGAATACAG GTCAACTNNNCTAGCGTTAC	6364
TGCAGGACCAGAGAATTCGAATACAG AGGCCCTNNNCTAGCGTTAC	5885	TGCAGGACCAGAGAATTCGAATACAT GCCGATANNNCTAGCGTTAC	6125	TGCAGGACCAGAGAATTCGAATACAT GACGTGTNNNCTAGCGTTAC	6365
TGCAGGACCAGAGAATTCGAATACAC TTCCTAGNNNCTAGCGTTAC	5886	TGCAGGACCAGAGAATTCGAATACAC AAAGCCTNNNCTAGCGTTAC	6126	TGCAGGACCAGAGAATTCGAATACAT TACAACANNNCTAGCGTTAC	6366
TGCAGGACCAGAGAATTCGAATACAC GCAGAAANNNCTAGCGTTAC	5887	TGCAGGACCAGAGAATTCGAATACAA CTGACGTNNNCTAGCGTTAC	6127	TGCAGGACCAGAGAATTCGAATACAA AATGTTCNNNCTAGCGTTAC	6367
TGCAGGACCAGAGAATTCGAATACAT GTGCGTANNNCTAGCGTTAC	5888	TGCAGGACCAGAGAATTCGAATACAA AGCTCGTNNNCTAGCGTTAC	6128	TGCAGGACCAGAGAATTCGAATACAT TATAACGNNNCTAGCGTTAC	6368
TGCAGGACCAGAGAATTCGAATACAC GATGGAANNNGATCGACATG	5889	TGCAGGACCAGAGAATTCGAATACAG GATCGAANNNGATCGACATG	6129	TGCAGGACCAGAGAATTCGAATACAT CCGGATANNNGATCGACATG	6369
TGCAGGACCAGAGAATTCGAATACAC CAATTAANNNGATCGACATG	5890	TGCAGGACCAGAGAATTCGAATACAT CGCAACANNNGATCGACATG	6130	TGCAGGACCAGAGAATTCGAATACAA GCCCTTTNNNGATCGACATG	6370
TGCAGGACCAGAGAATTCGAATACAC ATAGGCTNNNGATCGACATG	5891	TGCAGGACCAGAGAATTCGAATACAC CGACTAANNNGATCGACATG	6131	TGCAGGACCAGAGAATTCGAATACAG TACACTGNNNGATCGACATG	6371
TGCAGGACCAGAGAATTCGAATACAA AAAAATTNNNGATCGACATG	5892	TGCAGGACCAGAGAATTCGAATACAG ACCGTTANNNGATCGACATG	6132	TGCAGGACCAGAGAATTCGAATACAC GTGTAGTNNNGATCGACATG	6372
TGCAGGACCAGAGAATTCGAATACAA ATACACTNNNGATCGACATG	5893	TGCAGGACCAGAGAATTCGAATACAA TGCCCTTNNNGATCGACATG	6133	TGCAGGACCAGAGAATTCGAATACAG GAAAGTCNNNGATCGACATG	6373
TGCAGGACCAGAGAATTCGAATACAA ATCGAAANNNGATCGACATG	5894	TGCAGGACCAGAGAATTCGAATACAT CGAAACCNNNGATCGACATG	6134	TGCAGGACCAGAGAATTCGAATACAT TCTGCGTNNNGATCGACATG	6374
TGCAGGACCAGAGAATTCGAATACAT CTATTACNNNGATCGACATG	5895	TGCAGGACCAGAGAATTCGAATACAG ACCTTCTNNNGATCGACATG	6135	TGCAGGACCAGAGAATTCGAATACAT ACTCGGANNNGATCGACATG	6375
TGCAGGACCAGAGAATTCGAATACAA CCCGATANNNGATCGACATG	5896	TGCAGGACCAGAGAATTCGAATACAC TACCCTANNNGATCGACATG	6136	TGCAGGACCAGAGAATTCGAATACAC GTCCAAANNNGATCGACATG	6376
TGCAGGACCAGAGAATTCGAATACAG AAACGCANNNGATCGACATG	5897	TGCAGGACCAGAGAATTCGAATACAA TGCCTTCNNNGATCGACATG	6137	TGCAGGACCAGAGAATTCGAATACAT TGAACGNNNGATCGACATG	6377
TGCAGGACCAGAGAATTCGAATACAG TGATCGTNNNGATCGACATG	5898	TGCAGGACCAGAGAATTCGAATACAG CGACTATNNNGATCGACATG	6138	TGCAGGACCAGAGAATTCGAATACAG GCCGCTANNNGATCGACATG	6378
TGCAGGACCAGAGAATTCGAATACAC GCAGCCANNNGATCGACATG	5899	TGCAGGACCAGAGAATTCGAATACAG GCATTCANNNGATCGACATG	6139	TGCAGGACCAGAGAATTCGAATACAG ATACGTCNNNGATCGACATG	6379

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池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT GACCATGNNNGATCGACATG	5900	TGCAGGACCAGAGAATTCGAATACAG CTAGAAGNNNGATCGACATG	6140	TGCAGGACCAGAGAATTCGAATACAA TTCAACANNNGATCGACATG	6380
TGCAGGACCAGAGAATTCGAATACAG GTCCACGNNNGATCGACATG	5901	TGCAGGACCAGAGAATTCGAATACAT TTATAAANNNGATCGACATG	6141	TGCAGGACCAGAGAATTCGAATACAG TGTGCATNNNGATCGACATG	6381
TGCAGGACCAGAGAATTCGAATACAA AGCATAANNNGATCGACATG	5902	TGCAGGACCAGAGAATTCGAATACAT CCCTACANNNGATCGACATG	6142	TGCAGGACCAGAGAATTCGAATACAG CCATAGTNNNGATCGACATG	6382
TGCAGGACCAGAGAATTCGAATACAG ACAGGCGNNNGATCGACATG	5903	TGCAGGACCAGAGAATTCGAATACAA CGTCTAGNNNGATCGACATG	6143	TGCAGGACCAGAGAATTCGAATACAC TCATCTCNNNGATCGACATG	6383
TGCAGGACCAGAGAATTCGAATACAA CGGTAGANNNGATCGACATG	5904	TGCAGGACCAGAGAATTCGAATACAG AGCTTTGNNNGATCGACATG	6144	TGCAGGACCAGAGAATTCGAATACAA ACCGACTNNNGATCGACATG	6384
TGCAGGACCAGAGAATTCGAATACAT CATTACTNNNGATCGACATG	5905	TGCAGGACCAGAGAATTCGAATACAA GAGCGGCNNNGATCGACATG	6145	TGCAGGACCAGAGAATTCGAATACAC ATCGCCCNNNGATCGACATG	6385
TGCAGGACCAGAGAATTCGAATACAC GAAAATANNNGATCGACATG	5906	TGCAGGACCAGAGAATTCGAATACAC ATATACANNNGATCGACATG	6146	TGCAGGACCAGAGAATTCGAATACAT AGGATCCNNNGATCGACATG	6386
TGCAGGACCAGAGAATTCGAATACAT GGAAGGTNNNGATCGACATG	5907	TGCAGGACCAGAGAATTCGAATACAA AGGCTAGNNNGATCGACATG	6147	TGCAGGACCAGAGAATTCGAATACAA TGGCGTTNNNGATCGACATG	6387
TGCAGGACCAGAGAATTCGAATACAC TGTTTTANNNGATCGACATG	5908	TGCAGGACCAGAGAATTCGAATACAT ATCGACGNNNGATCGACATG	6148	TGCAGGACCAGAGAATTCGAATACAC TAAATTGNNNGATCGACATG	6388
TGCAGGACCAGAGAATTCGAATACAC GGATTTGNNNGATCGACATG	5909	TGCAGGACCAGAGAATTCGAATACAA GACGTCTNNNGATCGACATG	6149	TGCAGGACCAGAGAATTCGAATACAA CTACATANNNGATCGACATG	6389
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TGCAGGACCAGAGAATTCGAATACAA TGCCTCTNNNGATCGACATG	5911	TGCAGGACCAGAGAATTCGAATACAG CCTGCAGNNNGATCGACATG	6151	TGCAGGACCAGAGAATTCGAATACAG ATGTGAGNNNGATCGACATG	6391
TGCAGGACCAGAGAATTCGAATACAA GAGAAGGNNNGATCGACATG	5912	TGCAGGACCAGAGAATTCGAATACAC GTAACGTNNNGATCGACATG	6152	TGCAGGACCAGAGAATTCGAATACAA GGCCAAANNNGATCGACATG	6392
TGCAGGACCAGAGAATTCGAATACAT CATGGTGNNNGATCGACATG	5913	TGCAGGACCAGAGAATTCGAATACAA TCTTATCNNNGATCGACATG	6153	TGCAGGACCAGAGAATTCGAATACAC CAAGCTANNNGATCGACATG	6393
TGCAGGACCAGAGAATTCGAATACAC TGGAGCCNNNGATCGACATG	5914	TGCAGGACCAGAGAATTCGAATACAA CGTTTGGNNNGATCGACATG	6154	TGCAGGACCAGAGAATTCGAATACAA GGAGATCNNNGATCGACATG	6394
TGCAGGACCAGAGAATTCGAATACAC TGTTAGGNNNGATCGACATG	5915	TGCAGGACCAGAGAATTCGAATACAG ATTAAAGNNNGATCGACATG	6155	TGCAGGACCAGAGAATTCGAATACAC CTCCGACNNNGATCGACATG	6395
TGCAGGACCAGAGAATTCGAATACAC TGGTTCTNNNGATCGACATG	5916	TGCAGGACCAGAGAATTCGAATACAT TGCCAGANNNGATCGACATG	6156	TGCAGGACCAGAGAATTCGAATACAC GCTGTGGNNNGATCGACATG	6396
TGCAGGACCAGAGAATTCGAATACAC AAAGTCCNNNGATCGACATG	5917	TGCAGGACCAGAGAATTCGAATACAC GGCATATNNNGATCGACATG	6157	TGCAGGACCAGAGAATTCGAATACAT ACCGCCCNNNGATCGACATG	6397
TGCAGGACCAGAGAATTCGAATACAC GTAGCCGNNNGATCGACATG	5918	TGCAGGACCAGAGAATTCGAATACAG GTCAGCCNNNGATCGACATG	6158	TGCAGGACCAGAGAATTCGAATACAC GTCGCCTNNNGATCGACATG	6398
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TGCAGGACCAGAGAATTCGAATACAC TAATGTTNNNGATCGACATG	5920	TGCAGGACCAGAGAATTCGAATACAC GCACGGTNNNGATCGACATG	6160	TGCAGGACCAGAGAATTCGAATACAG CCTGGACNNNGATCGACATG	6400
TGCAGGACCAGAGAATTCGAATACAG ACTTAATNNNGATCGACATG	5921	TGCAGGACCAGAGAATTCGAATACAT GCTTCGTNNNGATCGACATG	6161	TGCAGGACCAGAGAATTCGAATACAA CTTGGACNNNGATCGACATG	6401
TGCAGGACCAGAGAATTCGAATACAA TCACAATNNNGATCGACATG	5922	TGCAGGACCAGAGAATTCGAATACAA GCACTGTNNNGATCGACATG	6162	TGCAGGACCAGAGAATTCGAATACAT GTTGCCTNNNGATCGACATG	6402
TGCAGGACCAGAGAATTCGAATACAG AGCCTGCNNNGATCGACATG	5923	TGCAGGACCAGAGAATTCGAATACAC TTACAAANNNGATCGACATG	6163	TGCAGGACCAGAGAATTCGAATACAC GGCACGTNNNGATCGACATG	6403
TGCAGGACCAGAGAATTCGAATACAC TCTAGGANNNGATCGACATG	5924	TGCAGGACCAGAGAATTCGAATACAC GATGGCCNNNGATCGACATG	6164	TGCAGGACCAGAGAATTCGAATACAA GGTGTGANNNGATCGACATG	6404
TGCAGGACCAGAGAATTCGAATACAG GTGAGATNNNGATCGACATG	5925	TGCAGGACCAGAGAATTCGAATACAC ACCGGCANNNGATCGACATG	6165	TGCAGGACCAGAGAATTCGAATACAA ACGACGANNNGATCGACATG	6405
TGCAGGACCAGAGAATTCGAATACAA GGTTGCTNNNGATCGACATG	5926	TGCAGGACCAGAGAATTCGAATACAG CCATAACNNNGATCGACATG	6166	TGCAGGACCAGAGAATTCGAATACAC ATCACTCNNNGATCGACATG	6406
TGCAGGACCAGAGAATTCGAATACAG AGGTGCGNNNGATCGACATG	5927	TGCAGGACCAGAGAATTCGAATACAT GAAGTCCNNNGATCGACATG	6167	TGCAGGACCAGAGAATTCGAATACAT AATGCTANNNGATCGACATG	6407
TGCAGGACCAGAGAATTCGAATACAA GTCAGACNNNGATCGACATG	5928	TGCAGGACCAGAGAATTCGAATACAG CAACACTNNNGATCGACATG	6168	TGCAGGACCAGAGAATTCGAATACAC GCCTTGCNNNGATCGACATG	6408
TGCAGGACCAGAGAATTCGAATACAC AATGTATNNNGATCGACATG	5929	TGCAGGACCAGAGAATTCGAATACAA CGCTTCTNNNGATCGACATG	6169	TGCAGGACCAGAGAATTCGAATACAT GATCAGCNNNGATCGACATG	6409
TGCAGGACCAGAGAATTCGAATACAA ACCATTANNNGATCGACATG	5930	TGCAGGACCAGAGAATTCGAATACAT ACCGGCGNNNGATCGACATG	6170	TGCAGGACCAGAGAATTCGAATACAC TTCGGAANNNGATCGACATG	6410
TGCAGGACCAGAGAATTCGAATACAT GGCGCTGNNNGATCGACATG	5931	TGCAGGACCAGAGAATTCGAATACAT GCTAATANNNGATCGACATG	6171	TGCAGGACCAGAGAATTCGAATACAC GCAAATCNNNGATCGACATG	6411
TGCAGGACCAGAGAATTCGAATACAC GCCCTGTNNNGATCGACATG	5932	TGCAGGACCAGAGAATTCGAATACAT AAGGAGCNNNGATCGACATG	6172	TGCAGGACCAGAGAATTCGAATACAA GAGAACCNNNGATCGACATG	6412

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池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT AGCCGTANNNGATCGACATG	5933	TGCAGGACCAGAGAATTCGAATACAT AGTCCGANNNGATCGACATG	6173	TGCAGGACCAGAGAATTCGAATACAT CGACGATNNNGATCGACATG	6413
TGCAGGACCAGAGAATTCGAATACAG GATAGTGNNNGATCGACATG	5934	TGCAGGACCAGAGAATTCGAATACAC TATCCTGNNNGATCGACATG	6174	TGCAGGACCAGAGAATTCGAATACAC AGCAAGANNNGATCGACATG	6414
TGCAGGACCAGAGAATTCGAATACAT AAGGCAGNNNGATCGACATG	5935	TGCAGGACCAGAGAATTCGAATACAT TTGGTCCNNNGATCGACATG	6175	TGCAGGACCAGAGAATTCGAATACAC AAAGTAANNNGATCGACATG	6415
TGCAGGACCAGAGAATTCGAATACAA GGTCCTANNNGATCGACATG	5936	TGCAGGACCAGAGAATTCGAATACAG CCTTTCANNNGATCGACATG	6176	TGCAGGACCAGAGAATTCGAATACAG AAATCAANNNGATCGACATG	6416
TGCAGGACCAGAGAATTCGAATACAA ACTGGAGNNNGATCGACATG	5937	TGCAGGACCAGAGAATTCGAATACAG TGTTCGANNNGATCGACATG	6177	TGCAGGACCAGAGAATTCGAATACAC TCCTGATNNNGATCGACATG	6417
TGCAGGACCAGAGAATTCGAATACAT TGTTGTTNNNGATCGACATG	5938	TGCAGGACCAGAGAATTCGAATACAA CTGTCAGNNNGATCGACATG	6178	TGCAGGACCAGAGAATTCGAATACAA CTATAGTNNNGATCGACATG	6418
TGCAGGACCAGAGAATTCGAATACAG CGAAGCGNNNGATCGACATG	5939	TGCAGGACCAGAGAATTCGAATACAA TCTGACGNNNGATCGACATG	6179	TGCAGGACCAGAGAATTCGAATACAG GTAGTTCNNNGATCGACATG	6419
TGCAGGACCAGAGAATTCGAATACAA GATCCGTNNNGATCGACATG	5940	TGCAGGACCAGAGAATTCGAATACAT ACCTCGTNNNGATCGACATG	6180	TGCAGGACCAGAGAATTCGAATACAC GGAACTTNNNGATCGACATG	6420
TGCAGGACCAGAGAATTCGAATACAA TACCGTGNNNGATCGACATG	5941	TGCAGGACCAGAGAATTCGAATACAT GCATACGNNNGATCGACATG	6181	TGCAGGACCAGAGAATTCGAATACAG GATCTGTNNNGATCGACATG	6421
TGCAGGACCAGAGAATTCGAATACAA ATCATGTNNNGATCGACATG	5942	TGCAGGACCAGAGAATTCGAATACAC AGGTAAGNNNGATCGACATG	6182	TGCAGGACCAGAGAATTCGAATACAA TTCCGCTNNNGATCGACATG	6422
TGCAGGACCAGAGAATTCGAATACAT GTTTTGTNNNGATCGACATG	5943	TGCAGGACCAGAGAATTCGAATACAG GACCAAANNNGATCGACATG	6183	TGCAGGACCAGAGAATTCGAATACAT TTCTACANNNGATCGACATG	6423
TGCAGGACCAGAGAATTCGAATACAG GATACAGNNNGATCGACATG	5944	TGCAGGACCAGAGAATTCGAATACAG GTCGCCANNNGATCGACATG	6184	TGCAGGACCAGAGAATTCGAATACAT CCCAGCCNNNGATCGACATG	6424
TGCAGGACCAGAGAATTCGAATACAG TTCGTAGNNNGATCGACATG	5945	TGCAGGACCAGAGAATTCGAATACAA TGGAAGCNNNGATCGACATG	6185	TGCAGGACCAGAGAATTCGAATACAC TTACCACNNNGATCGACATG	6425
TGCAGGACCAGAGAATTCGAATACAG GAGATCANNNGATCGACATG	5946	TGCAGGACCAGAGAATTCGAATACAC ATACGACNNNGATCGACATG	6186	TGCAGGACCAGAGAATTCGAATACAA CCTTCTGNNNGATCGACATG	6426
TGCAGGACCAGAGAATTCGAATACAC TTTGTTANNNGATCGACATG	5947	TGCAGGACCAGAGAATTCGAATACAT TCAGCGANNNGATCGACATG	6187	TGCAGGACCAGAGAATTCGAATACAC GTGGTCGNNNGATCGACATG	6427
TGCAGGACCAGAGAATTCGAATACAG TGAACCTNNNGATCGACATG	5948	TGCAGGACCAGAGAATTCGAATACAC TGCGGTGNNNGATCGACATG	6188	TGCAGGACCAGAGAATTCGAATACAC CAAACTGNNNGATCGACATG	6428
TGCAGGACCAGAGAATTCGAATACAC CTACAGANNNTGCATCAGGT	5949	TGCAGGACCAGAGAATTCGAATACAC AGTACTGNNNTGCATCAGGT	6189	TGCAGGACCAGAGAATTCGAATACAC TCACGCCNNNTGCATCAGGT	6429
TGCAGGACCAGAGAATTCGAATACAG CATCGATNNNTGCATCAGGT	5950	TGCAGGACCAGAGAATTCGAATACAG ATCGAAGNNNTGCATCAGGT	6190	TGCAGGACCAGAGAATTCGAATACAG ACGAGCGNNNTGCATCAGGT	6430
TGCAGGACCAGAGAATTCGAATACAT ACTGCTCNNNTGCATCAGGT	5951	TGCAGGACCAGAGAATTCGAATACAT CAAACGCNNNTGCATCAGGT	6191	TGCAGGACCAGAGAATTCGAATACAA GAATGGCNNNTGCATCAGGT	6431
TGCAGGACCAGAGAATTCGAATACAC CTGTTGTNNNTGCATCAGGT	5952	TGCAGGACCAGAGAATTCGAATACAT TTCAATCNNNTGCATCAGGT	6192	TGCAGGACCAGAGAATTCGAATACAC CAGTCCCNNNTGCATCAGGT	6432
TGCAGGACCAGAGAATTCGAATACAG AGTCGAANNNTGCATCAGGT	5953	TGCAGGACCAGAGAATTCGAATACAG AGATGGTNNNTGCATCAGGT	6193	TGCAGGACCAGAGAATTCGAATACAA AAGTATGNNNTGCATCAGGT	6433
TGCAGGACCAGAGAATTCGAATACAT TGACCAGNNNTGCATCAGGT	5954	TGCAGGACCAGAGAATTCGAATACAA GGCTCATNNNTGCATCAGGT	6194	TGCAGGACCAGAGAATTCGAATACAC GTACGTANNNTGCATCAGGT	6434
TGCAGGACCAGAGAATTCGAATACAA TGGTTATNNNTGCATCAGGT	5955	TGCAGGACCAGAGAATTCGAATACAT GGCCGCANNNTGCATCAGGT	6195	TGCAGGACCAGAGAATTCGAATACAC AGCGCCANNNTGCATCAGGT	6435
TGCAGGACCAGAGAATTCGAATACAG CGCTCAGNNNTGCATCAGGT	5956	TGCAGGACCAGAGAATTCGAATACAT AACTGCGNNNTGCATCAGGT	6196	TGCAGGACCAGAGAATTCGAATACAG CTCTCCGNNNTGCATCAGGT	6436
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TGCAGGACCAGAGAATTCGAATACAT TACCACCNNNTGCATCAGGT	5958	TGCAGGACCAGAGAATTCGAATACAA CTTAATGNNNTGCATCAGGT	6198	TGCAGGACCAGAGAATTCGAATACAG AGAGTGTNNNTGCATCAGGT	6438
TGCAGGACCAGAGAATTCGAATACAG TATAACTNNNTGCATCAGGT	5959	TGCAGGACCAGAGAATTCGAATACAC ACCTGCCNNNTGCATCAGGT	6199	TGCAGGACCAGAGAATTCGAATACAA TGGAGTGNNNTGCATCAGGT	6439
TGCAGGACCAGAGAATTCGAATACAG CCCGTGANNNTGCATCAGGT	5960	TGCAGGACCAGAGAATTCGAATACAT ATGCTTTNNNTGCATCAGGT	6200	TGCAGGACCAGAGAATTCGAATACAT CGGCCGANNNTGCATCAGGT	6440
TGCAGGACCAGAGAATTCGAATACAC TGATGACNNNTGCATCAGGT	5961	TGCAGGACCAGAGAATTCGAATACAA GGTGCAANNNTGCATCAGGT	6201	TGCAGGACCAGAGAATTCGAATACAA TCGATTANNNTGCATCAGGT	6441
TGCAGGACCAGAGAATTCGAATACAC ATGGCATNNNTGCATCAGGT	5962	TGCAGGACCAGAGAATTCGAATACAC GGCTAATNNNTGCATCAGGT	6202	TGCAGGACCAGAGAATTCGAATACAC CCAACAANNNTGCATCAGGT	6442
TGCAGGACCAGAGAATTCGAATACAA TGATATCNNNTGCATCAGGT	5963	TGCAGGACCAGAGAATTCGAATACAT AGCAAAANNNTGCATCAGGT	6203	TGCAGGACCAGAGAATTCGAATACAT GTAGATTNNNTGCATCAGGT	6443
TGCAGGACCAGAGAATTCGAATACAT GTAAAAGNNNTGCATCAGGT	5964	TGCAGGACCAGAGAATTCGAATACAA GCAAGCANNNTGCATCAGGT	6204	TGCAGGACCAGAGAATTCGAATACAA CCGGAGGNNNTGCATCAGGT	6444
TGCAGGACCAGAGAATTCGAATACAC GTTGCCGNNNTGCATCAGGT	5965	TGCAGGACCAGAGAATTCGAATACAA TAGTACTNNNTGCATCAGGT	6205	TGCAGGACCAGAGAATTCGAATACAC ACCTGAANNNTGCATCAGGT	6445

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池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG AGGCACGNNNTGCATCAGGT	5966	TGCAGGACCAGAGAATTCGAATACAC CCATGTTNNNTGCATCAGGT	6206	TGCAGGACCAGAGAATTCGAATACAA CATGTGCNNNTGCATCAGGT	6446
TGCAGGACCAGAGAATTCGAATACAC CTGAGCGNNNTGCATCAGGT	5967	TGCAGGACCAGAGAATTCGAATACAG AGCAATGNNNTGCATCAGGT	6207	TGCAGGACCAGAGAATTCGAATACAC AGGATCTNNNTGCATCAGGT	6447
TGCAGGACCAGAGAATTCGAATACAG GTTGCTANNNTGCATCAGGT	5968	TGCAGGACCAGAGAATTCGAATACAA ATACCTANNNTGCATCAGGT	6208	TGCAGGACCAGAGAATTCGAATACAC GTTTGTCNNNTGCATCAGGT	6448
TGCAGGACCAGAGAATTCGAATACAG TCAAAGGNNNTGCATCAGGT	5969	TGCAGGACCAGAGAATTCGAATACAA ATATTGCNNNTGCATCAGGT	6209	TGCAGGACCAGAGAATTCGAATACAA AATCAAGNNNTGCATCAGGT	6449
TGCAGGACCAGAGAATTCGAATACAA CGTATGCNNNTGCATCAGGT	5970	TGCAGGACCAGAGAATTCGAATACAA ATCCATANNNTGCATCAGGT	6210	TGCAGGACCAGAGAATTCGAATACAT CAACATANNNTGCATCAGGT	6450
TGCAGGACCAGAGAATTCGAATACAC GAGCGGANNNTGCATCAGGT	5971	TGCAGGACCAGAGAATTCGAATACAT CCATTTANNNTGCATCAGGT	6211	TGCAGGACCAGAGAATTCGAATACAA TGAAGGCNNNTGCATCAGGT	6451
TGCAGGACCAGAGAATTCGAATACAT TTTGCCGNNNTGCATCAGGT	5972	TGCAGGACCAGAGAATTCGAATACAG AGGTTCTNNNTGCATCAGGT	6212	TGCAGGACCAGAGAATTCGAATACAC AAGTGGANNNTGCATCAGGT	6452
TGCAGGACCAGAGAATTCGAATACAA AGTCTGCNNNTGCATCAGGT	5973	TGCAGGACCAGAGAATTCGAATACAG TGATACCNNNTGCATCAGGT	6213	TGCAGGACCAGAGAATTCGAATACAA GCAAAATNNNTGCATCAGGT	6453
TGCAGGACCAGAGAATTCGAATACAC TTCCTTCNNNTGCATCAGGT	5974	TGCAGGACCAGAGAATTCGAATACAA CCTTGCTNNNTGCATCAGGT	6214	TGCAGGACCAGAGAATTCGAATACAA CAGATCCNNNTGCATCAGGT	6454
TGCAGGACCAGAGAATTCGAATACAA TGTGAAANNNTGCATCAGGT	5975	TGCAGGACCAGAGAATTCGAATACAT ATCAAGTNNNTGCATCAGGT	6215	TGCAGGACCAGAGAATTCGAATACAT ACGCCTTNNNTGCATCAGGT	6455
TGCAGGACCAGAGAATTCGAATACAG CCGTGGTNNNTGCATCAGGT	5976	TGCAGGACCAGAGAATTCGAATACAA CTTAGGCNNNTGCATCAGGT	6216	TGCAGGACCAGAGAATTCGAATACAA GCGCTATNNNTGCATCAGGT	6456
TGCAGGACCAGAGAATTCGAATACAC AGAGGCGNNNTGCATCAGGT	5977	TGCAGGACCAGAGAATTCGAATACAA CTGTTCCNNNTGCATCAGGT	6217	TGCAGGACCAGAGAATTCGAATACAA GTGATGCNNNTGCATCAGGT	6457
TGCAGGACCAGAGAATTCGAATACAT TTGATCTNNNTGCATCAGGT	5978	TGCAGGACCAGAGAATTCGAATACAG GATCCATNNNTGCATCAGGT	6218	TGCAGGACCAGAGAATTCGAATACAC GGATGAANNNTGCATCAGGT	6458
TGCAGGACCAGAGAATTCGAATACAG CGTCGACNNNTGCATCAGGT	5979	TGCAGGACCAGAGAATTCGAATACAC CACTCCGNNNTGCATCAGGT	6219	TGCAGGACCAGAGAATTCGAATACAG ACATAGGNNNTGCATCAGGT	6459
TGCAGGACCAGAGAATTCGAATACAG GATATAANNNTGCATCAGGT	5980	TGCAGGACCAGAGAATTCGAATACAG CAAGAGTNNNTGCATCAGGT	6220	TGCAGGACCAGAGAATTCGAATACAA TTGCGTGNNNTGCATCAGGT	6460
TGCAGGACCAGAGAATTCGAATACAA AATTTTANNNTGCATCAGGT	5981	TGCAGGACCAGAGAATTCGAATACAA CCGTCTTNNNTGCATCAGGT	6221	TGCAGGACCAGAGAATTCGAATACAC TACAGTGNNNTGCATCAGGT	6461
TGCAGGACCAGAGAATTCGAATACAA GCCCGTGNNNTGCATCAGGT	5982	TGCAGGACCAGAGAATTCGAATACAG GCTTAGTNNNTGCATCAGGT	6222	TGCAGGACCAGAGAATTCGAATACAC CGTCCACNNNTGCATCAGGT	6462
TGCAGGACCAGAGAATTCGAATACAC AATARAGNNNTGCATCAGGT	5983	TGCAGGACCAGAGAATTCGAATACAC CTAAGCANNNTGCATCAGGT	6223	TGCAGGACCAGAGAATTCGAATACAA AGCCCATNNNTGCATCAGGT	6463
TGCAGGACCAGAGAATTCGAATACAG CGACATTNNNTGCATCAGGT	5984	TGCAGGACCAGAGAATTCGAATACAG CGCGAAGNNNTGCATCAGGT	6224	TGCAGGACCAGAGAATTCGAATACAC GAGGCCTNNNTGCATCAGGT	6464
TGCAGGACCAGAGAATTCGAATACAC AGAGAGTNNNTGCATCAGGT	5985	TGCAGGACCAGAGAATTCGAATACAC ATTCTTANNNTGCATCAGGT	6225	TGCAGGACCAGAGAATTCGAATACAA CCTATCCNNNTGCATCAGGT	6465
TGCAGGACCAGAGAATTCGAATACAC TTCACACNNNTGCATCAGGT	5986	TGCAGGACCAGAGAATTCGAATACAA CTACGGTNNNTGCATCAGGT	6226	TGCAGGACCAGAGAATTCGAATACAA GGCGAGCNNNTGCATCAGGT	6466
TGCAGGACCAGAGAATTCGAATACAT TAAGCTANNNTGCATCAGGT	5987	TGCAGGACCAGAGAATTCGAATACAC CGGAGCTNNNTGCATCAGGT	6227	TGCAGGACCAGAGAATTCGAATACAG AGAACTGNNNTGCATCAGGT	6467
TGCAGGACCAGAGAATTCGAATACAG TGACCGCNNNTGCATCAGGT	5988	TGCAGGACCAGAGAATTCGAATACAG TACTTAANNNTGCATCAGGT	6228	TGCAGGACCAGAGAATTCGAATACAT GGTGTTGNNNTGCATCAGGT	6468
TGCAGGACCAGAGAATTCGAATACAC CGATATGNNNTGCATCAGGT	5989	TGCAGGACCAGAGAATTCGAATACAT GCCGCTCNNNTGCATCAGGT	6229	TGCAGGACCAGAGAATTCGAATACAC TAAATCANNNTGCATCAGGT	6469
TGCAGGACCAGAGAATTCGAATACAT AGCATTANNNTGCATCAGGT	5990	TGCAGGACCAGAGAATTCGAATACAG CGACTTANNNTGCATCAGGT	6230	TGCAGGACCAGAGAATTCGAATACAA TTTCCGCNNNTGCATCAGGT	6470
TGCAGGACCAGAGAATTCGAATACAC TAGGCCGNNNTGCATCAGGT	5991	TGCAGGACCAGAGAATTCGAATACAA TGGCAAGNNNTGCATCAGGT	6231	TGCAGGACCAGAGAATTCGAATACAC CTCCATANNNTGCATCAGGT	6471
TGCAGGACCAGAGAATTCGAATACAT TAGTAACNNNTGCATCAGGT	5992	TGCAGGACCAGAGAATTCGAATACAC GGAGGTGNNNTGCATCAGGT	6232	TGCAGGACCAGAGAATTCGAATACAT TACTACTNNNTGCATCAGGT	6472
TGCAGGACCAGAGAATTCGAATACAT ATCACGGNNNTGCATCAGGT	5993	TGCAGGACCAGAGAATTCGAATACAA CATTAACNNNTGCATCAGGT	6233	TGCAGGACCAGAGAATTCGAATACAT CGTTTATNNNTGCATCAGGT	6473
TGCAGGACCAGAGAATTCGAATACAC GATTCTCNNNTGCATCAGGT	5994	TGCAGGACCAGAGAATTCGAATACAT AGGAAATNNNTGCATCAGGT	6234	TGCAGGACCAGAGAATTCGAATACAA TTCAATGNNNTGCATCAGGT	6474
TGCAGGACCAGAGAATTCGAATACAG AGGAAGANNNTGCATCAGGT	5995	TGCAGGACCAGAGAATTCGAATACAC CTAAGTGNNNTGCATCAGGT	6235	TGCAGGACCAGAGAATTCGAATACAA ACCACACNNNTGCATCAGGT	6475
TGCAGGACCAGAGAATTCGAATACAT GTCTGCTNNNTGCATCAGGT	5996	TGCAGGACCAGAGAATTCGAATACAT AGACGCTNNNTGCATCAGGT	6236	TGCAGGACCAGAGAATTCGAATACAT ACCCGCCNNNTGCATCAGGT	6476
TGCAGGACCAGAGAATTCGAATACAA ATACTCANNNTGCATCAGGT	5997	TGCAGGACCAGAGAATTCGAATACAG TGAAGCANNNTGCATCAGGT	6237	TGCAGGACCAGAGAATTCGAATACAC CATGGCGNNNTGCATCAGGT	6477
TGCAGGACCAGAGAATTCGAATACAT AGTTCCCNNNTGCATCAGGT	5998	TGCAGGACCAGAGAATTCGAATACAG GACGCAGNNNTGCATCAGGT	6238	TGCAGGACCAGAGAATTCGAATACAC CTGAGTANNNTGCATCAGGT	6478

图20G

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA ATTCGTANNNTGCATCAGGT	5999	TGCAGGACCAGAGAATTCGAATACAT TTTACGTNNNTGCATCAGGT	6239	TGCAGGACCAGAGAATTCGAATACAG GATGTCTNNNTGCATCAGGT	6479
TGCAGGACCAGAGAATTCGAATACAG CTGATTGNNNTGCATCAGGT	6000	TGCAGGACCAGAGAATTCGAATACAG ATGATTTNNNTGCATCAGGT	6240	TGCAGGACCAGAGAATTCGAATACAA AGACCCTNNNTGCATCAGGT	6480
TGCAGGACCAGAGAATTCGAATACAT ACCCGAANNNTGCATCAGGT	6001	TGCAGGACCAGAGAATTCGAATACAA CGGAATGNNNTGCATCAGGT	6241	TGCAGGACCAGAGAATTCGAATACAG TACTTGGNNNTGCATCAGGT	6481
TGCAGGACCAGAGAATTCGAATACAA GGCCATTNNNTGCATCAGGT	6002	TGCAGGACCAGAGAATTCGAATACAA ATGGCAGNNNTGCATCAGGT	6242	TGCAGGACCAGAGAATTCGAATACAT CCCTCTTNNNTGCATCAGGT	6482
TGCAGGACCAGAGAATTCGAATACAG CTCCCCANNNTGCATCAGGT	6003	TGCAGGACCAGAGAATTCGAATACAC GACTGATNNNTGCATCAGGT	6243	TGCAGGACCAGAGAATTCGAATACAT ACTTACTNNNTGCATCAGGT	6483
TGCAGGACCAGAGAATTCGAATACAT GAACGCTNNNTGCATCAGGT	6004	TGCAGGACCAGAGAATTCGAATACAA AAGATACNNNTGCATCAGGT	6244	TGCAGGACCAGAGAATTCGAATACAG GTTTTCCNNNTGCATCAGGT	6484
TGCAGGACCAGAGAATTCGAATACAC GAGGCAGNNNTGCATCAGGT	6005	TGCAGGACCAGAGAATTCGAATACAA CGGCATTNNNTGCATCAGGT	6245	TGCAGGACCAGAGAATTCGAATACAG GATCACTNNNTGCATCAGGT	6485
TGCAGGACCAGAGAATTCGAATACAG GTGCTATNNNTGCATCAGGT	6006	TGCAGGACCAGAGAATTCGAATACAC CACGCTCNNNTGCATCAGGT	6246	TGCAGGACCAGAGAATTCGAATACAT TGATGGCNNNTGCATCAGGT	6486
TGCAGGACCAGAGAATTCGAATACAA ATTGCCGNNNTGCATCAGGT	6007	TGCAGGACCAGAGAATTCGAATACAA ACCACTGNNNTGCATCAGGT	6247	TGCAGGACCAGAGAATTCGAATACAC CACATTCNNNTGCATCAGGT	6487
TGCAGGACCAGAGAATTCGAATACAG GCCGACTNNNTGCATCAGGT	6008	TGCAGGACCAGAGAATTCGAATACAG TCGAGTTNNNTGCATCAGGT	6248	TGCAGGACCAGAGAATTCGAATACAC AAAAAGTNNNTGCATCAGGT	6488

图20H

池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACAGTATTANNNACGTATGCCA	6489	TGCAGGACCAGAGAATTCGAATA CAGCTGACCGNNNACGTATGCCA	6729	TGCAGGACCAGAGAATTCGAATA CATATTCGTTNNNACGTATGCCA	6969
TGCAGGACCAGAGAATTCGAATA CAGTACTAATNNNACGTATGCCA	6490	TGCAGGACCAGAGAATTCGAATA CACCAGCATANNNACGTATGCCA	6730	TGCAGGACCAGAGAATTCGAATA CACCATTAAANNNACGTATGCCA	6970
TGCAGGACCAGAGAATTCGAATA CATTTATGCTNNNACGTATGCCA	6491	TGCAGGACCAGAGAATTCGAATA CACGAAGGATNNNACGTATGCCA	6731	TGCAGGACCAGAGAATTCGAATA CAGTTGGCGCNNNACGTATGCCA	6971
TGCAGGACCAGAGAATTCGAATA CAGTCATCCTNNNACGTATGCCA	6492	TGCAGGACCAGAGAATTCGAATA CACGACGAGGNNNACGTATGCCA	6732	TGCAGGACCAGAGAATTCGAATA CACTGGCGTGNNNACGTATGCCA	6972
TGCAGGACCAGAGAATTCGAATA CACGAATAAANNNACGTATGCCA	6493	TGCAGGACCAGAGAATTCGAATA CATATAACCANNNACGTATGCCA	6733	TGCAGGACCAGAGAATTCGAATA CAAATACCCGNNNACGTATGCCA	6973
TGCAGGACCAGAGAATTCGAATA CAGACGTATCNNNACGTATGCCA	6494	TGCAGGACCAGAGAATTCGAATA CAGTGGTTTGNNNACGTATGCCA	6734	TGCAGGACCAGAGAATTCGAATA CACACAAACCNNNACGTATGCCA	6974
TGCAGGACCAGAGAATTCGAATA CAAATTCACANNNACGTATGCCA	6495	TGCAGGACCAGACAATTCGAATA CAGTTGCGATNNNACGTATGCCA	6735	TGCAGGACCAGAGAATTCGAATA CAATTAATATNNNACGTATGCCA	6975
TGCAGGACCAGAGAATTCGAATA CAAATCCGCANNNACGTATGCCA	6496	TGCAGGACCAGAGAATTCGAATA CAATACCCTCNNNACGTATGCCA	6736	TGCAGGACCAGAGAATTCGAATA CAGATTAGCCNNNACGTATGCCA	6976
TGCAGGACCAGAGAATTCGAATA CAACCTATTTNNNACGTATGCCA	6497	TGCAGGACCAGAGAATTCGAATA CACTCGAAGTNNNACGTATGCCA	6737	TGCAGGACCAGAGAATTCGAATA CAGACAAAATNNNACGTATGCCA	6977
TGCAGGACCAGAGAATTCGAATA CAGCTTACTCNNNACGTATGCCA	6498	TGCAGGACCAGAGAATTCGAATA CACAGGCCGTNNNACGTATGCCA	6738	TGCAGGACCAGAGAATTCGAATA CAAATATTTANNNACGTATGCCA	6978
TGCAGGACCAGAGAATTCGAATA CATTGGATGCNNNACGTATGCCA	6499	TGCAGGACCAGAGAATTCGAATA CAATAGTCATNNNACGTATGCCA	6739	TGCAGGACCAGAGAATTCGAATA CAAAAAGTCANNNACGTATGCCA	6979
TGCAGGACCAGAGAATTCGAATA CAGCGGACGANNNACGTATGCCA	6500	TGCAGGACCAGAGAATTCGAATA CACTCCGTCGNNNACGTATGCCA	6740	TGCAGGACCAGAGAATTCGAATA CAGTCTATAANNNACGTATGCCA	6980
TGCAGGACCAGAGAATTCGAATA CAACAAGTTTNNNACGTATGCCA	6501	TGCAGGACCAGAGAATTCGAATA CAGTGCCGTGNNNACGTATGCCA	6741	TGCAGGACCAGAGAATTCGAATA CAAAAAACGTNNNACGTATGCCA	6981
TGCAGGACCAGAGAATTCGAATA CATATCTCATNNNACGTATGCCA	6502	TGCAGGACCAGAGAATTCGAATA CAAGTAAAGTNNNACGTATGCCA	6742	TGCAGGACCAGAGAATTCGAATA CATTGCTCTGNNNACGTATGCCA	6982
TGCAGGACCAGAGAATTCGAATA CAGGTTTGGTNNNACGTATGCCA	6503	TGCAGGACCAGAGAATTCGAATA CATATTGCAANNNACGTATGCCA	6743	TGCAGGACCAGAGAATTCGAATA CAATGATGAANNNACGTATGCCA	6983
TGCAGGACCAGAGAATTCGAATA CATAATTCCTNNNACGTATGCCA	6504	TGCAGGACCAGAGAATTCGAATA CAACCCAGCGNNNACGTATGCCA	6744	TGCAGGACCAGAGAATTCGAATA CATCCCTGTANNNACGTATGCCA	6984
TGCAGGACCAGAGAATTCGAATA CAACGTCGTANNNACGTATGCCA	6505	TGCAGGACCAGAGAATTCGAATA CATGTCAAATNNNACGTATGCCA	6745	TGCAGGACCAGAGAATTCGAATA CAACATCCGANNNACGTATGCCA	6985
TGCAGGACCAGAGAATTCGAATA CAGAAGCTAGNNNACGTATGCCA	6506	TGCAGGACCAGAGAATTCGAATA CAGTGAAACGNNNACGTATGCCA	6746	TGCAGGACCAGAGAATTCGAATA CATTAGATCANNNACGTATGCCA	6986
TGCAGGACCAGAGAATTCGAATA CAACGAATCCNNNACGTATGCCA	6507	TGCAGGACCAGAGAATTCGAATA CAAGCGGATANNNACGTATGCCA	6747	TGCAGGACCAGAGAATTCGAATA CACGCCTACCNNNACGTATGCCA	6987
TGCAGGACCAGAGAATTCGAATA CATCTTAATCNNNACGTATGCCA	6508	TGCAGGACCAGAGAATTCGAATA CAACGCAGTTNNNACGTATGCCA	6748	TGCAGGACCAGAGAATTCGAATA CACTCTAACCNNNACGTATGCCA	6988
TGCAGGACCAGAGAATTCGAATA CAGCTTTTCGNNNACGTATGCCA	6509	TGCAGGACCAGAGAATTCGAATA CATAAGGATANNNACGTATGCCA	6749	TGCAGGACCAGAGAATTCGAATA CACGTCATCTNNNACGTATGCCA	6989
TGCAGGACCAGAGAATTCGAATA CATGCTGAGTNNNACGTATGCCA	6510	TGCAGGACCAGAGAATTCGAATA CATAGTGGAGNNNACGTATGCCA	6750	TGCAGGACCAGAGAATTCGAATA CACACCTATCNNNACGTATGCCA	6990
TGCAGGACCAGAGAATTCGAATA CACGTTGCAANNNACGTATGCCA	6511	TGCAGGACCAGAGAATTCGAATA CATGTGGAAGNNNACGTATGCCA	6751	TGCAGGACCAGAGAATTCGAATA CATCGCTATCNNNACGTATGCCA	6991
TGCAGGACCAGAGAATTCGAATA CACAGTACGTNNNACGTATGCCA	6512	TGCAGGACCAGAGAATTCGAATA CACCCACGTCNNNACGTATGCCA	6752	TGCAGGACCAGAGAATTCGAATA CAGAAGGCCGNNNACGTATGCCA	6992
TGCAGGACCAGAGAATTCGAATA CATGGATTTANNNACGTATGCCA	6513	TGCAGGACCAGAGAATTCGAATA CAGTAACGGANNNACGTATGCCA	6753	TGCAGGACCAGAGAATTCGAATA CAGTTTTCGCNNNACGTATGCCA	6993
TGCAGGACCAGAGAATTCGAATA CAGTGTAGAGNNNACGTATGCCA	6514	TGCAGGACCAGAGAATTCGAATA CATTCTACATNNNACGTATGCCA	6754	TGCAGGACCAGAGAATTCGAATA CAAGTGGCCCNNNACGTATGCCA	6994
TGCAGGACCAGAGAATTCGAATA CACTTTAGAANNNACGTATGCCA	6515	TGCAGGACCAGAGAATTCGAATA CATCAATGATNNNACGTATGCCA	6755	TGCAGGACCAGAGAATTCGAATA CAAGCCATACNNNACGTATGCCA	6995
TGCAGGACCAGAGAATTCGAATA CAATATAGTCNNNACGTATGCCA	6516	TGCAGGACCAGAGAATTCGAATA CATCGCGAATNNNACGTATGCCA	6756	TGCAGGACCAGAGAATTCGAATA CAATTCCGAGNNNACGTATGCCA	6996
TGCAGGACCAGAGAATTCGAATA CAGTAGAGCANNNACGTATGCCA	6517	TGCAGGACCAGAGAATTCGAATA CATAATGACTNNNACGTATGCCA	6757	TGCAGGACCAGAGAATTCGAATA CACAACCGATNNNACGTATGCCA	6997
TGCAGGACCAGAGAATTCGAATA CATAAATACCNNNACGTATGCCA	6518	TGCAGGACCAGAGAATTCGAATA CACAGGTTTGNNNACGTATGCCA	6758	TGCAGGACCAGAGAATTCGAATA CAAAGTATGANNNACGTATGCCA	6998
TGCAGGACCAGAGAATTCGAATA CACAGGACAANNNACGTATGCCA	6519	TGCAGGACCAGAGAATTCGAATA CATTCGGCTTNNNACGTATGCCA	6759	TGCAGGACCAGAGAATTCGAATA CAATCTGCCTNNNACGTATGCCA	6999
TGCAGGACCAGAGAATTCGAATA CAATATCACANNNACGTATGCCA	6520	TGCAGGACCAGAGAATTCGAATA CACCTTATTANNNACGTATGCCA	6760	TGCAGGACCAGAGAATTCGAATA CACTCATTTANNNACGTATGCCA	7000
TGCAGGACCAGAGAATTCGAATA CATGAATCATNNNACGTATGCCA	6521	TGCAGGACCAGAGAATTCGAATA CATAGCATGCNNNACGTATGCCA	6761	TGCAGGACCAGAGAATTCGAATA CATAAATCACNNNACGTATGCCA	7001

图21A

池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACTACGTAGNNNACGTATGCCA	6522	TGCAGGACCAGAGAATTCGAATA CAAAAACGCGNNNACGTATGCCA	6762	TGCAGGACCAGAGAATTCGAATA CACCGAGACCNNNACGTATGCCA	7002
TGCAGGACCAGAGAATTCGAATA CAGTACATCGNNNACGTATGCCA	6523	TGCAGGACCAGAGAATTCGAATA CATAGCTGACNNNACGTATGCCA	6763	TGCAGGACCAGAGAATTCGAATA CATCGCCCACNNNACGTATGCCA	7003
TGCAGGACCAGAGAATTCGAATA CACGCAGTGCNNNACGTATGCCA	6524	TGCAGGACCAGAGAATTCGAATA CACTACCCCGNNNACGTATGCCA	6764	TGCAGGACCAGAGAATTCGAATA CAACGACTTGNNNACGTATGCCA	7004
TGCAGGACCAGAGAATTCGAATA CAAACAAAGTNNNACGTATGCCA	6525	TGCAGGACCAGAGAATTCGAATA CAAGCTGTCANNNACGTATGCCA	6765	TGCAGGACCAGAGAATTCGAATA CAGTTTAGCGNNNACGTATGCCA	7005
TGCAGGACCAGAGAATTCGAATA CAAAACTTCANNNACGTATGCCA	6526	TGCAGGACCAGAGAATTCGAATA CACCCTCAGCNNNACGTATGCCA	6766	TGCAGGACCAGAGAATTCGAATA CAGTTTCAAANNNACGTATGCCA	7006
TGCAGGACCAGAGAATTCGAATA CAAGGAGCCGNNNACGTATGCCA	6527	TGCAGGACCAGAGAATTCGAATA CACACGTTCTNNNACGTATGCCA	6767	TGCAGGACCAGAGAATTCGAATA CAGAATGCGANNNACGTATGCCA	7007
TGCAGGACCAGAGAATTCGAATA CACGTGACATNNNACGTATGCCA	6528	TGCAGGACCAGAGAATTCGAATA CAACGGAACANNNACGTATGCCA	6768	TGCAGGACCAGAGAATTCGAATA CAACCCGTAANNNACGTATGCCA	7008
TGCAGGACCAGAGAATTCGAATA CAATACATCANNNACGTATGCCA	6529	TGCAGGACCAGAGAATTCGAATA CACATCATTANNNACGTATGCCA	6769	TGCAGGACCAGAGAATTCGAATA CAGTCACCAANNNACGTATGCCA	7009
TGCAGGACCAGAGAATTCGAATA CAAATAACCTNNNACGTATGCCA	6530	TGCAGGACCAGAGAATTCGAATA CACTAGAACCNNNACGTATGCCA	6770	TGCAGGACCAGAGAATTCGAATA CATTGGACTGNNNACGTATGCCA	7010
TGCAGGACCAGAGAATTCGAATA CACCAGCTTTNNNACGTATGCCA	6531	TGCAGGACCAGAGAATTCGAATA CATTTAGGTANNNACGTATGCCA	6771	TGCAGGACCAGAGAATTCGAATA CAAAGCTTGCNNNACGTATGCCA	7011
TGCAGGACCAGAGAATTCGAATA CATCCGTTTGNNNACGTATGCCA	6532	TGCAGGACCAGAGAATTCGAATA CATGATATTGNNNACGTATGCCA	6772	TGCAGGACCAGAGAATTCGAATA CATTATTTATNNNACGTATGCCA	7012
TGCAGGACCAGAGAATTCGAATA CACAGTCGGCNNNACGTATGCCA	6533	TGCAGGACCAGAGAATTCGAATA CAGCGAAAACNNNACGTATGCCA	6773	TGCAGGACCAGAGAATTCGAATA CATACAATGTNNNACGTATGCCA	7013
TGCAGGACCAGAGAATTCGAATA CATGATCGGTNNNACGTATGCCA	6534	TGCAGGACCAGAGAATTCGAATA CAACTAACGCNNNACGTATGCCA	6774	TGCAGGACCAGAGAATTCGAATA CAAAAGTGGCNNNACGTATGCCA	7014
TGCAGGACCAGAGAATTCGAATA CAACACACACNNNACGTATGCCA	6535	TGCAGGACCAGAGAATTCGAATA CATACTTGCCNNNACGTATGCCA	6775	TGCAGGACCAGAGAATTCGAATA CAGCTGCTCCNNNACGTATGCCA	7015
TGCAGGACCAGAGAATTCGAATA CATCACGCAANNNACGTATGCCA	6536	TGCAGGACCAGAGAATTCGAATA CACGTGCTAANNNACGTATGCCA	6776	TGCAGGACCAGAGAATTCGAATA CAGCTGATACNNNACGTATGCCA	7016
TGCAGGACCAGAGAATTCGAATA CATCGTACTCNNNACGTATGCCA	6537	TGCAGGACCAGAGAATTCGAATA CAAAACAGTANNNACGTATGCCA	6777	TGCAGGACCAGAGAATTCGAATA CACTTTCATTNNNACGTATGCCA	7017
TGCAGGACCAGAGAATTCGAATA CATTCAGACGNNNACGTATGCCA	6538	TGCAGGACCAGAGAATTCGAATA CAGCATCATGNNNACGTATGCCA	6778	TGCAGGACCAGAGAATTCGAATA CACTTGTGAGNNNACGTATGCCA	7018
TGCAGGACCAGAGAATTCGAATA CAGCGCACGTNNNACGTATGCCA	6539	TGCAGGACCAGAGAATTCGAATA CAACCTCGAANNNACGTATGCCA	6779	TGCAGGACCAGAGAATTCGAATA CAACTTCCGTNNNACGTATGCCA	7019
TGCAGGACCAGAGAATTCGAATA CACCAGACATNNNACGTATGCCA	6540	TGCAGGACCAGAGAATTCGAATA CAACAGCTACNNNACGTATGCCA	6780	TGCAGGACCAGAGAATTCGAATA CACAAGATCCNNNACGTATGCCA	7020
TGCAGGACCAGAGAATTCGAATA CATATTGATGNNNACGTATGCCA	6541	TGCAGGACCAGAGAATTCGAATA CACGTCAACANNNACGTATGCCA	6781	TGCAGGACCAGAGAATTCGAATA CAGTCGCCTCNNNACGTATGCCA	7021
TGCAGGACCAGAGAATTCGAATA CACGAGATAGNNNACGTATGCCA	6542	TGCAGGACCAGAGAATTCGAATA CACCGGCCCCNNNACGTATGCCA	6782	TGCAGGACCAGAGAATTCGAATA CAGTGGTGAANNNACGTATGCCA	7022
TGCAGGACCAGAGAATTCGAATA CAATACGAAANNNACGTATGCCA	6543	TGCAGGACCAGAGAATTCGAATA CATCGCGTGGNNNACGTATGCCA	6783	TGCAGGACCAGAGAATTCGAATA CAAGTAAGTANNNACGTATGCCA	7023
TGCAGGACCAGAGAATTCGAATA CAGATGAGACNNNACGTATGCCA	6544	TGCAGGACCAGAGAATTCGAATA CAAAGACTGGNNNACGTATGCCA	6784	TGCAGGACCAGAGAATTCGAATA CAATTTATTTNNNACGTATGCCA	7024
TGCAGGACCAGAGAATTCGAATA CATACAATCANNNACGTATGCCA	6545	TGCAGGACCAGAGAATTCGAATA CAGCAATGAGNNNACGTATGCCA	6785	TGCAGGACCAGAGAATTCGAATA CAGGAATCGANNNACGTATGCCA	7025
TGCAGGACCAGAGAATTCGAATA CATTTAATAANNNACGTATGCCA	6546	TGCAGGACCAGAGAATTCGAATA CAAGGAGCTANNNACGTATGCCA	6786	TGCAGGACCAGAGAATTCGAATA CACGTGCTTTNNNACGTATGCCA	7026
TGCAGGACCAGAGAATTCGAATA CAGCGCGTCANNNACGTATGCCA	6547	TGCAGGACCAGAGAATTCGAATA CACCTGAGATNNNACGTATGCCA	6787	TGCAGGACCAGAGAATTCGAATA CAGTTAAAGTNNNACGTATGCCA	7027
TGCAGGACCAGAGAATTCGAATA CACGATGATCNNNACGTATGCCA	6548	TGCAGGACCAGAGAATTCGAATA CAACGGAGGCNNNACGTATGCCA	6788	TGCAGGACCAGAGAATTCGAATA CAATCTTAAGNNNACGTATGCCA	7028
TGCAGGACCAGAGAATTCGAATA CACCGAAGCCNNNCTAGCGTTAC	6549	TGCAGGACCAGAGAATTCGAATA CAGATCGGCCNNNCTAGCGTTAC	6789	TGCAGGACCAGAGAATTCGAATA CAAACTCAGCNNNCTAGCGTTAC	7029
TGCAGGACCAGAGAATTCGAATA CACCAAACACNNNCTAGCGTTAC	6550	TGCAGGACCAGAGAATTCGAATA CATGCTGCAANNNCTAGCGTTAC	6790	TGCAGGACCAGAGAATTCGAATA CAACGAAAGCNNNCTAGCGTTAC	7030
TGCAGGACCAGAGAATTCGAATA CAGGTCTTCTNNNCTAGCGTTAC	6551	TGCAGGACCAGAGAATTCGAATA CATCGGAATCNNNCTAGCGTTAC	6791	TGCAGGACCAGAGAATTCGAATA CAGCGTAATCNNNCTAGCGTTAC	7031
TGCAGGACCAGAGAATTCGAATA CACCTCGGTCNNNCTAGCGTTAC	6552	TGCAGGACCAGAGAATTCGAATA CAGACGGCTCNNNCTAGCGTTAC	6792	TGCAGGACCAGAGAATTCGAATA CAAGGTGGTANNNCTAGCGTTAC	7032
TGCAGGACCAGAGAATTCGAATA CACCGCTGGANNNCTAGCGTTAC	6553	TGCAGGACCAGAGAATTCGAATA CAAGTTGGAGNNNCTAGCGTTAC	6793	TGCAGGACCAGAGAATTCGAATA CACTTGAGTGNNNCTAGCGTTAC	7033
TGCAGGACCAGAGAATTCGAATA CAACCACCTTNNNCTAGCGTTAC	6554	TGCAGGACCAGAGAATTCGAATA CAAGTACGTCNNNCTAGCGTTAC	6794	TGCAGGACCAGAGAATTCGAATA CACTCGCCGTNNNCTAGCGTTAC	7034

图21B

池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATCTAAGTANNNCTAGCGTTAC	6555	TGCAGGACCAGAGAATTCGAATA CACGATTAATNNNCTAGCGTTAC	6795	TGCAGGACCAGAGAATTCGAATA CAGGCCTAATNNNCTAGCGTTAC	7035
TGCAGGACCAGAGAATTCGAATA CAATTATAATNNNCTAGCGTTAC	6556	TGCAGGACCAGAGAATTCGAATA CATTACGCCTNNNCTAGCGTTAC	6796	TGCAGGACCAGAGAATTCGAATA CAACCCCCTGNNNCTAGCGTTAC	7036
TGCAGGACCAGAGAATTCGAATA CATGGACGGCNNNCTAGCGTTAC	6557	TGCAGGACCAGAGAATTCGAATA CAAGGAGTTGNNNCTAGCGTTAC	6797	TGCAGGACCAGAGAATTCGAATA CACCCTATCANNNCTAGCGTTAC	7037
TGCAGGACCAGAGAATTCGAATA CACTTCATTANNNCTAGCGTTAC	6558	TGCAGGACCAGAGAATTCGAATA CAGTACACCANNNCTAGCGTTAC	6798	TGCAGGACCAGAGAATTCGAATA CATAGAACAANNNCTAGCGTTAC	7038
TGCAGGACCAGAGAATTCGAATA CAACGCACTANNNCTAGCGTTAC	6559	TGCAGGACCAGAGAATTCGAATA CAGGAAAATTNNNCTAGCGTTAC	6799	TGCAGGACCAGAGAATTCGAATA CACCGGAGGANNNCTAGCGTTAC	7039
TGCAGGACCAGAGAATTCGAATA CATCATGGCANNNCTAGCGTTAC	6560	TGCAGGACCAGAGAATTCGAATA CACGGTTCTTNNNCTAGCGTTAC	6800	TGCAGGACCAGAGAATTCGAATA CAATGAACAANNNCTAGCGTTAC	7040
TGCAGGACCAGAGAATTCGAATA CAGGCTTAACNNNCTAGCGTTAC	6561	TGCAGGACCAGAGAATTCGAATA CAGGTCGACCNNNCTAGCGTTAC	6801	TGCAGGACCAGAGAATTCGAATA CATTCGAAGCNNNCTAGCGTTAC	7041
TGCAGGACCAGAGAATTCGAATA CAATGGTATTNNNCTAGCGTTAC	6562	TGCAGGACCAGAGAATTCGAATA CATTCGCTCANNNCTAGCGTTAC	6802	TGCAGGACCAGAGAATTCGAATA CAAACAACAANNNCTAGCGTTAC	7042
TGCAGGACCAGAGAATTCGAATA CAGTATGCTGNNNCTAGCGTTAC	6563	TGCAGGACCAGAGAATTCGAATA CACGCAGCGTNNNCTAGCGTTAC	6803	TGCAGGACCAGAGAATTCGAATA CATCCTTTGGNNNCTAGCGTTAC	7043
TGCAGGACCAGAGAATTCGAATA CAATCGTGGTNNNCTAGCGTTAC	6564	TGCAGGACCAGAGAATTCGAATA CAGCTGTGCGNNNCTAGCGTTAC	6804	TGCAGGACCAGAGAATTCGAATA CAAAACGAATNNNCTAGCGTTAC	7044
TGCAGGACCAGAGAATTCGAATA CAGCTTAGGTNNNCTAGCGTTAC	6565	TGCAGGACCAGAGAATTCGAATA CACACCAGTANNNCTAGCGTTAC	6805	TGCAGGACCAGAGAATTCGAATA CATCCAGTGANNNCTAGCGTTAC	7045
TGCAGGACCAGAGAATTCGAATA CATCTGTATTNNNCTAGCGTTAC	6566	TGCAGGACCAGAGAATTCGAATA CAATCATTGANNNCTAGCGTTAC	6806	TGCAGGACCAGAGAATTCGAATA CACTTCAAAANNNCTAGCGTTAC	7046
TGCAGGACCAGAGAATTCGAATA CAGGATAGCANNNCTAGCGTTAC	6567	TGCAGGACCAGAGAATTCGAATA CATAATCATGNNNCTAGCGTTAC	6807	TGCAGGACCAGAGAATTCGAATA CATATCTAGANNNCTAGCGTTAC	7047
TGCAGGACCAGAGAATTCGAATA CATTCACTCGNNNCTAGCGTTAC	6568	TGCAGGACCAGAGAATTCGAATA CAGTTGACCANNNCTAGCGTTAC	6808	TGCAGGACCAGAGAATTCGAATA CAAACGGCTTNNNCTAGCGTTAC	7048
TGCAGGACCAGAGAATTCGAATA CATTCGGACANNNCTAGCGTTAC	6569	TGCAGGACCAGAGAATTCGAATA CAACTCATGGNNNCTAGCGTTAC	6809	TGCAGGACCAGAGAATTCGAATA CAACTTTTCANNNCTAGCGTTAC	7049
TGCAGGACCAGAGAATTCGAATA CACGGTCGGTNNNCTAGCGTTAC	6570	TGCAGGACCAGAGAATTCGAATA CACCCAGTTTNNNCTAGCGTTAC	6810	TGCAGGACCAGAGAATTCGAATA CAAGTGCTTGNNNCTAGCGTTAC	7050
TGCAGGACCAGAGAATTCGAATA CAAGATCGCTNNNCTAGCGTTAC	6571	TGCAGGACCAGAGAATTCGAATA CATCAAGGAGNNNCTAGCGTTAC	6811	TGCAGGACCAGAGAATTCGAATA CAATGGTCCANNNCTAGCGTTAC	7051
TGCAGGACCAGAGAATTCGAATA CAGCATTCGANNNCTAGCGTTAC	6572	TGCAGGACCAGAGAATTCGAATA CAAACGCTTGNNNCTAGCGTTAC	6812	TGCAGGACCAGAGAATTCGAATA CAGCCCCCTANNNCTAGCGTTAC	7052
TGCAGGACCAGAGAATTCGAATA CACGCTGATANNNCTAGCGTTAC	6573	TGCAGGACCAGAGAATTCGAATA CACTTATATCNNNCTAGCGTTAC	6813	TGCAGGACCAGAGAATTCGAATA CAGTTGCTCTNNNCTAGCGTTAC	7053
TGCAGGACCAGAGAATTCGAATA CACGGTTAACNNNCTAGCGTTAC	6574	TGCAGGACCAGAGAATTCGAATA CAAGTGTCCANNNCTAGCGTTAC	6814	TGCAGGACCAGAGAATTCGAATA CAGCATATATNNNCTAGCGTTAC	7054
TGCAGGACCAGAGAATTCGAATA CAAATGTCATNNNCTAGCGTTAC	6575	TGCAGGACCAGAGAATTCGAATA CAAGCGACGGNNNCTAGCGTTAC	6815	TGCAGGACCAGAGAATTCGAATA CAGGTCTTGANNNCTAGCGTTAC	7055
TGCAGGACCAGAGAATTCGAATA CAGCAAGACANNNCTAGCGTTAC	6576	TGCAGGACCAGAGAATTCGAATA CACTGTCCCGNNNCTAGCGTTAC	6816	TGCAGGACCAGAGAATTCGAATA CAACTATTTCNNNCTAGCGTTAC	7056
TGCAGGACCAGAGAATTCGAATA CACCAGCCTCNNNCTAGCGTTAC	6577	TGCAGGACCAGAGAATTCGAATA CAACTCACCTNNNCTAGCGTTAC	6817	TGCAGGACCAGAGAATTCGAATA CACTTAAAACNNNCTAGCGTTAC	7057
TGCAGGACCAGAGAATTCGAATA CACTTGTTCGNNNCTAGCGTTAC	6578	TGCAGGACCAGAGAATTCGAATA CAAAATTCGANNNCTAGCGTTAC	6818	TGCAGGACCAGAGAATTCGAATA CATCGCAGCGNNNCTAGCGTTAC	7058
TGCAGGACCAGAGAATTCGAATA CATATCGGTGNNNCTAGCGTTAC	6579	TGCAGGACCAGAGAATTCGAATA CAGTAATATCNNNCTAGCGTTAC	6819	TGCAGGACCAGAGAATTCGAATA CAGATTCGACNNNCTAGCGTTAC	7059
TGCAGGACCAGAGAATTCGAATA CACTGGCATANNNCTAGCGTTAC	6580	TGCAGGACCAGAGAATTCGAATA CACAAGAAATNNNCTAGCGTTAC	6820	TGCAGGACCAGAGAATTCGAATA CATGGCCGTGNNNCTAGCGTTAC	7060
TGCAGGACCAGAGAATTCGAATA CATGCAGGCCNNNCTAGCGTTAC	6581	TGCAGGACCAGAGAATTCGAATA CAATTCCCCANNNCTAGCGTTAC	6821	TGCAGGACCAGAGAATTCGAATA CAAAGGCATGNNNCTAGCGTTAC	7061
TGCAGGACCAGAGAATTCGAATA CATTCGTCCTNNNCTAGCGTTAC	6582	TGCAGGACCAGAGAATTCGAATA CAGTCTTAGCNNNCTAGCGTTAC	6822	TGCAGGACCAGAGAATTCGAATA CAATGATCTANNNCTAGCGTTAC	7062
TGCAGGACCAGAGAATTCGAATA CATAACGGAGNNNCTAGCGTTAC	6583	TGCAGGACCAGAGAATTCGAATA CATACCAGCANNNCTAGCGTTAC	6823	TGCAGGACCAGAGAATTCGAATA CATCGGCAATNNNCTAGCGTTAC	7063
TGCAGGACCAGAGAATTCGAATA CAGAGTGGATNNNCTAGCGTTAC	6584	TGCAGGACCAGAGAATTCGAATA CACACGCCTCNNNCTAGCGTTAC	6824	TGCAGGACCAGAGAATTCGAATA CAATCCGCTTNNNCTAGCGTTAC	7064
TGCAGGACCAGAGAATTCGAATA CATCGTAAATNNNCTAGCGTTAC	6585	TGCAGGACCAGAGAATTCGAATA CAAATCGAGGNNNCTAGCGTTAC	6825	TGCAGGACCAGAGAATTCGAATA CAGAAGTGGTNNNCTAGCGTTAC	7065
TGCAGGACCAGAGAATTCGAATA CACAACGACTNNNCTAGCGTTAC	6586	TGCAGGACCAGAGAATTCGAATA CACATACAATNNNCTAGCGTTAC	6826	TGCAGGACCAGAGAATTCGAATA CAGGAACAGTNNNCTAGCGTTAC	7066
TGCAGGACCAGAGAATTCGAATA CAGCACCCCTNNNCTAGCGTTAC	6587	TGCAGGACCAGAGAATTCGAATA CATTATGTTCNNNCTAGCGTTAC	6827	TGCAGGACCAGAGAATTCGAATA CACTAAACATNNNCTAGCGTTAC	7067

图21C

池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGATAATTCNNNCTAGCGTTAC	6588	TGCAGGACCAGAGAATTCGAATA CAGTCTGTCTNNNCTAGCGTTAC	6828	TGCAGGACCAGAGAATTCGAATA CAAAGGAGTCNNNCTAGCGTTAC	7068
TGCAGGACCAGAGAATTCGAATA CAAACTCAATNNNCTAGCGTTAC	6589	TGCAGGACCAGAGAATTCGAATA CAGTCTGAACNNNCTAGCGTTAC	6829	TGCAGGACCAGAGAATTCGAATA CATCCATGTCNNNCTAGCGTTAC	7069
TGCAGGACCAGAGAATTCGAATA CATCAAAACTNNNCTAGCGTTAC	6590	TGCAGGACCAGAGAATTCGAATA CAAGGTGCGGNNNCTAGCGTTAC	6830	TGCAGGACCAGAGAATTCGAATA CAGTACGAGANNNCTAGCGTTAC	7070
TGCAGGACCAGAGAATTCGAATA CAATTATTCCNNNCTAGCGTTAC	6591	TGCAGGACCAGAGAATTCGAATA CACAGAAACGNNNCTAGCGTTAC	6831	TGCAGGACCAGAGAATTCGAATA CAGGCCAGCTNNNCTAGCGTTAC	7071
TGCAGGACCAGAGAATTCGAATA CACTTCTTGGNNNCTAGCGTTAC	6592	TGCAGGACCAGAGAATTCGAATA CATCTGTTGCNNNCTAGCGTTAC	6832	TGCAGGACCAGAGAATTCGAATA CAGTCCGATANNNCTAGCGTTAC	7072
TGCAGGACCAGAGAATTCGAATA CATAAGTAAGNNNCTAGCGTTAC	6593	TGCAGGACCAGAGAATTCGAATA CACGATGGTTNNNCTAGCGTTAC	6833	TGCAGGACCAGAGAATTCGAATA CATGTTACAANNNCTAGCGTTAC	7073
TGCAGGACCAGAGAATTCGAATA CACTAACCCTNNNCTAGCGTTAC	6594	TGCAGGACCAGAGAATTCGAATA CAATAATATTNNNCTAGCGTTAC	6834	TGCAGGACCAGAGAATTCGAATA CACATTCCACNNNCTAGCGTTAC	7074
TGCAGGACCAGAGAATTCGAATA CAATAGCGTCNNNCTAGCGTTAC	6595	TGCAGGACCAGAGAATTCGAATA CAATCGACGTNNNCTAGCGTTAC	6835	TGCAGGACCAGAGAATTCGAATA CATGTTGAATNNNCTAGCGTTAC	7075
TGCAGGACCAGAGAATTCGAATA CAAAGGTAATNNNCTAGCGTTAC	6596	TGCAGGACCAGAGAATTCGAATA CAGAGGAAAGNNNCTAGCGTTAC	6836	TGCAGGACCAGAGAATTCGAATA CAAGAAACGCNNNCTAGCGTTAC	7076
TGCAGGACCAGAGAATTCGAATA CATCACGTAGNNNCTAGCGTTAC	6597	TGCAGGACCAGAGAATTCGAATA CAATTACACANNNCTAGCGTTAC	6837	TGCAGGACCAGAGAATTCGAATA CATCCGACCCNNNCTAGCGTTAC	7077
TGCAGGACCAGAGAATTCGAATA CAAACCATATNNNCTAGCGTTAC	6598	TGCAGGACCAGAGAATTCGAATA CAGGACCTGCNNNCTAGCGTTAC	6838	TGCAGGACCAGAGAATTCGAATA CACACTAGTGNNNCTAGCGTTAC	7078
TGCAGGACCAGAGAATTCGAATA CAGACGAGTANNNCTAGCGTTAC	6599	TGCAGGACCAGAGAATTCGAATA CAACGTAGAGNNNCTAGCGTTAC	6839	TGCAGGACCAGAGAATTCGAATA CAACCGGCGTNNNCTAGCGTTAC	7079
TGCAGGACCAGAGAATTCGAATA CAATAAATTTNNNCTAGCGTTAC	6600	TGCAGGACCAGAGAATTCGAATA CACACGGCGTNNNCTAGCGTTAC	6840	TGCAGGACCAGAGAATTCGAATA CACTTGCTACNNNCTAGCGTTAC	7080
TGCAGGACCAGAGAATTCGAATA CAGAGCTAAGNNNCTAGCGTTAC	6601	TGCAGGACCAGAGAATTCGAATA CAATTACGTANNNCTAGCGTTAC	6841	TGCAGGACCAGAGAATTCGAATA CATTGCAGTGNNNCTAGCGTTAC	7081
TGCAGGACCAGAGAATTCGAATA CAGCGGATCCNNNCTAGCGTTAC	6602	TGCAGGACCAGAGAATTCGAATA CATATGTTGANNNCTAGCGTTAC	6842	TGCAGGACCAGAGAATTCGAATA CAAATGAAGTNNNCTAGCGTTAC	7082
TGCAGGACCAGAGAATTCGAATA CATTCATAGANNNCTAGCGTTAC	6603	TGCAGGACCAGAGAATTCGAATA CACAGACTCANNNCTAGCGTTAC	6843	TGCAGGACCAGAGAATTCGAATA CACTCGCCCANNNCTAGCGTTAC	7083
TGCAGGACCAGAGAATTCGAATA CATTAAGCATNNNCTAGCGTTAC	6604	TGCAGGACCAGAGAATTCGAATA CACGGATGCCNNNCTAGCGTTAC	6844	TGCAGGACCAGAGAATTCGAATA CAGTGGACCCNNNCTAGCGTTAC	7084
TGCAGGACCAGAGAATTCGAATA CATCGAGCGCNNNCTAGCGTTAC	6605	TGCAGGACCAGAGAATTCGAATA CATACATCTTNNNCTAGCGTTAC	6845	TGCAGGACCAGAGAATTCGAATA CAACGACTCANNNCTAGCGTTAC	7085
TGCAGGACCAGAGAATTCGAATA CATCGCACCCNNNCTAGCGTTAC	6606	TGCAGGACCAGAGAATTCGAATA CACTTCGTGTNNNCTAGCGTTAC	6846	TGCAGGACCAGAGAATTCGAATA CAACAACTTANNNCTAGCGTTAC	7086
TGCAGGACCAGAGAATTCGAATA CACTTGGACANNNCTAGCGTTAC	6607	TGCAGGACCAGAGAATTCGAATA CAGAACGCGGNNNCTAGCGTTAC	6847	TGCAGGACCAGAGAATTCGAATA CATCTGGTAGNNNCTAGCGTTAC	7087
TGCAGGACCAGAGAATTCGAATA CATTCCAGTCNNNCTAGCGTTAC	6608	TGCAGGACCAGAGAATTCGAATA CATCGGATTGNNNCTAGCGTTAC	6848	TGCAGGACCAGAGAATTCGAATA CACTATGGCANNNCTAGCGTTAC	7088
TGCAGGACCAGAGAATTCGAATA CAGTTTTTACNNNGATCGACATG	6609	TGCAGGACCAGAGAATTCGAATA CAAGACAAATNNNGATCGACATG	6849	TGCAGGACCAGAGAATTCGAATA CAACCCGCGANNNGATCGACATG	7089
TGCAGGACCAGAGAATTCGAATA CAAACTTAGTNNNGATCGACATG	6610	TGCAGGACCAGAGAATTCGAATA CACGAAGTAGNNNGATCGACATG	6850	TGCAGGACCAGAGAATTCGAATA CACGCGGTACNNNGATCGACATG	7090
TGCAGGACCAGAGAATTCGAATA CACGCGCGCGNNNGATCGACATG	6611	TGCAGGACCAGAGAATTCGAATA CAAAAGAGCCNNNGATCGACATG	6851	TGCAGGACCAGAGAATTCGAATA CACACATCAGNNNGATCGACATG	7091
TGCAGGACCAGAGAATTCGAATA CAAACTGTTANNNGATCGACATG	6612	TGCAGGACCAGAGAATTCGAATA CATGAGTGGANNNGATCGACATG	6852	TGCAGGACCAGAGAATTCGAATA CATAGACACCNNNGATCGACATG	7092
TGCAGGACCAGAGAATTCGAATA CAGTAAGTTTNNNGATCGACATG	6613	TGCAGGACCAGAGAATTCGAATA CACGCTCCCANNNGATCGACATG	6853	TGCAGGACCAGAGAATTCGAATA CAATGTAAAGNNNGATCGACATG	7093
TGCAGGACCAGAGAATTCGAATA CACTTAGCAGNNNGATCGACATG	6614	TGCAGGACCAGAGAATTCGAATA CAACACTTCCNNNGATCGACATG	6854	TGCAGGACCAGAGAATTCGAATA CAATCCTCTGNNNGATCGACATG	7094
TGCAGGACCAGAGAATTCGAATA CAACTTTCCGNNNGATCGACATG	6615	TGCAGGACCAGAGAATTCGAATA CAGCAGTCATNNNGATCGACATG	6855	TGCAGGACCAGAGAATTCGAATA CAGTCGTCCCNNNGATCGACATG	7095
TGCAGGACCAGAGAATTCGAATA CACTCCTCTTNNNGATCGACATG	6616	TGCAGGACCAGAGAATTCGAATA CACCATATGGNNNGATCGACATG	6856	TGCAGGACCAGAGAATTCGAATA CAACTTGCAGNNNGATCGACATG	7096
TGCAGGACCAGAGAATTCGAATA CAAGATAATGNNNGATCGACATG	6617	TGCAGGACCAGAGAATTCGAATA CAATGCGCCGNNNGATCGACATG	6857	TGCAGGACCAGAGAATTCGAATA CAGAGCGCTCNNNGATCGACATG	7097
TGCAGGACCAGAGAATTCGAATA CACAGCCCTCNNNGATCGACATG	6618	TGCAGGACCAGAGAATTCGAATA CAGTTGAACCNNNGATCGACATG	6858	TGCAGGACCAGAGAATTCGAATA CATCGCCAGGNNNGATCGACATG	7098
TGCAGGACCAGAGAATTCGAATA CACGTAATTANNNGATCGACATG	6619	TGCAGGACCAGAGAATTCGAATA CAAAGGTTGGNNNGATCGACATG	6859	TGCAGGACCAGAGAATTCGAATA CACGATGCCGNNNGATCGACATG	7099
TGCAGGACCAGAGAATTCGAATA CAGTTCGTTCNNNGATCGACATG	6620	TGCAGGACCAGAGAATTCGAATA CAGCACGCTGNNNGATCGACATG	6860	TGCAGGACCAGAGAATTCGAATA CAACCCCCACNNNGATCGACATG	7100

图21D

池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATTCCGTCANNNGATCGACATG	6621	TGCAGGACCAGAGAATTCGAATA CAGCTCATAGNNNGATCGACATG	6861	TGCAGGACCAGAGAATTCGAATA CATCATTTCANNNGATCGACATG	7101
TGCAGGACCAGAGAATTCGAATA CAACGACGTTNNNGATCGACATG	6622	TGCAGGACCAGAGAATTCGAATA CAACAGTCTGNNNGATCGACATG	6862	TGCAGGACCAGAGAATTCGAATA CATGCCGGTGNNNGATCGACATG	7102
TGCAGGACCAGAGAATTCGAATA CAAAGTAGCGNNNGATCGACATG	6623	TGCAGGACCAGAGAATTCGAATA CATTTAAGTGNNNGATCGACATG	6863	TGCAGGACCAGAGAATTCGAATA CACGCAAGAANNNGATCGACATG	7103
TGCAGGACCAGAGAATTCGAATA CAAGTGAAGCNNNGATCGACATG	6624	TGCAGGACCAGAGAATTCGAATA CAGATTAATCNNNGATCGACATG	6864	TGCAGGACCAGAGAATTCGAATA CATAGACCACNNNGATCGACATG	7104
TGCAGGACCAGAGAATTCGAATA CATTCTCATANNNGATCGACATG	6625	TGCAGGACCAGAGAATTCGAATA CAGAGMAAGGNNNGATCGACATG	6865	TGCAGGACCAGAGAATTCGAATA CAACCGAAGANNNGATCGACATG	7105
TGCAGGACCAGAGAATTCGAATA CAAGTAGAGCNNNGATCGACATG	6626	TGCAGGACCAGAGAATTCGAATA CAACATTCGGNNNGATCGACATG	6866	TGCAGGACCAGAGAATTCGAATA CATCTTGTTANNNGATCGACATG	7106
TGCAGGACCAGAGAATTCGAATA CATCCCGATTNNNGATCGACATG	6627	TGCAGGACCAGAGAATTCGAATA GATTGCGTCTNNNGATCGACATG	6867	TGCAGGACCAGAGAATTCGAATA CACAGACTGTNNNGATCGACATG	7107
TGCAGGACCAGAGAATTCGAATA CACAAGGTCTNNNGATCGACATG	6628	TGCAGGACCAGAGAATTCGAATA CAGCTCACAANNNGATCGACATG	6868	TGCAGGACCAGAGAATTCGAATA CAGATCTGCANNNGATCGACATG	7108
TGCAGGACCAGAGAATTCGAATA CAGAGTATGGNNNGATCGACATG	6629	TGCAGGACCAGAGAATTCGAATA CACGTTAACGNNNGATCGACATG	6869	TGCAGGACCAGAGAATTCGAATA CATCGAAGGANNNGATCGACATG	7109
TGCAGGACCAGAGAATTCGAATA CACCGCAGTGNNNGATCGACATG	6630	TGCAGGACCAGAGAATTCGAATA CAGTACGTTGNNNGATCGACATG	6870	TGCAGGACCAGAGAATTCGAATA CACGGAGCAGNNNGATCGACATG	7110
TGCAGGACCAGAGAATTCGAATA CAGAAGCTCTNNNGATCGACATG	6631	TGCAGGACCAGAGAATTCGAATA CATGCTCAGANNNGATCGACATG	6871	TGCAGGACCAGAGAATTCGAATA CACACCGGACNNNGATCGACATG	7111
TGCAGGACCAGAGAATTCGAATA CAGTGCAAGANNNGATCGACATG	6632	TGCAGGACCAGAGAATTCGAATA CATACCAAATNNNGATCGACATG	6872	TGCAGGACCAGAGAATTCGAATA CAATAACGTTNNNGATCGACATG	7112
TGCAGGACCAGAGAATTCGAATA CAAACGGTAGNNNGATCGACATG	6633	TGCAGGACCAGAGAATTCGAATA CACCATGATGNNNGATCGACATG	6873	TGCAGGACCAGAGAATTCGAATA CATGTCTGGANNNGATCGACATG	7113
TGCAGGACCAGAGAATTCGAATA CACTTCGACTNNNGATCGACATG	6634	TGCAGGACCAGAGAATTCGAATA CATATATGCANNNGATCGACATG	6874	TGCAGGACCAGAGAATTCGAATA CATATGGACCNNNGATCGACATG	7114
TGCAGGACCAGACAATTCGAATA CACCGACGACNNNGATCGACATG	6635	TGCAGGACCAGAGAATTCGAATA CACCGCTTATNNNGATCGACATG	6875	TGCAGGACCAGAGAATTCGAATA CACAACTTGGNNNGATCGACATG	7115
TGCAGGACCAGAGAATTCGAATA CACTACACTCNNNGATCGACATG	6636	TGCAGGACCAGAGAATTCGAATA CAGGCGTCACNNNGATCGACATG	6876	TGCAGGACCAGAGAATTCGAATA CACAATCGACNNNGATCGACATG	7116
TGCAGGACCAGAGAATTCGAATA CAAGCTAAGGNNNGATCGACATG	6637	TGCAGGACCAGAGAATTCGAATA CAGGCATAAGNNNGATCGACATG	6877	TGCAGGACCAGAGAATTCGAATA CAGCAAGCGGNNNGATCGACATG	7117
TGCAGGACCAGAGAATTCGAATA CAGAGTATCCNNNGATCGACATG	6638	TGCAGGACCAGAGAATTCGAATA CAGAATTTGTNNNGATCGACATG	6878	TGCAGGACCAGAGAATTCGAATA CAGCCAACGCNNNGATCGACATG	7118
TGCAGGACCAGAGAATTCGAATA CATCCTACCANNNGATCGACATG	6639	TGCAGGACCAGAGAATTCGAATA CATCTTGACCNNNGATCGACATG	6879	TGCAGGACCAGAGAATTCGAATA CATCGTTAAANNNGATCGACATG	7119
TGCAGGACCAGAGAATTCGAATA CATTTTTCTCNNNGATCGACATG	6640	TGCAGGACCAGAGAATTCGAATA CAACACCTAGNNNGATCGACATG	6880	TGCAGGACCAGAGAATTCGAATA CACTAGCGTANNNGATCGACATG	7120
TGCAGGACCAGAGAATTCGAATA CACGGATAAGNNNGATCGACATG	6641	TGCAGGACCAGAGAATTCGAATA CAATCTCACCNNNGATCGACATG	6881	TGCAGGACCAGAGAATTCGAATA CACTGAGTTGNNNGATCGACATG	7121
TGCAGGACCAGAGAATTCGAATA CACAAATCGCNNNGATCGACATG	6642	TGCAGGACCAGAGAATTCGAATA CATTGAGATTNNNGATCGACATG	6882	TGCAGGACCAGAGAATTCGAATA CATGGCGCGTNNNGATCGACATG	7122
TGCAGGACCAGAGAATTCGAATA CAGTGTCGGCNNNGATCGACATG	6643	TGCAGGACCAGAGAATTCGAATA CATCAACCAGNNNGATCGACATG	6883	TGCAGGACCAGAGAATTCGAATA CAGTGACTTGNNNGATCGACATG	7123
TGCAGGACCAGACAATTCGAATA CAAAGCTATTNNNGATCGACATG	6644	TGCAGGACCAGAGAATTCGAATA CATTTGACGGNNNGATCGACATG	6884	TGCAGGACCAGAGAATTCGAATA CACTGCGAATNNNGATCGACATG	7124
TGCAGGACCAGAGAATTCGAATA CAACCGGACCNNNGATCGACATG	6645	TGCAGGACCAGAGAATTCGAATA CAGTTCATTTNNNGATCGACATG	6885	TGCAGGACCAGAGAATTCGAATA CACATGACACNNNGATCGACATG	7125
TGCAGGACCAGAGAATTCGAATA CATTAAATGCNNNGATCGACATG	6646	TGCAGGACCAGAGAATTCGAATA CAGAGTGGTANNNGATCGACATG	6886	TGCAGGACCAGAGAATTCGAATA CAGCGATTTGNNNGATCGACATG	7126
TGCAGGACCAGAGAATTCGAATA CACTGCAAGTNNNGATCGACATG	6647	TGCAGGACCAGAGAATTCGAATA CAAGTTGCTGNNNGATCGACATG	6887	TGCAGGACCAGAGAATTCGAATA CAACTAGGAGNNNGATCGACATG	7127
TGCAGGACCAGAGAATTCGAATA CACCCTTAACNNNGATCGACATG	6648	TGCAGGACCAGAGAATTCGAATA CAGATTTTAGNNNGATCGACATG	6888	TGCAGGACCAGAGAATTCGAATA CAGCGCAGCTNNNGATCGACATG	7128
TGCAGGACCAGAGAATTCGAATA CAAGTGAGACNNNGATCGACATG	6649	TGCAGGACCAGAGAATTCGAATA CACTAACAATNNNGATCGACATG	6889	TGCAGGACCAGAGAATTCGAATA CACACAGCCGNNNGATCGACATG	7129
TGCAGGACCAGAGAATTCGAATA CATATTAGACNNNGATCGACATG	6650	TGCAGGACCAGAGAATTCGAATA CAAGCTGATCNNNGATCGACATG	6890	TGCAGGACCAGAGAATTCGAATA CAGCCTTGTTNNNGATCGACATG	7130
TGCAGGACCAGAGAATTCGAATA CAGTTGGCTANNNGATCGACATG	6651	TGCAGGACCAGAGAATTCGAATA CACGACGGCTNNNGATCGACATG	6891	TGCAGGACCAGAGAATTCGAATA CAAATATCGTNNNGATCGACATG	7131
TGCAGGACCAGAGAATTCGAATA CATCGCTAAGNNNGATCGACATG	6652	TGCAGGACCAGAGAATTCGAATA CACGGCGTACNNNGATCGACATG	6892	TGCAGGACCAGAGAATTCGAATA CACCGAAAGANNNGATCGACATG	7132
TGCAGGACCAGAGAATTCGAATA CAAGCCCCTCNNNGATCGACATG	6653	TGCAGGACCAGAGAATTCGAATA CATTGCAGGTNNNGATCGACATG	6893	TGCAGGACCAGAGAATTCGAATA CACAAAGGTGNNNGATCGACATG	7133

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池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATTACGAATNNNGATCGACATG	6654	TGCAGGACCAGAGAATTCGAATA CATGAGCTGTNNNGATCGACATG	6894	TGCAGGACCAGAGAATTCGAATA CAAAATCCATNNNGATCGACATG	7134
TGCAGGACCAGAGAATTCGAATA CAGGCCACCANNNGATCGACATG	6655	TGCAGGACCAGAGAATTCGAATA CAAGTCTCAGNNNGATCGACATG	6895	TGCAGGACCAGAGAATTCGAATA CAAACAATCTNNNGATCGACATG	7135
TGCAGGACCAGAGAATTCGAATA CATCCTTATANNNGATCGACATG	6656	TGCAGGACCAGAGAATTCGAATA CAATTCCTTANNNGATCGACATG	6896	TGCAGGACCAGAGAATTCGAATA CACATTGGCANNNGATCGACATG	7136
TGCAGGACCAGAGAATTCGAATA CATCAGTCTCNNNGATCGACATG	6657	TGCAGGACCAGAGAATTCGAATA CAGAGAGAGANNNGATCGACATG	6897	TGCAGGACCAGAGAATTCGAATA CACTACAACGNNNGATCGACATG	7137
TGCAGGACCAGAGAATTCGAATA CACGACTTCTNNNGATCGACATG	6658	TGCAGGACCAGAGAATTCGAATA CAGCAGAGCGNNNGATCGACATG	6898	TGCAGGACCAGAGAATTCGAATA CAATCGAGAGNNNGATCGACATG	7138
TGCAGGACCAGAGAATTCGAATA CAAGGTAACGNNNGATCGACATG	6659	TGCAGGACCAGAGAATTCGAATA CAGGCACTATNNNGATCGACATG	6899	TGCAGGACCAGAGAATTCGAATA CACGCGTCCTNNNGATCGACATG	7139
TGCAGGACCAGAGAATTCGAATA CAAGACACTCNNNGATCGACATG	6660	TGCAGGACCAGAGAATTCGAATA CAGACCTCAANNNGATCGACATG	6900	TGCAGGACCAGAGAATTCGAATA CATTACGTTTNNNGATCGACATG	7140
TGCAGGACCAGAGAATTCGAATA CAGGCTTCGGNNNGATCGACATG	6661	TGCAGGACCAGAGAATTCGAATA CAAATAACTCNNNGATCGACATG	6901	TGCAGGACCAGAGAATTCGAATA CAGTAGTCGTNNNGATCGACATG	7141
TGCAGGACCAGAGAATTCGAATA CACAATTCGGNNNGATCGACATG	6662	TGCAGGACCAGAGAATTCGAATA CATCATATTCNNNGATCGACATG	6902	TGCAGGACCAGAGAATTCGAATA CATGCCTCGCNNNGATCGACATG	7142
TGCAGGACCAGAGAATTCGAATA CAGGCTCTGGNNNGATCGACATG	6663	TGCAGGACCAGAGAATTCGAATA CAGATAGAATNNNGATCGACATG	6903	TGCAGGACCAGAGAATTCGAATA CAATACATTGNNNGATCGACATG	7143
TGCAGGACCAGAGAATTCGAATA CATCTCTGACNNNGATCGACATG	6664	TGCAGGACCAGAGAATTCGAATA CACCTGGACGNNNGATCGACATG	6904	TGCAGGACCAGAGAATTCGAATA CATATAAAAANNNGATCGACATG	7144
TGCAGGACCAGAGAATTCGAATA CAGAGTAGGTNNNGATCGACATG	6665	TGCAGGACCAGAGAATTCGAATA CATAACCCAGNNNGATCGACATG	6905	TGCAGGACCAGAGAATTCGAATA CATACCTGCTNNNGATCGACATG	7145
TGCAGGACCAGAGAATTCGAATA CAATTTTTTANNNGATCGACATG	6666	TGCAGGACCAGAGAATTCGAATA CAGCAGCCGTNNNGATCGACATG	6906	TGCAGGACCAGAGAATTCGAATA CATGAGAACGNNNGATCGACATG	7146
TGCAGGACCAGAGAATTCGAATA CAATTTCTACNNNGATCGACATG	6667	TGCAGGACCAGAGAATTCGAATA CACAGACCGCNNNGATCGACATG	6907	TGCAGGACCAGAGAATTCGAATA CAGGAACTGANNNGATCGACATG	7147
TGCAGGACCAGAGAATTCGAATA CAAACGCTGTNNNGATCGACATG	6668	TGCAGGACCAGAGAATTCGAATA CATTAAGAAGNNNGATCGACATG	6908	TGCAGGACCAGAGAATTCGAATA CAAGAGCGCGNNNGATCGACATG	7148
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TGCAGGACCAGAGAATTCGAATA CATAACGATTNNNTGCATCAGGT	6670	TGCAGGACCAGAGAATTCGAATA CACCACAGGCNNNTGCATCAGGT	6910	TGCAGGACCAGAGAATTCGAATA CATCCCCTAANNNTGCATCAGGT	7150
TGCAGGACCAGAGAATTCGAATA CAGCCCAGCANNNTGCATCAGGT	6671	TGCAGGACCAGAGAATTCGAATA CAGTCAGGCCNNNTGCATCAGGT	6911	TGCAGGACCAGAGAATTCGAATA CATCGGCATANNNTGCATCAGGT	7151
TGCAGGACCAGAGAATTCGAATA CAACAAACGGNNNTGCATCAGGT	6672	TGCAGGACCAGAGAATTCGAATA CAGTCGGCACNNNTGCATCAGGT	6912	TGCAGGACCAGAGAATTCGAATA CACGCCTCCANNNTGCATCAGGT	7152
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TGCAGGACCAGAGAATTCGAATA CACGGATCGCNNNTGCATCAGGT	6674	TGCAGGACCAGAGAATTCGAATA CACATTATTCNNNTGCATCAGGT	6914	TGCAGGACCAGAGAATTCGAATA CAAAGGTTCCNNNTGCATCAGGT	7154
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TGCAGGACCAGAGAATTCGAATA CAACCTAAATNNNTGCATCAGGT	6676	TGCAGGACCAGAGAATTCGAATA CAAATTCTCTNNNTGCATCAGGT	6916	TGCAGGACCAGAGAATTCGAATA CAAGGCATTCNNNTGCATCAGGT	7156
TGCAGGACCAGAGAATTCGAATA CACGTATCGANNNTGCATCAGGT	6677	TGCAGGACCAGAGAATTCGAATA CAGCCATCGGNNNTGCATCAGGT	6917	TGCAGGACCAGAGAATTCGAATA CACACCAGCGNNNTGCATCAGGT	7157
TGCAGGACCAGAGAATTCGAATA CATCAGATATNNNTGCATCAGGT	6678	TGCAGGACCAGAGAATTCGAATA CATATAATTANNNTGCATCAGGT	6918	TGCAGGACCAGAGAATTCGAATA CATATGCGTGNNNTGCATCAGGT	7158
TGCAGGACCAGAGAATTCGAATA CAGCGACCGTNNNTGCATCAGGT	6679	TGCAGGACCAGAGAATTCGAATA CAACGAACAGNNNTGCATCAGGT	6919	TGCAGGACCAGAGAATTCGAATA CAGCATAGCTNNNTGCATCAGGT	7159
TGCAGGACCAGAGAATTCGAATA CATCAGACTGNNNTGCATCAGGT	6680	TGCAGGACCAGAGAATTCGAATA CAAGGCCCGTNNNTGCATCAGGT	6920	TGCAGGACCAGAGAATTCGAATA CATCACTAGGNNNTGCATCAGGT	7160
TGCAGGACCAGAGAATTCGAATA CAATGCACGTNNNTGCATCAGGT	6681	TGCAGGACCAGAGAATTCGAATA CACAAAGAGCNNNTGCATCAGGT	6921	TGCAGGACCAGAGAATTCGAATA CAGCCGAGCTNNNTGCATCAGGT	7161
TGCAGGACCAGAGAATTCGAATA CATCTACTGCNNNTGCATCAGGT	6682	TGCAGGACCAGAGAATTCGAATA CATTCAGGACNNNTGCATCAGGT	6922	TGCAGGACCAGAGAATTCGAATA CAACTGCCAANNNTGCATCAGGT	7162
TGCAGGACCAGAGAATTCGAATA CACTCGTTGTNNNTGCATCAGGT	6683	TGCAGGACCAGAGAATTCGAATA CAAGCACGCCNNNTGCATCAGGT	6923	TGCAGGACCAGAGAATTCGAATA CACCGACAATNNNTGCATCAGGT	7163
TGCAGGACCAGAGAATTCGAATA CACTGTGTAGNNNTGCATCAGGT	6684	TGCAGGACCAGAGAATTCGAATA CAGACACATCNNNTGCATCAGGT	6924	TGCAGGACCAGAGAATTCGAATA CACAGGCCCANNNTGCATCAGGT	7164
TGCAGGACCAGAGAATTCGAATA CAGCTTGCTTNNNTGCATCAGGT	6685	TGCAGGACCAGAGAATTCGAATA CACGATACACNNNTGCATCAGGT	6925	TGCAGGACCAGAGAATTCGAATA CACAACCCCCNNNTGCATCAGGT	7165
TGCAGGACCAGAGAATTCGAATA CACTTTTCTTNNNTGCATCAGGT	6686	TGCAGGACCAGAGAATTCGAATA CAATACGCGTNNNTGCATCAGGT	6926	TGCAGGACCAGAGAATTCGAATA CAAAGACGACNNNTGCATCAGGT	7166

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池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
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TGCAGGACCAGAGAATTCGAATA CAATCCAGCANNNTGCATCAGGT	6688	TGCAGGACCAGAGAATTCGAATA CACTCTCTCTNNNTGCATCAGGT	6928	TGCAGGACCAGAGAATTCGAATA CAATAGGCCTNNNTGCATCAGGT	7168
TGCAGGACCAGAGAATTCGAATA CAAACCGCTANNNTGCATCAGGT	6689	TGCAGGACCAGAGAATTCGAATA CACAATGAGGNNNTGCATCAGGT	6929	TGCAGGACCAGAGAATTCGAATA CATTGGATATNNNTGCATCAGGT	7169
TGCAGGACCAGAGAATTCGAATA CACGCCTGTCNNNTGCATCAGGT	6690	TGCAGGACCAGAGAATTCGAATA CACACAGTGTNNNTGCATCAGGT	6930	TGCAGGACCAGAGAATTCGAATA CACTATCGCTNNNTGCATCAGGT	7170
TGCAGGACCAGAGAATTCGAATA CATAAGGCCTNNNTGCATCAGGT	6691	TGCAGGACCAGAGAATTCGAATA CAAACATACTNNNTGCATCAGGT	6931	TGCAGGACCAGAGAATTCGAATA CACTCTTGACNNNTGCATCAGGT	7171
TGCAGGACCAGAGAATTCGAATA CATGTCATGGNNNTGCATCAGGT	6692	TGCAGGACCAGAGAATTCGAATA CACGGCATCGNNNTGCATCAGGT	6932	TGCAGGACCAGAGAATTCGAATA CAAATTAGGANNNTGCATCAGGT	7172
TGCAGGACCAGAGAATTCGAATA CATAGCAGTCNNNTGCATCAGGT	6693	TGCAGGACCAGAGAATTCGAATA CAAGTAGATANNNTGCATCAGGT	6933	TGCAGGACCAGAGAATTCGAATA CACGTTGCTTNNNTGCATCAGGT	7173
TGCAGGACCAGAGAATTCGAATA CAGCGCTGACNNNTGCATCAGGT	6694	TGCAGGACCAGAGAATTCGAATA CAGCGATCCGNNNTGCATCAGGT	6934	TGCAGGACCAGAGAATTCGAATA CATTTCCCCTNNNTGCATCAGGT	7174
TGCAGGACCAGAGAATTCGAATA CATATATCCTNNNTGCATCAGGT	6695	TGCAGGACCAGAGAATTCGAATA CAATTAAATTNNNTGCATCAGGT	6935	TGCAGGACCAGAGAATTCGAATA CAACTACCTCNNNTGCATCAGGT	7175
TGCAGGACCAGAGAATTCGAATA CACACGAAAGNNNTGCATCAGGT	6696	TGCAGGACCAGAGAATTCGAATA CAAGATTCATNNNTGCATCAGGT	6936	TGCAGGACCAGAGAATTCGAATA CAACTCTGCTNNNTGCATCAGGT	7176
TGCAGGACCAGAGAATTCGAATA CAATAAGTCTNNNTGCATCAGGT	6697	TGCAGGACCAGAGAATTCGAATA CATCACCTGTNNNTGCATCAGGT	6937	TGCAGGACCAGAGAATTCGAATA CACTACCTCANNNTGCATCAGGT	7177
TGCAGGACCAGAGAATTCGAATA CAGCTGTCCCNNNTGCATCAGGT	6698	TGCAGGACCAGAGAATTCGAATA CACAAATACTNNNTGCATCAGGT	6938	TGCAGGACCAGAGAATTCGAATA CAACTGCTAGNNNTGCATCAGGT	7178
TGCAGGACCAGAGAATTCGAATA CAATGACCTGNNNTGCATCAGGT	6699	TGCAGGACCAGAGAATTCGAATA CATTTAGCAANNNTGCATCAGGT	6939	TGCAGGACCAGAGAATTCGAATA CACGCGCAGTNNNTGCATCAGGT	7179
TGCAGGACCAGAGAATTCGAATA CAATACCCCTNNNTGCATCAGGT	6700	TGCAGGACCAGAGAATTCGAATA CATCCTAGTGNNNTGCATCAGGT	6940	TGCAGGACCAGAGAATTCGAATA CAGGCTTTCTNNNTGCATCAGGT	7180
TGCAGGACCAGAGAATTCGAATA CATGAGGTAGNNNTGCATCAGGT	6701	TGCAGGACCAGAGAATTCGAATA CATAAAGAGTNNNTGCATCAGGT	6941	TGCAGGACCAGAGAATTCGAATA CACTGGACTANNNTGCATCAGGT	7181
TGCAGGACCAGAGAATTCGAATA CACGAATCTGNNNTGCATCAGGT	6702	TGCAGGACCAGAGAATTCGAATA CACATGCACANNNTGCATCAGGT	6942	TGCAGGACCAGAGAATTCGAATA CAACATCAGCNNNTGCATCAGGT	7182
TGCAGGACCAGAGAATTCGAATA CAGCCGACGTNNNTGCATCAGGT	6703	TGCAGGACCAGAGAATTCGAATA CATTTCAACTNNNTGCATCAGGT	6943	TGCAGGACCAGAGAATTCGAATA CATCAGTTCCNNNTGCATCAGGT	7183
TGCAGGACCAGAGAATTCGAATA CATTCAAACANNNTGCATCAGGT	6704	TGCAGGACCAGAGAATTCGAATA CACTGATGTGNNNTGCATCAGGT	6944	TGCAGGACCAGAGAATTCGAATA CATCACGATGNNNTGCATCAGGT	7184
TGCAGGACCAGAGAATTCGAATA CAAGGCTTACNNNTGCATCAGGT	6705	TGCAGGACCAGAGAATTCGAATA CACCCGTTCGNNNTGCATCAGGT	6945	TGCAGGACCAGAGAATTCGAATA CAGTATGCACNNNTGCATCAGGT	7185
TGCAGGACCAGAGAATTCGAATA CAAAAACGGCNNNTGCATCAGGT	6706	TGCAGGACCAGAGAATTCGAATA CACATAAGAANNNTGCATCAGGT	6946	TGCAGGACCAGAGAATTCGAATA CATCAGGCGCNNNTGCATCAGGT	7186
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TGCAGGACCAGAGAATTCGAATA CAATGGCGAANNNTGCATCAGGT	6708	TGCAGGACCAGAGAATTCGAATA CACTGACGATNNNTGCATCAGGT	6948	TGCAGGACCAGAGAATTCGAATA CAGGTCGGAGNNNTGCATCAGGT	7188
TGCAGGACCAGAGAATTCGAATA CAACCAAGAGNNNTGCATCAGGT	6709	TGCAGGACCAGAGAATTCGAATA CAACTTTCTANNNTGCATCAGGT	6949	TGCAGGACCAGAGAATTCGAATA CAATAAGGCGNNNTGCATCAGGT	7189
TGCAGGACCAGAGAATTCGAATA CACAAAGGCTNNNTGCATCAGGT	6710	TGCAGGACCAGAGAATTCGAATA CACACATAGCNNNTGCATCAGGT	6950	TGCAGGACCAGAGAATTCGAATA CAAGCCGACCNNNTGCATCAGGT	7190
TGCAGGACCAGAGAATTCGAATA CACGCTTTCANNNTGCATCAGGT	6711	TGCAGGACCAGAGAATTCGAATA CATTAGTCAANNNTGCATCAGGT	6951	TGCAGGACCAGAGAATTCGAATA CACATGTCAGNNNTGCATCAGGT	7191
TGCAGGACCAGAGAATTCGAATA CATCCAGGCGNNNTGCATCAGGT	6712	TGCAGGACCAGAGAATTCGAATA CATGGTCGCGNNNTGCATCAGGT	6952	TGCAGGACCAGAGAATTCGAATA CATTTTAGCTNNNTGCATCAGGT	7192
TGCAGGACCAGAGAATTCGAATA CATTGAAATCNNNTGCATCAGGT	6713	TGCAGGACCAGAGAATTCGAATA CATTCTGACCNNNTGCATCAGGT	6953	TGCAGGACCAGAGAATTCGAATA CATCGAGTTGNNNTGCATCAGGT	7193
TGCAGGACCAGAGAATTCGAATA CACCTGCTGCNNNTGCATCAGGT	6714	TGCAGGACCAGAGAATTCGAATA CATAAAACCTNNNTGCATCAGGT	6954	TGCAGGACCAGAGAATTCGAATA CAGCCACCTCNNNTGCATCAGGT	7194
TGCAGGACCAGAGAATTCGAATA CACGAATGAGNNNTGCATCAGGT	6715	TGCAGGACCAGAGAATTCGAATA CAACTATAACNNNTGCATCAGGT	6955	TGCAGGACCAGAGAATTCGAATA CATGTTGTGGNNNTGCATCAGGT	7195
TGCAGGACCAGAGAATTCGAATA CATGTGTTAANNNTGCATCAGGT	6716	TGCAGGACCAGAGAATTCGAATA CATATGATGTNNNTGCATCAGGT	6956	TGCAGGACCAGAGAATTCGAATA CAGTTGTGTGNNNTGCATCAGGT	7196
TGCAGGACCAGAGAATTCGAATA CATTCAAAACNNNTGCATCAGGT	6717	TGCAGGACCAGAGAATTCGAATA CATCACCGCCNNNTGCATCAGGT	6957	TGCAGGACCAGAGAATTCGAATA CACGTGAACTNNNTGCATCAGGT	7197
TGCAGGACCAGAGAATTCGAATA CACAGCCCAGNNNTGCATCAGGT	6718	TGCAGGACCAGAGAATTCGAATA CAAGGTTATTNNNTGCATCAGGT	6958	TGCAGGACCAGAGAATTCGAATA CAAAGGCTCTNNNTGCATCAGGT	7198
TGCAGGACCAGAGAATTCGAATA CAGACAGTAGNNNTGCATCAGGT	6719	TGCAGGACCAGAGAATTCGAATA CAAGCAGCTTNNNTGCATCAGGT	6959	TGCAGGACCAGAGAATTCGAATA CATATTCTTGNNNTGCATCAGGT	7199

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池-28	SEQ ID NO:	池-29	SEQ ID NO:	池-30	SEQ ID NO:
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TGCAGGACCAGAGAATTCGAATA CATAATCCAANNNTGCATCAGGT	6721	TGCAGGACCAGAGAATTCGAATA CACACACTTCNNNTGCATCAGGT	6961	TGCAGGACCAGAGAATTCGAATA CACCAAGACTNNNTGCATCAGGT	7201
TGCAGGACCAGAGAATTCGAATA CACGTACAACNNNTGCATCAGGT	6722	TGCAGGACCAGAGAATTCGAATA CAAAAAAACCNNNTGCATCAGGT	6962	TGCAGGACCAGAGAATTCGAATA CAAGTTCCAGNNNTGCATCAGGT	7202
TGCAGGACCAGAGAATTCGAATA CAATATTCGANNNTGCATCAGGT	6723	TGCAGGACCAGAGAATTCGAATA CATACAGCCANNNTGCATCAGGT	6963	TGCAGGACCAGAGAATTCGAATA CAAACCAGTCNNNTGCATCAGGT	7203
TGCAGGACCAGAGAATTCGAATA CATAATTATANNNTGCATCAGGT	6724	TGCAGGACCAGAGAATTCGAATA CAATGAAAACNNNTGCATCAGGT	6964	TGCAGGACCAGAGAATTCGAATA CATGGCTCAANNNTGCATCAGGT	7204
TGCAGGACCAGAGAATTCGAATA CAGATGCAGANNNTGCATCAGGT	6725	TGCAGGACCAGAGAATTCGAATA CAGTGATGCTNNNTGCATCAGGT	6965	TGCAGGACCAGAGAATTCGAATA CATCTTTATGNNNTGCATCAGGT	7205
TGCAGGACCAGAGAATTCGAATA CAGGAGCCAGNNNTGCATCAGGT	6726	TGCAGGACCAGAGAATTCGAATA CATTAACAGTNNNTGCATCAGGT	6966	TGCAGGACCAGAGAATTCGAATA CAGGTGACTTNNNTGCATCAGGT	7206
TGCAGGACCAGAGAATTCGAATA CAGCGAGTTTNNNTGCATCAGGT	6727	TGCAGGACCAGAGAATTCGAATA CACAACCGCGNNNTGCATCAGGT	6967	TGCAGGACCAGAGAATTCGAATA CATCCTAACCNNNTGCATCAGGT	7207
TGCAGGACCAGAGAATTCGAATA CAAAGTGACGNNNTGCATCAGGT	6728	TGCAGGACCAGAGAATTCGAATA CATGTGCCCCNNNTGCATCAGGT	6968	TGCAGGACCAGAGAATTCGAATA CAGCGTAAAGNNNTGCATCAGGT	7208

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池-31	SEQ ID NO:	池-32	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATAC ATGGTCCAANNNACGTATGCCA	7209	TGCAGGACCAGAGAATTCGAATA CATTCCAATTNNNACGTATGCCA	7449
TGCAGGACCAGAGAATTCGAATAC AGTACTCAGNNNACGTATGCCA	7210	TGCAGGACCAGAGAATTCGAATA CATGTACAGCNNNACGTATGCCA	7450
TGCAGGACCAGAGAATTCGAATAC AGAAGCCCCNNNACGTATGCCA	7211	TGCAGGACCAGAGAATTCGAATA CACAGGAGCGNNNACGTATGCCA	7451
TGCAGGACCAGAGAATTCGAATAC ATTAACCGGNNNACGTATGCCA	7212	TGCAGGACCAGAGAATTCGAATA CAATGCGTTGNNNACGTATGCCA	7452
TGCAGGACCAGAGAATTCGAATAC ATAACCTGGNNNACGTATGCCA	7213	TGCAGGACCAGAGAATTCGAATA CATATTTTCGNNNACGTATGCCA	7453
TGCAGGACCAGAGAATTCGAATAC AGTCGACTANNNACGTATGCCA	7214	TGCAGGACCAGAGAATTCGAATA CAAATTCCCCNNNACGTATGCCA	7454
TGCAGGACCAGAGAATTCGAATAC ACCAAACGTNNNACGTATGCCA	7215	TGCAGGACCAGAGAATTCGAATA CATCTGACGANNNACGTATGCCA	7455
TGCAGGACCAGAGAATTCGAATAC AACGTATCGNNNACGTATGCCA	7216	TGCAGGACCAGAGAATTCGAATA CACCGCGCTTNNNACGTATGCCA	7456
TGCAGGACCAGAGAATTCGAATAC ACACGGCCANNNACGTATGCCA	7217	TGCAGGACCAGAGAATTCGAATA CAAAACACCCNNNACGTATGCCA	7457
TGCAGGACCAGAGAATTCGAATAC AAGGTTTGCNNNACGTATGCCA	7218	TGCAGGACCAGAGAATTCGAATA CAGGTTGTGTNNNACGTATGCCA	7458
TGCAGGACCAGAGAATTCGAATAC ACGACGCGTNNNACGTATGCCA	7219	TGCAGGACCAGAGAATTCGAATA CAACTAACGNNNACGTATGCCA	7459
TGCAGGACCAGAGAATTCGAATAC ACCGACGTGNNNACGTATGCCA	7220	TGCAGGACCAGAGAATTCGAATA CATCAGGAGANNNACGTATGCCA	7460
TGCAGGACCAGAGAATTCGAATAC ACAGTTTTTNNNACGTATGCCA	7221	TGCAGGACCAGAGAATTCGAATA CAGTCTGCGGNNNACGTATGCCA	7461
TGCAGGACCAGAGAATTCGAATAC ATGCCCGGANNNACGTATGCCA	7222	TGCAGGACCAGAGAATTCGAATA CAACTGGCGCNNNACGTATGCCA	7462
TGCAGGACCAGAGAATTCGAATAC AGCCACTCCNNNACGTATGCCA	7223	TGCAGGACCAGAGAATTCGAATA CACGACTCTTNNNACGTATGCCA	7463
TGCAGGACCAGAGAATTCGAATAC AGACGAAGTNNNACGTATGCCA	7224	TGCAGGACCAGAGAATTCGAATA CAGCGAAGGCNNNACGTATGCCA	7464
TGCAGGACCAGAGAATTCGAATAC AGGTTCCTTNNNACGTATGCCA	7225	TGCAGGACCAGAGAATTCGAATA CAGGCGCCGCNNNACGTATGCCA	7465
TGCAGGACCAGAGAATTCGAATAC ACCGGAATTNNNACGTATGCCA	7226	TGCAGGACCAGAGAATTCGAATA CAGAGCACCCNNNACGTATGCCA	7466
TGCAGGACCAGAGAATTCGAATAC ATCGGCAGCNNNACGTATGCCA	7227	TGCAGGACCAGAGAATTCGAATA CACCCAAAGTNNNACGTATGCCA	7467
TGCAGGACCAGAGAATTCGAATAC AGCTAGAGANNNACGTATGCCA	7228	TGCAGGACCAGAGAATTCGAATA CACGGAATAGNNNACGTATGCCA	7468
TGCAGGACCAGAGAATTCGAATAC ACCACTTACNNNACGTATGCCA	7229	TGCAGGACCAGAGAATTCGAATA CAAGTAAGATNNNACGTATGCCA	7469
TGCAGGACCAGAGAATTCGAATAC AACCACCGGNNNACGTATGCCA	7230	TGCAGGACCAGAGAATTCGAATA CATCTCACACNNNACGTATGCCA	7470
TGCAGGACCAGAGAATTCGAATAC AGAAACATANNNACGTATGCCA	7231	TGCAGGACCAGAGAATTCGAATA CAGGCCCCAANNNACGTATGCCA	7471
TGCAGGACCAGAGAATTCGAATAC AGCTGAAAGNNNACGTATGCCA	7232	TGCAGGACCAGAGAATTCGAATA CAGGATTTGCNNNACGTATGCCA	7472
TGCAGGACCAGAGAATTCGAATAC ATAAGAAGTNNNACGTATGCCA	7233	TGCAGGACCAGAGAATTCGAATA CAAATGACAANNNACGTATGCCA	7473
TGCAGGACCAGAGAATTCGAATAC ACGTGACTANNNACGTATGCCA	7234	TGCAGGACCAGAGAATTCGAATA CATAAAAAATNNNACGTATGCCA	7474
TGCAGGACCAGAGAATTCGAATAC ATTAAGATCNNNACGTATGCCA	7235	TGCAGGACCAGAGAATTCGAATA CATAATGGCCNNNACGTATGCCA	7475
TGCAGGACCAGAGAATTCGAATAC ATGGATCACNNNACGTATGCCA	7236	TGCAGGACCAGAGAATTCGAATA CAGTTGCTTCNNNACGTATGCCA	7476
TGCAGGACCAGAGAATTCGAATAC ACCGAGCTGNNNACGTATGCCA	7237	TGCAGGACCAGAGAATTCGAATA CACGTTTCACNNNACGTATGCCA	7477
TGCAGGACCAGAGAATTCGAATAC ACTCATAAANNNACGTATGCCA	7238	TGCAGGACCAGAGAATTCGAATA CAGAACAAATNNNACGTATGCCA	7478
TGCAGGACCAGAGAATTCGAATAC ACTCTACTGNNNACGTATGCCA	7239	TGCAGGACCAGAGAATTCGAATA CAATAGAAGTNNNACGTATGCCA	7479
TGCAGGACCAGAGAATTCGAATAC AAGGTGAGTNNNACGTATGCCA	7240	TGCAGGACCAGAGAATTCGAATA CAGTAAGGCANNNACGTATGCCA	7480
TGCAGGACCAGAGAATTCGAATAC AGAACACTCNNNACGTATGCCA	7241	TGCAGGACCAGAGAATTCGAATA CAGAGATGCANNNACGTATGCCA	7481

图22A

池-31	SEQ ID NO:	池-32	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATAC AGGCAGAGCNNNACGTATGCCA	7242	TGCAGGACCAGAGAATTCGAATA CACACCATCTNNNACGTATGCCA	7482
TGCAGGACCAGAGAATTCGAATAC ATTTCCAGCNNNACGTATGCCA	7243	TGCAGGACCAGAGAATTCGAATA CAGATACACCNNNACGTATGCCA	7483
TGCAGGACCAGAGAATTCGAATAC ACCCATCATNNNACGTATGCCA	7244	TGCAGGACCAGAGAATTCGAATA CAGATACTGCNNNACGTATGCCA	7484
TGCAGGACCAGAGAATTCGAATAC AATCAGCGTNNNACGTATGCCA	7245	TGCAGGACCAGAGAATTCGAATA CACGTAACTGNNNACGTATGCCA	7485
TGCAGGACCAGAGAATTCGAATAC ATGAAAAACNNNACGTATGCCA	7246	TGCAGGACCAGAGAATTCGAATA CATCCTCTTCNNNACGTATGCCA	7486
TGCAGGACCAGAGAATTCGAATAC AATGCGGAANNNACGTATGCCA	7247	TGCAGGACCAGAGAATTCGAATA CATGCGGTCGNNNACGTATGCCA	7487
TGCAGGACCAGAGAATTCGAATAC ACGGATTCANNNACGTATGCCA	7248	TGCAGGACCAGAGAATTCGAATA CAACAGGAACNNNACGTATGCCA	7488
TGCAGGACCAGAGAATTCGAATAC AGTCATACGNNNACGTATGCCA	7249	TGCAGGACCAGAGAATTCGAATA CAAAAATTTTNNNACGTATGCCA	7489
TGCAGGACCAGAGAATTCGAATAC AACCTGCTTNNNACGTATGCCA	7250	TGCAGGACCAGAGAATTCGAATA CAAAGTCACCNNNACGTATGCCA	7490
TGCAGGACCAGAGAATTCGAATAC AGTTGTGCANNNACGTATGCCA	7251	TGCAGGACCAGAGAATTCGAATA CATCTACGAGNNNACGTATGCCA	7491
TGCAGGACCAGAGAATTCGAATAC AGAAATCGGNNNACGTATGCCA	7252	TGCAGGACCAGAGAATTCGAATA CAGATCTTCCNNNACGTATGCCA	7492
TGCAGGACCAGAGAATTCGAATAC AAAGTTAGANNNACGTATGCCA	7253	TGCAGGACCAGAGAATTCGAATA CAGGACACCCNNNACGTATGCCA	7493
TGCAGGACCAGAGAATTCGAATAC ATGTAACGCNNNACGTATGCCA	7254	TGCAGGACCAGAGAATTCGAATA CAATAGGTGGNNNACGTATGCCA	7494
TGCAGGACCAGAGAATTCGAATAC AGTTTTGAANNNACGTATGCCA	7255	TGCAGGACCAGAGAATTCGAATA CACCATCGCCNNNACGTATGCCA	7495
TGCAGGACCAGAGAATTCGAATAC ACAAACTGCNNNACGTATGCCA	7256	TGCAGGACCAGAGAATTCGAATA CATGATCTCCNNNACGTATGCCA	7496
TGCAGGACCAGAGAATTCGAATAC AGCCTGAGCNNNACGTATGCCA	7257	TGCAGGACCAGAGAATTCGAATA CACGCGAATTNNNACGTATGCCA	7497
TGCAGGACCAGAGAATTCGAATAC ATCTTCCAGNNNACGTATGCCA	7258	TGCAGGACCAGAGAATTCGAATA CATATATAATNNNACGTATGCCA	7498
TGCAGGACCAGAGAATTCGAATAC ATACCCTACNNNACGTATGCCA	7259	TGCAGGACCAGAGAATTCGAATA CATATCGCCTNNNACGTATGCCA	7499
TGCAGGACCAGAGAATTCGAATAC ATCATAGATNNNACGTATGCCA	7260	TGCAGGACCAGAGAATTCGAATA CATTACGAGCNNNACGTATGCCA	7500
TGCAGGACCAGAGAATTCGAATAC AGTATAGAANNNACGTATGCCA	7261	TGCAGGACCAGAGAATTCGAATA CAGGTTTCTCNNNACGTATGCCA	7501
TGCAGGACCAGAGAATTCGAATAC ACCCTAAAGNNNACGTATGCCA	7262	TGCAGGACCAGAGAATTCGAATA CACTTGCAGANNNACGTATGCCA	7502
TGCAGGACCAGAGAATTCGAATAC AGCGGTTTANNNACGTATGCCA	7263	TGCAGGACCAGAGAATTCGAATA CAGACATTTANNNACGTATGCCA	7503
TGCAGGACCAGAGAATTCGAATAC ATAGCTCAGNNNACGTATGCCA	7264	TGCAGGACCAGAGAATTCGAATA CAACACGAGANNNACGTATGCCA	7504
TGCAGGACCAGAGAATTCGAATAC ACCGTCCCANNNACGTATGCCA	7265	TGCAGGACCAGAGAATTCGAATA CATTGCCCGCNNNACGTATGCCA	7505
TGCAGGACCAGAGAATTCGAATAC AAGTGCGAANNNACGTATGCCA	7266	TGCAGGACCAGAGAATTCGAATA CACAGTCCTTNNNACGTATGCCA	7506
TGCAGGACCAGAGAATTCGAATAC ATGAGCTTGNNNACGTATGCCA	7267	TGCAGGACCAGAGAATTCGAATA CAGCATTTGGNNNACGTATGCCA	7507
TGCAGGACCAGAGAATTCGAATAC ATATCGTGGNNNACGTATGCCA	7268	TGCAGGACCAGAGAATTCGAATA CAGGATATCCNNNACGTATGCCA	7508
TGCAGGACCAGAGAATTCGAATAC ATCAGACACNNNCTAGCGTTAC	7269	TGCAGGACCAGAGAATTCGAATA CACCAGGAGGNNNCTAGCGTTAC	7509
TGCAGGACCAGAGAATTCGAATAC ATACCCTTGNNNCTAGCGTTAC	7270	TGCAGGACCAGAGAATTCGAATA CATCGCCTTANNNCTAGCGTTAC	7510
TGCAGGACCAGAGAATTCGAATAC ACATCGAGTNNNCTAGCGTTAC	7271	TGCAGGACCAGAGAATTCGAATA CATTACCCGTNNNCTAGCGTTAC	7511
TGCAGGACCAGAGAATTCGAATAC ATGAATCTANNNCTAGCGTTAC	7272	TGCAGGACCAGAGAATTCGAATA CAATCACCTCNNNCTAGCGTTAC	7512
TGCAGGACCAGAGAATTCGAATAC AAGTGGAGTNNNCTAGCGTTAC	7273	TGCAGGACCAGAGAATTCGAATA CACCAATTCCNNNCTAGCGTTAC	7513
TGCAGGACCAGAGAATTCGAATAC ACTGAAGGANNNCTAGCGTTAC	7274	TGCAGGACCAGAGAATTCGAATA CATGCGTGATNNNCTAGCGTTAC	7514

图22B

池-31	SEQ ID NO:	池-32	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATAC AAATCAGTTNNNCTAGCGTTAC	7275	TGCAGGACCAGAGAATTCGAATA CACTCGGCCTNNNCTAGCGTTAC	7515
TGCAGGACCAGAGAATTCGAATAC ACGCAGGCTNNNCTAGCGTTAC	7276	TGCAGGACCAGAGAATTCGAATA CAAGGAATTANNNCTAGCGTTAC	7516
TGCAGGACCAGAGAATTCGAATAC ACGGTGCACNNNCTAGCGTTAC	7277	TGCAGGACCAGAGAATTCGAATA CACCCTACATNNNCTAGCGTTAC	7517
TGCAGGACCAGAGAATTCGAATAC ACGTATCAGNNNCTAGCGTTAC	7278	TGCAGGACCAGAGAATTCGAATA CACGGTTTAGNNNCTAGCGTTAC	7518
TGCAGGACCAGAGAATTCGAATAC ATAACGCTGNNNCTAGCGTTAC	7279	TGCAGGACCAGAGAATTCGAATA CATCGTATAANNNCTAGCGTTAC	7519
TGCAGGACCAGAGAATTCGAATAC AACCGTACANNNCTAGCGTTAC	7280	TGCAGGACCAGAGAATTCGAATA CATAAGCAAANNNCTAGCGTTAC	7520
TGCAGGACCAGAGAATTCGAATAC AGCTTAGTGNNNCTAGCGTTAC	7281	TGCAGGACCAGAGAATTCGAATA CACGGTCTGGNNNCTAGCGTTAC	7521
TGCAGGACCAGAGAATTCGAATAC ACGAACGCCNNNCTAGCGTTAC	7282	TGCAGGACCAGAGAATTCGAATA CACCACAGTANNNCTAGCGTTAC	7522
TGCAGGACCAGAGAATTCGAATAC AGTATCGTGNNNCTAGCGTTAC	7283	TGCAGGACCAGAGAATTCGAATA CAACCACTAGNNNCTAGCGTTAC	7523
TGCAGGACCAGAGAATTCGAATAC ATACAAATCNNNCTAGCGTTAC	7284	TGCAGGACCAGAGAATTCGAATA CACGCAAACTNNNCTAGCGTTAC	7524
TGCAGGACCAGAGAATTCGAATAC ACGTCCTTANNNCTAGCGTTAC	7285	TGCAGGACCAGAGAATTCGAATA CACTTCAACCNNNCTAGCGTTAC	7525
TGCAGGACCAGAGAATTCGAATAC AAGACCACTNNNCTAGCGTTAC	7286	TGCAGGACCAGAGAATTCGAATA CAGAGAGGCCNNNCTAGCGTTAC	7526
TGCAGGACCAGAGAATTCGAATAC AACAAGGTGNNNCTAGCGTTAC	7287	TGCAGGACCAGAGAATTCGAATA CAATATTGGTNNNCTAGCGTTAC	7527
TGCAGGACCAGAGAATTCGAATAC AATACTTGANNNCTAGCGTTAC	7288	TGCAGGACCAGAGAATTCGAATA CACTATATGANNNCTAGCGTTAC	7528
TGCAGGACCAGAGAATTCGAATAC ACTTCCGATNNNCTAGCGTTAC	7289	TGCAGGACCAGAGAATTCGAATA CAATCTTGTTNNNCTAGCGTTAC	7529
TGCAGGACCAGAGAATTCGAATAC ACGTCTTGTNNNCTAGCGTTAC	7290	TGCAGGACCAGAGAATTCGAATA CATAAAGGCGNNNCTAGCGTTAC	7530
TGCAGGACCAGAGAATTCGAATAC AAAGTGGTGNNNCTAGCGTTAC	7291	TGCAGGACCAGAGAATTCGAATA CACCATTTGCNNNCTAGCGTTAC	7531
TGCAGGACCAGAGAATTCGAATAC ATCGGTGGCNNNCTAGCGTTAC	7292	TGCAGGACCAGAGAATTCGAATA CATACCCCTANNNCTAGCGTTAC	7532
TGCAGGACCAGAGAATTCGAATAC AAAAATCAGNNNCTAGCGTTAC	7293	TGCAGGACCAGAGAATTCGAATA CAAGAACCGANNNCTAGCGTTAC	7533
TGCAGGACCAGAGAATTCGAATAC ATCCCGCGTNNNCTAGCGTTAC	7294	TGCAGGACCAGAGAATTCGAATA CAACGATAGGNNNCTAGCGTTAC	7534
TGCAGGACCAGAGAATTCGAATAC AGGCACGCTNNNCTAGCGTTAC	7295	TGCAGGACCAGAGAATTCGAATA CAGGCGCCATNNNCTAGCGTTAC	7535
TGCAGGACCAGAGAATTCGAATAC AGCTGTCTTNNNCTAGCGTTAC	7296	TGCAGGACCAGAGAATTCGAATA CAAAAATCTCNNNCTAGCGTTAC	7536
TGCAGGACCAGAGAATTCGAATAC AAGCATAAANNNCTAGCGTTAC	7297	TGCAGGACCAGAGAATTCGAATA CAGACTAGCTNNNCTAGCGTTAC	7537
TGCAGGACCAGAGAATTCGAATAC ATGCGAATCNNNCTAGCGTTAC	7298	TGCAGGACCAGAGAATTCGAATA CACGTGAGTTNNNCTAGCGTTAC	7538
TGCAGGACCAGAGAATTCGAATAC ACGTTTCGTNNNCTAGCGTTAC	7299	TGCAGGACCAGAGAATTCGAATA CACCCGCTGTNNNCTAGCGTTAC	7539
TGCAGGACCAGAGAATTCGAATAC AGCACTCTTNNNCTAGCGTTAC	7300	TGCAGGACCAGAGAATTCGAATA CAAAAACTTCNNNCTAGCGTTAC	7540
TGCAGGACCAGAGAATTCGAATAC ACTCGCTGCNNNCTAGCGTTAC	7301	TGCAGGACCAGAGAATTCGAATA CAAGTAACGGNNNCTAGCGTTAC	7541
TGCAGGACCAGAGAATTCGAATAC ACATACAGCNNNCTAGCGTTAC	7302	TGCAGGACCAGAGAATTCGAATA CAATCAACATNNNCTAGCGTTAC	7542
TGCAGGACCAGAGAATTCGAATAC AGAGCAAACNNNCTAGCGTTAC	7303	TGCAGGACCAGAGAATTCGAATA CACTTTTGATNNNCTAGCGTTAC	7543
TGCAGGACCAGAGAATTCGAATAC AGCTTCCATNNNCTAGCGTTAC	7304	TGCAGGACCAGAGAATTCGAATA CAGTGTACCANNNCTAGCGTTAC	7544
TGCAGGACCAGAGAATTCGAATAC ACCTAATTTNNNCTAGCGTTAC	7305	TGCAGGACCAGAGAATTCGAATA CATGCACACANNNCTAGCGTTAC	7545
TGCAGGACCAGAGAATTCGAATAC AAGCCCGACNNNCTAGCGTTAC	7306	TGCAGGACCAGAGAATTCGAATA CATATACTTCNNNCTAGCGTTAC	7546
TGCAGGACCAGAGAATTCGAATAC ATGGTGAAGNNNCTAGCGTTAC	7307	TGCAGGACCAGAGAATTCGAATA CAGAAACTAANNNCTAGCGTTAC	7547

图22C

池-31	SEQ ID NO:	池-32	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATAC AATCGCTGANNNCTAGCGTTAC	7308	TGCAGGACCAGAGAATTCGAATA CAATCTCGAGNNNCTAGCGTTAC	7548
TGCAGGACCAGAGAATTCGAATAC ATTACTGCCNNNCTAGCGTTAC	7309	TGCAGGACCAGAGAATTCGAATA CAATGTCTGGNNNCTAGCGTTAC	7549
TGCAGGACCAGAGAATTCGAATAC AGGAGGCCANNNCTAGCGTTAC	7310	TGCAGGACCAGAGAATTCGAATA CAAGACATGGNNNCTAGCGTTAC	7550
TGCAGGACCAGAGAATTCGAATAC ATACCTGTCNNNCTAGCGTTAC	7311	TGCAGGACCAGAGAATTCGAATA CACGGCAATTNNNCTAGCGTTAC	7551
TGCAGGACCAGAGAATTCGAATAC AATATGCTANNNCTAGCGTTAC	7312	TGCAGGACCAGAGAATTCGAATA CATAATGTTGNNNCTAGCGTTAC	7552
TGCAGGACCAGAGAATTCGAATAC AGATCACCANNNCTAGCGTTAC	7313	TGCAGGACCAGAGAATTCGAATA CAGCGAGGACNNNCTAGCGTTAC	7553
TGCAGGACCAGAGAATTCGAATAC AGCGGAACGNNNCTAGCGTTAC	7314	TGCAGGACCAGAGAATTCGAATA CACGAACATCNNNCTAGCGTTAC	7554
TGCAGGACCAGAGAATTCGAATAC AAATCCTTTNNNCTAGCGTTAC	7315	TGCAGGACCAGAGAATTCGAATA CAGCATGTACNNNCTAGCGTTAC	7555
TGCAGGACCAGAGAATTCGAATAC ATACTATAGNNNCTAGCGTTAC	7316	TGCAGGACCAGAGAATTCGAATA CAGCAACTGTNNNCTAGCGTTAC	7556
TGCAGGACCAGAGAATTCGAATAC AGTCTGTAGNNNCTAGCGTTAC	7317	TGCAGGACCAGAGAATTCGAATA CAGTACTCTCNNNCTAGCGTTAC	7557
TGCAGGACCAGAGAATTCGAATAC AGACTATCGNNNCTAGCGTTAC	7318	TGCAGGACCAGAGAATTCGAATA CAGGCTAAAGNNNCTAGCGTTAC	7558
TGCAGGACCAGAGAATTCGAATAC AAGGATTAANNNCTAGCGTTAC	7319	TGCAGGACCAGAGAATTCGAATA CACCCTTTGANNNCTAGCGTTAC	7559
TGCAGGACCAGAGAATTCGAATAC ATTACATCTNNNCTAGCGTTAC	7320	TGCAGGACCAGAGAATTCGAATA CACGCAGGAGNNNCTAGCGTTAC	7560
TGCAGGACCAGAGAATTCGAATAC ATTTGGCAGNNNCTAGCGTTAC	7321	TGCAGGACCAGAGAATTCGAATA CAGTAAGAATNNNCTAGCGTTAC	7561
TGCAGGACCAGAGAATTCGAATAC ACAGTATGCNNNCTAGCGTTAC	7322	TGCAGGACCAGAGAATTCGAATA CATGATTACANNNCTAGCGTTAC	7562
TGCAGGACCAGAGAATTCGAATAC ATTCGATCCNNNCTAGCGTTAC	7323	TGCAGGACCAGAGAATTCGAATA CACAAAAATGNNNCTAGCGTTAC	7563
TGCAGGACCAGAGAATTCGAATAC AAATCCCCTNNNCTAGCGTTAC	7324	TGCAGGACCAGAGAATTCGAATA CACCGTGGTGNNNCTAGCGTTAC	7564
TGCAGGACCAGAGAATTCGAATAC ACTCTCCCCNNNCTAGCGTTAC	7325	TGCAGGACCAGAGAATTCGAATA CAAACGTTATNNNCTAGCGTTAC	7565
TGCAGGACCAGAGAATTCGAATAC ACAATTAACNNNCTAGCGTTAC	7326	TGCAGGACCAGAGAATTCGAATA CAGCTTGCAANNNCTAGCGTTAC	7566
TGCAGGACCAGAGAATTCGAATAC AATTTTGCTNNNCTAGCGTTAC	7327	TGCAGGACCAGAGAATTCGAATA CATTAGTCGGNNNCTAGCGTTAC	7567
TGCAGGACCAGAGAATTCGAATAC AATAAATCCNNNCTAGCGTTAC	7328	TGCAGGACCAGAGAATTCGAATA CAACGGCCGTNNNCTAGCGTTAC	7568
TGCAGGACCAGAGAATTCGAATAC ATACTCGTCNNNGATCGACATG	7329	TGCAGGACCAGAGAATTCGAATA CAGCGTGAAANNNGATCGACATG	7569
TGCAGGACCAGAGAATTCGAATAC AATGCGAAGNNNGATCGACATG	7330	TGCAGGACCAGAGAATTCGAATA CATGCCTGCCNNNGATCGACATG	7570
TGCAGGACCAGAGAATTCGAATAC ATGCGCAGCNNNGATCGACATG	7331	TGCAGGACCAGAGAATTCGAATA CATCGACGCGNNNGATCGACATG	7571
TGCAGGACCAGAGAATTCGAATAC ATGGTAAAANNNGATCGACATG	7332	TGCAGGACCAGAGAATTCGAATA CATCATCCTGNNNGATCGACATG	7572
TGCAGGACCAGAGAATTCGAATAC ACACTCCATNNNGATCGACATG	7333	TGCAGGACCAGAGAATTCGAATA CAGTCAGTCANNNGATCGACATG	7573
TGCAGGACCAGAGAATTCGAATAC ACCTATGGANNNGATCGACATG	7334	TGCAGGACCAGAGAATTCGAATA CACCGGTGACNNNGATCGACATG	7574
TGCAGGACCAGAGAATTCGAATAC AATGCTGCTNNNGATCGACATG	7335	TGCAGGACCAGAGAATTCGAATA CATATCGCGANNNGATCGACATG	7575
TGCAGGACCAGAGAATTCGAATAC AGATTGAAANNNGATCGACATG	7336	TGCAGGACCAGAGAATTCGAATA CAGACGCGTCNNNGATCGACATG	7576
TGCAGGACCAGAGAATTCGAATAC AACACCCAANNNGATCGACATG	7337	TGCAGGACCAGAGAATTCGAATA CAGAACAGACNNNGATCGACATG	7577
TGCAGGACCAGAGAATTCGAATAC ACCGGCATGNNNGATCGACATG	7338	TGCAGGACCAGAGAATTCGAATA CAGTGTGTGTNNNGATCGACATG	7578
TGCAGGACCAGAGAATTCGAATAC ATCCGATTCNNNGATCGACATG	7339	TGCAGGACCAGAGAATTCGAATA CAGATTGCGTNNNGATCGACATG	7579
TGCAGGACCAGAGAATTCGAATAC AGAATCCTGNNNGATCGACATG	7340	TGCAGGACCAGAGAATTCGAATA CAGTAGATTTNNNGATCGACATG	7580

图22D

池-31	SEQ ID NO:	池-32	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATAC ATTTCGTCGNNNGATCGACATG	7341	TGCAGGACCAGAGAATTCGAATA CAGCTTGAGTNNNGATCGACATG	7581
TGCAGGACCAGAGAATTCGAATAC ACTTCACTGNNNGATCGACATG	7342	TGCAGGACCAGAGAATTCGAATA CACGCAACGCNNNGATCGACATG	7582
TGCAGGACCAGAGAATTCGAATAC ACCCTATTGNNNGATCGACATG	7343	TGCAGGACCAGAGAATTCGAATA CACCTAATGGNNNGATCGACATG	7583
TGCAGGACCAGAGAATTCGAATAC AAGTAGTAANNNGATCGACATG	7344	TGCAGGACCAGAGAATTCGAATA CAGACAGGATNNNGATCGACATG	7584
TGCAGGACCAGAGAATTCGAATAC ACACCGTAANNNGATCGACATG	7345	TGCAGGACCAGAGAATTCGAATA CACTTCCCTTNNNGATCGACATG	7585
TGCAGGACCAGAGAATTCGAATAC ATGTTTCCGNNNGATCGACATG	7346	TGCAGGACCAGAGAATTCGAATA CATAAGAGATNNNGATCGACATG	7586
TGCAGGACCAGAGAATTCGAATAC AGCTGGACCNNNGATCGACATG	7347	TGCAGGACCAGAGAATTCGAATA CAACCGAATCNNNGATCGACATG	7587
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图22E

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TGCAGGACCAGAGAATTCGAATAC ACCCCATATNNNGATCGACATG	7378	TGCAGGACCAGAGAATTCGAATA CAGGCGTTGCNNNGATCGACATG	7618
TGCAGGACCAGAGAATTCGAATAC AGATAGGTGNNNGATCGACATG	7379	TGCAGGACCAGAGAATTCGAATA CAGCATCTCTNNNGATCGACATG	7619
TGCAGGACCAGAGAATTCGAATAC AAAATAACGNNNGATCGACATG	7380	TGCAGGACCAGAGAATTCGAATA CAACTCTCCANNNGATCGACATG	7620
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图22F

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图22G

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TGCAGGACCAGAGAATTCGAATAC AATATCGTANNNTGCATCAGGT	7441	TGCAGGACCAGAGAATTCGAATA CAGACCATTGNNNTGCATCAGGT	7681
TGCAGGACCAGAGAATTCGAATAC AACCTCTCANNNTGCATCAGGT	7442	TGCAGGACCAGAGAATTCGAATA CACCGCGTAGNNNTGCATCAGGT	7682
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TGCAGGACCAGAGAATTCGAATAC ACGGATTGTNNNTGCATCAGGT	7447	TGCAGGACCAGAGAATTCGAATA CAGTCTCTACNNNTGCATCAGGT	7687
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图22H

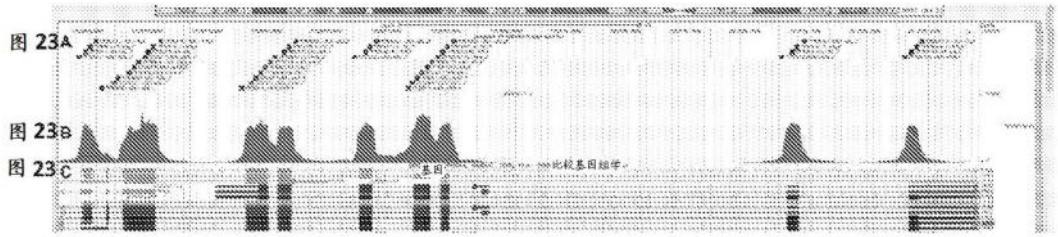


图23

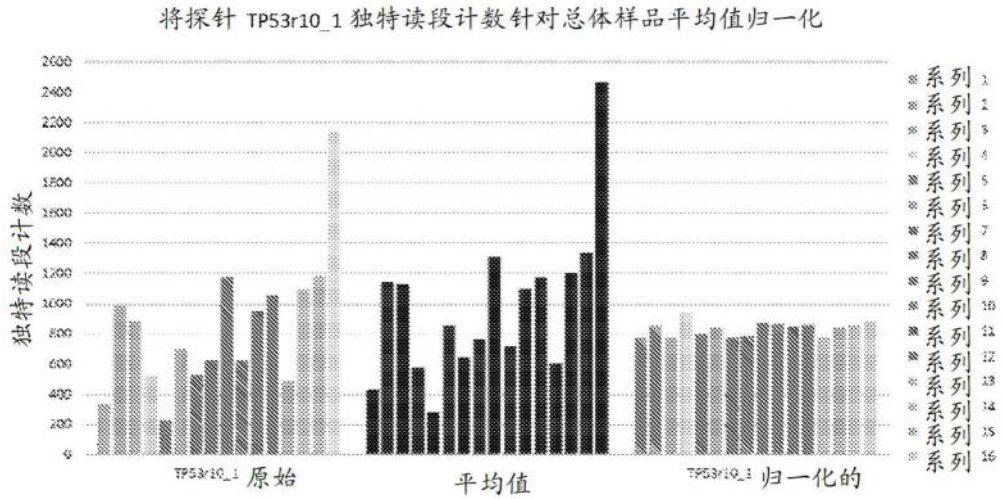


图 24A 图 24B 图 24C

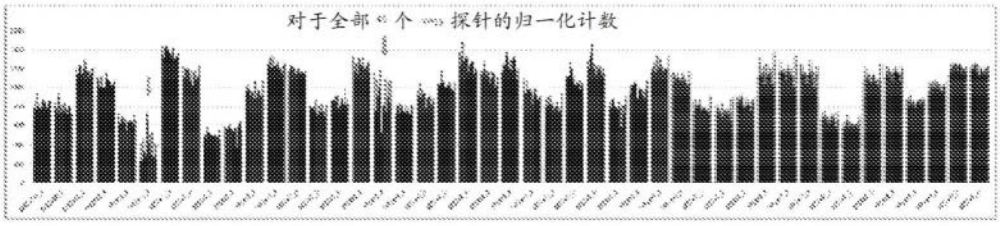


图25

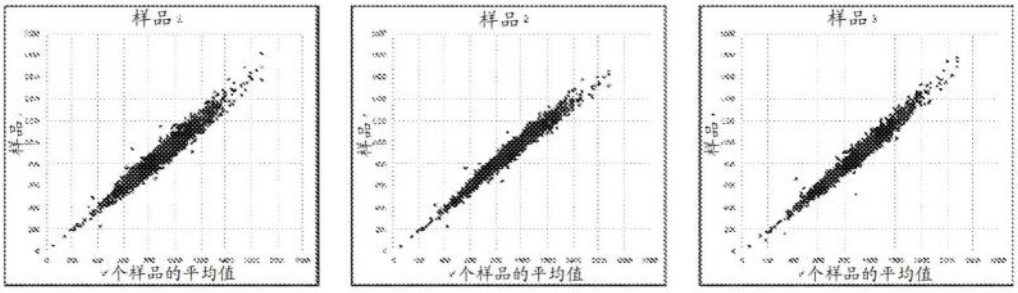


图26

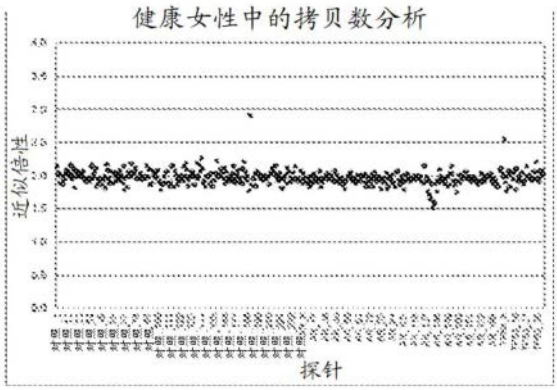


图27A

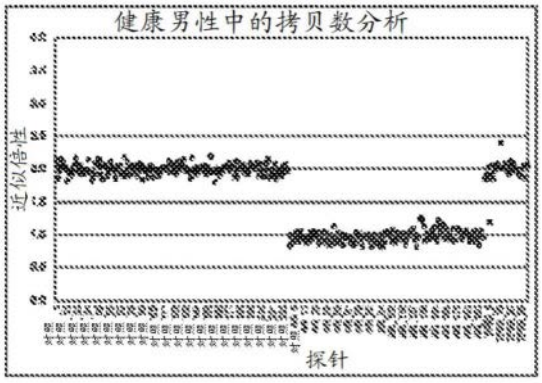


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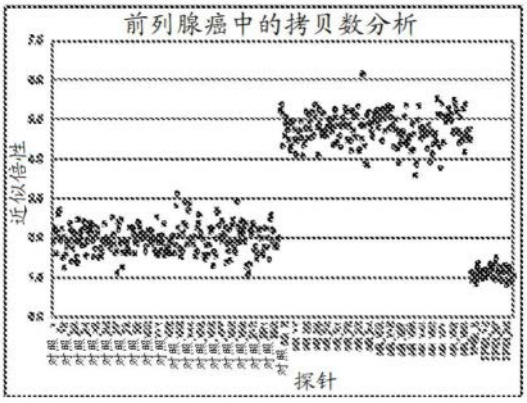


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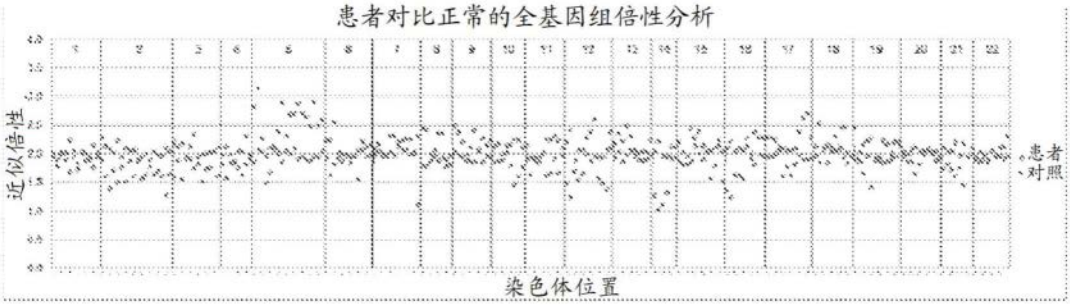


图28

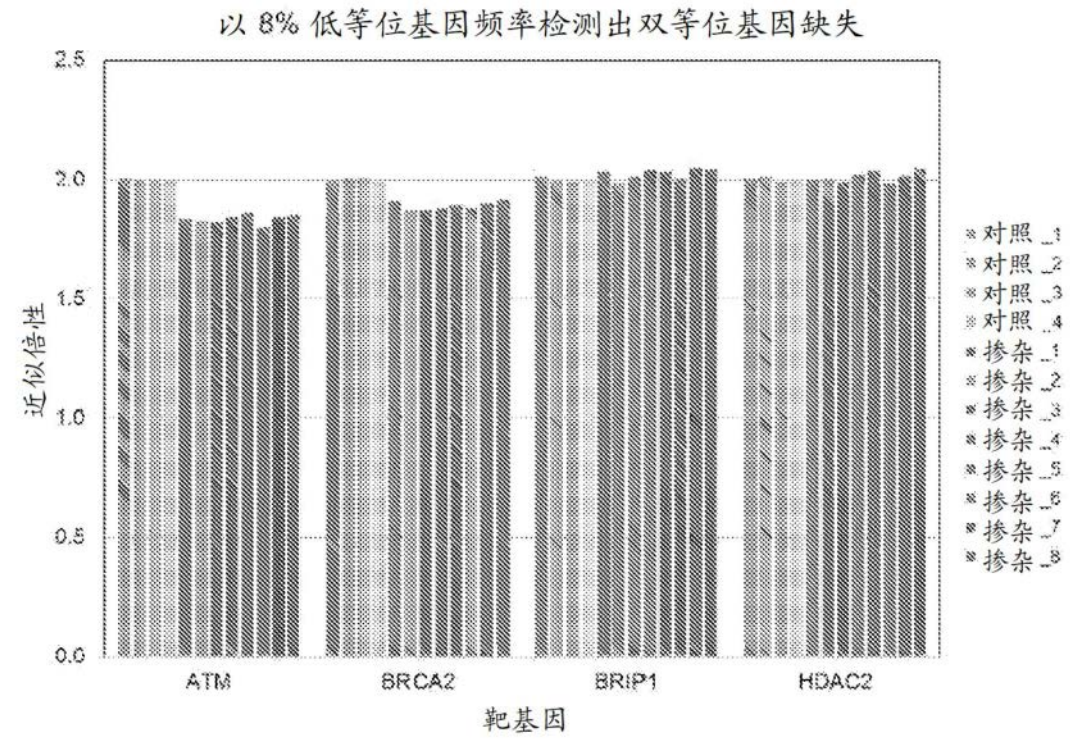

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近似倍性
2.5
2.0
1.5
1.0
0.5
0.0
ATM
SRCA2
BRIP1
HDAC2
靶基因
对照_1
对照_2
对照_3
对照_4
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掺杂_2
掺杂_3
掺杂_4
掺杂_5
掺杂_6
掺杂_7
掺杂_8

图29