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(73) 专利权人 分析生物科学有限公司
地址 美国华盛顿州

(72) 发明人 克里斯多弗·K·雷蒙德 林继力
珍妮弗·埃尔南德斯

(74) 专利代理机构 北京英赛嘉华知识产权代理
有限责任公司 11204
专利代理师 王达佐 洪欣

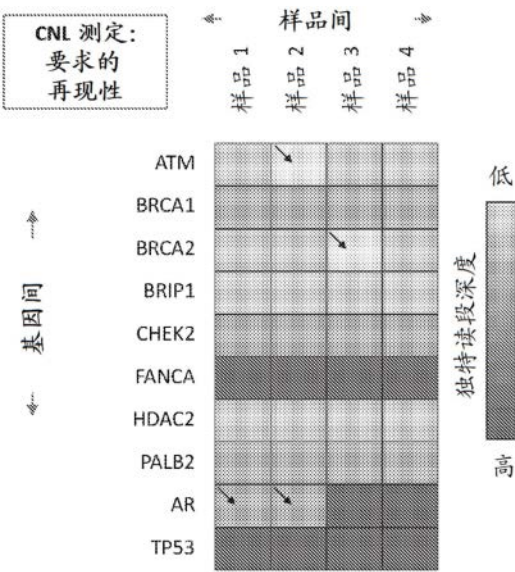
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(54) 发明名称
用于检测DNA样品中基因组拷贝变化的方法

(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。



1. 一种从测试样品捕获DNA靶区域的方法,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;以及

(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;

其中所述衔接子选自衔接子组,其中所述衔接子组中的每个衔接子包含选自独特的样品标签区的池的样品标签区,其中所述池选自多个池,并且其中所选择的池是测试样品独特的;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;

其中所述样品标签区鉴定所述测试样品;并且

其中所述锚定区包含能够附接至所述基因组DNA片段的多核苷酸序列;

从而从所述测试样品捕获DNA靶区域。

2. 如权利要求1所述的方法,其中所述DNA靶区域包括单核苷酸变异、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。

3. 如权利要求1-2中任一项所述的方法,其中所述测试样品是组织活检。

4. 如权利要求1-3中任一项所述的方法,其中所述基因组DNA是无细胞DNA或细胞DNA。

5. 如权利要求4所述的方法,其中所述基因组DNA是从所述测试样品分离的无细胞DNA;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。

6. 如权利要求1-3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:

(i) 从所述测试样品分离细胞DNA;

(ii) 使所述细胞DNA片段化以获得所述基因组DNA片段。

7. 如权利要求6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。

8. 如权利要求6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。

9. 如权利要求8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。

10. 如前述权利要求中任一项所述的方法,其中所述样品标签区还包含有助于鉴定独特基因组DNA片段的独特分子标识符。

11. 如前述权利要求中任一项所述的方法,其中所述扩增区的长度为10至50个核苷酸。

12. 如前述权利要求中任一项所述的方法,其中所述扩增区的长度为20至30个核苷酸。

13. 如前述权利要求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。

14. 如前述权利要求中任一项所述的方法,其中所述样品标签区的长度为5至50个核苷酸。

15. 如权利要求14所述的方法,其中所述样品标签区的长度为5至15个核苷酸。

16. 如权利要求14所述的方法,其中所述样品标签区的长度为8个核苷酸。

17. 如权利要求10-16中任一项所述的方法,其中所述衔接子包含独特分子标识符倍增器,所述独特分子标识符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。

18. 如权利要求17所述的方法,其中所述独特分子标识符倍增器的长度为1至5个核苷酸。

19. 如权利要求17所述的方法,其中所述独特分子标识符倍增器的长度为3个核苷酸。

20. 如前述权利要求中任一项所述的方法,其中所述锚定区的长度为1至50个核苷酸。

21. 如权利要求20所述的方法,其中所述锚定区的长度为5至25个核苷酸。

22. 如权利要求20或21所述的方法,其中所述锚定区的长度为10个核苷酸。

23. 如前述权利要求中任一项所述的方法,其中步骤(a)包括将第一衔接子附接至基因组DNA片段的一端,并且将第二衔接子附接至所述DNA片段的另一端。

24. 如权利要求23所述的方法,其中在将所述基因组DNA片段附接至所述第一衔接子和所述第二衔接子之前,对所述基因组DNA片段进行末端修复。

25. 如权利要求23所述的方法,其中所述衔接子组中的每个衔接子的扩增区包含相同的核苷酸序列。

26. 如权利要求24或25所述的方法,其中所述衔接子组中的每个衔接子的样品标签区包含2至1,000个独特的核苷酸序列中的一个核苷酸序列。

27. 如权利要求26所述的方法,其中所述衔接子组中的每个衔接子的样品标签区包含50至500个独特的核苷酸序列中的一个核苷酸序列。

28. 如权利要求26所述的方法,其中所述衔接子组中的每个衔接子的样品标签区包含100至400个独特的核苷酸序列中的一个核苷酸序列。

29. 如权利要求26所述的方法,其中所述衔接子组中的每个衔接子的样品标签区包含200至300个独特的核苷酸序列中的一个核苷酸序列。

30. 如权利要求26所述的方法,其中所述衔接子组中的每个衔接子的样品标签区包含240个核苷酸序列中的一个核苷酸序列。

31. 如权利要求26-30中任一项所述的方法,其中所述独特的核苷酸序列中的每个序列与所述独特的核苷酸序列的任何其他序列相隔的汉明距离为至少二。

32. 如权利要求24-31中任一项所述的方法,其中所述衔接子组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独特分子标识符倍增器。

33. 如权利要求24-32中任一项所述的方法,其中所述衔接子组中的每一个包含与所述样品标签区相邻的独特分子标识符倍增器。

34. 如权利要求32或33所述的方法,其中所述衔接子组中的每个衔接子的所述独特分子标识符倍增器的长度为1至5个核苷酸。

35. 如权利要求34所述的方法,其中所述衔接子组中的每个衔接子的所述独特分子标识符倍增器的长度为三个核苷酸。

36. 如权利要求24-35中任一项所述的方法,其中所述衔接子组包含四个锚定区,其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个,并且其中给定序列中的每个样品标签区与给定序列的四个锚定区中的一个配对。

37. 如权利要求23或24所述的方法,其中所述衔接子组中的每个衔接子的扩增区与所述衔接子组中的每个其他衔接子的扩增区相同;

其中所述衔接子组中的每个衔接子的样品标签区的长度为8个核苷酸,其中每个样品标签区的核苷酸序列与所述衔接子组的样品标签区的任何其他核苷酸序列相隔的汉明距

离为至少二，

其中所述衔接子组中的每一个衔接子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独特分子标识符倍增器，其中所述衔接子组中的每个衔接子的所述独特分子标识符倍增器的长度为三个核苷酸，并且其中给定序列的独特分子标识符倍增器与所述衔接子组的每个样品标签区配对，

其中所述衔接子组包含四个锚定区，其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个，并且其中给定序列中的每个样品区与给定序列的四个锚定区中的一个配对。

38. 如权利要求23-37中任一项所述的方法，其中将所述基因组DNA片段附接至第一衔接子和第二衔接子的步骤包括：

(i) 将包含锚定区的至少一部分的寡核苷酸附接至所述基因组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；以及

(ii) 在适合于DNA连接的条件下，使与所述附接链附接的基因组DNA片段与编码全长衔接子序列的DNA寡核苷酸、T4多核苷酸激酶、Taq DNA连接酶和全长Bst聚合酶接触；

从而将所述第一衔接子和所述第二衔接子附接至所述基因组DNA片段。

39. 如权利要求23-38中任一项所述的方法，其中所述基因组DNA片段是无细胞DNA。

40. 如权利要求23-39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。

41. 如前述权利要求中任一项所述的方法，其还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。

42. 如前述权利要求中任一项所述的方法，其还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，从而进行引物延伸和/或对包含来自所述基因组DNA文库的目标区域的DNA文库片段的扩增。

43. 如前述权利要求中任一项所述的方法，其还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，从而进行引物延伸和对包含来自所述基因组DNA文库的目标区域的所述DNA文库片段的扩增。

44. 如前述权利要求中任一项所述的方法，其还包括对包含所述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。

45. 如前述权利要求中任一项所述的方法，其包括对包含所述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。

46. 如权利要求45所述的方法，其中所述独特分子标识元件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。

47. 如权利要求46所述的方法，其中包含相同独特分子标识元件的测序读段被鉴定为独特基因组序列。

48. 如权利要求46-47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。

49. 如权利要求48所述的方法，其中测定所述原始基因组深度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独特基因组序列的平均数目。

50. 如权利要求49所述的方法,其中与高度可变数目的独特基因组序列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。

51. 如权利要求49所述的方法,其还包括计算样品的原始基因组深度,其包括计算所述样品中针对所有捕获探针的所有原始基因组深度的数值平均值。

52. 如权利要求49所述的方法,其中在计算样品的原始基因组深度中不包括针对噪声探针的原始基因组深度值。

53. 如权利要求48-52中任一项所述的方法,其中通过将针对每个捕获探针的原始基因组深度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原始基因组深度归一化,其包括

(i) 使样品中的每个捕获探针原始基因组深度乘以归一化常数,其中所述归一化常数包括任何实数;以及

(ii) 使(i)的乘积除以针对相应样品计算的原始基因组深度;或

(iii) 使(i)的乘积除以从探针子集计算的平均原始基因组深度。

54. 如权利要求53所述的方法,其中所述探针子集是对照探针组。

55. 如前述权利要求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。

56. 如权利要求55所述的方法,其中所述基因是BRCA2、ATM、BRCA1、BRIP1、CHEK2、FANCA、HDAC2和/或PALB2。

57. 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,

其中所述衔接子选自衔接子组,其中所述衔接子组中的每个衔接子包含选自独特的样品标签区的池的样品标签区,其中所述池选自多个池,并且其中所选择的池是测试样品独特的;

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;

其中所述样品标签区识别所述测试样品;并且

其中所述锚定区包含能够附接至所述基因组DNA片段的多核苷酸序列。

58. 如权利要求57所述的基因组DNA文库,其中所述样品标签区还包含独特分子标识符,其中所述独特分子标识符有助于鉴定独特基因组DNA片段。

59. 如权利要求57或58所述的基因组DNA文库,其中所述扩增区的长度为10至50个核苷酸。

60. 如权利要求59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。

61. 如前述权利要求中任一项所述的基因组DNA文库,其中所述样品标签区的长度为5至50个核苷酸。

62. 如权利要求61所述的基因组DNA文库,其中所述样品标签区的长度为8个核苷酸。

63. 如权利要求57-62中任一项所述的基因组DNA文库,其中所述衔接子包含独特分子标识符倍增器,并且所述独特分子标识符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。

64. 如权利要求63所述的基因组DNA文库,其中所述独特分子标识符倍增器的长度为1

至5个核苷酸。

65. 如前述权利要求中任一项所述的基因组DNA文库,其中所述锚定区的长度为1至50个核苷酸。

66. 如权利要求65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。

67. 如权利要求57-66中任一项所述的基因组DNA文库,其中所述衔接子组中的每个衔接子的扩增区与所述衔接子组中的每个其他衔接子的扩增区相同。

68. 如权利要求57-67中任一项所述的基因组DNA文库,其中每个独特的样品标签区序列与任何其他独特的样品标签区序列相隔的汉明距离为至少二。

69. 如权利要求57-68中任一项所述的基因组DNA文库,其中所述衔接子组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独特分子标识符倍增器。

70. 如权利要求57-68中任一项所述的基因组DNA文库,其中所述衔接子组中的每一个包含与所述样品标签区相邻的独特分子标识符倍增器。

71. 如权利要求57-70中任一项所述的基因组DNA文库,其中所述衔接子组包含四个锚定区,其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个,并且其中给定序列中的每个样品区与给定序列的四个锚定区中的一个配对。

72. 如权利要求57所述的基因组DNA文库,其中所述衔接子组中的每个衔接子的扩增区与所述衔接子组中的每个其他衔接子的扩增区相同;

其中所述样品标签区的池的每个样品标签区的长度为8个核苷酸,其中每个独特的样品标签区序列与任何其他独特的样品标签区序列相隔的汉明距离为至少二;

其中所述衔接子组中的每一个衔接子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独特分子标识符倍增器,其中所述衔接子组中的每个衔接子的所述独特分子标识符倍增器的长度为三个核苷酸,并且其中给定序列的独特分子标识符倍增器与所述衔接子组的每个样品标签区配对;

其中所述衔接子组包含四个锚定区,其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个;并且

其中给定序列的每个样品区与给定序列的四个锚定区中的一个配对。

73. 如权利要求57-72中任一项所述的基因组DNA文库,其中所述基因组DNA片段是无细胞DNA。

74. 多个基因组DNA文库,其包含多于一个根据权利要求57-73中任一项所述的基因组文库。

75. 如权利要求74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。

76. 如权利要求74或75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。

77. 一种用于捕获无细胞DNA的DNA靶区域的方法,其包括:

(a) 生成如权利要求57-76中任一项所述的DNA文库;以及

(b) 使所述无细胞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；

从而捕获所述DNA靶区域。

78. 如权利要求57-73中任一项所述的基因组DNA文库，其中所述样品标签区识别与其附接的基因组DNA片段。

79. 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；

其中所述衔接子组中的每个衔接子包含选自独特的样品标签区的池的样品标签区，其中所述池选自多个池，并且其中所选择的池是测试样品独特的；

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；

其中所述样品标签区识别所述测试样品；并且

其中所述锚定区包含能够附接至所述基因组DNA片段的多核苷酸序列。

80. 如权利要求79所述的衔接子组，其中所述样品标签区还包含独特分子标识符，其中所述独特分子标识符有助于鉴定独特基因组DNA片段。

81. 如权利要求79或80所述的衔接子组，其中所述扩增区的长度为10至50个核苷酸。

82. 如权利要求79-81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。

83. 如前述权利要求中任一项所述的衔接子组，其中所述样品标签区的长度为5至50个核苷酸。

84. 如权利要求83所述的衔接子组，其中所述样品标签区的长度为8个核苷酸。

85. 如权利要求79-84中任一项所述的衔接子组，其中所述衔接子包含独特分子标识符倍增器，并且所述独特分子标识符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。

86. 如权利要求85所述的衔接子组，其中所述独特分子标识符倍增器的长度为1至5个核苷酸。

87. 如权利要求79-86所述的衔接子组，其中所述锚定区的长度为1至50个核苷酸。

88. 如权利要求87所述的衔接子组，其中所述锚定区的长度为10个核苷酸。

89. 如权利要求79-88中任一项所述的衔接子组，其中所述衔接子组中的每个衔接子的扩增区与所述衔接子组中的每个其他衔接子的扩增区相同。

90. 如权利要求89所述的衔接子组，其中每个独特的样品标签区序列与任何其他独特的样品标签区序列相隔的汉明距离为至少二。

91. 如权利要求79-90中任一项所述的衔接子组，其中所述衔接子组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独特分子标识符倍增器。

92. 如权利要求79-90中任一项所述的衔接子组，其中所述衔接子组中的每一个包含与所述样品标签区相邻的独特分子标识符倍增器。

93. 如权利要求92所述的衔接子组，其中所述衔接子组包含四个锚定区，其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个，并且其中给定序列中的每个样品区与给定序列的四个锚定区中的一个配对。

94. 如权利要求79-93中任一项所述的衔接子组，其中所述衔接子组中的每个衔接子的

扩增区与所述衔接子组中的每个其他衔接子的扩增区相同；

其中每个衔接子的样品标签区的长度为8个核苷酸，其中每个独特的样品标签区序列与任何其他独特的样品标签区序列相隔的汉明距离为至少二；

其中所述衔接子组中的每一个衔接子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独特分子标识符倍增器，其中所述衔接子组中的每个衔接子的所述独特分子标识符倍增器的长度为三个核苷酸，其中给定序列的所述独特分子标识符倍增器与给定序列的一个样品标签区配对；

其中所述衔接子组包含四个锚定区，其中所述衔接子组的每个衔接子包含所述四个锚定区中的一个；并且

其中给定序列的每个样品区与给定序列的四个锚定区中的一个配对。

95. 如权利要求79-94中任一项所述的衔接子组，其中所述样品标签区识别与其附接的基因组DNA片段。

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_02W0_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'磷酸化衔接链,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,并且其中所述衔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)。在某些实施方案中,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。在某些实施方案中,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)。在某些实施方案中,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。在某些实施方案中,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。在某些实施方案中,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。在某些实施方案中,在计算样品的RGD中不包括针对噪声探针的RGD值。

[0030] 在某些实施方案中,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。在某些实施方案中,所述探针子集是对照探针组。

[0031] 在某些实施方案中,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。在某些实施方案中,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 Δ ATM和 Δ BRCA2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 Δ ATM和 Δ BRCA2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 $\times$ 常数 $\div$ 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($[\text{样品}_Z\text{的探针}_Y\text{的独特读段计数}] \times 2 \div [\text{多个对照样品的探针}_Y\text{的平均独特读段计数}]$)。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 Δ ATM)和来自NA09596(单等位基因 Δ BRCA2)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:通过生成由衔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($\geq 10,000$)。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)可以相对于源自同一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,Greenhouse Associates and Wiley-Interscience;Glover,DNA Cloning:A Practical Approach,第I和II卷(IRL Press,Oxford,1985);Anand,Techniques for the Analysis of Complex 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 $\pm 15\%$ 、 $\pm 10\%$ 、 $\pm 9\%$ 、 $\pm 8\%$ 、 $\pm 7\%$ 、 $\pm 6\%$ 、 $\pm 5\%$ 、 $\pm 4\%$ 、 $\pm 3\%$ 、 $\pm 2\%$ 或 $\pm 1\%$ 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 $\leq 2\%$ 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65,536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衔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,衔接步骤包括将衔接子模块衔接/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衔接至片段化的末端修复的DNA的各端。

[0145] 在一些实施方案中,将多个衔接子种类衔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,将多个衔接子种类衔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衔接,所述样品标签序列全部不同于衔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,多个衔接子种类衔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,将多个衔接子种类衔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 $240 \times 64 = 15,360$ 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“衔接链”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 $T_m \geq 55^\circ\text{C}$ 。

[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的平均大小约为约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核苷酸内、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cDNA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制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,诊断或监测医疗病症,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,薏仁米)、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、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、肝细胞癌、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、SLC01B3、SMAD2、SMAD3、SMAD4、SMARCA4、SMARCB1、SMO、SOD2、SOX10、SOX2、SRC、STK11、SULT1A1、TBX22、TET2、TGFB2、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、柚原蛋白、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1B(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)、SLC01B1(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,优选苯酚,成员1)、TPMT(硫嘌呤S-甲基转移酶)、TYMS(胸苷酸合成酶)、UGT1A1(UDP葡萄糖醛酸基转移酶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)、莫洛尼鼠白血病毒(M-MuLV)、莫洛尼鼠肉瘤病毒(MoMSV)、Harvey鼠肉瘤病毒(HaMuSV)、鼠乳腺癌病毒(MuMTV)、长臂猿白血病毒(GaLV)、猫白血病毒(FLV)、泡沫病毒属、Friend鼠白血病毒、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)、Bunyaviridae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methyldamelamine,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 resins;氮芥如苯丁酸氮芥、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aclacinomycin、放线菌素、anthramycin、重氮丝氨酸、博来霉素、cactinomycin、卡里奇霉素、carabycin、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;醋葡萄糖内酯;醛磷酰胺糖苷;氨基乙酰丙酸;安吡啶;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;米托胍脲;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-巯鸟嘌呤;硫嘌呤;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W0 2016/028316的全部内容通过引用特别并入。

[0254] 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。

[0255] 实施例

[0256] 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

[0257] 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 Δ ATM或 Δ BRCA2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。

[0258] 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, Δ ATM) 的杂合缺失的永生化细胞分离的基因组DNA和带有BRCA2 (NA02718, Δ BRCA2) 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。 Δ ATM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。

[0259] 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% Δ ATM DNA (男性) 在女性DNA中;样品3,5% Δ BRCA2 DNA (女性) 在女性DNA中;样品4,纯女性DNA)。

[0260] 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。

[0261] 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 Δ ATM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。

[0262] 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。

[0263] 实施例2:来自健康供体和癌症患者的cfDNA的拷贝数分析

[0264] 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。

[0265] 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。

[0266] 表1:连接锚定寡核苷酸

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
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

[0268] *[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

[0269] **/5Phos/表示5'磷酸基团化学加成至5'碱基位置

[0270] 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。

[0271] 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。

[0272] 表2:TP53探针

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	GTGGCCCCTGCACCAGCAGCTCCTACACCGGCGGCCCTG	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

[0273]

[0274]

TP53_23	CATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCA	7711
TP53_24	CCAGGGTCCCCAGGCCTCTGATTCTCACTGATTGCTCTT	7712
TP53_25	GAGGGCCACTGACAACCACCTTAACCCCTCTCCCAGAG	7713
TP53_26	CCTCAGGCGGCTCATAGGGCACCACCACACTATGTCGAAA	7714
TP53_27	AGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACT	7715
TP53_28	CTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTG	7716
TP53_29	GAGGCAAGCAGAGGCTGGGGCAGCAGGCCAGTGTGCAG	7717
TP53_30	CCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTC	7718
TP53_31	ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCG	7719
TP53_32	GGACAGGTAGGACCTGATTTCTTACTGCCTCTTGCTTCT	7720
TP53_33	CTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCTGCTTG	7721
TP53_34	TCTCTTTTCTATCCTGAGTAGTGGTAATCTACTGGGACG	7722
TP53_35	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCT	7723
TP53_36	GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGG	7724
TP53_37	TCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTC	7725
TP53_38	TGCCTCAGATTCACTTTTATCACCTTCTTGCCTCTTTC	7726
TP53_39	GGCATTTTGAGTGTTAGACTGGAACTTTCCACTTGATAA	7727
TP53_40	CCTGAAGGGTGAAATATTCTCCATCCAGTGGTTTCTTCTT	7728
TP53_41	CCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCA	7729
TP53_42	CATCTTTTAACTCAGTACTGTGTATATACTTACTTCTCC	7730
TP53_43	ATGGCTTTCCAACCTAGGAAGGCAGGGGAGTAGGGCCAGG	7731
TP53_44	CCTGGAGTGAGCCCTGCTCCCCCTGGCTCCTTCCCAGCC	7732
TP53_45	TCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCA	7733

[0275] 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cDNA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。

[0276] 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示出了所有探针对于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。

[0277] 图25中通过45 TP53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。

[0278] 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”。

[0279] 表3:染色体对照探针

[0280]

名称	序列	SEQ ID NO:
Chr_1_1	GTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACA	7734
Chr_1_2	ATCCAAGGGGAGGAGATCAGTCCCCCTATTTGTATCGCAC	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	CAGCCTAGATATGATTCTCTCACTACCCTGTTCCATGGTTC	7743
Chr_1_11	AAAGAATGTGTTGGCTCATGATCAGACTTGAGCACTTGGG	7744
Chr_1_12	CCTAGGCTGTTGCTGCTGGACCTGTTTGTGCTTCATCACA	7745
Chr_2_1	CAGTTGACCCTTCAGCCACAGGGGTTTGAACTTTGAAGGA	7746
Chr_2_2	AGGACCTGAGTATGCACGTTTTTGGTATACTGGGTAGGGGT	7747
Chr_2_3	TATCAGCTGGGATGGTCCGGTCAGCAGCATTACCCTGTTT	7748
Chr_2_4	TGCCTGCTCAGCCCAGATTTCAGTCATGCTGGCCATAAAC	7749
Chr_2_5	CTGGGGGGTGAGGTTTGAAGTTTGAAGTGTGGGATGTGAGG	7750
Chr_2_6	CCAGCTTTTTTCAAGCTGGGAAAGTAATAACCCGTGTTG	7751
Chr_2_7	CCCAGCGCCCGTGGCTTTGGCTCCTCAGTCCCATTTAAAT	7752
Chr_2_8	TATACCACCAAGTCTACCTACTGCCTGCACATGCTATGGC	7753
Chr_2_9	GGTCAATCCGGCACTACTGGTTGTCCAAAGGGAGGTTACT	7754
Chr_2_10	AATCAAACATCAGGACCGCCACAGCACAGGTCAATGAAC	7755
Chr_2_11	GTGTCTCCTGGAGGTGCATGGGTGGTTTTTGAAC TTCATTG	7756
Chr_2_12	GACCCATGTAAGGGGTTGGGTTATGTTCTCCTTTTGCCA	7757
Chr_2_13	TCACTGACATGCGAAGCTGGGAACGAGAAAATGCACATCC	7758
Chr_2_14	TCCTACAGTGCTTAGGGATGAATCTGGCAAAGAAGGATGC	7759
Chr_2_15	GAAAGCAGTCCTTACCACAAGAAGACCCCGATGTGGTGGT	7760
Chr_2_16	ATTGCTCACTGGCTGGCTTGCAATTTGGTATGCGATTGGGA	7761
Chr_2_17	GTCCCTGGGACCATCTGTGCATTGTTCTTGTA ACTGGAAA	7762
Chr_2_18	GACCGAATGGCGAACGCAGTGAATAGATCAGGAGGGAAAA	7763

[0281]

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	GGGCTTCGGTTTTTGGCGAAGGTGCTCACAATCTTGATATC	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	TGTGAGCGTACTTTCTCCCCAGGTTGAAGAGGAATGAGT	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	GACAGAACTTTCATACCCAAGAGCTGCTTTCTCAGCTGGA	7781
Chr_4_7	CAGGCAACTTTGGCAAGACCAAGTCAGCCTTCTCATCTCT	7782
Chr_4_8	CCCTTGCTACCATCACTGTTGTCATCTGTGCTTGCATTCC	7783
Chr_5_1	AGGTCTCACTCCAAGTCCCCCTGTATTAGAGCTAGGCTGC	7784
Chr_5_2	GAAACCATGCGGGATTATCTTTGTGTCAGAGTGGAGCGGCA	7785
Chr_5_3	TATGAAATTAGGCGGTGGTTGGACGTGACTGTGTGTTGAC	7786
Chr_5_4	TGAAACTTGCATGACATACTGCGGCTGCCCATTCCTAGG	7787
Chr_5_5	TGCTTCTTGTATTATAACTCCCCTGGCCACCATCTCGGGCT	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	GGAGACAACCTTAGGAGGTTATCTAGACCATTCCTCGCCTTC	7795
Chr_5_13	GTGTTTCCTCCCAGCATGCACTTTGTGGCTGCCTTTCTTT	7796
Chr_5_14	TGGCTTGTGTAGCGTGTTTCATTTTGGAACCTTGGAGCCG	7797
Chr_5_15	GACACCTCTGGTGCAGTTTGTAGGCTGGCCGGGAAGGGAT	7798
Chr_5_16	GTTTCAGATCTTGCAATGGGAGGGATCGACTCGGCCCTTT	7799
Chr_5_17	TGCCTAAATCAGAAATGGGCTACTTCCCTTGGCCACATCC	7800
Chr_5_18	CAATCTACCACCTCAAGGTTACGCGTGGATTCTACACCT	7801

[0282]

Chr_6_1	GAGTTTTTCTTTCAGGTAGTCTGAGATGGCCCGCACCAAG	7802
Chr_6_2	TACTATAAAGAAGGCACCTCTAGGCTTGGCAAGCACACGT	7803
Chr_6_3	GGCAGATTCGATGGGACTTTAGACACTTGCTTTGCTCCCT	7804
Chr_6_4	CAAATGTCCCATGCAAAACATGTCCCGCACTGTGTGGTAA	7805
Chr_6_5	ACATGTGTAATCTTCTTCTCCTAGGGCGGCAGAACTCATG	7806
Chr_6_6	CCCGAGGAAAGCTCCTCTTTGCTGACTGTAATGTACTGCA	7807
Chr_6_7	GAGGACAGCATTCGCATATCAGGTCGAAATTTCTCCGCGA	7808
Chr_6_8	GTCCAGCTTTCATCCTTGATCCTGCTACTCTAGGCTCTCC	7809
Chr_6_9	ACTGATGGTGTTCACCTTGACCATCAGGTCTGATGGAGGA	7810
Chr_6_10	AATTGGTTCACAAAGCGTCGGGTGATCCAGTAACAGTCGA	7811
Chr_6_11	CAGAACTCTGCTCTAACGCCAAGCCTTCAATATGTCTTCG	7812
Chr_7_1	CAATTCTTACCATCCACAAAATGGATCCAGACAACGTTC	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	AAAAC TAACCAGTAAGTACAGGAGGGACCGAGAGGCATC	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

[0283]

Chr_9_7	TGCTGCAGTGTCTCGAAGAAACCTACCTGCGTTTCTTAGAA	7840
Chr_9_8	CATCATACCTATGGCATAGCCATCAGGGCACTGCAGTTTG	7841
Chr_9_9	TATATCTCACGTGACCGAGGATGGGTCGTGGGCATTACACA	7842
Chr_9_10	GAAATGGCCATCTATAGGTGGGAACCACTCCAGTGTACACA	7843
Chr_10_1	GGAAACCTTTTCAGTCTCTACTAGAAGCGCGGAGAGAACTC	7844
Chr_10_2	TCTGGCCGGCATTTCATTTAAGGCCTAAGGATGAAGGCGGT	7845
Chr_10_3	AGATACCCTATCGTTTCCTTATCTCAGCGAAACAACCTCCCC	7846
Chr_10_4	CGCAACTCCTCCAGATCGCAGTGGTGCTTCTTCACTTTCA	7847
Chr_10_5	TGATTCCATGGTTGCCCGTATACTCCATAAGGCGGTACTT	7848
Chr_10_6	ATACCATATCCGGCTTGTTAGGAGGAGGTATTACAGGGG	7849
Chr_10_7	GTACCTGTTAACCCAGACGCAATTCCTCCACAGTACACAG	7850
Chr_11_1	ATGTGACACTTGCATCCAGGGAGGTCACCATCTGTGTATG	7851
Chr_11_2	CTAGGTCCTGAAGAGGTGGCAAGGAACCAGGACAGAACAT	7852
Chr_11_3	TCTGTCATTGGTGACGCCATCTAGACTCTTGGCTTTGGGA	7853
Chr_11_4	AAGGTATAGAGCTGGGCGGCTTTCTCGTTATAGGTGGAG	7854
Chr_11_5	CTCCTACGTAGCCGGGTAGAACTTATGGCAGAAGTCAGG	7855
Chr_11_6	TGGATTCCCAGGGTTAATTGTGACCCATTGCAGGAAGGTG	7856
Chr_11_7	AATGCTGTCCTACTATGGTCTGTACCTGTCCCAGAGGTGG	7857
Chr_11_8	GTGCACCTGGAGAGCATAACAGGGCACTGACTTGTAGATCA	7858
Chr_11_9	TTCCATCTCGCATAACCTGCCCTAAACTCTTCTCGGTTT	7859
Chr_11_10	ATGAAGGCCTGCTTTGAGTTATCAGATAGGAAGGGGCCAG	7860
Chr_11_11	AGGTCATGTCCCCTTTTGGCTGAACCTAGTTTTGCCCAA	7861
Chr_12_1	CTGCATTCTCCATGAGTAGAGTACGAGCCTCATGTTGGTA	7862
Chr_12_2	AAGGCTGTCTTCACCAACTGGGTAGGTGTGGATCAAGACC	7863
Chr_12_3	CTGACTTTGGTGTGGGGAGTCGGTGGTCCTTCTTCCATT	7864
Chr_12_4	ACTGCAGAGGACCAGACTGGGAAAACAACGATATGGCAGG	7865
Chr_12_5	CCTGGCTTAGAAGTCTGGCCGGTCCTTCTTCAGCTTCTTA	7866
Chr_12_6	AATCTCAGAAAGAGTTCTTGGGACCATGGCAAATGGTGGC	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	ATTTCCCATGCGAGAGGTAGCTTGCCAGGCTGTTGGATA	7873
Chr_13_2	TTCCATGCCGAGTCCTGATGGAACTAGCACTGAAAGACC	7874
Chr_13_3	TCACGGGAGCTTCTTCACTGAGTTCTGCGAATCTGAAGC	7875
Chr_13_4	TTTCCAGAGATGAAGCACTACCCAGTCTTACCCAAGTTCTG	7876
Chr_13_5	CCACCGAGAACAGTGATGAAGGACTTAAAGTGAGAGATGG	7877

[0284]

Chr_13_6	GTTCACTCGTCGGTTTTTCACCAACCACAGACTAGCCTCA	7878
Chr_13_7	ACGCAGCTGTGTTGAGTGCACAGGAAGCTCTTAGGGTTAA	7879
Chr_13_8	TCTCAGTGAACAGAGGGGCTCACTGAGAGGACTTTGAATAC	7880
Chr_13_9	ATGGCACAGGCCACATACTGGAATGAATGACGGGCTTCAT	7881
Chr_13_10	TGCTGCTTGATGGTGGCATCACTGTCCCCTCATTCCATGA	7882
Chr_14_1	GGACACATGTGGACAGTGTGAAACCTCAGAACACTAACCC	7883
Chr_14_2	AAGTTCTTATCCTTAGGGACCCAGCGGAGACCTTGTTCT	7884
Chr_14_3	CGACGATGCCTGGGAATAGGATCCATGGGATTGATGAGAA	7885
Chr_14_4	GGGAGCCATGAAGATTTCTCCAGCTCCTGAGGAACTTTG	7886
Chr_14_5	TCTGGTCCTCAAGTCCTCAGCTGTAGAAGTTCTCATTGCG	7887
Chr_14_6	TGCCAACCTGGAAACTGGCTTGTGTGTCCACAACAGAAA	7888
Chr_15_1	TAGGTGACAGCACTGTCCTTTCCCTGCCATTTGCAGGGAA	7889
Chr_15_2	TTCTTCTAGATGGCAGACATTGTTGAGGCCTCCCGTACCT	7890
Chr_15_3	AGAGAGCTGCGAGACAAGACTTGGAGTGCGACAAGATTTCT	7891
Chr_15_4	TTCAATCAGGTACTCCGAGTTCCTTGGAGGCCAAAAGGA	7892
Chr_15_5	AGGAATATGGGGTCCATCTGAGACTCGCAAGTGATGATAC	7893
Chr_15_6	GATCTCCAGGACCAGCTCTCAGAAATGCACGATGAACTGG	7894
Chr_15_7	ACAGTGTGATGGAGCAGCAGTCCAAGTTCATCCTCCAAGA	7895
Chr_15_8	AAGATGACAGGATCCAGGAAACAAGACGCATGGGCCAGAA	7896
Chr_15_9	AAAGAGTGGGTCTGTAAATAATCAGGCCGAGACCACCAGC	7897
Chr_15_10	CACCCTTGTTTCGTGGCCCTTGCTTGGTAAACTGGTATCCA	7898
Chr_15_11	CCCAAGTATGGGTGAGGATGCTAGAAATGCCACATAATG	7899
Chr_15_12	AAGACTGTCATTGGTAGGTCATGATCCTTGGCAGCATGAC	7900
Chr_16_1	GTGGGGACGGTCATTATCAGCTTTCTGGACACACAGACAG	7901
Chr_16_2	TGAGAGGCCAAAGAATATCAGTTGACTCTGGATCAGGGGC	7902
Chr_16_3	GAGGCTTTTTAGGGCAGCGAGAAAACGGGAAC TTCATTCC	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	GCAACGTCAACAAC TACTACGTGCACAAGCGCCTCTACTG	7911
Chr_17_1	GCGGATGTCGTTATGGGACAGGTACAAGTAGATAAGTTGC	7912
Chr_17_2	GTGGTCACCATCTCTTCAAACCATTTGGACTGGGCCTGGT	7913
Chr_17_3	AAGCCAAGGAGTTCTGAGAGAGCTTAGCTAAGTTCTTCGC	7914
Chr_17_4	TTTTTTAGTACCCCACTGTGTAAGACCAACTGAGGGTGGC	7915

[0285]

Chr_17_5	GTTGTCATTGGGGCTATAGACATAAGCACCTTCCGGAATC	7916
Chr_17_6	CTGAGTGTGCGAGGGGAAGATATTGGTGAAGACCTGTTCT	7917
Chr_17_7	GTCAGACCCTGTCTCGTCTCCTTTACCTTGTCTCGATTT	7918
Chr_17_8	TAAACTATGCTCGCCACCACTCAGCACTCACCTCTTGGGC	7919
Chr_17_9	GGCAACTTCCTGAGACAGATCGGTAAAAACAACCCCTTCT	7920
Chr_17_10	TCAACTGTATTTTCATCAGAGAGATGTGGCTTTCCCAGACA	7921
Chr_17_11	GTTTCCCTCATGTTCCCCCAGGTTCTGTCAGGTGAAGCTG	7922
Chr_18_1	TTAACCCATCTCTACCCGTCCTGTGTCAAGAACGGAGGCT	7923
Chr_18_2	CTGCCCCAAAATAGAAACCGAGGTTCTCCGTGACCTACATC	7924
Chr_18_3	TTCTTTTGACAGTAACAGCGGGAACATGAAGCCGCCACTCT	7925
Chr_18_4	TGGTTTGCCAGTTCAGACACCCAGCCAAATTGCCCTCTCA	7926
Chr_18_5	TAGTGCAGCTGGCTTTGAGCCTGTTCCCGAATGTTTCAGAT	7927
Chr_18_6	AGGGTAATAGCACCAAGCTCTAGTCTACCCACCTCTCTGA	7928
Chr_18_7	CCGCATCTCTGGAGTAGGAATTGATCAGCCACCATATGGG	7929
Chr_18_8	CTATGAGCATACTGGGGAGGGAAACCTCTAAGCGGAACCT	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	TCTGTCTCACCGGTCCCTTCACTTCTAGGCAACTGTAGAT	7937
Chr_19_5	ATATCATGGTCTGTATCCCCAGGTACCTTGACACAGGCC	7938
Chr_19_6	CTCTCCGCCTTTCTTTAGACCTGAGCATGCAGAATTCCGA	7939
Chr_19_7	AAGGCATTTAAATGGGACAGCGTCCCATGCGTGACTTCTC	7940
Chr_19_8	TCTTTCTAACAGACGAACAGCCTACACCTACAACCCCGAG	7941
Chr_19_9	GTCCCAGCCCCAAAAGCATCTTGGGTAAGGATTTGGGATCA	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	GTGCACTGTCAGATCTTGGAACGGCCAAAGGATTTTTCC	7951
Chr_20_8	CATTTTGAGGAGGCTGCTAATTAAGGCTGAGGGCCATCA	7952
Chr_20_9	TCAATGGTAGACTGGAGTACCTTGCCAGGGCAGAGAAAAA	7953

[0286]

Chr_20_10	CTCCTCCAGGAGCTGGCAGCATCAAGACCCCACTTCGCTT	7954
Chr_21_1	AAATAATAGCAGGCGTTGAGATGTCCCTTCCCCAGCACTC	7955
Chr_21_2	AAGTCTGACAGCATCTGCTTGAAGTGAAGCACAGTGATGG	7956
Chr_21_3	ATTCGTGATGGCGCTCATTTCATAAAGGACGACAGGTCA	7957
Chr_21_4	GAAGAGTGAATTCCCGCTTCTGCGCCAACATTCTGTTTCC	7958
Chr_21_5	ACAGGTGAAGTCTTTGCGTGCCTCCCTGTTGGACTCAAAT	7959
Chr_21_6	TAATGATATTCTGGCACAAGGAGCAGAGCCCCTCTTCTTC	7960
Chr_21_7	AGACCCAGCCTACCTGCATGATCTCTTGTACAGCTTTGCA	7961
Chr_21_8	TCATGGAACATGGGCCTTGCAAAGGGGTCAAGATCACAAAC	7962
Chr_21_9	GTCAAAAAGGTCCAATCAGCTAGAGACTAGGCCAGACCCA	7963
Chr_22_1	TGTGACCACCCTAAAGGGAGGGCAGAAGCCGAGTCACCCT	7964
Chr_22_2	ACGCCCTCCACCTGCTGCTAGGACTCCCCTCCCAAACAAAG	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

[0287] 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。

[0288] 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。

[0289] 测量了相对于健康对照(褐色点)的去势抗性前列腺癌患者样品(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。

[0290] 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。

[0291] 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杂样品。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。

[0292] 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W0 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。

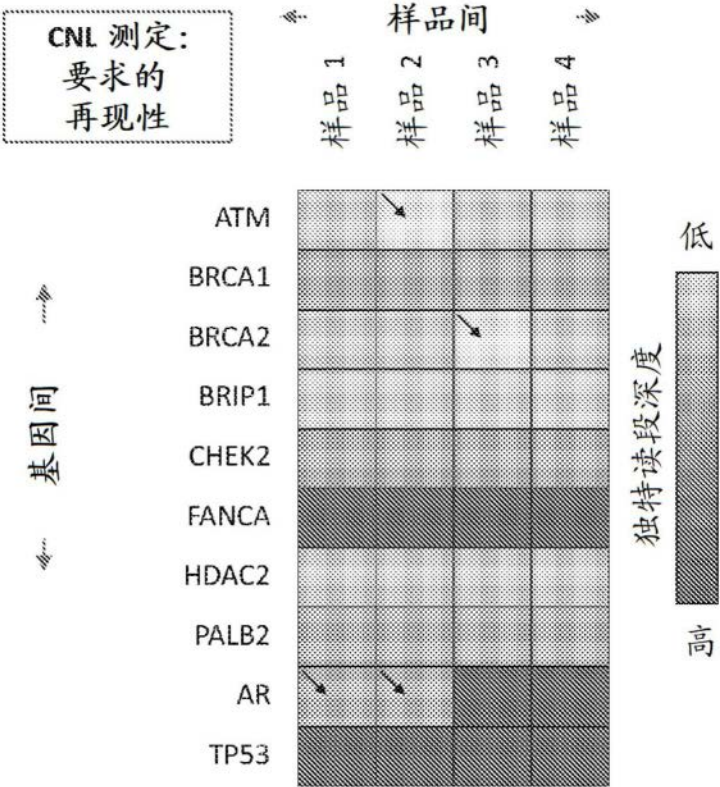


图1

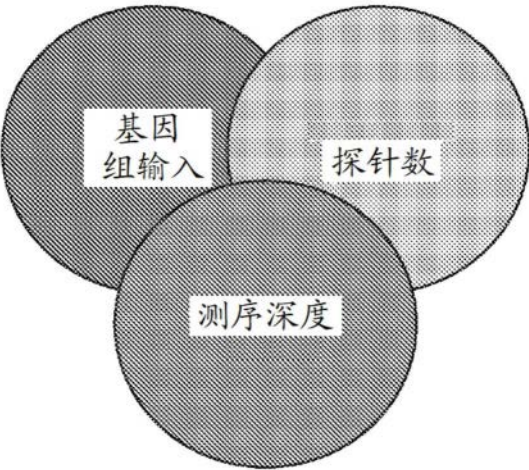


图2

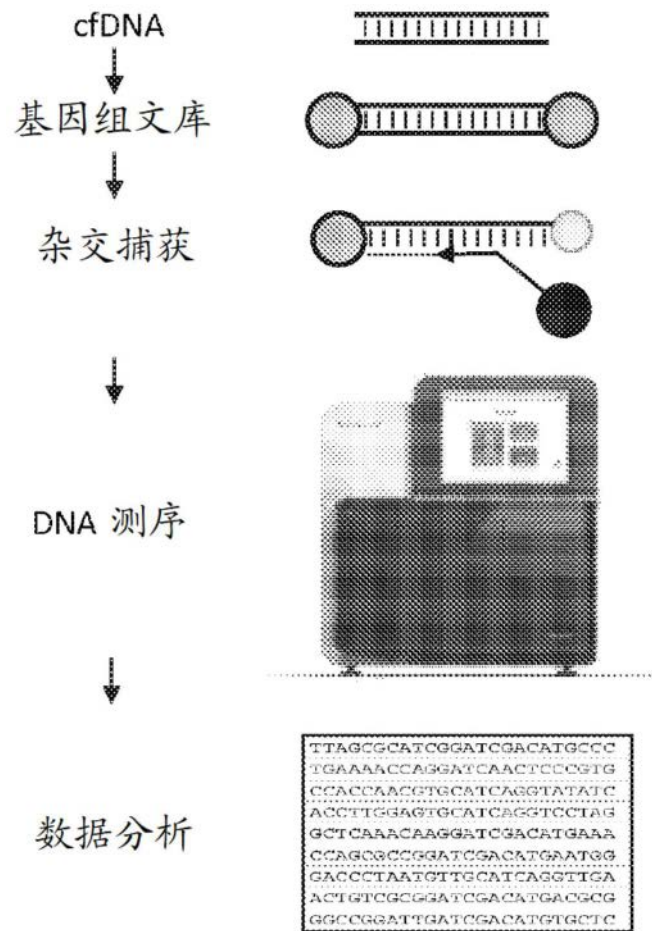


图3

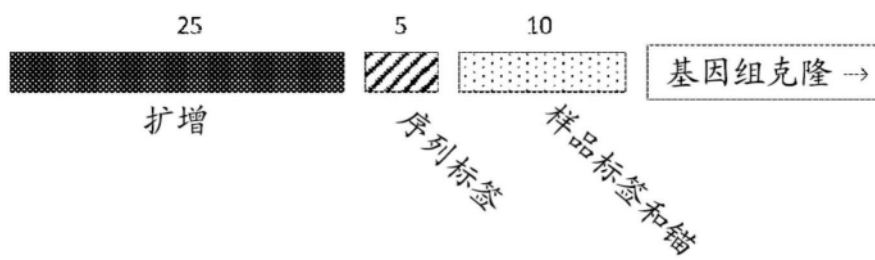


图4A

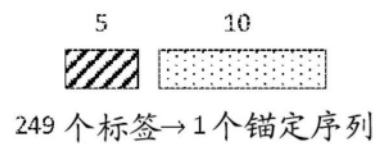


图4B

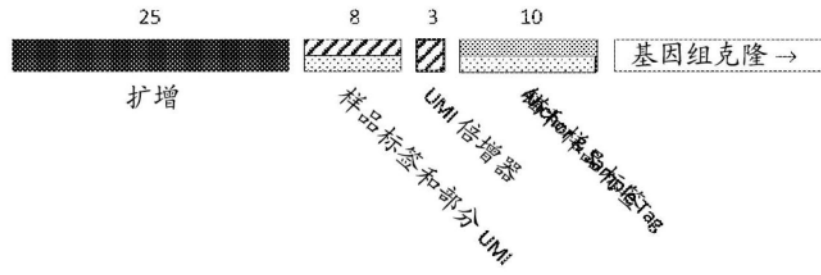


图4C

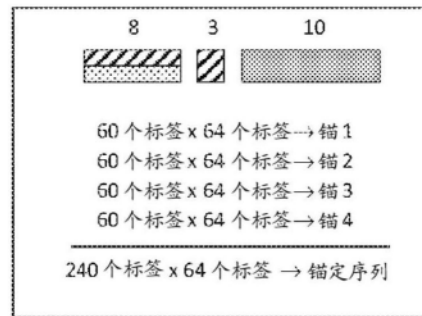


图4D



图4E

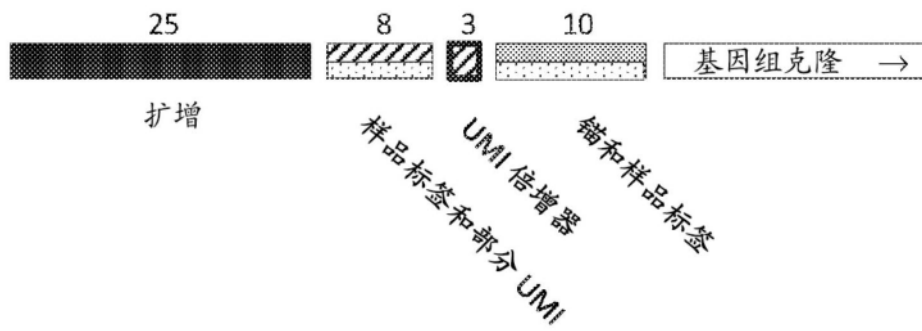


图5A

移动 UMI 倍增器以增加独特标签的数目

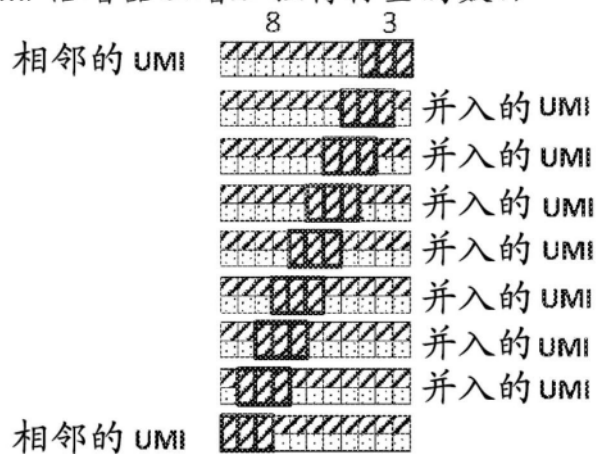


图5B

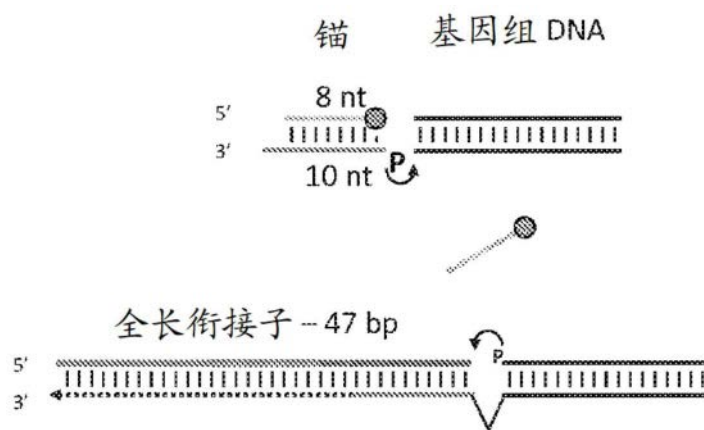


图6

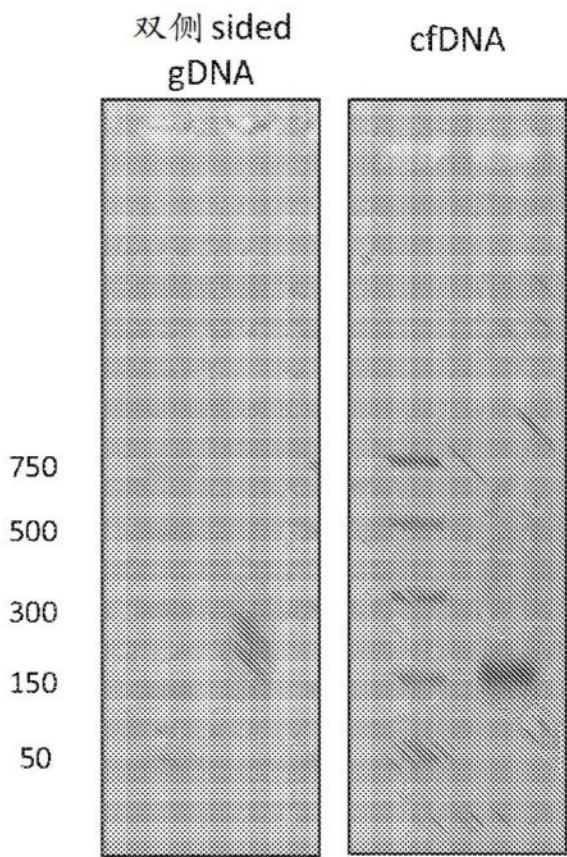


图7

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

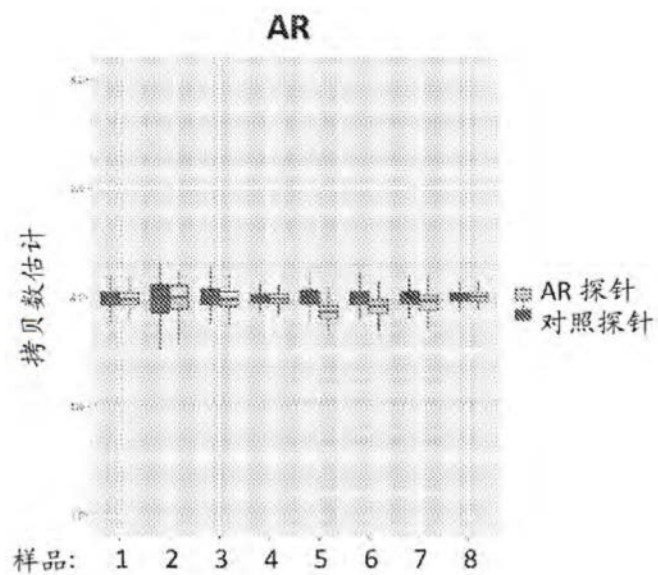


图8B

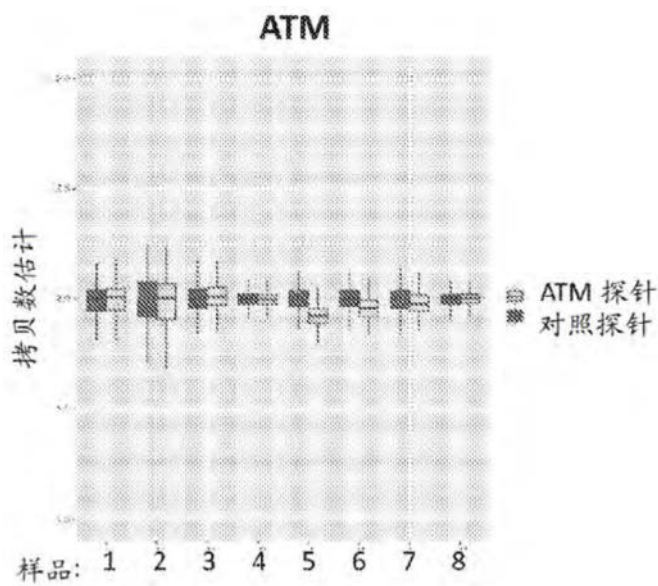


图8C

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

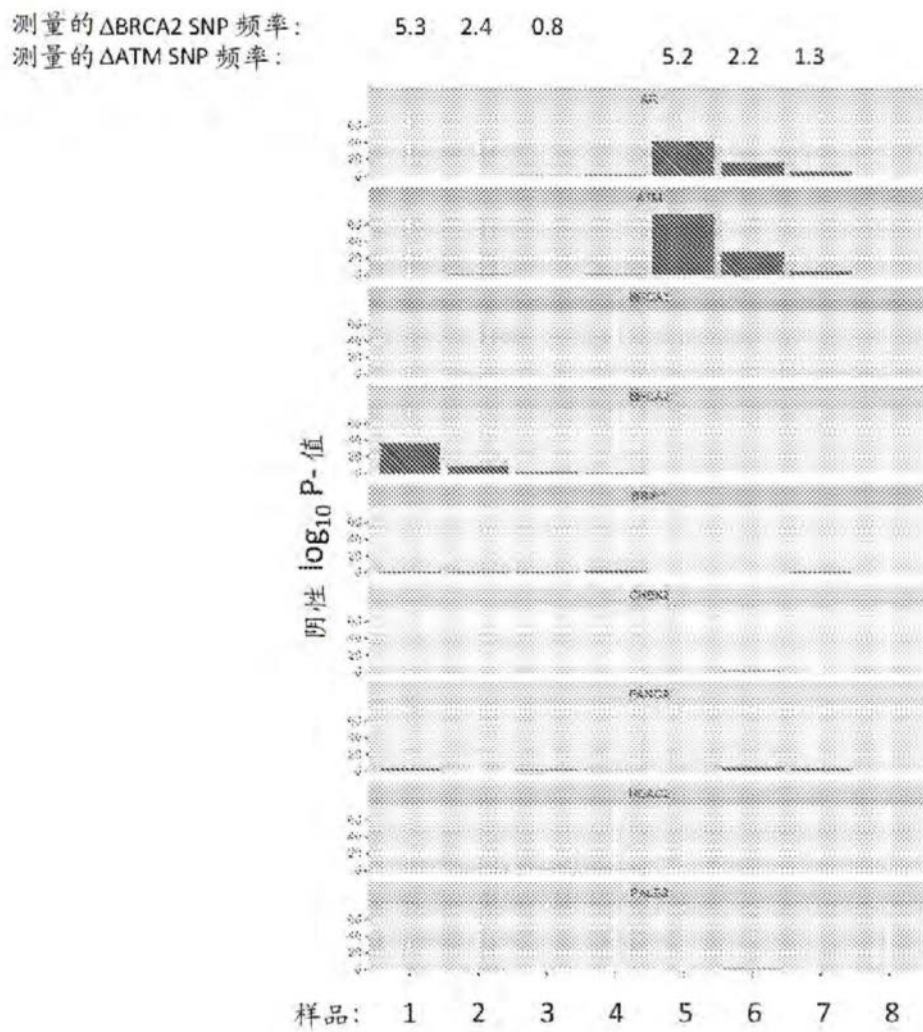


图9B

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

测量的 Δ ATM SNP 频率：
测量的 Δ BRCA2 SNP 频率：

5.5 2.5

7.2 2.6

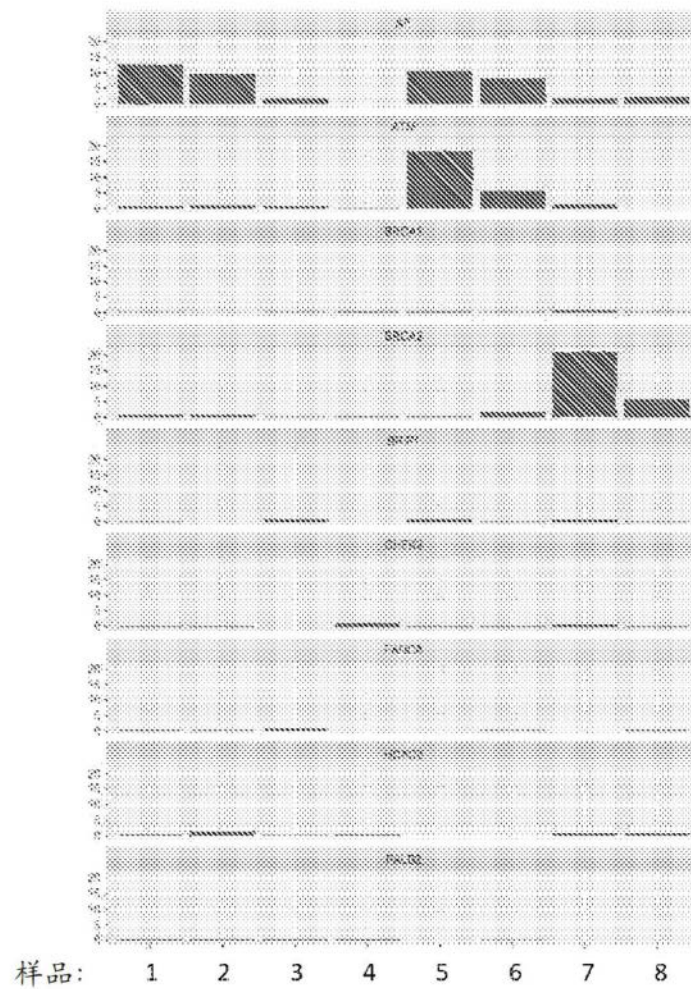


图10B



图11A

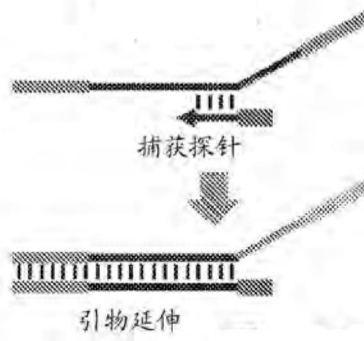


图11B

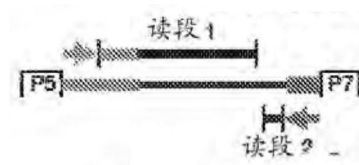


图11C

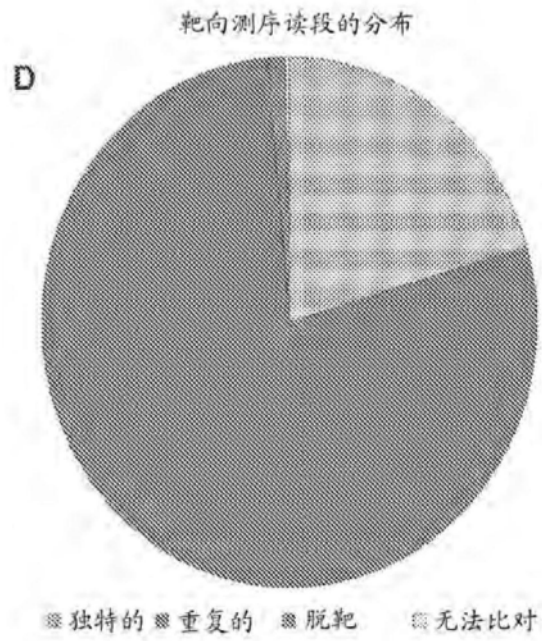


图11D

池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCAGAGAAATCGAATA	9	TGCAGGACCAGAGAAATCGAATA	249	TGCAGGACCAGAGAAATCGAATA	489
CACGAGCTTANNNNACGTATGCCA		CACCGTGTGNNNNACGTATGCCA		CAACGTCAACNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	10	TGCAGGACCAGAGAAATCGAATA	250	TGCAGGACCAGAGAAATCGAATA	490
CATTGCTGACNNNNACGTATGCCA		CATATCAATGNNNNACGTATGCCA		CAGTGTCTAGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	11	TGCAGGACCAGAGAAATCGAATA	251	TGCAGGACCAGAGAAATCGAATA	491
CATATATACNNNNACGTATGCCA		CACCTGCAATNNNNACGTATGCCA		CAGCGCCCACTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	12	TGCAGGACCAGAGAAATCGAATA	252	TGCAGGACCAGAGAAATCGAATA	492
CATCAGCMTGNNNNACGTATGCCA		CATTCGGAATNNNNACGTATGCCA		CAGCTCTGANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	13	TGCAGGACCAGAGAAATCGAATA	253	TGCAGGACCAGAGAAATCGAATA	493
CAACTGTAGCNNNNACGTATGCCA		CACCTGTCCANNNNACGTATGCCA		CAAGACTTGCNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	14	TGCAGGACCAGAGAAATCGAATA	254	TGCAGGACCAGAGAAATCGAATA	494
CAATATATGANNNNACGTATGCCA		CATCAGCATTTNNNNACGTATGCCA		CAGATGCTCINNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	15	TGCAGGACCAGAGAAATCGAATA	255	TGCAGGACCAGAGAAATCGAATA	495
CAATGAGCTTTNNNNACGTATGCCA		CAGCGTGGCTNNNNACGTATGCCA		CAATGTGAATNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	16	TGCAGGACCAGAGAAATCGAATA	256	TGCAGGACCAGAGAAATCGAATA	496
CAAAAATGCTNNNNACGTATGCCA		CACCGAGTAANNNNACGTATGCCA		CACAGGCGCTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	17	TGCAGGACCAGAGAAATCGAATA	257	TGCAGGACCAGAGAAATCGAATA	497
CAGGTTCCGCGNNNNACGTATGCCA		CAGGTGTCGCGNNNNACGTATGCCA		CAATGCCAAGTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	18	TGCAGGACCAGAGAAATCGAATA	258	TGCAGGACCAGAGAAATCGAATA	498
CAACGTGCAATNNNNACGTATGCCA		CATATTTGTAGNNNNACGTATGCCA		CAAGTGGTTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	19	TGCAGGACCAGAGAAATCGAATA	259	TGCAGGACCAGAGAAATCGAATA	499
CACCGCTCATNNNNACGTATGCCA		CATAGTATTGNNNNACGTATGCCA		CACCAAGCGCINNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	20	TGCAGGACCAGAGAAATCGAATA	260	TGCAGGACCAGAGAAATCGAATA	500
CAGTAAGCCTNNNNACGTATGCCA		CAAGCGCTTANNNNACGTATGCCA		CACAGTTATANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	21	TGCAGGACCAGAGAAATCGAATA	261	TGCAGGACCAGAGAAATCGAATA	501
CAAGTAATAGNNNNACGTATGCCA		CAATGAGGTTNNNNACGTATGCCA		CACGGAAGCGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	22	TGCAGGACCAGAGAAATCGAATA	262	TGCAGGACCAGAGAAATCGAATA	502
CAAAATGCCANNNNACGTATGCCA		CACCTTCGGTTNNNNACGTATGCCA		CAATGGCTACINNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	23	TGCAGGACCAGAGAAATCGAATA	263	TGCAGGACCAGAGAAATCGAATA	503
CAAGTGCATGNNNNACGTATGCCA		CAAGACGGATNNNNACGTATGCCA		CAATCGCATGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	24	TGCAGGACCAGAGAAATCGAATA	264	TGCAGGACCAGAGAAATCGAATA	504
CAGAGATATGNNNNACGTATGCCA		CATCTGTCTGNNNNACGTATGCCA		CAATATCTTTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	25	TGCAGGACCAGAGAAATCGAATA	265	TGCAGGACCAGAGAAATCGAATA	505
CAGTCCAGCANNNNACGTATGCCA		CAATCAGCGTTNNNNACGTATGCCA		CAATGAAGCAGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	26	TGCAGGACCAGAGAAATCGAATA	266	TGCAGGACCAGAGAAATCGAATA	506
CATCTCAGAGNNNNACGTATGCCA		CACGTAAAGGNNNNACGTATGCCA		CAGACCCAGCGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	27	TGCAGGACCAGAGAAATCGAATA	267	TGCAGGACCAGAGAAATCGAATA	507
CAAAACCTAANNNNACGTATGCCA		CAAGAAAGAAANNNNACGTATGCCA		CAAGATTAAGANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	28	TGCAGGACCAGAGAAATCGAATA	268	TGCAGGACCAGAGAAATCGAATA	508
CACATACCAAGNNNNACGTATGCCA		CACGTAGCTTNNNNACGTATGCCA		CAAGATCTATNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	29	TGCAGGACCAGAGAAATCGAATA	269	TGCAGGACCAGAGAAATCGAATA	509
CAATGTGACTNNNNACGTATGCCA		CAGGTACCTAANNNNACGTATGCCA		CAACGTACACNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	30	TGCAGGACCAGAGAAATCGAATA	270	TGCAGGACCAGAGAAATCGAATA	510
CACCTCCTATGNNNNACGTATGCCA		CAGAAACCAANNNNACGTATGCCA		CAACGTTACANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	31	TGCAGGACCAGAGAAATCGAATA	271	TGCAGGACCAGAGAAATCGAATA	511
CAATCATGATNNNNACGTATGCCA		CACATATACNNNNACGTATGCCA		CAAAAACCTATNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	32	TGCAGGACCAGAGAAATCGAATA	272	TGCAGGACCAGAGAAATCGAATA	512
CAATGACGGTTNNNNACGTATGCCA		CAACGGACCAANNNNACGTATGCCA		CACCTGATTTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	33	TGCAGGACCAGAGAAATCGAATA	273	TGCAGGACCAGAGAAATCGAATA	513
CAGTCCGCGTNNNNACGTATGCCA		CAATCCAGTNNNNACGTATGCCA		CATGAATATCINNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	34	TGCAGGACCAGAGAAATCGAATA	274	TGCAGGACCAGAGAAATCGAATA	514
CAGTTACCTTNNNNACGTATGCCA		CAGGACAACANNNNACGTATGCCA		CAACTGCGCGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	35	TGCAGGACCAGAGAAATCGAATA	275	TGCAGGACCAGAGAAATCGAATA	515
CACCTTAACCGNNNNACGTATGCCA		CAGAAAGTTANNNNACGTATGCCA		CAGAACGACANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	36	TGCAGGACCAGAGAAATCGAATA	276	TGCAGGACCAGAGAAATCGAATA	516
CACGCTCCTGNNNNACGTATGCCA		CAAAACAGGNNNNACGTATGCCA		CATATATTGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	37	TGCAGGACCAGAGAAATCGAATA	277	TGCAGGACCAGAGAAATCGAATA	517
CATCTCGGTTNNNNACGTATGCCA		CACCGAAGTNNNNACGTATGCCA		CATAGATGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	38	TGCAGGACCAGAGAAATCGAATA	278	TGCAGGACCAGAGAAATCGAATA	518
CAGGTGAGCINNNNACGTATGCCA		CATTCACCAANNNNACGTATGCCA		CAGCAAGTAGNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	39	TGCAGGACCAGAGAAATCGAATA	279	TGCAGGACCAGAGAAATCGAATA	519
CACGCTTCGCGNNNNACGTATGCCA		CATCGAGAGANNNNACGTATGCCA		CAAAACGACCTNNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	40	TGCAGGACCAGAGAAATCGAATA	280	TGCAGGACCAGAGAAATCGAATA	520
CAATCCACACNNNNACGTATGCCA		CACGATGTGANNNNACGTATGCCA		CAGTACACTCINNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATA	41	TGCAGGACCAGAGAAATCGAATA	281	TGCAGGACCAGAGAAATCGAATA	521
CATAGCACTGNNNNACGTATGCCA		CACGGCAGGANNNNACGTATGCCA		CATATGCGGTTNNNNACGTATGCCA	

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATA CACTGGCTTNNNACGTATGCCA	42	TGCAGGACCCAGAGAAATTCGAATA CAAGAACCAGNNNACGTATGCCA	282	TGCAGGACCCAGAGAAATTCGAATA CAATAATAGNNNACGTATGCCA	522
TGCAGGACCCAGAGAAATTCGAATA CAGCAAAATGNNNACGTATGCCA	43	TGCAGGACCCAGAGAAATTCGAATA CAGATTTTGANNNACGTATGCCA	283	TGCAGGACCCAGAGAAATTCGAATA CAGTTACTANNNACGTATGCCA	523
TGCAGGACCCAGAGAAATTCGAATA CAGGATGACANNNACGTATGCCA	44	TGCAGGACCCAGAGAAATTCGAATA CAARCACTGNNNACGTATGCCA	284	TGCAGGACCCAGAGAAATTCGAATA CACCTTTGTANNNACGTATGCCA	524
TGCAGGACCCAGAGAAATTCGAATA CAGCCCTCACTNNNACGTATGCCA	45	TGCAGGACCCAGAGAAATTCGAATA CAACCTCTACNNNACGTATGCCA	285	TGCAGGACCCAGAGAAATTCGAATA CAACATTTCTNNNACGTATGCCA	525
TGCAGGACCCAGAGAAATTCGAATA CACTAGCCGNNNACGTATGCCA	46	TGCAGGACCCAGAGAAATTCGAATA CAGGCGTTTANNNACGTATGCCA	286	TGCAGGACCCAGAGAAATTCGAATA CACCGACTTNNNACGTATGCCA	526
TGCAGGACCCAGAGAAATTCGAATA CACCTCTCTNNNACGTATGCCA	47	TGCAGGACCCAGAGAAATTCGAATA CAOCCGAAAGCNNNACGTATGCCA	287	TGCAGGACCCAGAGAAATTCGAATA CAATATGAACNNNACGTATGCCA	527
TGCAGGACCCAGAGAAATTCGAATA CACTAGCCGNNNACGTATGCCA	48	TGCAGGACCCAGAGAAATTCGAATA CACTACCTTACNNNACGTATGCCA	288	TGCAGGACCCAGAGAAATTCGAATA CATCTCTTTCTNNNACGTATGCCA	528
TGCAGGACCCAGAGAAATTCGAATA CAGCAATGCTNNNACGTATGCCA	49	TGCAGGACCCAGAGAAATTCGAATA CACTTACGCGNNNACGTATGCCA	289	TGCAGGACCCAGAGAAATTCGAATA CAATAGGTTTNNNACGTATGCCA	529
TGCAGGACCCAGAGAAATTCGAATA CAAAATGCTTNNNACGTATGCCA	50	TGCAGGACCCAGAGAAATTCGAATA CAAGGTATGNNNACGTATGCCA	290	TGCAGGACCCAGAGAAATTCGAATA CACGACGTTANNNACGTATGCCA	530
TGCAGGACCCAGAGAAATTCGAATA CACTACTAACNNNACGTATGCCA	51	TGCAGGACCCAGAGAAATTCGAATA CAACTACAAATNNNACGTATGCCA	291	TGCAGGACCCAGAGAAATTCGAATA CAAGCATAGGNNNACGTATGCCA	531
TGCAGGACCCAGAGAAATTCGAATA CACCTCGGACNNNACGTATGCCA	52	TGCAGGACCCAGAGAAATTCGAATA CACTCTCTCAANNNACGTATGCCA	292	TGCAGGACCCAGAGAAATTCGAATA CACTCGCATCTNNNACGTATGCCA	532
TGCAGGACCCAGAGAAATTCGAATA CAGCAACTTNNNACGTATGCCA	53	TGCAGGACCCAGAGAAATTCGAATA CAGRTACAAANNNACGTATGCCA	293	TGCAGGACCCAGAGAAATTCGAATA CAGGACGCCANNNACGTATGCCA	533
TGCAGGACCCAGAGAAATTCGAATA CACCGTGGAGNNNACGTATGCCA	54	TGCAGGACCCAGAGAAATTCGAATA CAACCAACACNNNACGTATGCCA	294	TGCAGGACCCAGAGAAATTCGAATA CAACGCGCCGNNNACGTATGCCA	534
TGCAGGACCCAGAGAAATTCGAATA CAGTAACCGTNNNACGTATGCCA	55	TGCAGGACCCAGAGAAATTCGAATA CAACCCACTTNNNACGTATGCCA	295	TGCAGGACCCAGAGAAATTCGAATA CACTCTCGATNNNACGTATGCCA	535
TGCAGGACCCAGAGAAATTCGAATA CATAGTTTNNNACGTATGCCA	56	TGCAGGACCCAGAGAAATTCGAATA CACTTAAGCGNNNACGTATGCCA	296	TGCAGGACCCAGAGAAATTCGAATA CAOCTTACGNNNACGTATGCCA	536
TGCAGGACCCAGAGAAATTCGAATA CACTGTGCTNNNACGTATGCCA	57	TGCAGGACCCAGAGAAATTCGAATA CACTTAAGCGNNNACGTATGCCA	297	TGCAGGACCCAGAGAAATTCGAATA CACTTTCTAACTNNNACGTATGCCA	537
TGCAGGACCCAGAGAAATTCGAATA CATCTCGAGTNNNACGTATGCCA	58	TGCAGGACCCAGAGAAATTCGAATA CAOCAAATCCANNNACGTATGCCA	298	TGCAGGACCCAGAGAAATTCGAATA CAAAAAGACTNNNACGTATGCCA	538
TGCAGGACCCAGAGAAATTCGAATA CACCTCCACGNNNACGTATGCCA	59	TGCAGGACCCAGAGAAATTCGAATA CACAACTAATNNNACGTATGCCA	299	TGCAGGACCCAGAGAAATTCGAATA CATCCTAGCTNNNACGTATGCCA	539
TGCAGGACCCAGAGAAATTCGAATA CAGAGACTAGNNNACGTATGCCA	60	TGCAGGACCCAGAGAAATTCGAATA CATCACACCTNNNACGTATGCCA	300	TGCAGGACCCAGAGAAATTCGAATA CAACCAAAAGNNNACGTATGCCA	540
TGCAGGACCCAGAGAAATTCGAATA CATGAACTATNNNACGTATGCCA	61	TGCAGGACCCAGAGAAATTCGAATA CAGACCGTCTGNNNACGTATGCCA	301	TGCAGGACCCAGAGAAATTCGAATA CAACGAGTTNNNACGTATGCCA	541
TGCAGGACCCAGAGAAATTCGAATA CAGTTGATANNNACGTATGCCA	62	TGCAGGACCCAGAGAAATTCGAATA CACTTTAAGANNNACGTATGCCA	302	TGCAGGACCCAGAGAAATTCGAATA CACTATGGTNNNACGTATGCCA	542
TGCAGGACCCAGAGAAATTCGAATA CATCCACTCANNNACGTATGCCA	63	TGCAGGACCCAGAGAAATTCGAATA CATGTGATANNNACGTATGCCA	303	TGCAGGACCCAGAGAAATTCGAATA CAOCCACCTGNNNACGTATGCCA	543
TGCAGGACCCAGAGAAATTCGAATA CAGTGAGCTNNNACGTATGCCA	64	TGCAGGACCCAGAGAAATTCGAATA CAACCCAAATGNNNACGTATGCCA	304	TGCAGGACCCAGAGAAATTCGAATA CAGAAATCGCTNNNACGTATGCCA	544
TGCAGGACCCAGAGAAATTCGAATA CACTAGCGGANNNACGTATGCCA	65	TGCAGGACCCAGAGAAATTCGAATA CAACGTGTACNNNACGTATGCCA	305	TGCAGGACCCAGAGAAATTCGAATA CAAGTGTATNNNACGTATGCCA	545
TGCAGGACCCAGAGAAATTCGAATA CACACCTCCGNNNACGTATGCCA	66	TGCAGGACCCAGAGAAATTCGAATA CAATGAATGNNNACGTATGCCA	306	TGCAGGACCCAGAGAAATTCGAATA CAACGCGTGGNNNACGTATGCCA	546
TGCAGGACCCAGAGAAATTCGAATA CAAAAGAAANNNACGTATGCCA	67	TGCAGGACCCAGAGAAATTCGAATA CATCTCTGTTNNNACGTATGCCA	307	TGCAGGACCCAGAGAAATTCGAATA CACTCTGTTNNNACGTATGCCA	547
TGCAGGACCCAGAGAAATTCGAATA CAGAACTCTNNNACGTATGCCA	68	TGCAGGACCCAGAGAAATTCGAATA CAGTAACAGGNNNACGTATGCCA	308	TGCAGGACCCAGAGAAATTCGAATA CACTTGTAGATNNNACGTATGCCA	548
TGCAGGACCCAGAGAAATTCGAATA CAGAAATAACANNNACGTATGCCA	69	TGCAGGACCCAGAGAAATTCGAATA CAACTCTGTTANNNACGTATGCCA	309	TGCAGGACCCAGAGAAATTCGAATA CAGCCGCACTNNNACGTATGCCA	549
TGCAGGACCCAGAGAAATTCGAATA CAGCTCTGCTNNNACGTATGCCA	70	TGCAGGACCCAGAGAAATTCGAATA CAACGCTTACNNNACGTATGCCA	310	TGCAGGACCCAGAGAAATTCGAATA CAAGTGACGANNNACGTATGCCA	550
TGCAGGACCCAGAGAAATTCGAATA CACCCGCACTNNNACGTATGCCA	71	TGCAGGACCCAGAGAAATTCGAATA CATCGAAGCTGNNNACGTATGCCA	311	TGCAGGACCCAGAGAAATTCGAATA CAATACCTCCNNNACGTATGCCA	551
TGCAGGACCCAGAGAAATTCGAATA CACCAAGCATANNNACGTATGCCA	72	TGCAGGACCCAGAGAAATTCGAATA CATAGCTAATNNNACGTATGCCA	312	TGCAGGACCCAGAGAAATTCGAATA CACTTTTTCANNNACGTATGCCA	552
TGCAGGACCCAGAGAAATTCGAATA CAGCGTACATNNNACGTATGCCA	73	TGCAGGACCCAGAGAAATTCGAATA CAOCCGATANNNACGTATGCCA	313	TGCAGGACCCAGAGAAATTCGAATA CAATATCATGNNNACGTATGCCA	553
TGCAGGACCCAGAGAAATTCGAATA GACCATATCCNNNACGTATGCCA	74	TGCAGGACCCAGAGAAATTCGAATA CAATGTATGANNNACGTATGCCA	314	TGCAGGACCCAGAGAAATTCGAATA CATACATATGNNNACGTATGCCA	554

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池 -1	SEQ ID NO:	池 -2	SEQ ID NO:	池 -3	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATA	73	TGCAGGACCCAGAGAAATTCGAATA	315	TGCAGGACCCAGAGAAATTCGAATA	553
CACATACCGTNNNNCTAGCGTTAC		CATCGCGATANNNNCTAGCGTTAC		CAACTTTTGTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	76	TGCAGGACCCAGAGAAATTCGAATA	316	TGCAGGACCCAGAGAAATTCGAATA	556
CAATATAGCTNNNNCTAGCGTTAC		CACACAGCTNNNNCTAGCGTTAC		CATATATGACNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	77	TGCAGGACCCAGAGAAATTCGAATA	317	TGCAGGACCCAGAGAAATTCGAATA	557
CAACAGGTATNNNNCTAGCGTTAC		CAACGGTGCNNNNCTAGCGTTAC		CAACAGACAGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	78	TGCAGGACCCAGAGAAATTCGAATA	318	TGCAGGACCCAGAGAAATTCGAATA	558
CACAACTGANNNNCTAGCGTTAC		CACTTAGGCMNNNNCTAGCGTTAC		CAGCTGCTATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	79	TGCAGGACCCAGAGAAATTCGAATA	319	TGCAGGACCCAGAGAAATTCGAATA	559
CATGATGGTNNNNCTAGCGTTAC		CATGCGATGNNNNCTAGCGTTAC		CACCGAAACTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	80	TGCAGGACCCAGAGAAATTCGAATA	320	TGCAGGACCCAGAGAAATTCGAATA	560
CAGGAGCCGANNNNCTAGCGTTAC		CAATGGTGCNNNNCTAGCGTTAC		CAGCTAGGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	81	TGCAGGACCCAGAGAAATTCGAATA	321	TGCAGGACCCAGAGAAATTCGAATA	561
CAATGCGCCNNNNCTAGCGTTAC		CAACCCGAGNNNNCTAGCGTTAC		CAGCTTCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	82	TGCAGGACCCAGAGAAATTCGAATA	322	TGCAGGACCCAGAGAAATTCGAATA	562
CATGCTGTAGNNNNCTAGCGTTAC		CAGCAGACCGNNNNCTAGCGTTAC		CAACAGCATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	85	TGCAGGACCCAGAGAAATTCGAATA	323	TGCAGGACCCAGAGAAATTCGAATA	563
CAGGATTGACNNNNCTAGCGTTAC		CACCTGGCAGNNNNCTAGCGTTAC		CAACGAGACTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	84	TGCAGGACCCAGAGAAATTCGAATA	324	TGCAGGACCCAGAGAAATTCGAATA	564
CATTTGTATNNNNCTAGCGTTAC		CAGAGAGTGNNNNNCTAGCGTTAC		CAATCATATGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	85	TGCAGGACCCAGAGAAATTCGAATA	325	TGCAGGACCCAGAGAAATTCGAATA	565
CACATATGGCNNNNCTAGCGTTAC		CACGTTCTATNNNNCTAGCGTTAC		CATGAGATTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	86	TGCAGGACCCAGAGAAATTCGAATA	326	TGCAGGACCCAGAGAAATTCGAATA	566
CAGCATGAAANNNNCTAGCGTTAC		CAGAGGTGANNNNCTAGCGTTAC		CAGCGCGCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	87	TGCAGGACCCAGAGAAATTCGAATA	327	TGCAGGACCCAGAGAAATTCGAATA	567
CACAGGAAACNNNNCTAGCGTTAC		CATTCTCTCCNNNNCTAGCGTTAC		CAAGGCGCAGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	88	TGCAGGACCCAGAGAAATTCGAATA	328	TGCAGGACCCAGAGAAATTCGAATA	568
CACCTTAGCANNNNCTAGCGTTAC		CACCTGTCTNNNNCTAGCGTTAC		CAGTAGACACNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	89	TGCAGGACCCAGAGAAATTCGAATA	329	TGCAGGACCCAGAGAAATTCGAATA	569
CAACCTTAGCTNNNNCTAGCGTTAC		CACCTCAGCAANNNNCTAGCGTTAC		CAAGATTTCANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	90	TGCAGGACCCAGAGAAATTCGAATA	330	TGCAGGACCCAGAGAAATTCGAATA	570
CACCATTTCTNNNNCTAGCGTTAC		CATCTTATCTNNNNCTAGCGTTAC		CATGCACTCTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	91	TGCAGGACCCAGAGAAATTCGAATA	331	TGCAGGACCCAGAGAAATTCGAATA	571
CATCTGGTTCTNNNNCTAGCGTTAC		CATCTGGCAGNNNNCTAGCGTTAC		CACCTCAGAGTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	92	TGCAGGACCCAGAGAAATTCGAATA	332	TGCAGGACCCAGAGAAATTCGAATA	572
CACACCTGTNNNNCTAGCGTTAC		CACCTTTCTGNNNNCTAGCGTTAC		CACCTCTGTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	93	TGCAGGACCCAGAGAAATTCGAATA	333	TGCAGGACCCAGAGAAATTCGAATA	573
CAAGAGAGGANNNNCTAGCGTTAC		CAATGTGAGGNNNNCTAGCGTTAC		CATTATCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	94	TGCAGGACCCAGAGAAATTCGAATA	334	TGCAGGACCCAGAGAAATTCGAATA	574
CAATGCGCCGNNNNCTAGCGTTAC		CAACAAACATNNNNCTAGCGTTAC		CAGCGGTTGCMNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	95	TGCAGGACCCAGAGAAATTCGAATA	335	TGCAGGACCCAGAGAAATTCGAATA	575
CATAGGCTGTNNNNCTAGCGTTAC		CAGAGAGACNNNNCTAGCGTTAC		CAACTTCTCTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	96	TGCAGGACCCAGAGAAATTCGAATA	336	TGCAGGACCCAGAGAAATTCGAATA	576
CAGAAAGACNNNNCTAGCGTTAC		CACCTTCAGGANNNNCTAGCGTTAC		CATTGTAGGCMNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	97	TGCAGGACCCAGAGAAATTCGAATA	337	TGCAGGACCCAGAGAAATTCGAATA	577
CATCATTTGTNNNNCTAGCGTTAC		CATCTCTGGNNNNCTAGCGTTAC		CATGACCCCAANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	98	TGCAGGACCCAGAGAAATTCGAATA	338	TGCAGGACCCAGAGAAATTCGAATA	578
CATCGAAACANNNNCTAGCGTTAC		CACCTTCTCTNNNNCTAGCGTTAC		CACCTCTGTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	99	TGCAGGACCCAGAGAAATTCGAATA	339	TGCAGGACCCAGAGAAATTCGAATA	579
CAAGCTTAGCANNNNCTAGCGTTAC		CAATAGTATGNNNNCTAGCGTTAC		CAAGGCACTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	100	TGCAGGACCCAGAGAAATTCGAATA	340	TGCAGGACCCAGAGAAATTCGAATA	580
CACCTCGGTTNNNNCTAGCGTTAC		CAGCATAGAGNNNNCTAGCGTTAC		CACCTATGATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	101	TGCAGGACCCAGAGAAATTCGAATA	341	TGCAGGACCCAGAGAAATTCGAATA	581
CAAAATGCTTNNNNCTAGCGTTAC		CATAGCTCTNNNNCTAGCGTTAC		CACAGGTGCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	102	TGCAGGACCCAGAGAAATTCGAATA	342	TGCAGGACCCAGAGAAATTCGAATA	582
CATACACGTTNNNNCTAGCGTTAC		CAAGCAAGTANNNNCTAGCGTTAC		CATTCTTTTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	103	TGCAGGACCCAGAGAAATTCGAATA	343	TGCAGGACCCAGAGAAATTCGAATA	583
CAATCTCTGNNNNCTAGCGTTAC		CACATCTCTNNNNCTAGCGTTAC		CATTTCGCGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	104	TGCAGGACCCAGAGAAATTCGAATA	344	TGCAGGACCCAGAGAAATTCGAATA	584
CAGTAATGCTNNNNCTAGCGTTAC		CAAGAGATTANNNNCTAGCGTTAC		CAAGCCTGTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	105	TGCAGGACCCAGAGAAATTCGAATA	345	TGCAGGACCCAGAGAAATTCGAATA	585
CATTGCGCGNNNNCTAGCGTTAC		CAATCGAAGANNNNCTAGCGTTAC		CAAGCGCACTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	106	TGCAGGACCCAGAGAAATTCGAATA	346	TGCAGGACCCAGAGAAATTCGAATA	586
CAGTCAGGANNNNCTAGCGTTAC		CAGGAGTACANNNNCTAGCGTTAC		CATGTTGAGCMMNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	107	TGCAGGACCCAGAGAAATTCGAATA	347	TGCAGGACCCAGAGAAATTCGAATA	587
CAGTTAAAGNNNNCTAGCGTTAC		CAATAGCAGGNNNNCTAGCGTTAC		CAAAAAGTTGNNNNCTAGCGTTAC	

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池-1	SEQ ID NO.	池-2	SEQ ID NO.	池-3	SEQ ID NO.
TGCAGGACCAGAGAAATTCGAATA	108	TGCAGGACCAGAGAAATTCGAATA	348	TGCAGGACCAGAGAAATTCGAATA	588
CATGTCATAANNCTAGCGTTAC		CATGTAATTGNNCTAGCGTTAC		CACGCTGCCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	109	TGCAGGACCAGAGAAATTCGAATA	349	TGCAGGACCAGAGAAATTCGAATA	589
CACCTTGAAATNNCTAGCGTTAC		CAGTTCGCCGNNCTAGCGTTAC		CACAGCGCTGNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	110	TGCAGGACCAGAGAAATTCGAATA	350	TGCAGGACCAGAGAAATTCGAATA	590
CATGTGGCATNNCTAGCGTTAC		CATAGATTTGNNCTAGCGTTAC		CAAGCTAAGCNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	111	TGCAGGACCAGAGAAATTCGAATA	351	TGCAGGACCAGAGAAATTCGAATA	591
CATCTACACNNCTAGCGTTAC		CAAGGACAGNNCTAGCGTTAC		CAACGGCTGNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	112	TGCAGGACCAGAGAAATTCGAATA	352	TGCAGGACCAGAGAAATTCGAATA	592
CATGATGCTNNCTAGCGTTAC		CACCTGCTGNNCTAGCGTTAC		CATAGTTCAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	113	TGCAGGACCAGAGAAATTCGAATA	353	TGCAGGACCAGAGAAATTCGAATA	593
CATCTAGCCTNNCTAGCGTTAC		CACCTTGTATNNCTAGCGTTAC		CAATGTAGCNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	114	TGCAGGACCAGAGAAATTCGAATA	354	TGCAGGACCAGAGAAATTCGAATA	594
CAATAAAGCANNCTAGCGTTAC		CACGTACGNNCTAGCGTTAC		CAAGAAACANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	115	TGCAGGACCAGAGAAATTCGAATA	355	TGCAGGACCAGAGAAATTCGAATA	595
CATGCTAAANNCTAGCGTTAC		CAGTTTGCCANNCTAGCGTTAC		CAGAAACGNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	116	TGCAGGACCAGAGAAATTCGAATA	356	TGCAGGACCAGAGAAATTCGAATA	596
CACATGACGTTNNCTAGCGTTAC		CATGCTCTGNNCTAGCGTTAC		CACGCTATACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	117	TGCAGGACCAGAGAAATTCGAATA	357	TGCAGGACCAGAGAAATTCGAATA	597
CACCTTATCATNNCTAGCGTTAC		CATCAGTATANNCTAGCGTTAC		CATAACATACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	118	TGCAGGACCAGAGAAATTCGAATA	358	TGCAGGACCAGAGAAATTCGAATA	598
CACGGCTGANNCTAGCGTTAC		CACCCAGGTANNCTAGCGTTAC		CACCTGCTATCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	119	TGCAGGACCAGAGAAATTCGAATA	359	TGCAGGACCAGAGAAATTCGAATA	599
CACGTCMAATGNNCTAGCGTTAC		CAAGGCTAANNCTAGCGTTAC		CACGGCAACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	120	TGCAGGACCAGAGAAATTCGAATA	360	TGCAGGACCAGAGAAATTCGAATA	600
CACCTTATCTNNCTAGCGTTAC		CAAGATGCCANNCTAGCGTTAC		CACAAAAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	121	TGCAGGACCAGAGAAATTCGAATA	361	TGCAGGACCAGAGAAATTCGAATA	601
CAGGAGGATANNCTAGCGTTAC		CAGCATCGCANNCTAGCGTTAC		CACGTTAGCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	122	TGCAGGACCAGAGAAATTCGAATA	362	TGCAGGACCAGAGAAATTCGAATA	602
CAATTGTCNNCTAGCGTTAC		CAGCTCTGGAANNCTAGCGTTAC		CACCTTAATCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	123	TGCAGGACCAGAGAAATTCGAATA	363	TGCAGGACCAGAGAAATTCGAATA	603
CAAGCTGCANNCTAGCGTTAC		CAAGCTGTACNNCTAGCGTTAC		CATGTGGCCNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	124	TGCAGGACCAGAGAAATTCGAATA	364	TGCAGGACCAGAGAAATTCGAATA	604
CACGAGGTCNNCTAGCGTTAC		CAGAGGCGCANNCTAGCGTTAC		CATGTAGACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	125	TGCAGGACCAGAGAAATTCGAATA	365	TGCAGGACCAGAGAAATTCGAATA	605
CACGGGACANNCTAGCGTTAC		CATGGTGGANNCTAGCGTTAC		CATACCGCATGNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	126	TGCAGGACCAGAGAAATTCGAATA	366	TGCAGGACCAGAGAAATTCGAATA	606
CATGGCGCTNNCTAGCGTTAC		CACGGTGTANNCTAGCGTTAC		CATTGCCCGNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	127	TGCAGGACCAGAGAAATTCGAATA	367	TGCAGGACCAGAGAAATTCGAATA	607
CAGTTTACGANNCTAGCGTTAC		CATCGCGACNNCTAGCGTTAC		CATGCTTCTNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	128	TGCAGGACCAGAGAAATTCGAATA	368	TGCAGGACCAGAGAAATTCGAATA	608
CATTTATCATNNCTAGCGTTAC		CAGCTGTGTANNCTAGCGTTAC		CAAAACGCTANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	129	TGCAGGACCAGAGAAATTCGAATA	369	TGCAGGACCAGAGAAATTCGAATA	609
CACCTTCTCANNCTAGCGTTAC		CAACGTGCGCANNCTAGCGTTAC		CAGGCTATACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	130	TGCAGGACCAGAGAAATTCGAATA	370	TGCAGGACCAGAGAAATTCGAATA	610
CAAAACGCTANNCTAGCGTTAC		CAATCAGCCANNCTAGCGTTAC		CAATTGCTTANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	131	TGCAGGACCAGAGAAATTCGAATA	371	TGCAGGACCAGAGAAATTCGAATA	611
CAACTTGTCCNNCTAGCGTTAC		CAGATACCTANNCTAGCGTTAC		CACAGGATGANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	132	TGCAGGACCAGAGAAATTCGAATA	372	TGCAGGACCAGAGAAATTCGAATA	612
CATTTGTATANNCTAGCGTTAC		CAATTTGCCANNCTAGCGTTAC		CACGTTATCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	133	TGCAGGACCAGAGAAATTCGAATA	373	TGCAGGACCAGAGAAATTCGAATA	613
CAGGACTGCGNNCTAGCGTTAC		CACCTTAAGTANNCTAGCGTTAC		CAGTTTCAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	134	TGCAGGACCAGAGAAATTCGAATA	374	TGCAGGACCAGAGAAATTCGAATA	614
CATGCTGCAANNCTAGCGTTAC		CATATGCCCTANNCTAGCGTTAC		CACAAATCTNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	135	TGCAGGACCAGAGAAATTCGAATA	375	TGCAGGACCAGAGAAATTCGAATA	615
CACAGAAATANNCTAGCGTTAC		CAACTTGACNNCTAGCGTTAC		CACCTGCAACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	136	TGCAGGACCAGAGAAATTCGAATA	376	TGCAGGACCAGAGAAATTCGAATA	616
CATCGGAGCANNCTAGCGTTAC		CAAGGAACANNCTAGCGTTAC		CAGGTGCCANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	137	TGCAGGACCAGAGAAATTCGAATA	377	TGCAGGACCAGAGAAATTCGAATA	617
CAATTTCTGNNCTAGCGTTAC		CATGAGCGAANNCTAGCGTTAC		CACGATAACNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	138	TGCAGGACCAGAGAAATTCGAATA	378	TGCAGGACCAGAGAAATTCGAATA	618
CAACTTGTANNCTAGCGTTAC		CATGCTGTGANNCTAGCGTTAC		CATTATGACANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	139	TGCAGGACCAGAGAAATTCGAATA	379	TGCAGGACCAGAGAAATTCGAATA	619
CACAGGCTGANNCTAGCGTTAC		CAGGTTCTGANNCTAGCGTTAC		CACGCTTACANNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	140	TGCAGGACCAGAGAAATTCGAATA	380	TGCAGGACCAGAGAAATTCGAATA	620
CAAACTCGCTNNCTAGCGTTAC		CAACAAACANNCTAGCGTTAC		CACCTTCTCANNCTAGCGTTAC	

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCCAGAGAAATCGAATA	141	TGCAGGACCCAGAGAAATCGAATA	381	TGCAGGACCCAGAGAAATCGAATA	621
CAGCCCTATCANNNGATCGACATG		CAAGCTAGANNNGATCGACATG		CAACCCAGCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	142	TGCAGGACCCAGAGAAATCGAATA	382	TGCAGGACCCAGAGAAATCGAATA	622
CACCGCTAAANNNGATCGACATG		CATTAAATATNNNGATCGACATG		CAGTAGCTGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	143	TGCAGGACCCAGAGAAATCGAATA	383	TGCAGGACCCAGAGAAATCGAATA	623
CAGTGAATGNNNGATCGACATG		CAAGGAGTCANNNGATCGACATG		CAGTTCCTAAANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	144	TGCAGGACCCAGAGAAATCGAATA	384	TGCAGGACCCAGAGAAATCGAATA	624
CATCTCTCANNNGATCGACATG		CACTGCACTGNNNGATCGACATG		CAGCGTTTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	145	TGCAGGACCCAGAGAAATCGAATA	385	TGCAGGACCCAGAGAAATCGAATA	625
CATCTCTAGNNNGATCGACATG		CAGCGGACAGNNNGATCGACATG		CAGTCTGCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	146	TGCAGGACCCAGAGAAATCGAATA	386	TGCAGGACCCAGAGAAATCGAATA	626
CACAGGCGCCNNNGATCGACATG		CACGCTCGTCNNNGATCGACATG		CAACAGAAATNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	147	TGCAGGACCCAGAGAAATCGAATA	387	TGCAGGACCCAGAGAAATCGAATA	627
CAGTCATTAANNNGATCGACATG		CATCTGATGNNNGATCGACATG		CATCTGCTATNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	148	TGCAGGACCCAGAGAAATCGAATA	388	TGCAGGACCCAGAGAAATCGAATA	628
CATCTGCTGANNNGATCGACATG		CAGGCTAGANNNGATCGACATG		CAGGCTGTGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	149	TGCAGGACCCAGAGAAATCGAATA	389	TGCAGGACCCAGAGAAATCGAATA	629
CACAGGCGANNNGATCGACATG		CACTGAGCCANNNGATCGACATG		CAGCAGTCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	150	TGCAGGACCCAGAGAAATCGAATA	390	TGCAGGACCCAGAGAAATCGAATA	630
CAAGGTTTCANNNGATCGACATG		CACACCCGTCNNNGATCGACATG		CAGTAACCCANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	151	TGCAGGACCCAGAGAAATCGAATA	391	TGCAGGACCCAGAGAAATCGAATA	631
CACGCTCTATNNNGATCGACATG		CATCTCTGANNNGATCGACATG		CACATCTGTANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	152	TGCAGGACCCAGAGAAATCGAATA	392	TGCAGGACCCAGAGAAATCGAATA	632
CATCTGCTGNNNGATCGACATG		CAGGCAACCCNNNGATCGACATG		CAAAACCGTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	153	TGCAGGACCCAGAGAAATCGAATA	393	TGCAGGACCCAGAGAAATCGAATA	633
CATCAGCACANNNGATCGACATG		CACAGTCTGANNNGATCGACATG		CAATCTGCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	154	TGCAGGACCCAGAGAAATCGAATA	394	TGCAGGACCCAGAGAAATCGAATA	634
CACGAACTACNNNGATCGACATG		CATCTACTCANNNGATCGACATG		CATCTAGCCANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	155	TGCAGGACCCAGAGAAATCGAATA	395	TGCAGGACCCAGAGAAATCGAATA	635
CATACCTAAANNNGATCGACATG		CATCTCATACNNNGATCGACATG		CAGGTCTACANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	156	TGCAGGACCCAGAGAAATCGAATA	396	TGCAGGACCCAGAGAAATCGAATA	636
CAGGTACCAANNNGATCGACATG		CAACCCGACNNNGATCGACATG		CAAGTGAACGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	157	TGCAGGACCCAGAGAAATCGAATA	397	TGCAGGACCCAGAGAAATCGAATA	637
CACAGGCTTNNNGATCGACATG		CAGGCAAACTNNNGATCGACATG		CATCTCTTANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	158	TGCAGGACCCAGAGAAATCGAATA	398	TGCAGGACCCAGAGAAATCGAATA	638
CAGAAACCTTNNNGATCGACATG		CAGGATCCGNNNGATCGACATG		CATGGCTTGANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	159	TGCAGGACCCAGAGAAATCGAATA	399	TGCAGGACCCAGAGAAATCGAATA	639
CATCTCGCATNNNGATCGACATG		CACCTCTCTTNNNGATCGACATG		CAATTACGCGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	160	TGCAGGACCCAGAGAAATCGAATA	400	TGCAGGACCCAGAGAAATCGAATA	640
CACCAATCTGNNNGATCGACATG		CATCTGTGCGNNNGATCGACATG		CATGGCTCTTNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	161	TGCAGGACCCAGAGAAATCGAATA	401	TGCAGGACCCAGAGAAATCGAATA	641
CAACCTTACNNNGATCGACATG		CACCTATCTCANNNGATCGACATG		CACACTCACTNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	162	TGCAGGACCCAGAGAAATCGAATA	402	TGCAGGACCCAGAGAAATCGAATA	642
CAGCGGTCTGNNNGATCGACATG		CAAGATGCTTNNNGATCGACATG		CACTTCAGGCGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	163	TGCAGGACCCAGAGAAATCGAATA	403	TGCAGGACCCAGAGAAATCGAATA	643
CAAAATCAACGNNNGATCGACATG		CAATTTGAGANNNGATCGACATG		CAACCAATCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	164	TGCAGGACCCAGAGAAATCGAATA	404	TGCAGGACCCAGAGAAATCGAATA	644
CAAAJAGTAGNNNGATCGACATG		CAGTGTCTGNNNGATCGACATG		CAACGTAAACNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	165	TGCAGGACCCAGAGAAATCGAATA	405	TGCAGGACCCAGAGAAATCGAATA	645
CAGGATCTANNNGATCGACATG		CAAAAGCAATANNNGATCGACATG		CAACGCTCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	166	TGCAGGACCCAGAGAAATCGAATA	406	TGCAGGACCCAGAGAAATCGAATA	646
CAAGCGCTGNNNGATCGACATG		CATTAGCGCANNNGATCGACATG		CATTCCGGAANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	167	TGCAGGACCCAGAGAAATCGAATA	407	TGCAGGACCCAGAGAAATCGAATA	647
CAGACCCGCTNNNGATCGACATG		CAAAACGATGNNNGATCGACATG		CACGCACTATNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	168	TGCAGGACCCAGAGAAATCGAATA	408	TGCAGGACCCAGAGAAATCGAATA	648
CACGCTAAAGNNNGATCGACATG		CAGCATGCAANNNGATCGACATG		CACAAATCTCANNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	169	TGCAGGACCCAGAGAAATCGAATA	409	TGCAGGACCCAGAGAAATCGAATA	649
CAAGGATGANNNGATCGACATG		CATCTCATATNNNGATCGACATG		CATCAGAGTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	170	TGCAGGACCCAGAGAAATCGAATA	410	TGCAGGACCCAGAGAAATCGAATA	650
CATTCTGGANNNGATCGACATG		CACTGCGCTTNNNGATCGACATG		CAAACTGTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	171	TGCAGGACCCAGAGAAATCGAATA	411	TGCAGGACCCAGAGAAATCGAATA	651
CAGCTCAACNNNGATCGACATG		CAEATTOGCAANNNGATCGACATG		CACTAGCATGNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	172	TGCAGGACCCAGAGAAATCGAATA	412	TGCAGGACCCAGAGAAATCGAATA	652
CATAAGCTTANNNGATCGACATG		CAATCTATCTNNNGATCGACATG		CAGATTAACTNNNGATCGACATG	
TGCAGGACCCAGAGAAATCGAATA	173	TGCAGGACCCAGAGAAATCGAATA	413	TGCAGGACCCAGAGAAATCGAATA	653
CACAGCCCTTNNNGATCGACATG		CAGTCACCCNNNGATCGACATG		CAGGCTAGGNNNGATCGACATG	

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池 -1	SEQ ID NO:	池 -2	SEQ ID NO:	池 -3	SEQ ID NO:
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CACCTTCCCGNNNGATCGACATG		CACCTTGTGANNNGATCGACATG		CAATACCGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	175	TGCAGGACCAGAGAATTGGAATA	415	TGCAGGACCAGAGAATTGGAATA	655
CAGTGAAGATNNNGATCGACATG		CAGGCTTCCGNNNGATCGACATG		CAABATGTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	176	TGCAGGACCAGAGAATTGGAATA	416	TGCAGGACCAGAGAATTGGAATA	656
CAGGCTTCCGNNNGATCGACATG		CACATCGATGNNNGATCGACATG		CAGGCGATCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	177	TGCAGGACCAGAGAATTGGAATA	417	TGCAGGACCAGAGAATTGGAATA	657
CAATTAATTCGNNNGATCGACATG		CAAGTCCGCGNNNGATCGACATG		CACTCCGCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	178	TGCAGGACCAGAGAATTGGAATA	418	TGCAGGACCAGAGAATTGGAATA	658
CAGTAATAGGNNNGATCGACATG		CAGATAGCGANNNGATCGACATG		CAGATAAGGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	179	TGCAGGACCAGAGAATTGGAATA	419	TGCAGGACCAGAGAATTGGAATA	659
CATACAAGCCNNNGATCGACATG		CATCTTTGGCNNNGATCGACATG		CAGGCATCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	180	TGCAGGACCAGAGAATTGGAATA	420	TGCAGGACCAGAGAATTGGAATA	660
CAAGGCGGANNNGATCGACATG		CATCTCATCGNNNGATCGACATG		CATCTTATGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	181	TGCAGGACCAGAGAATTGGAATA	421	TGCAGGACCAGAGAATTGGAATA	661
CAATACTTTCNNNGATCGACATG		CATGAGGCGCANNNGATCGACATG		CACGCGATCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	182	TGCAGGACCAGAGAATTGGAATA	422	TGCAGGACCAGAGAATTGGAATA	662
CACATGGATCANNNGATCGACATG		CAAGTCTCGANNNGATCGACATG		CAACCGGTCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	183	TGCAGGACCAGAGAATTGGAATA	423	TGCAGGACCAGAGAATTGGAATA	663
CAACCGGCTANNNGATCGACATG		CAAGGTATANNNGATCGACATG		CACACGATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	184	TGCAGGACCAGAGAATTGGAATA	424	TGCAGGACCAGAGAATTGGAATA	664
CAGTCTGAGANNNGATCGACATG		CAAGTCTCGCANNNGATCGACATG		CAAACTCCGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	185	TGCAGGACCAGAGAATTGGAATA	425	TGCAGGACCAGAGAATTGGAATA	665
CATBAATCTCANNNGATCGACATG		CATCAGATCCGNNNGATCGACATG		CAOCCCTTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	186	TGCAGGACCAGAGAATTGGAATA	426	TGCAGGACCAGAGAATTGGAATA	666
CATAACCCCTCANNNGATCGACATG		CAGCATACACNNNGATCGACATG		CATCTTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	187	TGCAGGACCAGAGAATTGGAATA	427	TGCAGGACCAGAGAATTGGAATA	667
CAGGCGCTTCGNNNGATCGACATG		CATCCACAGNNNGATCGACATG		CATATTTAAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	188	TGCAGGACCAGAGAATTGGAATA	428	TGCAGGACCAGAGAATTGGAATA	668
CACCGGACCCNNNGATCGACATG		CATCTGCTTANNNGATCGACATG		CATTAATGCGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	189	TGCAGGACCAGAGAATTGGAATA	429	TGCAGGACCAGAGAATTGGAATA	669
CATGGAAGTGNNGATCGACATG		CCACACCCGNNNGATCGACATG		CACCTTGTGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	190	TGCAGGACCAGAGAATTGGAATA	430	TGCAGGACCAGAGAATTGGAATA	670
CAAAAGTCTANNNGATCGACATG		CAGACCTCCGNNNGATCGACATG		CATACCGAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	191	TGCAGGACCAGAGAATTGGAATA	431	TGCAGGACCAGAGAATTGGAATA	671
CAATGAATAGNNNGATCGACATG		CATGGCATTNNNGATCGACATG		CAAGTCACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	192	TGCAGGACCAGAGAATTGGAATA	432	TGCAGGACCAGAGAATTGGAATA	672
CATCTCTCTCANNNGATCGACATG		CATCTCCGCGNNNGATCGACATG		CAGTTATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	193	TGCAGGACCAGAGAATTGGAATA	433	TGCAGGACCAGAGAATTGGAATA	673
CAOCCAGCCTNNNGATCGACATG		CAOCCAGGCTGNNNGATCGACATG		CATTTCCGAAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	194	TGCAGGACCAGAGAATTGGAATA	434	TGCAGGACCAGAGAATTGGAATA	674
CAAAACAAAGCANNNGATCGACATG		CAAAATATAANNNGATCGACATG		CACACATCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	195	TGCAGGACCAGAGAATTGGAATA	435	TGCAGGACCAGAGAATTGGAATA	675
CACGCTCACGNNNGATCGACATG		CAGCAATTTANNNGATCGACATG		CATTGGAAAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	196	TGCAGGACCAGAGAATTGGAATA	436	TGCAGGACCAGAGAATTGGAATA	676
CATGGTGATCANNNGATCGACATG		CAACTCACTGNNNGATCGACATG		CAGTCCGCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	197	TGCAGGACCAGAGAATTGGAATA	437	TGCAGGACCAGAGAATTGGAATA	677
CAGTTGCTAGNNNGATCGACATG		CAAGAGGCAANNNGATCGACATG		CATGAAGCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	198	TGCAGGACCAGAGAATTGGAATA	438	TGCAGGACCAGAGAATTGGAATA	678
CATCACCCTANNNGATCGACATG		CATAGGCTGNNNGATCGACATG		CAAAAGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	199	TGCAGGACCAGAGAATTGGAATA	439	TGCAGGACCAGAGAATTGGAATA	679
CAGACTCTGANNNGATCGACATG		CACACACAGTNNNGATCGACATG		CAGATGGAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	200	TGCAGGACCAGAGAATTGGAATA	440	TGCAGGACCAGAGAATTGGAATA	680
CACGTATGACNNNGATCGACATG		CATGATAGANNNGATCGACATG		CAGCCTCGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	201	TGCAGGACCAGAGAATTGGAATA	441	TGCAGGACCAGAGAATTGGAATA	681
CATGCAACCGNNNGATCGACATG		CAGACAACGANNNGATCGACATG		CAAAATAAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	202	TGCAGGACCAGAGAATTGGAATA	442	TGCAGGACCAGAGAATTGGAATA	682
CAACTGATGNNNGATCGACATG		CACTGCTCANNNGATCGACATG		CATTCCGCGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	203	TGCAGGACCAGAGAATTGGAATA	443	TGCAGGACCAGAGAATTGGAATA	683
CATACGTCCGNNNGATCGACATG		CAGTTTCCGANNNGATCGACATG		CATCTCTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	204	TGCAGGACCAGAGAATTGGAATA	444	TGCAGGACCAGAGAATTGGAATA	684
CACGGCCGCGNNNGATCGACATG		CATTCAATAGNNNGATCGACATG		CATTGTGGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	205	TGCAGGACCAGAGAATTGGAATA	445	TGCAGGACCAGAGAATTGGAATA	685
CAATCTTTGNNNGATCGACATG		CATAGCCATGNNNGATCGACATG		CATCCCATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	206	TGCAGGACCAGAGAATTGGAATA	446	TGCAGGACCAGAGAATTGGAATA	686
CATTGTACTNNNGATCGACATG		CAGTTGTAAANNNGATCGACATG		CAGTGTGACNNNGATCGACATG	

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池-1	SEQ ID NO:	池-2	SEQ ID NO:	池-3	SEQ ID NO:
TGCAGGACCCAGAGAATTTCGAATA	207	TGCAGGACCCAGAGAATTTCGAATA	447	TGCAGGACCCAGAGAATTTCGAATA	687
CATGTTAATGNNNTGCATCAGGT		CACCTGCACTNNNTGCATCAGGT		CATGCCCTAANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	208	TGCAGGACCCAGAGAATTTCGAATA	448	TGCAGGACCCAGAGAATTTCGAATA	688
CAAAACATTGNNNTGCATCAGGT		CATTAGAGCCNNNTGCATCAGGT		CACGCTGACGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	209	TGCAGGACCCAGAGAATTTCGAATA	449	TGCAGGACCCAGAGAATTTCGAATA	689
CACGCCCGAANNNTGCATCAGGT		CAGGCCCTACNNNTGCATCAGGT		CATGGTGGTTNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	210	TGCAGGACCCAGAGAATTTCGAATA	450	TGCAGGACCCAGAGAATTTCGAATA	690
CACAGCGCACNNNTGCATCAGGT		CAAAATGGACGNNNTGCATCAGGT		CACATCTTANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	211	TGCAGGACCCAGAGAATTTCGAATA	451	TGCAGGACCCAGAGAATTTCGAATA	691
CACAGAGTATCANNNTGCATCAGGT		CAAGACCTGTNNNTGCATCAGGT		CAATAAOCCTANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	212	TGCAGGACCCAGAGAATTTCGAATA	452	TGCAGGACCCAGAGAATTTCGAATA	692
CAATGGTGGANNNTGCATCAGGT		CACITACATNNNTGCATCAGGT		CAAGAGTGTNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	213	TGCAGGACCCAGAGAATTTCGAATA	453	TGCAGGACCCAGAGAATTTCGAATA	693
CATCACACTCANNNTGCATCAGGT		CATAAGAAACNNNTGCATCAGGT		CAAAATGGCGANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	214	TGCAGGACCCAGAGAATTTCGAATA	454	TGCAGGACCCAGAGAATTTCGAATA	694
CAGAAACGACNNNTGCATCAGGT		CAGATTCTTNNNTGCATCAGGT		CAGTCTCTTNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	215	TGCAGGACCCAGAGAATTTCGAATA	455	TGCAGGACCCAGAGAATTTCGAATA	695
CAGAGCTTTANNNTGCATCAGGT		CATCTAGGTGNNNTGCATCAGGT		CATGCCOCCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	216	TGCAGGACCCAGAGAATTTCGAATA	456	TGCAGGACCCAGAGAATTTCGAATA	696
CAGGCCCTTNNNTGCATCAGGT		CAGTGTCTTNNNTGCATCAGGT		CAGGAGCTCGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	217	TGCAGGACCCAGAGAATTTCGAATA	457	TGCAGGACCCAGAGAATTTCGAATA	697
CACAACTCTCANNNTGCATCAGGT		CATAAACTTNNNTGCATCAGGT		CAACTGAAOCNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	218	TGCAGGACCCAGAGAATTTCGAATA	458	TGCAGGACCCAGAGAATTTCGAATA	698
CATGTACTGNNNTGCATCAGGT		CAGACATCCANNNTGCATCAGGT		CATCTGATCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	219	TGCAGGACCCAGAGAATTTCGAATA	459	TGCAGGACCCAGAGAATTTCGAATA	699
CATTTGGCTCANNNTGCATCAGGT		CATAAGTCCGNNNTGCATCAGGT		CACACTTCCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	220	TGCAGGACCCAGAGAATTTCGAATA	460	TGCAGGACCCAGAGAATTTCGAATA	700
CAGAAATATANNNTGCATCAGGT		CAAGGCSCGANNNTGCATCAGGT		CAGATCCTGANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	221	TGCAGGACCCAGAGAATTTCGAATA	461	TGCAGGACCCAGAGAATTTCGAATA	701
CAGAACTCACNNNTGCATCAGGT		CAGAGCTCTANNNTGCATCAGGT		CAAGAAGTATNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	222	TGCAGGACCCAGAGAATTTCGAATA	462	TGCAGGACCCAGAGAATTTCGAATA	702
CACITACCGTNNNTGCATCAGGT		CATCATAATGNNNTGCATCAGGT		CNNACCCACANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	223	TGCAGGACCCAGAGAATTTCGAATA	463	TGCAGGACCCAGAGAATTTCGAATA	703
CATCTTTACANNNTGCATCAGGT		CAGGATGGTANNNTGCATCAGGT		CATGCCGAAANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	224	TGCAGGACCCAGAGAATTTCGAATA	464	TGCAGGACCCAGAGAATTTCGAATA	704
CACGAAGTCNNNTGCATCAGGT		CATAGCCTTNNNTGCATCAGGT		CAATCAGAGGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	225	TGCAGGACCCAGAGAATTTCGAATA	465	TGCAGGACCCAGAGAATTTCGAATA	705
CACITTTGGANNNTGCATCAGGT		CAATCCOCCGNNNTGCATCAGGT		CAGTCATATANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	226	TGCAGGACCCAGAGAATTTCGAATA	466	TGCAGGACCCAGAGAATTTCGAATA	706
CAGTTCTCTGNNNTGCATCAGGT		CAGATTGCTGNNNTGCATCAGGT		CAACCCACCCNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	227	TGCAGGACCCAGAGAATTTCGAATA	467	TGCAGGACCCAGAGAATTTCGAATA	707
CACCTTCAACNNNTGCATCAGGT		CAGTGAATGAGNNNTGCATCAGGT		CACCCACAGCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	228	TGCAGGACCCAGAGAATTTCGAATA	468	TGCAGGACCCAGAGAATTTCGAATA	708
CAAAATGCTNNNTGCATCAGGT		CAAGGAACGNNNTGCATCAGGT		CATGCTGACANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	229	TGCAGGACCCAGAGAATTTCGAATA	469	TGCAGGACCCAGAGAATTTCGAATA	709
CAATTCGCGATNNNTGCATCAGGT		CAECTCTTTNNNTGCATCAGGT		CAGCAGCATNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	230	TGCAGGACCCAGAGAATTTCGAATA	470	TGCAGGACCCAGAGAATTTCGAATA	710
CAGGCTCGTNNNTGCATCAGGT		CAGTAATCGCANNNTGCATCAGGT		CAGGCGATGGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	231	TGCAGGACCCAGAGAATTTCGAATA	471	TGCAGGACCCAGAGAATTTCGAATA	711
CAGACCCCTAANNNTGCATCAGGT		CACCTGTTATNNNTGCATCAGGT		CATTGATGGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	232	TGCAGGACCCAGAGAATTTCGAATA	472	TGCAGGACCCAGAGAATTTCGAATA	712
CACAAATTTNNNTGCATCAGGT		CACACACACANNNTGCATCAGGT		CATGGAGGCGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	233	TGCAGGACCCAGAGAATTTCGAATA	473	TGCAGGACCCAGAGAATTTCGAATA	713
CATTTTTCCNNNTGCATCAGGT		CATAAAATAANNNTGCATCAGGT		CAGTATPACANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	234	TGCAGGACCCAGAGAATTTCGAATA	474	TGCAGGACCCAGAGAATTTCGAATA	714
CATTTCACGANNNTGCATCAGGT		CAAACGCACTNNNTGCATCAGGT		CACGACAATCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	235	TGCAGGACCCAGAGAATTTCGAATA	475	TGCAGGACCCAGAGAATTTCGAATA	715
CAGTGGTCTANNNTGCATCAGGT		CACATATGATNNNTGCATCAGGT		CAGTGGCCACNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	236	TGCAGGACCCAGAGAATTTCGAATA	476	TGCAGGACCCAGAGAATTTCGAATA	716
CATTTCTAATCANNNTGCATCAGGT		CAGCGTCATANNNTGCATCAGGT		CATAOCCGCGNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	237	TGCAGGACCCAGAGAATTTCGAATA	477	TGCAGGACCCAGAGAATTTCGAATA	717
CAATTTGATTGNNNTGCATCAGGT		CATAAGCCTGNNNTGCATCAGGT		CAGCGAAGCANNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	238	TGCAGGACCCAGAGAATTTCGAATA	478	TGCAGGACCCAGAGAATTTCGAATA	718
CATGCAATAGCANNNTGCATCAGGT		CATAAGCACGNNNTGCATCAGGT		CACCAATGACNNNTGCATCAGGT	
TGCAGGACCCAGAGAATTTCGAATA	239	TGCAGGACCCAGAGAATTTCGAATA	479	TGCAGGACCCAGAGAATTTCGAATA	719
CAGACAGATGNNNTGCATCAGGT		CACCTGGAAACNNNTGCATCAGGT		CAAGCCTTCTNNNTGCATCAGGT	

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池-1	SEQ ID No:	池-2	SEQ ID No:	池-3	SEQ ID No:
TGCAGGACCAGAGAATTCGAATA CATGCTCTACNNNTGCATCAGGT	240	TGCAGGACCAGAGAATTCGAATA CAACCGAGANNNTGCATCAGGT	480	TGCAGGACCAGAGAATTCGAATA CATATCACCCNNNTGCATCAGGT	720
TGCAGGACCAGAGAATTCGAATA CATGCGATACNNNTGCATCAGGT	241	TGCAGGACCAGAGAATTCGAATA CACTATCTATNNNTGCATCAGGT	481	TGCAGGACCAGAGAATTCGAATA CACCTTATGCHNNTGCATCAGGT	721
TGCAGGACCAGAGAATTCGAATA CAACACTGCANNNTGCATCAGGT	242	TGCAGGACCAGAGAATTCGAATA CACAAATTAGNNNTGCATCAGGT	482	TGCAGGACCAGAGAATTCGAATA CATTAATGACNNNTGCATCAGGT	722
TGCAGGACCAGAGAATTCGAATA CAGTCACCTGNNNTGCATCAGGT	243	TGCAGGACCAGAGAATTCGAATA CACTAAACGNNNTGCATCAGGT	483	TGCAGGACCAGAGAATTCGAATA CACTACCTTGNNNTGCATCAGGT	723
TGCAGGACCAGAGAATTCGAATA CAATTGATTCNNNTGCATCAGGT	244	TGCAGGACCAGAGAATTCGAATA CATAGTAGANNNTGCATCAGGT	484	TGCAGGACCAGAGAATTCGAATA CAAGGATCTCNNNTGCATCAGGT	724
TGCAGGACCAGAGAATTCGAATA CAAACTTAGCNNNTGCATCAGGT	245	TGCAGGACCAGAGAATTCGAATA CAGCAAACTGNNNTGCATCAGGT	485	TGCAGGACCAGAGAATTCGAATA CAAAATCAANNNTGCATCAGGT	725
TGCAGGACCAGAGAATTCGAATA CAGGCGSATCANNNTGCATCAGGT	246	TGCAGGACCAGAGAATTCGAATA CACAAATTATNNNTGCATCAGGT	486	TGCAGGACCAGAGAATTCGAATA CAGAAATGACNNNTGCATCAGGT	726
TGCAGGACCAGAGAATTCGAATA CAAGGATCTNNNTGCATCAGGT	247	TGCAGGACCAGAGAATTCGAATA CACAACTGACNNNTGCATCAGGT	487	TGCAGGACCAGAGAATTCGAATA CAACTAGATGNNNTGCATCAGGT	727
TGCAGGACCAGAGAATTCGAATA CATACTGACNNNTGCATCAGGT	248	TGCAGGACCAGAGAATTCGAATA CATTCGTCGNNNTGCATCAGGT	488	TGCAGGACCAGAGAATTCGAATA CATTTTCGGNNNTGCATCAGGT	728

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACACAGAGAAATCGAATA	729	TGCAGGACACAGAGAAATCGAATA	969	TGCAGGACACAGAGAAATCGAATA	1209
CATATGCGGNNNACGTATGCCA		CAGCGATTACNNNNACGTATGCCA		CACAATGACNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	730	TGCAGGACACAGAGAAATCGAATA	970	TGCAGGACACAGAGAAATCGAATA	1210
CAGTTGACCTGNNNACGTATGCCA		CATAGTCCGTGNNNACGTATGCCA		CAGGTACGTANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	731	TGCAGGACACAGAGAAATCGAATA	971	TGCAGGACACAGAGAAATCGAATA	1211
CATCCTACACNNNNACGTATGCCA		CAGTTATPACNNNNACGTATGCCA		CAGCCAGTACNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	732	TGCAGGACACAGAGAAATCGAATA	972	TGCAGGACACAGAGAAATCGAATA	1212
CAGTACTCTGNNNACGTATGCCA		CATATCTTGANNNNACGTATGCCA		CACRATCCGNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	733	TGCAGGACACAGAGAAATCGAATA	973	TGCAGGACACAGAGAAATCGAATA	1213
CAGCTTCCGNNNNACGTATGCCA		CAACGTTGANNNNACGTATGCCA		CATTGGACACNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	734	TGCAGGACACAGAGAAATCGAATA	974	TGCAGGACACAGAGAAATCGAATA	1214
CAGATGCTGNNNACGTATGCCA		CAACTCTGANNNNACGTATGCCA		CANCAATGCGNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	735	TGCAGGACACAGAGAAATCGAATA	975	TGCAGGACACAGAGAAATCGAATA	1215
CAGTCCGCTGNNNACGTATGCCA		CAGGACTACTNNNNACGTATGCCA		CACCTTTATANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	736	TGCAGGACACAGAGAAATCGAATA	976	TGCAGGACACAGAGAAATCGAATA	1216
CATATGTCCGNNNNACGTATGCCA		CATCTGTCCGNNNNACGTATGCCA		CAGTGGCTGNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	737	TGCAGGACACAGAGAAATCGAATA	977	TGCAGGACACAGAGAAATCGAATA	1217
CATATTTGCTNNNNACGTATGCCA		CACCCCTAAGTNNNNACGTATGCCA		CATCTCCGTTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	738	TGCAGGACACAGAGAAATCGAATA	978	TGCAGGACACAGAGAAATCGAATA	1218
CAGTCCGCGNNNNACGTATGCCA		CATTGGAGAGNNNNACGTATGCCA		CAATGGCCATNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	739	TGCAGGACACAGAGAAATCGAATA	979	TGCAGGACACAGAGAAATCGAATA	1219
CAAGATGGCNNNNACGTATGCCA		CAGAATCAANNNNACGTATGCCA		CATTTGATAGNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	740	TGCAGGACACAGAGAAATCGAATA	980	TGCAGGACACAGAGAAATCGAATA	1220
CAGTCCCGAGNNNNACGTATGCCA		CAGTTCTGCTNNNNACGTATGCCA		CAGTCCCGGNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	741	TGCAGGACACAGAGAAATCGAATA	981	TGCAGGACACAGAGAAATCGAATA	1221
CAAGCTTTGCTNNNNACGTATGCCA		CAGTACACACNNNNACGTATGCCA		CAGGCTTCANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	742	TGCAGGACACAGAGAAATCGAATA	982	TGCAGGACACAGAGAAATCGAATA	1222
CATGCAAAAGNNNNACGTATGCCA		CAAGTCACTGNNNNACGTATGCCA		CACUTTTTTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	743	TGCAGGACACAGAGAAATCGAATA	983	TGCAGGACACAGAGAAATCGAATA	1223
CAAGGTGTAGNNNNACGTATGCCA		CACACGAGAGNNNNACGTATGCCA		CAACGCGCGGANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	744	TGCAGGACACAGAGAAATCGAATA	984	TGCAGGACACAGAGAAATCGAATA	1224
CACACAGAGTTNNNNACGTATGCCA		CATAGGCTCANNNNACGTATGCCA		CACCCCTAGCNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	745	TGCAGGACACAGAGAAATCGAATA	985	TGCAGGACACAGAGAAATCGAATA	1225
CACAGCGGCTNNNNACGTATGCCA		CAGGCCCTGNNNNACGTATGCCA		CACGGAGGCGANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	746	TGCAGGACACAGAGAAATCGAATA	986	TGCAGGACACAGAGAAATCGAATA	1226
CAAGGCTACGNNNNACGTATGCCA		CAGGCCATCCNNNNACGTATGCCA		CAGTATGAAATNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	747	TGCAGGACACAGAGAAATCGAATA	987	TGCAGGACACAGAGAAATCGAATA	1227
CAGAACCGANNNNACGTATGCCA		CATCGATTGNNNNACGTATGCCA		CAGACCGCGTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	748	TGCAGGACACAGAGAAATCGAATA	988	TGCAGGACACAGAGAAATCGAATA	1228
CAAGTACTCGNNNNACGTATGCCA		CATAGACACGNNNNACGTATGCCA		CATACCTAGTANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	749	TGCAGGACACAGAGAAATCGAATA	989	TGCAGGACACAGAGAAATCGAATA	1229
CAAAACAATTCNNNNACGTATGCCA		CAACTAAGTTNNNNACGTATGCCA		CAACCAGTGTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	750	TGCAGGACACAGAGAAATCGAATA	990	TGCAGGACACAGAGAAATCGAATA	1230
CAGTATTACNNNNACGTATGCCA		CAATGTTCGNNNNACGTATGCCA		CAGATGCGTANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	751	TGCAGGACACAGAGAAATCGAATA	991	TGCAGGACACAGAGAAATCGAATA	1231
CATGATTATGNNNNACGTATGCCA		CAAGCCCAATNNNNACGTATGCCA		CACCATATTTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	752	TGCAGGACACAGAGAAATCGAATA	992	TGCAGGACACAGAGAAATCGAATA	1232
CAGCAAACTNNNNACGTATGCCA		CAGTGAATTCNNNNACGTATGCCA		CAAAACCAACNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	753	TGCAGGACACAGAGAAATCGAATA	993	TGCAGGACACAGAGAAATCGAATA	1233
CAGATCTTANNNNACGTATGCCA		CAGTGCCTAACNNNNACGTATGCCA		CAGCACGAPANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	754	TGCAGGACACAGAGAAATCGAATA	994	TGCAGGACACAGAGAAATCGAATA	1234
CAGAGAGCGNNNNACGTATGCCA		CAGCCACGCGANNNNACGTATGCCA		CAACGACAGANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	755	TGCAGGACACAGAGAAATCGAATA	995	TGCAGGACACAGAGAAATCGAATA	1235
CAAGCCGAGANNNNACGTATGCCA		CAAGTCCGATNNNNACGTATGCCA		CAATACCATANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	756	TGCAGGACACAGAGAAATCGAATA	996	TGCAGGACACAGAGAAATCGAATA	1236
CAGGAGCGCTNNNNACGTATGCCA		CAGTTAAATCANNNNACGTATGCCA		CACCAGTTCTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	757	TGCAGGACACAGAGAAATCGAATA	997	TGCAGGACACAGAGAAATCGAATA	1237
CAGCTGCCCTNNNNACGTATGCCA		CAACTGAGTNNNNACGTATGCCA		CATTGCTGANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	758	TGCAGGACACAGAGAAATCGAATA	998	TGCAGGACACAGAGAAATCGAATA	1238
CACCTTTTCNNNNACGTATGCCA		CACCTCATGCGNNNNACGTATGCCA		CGGCCCATTTNNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	759	TGCAGGACACAGAGAAATCGAATA	999	TGCAGGACACAGAGAAATCGAATA	1239
CATTCGCAATNNNNACGTATGCCA		CAACCGAGATNNNNACGTATGCCA		CAAAACGCTCANNNNACGTATGCCA	
TGCAGGACACAGAGAAATCGAATA	760	TGCAGGACACAGAGAAATCGAATA	1000	TGCAGGACACAGAGAAATCGAATA	1240
CAATCGCATGNNNNACGTATGCCA		CAGGCGTCCANNNNACGTATGCCA		CAGTGTCTGNNNNACGTATGCCA	

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池 -4	SEQ ID NO:	池 -5	SEQ ID NO:	池 -6	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	761	TGCAGGACCAGAGAATTGGAATA	1001	TGCAGGACCAGAGAATTGGAATA	1241
CAGCATGCGCANNACGATAGCCA		CAGCATGCGCANNACGATAGCCA		CAGCATGCGCANNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	762	TGCAGGACCAGAGAATTGGAATA	1002	TGCAGGACCAGAGAATTGGAATA	1242
CATCATCGCTNNNACGATAGCCA		CAGGTCTTAGNNNACGATAGCCA		CATTCGCTTNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	763	TGCAGGACCAGAGAATTGGAATA	1003	TGCAGGACCAGAGAATTGGAATA	1243
CACGCTGCTNNNACGATAGCCA		CAGCCTGGATNNNACGATAGCCA		CACACGCAATNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	764	TGCAGGACCAGAGAATTGGAATA	1004	TGCAGGACCAGAGAATTGGAATA	1244
CAGGTTATTAANNACGATAGCCA		CAATCCCGAANNNACGATAGCCA		CAGGTTATCCNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	765	TGCAGGACCAGAGAATTGGAATA	1005	TGCAGGACCAGAGAATTGGAATA	1245
CAGAGTTAANNACGATAGCCA		CATTTACTCANNNACGATAGCCA		CAGGCAATAGANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	766	TGCAGGACCAGAGAATTGGAATA	1006	TGCAGGACCAGAGAATTGGAATA	1246
CATGAATTCNNNACGATAGCCA		CATCCACCGCANNNACGATAGCCA		CAGGCGCGCTNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	767	TGCAGGACCAGAGAATTGGAATA	1007	TGCAGGACCAGAGAATTGGAATA	1247
CACCTTACCTGNNNACGATAGCCA		CACACAGATTGNNNACGATAGCCA		CACAAATTCANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	768	TGCAGGACCAGAGAATTGGAATA	1008	TGCAGGACCAGAGAATTGGAATA	1248
CAGATTCGCTGNNNACGATAGCCA		CACATGGTCANNNACGATAGCCA		CATAATGCATNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	769	TGCAGGACCAGAGAATTGGAATA	1009	TGCAGGACCAGAGAATTGGAATA	1249
CAGGACACGGGNNNACGATAGCCA		CACCATTTCCGNNNACGATAGCCA		CAGCTCGCTCANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	770	TGCAGGACCAGAGAATTGGAATA	1010	TGCAGGACCAGAGAATTGGAATA	1250
CATCTCGCGCANNNACGATAGCCA		CATGTCGCGCANNNACGATAGCCA		CARATTTGTGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	771	TGCAGGACCAGAGAATTGGAATA	1011	TGCAGGACCAGAGAATTGGAATA	1251
CACCTTCGAGTNNNACGATAGCCA		CARACCAATACNNNACGATAGCCA		CATGAGACGCTNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	772	TGCAGGACCAGAGAATTGGAATA	1012	TGCAGGACCAGAGAATTGGAATA	1252
CATATAGTTACNNNACGATAGCCA		CATTTCGACGANNNACGATAGCCA		CAGGCAATACANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	773	TGCAGGACCAGAGAATTGGAATA	1013	TGCAGGACCAGAGAATTGGAATA	1253
CAGGCTCTGANNNACGATAGCCA		CACCTTTAGAGANNNACGATAGCCA		CAGTCTCTCANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	774	TGCAGGACCAGAGAATTGGAATA	1014	TGCAGGACCAGAGAATTGGAATA	1254
CATGCTTTATNNNACGATAGCCA		CACGCTCTTNNNACGATAGCCA		CAGTTCGCGAGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	775	TGCAGGACCAGAGAATTGGAATA	1015	TGCAGGACCAGAGAATTGGAATA	1255
CAGCCACTTTNNNACGATAGCCA		CACACGAGAGANNNACGATAGCCA		CATTTAGACANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	776	TGCAGGACCAGAGAATTGGAATA	1016	TGCAGGACCAGAGAATTGGAATA	1256
CATATCGGACNNNACGATAGCCA		CAGGCGCACACNNNACGATAGCCA		CACACCGCGTNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	777	TGCAGGACCAGAGAATTGGAATA	1017	TGCAGGACCAGAGAATTGGAATA	1257
CATTTCCACTNNNACGATAGCCA		CATCTGTGAGNNNACGATAGCCA		CATTTCTAGANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	778	TGCAGGACCAGAGAATTGGAATA	1018	TGCAGGACCAGAGAATTGGAATA	1258
CBAATTCGCTGNNNACGATAGCCA		CBAAGCCACGNNNACGATAGCCA		CACGACACGCGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	779	TGCAGGACCAGAGAATTGGAATA	1019	TGCAGGACCAGAGAATTGGAATA	1259
CACCGCCCTNNNACGATAGCCA		CACCCAGTTGANNNACGATAGCCA		CACGACCGCANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	780	TGCAGGACCAGAGAATTGGAATA	1020	TGCAGGACCAGAGAATTGGAATA	1260
CATAGCTAGCANNNACGATAGCCA		CACCTTGTAGCANNNACGATAGCCA		CACATATAGTNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	781	TGCAGGACCAGAGAATTGGAATA	1021	TGCAGGACCAGAGAATTGGAATA	1261
CAGCAACCTNNNACGATAGCCA		CAATATGCATNNNACGATAGCCA		CATGTGATACNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	782	TGCAGGACCAGAGAATTGGAATA	1022	TGCAGGACCAGAGAATTGGAATA	1262
CACGCTCTATNNNACGATAGCCA		CACCCAGGCGTNNNACGATAGCCA		CAATCTCTAANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	783	TGCAGGACCAGAGAATTGGAATA	1023	TGCAGGACCAGAGAATTGGAATA	1263
CAGCCACACGNNNACGATAGCCA		CAATGTCTTAGNNNACGATAGCCA		CATGATGAGGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	784	TGCAGGACCAGAGAATTGGAATA	1024	TGCAGGACCAGAGAATTGGAATA	1264
CAGGCTTCCNNNACGATAGCCA		CACCTGTCCGNNNACGATAGCCA		CAGCTCGACGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	785	TGCAGGACCAGAGAATTGGAATA	1025	TGCAGGACCAGAGAATTGGAATA	1265
CAGTTTACACNNNACGATAGCCA		CATTTTACCANNNACGATAGCCA		CATTAGCTAANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	786	TGCAGGACCAGAGAATTGGAATA	1026	TGCAGGACCAGAGAATTGGAATA	1266
CAGCATCTTCNNNACGATAGCCA		CATGCGCTGCNNNACGATAGCCA		CATGCTTTTANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	787	TGCAGGACCAGAGAATTGGAATA	1027	TGCAGGACCAGAGAATTGGAATA	1267
CAACCAATGTNNNACGATAGCCA		CACGCTTTGACNNNACGATAGCCA		CAATCACAGCANNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	788	TGCAGGACCAGAGAATTGGAATA	1028	TGCAGGACCAGAGAATTGGAATA	1268
CAGATCCCGCANNNACGATAGCCA		CAATTTATTTNNNACGATAGCCA		CAATCTCGGNNNACGATAGCCA	
TGCAGGACCAGAGAATTGGAATA	789	TGCAGGACCAGAGAATTGGAATA	1029	TGCAGGACCAGAGAATTGGAATA	1269
CAGCCCACTGNNNCTAGCGTTAC		CAGTSTGGANNNNCTAGCGTTAC		CACACACTGGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	790	TGCAGGACCAGAGAATTGGAATA	1030	TGCAGGACCAGAGAATTGGAATA	1270
CAGCGGTTGCTNNNCTAGCGTTAC		CAACTCGTAGNNNCTAGCGTTAC		CAATTTGTTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	791	TGCAGGACCAGAGAATTGGAATA	1031	TGCAGGACCAGAGAATTGGAATA	1271
CATACGCTGCANNNNCTAGCGTTAC		CATCGCGTCCNNNNCTAGCGTTAC		CAAGACACCGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	792	TGCAGGACCAGAGAATTGGAATA	1032	TGCAGGACCAGAGAATTGGAATA	1272
CACACCCACGNNNNCTAGCGTTAC		CAGCGTAATGNNNNCTAGCGTTAC		CACGCGAGAGNNNNCTAGCGTTAC	

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	793	TGCAGGACCAGAGAATTGGAATA	1032	TGCAGGACCAGAGAATTGGAATA	1273
CACACGGAGGNNNCTAGCGTTAC		CAGCGTGTANNNNCTAGCGTTAC		CATTAGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	794	TGCAGGACCAGAGAATTGGAATA	1034	TGCAGGACCAGAGAATTGGAATA	1274
CACCGTAAACNNNNCTAGCGTTAC		CACGAGAAACNNNNCTAGCGTTAC		CAAAAGACGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	795	TGCAGGACCAGAGAATTGGAATA	1035	TGCAGGACCAGAGAATTGGAATA	1275
CAGAGCTATGNNNNCTAGCGTTAC		CAATGGTCAGNNNNCTAGCGTTAC		CACGGAAACAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	796	TGCAGGACCAGAGAATTGGAATA	1036	TGCAGGACCAGAGAATTGGAATA	1276
CAAPAGGCAANNNNCTAGCGTTAC		CACTCAGCTANNNNCTAGCGTTAC		CACTGTGGAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	797	TGCAGGACCAGAGAATTGGAATA	1037	TGCAGGACCAGAGAATTGGAATA	1277
CAACAGAGCTNNNNCTAGCGTTAC		CAGGTAGCGGNNNNCTAGCGTTAC		CAGGCTTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	798	TGCAGGACCAGAGAATTGGAATA	1038	TGCAGGACCAGAGAATTGGAATA	1278
CACGTAGCAANNNNCTAGCGTTAC		CACCTGGTCCNNNNCTAGCGTTAC		CACCAATTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	799	TGCAGGACCAGAGAATTGGAATA	1039	TGCAGGACCAGAGAATTGGAATA	1279
CATCCCGAGCANNNNCTAGCGTTAC		CACAGCACCCGNNNNCTAGCGTTAC		CAGAGTCTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	800	TGCAGGACCAGAGAATTGGAATA	1040	TGCAGGACCAGAGAATTGGAATA	1280
CAGTACCTGANNNNCTAGCGTTAC		CACATTGTGNNNNCTAGCGTTAC		CAAACTGTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	801	TGCAGGACCAGAGAATTGGAATA	1041	TGCAGGACCAGAGAATTGGAATA	1281
CAAGAGAGGANNNNCTAGCGTTAC		CAAGGAACGTGNNNNCTAGCGTTAC		CAAGTGSCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	802	TGCAGGACCAGAGAATTGGAATA	1042	TGCAGGACCAGAGAATTGGAATA	1282
CAGTAACTCGNNNNCTAGCGTTAC		CAGTTATTAGNNNNCTAGCGTTAC		CAGGTTAACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	803	TGCAGGACCAGAGAATTGGAATA	1043	TGCAGGACCAGAGAATTGGAATA	1283
CAGGTACATCANNNNCTAGCGTTAC		CAAACTCTTCNNNNCTAGCGTTAC		CATTGTGTGTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	804	TGCAGGACCAGAGAATTGGAATA	1044	TGCAGGACCAGAGAATTGGAATA	1284
CAGTTAACTCGNNNNCTAGCGTTAC		CAGACCAATCCNNNNCTAGCGTTAC		CAAAATGGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	805	TGCAGGACCAGAGAATTGGAATA	1045	TGCAGGACCAGAGAATTGGAATA	1285
CAACGAGCTGNNNNCTAGCGTTAC		CAATCTAGATNNNNCTAGCGTTAC		CAGTGTAGGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	806	TGCAGGACCAGAGAATTGGAATA	1046	TGCAGGACCAGAGAATTGGAATA	1286
CAGTAACTCGNNNNCTAGCGTTAC		CAGCGACGTGNNNNCTAGCGTTAC		CAGTAAAGCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	807	TGCAGGACCAGAGAATTGGAATA	1047	TGCAGGACCAGAGAATTGGAATA	1287
CATCAGAGCTNNNNCTAGCGTTAC		CACACCCCGTNNNNCTAGCGTTAC		CAGTTTATGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	808	TGCAGGACCAGAGAATTGGAATA	1048	TGCAGGACCAGAGAATTGGAATA	1288
CACAGATACGNNNNCTAGCGTTAC		CACGCTTCGTNNNNCTAGCGTTAC		CAACGACTGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	809	TGCAGGACCAGAGAATTGGAATA	1049	TGCAGGACCAGAGAATTGGAATA	1289
CATACACTTCNNNNCTAGCGTTAC		CAGTGGACCAANNNNCTAGCGTTAC		CACCTAGTAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	810	TGCAGGACCAGAGAATTGGAATA	1050	TGCAGGACCAGAGAATTGGAATA	1290
CAGTGTAAAGNNNNCTAGCGTTAC		CATGCTTGTGNNNNCTAGCGTTAC		CAGGTTCTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	811	TGCAGGACCAGAGAATTGGAATA	1051	TGCAGGACCAGAGAATTGGAATA	1291
CAGCTTGAAGNNNNCTAGCGTTAC		CAAGTGTGTCNNNNCTAGCGTTAC		CATATCATCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	812	TGCAGGACCAGAGAATTGGAATA	1052	TGCAGGACCAGAGAATTGGAATA	1292
CAGTCCCTCGNNNNCTAGCGTTAC		CATATTGTCTNNNNCTAGCGTTAC		CAGTCCGGAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	813	TGCAGGACCAGAGAATTGGAATA	1053	TGCAGGACCAGAGAATTGGAATA	1293
CAATCCCTCGNNNNCTAGCGTTAC		CAATTTGACANNNNCTAGCGTTAC		CATCAGTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	814	TGCAGGACCAGAGAATTGGAATA	1054	TGCAGGACCAGAGAATTGGAATA	1294
CATGCCCCACNNNNCTAGCGTTAC		CACGCAACGNNNNCTAGCGTTAC		CAAGTSCCTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	815	TGCAGGACCAGAGAATTGGAATA	1055	TGCAGGACCAGAGAATTGGAATA	1295
CAGTATTATGNNNNCTAGCGTTAC		CACCGCGAGCANNNNCTAGCGTTAC		CAGTATGTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	816	TGCAGGACCAGAGAATTGGAATA	1056	TGCAGGACCAGAGAATTGGAATA	1296
CATIGATTGANNNNCTAGCGTTAC		CATTAGGCGTNNNNCTAGCGTTAC		CAGCAGCAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	817	TGCAGGACCAGAGAATTGGAATA	1057	TGCAGGACCAGAGAATTGGAATA	1297
CATGCGACCCNNNNCTAGCGTTAC		CATCGGAGCCNNNNCTAGCGTTAC		CAGCAGGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	818	TGCAGGACCAGAGAATTGGAATA	1058	TGCAGGACCAGAGAATTGGAATA	1298
CAGTGGTTCANNNNCTAGCGTTAC		CAGTCTACAGNNNNCTAGCGTTAC		CATGTAGGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	819	TGCAGGACCAGAGAATTGGAATA	1059	TGCAGGACCAGAGAATTGGAATA	1299
CACCGGCTGANNNNCTAGCGTTAC		CACCGGCTCTNNNNCTAGCGTTAC		CATACAGACCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	820	TGCAGGACCAGAGAATTGGAATA	1060	TGCAGGACCAGAGAATTGGAATA	1300
CACCTTCCGNNNNCTAGCGTTAC		CATTAAACTGNNNNCTAGCGTTAC		CACGATCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	821	TGCAGGACCAGAGAATTGGAATA	1061	TGCAGGACCAGAGAATTGGAATA	1301
CAGCTAAGTGNNNNCTAGCGTTAC		CAACAGAGACNNNNCTAGCGTTAC		CAGGCCAAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	822	TGCAGGACCAGAGAATTGGAATA	1062	TGCAGGACCAGAGAATTGGAATA	1302
CAGTGTCCANNNNCTAGCGTTAC		CAATCATGCGNNNNCTAGCGTTAC		CAGACATAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	823	TGCAGGACCAGAGAATTGGAATA	1063	TGCAGGACCAGAGAATTGGAATA	1303
CATGCACTGANNNNCTAGCGTTAC		CACGCACTAGNNNNCTAGCGTTAC		CACGCCACTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	824	TGCAGGACCAGAGAATTGGAATA	1064	TGCAGGACCAGAGAATTGGAATA	1304
CAGAACTTTNNNNCTAGCGTTAC		CAGTCCAGGTANNNNCTAGCGTTAC		CAGGCTAGGCGNNNNCTAGCGTTAC	

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池-4	SEQ ID No:	池-5	SEQ ID No:	池-6	SEQ ID No:
TGCAGGACCAGAGAAATCGAATA	825	TGCAGGACCAGAGAAATCGAATA	1065	TGCAGGACCAGAGAAATCGAATA	1305
CATGTGTAGCANNCTAGCGTTAC		CACTTTGCCANNCTAGCGTTAC		CATCGGCAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	826	TGCAGGACCAGAGAAATCGAATA	1066	TGCAGGACCAGAGAAATCGAATA	1306
CATGTACCTGNNNCTAGCGTTAC		CAAAATTCGANNCTAGCGTTAC		CACCTTATAGANNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	827	TGCAGGACCAGAGAAATCGAATA	1067	TGCAGGACCAGAGAAATCGAATA	1307
CATCTGCTAANNCTAGCGTTAC		CAGATCGCATNNCTAGCGTTAC		CAAGGCGGAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	828	TGCAGGACCAGAGAAATCGAATA	1068	TGCAGGACCAGAGAAATCGAATA	1308
CAATCGAATTNNNCTAGCGTTAC		CATGTGTTGNNNCTAGCGTTAC		CAGTAGCACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	829	TGCAGGACCAGAGAAATCGAATA	1069	TGCAGGACCAGAGAAATCGAATA	1309
CATTTTTCGNNNCTAGCGTTAC		CAGTAACATNNNCTAGCGTTAC		CAGCTGTCAANNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	830	TGCAGGACCAGAGAAATCGAATA	1070	TGCAGGACCAGAGAAATCGAATA	1310
CATCAGTCCNNNCTAGCGTTAC		CAACGCATCANNNCTAGCGTTAC		CAGTCCAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	831	TGCAGGACCAGAGAAATCGAATA	1071	TGCAGGACCAGAGAAATCGAATA	1311
CAGTGCACTNNNCTAGCGTTAC		CATAGGAAGCANNNCTAGCGTTAC		CATTCAATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	832	TGCAGGACCAGAGAAATCGAATA	1072	TGCAGGACCAGAGAAATCGAATA	1312
CAGTAGAAGCANNNCTAGCGTTAC		CAGCAATGTNNNCTAGCGTTAC		CACCCGATGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	833	TGCAGGACCAGAGAAATCGAATA	1073	TGCAGGACCAGAGAAATCGAATA	1313
CACAGCATTGNNNCTAGCGTTAC		CAGCGCGCATNNNCTAGCGTTAC		CATTAGTTGANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	834	TGCAGGACCAGAGAAATCGAATA	1074	TGCAGGACCAGAGAAATCGAATA	1314
CACGCGCTAGNNNCTAGCGTTAC		CACCTGAGCCGNNNCTAGCGTTAC		CAATTCAGAAPNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	835	TGCAGGACCAGAGAAATCGAATA	1075	TGCAGGACCAGAGAAATCGAATA	1315
CACAGTTTGNNNCTAGCGTTAC		CACCTGCTGCCNNNCTAGCGTTAC		CATTAGAACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	836	TGCAGGACCAGAGAAATCGAATA	1076	TGCAGGACCAGAGAAATCGAATA	1316
CATCCCAAGANNNCTAGCGTTAC		CAGTGGCGGANNNCTAGCGTTAC		CAGTGGCTATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	837	TGCAGGACCAGAGAAATCGAATA	1077	TGCAGGACCAGAGAAATCGAATA	1317
CATTAGGACNNNCTAGCGTTAC		CAAGGCTAGTNNNCTAGCGTTAC		CATTGGATCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	838	TGCAGGACCAGAGAAATCGAATA	1078	TGCAGGACCAGAGAAATCGAATA	1318
CAACAATTTGNNNCTAGCGTTAC		CAACTTTGTNNNCTAGCGTTAC		CACAGAGATANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	839	TGCAGGACCAGAGAAATCGAATA	1079	TGCAGGACCAGAGAAATCGAATA	1319
CATGCTCGAANNNCTAGCGTTAC		CAGCCATATGNNNCTAGCGTTAC		CANGCACTANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	840	TGCAGGACCAGAGAAATCGAATA	1080	TGCAGGACCAGAGAAATCGAATA	1320
CAGCGGCTAGNNNCTAGCGTTAC		CAAGCCTGGCNNNCTAGCGTTAC		CAACTAGACNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	841	TGCAGGACCAGAGAAATCGAATA	1081	TGCAGGACCAGAGAAATCGAATA	1321
CAAAATTAACNNNCTAGCGTTAC		CAACGTGTGNNNCTAGCGTTAC		CAATCAATTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	842	TGCAGGACCAGAGAAATCGAATA	1082	TGCAGGACCAGAGAAATCGAATA	1322
CACAGACCCGNNNCTAGCGTTAC		CATTTTCTGNNNCTAGCGTTAC		CAAGAACTCANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	843	TGCAGGACCAGAGAAATCGAATA	1083	TGCAGGACCAGAGAAATCGAATA	1323
CAGTGCAGATNNNCTAGCGTTAC		CAGCTGCCGANNNCTAGCGTTAC		CAGATTTCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	844	TGCAGGACCAGAGAAATCGAATA	1084	TGCAGGACCAGAGAAATCGAATA	1324
CAAAATTAANNNCTAGCGTTAC		CACAAATAGNNNCTAGCGTTAC		CAGTACCGANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	845	TGCAGGACCAGAGAAATCGAATA	1085	TGCAGGACCAGAGAAATCGAATA	1325
CACATGCCANNNCTAGCGTTAC		CACATAAGTANNNCTAGCGTTAC		CACCGCTAANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	846	TGCAGGACCAGAGAAATCGAATA	1086	TGCAGGACCAGAGAAATCGAATA	1326
CAGCATCCGNNNCTAGCGTTAC		CAAAATGATGNNNCTAGCGTTAC		CAAGTTGCTCANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	847	TGCAGGACCAGAGAAATCGAATA	1087	TGCAGGACCAGAGAAATCGAATA	1327
CAATATAAANNNCTAGCGTTAC		CACCTTGCTGNNNCTAGCGTTAC		CATCGCACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	848	TGCAGGACCAGAGAAATCGAATA	1088	TGCAGGACCAGAGAAATCGAATA	1328
CAGCCTCCGNNNCTAGCGTTAC		CAGATAGGCANNNCTAGCGTTAC		CATTGCTACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	849	TGCAGGACCAGAGAAATCGAATA	1089	TGCAGGACCAGAGAAATCGAATA	1329
CATCCAAACNNNGATCGACATG		CACAGATTATNNNGATCGACATG		CAATGAGATTANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	850	TGCAGGACCAGAGAAATCGAATA	1090	TGCAGGACCAGAGAAATCGAATA	1330
CAAAATGCGCANNNGATCGACATG		CAGTTACGCTNNNGATCGACATG		CAATCGTACNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	851	TGCAGGACCAGAGAAATCGAATA	1091	TGCAGGACCAGAGAAATCGAATA	1331
CACCTGTCCANNNGATCGACATG		CAACAGTTCCNNNGATCGACATG		CATGTCGTTCCNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	852	TGCAGGACCAGAGAAATCGAATA	1092	TGCAGGACCAGAGAAATCGAATA	1332
CAGCTGTCCANNNGATCGACATG		CAAACTGCCANNNGATCGACATG		CATGCTATANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	853	TGCAGGACCAGAGAAATCGAATA	1093	TGCAGGACCAGAGAAATCGAATA	1333
CAGTGAACCTNNNGATCGACATG		CAAGAAATCANNNGATCGACATG		CAGTGGATCANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	854	TGCAGGACCAGAGAAATCGAATA	1094	TGCAGGACCAGAGAAATCGAATA	1334
CACCTTTCCNNNGATCGACATG		CATGCTCCTANNNGATCGACATG		CATGCTCAANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	855	TGCAGGACCAGAGAAATCGAATA	1095	TGCAGGACCAGAGAAATCGAATA	1335
CAGAGAGCCGNNNGATCGACATG		CACAGAAATCANNNGATCGACATG		CAAGCGCTGTCNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	856	TGCAGGACCAGAGAAATCGAATA	1096	TGCAGGACCAGAGAAATCGAATA	1336
CACAGACAGANNNGATCGACATG		CACCTTGACANNNGATCGACATG		CACCTCCTCGNNNGATCGACATG	

图13D

池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAAATCGAATA	857	TGCAGGACCAGAGAAATCGAATA	1097	TGCAGGACCAGAGAAATCGAATA	1337
CATATATGACNNNGATCGACATG		CACGTGGTGTNNNGATCGACATG		CAGACTAATNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	858	TGCAGGACCAGAGAAATCGAATA	1098	TGCAGGACCAGAGAAATCGAATA	1338
CAGTCCGACGNNNGATCGACATG		CACGGATCTANNNGATCGACATG		CACRATAAGANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	859	TGCAGGACCAGAGAAATCGAATA	1099	TGCAGGACCAGAGAAATCGAATA	1339
CAACTGCATGNNNGATCGACATG		CAAAAAGAGNNNGATCGACATG		CATTACCGCNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	860	TGCAGGACCAGAGAAATCGAATA	1100	TGCAGGACCAGAGAAATCGAATA	1340
CATACCTAAANNNGATCGACATG		CAGCAGACATNNNGATCGACATG		CAGTGTATTANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	861	TGCAGGACCAGAGAAATCGAATA	1101	TGCAGGACCAGAGAAATCGAATA	1341
CAGCCAGATGNNNGATCGACATG		CACCGGACGNNNGATCGACATG		CAGGATGTANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	862	TGCAGGACCAGAGAAATCGAATA	1102	TGCAGGACCAGAGAAATCGAATA	1342
CAGGCAATGNNNGATCGACATG		CATGTTATGNNNGATCGACATG		CATIAATTCGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	863	TGCAGGACCAGAGAAATCGAATA	1103	TGCAGGACCAGAGAAATCGAATA	1343
CAGACGCTGNNNGATCGACATG		CAGCGAGACGNNNGATCGACATG		CAGGTCACACNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	864	TGCAGGACCAGAGAAATCGAATA	1104	TGCAGGACCAGAGAAATCGAATA	1344
CACCACTCAANNNGATCGACATG		CATTATCGAANNNGATCGACATG		CACGTGACACNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	865	TGCAGGACCAGAGAAATCGAATA	1105	TGCAGGACCAGAGAAATCGAATA	1345
CATTTTCGAANNNGATCGACATG		CAGTGCATGNNNGATCGACATG		CAGACCCGCTGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	866	TGCAGGACCAGAGAAATCGAATA	1106	TGCAGGACCAGAGAAATCGAATA	1346
CAGTTAGTTANNNGATCGACATG		CAGCTAATAANNNGATCGACATG		CAGGTCAACGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	867	TGCAGGACCAGAGAAATCGAATA	1107	TGCAGGACCAGAGAAATCGAATA	1347
GATCAGCTGNNNGATCGACATG		CAATCCAAATANNNGATCGACATG		CACCTTAGCTGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	868	TGCAGGACCAGAGAAATCGAATA	1108	TGCAGGACCAGAGAAATCGAATA	1348
CATCCGAGGNNNGATCGACATG		CATTCAAGGCGNNNGATCGACATG		CAGCTCGCTAANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	869	TGCAGGACCAGAGAAATCGAATA	1109	TGCAGGACCAGAGAAATCGAATA	1349
CATCTGCAANNNGATCGACATG		CATTATTAANNNGATCGACATG		CAGGCTAGTNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	870	TGCAGGACCAGAGAAATCGAATA	1110	TGCAGGACCAGAGAAATCGAATA	1350
CATCTAAGCGNNNGATCGACATG		CAAACTCTAANNNGATCGACATG		CAGAGAGTTGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	871	TGCAGGACCAGAGAAATCGAATA	1111	TGCAGGACCAGAGAAATCGAATA	1351
CACGTAGGAANNNGATCGACATG		CAGACTCCANNNGATCGACATG		CATAGAGGCGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	872	TGCAGGACCAGAGAAATCGAATA	1112	TGCAGGACCAGAGAAATCGAATA	1352
CACAGACTGNNNGATCGACATG		CACAGGCTGNNNGATCGACATG		CAGTTAATACNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	873	TGCAGGACCAGAGAAATCGAATA	1113	TGCAGGACCAGAGAAATCGAATA	1353
CATTCCGTGNNNGATCGACATG		CAGAGTCACTNNNGATCGACATG		CAGGTCGCGANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	874	TGCAGGACCAGAGAAATCGAATA	1114	TGCAGGACCAGAGAAATCGAATA	1354
CAGTGAACGANNNGATCGACATG		CAAGAACTGNNNGATCGACATG		CACTAACCATNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	875	TGCAGGACCAGAGAAATCGAATA	1115	TGCAGGACCAGAGAAATCGAATA	1355
CAGCTAAACGNNNGATCGACATG		CAGCGTATGNNNGATCGACATG		CAGTACGCTNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	876	TGCAGGACCAGAGAAATCGAATA	1116	TGCAGGACCAGAGAAATCGAATA	1356
CACATTTTCNNNGATCGACATG		CACCTAAATGNNNGATCGACATG		CAAAACGACGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	877	TGCAGGACCAGAGAAATCGAATA	1117	TGCAGGACCAGAGAAATCGAATA	1357
GATGAGGAAGNNNGATCGACATG		CATTAGCGTNNNGATCGACATG		CAGTAGGTTGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	878	TGCAGGACCAGAGAAATCGAATA	1118	TGCAGGACCAGAGAAATCGAATA	1358
CAGTAATCTNNNGATCGACATG		CACCGAGAGANNNGATCGACATG		CACCTTTTCNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	879	TGCAGGACCAGAGAAATCGAATA	1119	TGCAGGACCAGAGAAATCGAATA	1359
CATATCTCCGNNNGATCGACATG		CATCAGCCGANNNGATCGACATG		CATGACCCGANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	880	TGCAGGACCAGAGAAATCGAATA	1120	TGCAGGACCAGAGAAATCGAATA	1360
CAGCTACGCGNNNGATCGACATG		CACCGAATACNNNGATCGACATG		CAATCAGTTANNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	881	TGCAGGACCAGAGAAATCGAATA	1121	TGCAGGACCAGAGAAATCGAATA	1361
CAATATCTGANNNGATCGACATG		CAGCGGCAAGNNNGATCGACATG		CATAGTAAAGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	882	TGCAGGACCAGAGAAATCGAATA	1122	TGCAGGACCAGAGAAATCGAATA	1362
CATACTTAGANNNGATCGACATG		CATAAATCGNNNGATCGACATG		CACCGGATGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	883	TGCAGGACCAGAGAAATCGAATA	1123	TGCAGGACCAGAGAAATCGAATA	1363
CATCATTTGNNNGATCGACATG		CAAGGCTTCNNNGATCGACATG		CACACAGCATNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	884	TGCAGGACCAGAGAAATCGAATA	1124	TGCAGGACCAGAGAAATCGAATA	1364
CAGCGTGGAGNNNGATCGACATG		CATGCAATANNNGATCGACATG		CACAGGTACTNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	885	TGCAGGACCAGAGAAATCGAATA	1125	TGCAGGACCAGAGAAATCGAATA	1365
CATAGAGCCGNNNGATCGACATG		CACCTCTGCTNNNGATCGACATG		CACATAGCGNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	886	TGCAGGACCAGAGAAATCGAATA	1126	TGCAGGACCAGAGAAATCGAATA	1366
CAGGCGCTAANNNGATCGACATG		CATAGTGGTNNNGATCGACATG		CAGTACTGGTNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	887	TGCAGGACCAGAGAAATCGAATA	1127	TGCAGGACCAGAGAAATCGAATA	1367
CACATCTCAGNNNGATCGACATG		CAGAAACCTGNNNGATCGACATG		CAGCGAGTCTNNNGATCGACATG	
TGCAGGACCAGAGAAATCGAATA	888	TGCAGGACCAGAGAAATCGAATA	1128	TGCAGGACCAGAGAAATCGAATA	1368
CATGCGATCANNNGATCGACATG		CATGACTATANNNGATCGACATG		CACGTGCTGNNNGATCGACATG	

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATA	889	TGCAGGACCCAGAGAATTGGAATA	1129	TGCAGGACCCAGAGAATTGGAATA	1369
CACCGGAGGACNNNGATCGACATG		CACATGACTGNNNGATCGACATG		CACACTACCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	890	TGCAGGACCCAGAGAATTGGAATA	1130	TGCAGGACCCAGAGAATTGGAATA	1370
CAACTAATTGNNNGATCGACATG		CACCAAGCTCNNNGATCGACATG		CAGTCTATATNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	891	TGCAGGACCCAGAGAATTGGAATA	1131	TGCAGGACCCAGAGAATTGGAATA	1371
CATGCCCTAGANNNGATCGACATG		CACGCAATTGNNNGATCGACATG		CAATGACGCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	892	TGCAGGACCCAGAGAATTGGAATA	1132	TGCAGGACCCAGAGAATTGGAATA	1372
CACATATCCGTTNNNGATCGACATG		CAAGCCGGTNNNGATCGACATG		CAAGGCACCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	893	TGCAGGACCCAGAGAATTGGAATA	1133	TGCAGGACCCAGAGAATTGGAATA	1373
CATGCCAGGCGNNNGATCGACATG		CACCTGGCTNNNGATCGACATG		CAGGCAGGCGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	894	TGCAGGACCCAGAGAATTGGAATA	1134	TGCAGGACCCAGAGAATTGGAATA	1374
CAGCCGACGANNNGATCGACATG		CATTATGCAANNNGATCGACATG		CACCTATGTTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	895	TGCAGGACCCAGAGAATTGGAATA	1135	TGCAGGACCCAGAGAATTGGAATA	1375
CAAGACCCATNNNGATCGACATG		CATATTGAGNNNGATCGACATG		CATAAAATATNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	896	TGCAGGACCCAGAGAATTGGAATA	1136	TGCAGGACCCAGAGAATTGGAATA	1376
CATTGACCTCNNNGATCGACATG		CATGTTGGCTNNNGATCGACATG		CAGACACCACTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	897	TGCAGGACCCAGAGAATTGGAATA	1137	TGCAGGACCCAGAGAATTGGAATA	1377
CACCTTGCCTCANNNGATCGACATG		CATAGCATCGNNNGATCGACATG		CATAGATACCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	898	TGCAGGACCCAGAGAATTGGAATA	1138	TGCAGGACCCAGAGAATTGGAATA	1378
CAATTCCTCCANNNGATCGACATG		CATTGAGCGNNNGATCGACATG		CATACCTCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	899	TGCAGGACCCAGAGAATTGGAATA	1139	TGCAGGACCCAGAGAATTGGAATA	1379
CAAAACCCGACANNNGATCGACATG		CAAAACCCGACANNNGATCGACATG		CAGTCCGCCANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	900	TGCAGGACCCAGAGAATTGGAATA	1140	TGCAGGACCCAGAGAATTGGAATA	1380
CAGCGATCATNNNGATCGACATG		CATATGGCTNNNGATCGACATG		CACCTCTTAGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	901	TGCAGGACCCAGAGAATTGGAATA	1141	TGCAGGACCCAGAGAATTGGAATA	1381
CATAGACACGNNNGATCGACATG		CAAGCCTATGNNNGATCGACATG		CATAAGATTGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	902	TGCAGGACCCAGAGAATTGGAATA	1142	TGCAGGACCCAGAGAATTGGAATA	1382
CAGCCACTGNNNGATCGACATG		CACACTCTACNNNGATCGACATG		CACGCGTACGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	903	TGCAGGACCCAGAGAATTGGAATA	1143	TGCAGGACCCAGAGAATTGGAATA	1383
CAGGTTTGAANNNGATCGACATG		CAAAACTGAANNNGATCGACATG		CAGTGACCAANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	904	TGCAGGACCCAGAGAATTGGAATA	1144	TGCAGGACCCAGAGAATTGGAATA	1384
CAAACTTGGCNNNGATCGACATG		CACCTTCCGCGNNNGATCGACATG		CAAAAGACCGANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	905	TGCAGGACCCAGAGAATTGGAATA	1145	TGCAGGACCCAGAGAATTGGAATA	1385
CAACCTAATGNNNGATCGACATG		CAACCTGGCNNNGATCGACATG		CAAACTGATTGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	906	TGCAGGACCCAGAGAATTGGAATA	1146	TGCAGGACCCAGAGAATTGGAATA	1386
CAGCACAGGANNNGATCGACATG		CAGTACCTCAANNNGATCGACATG		CACCCCTCAANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	907	TGCAGGACCCAGAGAATTGGAATA	1147	TGCAGGACCCAGAGAATTGGAATA	1387
CATCTGTGAGNNNGATCGACATG		CAACCGCTANNNGATCGACATG		CAQCCTGAATNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	908	TGCAGGACCCAGAGAATTGGAATA	1148	TGCAGGACCCAGAGAATTGGAATA	1388
CAAGCTAACANNNGATCGACATG		CAAAACCGCTNNNGATCGACATG		CATCCGTAGTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	909	TGCAGGACCCAGAGAATTGGAATA	1149	TGCAGGACCCAGAGAATTGGAATA	1389
CATCTGAGCANNNGATCGACATG		CAGAGCCGAGCANNNGATCGACATG		CATCGCTCGGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	910	TGCAGGACCCAGAGAATTGGAATA	1150	TGCAGGACCCAGAGAATTGGAATA	1390
CAAGTGGAACTNNNGATCGACATG		CATTTATATANNNGATCGACATG		CACATCTCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	911	TGCAGGACCCAGAGAATTGGAATA	1151	TGCAGGACCCAGAGAATTGGAATA	1391
CAGAACTCGTNNNGATCGACATG		CAGCTAGGTTNNNGATCGACATG		CATAGAGACGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	912	TGCAGGACCCAGAGAATTGGAATA	1152	TGCAGGACCCAGAGAATTGGAATA	1392
CAGCAGGCGANNNGATCGACATG		CATTTGACTTNNNGATCGACATG		CAGCGGATGGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	913	TGCAGGACCCAGAGAATTGGAATA	1153	TGCAGGACCCAGAGAATTGGAATA	1393
CAGGCTCTCCANNNGATCGACATG		CAACAACTNNNGATCGACATG		CACCTCACCACTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	914	TGCAGGACCCAGAGAATTGGAATA	1154	TGCAGGACCCAGAGAATTGGAATA	1394
CAAAATACATCANNNGATCGACATG		CATTGCAATGNNNGATCGACATG		CAATGGTAAANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	915	TGCAGGACCCAGAGAATTGGAATA	1155	TGCAGGACCCAGAGAATTGGAATA	1395
CAAGCTCAAGNNNGATCGACATG		CAACAGCCANNNGATCGACATG		CATATCAACANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	916	TGCAGGACCCAGAGAATTGGAATA	1156	TGCAGGACCCAGAGAATTGGAATA	1396
CATCAGCGCCNNNGATCGACATG		CAGGTGCTGNNNGATCGACATG		CAAAAGTCAANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	917	TGCAGGACCCAGAGAATTGGAATA	1157	TGCAGGACCCAGAGAATTGGAATA	1397
CATTAGGTTGNNNGATCGACATG		CAAGGTGCTNNNGATCGACATG		CACAAAGCCANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	918	TGCAGGACCCAGAGAATTGGAATA	1158	TGCAGGACCCAGAGAATTGGAATA	1398
CAGTCTAGTNNNGATCGACATG		CAACACCGAANNNGATCGACATG		CACGATGACTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	919	TGCAGGACCCAGAGAATTGGAATA	1159	TGCAGGACCCAGAGAATTGGAATA	1399
CAAAAGGATTNNNGATCGACATG		CAGATCGGACNNNGATCGACATG		CACGATTGTGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATA	920	TGCAGGACCCAGAGAATTGGAATA	1160	TGCAGGACCCAGAGAATTGGAATA	1400
CATTTTAGCANNNGATCGACATG		CAGGAAGACTNNNGATCGACATG		CATTATCTGNNNGATCGACATG	

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池-4	SEQ ID NO:	池-5	SEQ ID NO:	池-6	SEQ ID NO:
TGCAGGACCAGAGAAATCGAATA	921	TGCAGGACCAGAGAAATCGAATA	1161	TGCAGGACCAGAGAAATCGAATA	1401
CAATTAACCTGANNNTGCATCAGGT		CAGGTAATGANNNTGCATCAGGT		CAGTATTGATNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	922	TGCAGGACCAGAGAAATCGAATA	1162	TGCAGGACCAGAGAAATCGAATA	1402
CATTTTACGNNNTGCATCAGGT		CAGGTAGAACNNNTGCATCAGGT		CAAGGAGGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	923	TGCAGGACCAGAGAAATCGAATA	1163	TGCAGGACCAGAGAAATCGAATA	1403
CAGTGGCGACNNNTGCATCAGGT		CAATATGAGANNNTGCATCAGGT		CAACTGCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	924	TGCAGGACCAGAGAAATCGAATA	1164	TGCAGGACCAGAGAAATCGAATA	1404
CAGAAATAGATTNNNTGCATCAGGT		CATGGAAATANNNTGCATCAGGT		CAAAATCTGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	925	TGCAGGACCAGAGAAATCGAATA	1165	TGCAGGACCAGAGAAATCGAATA	1405
CAGCTGAGCCNNNTGCATCAGGT		CATAACCAATNNNTGCATCAGGT		CACCATGTGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	926	TGCAGGACCAGAGAAATCGAATA	1166	TGCAGGACCAGAGAAATCGAATA	1406
CAACAGGCAANNNTGCATCAGGT		CAGTCTGATGNNNTGCATCAGGT		CACCCCTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	927	TGCAGGACCAGAGAAATCGAATA	1167	TGCAGGACCAGAGAAATCGAATA	1407
CAGACCCGACNNNTGCATCAGGT		CATTATGAGNNNTGCATCAGGT		CAGCTAGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	928	TGCAGGACCAGAGAAATCGAATA	1168	TGCAGGACCAGAGAAATCGAATA	1408
CACCTATTGANNNTGCATCAGGT		CAATGATTTGNNNTGCATCAGGT		CAACACCCGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	929	TGCAGGACCAGAGAAATCGAATA	1169	TGCAGGACCAGAGAAATCGAATA	1409
CAGTCTGCTGANNNTGCATCAGGT		CAGTCACTGTTNNNTGCATCAGGT		CAGCTGAGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	930	TGCAGGACCAGAGAAATCGAATA	1170	TGCAGGACCAGAGAAATCGAATA	1410
CAATTTAGCTGNNNTGCATCAGGT		CACTGCATACNNNTGCATCAGGT		CAAAATGCGTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	931	TGCAGGACCAGAGAAATCGAATA	1171	TGCAGGACCAGAGAAATCGAATA	1411
CATCGGCAANNNTGCATCAGGT		CAGCTAGCATNNNTGCATCAGGT		CAATTGCCAGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	932	TGCAGGACCAGAGAAATCGAATA	1172	TGCAGGACCAGAGAAATCGAATA	1412
CACGCGCGACNNNTGCATCAGGT		CAAAATCATGNNNTGCATCAGGT		CATTAAATTCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	933	TGCAGGACCAGAGAAATCGAATA	1173	TGCAGGACCAGAGAAATCGAATA	1413
CAGCTTGGCCNNNTGCATCAGGT		CAGCTCTCATNNNTGCATCAGGT		CARGCATATNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	934	TGCAGGACCAGAGAAATCGAATA	1174	TGCAGGACCAGAGAAATCGAATA	1414
CAACCAATCAANNNTGCATCAGGT		CAACTCGTTGNNNTGCATCAGGT		CACCCATTACNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	935	TGCAGGACCAGAGAAATCGAATA	1175	TGCAGGACCAGAGAAATCGAATA	1415
CAATGATGCGANNNTGCATCAGGT		CAAGTTCTGNNNTGCATCAGGT		CACCTCGTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	936	TGCAGGACCAGAGAAATCGAATA	1176	TGCAGGACCAGAGAAATCGAATA	1416
CACACAGTACNNNTGCATCAGGT		CAACTAGTATNNNTGCATCAGGT		CAGGTATCGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	937	TGCAGGACCAGAGAAATCGAATA	1177	TGCAGGACCAGAGAAATCGAATA	1417
CAATTCAGGTGNNNTGCATCAGGT		CAATTCGCGANNNTGCATCAGGT		CAGTACCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	938	TGCAGGACCAGAGAAATCGAATA	1178	TGCAGGACCAGAGAAATCGAATA	1418
CAGCTTCGCGNNNTGCATCAGGT		CACGAGCGCTNNNTGCATCAGGT		CACACTTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	939	TGCAGGACCAGAGAAATCGAATA	1179	TGCAGGACCAGAGAAATCGAATA	1419
CATTACTCTGNNNTGCATCAGGT		CAACGACCATNNNTGCATCAGGT		CAGAACTTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	940	TGCAGGACCAGAGAAATCGAATA	1180	TGCAGGACCAGAGAAATCGAATA	1420
CATAATGCTGNNNTGCATCAGGT		CATAAGTGANNNTGCATCAGGT		CATATTATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	941	TGCAGGACCAGAGAAATCGAATA	1181	TGCAGGACCAGAGAAATCGAATA	1421
CATACCATTTNNNTGCATCAGGT		CATCTGCGCGNNNTGCATCAGGT		CAGGCCGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	942	TGCAGGACCAGAGAAATCGAATA	1182	TGCAGGACCAGAGAAATCGAATA	1422
CACTCGCTANNNTGCATCAGGT		CAATTACTGTNNNTGCATCAGGT		CAGCAAAAGCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	943	TGCAGGACCAGAGAAATCGAATA	1183	TGCAGGACCAGAGAAATCGAATA	1423
CAAGCGGTAAANNNTGCATCAGGT		CAATATGTTGNNNTGCATCAGGT		CAGATAAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	944	TGCAGGACCAGAGAAATCGAATA	1184	TGCAGGACCAGAGAAATCGAATA	1424
CAGGAAACTGNNNTGCATCAGGT		CACGAGCGGTTNNNTGCATCAGGT		CACAGTATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	945	TGCAGGACCAGAGAAATCGAATA	1185	TGCAGGACCAGAGAAATCGAATA	1425
CAGGCGCAGCTNNNTGCATCAGGT		CACCGGTTGATNNNTGCATCAGGT		CACCTCACGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	946	TGCAGGACCAGAGAAATCGAATA	1186	TGCAGGACCAGAGAAATCGAATA	1426
CATCATTTGANNNTGCATCAGGT		CACCGTGCAGNNNTGCATCAGGT		CACCGTCAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	947	TGCAGGACCAGAGAAATCGAATA	1187	TGCAGGACCAGAGAAATCGAATA	1427
CACCGTGAAATNNNTGCATCAGGT		CAGTCTAAATNNNTGCATCAGGT		CAGGTTCTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	948	TGCAGGACCAGAGAAATCGAATA	1188	TGCAGGACCAGAGAAATCGAATA	1428
CACGGAAGCGNNNTGCATCAGGT		CAGTAATTACNNNTGCATCAGGT		CATTATATTTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	949	TGCAGGACCAGAGAAATCGAATA	1189	TGCAGGACCAGAGAAATCGAATA	1429
CAGTTTGAACNNNTGCATCAGGT		CACCTCCGCTNNNTGCATCAGGT		CAGGTTTACGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	950	TGCAGGACCAGAGAAATCGAATA	1190	TGCAGGACCAGAGAAATCGAATA	1430
CAGGCGGCTGNNNTGCATCAGGT		CAGAGCGTGGNNNTGCATCAGGT		CAGGACGATANNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	951	TGCAGGACCAGAGAAATCGAATA	1191	TGCAGGACCAGAGAAATCGAATA	1431
CAATTTGGCTGNNNTGCATCAGGT		CAATTTACTGNNNTGCATCAGGT		CAAGTCAAGGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATCGAATA	952	TGCAGGACCAGAGAAATCGAATA	1192	TGCAGGACCAGAGAAATCGAATA	1432
CATTGACGCTGNNNTGCATCAGGT		CACACACTGNNNTGCATCAGGT		CACACGACNNNTGCATCAGGT	

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池-4	SEQ ID No:	池-5	SEQ ID No:	池-6	SEQ ID No:
TGCAGGACCCAGAGAAATCGAATA	953	TGCAGGACCCAGAGAAATCGAATA	1193	TGCAGGACCCAGAGAAATCGAATA	1433
CATGGACGTTNNNTGCATCAGGT		CACCGCGCGNNNTGCATCAGGT		CAAGCCATGTTNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	954	TGCAGGACCCAGAGAAATCGAATA	1194	TGCAGGACCCAGAGAAATCGAATA	1434
CATGACACTCANNNTGCATCAGGT		CACCTAACCTGNNNTGCATCAGGT		CATTCCACTGNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	955	TGCAGGACCCAGAGAAATCGAATA	1195	TGCAGGACCCAGAGAAATCGAATA	1435
CAGTACCTGTNNNTGCATCAGGT		CAATTCAAGTTNNNTGCATCAGGT		CAACCCCTGTTNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	956	TGCAGGACCCAGAGAAATCGAATA	1196	TGCAGGACCCAGAGAAATCGAATA	1436
CAAGGTCCCGNNNTGCATCAGGT		CAATTGGCGTTNNNTGCATCAGGT		CACCCCTTTCTNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	957	TGCAGGACCCAGAGAAATCGAATA	1197	TGCAGGACCCAGAGAAATCGAATA	1437
CATTTCATCTANNNTGCATCAGGT		CATGATTTGANNNTGCATCAGGT		CPATGTTGANNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	958	TGCAGGACCCAGAGAAATCGAATA	1198	TGCAGGACCCAGAGAAATCGAATA	1438
CAGATAAAGTNNNTGCATCAGGT		CAACTGCCGNNNTGCATCAGGT		CACACTGCCGNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	959	TGCAGGACCCAGAGAAATCGAATA	1199	TGCAGGACCCAGAGAAATCGAATA	1439
CACAGGGAANNNTGCATCAGGT		CATTAAATCCTNNNTGCATCAGGT		CATTCCGTAANNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	960	TGCAGGACCCAGAGAAATCGAATA	1200	TGCAGGACCCAGAGAAATCGAATA	1440
CAGGTGAGGANNNTGCATCAGGT		CACCTACGCTTNNNTGCATCAGGT		CAACCCCTGCCNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	961	TGCAGGACCCAGAGAAATCGAATA	1201	TGCAGGACCCAGAGAAATCGAATA	1441
CACGTGATCANNNTGCATCAGGT		CATAGCTATANNNTGCATCAGGT		CAGTACCTAGNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	962	TGCAGGACCCAGAGAAATCGAATA	1202	TGCAGGACCCAGAGAAATCGAATA	1442
CATTGCGTTGANNNTGCATCAGGT		CATGCACTCTNNNTGCATCAGGT		CACGATATTNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	963	TGCAGGACCCAGAGAAATCGAATA	1203	TGCAGGACCCAGAGAAATCGAATA	1443
CATCGCTCCGNNNTGCATCAGGT		CAGTCTCTCCNNNTGCATCAGGT		CAGCCACCCGNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	964	TGCAGGACCCAGAGAAATCGAATA	1204	TGCAGGACCCAGAGAAATCGAATA	1444
CACCACTCAANNNTGCATCAGGT		CAGCCACCCGNNNTGCATCAGGT		CATACATCANNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	965	TGCAGGACCCAGAGAAATCGAATA	1205	TGCAGGACCCAGAGAAATCGAATA	1445
CACACATTCGNNNTGCATCAGGT		CATTATGTGANNNTGCATCAGGT		CAGCCAGAACNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	966	TGCAGGACCCAGAGAAATCGAATA	1206	TGCAGGACCCAGAGAAATCGAATA	1446
CAGGTATCTTNNNTGCATCAGGT		CAATACCTCCGNNNTGCATCAGGT		CAACGGATCTNNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	967	TGCAGGACCCAGAGAAATCGAATA	1207	TGCAGGACCCAGAGAAATCGAATA	1447
CATAAGATGANNNTGCATCAGGT		CAACTATGGCNNNTGCATCAGGT		CACGTTCTTANNNTGCATCAGGT	
TGCAGGACCCAGAGAAATCGAATA	968	TGCAGGACCCAGAGAAATCGAATA	1208	TGCAGGACCCAGAGAAATCGAATA	1448
CATTAAAAATTNNNTGCATCAGGT		CAACGGCTCGNNNTGCATCAGGT		CAATGCCAGTNNNTGCATCAGGT	

图13H

池-7	SEQ ID No.	池-8	SEQ ID No.	池-9	SEQ ID No.
TGCAGGACCCAGAGAAATTCGAATA	1449	TGCAGGACCCAGAGAAATTCGAATA	1489	TGCAGGACCCAGAGAAATTCGAATA	1529
CACAGGCTCCGNNNACGTATGCCA		CACATACCCAGNNNACGTATGCCA		CAGAACCCGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1450	TGCAGGACCCAGAGAAATTCGAATA	1490	TGCAGGACCCAGAGAAATTCGAATA	1530
CATTGAGCCGNNNACGTATGCCA		CATTATTGAGNNNACGTATGCCA		CAACCAATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1451	TGCAGGACCCAGAGAAATTCGAATA	1491	TGCAGGACCCAGAGAAATTCGAATA	1531
CACACAGAGANNNACGTATGCCA		CAACTGTGTGNNNACGTATGCCA		CAGACCGATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1452	TGCAGGACCCAGAGAAATTCGAATA	1492	TGCAGGACCCAGAGAAATTCGAATA	1532
CAGGACTCCGNNNACGTATGCCA		CAITGTATGNNNACGTATGCCA		CAATGTATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1453	TGCAGGACCCAGAGAAATTCGAATA	1493	TGCAGGACCCAGAGAAATTCGAATA	1533
CATTGGTTAANNNACGTATGCCA		CATTCTCGGNNNACGTATGCCA		CAGGAGAAGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1454	TGCAGGACCCAGAGAAATTCGAATA	1494	TGCAGGACCCAGAGAAATTCGAATA	1534
CATACTAAGANNNACGTATGCCA		CACCACTTAGNNNACGTATGCCA		CACTTATACANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1455	TGCAGGACCCAGAGAAATTCGAATA	1495	TGCAGGACCCAGAGAAATTCGAATA	1535
CAGTCCGAATGNNNACGTATGCCA		CAGGAACAATNNNACGTATGCCA		CACCTCGTAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1456	TGCAGGACCCAGAGAAATTCGAATA	1496	TGCAGGACCCAGAGAAATTCGAATA	1536
CAAGCGACGNNNACGTATGCCA		CATCCGAAGTNNNACGTATGCCA		CATAAGCATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1457	TGCAGGACCCAGAGAAATTCGAATA	1497	TGCAGGACCCAGAGAAATTCGAATA	1537
CAATCATGTAANNNACGTATGCCA		CAITGGCTCCNNNACGTATGCCA		CAAGGCGCTTNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1458	TGCAGGACCCAGAGAAATTCGAATA	1498	TGCAGGACCCAGAGAAATTCGAATA	1538
CAAAAGAGTTNNNACGTATGCCA		CACAGTCCGNNNACGTATGCCA		CATTAAACAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1459	TGCAGGACCCAGAGAAATTCGAATA	1499	TGCAGGACCCAGAGAAATTCGAATA	1539
CAAGGACCCGNNNACGTATGCCA		CACTCAACTGNNNACGTATGCCA		CATGGCCATANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1460	TGCAGGACCCAGAGAAATTCGAATA	1500	TGCAGGACCCAGAGAAATTCGAATA	1540
CATTGAAACANNNACGTATGCCA		CAGGCGGCTTNNNACGTATGCCA		CAGAGTGATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1461	TGCAGGACCCAGAGAAATTCGAATA	1501	TGCAGGACCCAGAGAAATTCGAATA	1541
CACCTCGACTTNNNACGTATGCCA		CAATGCGCTANNNACGTATGCCA		CACCTAATCCGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1462	TGCAGGACCCAGAGAAATTCGAATA	1502	TGCAGGACCCAGAGAAATTCGAATA	1542
CAGGCGAATTCNNNACGTATGCCA		CAAGTCCGGAANNNACGTATGCCA		CAAGGTAAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1463	TGCAGGACCCAGAGAAATTCGAATA	1503	TGCAGGACCCAGAGAAATTCGAATA	1543
CACCCCGCGNNNACGTATGCCA		CATGCTGGCGNNNACGTATGCCA		CAACAGTACGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1464	TGCAGGACCCAGAGAAATTCGAATA	1504	TGCAGGACCCAGAGAAATTCGAATA	1544
CAGATAAGCGNNNACGTATGCCA		CACTAAGCTGNNNACGTATGCCA		CAATGTGATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1465	TGCAGGACCCAGAGAAATTCGAATA	1505	TGCAGGACCCAGAGAAATTCGAATA	1545
CAGAAAGGATGNNNACGTATGCCA		CAGAAACAAANNNACGTATGCCA		CAGCTGCGANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1466	TGCAGGACCCAGAGAAATTCGAATA	1506	TGCAGGACCCAGAGAAATTCGAATA	1546
CAATATTATNNNACGTATGCCA		CAATGCAAAANNNACGTATGCCA		CACTTTTATGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1467	TGCAGGACCCAGAGAAATTCGAATA	1507	TGCAGGACCCAGAGAAATTCGAATA	1547
CATAAGCTATNNNACGTATGCCA		CAACGGCTCGNNNACGTATGCCA		CATCCCAAGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1468	TGCAGGACCCAGAGAAATTCGAATA	1508	TGCAGGACCCAGAGAAATTCGAATA	1548
CAACTCGCGNNNACGTATGCCA		CACACAGATAANNNACGTATGCCA		CAGACACTACNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1469	TGCAGGACCCAGAGAAATTCGAATA	1509	TGCAGGACCCAGAGAAATTCGAATA	1549
CAGGACTCGNNNACGTATGCCA		CATGTAGCCANNNACGTATGCCA		CAATACCGAGNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1470	TGCAGGACCCAGAGAAATTCGAATA	1510	TGCAGGACCCAGAGAAATTCGAATA	1550
CATCGGACTTNNNACGTATGCCA		CACTCTGCAANNNACGTATGCCA		CAGTTGAAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1471	TGCAGGACCCAGAGAAATTCGAATA	1511	TGCAGGACCCAGAGAAATTCGAATA	1551
CAGGAGGAGGNNNACGTATGCCA		CATTACCTTANNNACGTATGCCA		CAATTTCTTANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1472	TGCAGGACCCAGAGAAATTCGAATA	1512	TGCAGGACCCAGAGAAATTCGAATA	1552
CACAGGACGNNNACGTATGCCA		CAITCAATTCNNNACGTATGCCA		CAACGTTCAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1473	TGCAGGACCCAGAGAAATTCGAATA	1513	TGCAGGACCCAGAGAAATTCGAATA	1553
CAATCTCATGNNNACGTATGCCA		CAAGGTTCTGNNNACGTATGCCA		CAAAATACGAANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1474	TGCAGGACCCAGAGAAATTCGAATA	1514	TGCAGGACCCAGAGAAATTCGAATA	1554
CAAGGCGATANNNACGTATGCCA		CAATTTTAAANNNACGTATGCCA		CACCACTGANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1475	TGCAGGACCCAGAGAAATTCGAATA	1515	TGCAGGACCCAGAGAAATTCGAATA	1555
CACCTAGATGNNNACGTATGCCA		CATTGCAAGCANNNACGTATGCCA		CAATCCCTCANNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1476	TGCAGGACCCAGAGAAATTCGAATA	1516	TGCAGGACCCAGAGAAATTCGAATA	1556
CACCTACCATNNNACGTATGCCA		CACCCCACTGNNNACGTATGCCA		CACGTCCGCTNNNACGTATGCCA	

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池 -7	SEQ ID NO.	池 -8	SEQ ID NO.	池 -9	SEQ ID NO.
TGCAGGACCCAGAGAAATTCGAATA	1477	TGCAGGACCCAGAGAAATTCGAATA	1717	TGCAGGACCCAGAGAAATTCGAATA	1957
CAGACGCTCCANNNNACGTATGCCA		CAGCTTCTGNNNNACGTATGCCA		CATATACACANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1478	TGCAGGACCCAGAGAAATTCGAATA	1718	TGCAGGACCCAGAGAAATTCGAATA	1958
CAGGACCTAGNNNNACGTATGCCA		CAGGAACTCCNNNNACGTATGCCA		CAGCTGTATATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1479	TGCAGGACCCAGAGAAATTCGAATA	1719	TGCAGGACCCAGAGAAATTCGAATA	1959
CAGATCGGANNNNACGTATGCCA		CAGTGTAGGNNNNACGTATGCCA		CAGTCCAGANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1480	TGCAGGACCCAGAGAAATTCGAATA	1720	TGCAGGACCCAGAGAAATTCGAATA	1960
CAGCGCATTAANNNNACGTATGCCA		CAGATCGATCCNNNNACGTATGCCA		CAGCGCGCTGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1481	TGCAGGACCCAGAGAAATTCGAATA	1721	TGCAGGACCCAGAGAAATTCGAATA	1961
CATTAAAGTTGNNNNACGTATGCCA		CAGTAATAGANNNNACGTATGCCA		CATACGTCAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1482	TGCAGGACCCAGAGAAATTCGAATA	1722	TGCAGGACCCAGAGAAATTCGAATA	1962
CAGCGAGCTGNNNNACGTATGCCA		CAGCGAGCTGNNNNACGTATGCCA		CATGTCCTCANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1483	TGCAGGACCCAGAGAAATTCGAATA	1723	TGCAGGACCCAGAGAAATTCGAATA	1963
CAGGACCGCTGNNNNACGTATGCCA		CATTTGCTTANNNNACGTATGCCA		CAGCGTATATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1484	TGCAGGACCCAGAGAAATTCGAATA	1724	TGCAGGACCCAGAGAAATTCGAATA	1964
CAGTATTTCTNNNNACGTATGCCA		CATTTTCTGANNNNACGTATGCCA		CAGGACCCACNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1485	TGCAGGACCCAGAGAAATTCGAATA	1725	TGCAGGACCCAGAGAAATTCGAATA	1965
CAGGTCCTCCNNNNACGTATGCCA		CAGACGGAGCANNNNACGTATGCCA		CATCGCTCTANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1486	TGCAGGACCCAGAGAAATTCGAATA	1726	TGCAGGACCCAGAGAAATTCGAATA	1966
CAGCAAGCTCTGNNNNACGTATGCCA		CAGCCAGCGCANNNNACGTATGCCA		CAGCGAAGATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1487	TGCAGGACCCAGAGAAATTCGAATA	1727	TGCAGGACCCAGAGAAATTCGAATA	1967
CAGAGCACANNNNACGTATGCCA		CAGAGTATTTNNNNACGTATGCCA		CATTAGCGGTTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1488	TGCAGGACCCAGAGAAATTCGAATA	1728	TGCAGGACCCAGAGAAATTCGAATA	1968
CATCAAACTGNNNNACGTATGCCA		CAGCGCGCTANNNNACGTATGCCA		CATGAGCTCANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1489	TGCAGGACCCAGAGAAATTCGAATA	1729	TGCAGGACCCAGAGAAATTCGAATA	1969
CATTCGCGCTANNNNACGTATGCCA		CAGCTATGCGNNNNACGTATGCCA		CATACGCGTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1490	TGCAGGACCCAGAGAAATTCGAATA	1730	TGCAGGACCCAGAGAAATTCGAATA	1970
CATTTGACGNNNNACGTATGCCA		CATAGCAGCTNNNNACGTATGCCA		CATAGTGTATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1491	TGCAGGACCCAGAGAAATTCGAATA	1731	TGCAGGACCCAGAGAAATTCGAATA	1971
CAGTAAGCTTAANNNNACGTATGCCA		CAGCGCTGACNNNNACGTATGCCA		CAGATTAGGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1492	TGCAGGACCCAGAGAAATTCGAATA	1732	TGCAGGACCCAGAGAAATTCGAATA	1972
CAGGACCGGANNNNACGTATGCCA		CAGAAATACANNNNACGTATGCCA		CAGACCCACANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1493	TGCAGGACCCAGAGAAATTCGAATA	1733	TGCAGGACCCAGAGAAATTCGAATA	1973
CATGTCCGCGNNNNACGTATGCCA		CAGTAGATATNNNNACGTATGCCA		CAGTGGCTGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1494	TGCAGGACCCAGAGAAATTCGAATA	1734	TGCAGGACCCAGAGAAATTCGAATA	1974
CAGCCCGCAGANNNNACGTATGCCA		CAGTGTGCGNNNNACGTATGCCA		CATATGTTCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1495	TGCAGGACCCAGAGAAATTCGAATA	1735	TGCAGGACCCAGAGAAATTCGAATA	1975
CAGAGCGCGCANNNNACGTATGCCA		CAGTACGCAANNNNACGTATGCCA		CAGTGGTCGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1496	TGCAGGACCCAGAGAAATTCGAATA	1736	TGCAGGACCCAGAGAAATTCGAATA	1976
CAGCCATTGANNNNACGTATGCCA		CATTTCTGTANNNNACGTATGCCA		CAGTGACCGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1497	TGCAGGACCCAGAGAAATTCGAATA	1737	TGCAGGACCCAGAGAAATTCGAATA	1977
CATGAACACGNNNNACGTATGCCA		CAGCTCCCTCANNNNACGTATGCCA		CAGGCGTCTCANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1498	TGCAGGACCCAGAGAAATTCGAATA	1738	TGCAGGACCCAGAGAAATTCGAATA	1978
CAGAACTCCGTTNNNNACGTATGCCA		CAGACTTGACNNNNACGTATGCCA		CAGTCTAATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1499	TGCAGGACCCAGAGAAATTCGAATA	1739	TGCAGGACCCAGAGAAATTCGAATA	1979
CATTAACTCGANNNNACGTATGCCA		CAGTCTATGNNNNACGTATGCCA		CAGTCTGCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1500	TGCAGGACCCAGAGAAATTCGAATA	1740	TGCAGGACCCAGAGAAATTCGAATA	1980
CAGCGCAGCTCANNNNACGTATGCCA		CATCTCAGTANNNNACGTATGCCA		CAGGTTCTCANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1501	TGCAGGACCCAGAGAAATTCGAATA	1741	TGCAGGACCCAGAGAAATTCGAATA	1981
CAGCCCTTAGTNNNNACGTATGCCA		CAGGAAGATGNNNNACGTATGCCA		CAGTGAAGGTTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1502	TGCAGGACCCAGAGAAATTCGAATA	1742	TGCAGGACCCAGAGAAATTCGAATA	1982
CATTTCTCTGNNNNACGTATGCCA		CATTTTCCANNNNACGTATGCCA		CAGTTTAAAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1503	TGCAGGACCCAGAGAAATTCGAATA	1743	TGCAGGACCCAGAGAAATTCGAATA	1983
CATTCACGCGNNNNACGTATGCCA		CAGACCGGCTNNNNACGTATGCCA		CAGAAAGCAATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1504	TGCAGGACCCAGAGAAATTCGAATA	1744	TGCAGGACCCAGAGAAATTCGAATA	1984
CATTCAGGAGNNNNACGTATGCCA		CAGTTGTCAANNNNACGTATGCCA		CATGAAGCGANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	1505	TGCAGGACCCAGAGAAATTCGAATA	1745	TGCAGGACCCAGAGAAATTCGAATA	1985
CATTCACGCTGNNNNACGTATGCCA		CAGTCTAGGNNNNACGTATGCCA		CAGTACTGCTNNNNACGTATGCCA	

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACACAGAGAATTGGAATA	1506	TGCAGGACACAGAGAATTGGAATA	1746	TGCAGGACACAGAGAATTGGAATA	1986
CAATCCGCGTGNHNAAGTATGCCA		CAGCCTTACTNNNAAGTATGCCA		CAACTATGTANNNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1507	TGCAGGACACAGAGAATTGGAATA	1747	TGCAGGACACAGAGAATTGGAATA	1987
CAAAATTCGCGNNHNAAGTATGCCA		CAGCATGTGTNNHNAAGTATGCCA		CAGAACTTCGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1508	TGCAGGACACAGAGAATTGGAATA	1748	TGCAGGACACAGAGAATTGGAATA	1988
CAGGTTCATGAMHNAAGTATGCCA		CAGTACTGTGNNHNAAGTATGCCA		CAGGTTCGCGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1509	TGCAGGACACAGAGAATTGGAATA	1749	TGCAGGACACAGAGAATTGGAATA	1989
CACGTTTATGTNNHNAAGTATGCCA		CAATCTAACANNHNAAGTATGCCA		CAATCCAAATGTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1510	TGCAGGACACAGAGAATTGGAATA	1750	TGCAGGACACAGAGAATTGGAATA	1990
CAGTCCACGCGNNHNAAGTATGCCA		CAACGATTCGNNHNAAGTATGCCA		CAACTTGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1511	TGCAGGACACAGAGAATTGGAATA	1751	TGCAGGACACAGAGAATTGGAATA	1991
CAACGTTTGTGNNHNAAGTATGCCA		CAAAAGCTTANNHNAAGTATGCCA		CAATCGCTGCGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1512	TGCAGGACACAGAGAATTGGAATA	1752	TGCAGGACACAGAGAATTGGAATA	1992
CAATCCGCGTGNHNAAGTATGCCA		CAAGTAAAGANNHNAAGTATGCCA		CAATCCGCTGTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1513	TGCAGGACACAGAGAATTGGAATA	1753	TGCAGGACACAGAGAATTGGAATA	1993
CAAGGCGCGGNNHNAAGTATGCCA		CATCTGAGACNNHNAAGTATGCCA		CACGGTACTANNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1514	TGCAGGACACAGAGAATTGGAATA	1754	TGCAGGACACAGAGAATTGGAATA	1994
CAGGCAATAGNNHNAAGTATGCCA		CAATGGCGATTNNHNAAGTATGCCA		CAAGATATCTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1515	TGCAGGACACAGAGAATTGGAATA	1755	TGCAGGACACAGAGAATTGGAATA	1995
CAGGCTAGCGNNHNAAGTATGCCA		CACATCTTGTGNNHNAAGTATGCCA		CAATCAAGTGTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1516	TGCAGGACACAGAGAATTGGAATA	1756	TGCAGGACACAGAGAATTGGAATA	1996
CAATGTTCTATNNHNAAGTATGCCA		CATCTTGTGNNHNAAGTATGCCA		CAACCTCTCTANNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1517	TGCAGGACACAGAGAATTGGAATA	1757	TGCAGGACACAGAGAATTGGAATA	1997
CAATTAATATANNHNAAGTATGCCA		CAGCGAAGCAANNHNAAGTATGCCA		CAAGCAATTTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1518	TGCAGGACACAGAGAATTGGAATA	1758	TGCAGGACACAGAGAATTGGAATA	1998
CAATATGCTGNNHNAAGTATGCCA		CAGAGTAGACNNHNAAGTATGCCA		CAGCCCGCAANNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1519	TGCAGGACACAGAGAATTGGAATA	1759	TGCAGGACACAGAGAATTGGAATA	1999
CAGGTGGTTANNHNAAGTATGCCA		CAGCTCATGGANNHNAAGTATGCCA		CAACCAATGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1520	TGCAGGACACAGAGAATTGGAATA	1760	TGCAGGACACAGAGAATTGGAATA	2000
CAGGCTAGCGNNHNAAGTATGCCA		CATTCGCGCGNNHNAAGTATGCCA		CAGATGGGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1521	TGCAGGACACAGAGAATTGGAATA	1761	TGCAGGACACAGAGAATTGGAATA	2001
CAGACCTTGCANNHNAAGTATGCCA		CAATGGCCTAANNHNAAGTATGCCA		CAACCGCTGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1522	TGCAGGACACAGAGAATTGGAATA	1762	TGCAGGACACAGAGAATTGGAATA	2002
CAATCTATTCNNHNAAGTATGCCA		CAGGCGCAANNHNAAGTATGCCA		CAACCCACTTNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1523	TGCAGGACACAGAGAATTGGAATA	1763	TGCAGGACACAGAGAATTGGAATA	2003
CAAGGTAICGNNHNAAGTATGCCA		CAATAGAAACNNHNAAGTATGCCA		CAGGACCTGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1524	TGCAGGACACAGAGAATTGGAATA	1764	TGCAGGACACAGAGAATTGGAATA	2004
CAGGCGAACGNNHNAAGTATGCCA		CATCGGCTGTGNNHNAAGTATGCCA		CACTTTGATCNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1525	TGCAGGACACAGAGAATTGGAATA	1765	TGCAGGACACAGAGAATTGGAATA	2005
CAAGGATGTGNNHNAAGTATGCCA		CAGTGCTGTGNNHNAAGTATGCCA		CAAGGTATGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1526	TGCAGGACACAGAGAATTGGAATA	1766	TGCAGGACACAGAGAATTGGAATA	2006
CATCATGCTCNNHNAAGTATGCCA		CAATATGCCACNNHNAAGTATGCCA		CACATCCAGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1527	TGCAGGACACAGAGAATTGGAATA	1767	TGCAGGACACAGAGAATTGGAATA	2007
CAATGCTTATNNHNAAGTATGCCA		CAATCACTGTGNNHNAAGTATGCCA		CACACAACTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1528	TGCAGGACACAGAGAATTGGAATA	1768	TGCAGGACACAGAGAATTGGAATA	2008
CAAGGCGCAGNNHNAAGTATGCCA		CATCAGGACANNHNAAGTATGCCA		CATAAATGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1529	TGCAGGACACAGAGAATTGGAATA	1769	TGCAGGACACAGAGAATTGGAATA	2009
CAGCAGCTGTGNNHNAAGTATGCCA		CATGTTACGTGNNHNAAGTATGCCA		CAATCTACANNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1530	TGCAGGACACAGAGAATTGGAATA	1770	TGCAGGACACAGAGAATTGGAATA	2010
CAGCGAATGTGNNHNAAGTATGCCA		CAATACGCTGTGNNHNAAGTATGCCA		CAGCGAGATGTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1531	TGCAGGACACAGAGAATTGGAATA	1771	TGCAGGACACAGAGAATTGGAATA	2011
CAAAACAGACGNNHNAAGTATGCCA		CAACCTTTAGNNHNAAGTATGCCA		CAGTAGCCATGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1532	TGCAGGACACAGAGAATTGGAATA	1772	TGCAGGACACAGAGAATTGGAATA	2012
CAATCCAAACGNNHNAAGTATGCCA		CAATCTTGTGNNHNAAGTATGCCA		CAAGGCGCTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1533	TGCAGGACACAGAGAATTGGAATA	1773	TGCAGGACACAGAGAATTGGAATA	2013
CAAGGCGCATGNNHNAAGTATGCCA		CACTTTGACGNNHNAAGTATGCCA		CAGTAGACTGNNHNAAGTATGCCA	
TGCAGGACACAGAGAATTGGAATA	1534	TGCAGGACACAGAGAATTGGAATA	1774	TGCAGGACACAGAGAATTGGAATA	2014
CAGCTTAAGANNHNAAGTATGCCA		CAGTTCTGAGNNHNAAGTATGCCA		CAGGTATCTGNNHNAAGTATGCCA	

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池-7	SEQ ID NO.	池-8	SEQ ID NO.	池-9	SEQ ID NO.
TGCAGGACCAGAGAATTCGAATA	1535	TGCAGGACCAGAGAATTCGAATA	1775	TGCAGGACCAGAGAATTCGAATA	2015
CACATACCTCANNCTAGCGTTAC		CATGTTGCAGNNNCTAGCGTTAC		CAGGTTTTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1536	TGCAGGACCAGAGAATTCGAATA	1776	TGCAGGACCAGAGAATTCGAATA	2016
CAGCCAAATCANNNCTAGCGTTAC		CAAAACCAACNNNCTAGCGTTAC		CAACAGAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1537	TGCAGGACCAGAGAATTCGAATA	1777	TGCAGGACCAGAGAATTCGAATA	2017
CACCTTAGCCANNNCTAGCGTTAC		CATAAGCACCNNNCTAGCGTTAC		CACAGCACGCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1538	TGCAGGACCAGAGAATTCGAATA	1778	TGCAGGACCAGAGAATTCGAATA	2018
CACGCCACCAANNNCTAGCGTTAC		CAGATGTAAANNNCTAGCGTTAC		CAACCGTTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1539	TGCAGGACCAGAGAATTCGAATA	1779	TGCAGGACCAGAGAATTCGAATA	2019
CATTCCGGTANNNCTAGCGTTAC		CAGTTATGCCNNNCTAGCGTTAC		CAGGAAGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1540	TGCAGGACCAGAGAATTCGAATA	1780	TGCAGGACCAGAGAATTCGAATA	2020
CATTAGACATNNNCTAGCGTTAC		CAGCGCCGAANNNCTAGCGTTAC		CAGAGGATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1541	TGCAGGACCAGAGAATTCGAATA	1781	TGCAGGACCAGAGAATTCGAATA	2021
CAGGCATTACNNNCTAGCGTTAC		CAAGATTGTNNNCTAGCGTTAC		CACGGTTCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1542	TGCAGGACCAGAGAATTCGAATA	1782	TGCAGGACCAGAGAATTCGAATA	2022
CAAAACCAAAANNNCTAGCGTTAC		CACACAGCTANNNCTAGCGTTAC		CATCCACAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1543	TGCAGGACCAGAGAATTCGAATA	1783	TGCAGGACCAGAGAATTCGAATA	2023
CACCGCTCTANNNCTAGCGTTAC		CAACGGCAGGNNNCTAGCGTTAC		CAGAGACCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1544	TGCAGGACCAGAGAATTCGAATA	1784	TGCAGGACCAGAGAATTCGAATA	2024
CACCGATCTGNNNCTAGCGTTAC		CATACGGAGANNNCTAGCGTTAC		CAGTCCGAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1545	TGCAGGACCAGAGAATTCGAATA	1785	TGCAGGACCAGAGAATTCGAATA	2025
CAGCATGAGANNNCTAGCGTTAC		CATCTCGATGANNNCTAGCGTTAC		CATCGGCTCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1546	TGCAGGACCAGAGAATTCGAATA	1786	TGCAGGACCAGAGAATTCGAATA	2026
CAGTAAGTCCNNNCTAGCGTTAC		CATCCCCCINNINCTAGCGTTAC		CATCATTCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1547	TGCAGGACCAGAGAATTCGAATA	1787	TGCAGGACCAGAGAATTCGAATA	2027
CAAAAGCGAGTNNNCTAGCGTTAC		CACCATCTACNNNCTAGCGTTAC		CAGAACTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1548	TGCAGGACCAGAGAATTCGAATA	1788	TGCAGGACCAGAGAATTCGAATA	2028
CAGATCTGCGNNNCTAGCGTTAC		CAAAAGCAGGTNNNCTAGCGTTAC		CATAAATTTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1549	TGCAGGACCAGAGAATTCGAATA	1789	TGCAGGACCAGAGAATTCGAATA	2029
CACCGGTCACNNNCTAGCGTTAC		CAAAAGTCAANNNCTAGCGTTAC		CAGATTGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1550	TGCAGGACCAGAGAATTCGAATA	1790	TGCAGGACCAGAGAATTCGAATA	2030
CATCTCTCGCGNNNCTAGCGTTAC		CAATTCGACGNNNCTAGCGTTAC		CATGGCGCACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1551	TGCAGGACCAGAGAATTCGAATA	1791	TGCAGGACCAGAGAATTCGAATA	2031
CACATGTCCGANNNCTAGCGTTAC		CAACCCAGCGNNNCTAGCGTTAC		CAGAAATCAGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1552	TGCAGGACCAGAGAATTCGAATA	1792	TGCAGGACCAGAGAATTCGAATA	2032
CAAAACGGTTCNNNCTAGCGTTAC		CATAGTCGGTNNNCTAGCGTTAC		CAAGGCTATCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1553	TGCAGGACCAGAGAATTCGAATA	1793	TGCAGGACCAGAGAATTCGAATA	2033
CACCCCAATTNNNCTAGCGTTAC		CATGGGCATANNNCTAGCGTTAC		CATCTTGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1554	TGCAGGACCAGAGAATTCGAATA	1794	TGCAGGACCAGAGAATTCGAATA	2034
CACCGCTGTNNNCTAGCGTTAC		CATAGAACCCNNNCTAGCGTTAC		CAGCATTCGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1555	TGCAGGACCAGAGAATTCGAATA	1795	TGCAGGACCAGAGAATTCGAATA	2035
CAACTCTAAANNNCTAGCGTTAC		CAGGTTTGTGNNNCTAGCGTTAC		CATAGATTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1556	TGCAGGACCAGAGAATTCGAATA	1796	TGCAGGACCAGAGAATTCGAATA	2036
CAATGAGCTCNNNCTAGCGTTAC		CAAGATTGTNNNCTAGCGTTAC		CAGTTTGCCTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1557	TGCAGGACCAGAGAATTCGAATA	1797	TGCAGGACCAGAGAATTCGAATA	2037
CATCTAAGGCGNNNCTAGCGTTAC		CATTAGCGACNNNCTAGCGTTAC		CATCTTCGGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1558	TGCAGGACCAGAGAATTCGAATA	1798	TGCAGGACCAGAGAATTCGAATA	2038
CACAAATAGCGNNNCTAGCGTTAC		CAGATATATCNNNCTAGCGTTAC		CAAGTAGTCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1559	TGCAGGACCAGAGAATTCGAATA	1799	TGCAGGACCAGAGAATTCGAATA	2039
CATCTTGGTNNNCTAGCGTTAC		CAAACTGTGNNNCTAGCGTTAC		CAGGGTGTATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1560	TGCAGGACCAGAGAATTCGAATA	1800	TGCAGGACCAGAGAATTCGAATA	2040
CACAGAGCCANNNCTAGCGTTAC		CACGAATGGANNNCTAGCGTTAC		CAGTGTGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1561	TGCAGGACCAGAGAATTCGAATA	1801	TGCAGGACCAGAGAATTCGAATA	2041
CAGCTTGGATNNNCTAGCGTTAC		CAGTTCTGTTGNNNCTAGCGTTAC		CAAACTGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1562	TGCAGGACCAGAGAATTCGAATA	1802	TGCAGGACCAGAGAATTCGAATA	2042
CATTAATATCNNNCTAGCGTTAC		CATCGTGGTANNNCTAGCGTTAC		CAATAAATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	1563	TGCAGGACCAGAGAATTCGAATA	1803	TGCAGGACCAGAGAATTCGAATA	2043
CACCTAAATNNNCTAGCGTTAC		CAGCAAAATANNNCTAGCGTTAC		CAACGGCTGCGNNNCTAGCGTTAC	

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池-7	SEQ ID NO.	池-8	SEQ ID NO.	池-9	SEQ ID NO.
TGCAGGACCAGAGAAATCGAATA	1564	TGCAGGACCAGAGAAATCGAATA	1804	TGCAGGACCAGAGAAATCGAATA	2044
CAGAACCTGANNHCTAGCGTTAC		CAGAACTAANNHCTAGCGTTAC		CACGTTCGTANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1565	TGCAGGACCAGAGAAATCGAATA	1805	TGCAGGACCAGAGAAATCGAATA	2045
CAGAGGGCTGNNHCTAGCGTTAC		CATCGGAGTGNHCTAGCGTTAC		CAAGGGCTAANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1566	TGCAGGACCAGAGAAATCGAATA	1806	TGCAGGACCAGAGAAATCGAATA	2046
CAAGGTGATGNNHCTAGCGTTAC		CAGTCTGAGNNHCTAGCGTTAC		CATGCCATGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1567	TGCAGGACCAGAGAAATCGAATA	1807	TGCAGGACCAGAGAAATCGAATA	2047
CAACGGCTTANNHCTAGCGTTAC		CATCGGCGTGNHCTAGCGTTAC		CAAAAGCTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1568	TGCAGGACCAGAGAAATCGAATA	1808	TGCAGGACCAGAGAAATCGAATA	2048
CAGGTGCGTGNHCTAGCGTTAC		CAGATCGGCGNNHCTAGCGTTAC		CAAGGACGATHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1569	TGCAGGACCAGAGAAATCGAATA	1809	TGCAGGACCAGAGAAATCGAATA	2049
CAGAGATCAGNNHCTAGCGTTAC		CAGTGTATGNNHCTAGCGTTAC		CACCTGAGGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1570	TGCAGGACCAGAGAAATCGAATA	1810	TGCAGGACCAGAGAAATCGAATA	2050
CATACGATGNNHCTAGCGTTAC		CAAGTATTTGNNHCTAGCGTTAC		CATGCGATGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1571	TGCAGGACCAGAGAAATCGAATA	1811	TGCAGGACCAGAGAAATCGAATA	2051
CAAGTTATCANNHCTAGCGTTAC		CAGCTAAGGNNHCTAGCGTTAC		CAAGCGAAGCANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1572	TGCAGGACCAGAGAAATCGAATA	1812	TGCAGGACCAGAGAAATCGAATA	2052
CACAGTGTGNNHCTAGCGTTAC		CAAGCCAGCANNHCTAGCGTTAC		CATAGAGTGNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1573	TGCAGGACCAGAGAAATCGAATA	1813	TGCAGGACCAGAGAAATCGAATA	2053
CATACCGGCGNNHCTAGCGTTAC		CAAGTGTGNNHCTAGCGTTAC		CAAGCGAGANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1574	TGCAGGACCAGAGAAATCGAATA	1814	TGCAGGACCAGAGAAATCGAATA	2054
CAGTGTGTGNNHCTAGCGTTAC		CACATATTTGNNHCTAGCGTTAC		CACCTATTTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1575	TGCAGGACCAGAGAAATCGAATA	1815	TGCAGGACCAGAGAAATCGAATA	2055
CAGTGTGTTAANNHCTAGCGTTAC		CAGTGTATGNNHCTAGCGTTAC		CAGCGAGCGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1576	TGCAGGACCAGAGAAATCGAATA	1816	TGCAGGACCAGAGAAATCGAATA	2056
CAGCTCTAGNNHCTAGCGTTAC		CAATAGTATGNNHCTAGCGTTAC		CAAGGATTTAANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1577	TGCAGGACCAGAGAAATCGAATA	1817	TGCAGGACCAGAGAAATCGAATA	2057
CATGTGTGCTGNNHCTAGCGTTAC		CACCGCTGAGNNHCTAGCGTTAC		CAATATGTTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1578	TGCAGGACCAGAGAAATCGAATA	1818	TGCAGGACCAGAGAAATCGAATA	2058
CATATAGGCTGNNHCTAGCGTTAC		CATTATTTTANNHCTAGCGTTAC		CACATTAAGTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1579	TGCAGGACCAGAGAAATCGAATA	1819	TGCAGGACCAGAGAAATCGAATA	2059
CAAGAACGACNNHCTAGCGTTAC		CAACAAAGCANNHCTAGCGTTAC		CAGACGAGCANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1580	TGCAGGACCAGAGAAATCGAATA	1820	TGCAGGACCAGAGAAATCGAATA	2060
CATACGATATNNHCTAGCGTTAC		CATAAGTATGNNHCTAGCGTTAC		CACCGATAGTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1581	TGCAGGACCAGAGAAATCGAATA	1821	TGCAGGACCAGAGAAATCGAATA	2061
CATTAAGCTTANNHCTAGCGTTAC		CAGGACACGNNHCTAGCGTTAC		CAAGTATGTTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1582	TGCAGGACCAGAGAAATCGAATA	1822	TGCAGGACCAGAGAAATCGAATA	2062
CATTAAGCTTANNHCTAGCGTTAC		CAGTACCTCTGNNHCTAGCGTTAC		CATTTGCGCTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1583	TGCAGGACCAGAGAAATCGAATA	1823	TGCAGGACCAGAGAAATCGAATA	2063
CAGCACTGCTGNNHCTAGCGTTAC		CACGTGTGATGNNHCTAGCGTTAC		CAGTAGACGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1584	TGCAGGACCAGAGAAATCGAATA	1824	TGCAGGACCAGAGAAATCGAATA	2064
CACCTCTGACNNHCTAGCGTTAC		CAACAAAGCANNHCTAGCGTTAC		CAACGAACTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1585	TGCAGGACCAGAGAAATCGAATA	1825	TGCAGGACCAGAGAAATCGAATA	2065
CATTCGATCTGNNHCTAGCGTTAC		CAAGAGGCTAANNHCTAGCGTTAC		CACGTCTTTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1586	TGCAGGACCAGAGAAATCGAATA	1826	TGCAGGACCAGAGAAATCGAATA	2066
CATCACTGNNHCTAGCGTTAC		CARTTCAGTNNHCTAGCGTTAC		CAACACAGGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1587	TGCAGGACCAGAGAAATCGAATA	1827	TGCAGGACCAGAGAAATCGAATA	2067
CAATTTGCCCTGNNHCTAGCGTTAC		CACGTCTCAANNHCTAGCGTTAC		CAAGTCACTAANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1588	TGCAGGACCAGAGAAATCGAATA	1828	TGCAGGACCAGAGAAATCGAATA	2068
CATACATGTANNHCTAGCGTTAC		CAGGTAGCTTNNHCTAGCGTTAC		CAGAAAGAACNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1589	TGCAGGACCAGAGAAATCGAATA	1829	TGCAGGACCAGAGAAATCGAATA	2069
CAGACTTGTNNHCTAGCGTTAC		CATCCTTTGTNNHCTAGCGTTAC		CACCTAAGCTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1590	TGCAGGACCAGAGAAATCGAATA	1830	TGCAGGACCAGAGAAATCGAATA	2070
CAGTCCGACTNNHCTAGCGTTAC		CAGCCGACACNNHCTAGCGTTAC		CAAGACTTTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1591	TGCAGGACCAGAGAAATCGAATA	1831	TGCAGGACCAGAGAAATCGAATA	2071
CAACATGCTGNNHCTAGCGTTAC		CACTCAGCANNHCTAGCGTTAC		CAAGGACATGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATCGAATA	1592	TGCAGGACCAGAGAAATCGAATA	1832	TGCAGGACCAGAGAAATCGAATA	2072
CAGACACAGANNHCTAGCGTTAC		CAACAGTGTNNHCTAGCGTTAC		CAGGCGTAAANNHCTAGCGTTAC	

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池-7	SEQ ID NO.	池-8	SEQ ID NO.	池-9	SEQ ID NO.
TGCAGGACCAGAGAAATTCGAATA	1593	TGCAGGACCAGAGAAATTCGAATA	1833	TGCAGGACCAGAGAAATTCGAATA	2073
CACGCGTTTNNNGATCGACATG		CACGAGCGGNNNGATCGACATG		CAGTACCCAGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1594	TGCAGGACCAGAGAAATTCGAATA	1834	TGCAGGACCAGAGAAATTCGAATA	2074
CACCCAGAGCANNNGATCGACATG		CAACCGAAAGNNNGATCGACATG		CGCAATTTACNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1595	TGCAGGACCAGAGAAATTCGAATA	1835	TGCAGGACCAGAGAAATTCGAATA	2075
CACCGAGCGNNNGATCGACATG		CAGTTTGAGCANNNGATCGACATG		CAAAACACCCANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1596	TGCAGGACCAGAGAAATTCGAATA	1836	TGCAGGACCAGAGAAATTCGAATA	2076
CACCTTGCCNNNGATCGACATG		CAGTATCGGNNNGATCGACATG		CAAGTTATTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1597	TGCAGGACCAGAGAAATTCGAATA	1837	TGCAGGACCAGAGAAATTCGAATA	2077
CAGTTGATCGNNNGATCGACATG		CAATGTAGTNNNGATCGACATG		CACCTTCCTTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1598	TGCAGGACCAGAGAAATTCGAATA	1838	TGCAGGACCAGAGAAATTCGAATA	2078
CAGTGAATCGNNNGATCGACATG		CAAGACCTACNNNGATCGACATG		CAGCGCTCCGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1599	TGCAGGACCAGAGAAATTCGAATA	1839	TGCAGGACCAGAGAAATTCGAATA	2079
CACACGTTGANNNGATCGACATG		CATTTCGCGCANNNGATCGACATG		CAGAAACCCGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1600	TGCAGGACCAGAGAAATTCGAATA	1840	TGCAGGACCAGAGAAATTCGAATA	2080
CACATATCCGNNNGATCGACATG		CAGGACTCATNNNGATCGACATG		CAATTTGTATNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1601	TGCAGGACCAGAGAAATTCGAATA	1841	TGCAGGACCAGAGAAATTCGAATA	2081
CAGCGGACGANNNGATCGACATG		CAGTCCCGTNNNGATCGACATG		CAAGTTCTTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1602	TGCAGGACCAGAGAAATTCGAATA	1842	TGCAGGACCAGAGAAATTCGAATA	2082
CACCTTGATCANNNGATCGACATG		CAGCAAGCCGNNNGATCGACATG		CAGCAGCGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1603	TGCAGGACCAGAGAAATTCGAATA	1843	TGCAGGACCAGAGAAATTCGAATA	2083
CATATGCCGANNNGATCGACATG		CAAGCATCGGNNNGATCGACATG		CAGTATCGCTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1604	TGCAGGACCAGAGAAATTCGAATA	1844	TGCAGGACCAGAGAAATTCGAATA	2084
CAGTTGGTCANNNGATCGACATG		CAAGCAGCCGNNNGATCGACATG		CAGCAAGTGANNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1605	TGCAGGACCAGAGAAATTCGAATA	1845	TGCAGGACCAGAGAAATTCGAATA	2085
CACCTCTCGGNNNGATCGACATG		CAATCTCTATNNNGATCGACATG		CATAAGCATGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1606	TGCAGGACCAGAGAAATTCGAATA	1846	TGCAGGACCAGAGAAATTCGAATA	2086
CATGGTACGANNNGATCGACATG		CATPATGCCGNNNGATCGACATG		CAGCAATCTGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1607	TGCAGGACCAGAGAAATTCGAATA	1847	TGCAGGACCAGAGAAATTCGAATA	2087
CACCTCGGCTNNNGATCGACATG		CACAGCGGANNNGATCGACATG		CAGTCCAGGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1608	TGCAGGACCAGAGAAATTCGAATA	1848	TGCAGGACCAGAGAAATTCGAATA	2088
CAGCGACCGANNNGATCGACATG		CAGCGAATGANNNNGATCGACATG		CAGGTTTATANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1609	TGCAGGACCAGAGAAATTCGAATA	1849	TGCAGGACCAGAGAAATTCGAATA	2089
CACCGTGATNNNGATCGACATG		CAAGCGTACTNNNGATCGACATG		CAAGCTTGCGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1610	TGCAGGACCAGAGAAATTCGAATA	1850	TGCAGGACCAGAGAAATTCGAATA	2090
CAATTTCTTANNNGATCGACATG		CAGCCAGGCAANNNGATCGACATG		CACCAACCGCANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1611	TGCAGGACCAGAGAAATTCGAATA	1851	TGCAGGACCAGAGAAATTCGAATA	2091
CACCTGTCAAGNNNGATCGACATG		CAGGCTTGTGNNNGATCGACATG		CATGGAAGACANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1612	TGCAGGACCAGAGAAATTCGAATA	1852	TGCAGGACCAGAGAAATTCGAATA	2092
CAATTAACGNNNGATCGACATG		CACCTAGGCGNNNGATCGACATG		CAATTTGAAGANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1613	TGCAGGACCAGAGAAATTCGAATA	1853	TGCAGGACCAGAGAAATTCGAATA	2093
CAATAATCGNNNGATCGACATG		CACCGTTTTCNNNGATCGACATG		CATTTTCAANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1614	TGCAGGACCAGAGAAATTCGAATA	1854	TGCAGGACCAGAGAAATTCGAATA	2094
CAATAGACTTNNNGATCGACATG		CAGACCGACGNNNGATCGACATG		CAACGAACCTGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1615	TGCAGGACCAGAGAAATTCGAATA	1855	TGCAGGACCAGAGAAATTCGAATA	2095
CACCTGATGANNNGATCGACATG		CAACTTATGANNNGATCGACATG		CAAGGCGCTCANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1616	TGCAGGACCAGAGAAATTCGAATA	1856	TGCAGGACCAGAGAAATTCGAATA	2096
CAGCCGACGANNNGATCGACATG		CAAGATCAANNNGATCGACATG		CATTGGAGCTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1617	TGCAGGACCAGAGAAATTCGAATA	1857	TGCAGGACCAGAGAAATTCGAATA	2097
CACCAATATGNNNGATCGACATG		CATACTTCCGNNNGATCGACATG		CAACAGACAGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1618	TGCAGGACCAGAGAAATTCGAATA	1858	TGCAGGACCAGAGAAATTCGAATA	2098
CAGTCAATCGNNNGATCGACATG		CACGTTAGACNNNGATCGACATG		CATTCGTCAGNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1619	TGCAGGACCAGAGAAATTCGAATA	1859	TGCAGGACCAGAGAAATTCGAATA	2099
CATCAGCCCGNNNGATCGACATG		CAGGAGTTAGNNNGATCGACATG		CATTATGTCNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1620	TGCAGGACCAGAGAAATTCGAATA	1860	TGCAGGACCAGAGAAATTCGAATA	2100
CAGCAATTCNNNGATCGACATG		CAGACCTCTNNNGATCGACATG		CAGTCAGCATNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	1621	TGCAGGACCAGAGAAATTCGAATA	1861	TGCAGGACCAGAGAAATTCGAATA	2101
CAGTGAATCGNNNGATCGACATG		CAGCCCGCAANNNGATCGACATG		CACATTCTGNNNGATCGACATG	

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池-7	SEQ ID NO.	池-8	SEQ ID NO.	池-9	SEQ ID NO.
TGCAGGACCCAGAGAAATTCGAATA	1622	TGCAGGACCCAGAGAAATTCGAATA	1862	TGCAGGACCCAGAGAAATTCGAATA	2102
CACCGATTATNNNGATCGACATG		CAGAACCCATNNNGATCGACATG		CAGAAATTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1623	TGCAGGACCCAGAGAAATTCGAATA	1863	TGCAGGACCCAGAGAAATTCGAATA	2103
CACAAATCCGANNNGATCGACATG		CACCACTGCCNNNGATCGACATG		CATCGTCCGTTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1624	TGCAGGACCCAGAGAAATTCGAATA	1864	TGCAGGACCCAGAGAAATTCGAATA	2104
CAGGCAATGANNNGATCGACATG		CACAAATTCNNNGATCGACATG		CATTGTGGCANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1625	TGCAGGACCCAGAGAAATTCGAATA	1865	TGCAGGACCCAGAGAAATTCGAATA	2105
CACGTCTCAGANNNGATCGACATG		CACGGTCCGANNNGATCGACATG		CACCTGGACNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1626	TGCAGGACCCAGAGAAATTCGAATA	1866	TGCAGGACCCAGAGAAATTCGAATA	2106
CACAGACCTANNNGATCGACATG		CATTTCGCACNNNGATCGACATG		CACGTTCTTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1627	TGCAGGACCCAGAGAAATTCGAATA	1867	TGCAGGACCCAGAGAAATTCGAATA	2107
GCATCATCGNNNGATCGACATG		CAGGATAAGCANNNGATCGACATG		CACAAACCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1628	TGCAGGACCCAGAGAAATTCGAATA	1868	TGCAGGACCCAGAGAAATTCGAATA	2108
CAGAAACGATNNNGATCGACATG		CACCTGGCAGNNNGATCGACATG		CATAACCCGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1629	TGCAGGACCCAGAGAAATTCGAATA	1869	TGCAGGACCCAGAGAAATTCGAATA	2109
CATCGGTGATNNNGATCGACATG		CACCTGAAANNNGATCGACATG		CACCTACCGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1630	TGCAGGACCCAGAGAAATTCGAATA	1870	TGCAGGACCCAGAGAAATTCGAATA	2110
CATTTCGAATNNNGATCGACATG		CAGGTCTTTNNNGATCGACATG		CAGACAGGTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1631	TGCAGGACCCAGAGAAATTCGAATA	1871	TGCAGGACCCAGAGAAATTCGAATA	2111
CATTAAACGATNNNGATCGACATG		CAGGTGTTACNNNGATCGACATG		CAGTTCGTATCANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1632	TGCAGGACCCAGAGAAATTCGAATA	1872	TGCAGGACCCAGAGAAATTCGAATA	2112
CATGTACGTGNNNGATCGACATG		CATATCCGCTNNNGATCGACATG		CACGGGCTCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1633	TGCAGGACCCAGAGAAATTCGAATA	1873	TGCAGGACCCAGAGAAATTCGAATA	2113
CAGCGGTGCTNNNGATCGACATG		CAGCGTGAGNNNGATCGACATG		CATTGATTCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1634	TGCAGGACCCAGAGAAATTCGAATA	1874	TGCAGGACCCAGAGAAATTCGAATA	2114
CACCATATANNNGATCGACATG		CAGCGGTTCCNNNGATCGACATG		CATAATGTCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1635	TGCAGGACCCAGAGAAATTCGAATA	1875	TGCAGGACCCAGAGAAATTCGAATA	2115
CAGAAATTCGANNNGATCGACATG		CATTACCCANNNGATCGACATG		CAGAGTTAAANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1636	TGCAGGACCCAGAGAAATTCGAATA	1876	TGCAGGACCCAGAGAAATTCGAATA	2116
CAGTATCAGNNNGATCGACATG		CAGACCCCTCANNNGATCGACATG		CAGGACCATNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1637	TGCAGGACCCAGAGAAATTCGAATA	1877	TGCAGGACCCAGAGAAATTCGAATA	2117
CACCTTAGGANNNGATCGACATG		CATATGAGGNNNGATCGACATG		CATTGGCCGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1638	TGCAGGACCCAGAGAAATTCGAATA	1878	TGCAGGACCCAGAGAAATTCGAATA	2118
CATAAAAACNNNGATCGACATG		CAGACGGTCCNNNGATCGACATG		CAGAACTTTANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1639	TGCAGGACCCAGAGAAATTCGAATA	1879	TGCAGGACCCAGAGAAATTCGAATA	2119
CATGCACTCTNNNGATCGACATG		CACCTACACANNNGATCGACATG		CACCAAAACNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1640	TGCAGGACCCAGAGAAATTCGAATA	1880	TGCAGGACCCAGAGAAATTCGAATA	2120
CACAGCCTGNNNGATCGACATG		CATGACTACNNNGATCGACATG		CATAACACGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1641	TGCAGGACCCAGAGAAATTCGAATA	1881	TGCAGGACCCAGAGAAATTCGAATA	2121
CACACACTAGNNNGATCGACATG		CAGGACGTTNNNGATCGACATG		CAGGTAGAATNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1642	TGCAGGACCCAGAGAAATTCGAATA	1882	TGCAGGACCCAGAGAAATTCGAATA	2122
CACGTATCTNNNGATCGACATG		CAAAGCCTCANNNGATCGACATG		CAGTACTACGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1643	TGCAGGACCCAGAGAAATTCGAATA	1883	TGCAGGACCCAGAGAAATTCGAATA	2123
CATGGCTTAGNNNGATCGACATG		CACCTTAAAGNNNGATCGACATG		CATTCTATGANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1644	TGCAGGACCCAGAGAAATTCGAATA	1884	TGCAGGACCCAGAGAAATTCGAATA	2124
CACCTGTCATCANNNGATCGACATG		CATTGTATCANNNGATCGACATG		CACCTAAGCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1645	TGCAGGACCCAGAGAAATTCGAATA	1885	TGCAGGACCCAGAGAAATTCGAATA	2125
CATCCAGACNNNGATCGACATG		CACGTGATTTNNNGATCGACATG		CACCAAGGCTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1646	TGCAGGACCCAGAGAAATTCGAATA	1886	TGCAGGACCCAGAGAAATTCGAATA	2126
CACGAGTACTNNNGATCGACATG		CATTAAITGNNNGATCGACATG		CAGAGGACGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1647	TGCAGGACCCAGAGAAATTCGAATA	1887	TGCAGGACCCAGAGAAATTCGAATA	2127
CAGATCGAGNNNGATCGACATG		CACAGGTTCCNNNGATCGACATG		CACTACTCGTNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1648	TGCAGGACCCAGAGAAATTCGAATA	1888	TGCAGGACCCAGAGAAATTCGAATA	2128
CAGAACTACNNNGATCGACATG		CAGCATCTAGNNNGATCGACATG		CAGTACTGANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1649	TGCAGGACCCAGAGAAATTCGAATA	1889	TGCAGGACCCAGAGAAATTCGAATA	2129
CAGCCGACCCANNNGATCGACATG		CATTGTCTATNNNGATCGACATG		CACCAACCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	1650	TGCAGGACCCAGAGAAATTCGAATA	1890	TGCAGGACCCAGAGAAATTCGAATA	2130
CACAGCACTNNNGATCGACATG		CACATGCTCTNNNGATCGACATG		CATGTGTGACNNNGATCGACATG	

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池-7	SEQ ID NO:	池-8	SEQ ID NO:	池-9	SEQ ID NO:
TGCAGGACCAGAGAAATTCGAATA	1651	TGCAGGACCAGAGAAATTCGAATA	1891	TGCAGGACCAGAGAAATTCGAATA	2131
CAGTGCACATANNNTGCATCAGGT		CACATTCACAAANNNTGCATCAGGT		CACACCCCTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1652	TGCAGGACCAGAGAAATTCGAATA	1892	TGCAGGACCAGAGAAATTCGAATA	2132
CAATCTATTGNNNTGCATCAGGT		CACAAACCCCTGNNNTGCATCAGGT		CATGGCCATTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1653	TGCAGGACCAGAGAAATTCGAATA	1893	TGCAGGACCAGAGAAATTCGAATA	2133
CNAGTATGTTNNNTGCATCAGGT		CATGATCAATTNNNTGCATCAGGT		CAATTCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1654	TGCAGGACCAGAGAAATTCGAATA	1894	TGCAGGACCAGAGAAATTCGAATA	2134
CAGGTTCTTCNNNTGCATCAGGT		CAATACGATCNNNTGCATCAGGT		CATTGCTTTANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1655	TGCAGGACCAGAGAAATTCGAATA	1895	TGCAGGACCAGAGAAATTCGAATA	2135
CATAGTGCCTNNNTGCATCAGGT		CAGGACCCGANNNTGCATCAGGT		CAGCACCAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1656	TGCAGGACCAGAGAAATTCGAATA	1896	TGCAGGACCAGAGAAATTCGAATA	2136
CACCAACTTCNNNTGCATCAGGT		CACCCCTAATTNNNTGCATCAGGT		CACGAATGTCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1657	TGCAGGACCAGAGAAATTCGAATA	1897	TGCAGGACCAGAGAAATTCGAATA	2137
CAAGTTCAATNNNTGCATCAGGT		CACCTCAAGCANNNTGCATCAGGT		CATGGCTAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1658	TGCAGGACCAGAGAAATTCGAATA	1898	TGCAGGACCAGAGAAATTCGAATA	2138
CATTGTTGCGNNNTGCATCAGGT		CAGTTCGTACNNNTGCATCAGGT		CACTGTTATANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1659	TGCAGGACCAGAGAAATTCGAATA	1899	TGCAGGACCAGAGAAATTCGAATA	2139
CAGTCAATGCANNNTGCATCAGGT		CATTTCGCCANNNTGCATCAGGT		CATTCTCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1660	TGCAGGACCAGAGAAATTCGAATA	1900	TGCAGGACCAGAGAAATTCGAATA	2140
CAGCTGTAATANNNTGCATCAGGT		CAGGAAGGTANNNTGCATCAGGT		CATCACTAANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1661	TGCAGGACCAGAGAAATTCGAATA	1901	TGCAGGACCAGAGAAATTCGAATA	2141
CATTTCGGCCNNNTGCATCAGGT		CAGGCCCTTGNNNTGCATCAGGT		CATTACAGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1662	TGCAGGACCAGAGAAATTCGAATA	1902	TGCAGGACCAGAGAAATTCGAATA	2142
CATCTCTCTGNNNTGCATCAGGT		CACCAATATCANNNTGCATCAGGT		CATCTCTGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1663	TGCAGGACCAGAGAAATTCGAATA	1903	TGCAGGACCAGAGAAATTCGAATA	2143
CACCTTCGCCGNNNTGCATCAGGT		CATCACAACGNNNTGCATCAGGT		CATCGCCTAANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1664	TGCAGGACCAGAGAAATTCGAATA	1904	TGCAGGACCAGAGAAATTCGAATA	2144
CNACAGATTNNNTGCATCAGGT		CACCTGTACGNNNTGCATCAGGT		CAAGGAGCATNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1665	TGCAGGACCAGAGAAATTCGAATA	1905	TGCAGGACCAGAGAAATTCGAATA	2145
CACAGGACCAAGNNNTGCATCAGGT		CATCTCAATTNNNTGCATCAGGT		CAGGAATACGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1666	TGCAGGACCAGAGAAATTCGAATA	1906	TGCAGGACCAGAGAAATTCGAATA	2146
CACAGGACACANNNTGCATCAGGT		CAGGGCTCTANNNTGCATCAGGT		CATGAGACGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1667	TGCAGGACCAGAGAAATTCGAATA	1907	TGCAGGACCAGAGAAATTCGAATA	2147
CAGACCGAGGNNNTGCATCAGGT		CACCTTACCANNNTGCATCAGGT		CACCACCAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1668	TGCAGGACCAGAGAAATTCGAATA	1908	TGCAGGACCAGAGAAATTCGAATA	2148
CACCTATTAANNNTGCATCAGGT		CAGATTCCTCANNNTGCATCAGGT		CAAGCTCATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1669	TGCAGGACCAGAGAAATTCGAATA	1909	TGCAGGACCAGAGAAATTCGAATA	2149
CACCTAACCTNNNTGCATCAGGT		CATGCCCTGTTNNNTGCATCAGGT		CATATACCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1670	TGCAGGACCAGAGAAATTCGAATA	1910	TGCAGGACCAGAGAAATTCGAATA	2150
CATTTAGCGNNNTGCATCAGGT		CATCACCACGNNNTGCATCAGGT		CAGATGCCATNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1671	TGCAGGACCAGAGAAATTCGAATA	1911	TGCAGGACCAGAGAAATTCGAATA	2151
CATTAACCATNNNTGCATCAGGT		CACCTTCGGCANNNTGCATCAGGT		CATTGAGCTGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1672	TGCAGGACCAGAGAAATTCGAATA	1912	TGCAGGACCAGAGAAATTCGAATA	2152
CAGCTAAGTNNNTGCATCAGGT		CACAAACGAGNNNTGCATCAGGT		CATAAATGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1673	TGCAGGACCAGAGAAATTCGAATA	1913	TGCAGGACCAGAGAAATTCGAATA	2153
CAGTACAGAGNNNTGCATCAGGT		CACCCATTCTNNNTGCATCAGGT		CAACATGAAANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1674	TGCAGGACCAGAGAAATTCGAATA	1914	TGCAGGACCAGAGAAATTCGAATA	2154
CACCGGACCAANNNTGCATCAGGT		CACGCCATATNNNTGCATCAGGT		CATTCGGAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1675	TGCAGGACCAGAGAAATTCGAATA	1915	TGCAGGACCAGAGAAATTCGAATA	2155
CACCTCTAGTNNNTGCATCAGGT		CATCATCATNNNTGCATCAGGT		CAGTTCTCTGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1676	TGCAGGACCAGAGAAATTCGAATA	1916	TGCAGGACCAGAGAAATTCGAATA	2156
CAGCCCTGTTNNNTGCATCAGGT		CATATTGAGTNNNTGCATCAGGT		CACACATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1677	TGCAGGACCAGAGAAATTCGAATA	1917	TGCAGGACCAGAGAAATTCGAATA	2157
CACCCAGCTGNNNTGCATCAGGT		CAATTCTGCGNNNTGCATCAGGT		CATGGTCCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1678	TGCAGGACCAGAGAAATTCGAATA	1918	TGCAGGACCAGAGAAATTCGAATA	2158
CACCCCTCTGNNNTGCATCAGGT		CATATAGCTANNNTGCATCAGGT		CATACCGAGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	1679	TGCAGGACCAGAGAAATTCGAATA	1919	TGCAGGACCAGAGAAATTCGAATA	2159
CACCCAGGTGNNNTGCATCAGGT		CAGAGCGGACNNNTGCATCAGGT		CAGGCGTGANNNTGCATCAGGT	

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池-7	SEQ ID NO.	池-8	SEQ ID NO.	池-9	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATA CAGCGTGGTGNNTGCATCAGGT	1680	TGCAGGACCAGAGAATTGGAATA CAACCTTTACNNNTGCATCAGGT	1920	TGCAGGACCAGAGAATTGGAATA CATCTAACGGNNNTGCATCAGGT	2160
TGCAGGACCAGAGAATTGGAATA CACCGACGCANNTGCATCAGGT	1681	TGCAGGACCAGAGAATTGGAATA CAGGTCAAAANNTGCATCAGGT	1921	TGCAGGACCAGAGAATTGGAATA CATATAGCATNNNTGCATCAGGT	2161
TGCAGGACCAGAGAATTGGAATA CAITACCGGANNTGCATCAGGT	1682	TGCAGGACCAGAGAATTGGAATA CATCTAACGGNNNTGCATCAGGT	1922	TGCAGGACCAGAGAATTGGAATA CAGGCTCCGTHNNTGCATCAGGT	2162
TGCAGGACCAGAGAATTGGAATA CATCTTTCGGNNNTGCATCAGGT	1683	TGCAGGACCAGAGAATTGGAATA CRCRAATGTTHNNTGCATCAGGT	1923	TGCAGGACCAGAGAATTGGAATA CAATACATGTNNNTGCATCAGGT	2163
TGCAGGACCAGAGAATTGGAATA CACACAATTANNNTGCATCAGGT	1684	TGCAGGACCAGAGAATTGGAATA CATGGCTTTNNNTGCATCAGGT	1924	TGCAGGACCAGAGAATTGGAATA CAGGCTCGCANNTGCATCAGGT	2164
TGCAGGACCAGAGAATTGGAATA CACCTACATNNNTGCATCAGGT	1685	TGCAGGACCAGAGAATTGGAATA CARGGCTGTNNNTGCATCAGGT	1925	TGCAGGACCAGAGAATTGGAATA CAGTTTAGTANNNTGCATCAGGT	2165
TGCAGGACCAGAGAATTGGAATA CAATTACTGANNNTGCATCAGGT	1686	TGCAGGACCAGAGAATTGGAATA CAAACTATTGNNTGCATCAGGT	1926	TGCAGGACCAGAGAATTGGAATA CACTGAAATTNNNTGCATCAGGT	2166
TGCAGGACCAGAGAATTGGAATA CATTTTTCGANNNTGCATCAGGT	1687	TGCAGGACCAGAGAATTGGAATA CAATGTATTGNNTGCATCAGGT	1927	TGCAGGACCAGAGAATTGGAATA CAAAACACCTGNNNTGCATCAGGT	2167
TGCAGGACCAGAGAATTGGAATA CAAGGTGCTTHNNTGCATCAGGT	1688	TGCAGGACCAGAGAATTGGAATA CAGCTCGCGANNNTGCATCAGGT	1928	TGCAGGACCAGAGAATTGGAATA CAGGAAACGNNNTGCATCAGGT	2168

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池 -10	SEQ ID NO:	池 -11	SEQ ID NO:	池 -12	SEQ ID NO:
TGCAGGACCAGAGAAATCGAATACAG	2169	TGCAGGACCAGAGAAATCGAATACAA	2409	TGCAGGACCAGAGAAATCGAATACAT	2649
CTCTCGNNNACGTATGCCA		TACGTTANNNNACGTATGCCA		TGAGGAANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2170	TGCAGGACCAGAGAAATCGAATACAA	2410	TGCAGGACCAGAGAAATCGAATACAA	2650
TGCTACGNNNACGTATGCCA		ACTAGCCNNNACGTATGCCA		ATATCGANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2171	TGCAGGACCAGAGAAATCGAATACAC	2411	TGCAGGACCAGAGAAATCGAATACAA	2651
ACTCTCGNNNACGTATGCCA		GGATTACNNNACGTATGCCA		TGGACCTNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAC	2172	TGCAGGACCAGAGAAATCGAATACAG	2412	TGCAGGACCAGAGAAATCGAATACAG	2652
GCTCGGANNNACGTATGCCA		CACCGCTNNNACGTATGCCA		CCAATCTNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2173	TGCAGGACCAGAGAAATCGAATACAC	2413	TGCAGGACCAGAGAAATCGAATACAC	2653
CGCTTACNNNACGTATGCCA		GTAAATNNNACGTATGCCA		TAAATAANNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2174	TGCAGGACCAGAGAAATCGAATACAG	2414	TGCAGGACCAGAGAAATCGAATACAA	2654
AGCACGNNNACGTATGCCA		GCTAGTTNNNACGTATGCCA		TACATACNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2175	TGCAGGACCAGAGAAATCGAATACAT	2415	TGCAGGACCAGAGAAATCGAATACAT	2655
GTCTCGANNNACGTATGCCA		CAGAAAGNNNACGTATGCCA		ATGGCCANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2176	TGCAGGACCAGAGAAATCGAATACAA	2416	TGCAGGACCAGAGAAATCGAATACAA	2656
CTCCGCTNNNACGTATGCCA		CCAATCGNNNACGTATGCCA		TGATGCCNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2177	TGCAGGACCAGAGAAATCGAATACAT	2417	TGCAGGACCAGAGAAATCGAATACAA	2657
TGGCACNNNACGTATGCCA		CGACAAANNNACGTATGCCA		GGTAGGTNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2178	TGCAGGACCAGAGAAATCGAATACAG	2418	TGCAGGACCAGAGAAATCGAATACAT	2658
CACATCGNNNACGTATGCCA		TGCTACANNNACGTATGCCA		CCCTAGTNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2179	TGCAGGACCAGAGAAATCGAATACAG	2419	TGCAGGACCAGAGAAATCGAATACAG	2659
ATAACGANNNACGTATGCCA		CCAGAGNNNACGTATGCCA		TATTTGANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2180	TGCAGGACCAGAGAAATCGAATACAG	2420	TGCAGGACCAGAGAAATCGAATACAA	2660
GTATAGNNNACGTATGCCA		ATAGTATNNNACGTATGCCA		GTGAATANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2181	TGCAGGACCAGAGAAATCGAATACAT	2421	TGCAGGACCAGAGAAATCGAATACAA	2661
AGACCTGNNNACGTATGCCA		AAATGTCNNNACGTATGCCA		ATGGCACNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2182	TGCAGGACCAGAGAAATCGAATACAG	2422	TGCAGGACCAGAGAAATCGAATACAG	2662
CCCGGTANNNACGTATGCCA		CGTGGTNNNACGTATGCCA		TCCCCANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2183	TGCAGGACCAGAGAAATCGAATACAT	2423	TGCAGGACCAGAGAAATCGAATACAG	2663
CCCTCGANNNACGTATGCCA		TTGAAACNNNACGTATGCCA		CCCACTCNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2184	TGCAGGACCAGAGAAATCGAATACAT	2424	TGCAGGACCAGAGAAATCGAATACAG	2664
TGGCATCGNNNACGTATGCCA		AACTATGNNNACGTATGCCA		AGATATANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2185	TGCAGGACCAGAGAAATCGAATACAT	2425	TGCAGGACCAGAGAAATCGAATACAG	2665
AGGATCGNNNACGTATGCCA		CAGATGNNNACGTATGCCA		CACTACANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2186	TGCAGGACCAGAGAAATCGAATACAG	2426	TGCAGGACCAGAGAAATCGAATACAA	2666
TGCAATCGNNNACGTATGCCA		TCACACGNNNACGTATGCCA		CTTTGCGNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2187	TGCAGGACCAGAGAAATCGAATACAA	2427	TGCAGGACCAGAGAAATCGAATACAG	2667
CCCTCTNNNACGTATGCCA		TAAAGTGGNNNACGTATGCCA		TGAGGCCNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2188	TGCAGGACCAGAGAAATCGAATACAA	2428	TGCAGGACCAGAGAAATCGAATACAA	2668
TTGAGGTNNNACGTATGCCA		GAGCAGTNNNACGTATGCCA		AGTAGGCCNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2189	TGCAGGACCAGAGAAATCGAATACAT	2429	TGCAGGACCAGAGAAATCGAATACAG	2669
ACATCGANNNACGTATGCCA		ATGTGCTNNNACGTATGCCA		CTTCTACNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2190	TGCAGGACCAGAGAAATCGAATACAG	2430	TGCAGGACCAGAGAAATCGAATACAT	2670
CGAACCGNNNACGTATGCCA		CAGAGATNNNACGTATGCCA		GGAGGATNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2191	TGCAGGACCAGAGAAATCGAATACAT	2431	TGCAGGACCAGAGAAATCGAATACAG	2671
CCACACGNNNACGTATGCCA		CTCACGNNNACGTATGCCA		CTAACANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2192	TGCAGGACCAGAGAAATCGAATACAG	2432	TGCAGGACCAGAGAAATCGAATACAA	2672
CGTAAABNNNACGTATGCCA		CCCTTGGNNNACGTATGCCA		CGCTTACNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2193	TGCAGGACCAGAGAAATCGAATACAG	2433	TGCAGGACCAGAGAAATCGAATACAG	2673
TAGAGTGGNNNACGTATGCCA		AGTGGCCNNNACGTATGCCA		TCTTGTGNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2194	TGCAGGACCAGAGAAATCGAATACAG	2434	TGCAGGACCAGAGAAATCGAATACAG	2674
CACATAGNNNACGTATGCCA		TGATCGANNNACGTATGCCA		AGAGGCTNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2195	TGCAGGACCAGAGAAATCGAATACAT	2435	TGCAGGACCAGAGAAATCGAATACAG	2675
CTGTGCTNNNACGTATGCCA		GGTAGGNNNACGTATGCCA		CTGATGANNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAT	2196	TGCAGGACCAGAGAAATCGAATACAG	2436	TGCAGGACCAGAGAAATCGAATACAT	2676
AGTACATNNNACGTATGCCA		TACGGCCNNNACGTATGCCA		CGATACGNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2197	TGCAGGACCAGAGAAATCGAATACAG	2437	TGCAGGACCAGAGAAATCGAATACAA	2677
CGGACACNNNACGTATGCCA		CATCGCGNNNACGTATGCCA		AGAATGNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2198	TGCAGGACCAGAGAAATCGAATACAG	2438	TGCAGGACCAGAGAAATCGAATACAT	2678
TAAAGCTGNNNACGTATGCCA		AACTAGGNNNACGTATGCCA		CGGCTCGNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAA	2199	TGCAGGACCAGAGAAATCGAATACAG	2439	TGCAGGACCAGAGAAATCGAATACAA	2679
CTTGCTGNNNACGTATGCCA		ATCAAAATNNNACGTATGCCA		AGTCAATNNNACGTATGCCA	
TGCAGGACCAGAGAAATCGAATACAG	2200	TGCAGGACCAGAGAAATCGAATACAG	2440	TGCAGGACCAGAGAAATCGAATACAT	2680
GAGCTGGNNNACGTATGCCA		ACTGGTNNNACGTATGCCA		GTAAATGNNNACGTATGCCA	

图15A

池 -10	SEQ ID NO.	池 -11	SEQ ID NO.	池 -12	SEQ ID NO.
TGCAGGACCAGAGAAATTCGAATACAT	2201	TGCAGGACCAGAGAAATTCGAATACAG	2441	TGCAGGACCAGAGAAATTCGAATACAA	2681
SAGGATGNNNACGTATGCCA		CAAAATTNNNACGTATGCCA		TCTACCCNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2202	TGCAGGACCAGAGAAATTCGAATACAT	2442	TGCAGGACCAGAGAAATTCGAATACAT	2682
TCGGTCCNNNACGTATGCCA		TAGTGTANNNACGTATGCCA		GCACGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2203	TGCAGGACCAGAGAAATTCGAATACAG	2443	TGCAGGACCAGAGAAATTCGAATACAG	2683
TGCTCGNNNACGTATGCCA		ATGAAATNNNACGTATGCCA		AGTGTTCNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAA	2204	TGCAGGACCAGAGAAATTCGAATACAT	2444	TGCAGGACCAGAGAAATTCGAATACAA	2684
GACTGCNNNACGTATGCCA		TCCCGANNNACGTATGCCA		ACAGCGTNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2205	TGCAGGACCAGAGAAATTCGAATACAT	2445	TGCAGGACCAGAGAAATTCGAATACAG	2685
TTGGTACNNNACGTATGCCA		CCTCCTTNNNACGTATGCCA		GACGACGNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2206	TGCAGGACCAGAGAAATTCGAATACAG	2446	TGCAGGACCAGAGAAATTCGAATACAA	2686
TCAGTCCNNNACGTATGCCA		CCCATTTNNNACGTATGCCA		TTCCGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2207	TGCAGGACCAGAGAAATTCGAATACAG	2447	TGCAGGACCAGAGAAATTCGAATACAG	2687
TAACAAANNNACGTATGCCA		TTTGTTCNNNACGTATGCCA		GTCTCAANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2208	TGCAGGACCAGAGAAATTCGAATACAT	2448	TGCAGGACCAGAGAAATTCGAATACAG	2688
AACTGSTNNNACGTATGCCA		ATCCGTNNNACGTATGCCA		ACCATGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2209	TGCAGGACCAGAGAAATTCGAATACAT	2449	TGCAGGACCAGAGAAATTCGAATACAG	2689
GGATACGNNNACGTATGCCA		TCGGTGANNNACGTATGCCA		AAACGGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAA	2210	TGCAGGACCAGAGAAATTCGAATACAG	2450	TGCAGGACCAGAGAAATTCGAATACAA	2690
TGCAGGACCAGAGAAATTCGAATACAA		GTAGGANNNACGTATGCCA		GAGCGTANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAA	2211	TGCAGGACCAGAGAAATTCGAATACAG	2451	TGCAGGACCAGAGAAATTCGAATACAG	2691
GTCCCTGNNNACGTATGCCA		TTCTTTNNNACGTATGCCA		CCCTGACNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAA	2212	TGCAGGACCAGAGAAATTCGAATACAG	2452	TGCAGGACCAGAGAAATTCGAATACAG	2692
ATAGTTCHNNACGTATGCCA		ACTTTTNNNACGTATGCCA		CAGATTGNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2213	TGCAGGACCAGAGAAATTCGAATACAG	2453	TGCAGGACCAGAGAAATTCGAATACAT	2693
GAAGGACNNNACGTATGCCA		GTTAAGNNNACGTATGCCA		GTGTATNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2214	TGCAGGACCAGAGAAATTCGAATACAA	2454	TGCAGGACCAGAGAAATTCGAATACAA	2694
CAACCCGNNNACGTATGCCA		TCACGTTNNNACGTATGCCA		TTTGTGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2215	TGCAGGACCAGAGAAATTCGAATACAG	2455	TGCAGGACCAGAGAAATTCGAATACAG	2695
AAATGGAANNNACGTATGCCA		ATTTAGNNNACGTATGCCA		TAGCGTTNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2216	TGCAGGACCAGAGAAATTCGAATACAG	2456	TGCAGGACCAGAGAAATTCGAATACAG	2696
CAAAATANNNACGTATGCCA		ACGGCGANNNACGTATGCCA		ACGTGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2217	TGCAGGACCAGAGAAATTCGAATACAG	2457	TGCAGGACCAGAGAAATTCGAATACAA	2697
ACCCCTCCHNNACGTATGCCA		TGAAATCCHNNACGTATGCCA		ACAGCGANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2218	TGCAGGACCAGAGAAATTCGAATACAT	2458	TGCAGGACCAGAGAAATTCGAATACAA	2698
CCCGGTCCHNNACGTATGCCA		TGTGTAAANNNACGTATGCCA		AAATGCGNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2219	TGCAGGACCAGAGAAATTCGAATACAG	2459	TGCAGGACCAGAGAAATTCGAATACAT	2699
CAATTCGANNNACGTATGCCA		CCCGTGANNNACGTATGCCA		ACCAAGCCHNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2220	TGCAGGACCAGAGAAATTCGAATACAA	2460	TGCAGGACCAGAGAAATTCGAATACAG	2700
CCCTTAANNNACGTATGCCA		ACCAAGCCHNNNACGTATGCCA		GACCCCTCCHNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2221	TGCAGGACCAGAGAAATTCGAATACAT	2461	TGCAGGACCAGAGAAATTCGAATACAA	2701
ACCCGCGANNNACGTATGCCA		CGTTTGCNNNACGTATGCCA		CACCCCTTNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2222	TGCAGGACCAGAGAAATTCGAATACAG	2462	TGCAGGACCAGAGAAATTCGAATACAG	2702
ATCTGACNNNACGTATGCCA		TATTCGCGNNNACGTATGCCA		TGTTCGCGNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2223	TGCAGGACCAGAGAAATTCGAATACAA	2463	TGCAGGACCAGAGAAATTCGAATACAA	2703
CATGTTGNNNACGTATGCCA		ACAGATANNNACGTATGCCA		CCCGCCANNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2224	TGCAGGACCAGAGAAATTCGAATACAG	2464	TGCAGGACCAGAGAAATTCGAATACAT	2704
AGCACGTHNNNACGTATGCCA		TATTAATCCHNNNACGTATGCCA		GTACAAATNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2225	TGCAGGACCAGAGAAATTCGAATACAT	2465	TGCAGGACCAGAGAAATTCGAATACAG	2705
GTCCAAATNNNACGTATGCCA		CCCAATCCHNNNACGTATGCCA		ATCTAGCCHNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAA	2226	TGCAGGACCAGAGAAATTCGAATACAG	2466	TGCAGGACCAGAGAAATTCGAATACAG	2706
CCCTCTAHHNNACGTATGCCA		TAAAGTTNNNACGTATGCCA		CAGTCTTNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAT	2227	TGCAGGACCAGAGAAATTCGAATACAA	2467	TGCAGGACCAGAGAAATTCGAATACAG	2707
TACGACGNNNACGTATGCCA		GUTAAATNNNACGTATGCCA		CTGCAATNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2228	TGCAGGACCAGAGAAATTCGAATACAT	2468	TGCAGGACCAGAGAAATTCGAATACAG	2708
ATATCGGNNNACGTATGCCA		TGTTATCCHNNNACGTATGCCA		AGAGATCCHNNNACGTATGCCA	
TGCAGGACCAGAGAAATTCGAATACAG	2229	TGCAGGACCAGAGAAATTCGAATACAT	2469	TGCAGGACCAGAGAAATTCGAATACAA	2709
GCATATGNNNCTAGCGTTAC		AGTACGCHNNCTAGCGTTAC		CAAUTGCHNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATACAT	2230	TGCAGGACCAGAGAAATTCGAATACAG	2470	TGCAGGACCAGAGAAATTCGAATACAT	2710
ACGAGGANNNCTAGCGTTAC		AGCGTAATNNNCTAGCGTTAC		CCCGAATNNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATACAT	2231	TGCAGGACCAGAGAAATTCGAATACAG	2471	TGCAGGACCAGAGAAATTCGAATACAT	2711
CTTACATNNNCTAGCGTTAC		ATTAGTANNNCTAGCGTTAC		AAAGACANNNCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATACAG	2232	TGCAGGACCAGAGAAATTCGAATACAG	2472	TGCAGGACCAGAGAAATTCGAATACAG	2712
CGTCTGCHNNCTAGCGTTAC		CTCTAACHNNCTAGCGTTAC		CGTTGCHNNCTAGCGTTAC	

图15B

池-10	SEQ ID NO.	池-11	SEQ ID NO.	池-12	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATACAT	2233	TGCAGGACCAGAGAATTGGAATACAT	2473	TGCAGGACCAGAGAATTGGAATACAT	2713
AATCCGNNNNCTAGCGTTAC		AGTGTCNNNNCTAGCGTTAC		TACACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2234	TGCAGGACCAGAGAATTGGAATACAC	2474	TGCAGGACCAGAGAATTGGAATACAC	2714
AGCATACNNNNCTAGCGTTAC		GCAGAGGNNNNCTAGCGTTAC		TCCACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2235	TGCAGGACCAGAGAATTGGAATACAC	2475	TGCAGGACCAGAGAATTGGAATACAC	2715
TTCTCCNNNNCTAGCGTTAC		CGGTTCCNNNNCTAGCGTTAC		GAACCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2236	TGCAGGACCAGAGAATTGGAATACAA	2476	TGCAGGACCAGAGAATTGGAATACAA	2716
TTTCTCCNNNNCTAGCGTTAC		CACAGTNNNNCTAGCGTTAC		CGTCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2237	TGCAGGACCAGAGAATTGGAATACAA	2477	TGCAGGACCAGAGAATTGGAATACAA	2717
AATCGAANNNNCTAGCGTTAC		GATGAANNNNCTAGCGTTAC		AGTATCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2238	TGCAGGACCAGAGAATTGGAATACAA	2478	TGCAGGACCAGAGAATTGGAATACAA	2718
GATTATCNNNNCTAGCGTTAC		GTGAATCNNNNCTAGCGTTAC		TAGTCTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2239	TGCAGGACCAGAGAATTGGAATACAG	2479	TGCAGGACCAGAGAATTGGAATACAT	2719
TTTCAACNNNNCTAGCGTTAC		TATGTCCNNNNCTAGCGTTAC		ACCTTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2240	TGCAGGACCAGAGAATTGGAATACAA	2480	TGCAGGACCAGAGAATTGGAATACAA	2720
TTACATGNNNNCTAGCGTTAC		ATACTACNNNNCTAGCGTTAC		ACCAAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2241	TGCAGGACCAGAGAATTGGAATACAT	2481	TGCAGGACCAGAGAATTGGAATACAT	2721
CCATCCCTNNNNCTAGCGTTAC		TCGGATCNNNNCTAGCGTTAC		CACTCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2242	TGCAGGACCAGAGAATTGGAATACAT	2482	TGCAGGACCAGAGAATTGGAATACAA	2722
AGACTACNNNNCTAGCGTTAC		ACRTTAGNNNNCTAGCGTTAC		CCAGATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2243	TGCAGGACCAGAGAATTGGAATACAT	2483	TGCAGGACCAGAGAATTGGAATACAT	2723
ATTGGTGNNNNNCTAGCGTTAC		GGCCCGANNNNCTAGCGTTAC		GGCGTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2244	TGCAGGACCAGAGAATTGGAATACAG	2484	TGCAGGACCAGAGAATTGGAATACAG	2724
AGACCGTTNNNNCTAGCGTTAC		TTGASTCNNNNCTAGCGTTAC		GAGGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2245	TGCAGGACCAGAGAATTGGAATACAG	2485	TGCAGGACCAGAGAATTGGAATACAT	2725
CGGGCCGNNNNCTAGCGTTAC		TTAGCACNNNNCTAGCGTTAC		CGTCCATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2246	TGCAGGACCAGAGAATTGGAATACAA	2486	TGCAGGACCAGAGAATTGGAATACAC	2726
NACACACNNNNCTAGCGTTAC		GTCCCTCNNNNCTAGCGTTAC		GACCTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2247	TGCAGGACCAGAGAATTGGAATACAC	2487	TGCAGGACCAGAGAATTGGAATACAA	2727
GACGTCGNNNNCTAGCGTTAC		ATCGAGANNNNCTAGCGTTAC		GATTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2248	TGCAGGACCAGAGAATTGGAATACAA	2488	TGCAGGACCAGAGAATTGGAATACAA	2728
AGACTATNNNNCTAGCGTTAC		ATCGTCGNNNNCTAGCGTTAC		CTCGAACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2249	TGCAGGACCAGAGAATTGGAATACAA	2489	TGCAGGACCAGAGAATTGGAATACAA	2729
CCAGGAANNNNCTAGCGTTAC		CTCGAANNNNCTAGCGTTAC		GACCATCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2250	TGCAGGACCAGAGAATTGGAATACAT	2490	TGCAGGACCAGAGAATTGGAATACAG	2730
TCCATATNNNNCTAGCGTTAC		CAGGCTTNNNNCTAGCGTTAC		AACTTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2251	TGCAGGACCAGAGAATTGGAATACAT	2491	TGCAGGACCAGAGAATTGGAATACAA	2731
GCACCGANNNNCTAGCGTTAC		TGCGCTCANNNNCTAGCGTTAC		CCAGCGCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2252	TGCAGGACCAGAGAATTGGAATACAG	2492	TGCAGGACCAGAGAATTGGAATACAT	2732
GCACCGANNNNCTAGCGTTAC		GACCCACNNNNCTAGCGTTAC		ACCTCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2253	TGCAGGACCAGAGAATTGGAATACAT	2493	TGCAGGACCAGAGAATTGGAATACAC	2733
CCAGTAANNNNCTAGCGTTAC		TCTCCAGNNNNCTAGCGTTAC		GGAGCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2254	TGCAGGACCAGAGAATTGGAATACAG	2494	TGCAGGACCAGAGAATTGGAATACAA	2734
TCCACACGNNNNCTAGCGTTAC		TCCTCGCNNNNCTAGCGTTAC		CCGGAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2255	TGCAGGACCAGAGAATTGGAATACAA	2495	TGCAGGACCAGAGAATTGGAATACAG	2735
AGATCTGNNNNCTAGCGTTAC		ATAGTCTNNNNCTAGCGTTAC		GATCGCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2256	TGCAGGACCAGAGAATTGGAATACAG	2496	TGCAGGACCAGAGAATTGGAATACAA	2736
GAJATTCNNNNCTAGCGTTAC		CTGGATTNNNNCTAGCGTTAC		TCAAGCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	2257	TGCAGGACCAGAGAATTGGAATACAT	2497	TGCAGGACCAGAGAATTGGAATACAA	2737
TCTTTCCNNNNCTAGCGTTAC		TCGTCAANNNNCTAGCGTTAC		ACTCTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2258	TGCAGGACCAGAGAATTGGAATACAA	2498	TGCAGGACCAGAGAATTGGAATACAT	2738
CCATCTAANNNNCTAGCGTTAC		TTATGACNNNNCTAGCGTTAC		ATGAGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2259	TGCAGGACCAGAGAATTGGAATACAT	2499	TGCAGGACCAGAGAATTGGAATACAA	2739
TAAGGTCCNNNNCTAGCGTTAC		TTTAGAANNNNCTAGCGTTAC		GGCGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2260	TGCAGGACCAGAGAATTGGAATACAG	2500	TGCAGGACCAGAGAATTGGAATACAA	2740
ACCGACGNNNNCTAGCGTTAC		ATATACTNNNNCTAGCGTTAC		GAATTAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2261	TGCAGGACCAGAGAATTGGAATACAG	2501	TGCAGGACCAGAGAATTGGAATACAG	2741
TTTAGATNNNNCTAGCGTTAC		CTACCCGNNNNCTAGCGTTAC		ATTAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2262	TGCAGGACCAGAGAATTGGAATACAA	2502	TGCAGGACCAGAGAATTGGAATACAT	2742
CCGCTCCNNNNCTAGCGTTAC		ACCTTTTNNNNCTAGCGTTAC		ATTTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2263	TGCAGGACCAGAGAATTGGAATACAA	2503	TGCAGGACCAGAGAATTGGAATACAG	2743
TAATCCGNNNNCTAGCGTTAC		CTGTATNNNNCTAGCGTTAC		CTGTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	2264	TGCAGGACCAGAGAATTGGAATACAT	2504	TGCAGGACCAGAGAATTGGAATACAG	2744
ATTTCGANNNNCTAGCGTTAC		CCACCGNNNNCTAGCGTTAC		CTTACGANNNNCTAGCGTTAC	

图15C

池-10	SEQ ID NO.	池-11	SEQ ID NO.	池-12	SEQ ID NO.
TGCAGGACCCAGAGAATTGGAATACAA	2265	TGCAGGACCCAGAGAATTGGAATACAC	2505	TGCAGGACCCAGAGAATTGGAATACAC	2745
ACCGTGTNNNCTAGCGTTAC		GCCTGTNNNCTAGCGTTAC		CCACGGANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2266	TGCAGGACCCAGAGAATTGGAATACAC	2506	TGCAGGACCCAGAGAATTGGAATACAT	2746
CCAAITCNNNCTAGCGTTAC		TATAACANNNCTAGCGTTAC		GGATCTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	2267	TGCAGGACCCAGAGAATTGGAATACAG	2507	TGCAGGACCCAGAGAATTGGAATACAT	2747
TGGTGGTNNNCTAGCGTTAC		ACTGACTNNNCTAGCGTTAC		CCACGAANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	2268	TGCAGGACCCAGAGAATTGGAATACAC	2508	TGCAGGACCCAGAGAATTGGAATACAT	2748
GCTTAGGNNNCTAGCGTTAC		TGCCAGNNNCTAGCGTTAC		CAAGACNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2269	TGCAGGACCCAGAGAATTGGAATACAA	2509	TGCAGGACCCAGAGAATTGGAATACAG	2749
CACCCCHNNNCTAGCGTTAC		AGCCAGNNNCTAGCGTTAC		GCAGACNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAC	2270	TGCAGGACCCAGAGAATTGGAATACAC	2510	TGCAGGACCCAGAGAATTGGAATACAT	2750
CATTGAGNNNCTAGCGTTAC		GCCTTTGNNNCTAGCGTTAC		CTTTAGCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2271	TGCAGGACCCAGAGAATTGGAATACAT	2511	TGCAGGACCCAGAGAATTGGAATACAG	2751
CTTAACNNNCTAGCGTTAC		TTCCCTCNNNCTAGCGTTAC		CGTTTGANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	2272	TGCAGGACCCAGAGAATTGGAATACAG	2512	TGCAGGACCCAGAGAATTGGAATACAA	2752
ATAGACNNNCTAGCGTTAC		TTACTCGNNNCTAGCGTTAC		GGTACTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2273	TGCAGGACCCAGAGAATTGGAATACAA	2513	TGCAGGACCCAGAGAATTGGAATACAT	2753
AGTGTACNNNCTAGCGTTAC		TCCAGTCNNNCTAGCGTTAC		TCGTGTANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2274	TGCAGGACCCAGAGAATTGGAATACAT	2514	TGCAGGACCCAGAGAATTGGAATACAC	2754
CGCTTTNNNCTAGCGTTAC		TGTACGNNNCTAGCGTTAC		CGATGTANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	2275	TGCAGGACCCAGAGAATTGGAATACAG	2515	TGCAGGACCCAGAGAATTGGAATACAG	2755
GACTCAGNNNCTAGCGTTAC		ACCATTCNNNCTAGCGTTAC		TCGGTTANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2276	TGCAGGACCCAGAGAATTGGAATACAG	2516	TGCAGGACCCAGAGAATTGGAATACAG	2756
CTTAGTNNNCTAGCGTTAC		CCCTCTTNNNCTAGCGTTAC		GAACCCGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2277	TGCAGGACCCAGAGAATTGGAATACAT	2517	TGCAGGACCCAGAGAATTGGAATACAT	2757
AACATGANNNCTAGCGTTAC		GCATTAAANNNCTAGCGTTAC		TCGACTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2278	TGCAGGACCCAGAGAATTGGAATACAG	2518	TGCAGGACCCAGAGAATTGGAATACAT	2758
TAGGCTNNNCTAGCGTTAC		GTAGCGCHNNNCTAGCGTTAC		TCAGGCTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	2279	TGCAGGACCCAGAGAATTGGAATACAG	2519	TGCAGGACCCAGAGAATTGGAATACAG	2759
CCGCAGNNNCTAGCGTTAC		TCTCCTANNNCTAGCGTTAC		ACTTGAGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2280	TGCAGGACCCAGAGAATTGGAATACAT	2520	TGCAGGACCCAGAGAATTGGAATACAT	2760
GTACATTNNNCTAGCGTTAC		GGCGCGANNNCTAGCGTTAC		CACGCGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2281	TGCAGGACCCAGAGAATTGGAATACAG	2521	TGCAGGACCCAGAGAATTGGAATACAG	2761
GTCCGTANNNCTAGCGTTAC		AAATGATTNNNCTAGCGTTAC		ACTGTAGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2282	TGCAGGACCCAGAGAATTGGAATACAA	2522	TGCAGGACCCAGAGAATTGGAATACAA	2762
GACGACANNNCTAGCGTTAC		GGGAGGNNNCTAGCGTTAC		CCAAGCTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2283	TGCAGGACCCAGAGAATTGGAATACAT	2523	TGCAGGACCCAGAGAATTGGAATACAA	2763
AGTTCTANNNCTAGCGTTAC		TGAATAGNNNCTAGCGTTAC		CTGCAACNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	2284	TGCAGGACCCAGAGAATTGGAATACAA	2524	TGCAGGACCCAGAGAATTGGAATACAT	2764
CCGAACNNNCTAGCGTTAC		CCGCCAGNNNCTAGCGTTAC		AAACGGTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2285	TGCAGGACCCAGAGAATTGGAATACAG	2525	TGCAGGACCCAGAGAATTGGAATACAA	2765
GCAAITCNNNCTAGCGTTAC		CGGACAGNNNCTAGCGTTAC		CTTTGTANNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2286	TGCAGGACCCAGAGAATTGGAATACAA	2526	TGCAGGACCCAGAGAATTGGAATACAG	2766
TACACANNNCTAGCGTTAC		TAITCGANNNCTAGCGTTAC		ACGTTTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2287	TGCAGGACCCAGAGAATTGGAATACAA	2527	TGCAGGACCCAGAGAATTGGAATACAT	2767
CCAAITGNNNCTAGCGTTAC		TGTTGTANNNCTAGCGTTAC		TAAACCCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2288	TGCAGGACCCAGAGAATTGGAATACAG	2528	TGCAGGACCCAGAGAATTGGAATACAT	2768
TGCTTACNNNCTAGCGTTAC		ATTGTTANNNCTAGCGTTAC		TCGTAGCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	2289	TGCAGGACCCAGAGAATTGGAATACAG	2529	TGCAGGACCCAGAGAATTGGAATACAT	2769
AGCCAGGNNNGATCGACATG		TCCACGNNNGATCGACATG		GGCTAGTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2290	TGCAGGACCCAGAGAATTGGAATACAT	2530	TGCAGGACCCAGAGAATTGGAATACAG	2770
ACTCCTANNNGATCGACATG		GACTGACNNNGATCGACATG		CTTGTGCTNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2291	TGCAGGACCCAGAGAATTGGAATACAT	2531	TGCAGGACCCAGAGAATTGGAATACAG	2771
TTCTCTNNNGATCGACATG		GAITTAGNNNGATCGACATG		TAAATAGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2292	TGCAGGACCCAGAGAATTGGAATACAA	2532	TGCAGGACCCAGAGAATTGGAATACAG	2772
TGAGCTANNNGATCGACATG		CATACCTANNNGATCGACATG		GGTGTCCNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2293	TGCAGGACCCAGAGAATTGGAATACAA	2533	TGCAGGACCCAGAGAATTGGAATACAG	2773
TCCTGACANNNGATCGACATG		GCATCCANNNGATCGACATG		CTAGAGCANNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2294	TGCAGGACCCAGAGAATTGGAATACAA	2534	TGCAGGACCCAGAGAATTGGAATACAG	2774
TGACCCGNNNGATCGACATG		CGGCAANNNGATCGACATG		GACATAGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2295	TGCAGGACCCAGAGAATTGGAATACAG	2535	TGCAGGACCCAGAGAATTGGAATACAT	2775
TCATGGANNNGATCGACATG		TTTCTGNNNGATCGACATG		CTACACGNNNGATCGACATG	
TGCAGGACCCAGAGAATTGGAATACAG	2296	TGCAGGACCCAGAGAATTGGAATACAT	2536	TGCAGGACCCAGAGAATTGGAATACAG	2776
AACTCTANNNGATCGACATG		TAACTAGNNNGATCGACATG		AAACTGNNNGATCGACATG	

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池 -10	SEQ ID NO.	池 -11	SEQ ID NO.	池 -12	SEQ ID NO.
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TGCAGGACCCAGAGAAATCGAATACAC	2258	TGCAGGACCCAGAGAAATCGAATACAC	2538	TGCAGGACCCAGAGAAATCGAATACAG	2778
GGCGTGCNNINGATCGACATG		AGTATCANNINGATCGACATG		TCCAGTANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2259	TGCAGGACCCAGAGAAATCGAATACAC	2539	TGCAGGACCCAGAGAAATCGAATACAG	2779
CAGTCCGNNINGATCGACATG		CTGACANNINGATCGACATG		TCGAGACNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2300	TGCAGGACCCAGAGAAATCGAATACAC	2540	TGCAGGACCCAGAGAAATCGAATACAT	2780
GGCCCTGNNINGATCGACATG		GTGGCCANNINGATCGACATG		TTCAATCANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2301	TGCAGGACCCAGAGAAATCGAATACAG	2541	TGCAGGACCCAGAGAAATCGAATACAC	2781
CCGTCCGNNINGATCGACATG		CGTATACNNINGATCGACATG		AGCTGTANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2302	TGCAGGACCCAGAGAAATCGAATACAG	2542	TGCAGGACCCAGAGAAATCGAATACAA	2782
TCCTCCGNNINGATCGACATG		CGCTCCANNINGATCGACATG		CTGCTCTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2303	TGCAGGACCCAGAGAAATCGAATACAA	2543	TGCAGGACCCAGAGAAATCGAATACAA	2783
CTCCATTNNINGATCGACATG		CCGTTAGNNINGATCGACATG		AAGTTCTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2304	TGCAGGACCCAGAGAAATCGAATACAT	2544	TGCAGGACCCAGAGAAATCGAATACAG	2784
ACTCTTNNINGATCGACATG		GTACTTNNINGATCGACATG		AATCCAGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAT	2305	TGCAGGACCCAGAGAAATCGAATACAG	2545	TGCAGGACCCAGAGAAATCGAATACAG	2785
GTATCTANNINGATCGACATG		ATTATGANNINGATCGACATG		TCCCGCANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2306	TGCAGGACCCAGAGAAATCGAATACAC	2546	TGCAGGACCCAGAGAAATCGAATACAG	2786
AGTGTCTNNINGATCGACATG		AGACCCGNNINGATCGACATG		FAAATANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2307	TGCAGGACCCAGAGAAATCGAATACAT	2547	TGCAGGACCCAGAGAAATCGAATACAA	2787
TTCTAANNINGATCGACATG		AGCCANNINGATCGACATG		CCCTAAGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2308	TGCAGGACCCAGAGAAATCGAATACAT	2548	TGCAGGACCCAGAGAAATCGAATACAG	2788
AGACCCNNINGATCGACATG		CGAGTANNINGATCGACATG		GTCCATCANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAT	2309	TGCAGGACCCAGAGAAATCGAATACAG	2549	TGCAGGACCCAGAGAAATCGAATACAT	2789
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TGCAGGACCCAGAGAAATCGAATACAA	2310	TGCAGGACCCAGAGAAATCGAATACAC	2550	TGCAGGACCCAGAGAAATCGAATACAA	2790
TGTGCTGNNINGATCGACATG		CTTACACNNINGATCGACATG		AGTTCGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2311	TGCAGGACCCAGAGAAATCGAATACAT	2551	TGCAGGACCCAGAGAAATCGAATACAA	2791
CCAGGTGNNINGATCGACATG		AGCAGCCNNINGATCGACATG		TCAATGTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2312	TGCAGGACCCAGAGAAATCGAATACAC	2552	TGCAGGACCCAGAGAAATCGAATACAC	2792
AGCCAGGNNINGATCGACATG		CTTACTGNNINGATCGACATG		ATTGATNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2313	TGCAGGACCCAGAGAAATCGAATACAT	2553	TGCAGGACCCAGAGAAATCGAATACAG	2793
CTGAGCCNNINGATCGACATG		TACTCTANNINGATCGACATG		AGCGAANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2314	TGCAGGACCCAGAGAAATCGAATACAG	2554	TGCAGGACCCAGAGAAATCGAATACAC	2794
TAAGCCGNNINGATCGACATG		CGCCTACNNINGATCGACATG		ATSTTAANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAT	2315	TGCAGGACCCAGAGAAATCGAATACAC	2555	TGCAGGACCCAGAGAAATCGAATACAG	2795
TTGTCTANNINGATCGACATG		CTTAGAGNNINGATCGACATG		AACTTCGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2316	TGCAGGACCCAGAGAAATCGAATACAT	2556	TGCAGGACCCAGAGAAATCGAATACAC	2796
GGCTTTGNNINGATCGACATG		TCTATGTNNINGATCGACATG		CTCCGCCNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2317	TGCAGGACCCAGAGAAATCGAATACAT	2557	TGCAGGACCCAGAGAAATCGAATACAA	2797
CTATTTTNNINGATCGACATG		TTTACACNNINGATCGACATG		CGTAAANNINGATCGACATG	
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GCACCCANNINGATCGACATG		TGTTTTCNNINGATCGACATG		GTGTGTTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2319	TGCAGGACCCAGAGAAATCGAATACAG	2559	TGCAGGACCCAGAGAAATCGAATACAG	2799
CCCTCAANNINGATCGACATG		AAAGACCCNNINGATCGACATG		AAATAGTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2320	TGCAGGACCCAGAGAAATCGAATACAA	2560	TGCAGGACCCAGAGAAATCGAATACAG	2800
CCCATANNINGATCGACATG		CGTCCGNNINGATCGACATG		TCTATTTNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAT	2321	TGCAGGACCCAGAGAAATCGAATACAG	2561	TGCAGGACCCAGAGAAATCGAATACAT	2801
CTAATGNNINGATCGACATG		TTATACATNNINGATCGACATG		AGTAGCCNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2322	TGCAGGACCCAGAGAAATCGAATACAG	2562	TGCAGGACCCAGAGAAATCGAATACAG	2802
GCACCTACNNINGATCGACATG		AGTTCGNNINGATCGACATG		TACAAANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2323	TGCAGGACCCAGAGAAATCGAATACAC	2563	TGCAGGACCCAGAGAAATCGAATACAA	2803
ATTACAGNNINGATCGACATG		CTCGAANNINGATCGACATG		AGGTACGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2324	TGCAGGACCCAGAGAAATCGAATACAA	2564	TGCAGGACCCAGAGAAATCGAATACAT	2804
TGCTCCGNNINGATCGACATG		TGTCCGACNNINGATCGACATG		AGACTTANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAG	2325	TGCAGGACCCAGAGAAATCGAATACAT	2565	TGCAGGACCCAGAGAAATCGAATACAC	2805
CCGATTNNINGATCGACATG		AACAGCCNNINGATCGACATG		AGAGCAANNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2326	TGCAGGACCCAGAGAAATCGAATACAG	2566	TGCAGGACCCAGAGAAATCGAATACAA	2806
TGTCTANNINGATCGACATG		CCGAGTNNINGATCGACATG		CCCTCCGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAA	2327	TGCAGGACCCAGAGAAATCGAATACAA	2567	TGCAGGACCCAGAGAAATCGAATACAG	2807
CRAGGACNNINGATCGACATG		TCATAACNNINGATCGACATG		CTGTCTGNNINGATCGACATG	
TGCAGGACCCAGAGAAATCGAATACAC	2328	TGCAGGACCCAGAGAAATCGAATACAA	2568	TGCAGGACCCAGAGAAATCGAATACAA	2808
CGTAGTNNINGATCGACATG		AGGTCTGNNINGATCGACATG		GTCCCGCANNINGATCGACATG	

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池-10	SEQ ID NO:	池-11	SEQ ID NO:	池-12	SEQ ID NO:
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TGCAGGACCAGAGAATTGGAATACAG	2330	TGCAGGACCAGAGAATTGGAATACAA	2570	TGCAGGACCAGAGAATTGGAATACAC	2810
AGGCTANNNGATCGACATG		CGTACTGNNNGATCGACATG		CGGATGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	2331	TGCAGGACCAGAGAATTGGAATACAA	2571	TGCAGGACCAGAGAATTGGAATACAT	2811
TAACATAANNNGATCGACATG		TTAAGTCNNNGATCGACATG		CTATATCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	2332	TGCAGGACCAGAGAATTGGAATACAG	2572	TGCAGGACCAGAGAATTGGAATACAA	2812
GGCTAATNNNGATCGACATG		GTGAAAGNNNGATCGACATG		GACCTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	2333	TGCAGGACCAGAGAATTGGAATACAG	2573	TGCAGGACCAGAGAATTGGAATACAG	2813
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TGCAGGACCAGAGAATTGGAATACAG	2334	TGCAGGACCAGAGAATTGGAATACAT	2574	TGCAGGACCAGAGAATTGGAATACAG	2814
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TGCAGGACCAGAGAATTGGAATACAG	2335	TGCAGGACCAGAGAATTGGAATACAG	2575	TGCAGGACCAGAGAATTGGAATACAG	2815
TCTCAACNNNGATCGACATG		CCAGTGGNNNGATCGACATG		CCCATANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	2336	TGCAGGACCAGAGAATTGGAATACAT	2576	TGCAGGACCAGAGAATTGGAATACAA	2816
TGACAGGNNNGATCGACATG		CCAAGTNNNGATCGACATG		CTTTCAATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	2337	TGCAGGACCAGAGAATTGGAATACAT	2577	TGCAGGACCAGAGAATTGGAATACAT	2817
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TGCAGGACCAGAGAATTGGAATACAG	2338	TGCAGGACCAGAGAATTGGAATACAG	2578	TGCAGGACCAGAGAATTGGAATACAG	2818
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TGCAGGACCAGAGAATTGGAATACAG	2339	TGCAGGACCAGAGAATTGGAATACAG	2579	TGCAGGACCAGAGAATTGGAATACAG	2819
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TGCAGGACCAGAGAATTGGAATACAG	2348	TGCAGGACCAGAGAATTGGAATACAT	2588	TGCAGGACCAGAGAATTGGAATACAG	2828
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TGCAGGACCAGAGAATTGGAATACAG	2351	TGCAGGACCAGAGAATTGGAATACAT	2591	TGCAGGACCAGAGAATTGGAATACAA	2831
CACCTTCHNNNGATCAGGT		ATCCAGCCHNNNGATCAGGT		CTCGCTANNNTGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2352	TGCAGGACCAGAGAATTGGAATACAG	2592	TGCAGGACCAGAGAATTGGAATACAT	2832
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TGCAGGACCAGAGAATTGGAATACAA	2353	TGCAGGACCAGAGAATTGGAATACAT	2593	TGCAGGACCAGAGAATTGGAATACAT	2833
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TGCAGGACCAGAGAATTGGAATACAG	2354	TGCAGGACCAGAGAATTGGAATACAT	2594	TGCAGGACCAGAGAATTGGAATACAG	2834
TCTATCAGNNNTGATCAGGT		TGCCCTTCHNNNGATCAGGT		AAACTATNNNTGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	2355	TGCAGGACCAGAGAATTGGAATACAG	2595	TGCAGGACCAGAGAATTGGAATACAT	2835
TTCGGAGNNNTGATCAGGT		TGGAGTANNNTGATCAGGT		CACCTGTCHNNNGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2356	TGCAGGACCAGAGAATTGGAATACAG	2596	TGCAGGACCAGAGAATTGGAATACAA	2836
TGAGGATNNNTGATCAGGT		OCTCACCHNNNGATCAGGT		ACPAATGNNNTGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2357	TGCAGGACCAGAGAATTGGAATACAA	2597	TGCAGGACCAGAGAATTGGAATACAT	2837
CTATCCANNNTGATCAGGT		CACACCANNNTGATCAGGT		TTTCTTCHNNNGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2358	TGCAGGACCAGAGAATTGGAATACAA	2598	TGCAGGACCAGAGAATTGGAATACAG	2838
AAATGCTCHNNNTGATCAGGT		CCCCATINNNNTGATCAGGT		TTCACTCHNNNTGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2359	TGCAGGACCAGAGAATTGGAATACAA	2599	TGCAGGACCAGAGAATTGGAATACAA	2839
GCTGAANNNTGATCAGGT		TAGTCTANNNTGATCAGGT		GGTCTGTNNNTGATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	2360	TGCAGGACCAGAGAATTGGAATACAG	2600	TGCAGGACCAGAGAATTGGAATACAG	2840
TGCGACCHNNNTGATCAGGT		AAATGCTCHNNNTGATCAGGT		CAAAAGCCHNNNTGATCAGGT	

图15E

池 -10	SEQ ID No:	池 -11	SEQ ID No:	池 -12	SEQ ID No:
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
ACAGGTANNNTGCATCAGGT	2361	TAGATCGNNNTGCATCAGGT	2601	CGAGAGGNNNTGCATCAGGT	2841
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CGTTGCANNNTGCATCAGGT	2362	GCARCCNNNTGCATCAGGT	2602	TATITGCANNNTGCATCAGGT	2842
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TGAGACTNNNTGCATCAGGT	2363	GAGAGAANNNTGCATCAGGT	2603	CTCTGGTNNNTGCATCAGGT	2843
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
CGTTGCANNNTGCATCAGGT	2364	TTGTCTTNNNTGCATCAGGT	2604	TTGGAGGNNNTGCATCAGGT	2844
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
GAAGCTANNNTGCATCAGGT	2365	GGCATACNNNTGCATCAGGT	2605	ATCATTTNNNTGCATCAGGT	2845
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CGTTGATNNNTGCATCAGGT	2366	AGGCAATNNNTGCATCAGGT	2606	AGGTGATNNNTGCATCAGGT	2846
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
AGGCTCTNNNTGCATCAGGT	2367	CTCACGTNNNTGCATCAGGT	2607	CCCGTCAANNNTGCATCAGGT	2847
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GGTACCTNNNTGCATCAGGT	2368	TGGGTCANNNTGCATCAGGT	2608	ACAGGTANNNTGCATCAGGT	2848
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GTATCTNNNTGCATCAGGT	2369	JTAATGANNNTGCATCAGGT	2609	CGTTAGANNNTGCATCAGGT	2849
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
ACTTACGNNNTGCATCAGGT	2370	ACTCACGNNNTGCATCAGGT	2610	CTCTAGNNNTGCATCAGGT	2850
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
CTTCCACNNNTGCATCAGGT	2371	GCAGTGANNNNTGCATCAGGT	2611	GGCTTGTNNNTGCATCAGGT	2851
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CTTCTGANNNTGCATCAGGT	2372	AACTACTGNNNTGCATCAGGT	2612	GGAGTTCNNNTGCATCAGGT	2852
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GGCACANNNTGCATCAGGT	2373	AGGTCCNNNTGCATCAGGT	2613	CACCCAGNNNTGCATCAGGT	2853
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
TGTGAGTNNNTGCATCAGGT	2374	CTGGAAJNNNTGCATCAGGT	2614	GAATGCAANNNTGCATCAGGT	2854
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
GAGAGACNNNTGCATCAGGT	2375	AGAGGAGNNNTGCATCAGGT	2615	CATTACANNNTGCATCAGGT	2855
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
AATTGTGNNNTGCATCAGGT	2376	TGGAAGTNNNTGCATCAGGT	2616	GTCTCTGNNNTGCATCAGGT	2856
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TAATTGTNNNTGCATCAGGT	2377	GGGACTNNNTGCATCAGGT	2617	AGTGCCANNNTGCATCAGGT	2857
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
ATCATCTNNNTGCATCAGGT	2378	ACTTGTNNNTGCATCAGGT	2618	CAATGTGNNNTGCATCAGGT	2858
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GTGGATGNNNTGCATCAGGT	2379	ACTGACNNNTGCATCAGGT	2619	TTGAAATNNNTGCATCAGGT	2859
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TATCAGACHNNNTGCATCAGGT	2380	GGTGGTANNNTGCATCAGGT	2620	CACCTTCANNNTGCATCAGGT	2860
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
AGTTTCGNNNTGCATCAGGT	2381	TATTTTNNNTGCATCAGGT	2621	CCATTTCGNNNTGCATCAGGT	2861
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
AGAGATGNNNTGCATCAGGT	2382	CCCCATANNNTGCATCAGGT	2622	ACTCTCANNNTGCATCAGGT	2862
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
AGTCAACHNNNTGCATCAGGT	2383	AACTTGCNNNTGCATCAGGT	2623	AGCTGATNNNTGCATCAGGT	2863
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
TCGCTGTNNNTGCATCAGGT	2384	GAACCGTNNNTGCATCAGGT	2624	GAGCTCTNNNTGCATCAGGT	2864
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GTCCGAGNNNTGCATCAGGT	2385	GCATTGANNNTGCATCAGGT	2625	TGGATTGNNNTGCATCAGGT	2865
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CATGCAATNNNTGCATCAGGT	2386	GGGGTGTNNNTGCATCAGGT	2626	GCTATCCNNNTGCATCAGGT	2866
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
AAGTTCGNNNTGCATCAGGT	2387	CCGCCGNNNTGCATCAGGT	2627	ACGTTGTNNNTGCATCAGGT	2867
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
AAAGCACHNNNTGCATCAGGT	2388	AAAGCTACNNNTGCATCAGGT	2628	TTCACTCTNNNTGCATCAGGT	2868
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GGTGTCTNNNTGCATCAGGT	2389	GGTTCAANNNTGCATCAGGT	2629	GATTCAGNNNTGCATCAGGT	2869
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CGCAAGCHNNNTGCATCAGGT	2390	AACGTGTNNNTGCATCAGGT	2630	CGTGCATNNNTGCATCAGGT	2870
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TACACATANNNTGCATCAGGT	2391	TACTAGCNNNTGCATCAGGT	2631	GTGTTTTNNNTGCATCAGGT	2871
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CTCTCTGNNNTGCATCAGGT	2392	GAGTGTGNNNTGCATCAGGT	2632	GGCATCAANNNTGCATCAGGT	2872

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池 -10	SEQ ID NO.	池 -11	SEQ ID NO.	池 -12	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT	
GCCCCGNNNTGCATCAGGT	2393	AAACACGNNNTGCATCAGGT	2633	BAGCTGNNNTGCATCAGGT	2873
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TTAAICNNNTGCATCAGGT	2394	CATGCTNNNTGCATCAGGT	2634	CGGACTNNNTGCATCAGGT	2874
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CGTCGGNNNTGCATCAGGT	2395	ATTACGNNNTGCATCAGGT	2635	GAATTACNNNTGCATCAGGT	2875
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
GACAAATNNNTGCATCAGGT	2396	TAGATCCNNNTGCATCAGGT	2636	ACAGAGNNNTGCATCAGGT	2876
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
GTATANNNTGCATCAGGT	2397	GGCACGNNNTGCATCAGGT	2637	ATGTTCCNNNTGCATCAGGT	2877
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CTAAACNNNTGCATCAGGT	2398	AGCATAGNNNTGCATCAGGT	2638	CGCTACNNNTGCATCAGGT	2878
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CACTCGANNNTGCATCAGGT	2399	GTGTCTNNNTGCATCAGGT	2639	TACAGACNNNTGCATCAGGT	2879
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CATCGTNNNTGCATCAGGT	2400	CTTCGANNNTGCATCAGGT	2640	ATAGTGTNNNTGCATCAGGT	2880
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
TAAAGCGNNNTGCATCAGGT	2401	ATCAGCTNNNTGCATCAGGT	2641	GAGAGTTNNNTGCATCAGGT	2881
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
BAGCCCTNNNTGCATCAGGT	2402	CCACCTTNNNTGCATCAGGT	2642	ACATTTCTNNNTGCATCAGGT	2882
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
CATGTTNNNTGCATCAGGT	2403	GGCCACGNNNTGCATCAGGT	2643	ACAATGNNNTGCATCAGGT	2883
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GAAATAANNNTGCATCAGGT	2404	ACATCTCNNNTGCATCAGGT	2644	ATATTACNNNTGCATCAGGT	2884
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
ATGAAANNNTGCATCAGGT	2405	CTTTACNNNTGCATCAGGT	2645	GGCTTTNNNTGCATCAGGT	2885
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
GTGCCGNNNTGCATCAGGT	2406	CCCTAACNNNTGCATCAGGT	2646	CTGCTGNNNTGCATCAGGT	2886
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
CTGCTGNNNTGCATCAGGT	2407	CTCGACNNNTGCATCAGGT	2647	AGGCGCGNNNTGCATCAGGT	2887
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
BAGGTGNNNTGCATCAGGT	2408	GAGAGACNNNTGCATCAGGT	2648	CGGTGAANNNTGCATCAGGT	2888

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池 -13	SEQ ID NO:	池 -14	SEQ ID NO:	池 -15	SEQ ID NO:
TGCAGGACAGAGAATTGGAATACAC	2889	TGCAGGACAGAGAATTGGAATACAC	3129	TGCAGGACAGAGAATTGGAATACAG	3369
CACCGACGNNNACGTATGCCA		ATCGGTAMNNACGTATGCCA		TGTGATGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2890	TGCAGGACAGAGAATTGGAATACAT	3130	TGCAGGACAGAGAATTGGAATACAA	3370
ATCGCTGNNNACGTATGCCA		GGTGGGNNNACGTATGCCA		ARGCGGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2891	TGCAGGACAGAGAATTGGAATACAG	3131	TGCAGGACAGAGAATTGGAATACAT	3371
TGCGCGTNNNACGTATGCCA		TAAGTGGNNNACGTATGCCA		CGTGGATNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2892	TGCAGGACAGAGAATTGGAATACAG	3132	TGCAGGACAGAGAATTGGAATACAT	3372
GAGTAGGNNNACGTATGCCA		TTGTTGNNNACGTATGCCA		CACCGGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2893	TGCAGGACAGAGAATTGGAATACAA	3133	TGCAGGACAGAGAATTGGAATACAG	3373
CGTGGGNNNACGTATGCCA		GGGTTGNNNACGTATGCCA		CGGTTGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2894	TGCAGGACAGAGAATTGGAATACAG	3134	TGCAGGACAGAGAATTGGAATACAA	3374
TCCTGNNNACGTATGCCA		TACTGTGNNNACGTATGCCA		CACCGTNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2895	TGCAGGACAGAGAATTGGAATACAA	3135	TGCAGGACAGAGAATTGGAATACAG	3375
GGTATGNNNACGTATGCCA		GCAGCTNNNACGTATGCCA		CTCAGGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2896	TGCAGGACAGAGAATTGGAATACAG	3136	TGCAGGACAGAGAATTGGAATACAC	3376
TCACGTNNNACGTATGCCA		CGCTGTNNNACGTATGCCA		BAATCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2897	TGCAGGACAGAGAATTGGAATACAC	3137	TGCAGGACAGAGAATTGGAATACAT	3377
AGTAGGNNNACGTATGCCA		TCTCGGNNNACGTATGCCA		AAATATNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAC	2898	TGCAGGACAGAGAATTGGAATACAC	3138	TGCAGGACAGAGAATTGGAATACAC	3378
CGCTGTNNNACGTATGCCA		TACTGTGNNNACGTATGCCA		ATTAGCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2899	TGCAGGACAGAGAATTGGAATACAA	3139	TGCAGGACAGAGAATTGGAATACAG	3379
AAATATNNNACGTATGCCA		TAATGAGNNNACGTATGCCA		ACTACTGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2900	TGCAGGACAGAGAATTGGAATACAG	3140	TGCAGGACAGAGAATTGGAATACAG	3380
CACAGGNNNACGTATGCCA		CGTAGTNNNACGTATGCCA		TGCAGGACAGAGAATTGGAATACAG	3381
TGCAGGACAGAGAATTGGAATACAG	2901	TGCAGGACAGAGAATTGGAATACAA	3141	TGCAGGACAGAGAATTGGAATACAG	3382
GTGCGCTNNNACGTATGCCA		GCACACGNNNACGTATGCCA		GCTATTGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAC	2902	TGCAGGACAGAGAATTGGAATACAC	3142	TGCAGGACAGAGAATTGGAATACAG	3383
GTGACGNNNACGTATGCCA		TGTGTCTNNNACGTATGCCA		GTGTTGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2903	TGCAGGACAGAGAATTGGAATACAT	3143	TGCAGGACAGAGAATTGGAATACAT	3384
ACCGCTNNNACGTATGCCA		CCAAACGNNNACGTATGCCA		GGCTACNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2904	TGCAGGACAGAGAATTGGAATACAT	3144	TGCAGGACAGAGAATTGGAATACAA	3385
CAATTGNNNACGTATGCCA		GTCAAGCNNNACGTATGCCA		TCTTTCNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2905	TGCAGGACAGAGAATTGGAATACAA	3145	TGCAGGACAGAGAATTGGAATACAT	3386
GTGCGCAGNNNACGTATGCCA		GTGTCACNNNACGTATGCCA		CTGCTCINNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2906	TGCAGGACAGAGAATTGGAATACAC	3146	TGCAGGACAGAGAATTGGAATACAG	3387
AGGCGCAGNNNACGTATGCCA		GTCAAGNNNACGTATGCCA		CGAGCTNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2907	TGCAGGACAGAGAATTGGAATACAG	3147	TGCAGGACAGAGAATTGGAATACAA	3388
CTCGAGTNNNACGTATGCCA		TGAAGCINNACGTATGCCA		GCCGTGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAC	2908	TGCAGGACAGAGAATTGGAATACAT	3148	TGCAGGACAGAGAATTGGAATACAG	3389
CAATGAGNNNACGTATGCCA		TGGGCGCINNACGTATGCCA		ATAACCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2909	TGCAGGACAGAGAATTGGAATACAG	3149	TGCAGGACAGAGAATTGGAATACAC	3390
AGCACGNNNACGTATGCCA		TATTTGGNNNACGTATGCCA		GGAAACGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAC	2910	TGCAGGACAGAGAATTGGAATACAA	3150	TGCAGGACAGAGAATTGGAATACAG	3391
GCTTTGNNNACGTATGCCA		CAATAGNNNACGTATGCCA		TCCAGCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2911	TGCAGGACAGAGAATTGGAATACAC	3151	TGCAGGACAGAGAATTGGAATACAC	3392
GGATGCTNNNACGTATGCCA		TACCGCGNNNACGTATGCCA		CTCAGCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2912	TGCAGGACAGAGAATTGGAATACAT	3152	TGCAGGACAGAGAATTGGAATACAT	3393
CAATGGCINNACGTATGCCA		GTATACNNNACGTATGCCA		CGGCGCINNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2913	TGCAGGACAGAGAATTGGAATACAA	3153	TGCAGGACAGAGAATTGGAATACAC	3394
ACTACTNNNACGTATGCCA		GGCTACNNNACGTATGCCA		CGCCAGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2914	TGCAGGACAGAGAATTGGAATACAT	3154	TGCAGGACAGAGAATTGGAATACAG	3395
TCCGATGNNNACGTATGCCA		TCCCATGNNNACGTATGCCA		GCTGTTNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2915	TGCAGGACAGAGAATTGGAATACAT	3155	TGCAGGACAGAGAATTGGAATACAT	3396
NGATACGNNNACGTATGCCA		AGGCTTTNNNACGTATGCCA		TCTTATNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2916	TGCAGGACAGAGAATTGGAATACAG	3156	TGCAGGACAGAGAATTGGAATACAC	3397
CGTTTITNNNACGTATGCCA		GTTCACNNNACGTATGCCA		TTCTATNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2917	TGCAGGACAGAGAATTGGAATACAG	3157	TGCAGGACAGAGAATTGGAATACAT	3398
TTAGCGTNNNACGTATGCCA		ACGTTTNNNACGTATGCCA		CCCCGNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAG	2918	TGCAGGACAGAGAATTGGAATACAT	3158	TGCAGGACAGAGAATTGGAATACAT	3399
CGGCGCINNACGTATGCCA		GTGATNNNACGTATGCCA		GTCTACNNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAA	2919	TGCAGGACAGAGAATTGGAATACAA	3159	TGCAGGACAGAGAATTGGAATACAT	3400
TGCTCTGNNNACGTATGCCA		GTATTACNNNACGTATGCCA		GTATTANNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2920	TGCAGGACAGAGAATTGGAATACAG	3160	TGCAGGACAGAGAATTGGAATACAT	3401
TATCTACHNNACGTATGCCA		AGAACCHNNACGTATGCCA		GGTTTANNNACGTATGCCA	
TGCAGGACAGAGAATTGGAATACAT	2921	TGCAGGACAGAGAATTGGAATACAC	3161	TGCAGGACAGAGAATTGGAATACAG	3402
TCTATTGNNNACGTATGCCA		CTAATTNNNACGTATGCCA		AGACGGCINNACGTATGCCA	

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池 -13	SEQ ID No:	池 -14	SEQ ID No:	池 -15	SEQ ID No:
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CAGTACANNACGTATGCCA	2922	TTCACCTNNNACGTATGCCA	3162	GTGAGCGNNNACGTATGCCA	3402
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC	
CAGGATANNACGTATGCCA	2923	TCAACGTNNNACGTATGCCA	3163	AACAGTCNNNACGTATGCCA	3403
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
TATATACNNNACGTATGCCA	2924	CGTGTGNNNACGTATGCCA	3164	GTTCGANNNACGTATGCCA	3404
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
ATTACGNNNACGTATGCCA	2925	AAACCCANNNACGTATGCCA	3165	GTATTTNNNACGTATGCCA	3405
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
GTACAGNNNACGTATGCCA	2926	CCCTGTGNNNACGTATGCCA	3166	TACGTGNNNACGTATGCCA	3406
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
TAGGATCNNNACGTATGCCA	2927	GTAGCGTNNNACGTATGCCA	3167	CTAGCGNNNACGTATGCCA	3407
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
ACTAGANNNACGTATGCCA	2928	TCCATGNNNACGTATGCCA	3168	GAGCGGNNNACGTATGCCA	3408
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
CTTATCTNNNACGTATGCCA	2929	GCATGTTNNNACGTATGCCA	3169	GGCGCCGNNNACGTATGCCA	3409
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
AGGTCCGNNNACGTATGCCA	2930	GAATCCNNNACGTATGCCA	3170	AGCATGTNNNACGTATGCCA	3410
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA	
TGGAATJNNNACGTATGCCA	2931	CTTGTGTNNNACGTATGCCA	3171	GGCTAATNNNACGTATGCCA	3411
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC	
GTTCAGNNNACGTATGCCA	2932	AAACCCANNNACGTATGCCA	3172	TCAACCCNNNACGTATGCCA	3412
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
GCATCCGNNNACGTATGCCA	2933	GATACCTNNNACGTATGCCA	3173	CGGACCGNNNACGTATGCCA	3413
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
TATGGATNNNACGTATGCCA	2934	GGCGGAGNNNACGTATGCCA	3174	ACTGGGNNNACGTATGCCA	3414
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
CATCGTGHNNNACGTATGCCA	2935	ACTGTCTNNNACGTATGCCA	3175	CCCTCTGNNNACGTATGCCA	3415
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
AAGTAGTNNNACGTATGCCA	2936	TGGAGGCGNNNACGTATGCCA	3176	AGTTAACNNNACGTATGCCA	3416
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
AATAACCGNNNACGTATGCCA	2937	GTATCGCNNNACGTATGCCA	3177	GACTTCNNNACGTATGCCA	3417
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
TTCTCATNNNACGTATGCCA	2938	CGAGATCNNNACGTATGCCA	3178	CGGCATGNNNACGTATGCCA	3418
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAT	
CATCCCTNNNACGTATGCCA	2939	GGTAGTNNNACGTATGCCA	3179	GGAGTACNNNACGTATGCCA	3419
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAC	
GAAGATJNNNACGTATGCCA	2940	CGTATCTNNNACGTATGCCA	3180	TGTATTNNNACGTATGCCA	3420
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
ACATTATNNNACGTATGCCA	2941	ACGCACCTNNNACGTATGCCA	3181	AGAGCCANNNACGTATGCCA	3421
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
GATACGANNNACGTATGCCA	2942	CGATTGANNNACGTATGCCA	3182	GTGGAATHNNNACGTATGCCA	3422
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC	
TACATATNNNACGTATGCCA	2943	CTCTAAGNNNACGTATGCCA	3183	TGCTGAANNNACGTATGCCA	3423
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CATAGCGNNNACGTATGCCA	2944	GTGAGTANNNACGTATGCCA	3184	ATGGCAANNNACGTATGCCA	3424
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
TTGAACGNNNACGTATGCCA	2945	CCATATGANNNACGTATGCCA	3185	AGGTGGANNNACGTATGCCA	3425
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
TTCCCAJNNNACGTATGCCA	2946	CGGAGCGNNNACGTATGCCA	3186	ATGACTCNNNACGTATGCCA	3426
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
GAGCCCGNNNACGTATGCCA	2947	TGTGACANNNACGTATGCCA	3187	CTCTGTNNNACGTATGCCA	3427
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA	
TAATACNNNACGTATGCCA	2948	GTCCGTGNNNACGTATGCCA	3188	CGCAACTNNNACGTATGCCA	3428
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
ACGACAAJNNNACGTATGCCA	2949	TGCTGACNNNACGTATGCCA	3189	GAATGCTNNNACGTATGCCA	3429
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA	
GAATTATNNNACGTATGCCA	2950	CATGTCTNNNACGTATGCCA	3190	GGCPATCJNNNACGTATGCCA	3430
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
BCGCTGANNNACGTATGCCA	2951	CTTTTGGNNNACGTATGCCA	3191	CAGTTTJNNNACGTATGCCA	3431
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG	
CAATTAGNNNACGTATGCCA	2952	GGGTGANNNACGTATGCCA	3192	GGCAATCTNNNACGTATGCCA	3432
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
TGAGCAGJNNNACGTATGCCA	2953	CCCCCATNNNACGTATGCCA	3193	GCAGTGTNNNACGTATGCCA	3433
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
GACTTAAJNNNACGTATGCCA	2954	TCCTTTCGNNNACGTATGCCA	3194	GTCCATGNNNACGTATGCCA	3434

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池-13	SEQ ID No:	池-14	SEQ ID No:	池-15	SEQ ID No:
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
GAGAAATANNNCTAGCGTTAC	2955	TCCAGGANNNCTAGCGTTAC	3195	TATTCAINNNTAGCGTTAC	3435
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
TTTTTCTNNNCTAGCGTTAC	2956	ATGCATANNNCTAGCGTTAC	3196	TGGTCTNNNCTAGCGTTAC	3436
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAC	
TGCGATANNNCTAGCGTTAC	2957	AGAAATTNNNCTAGCGTTAC	3197	GTGTAGNNNCTAGCGTTAC	3437
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TCCATCGNNNCTAGCGTTAC	2958	CTCAATCNNNCTAGCGTTAC	3198	ACAGCGNNNCTAGCGTTAC	3438
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
GATATGANNNCTAGCGTTAC	2959	AAACAAANNNCTAGCGTTAC	3199	ACACCGTNNNCTAGCGTTAC	3439
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
AGCTACGNNNCTAGCGTTAC	2960	TGATGTNNNCTAGCGTTAC	3200	GTTAGCINNNTAGCGTTAC	3440
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA	
TACAGCGNNNCTAGCGTTAC	2961	GCCGTAAANNNCTAGCGTTAC	3201	TGCGCTNNNCTAGCGTTAC	3441
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
ACTACAGNNNCTAGCGTTAC	2962	GGCTCTAGNNNCTAGCGTTAC	3202	CTATGANNNCTAGCGTTAC	3442
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
TTTTAGNNNCTAGCGTTAC	2963	GCGTGTNNNCTAGCGTTAC	3203	GCGACGNNNCTAGCGTTAC	3443
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TTTCAGTNNNCTAGCGTTAC	2964	ACGTCATNNNCTAGCGTTAC	3204	GTCACAANNNCTAGCGTTAC	3444
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
CAGAACANNNCTAGCGTTAC	2965	GTATTAGNNNCTAGCGTTAC	3205	GCGATCGNNNCTAGCGTTAC	3445
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
GAGTAGANNNCTAGCGTTAC	2966	TGATTACNNNCTAGCGTTAC	3206	TTAGACNNNCTAGCGTTAC	3446
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT	
TCCGAGNNNCTAGCGTTAC	2967	CTCCGAANNNCTAGCGTTAC	3207	GCGGACNNNCTAGCGTTAC	3447
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
DGTATANNNCTAGCGTTAC	2968	TCTTCCNNNCTAGCGTTAC	3208	GTAAGACTNNNCTAGCGTTAC	3448
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
ACTCCGNNNCTAGCGTTAC	2969	CTCCTAGNNNCTAGCGTTAC	3209	GCCATAGNNNCTAGCGTTAC	3449
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
ACATTGNNNCTAGCGTTAC	2970	ACTTATANNNCTAGCGTTAC	3210	AATTACGNNNCTAGCGTTAC	3450
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TAGCATNNNCTAGCGTTAC	2971	AGAGTGAANNNCTAGCGTTAC	3211	GCGCGCNNNCTAGCGTTAC	3451
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
CAGACGANNNCTAGCGTTAC	2972	ATAAATTNNNCTAGCGTTAC	3212	AATATCANNNCTAGCGTTAC	3452
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
TGATCCGNNNCTAGCGTTAC	2973	CGGTGAGNNNCTAGCGTTAC	3213	TTAAGGANNNCTAGCGTTAC	3453
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
ATTATANNNCTAGCGTTAC	2974	GTCCCTTNNNCTAGCGTTAC	3214	TATACANNNCTAGCGTTAC	3454
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT	
AGTTTGHNNNCTAGCGTTAC	2975	GACTTATNNNCTAGCGTTAC	3215	ATTGACANNNCTAGCGTTAC	3455
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA	
GCCGCGNNNCTAGCGTTAC	2976	GGCACTANNNCTAGCGTTAC	3216	GGAATAINNNTAGCGTTAC	3456
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
CACACGANNNCTAGCGTTAC	2977	TTCCTATNNNCTAGCGTTAC	3217	TAGGACANNNCTAGCGTTAC	3457
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
AGTCGTTNNNCTAGCGTTAC	2978	TGATATANNNCTAGCGTTAC	3218	CCCAGTNNNCTAGCGTTAC	3458
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
GAGCCTTHNNNCTAGCGTTAC	2979	PAGCACTNNNCTAGCGTTAC	3219	CTACGTTNNNCTAGCGTTAC	3459
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
CTTCTANNNCTAGCGTTAC	2980	GCGATGNNNCTAGCGTTAC	3220	GGTGAGANNNCTAGCGTTAC	3460
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
TCATAGTNNNCTAGCGTTAC	2981	TCTCAATNNNCTAGCGTTAC	3221	TAGCACANNNCTAGCGTTAC	3461
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
AGCAATTNNNCTAGCGTTAC	2982	GCCACCCNNNCTAGCGTTAC	3222	CATGTANNNCTAGCGTTAC	3462
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
ATTGTANNNCTAGCGTTAC	2983	GACGGAANNNCTAGCGTTAC	3223	GACGAATNNNCTAGCGTTAC	3463
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TCCGCAANNNCTAGCGTTAC	2984	GAAACAGANNNCTAGCGTTAC	3224	GATGGCGNNNCTAGCGTTAC	3464
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
CTAGTCTNNNCTAGCGTTAC	2985	ATCTCGCNNNCTAGCGTTAC	3225	CCCRGTTNNNCTAGCGTTAC	3465
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
TAGGGTANNNCTAGCGTTAC	2986	GCAATCAGNNNCTAGCGTTAC	3226	GAGACAAANNNCTAGCGTTAC	3466
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
ATCAATCNNNCTAGCGTTAC	2987	CTAAGCANNNCTAGCGTTAC	3227	AATACCGNNNCTAGCGTTAC	3467

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池-13	SEQ ID NO.	池-14	SEQ ID NO.	池-15	SEQ ID NO.
TGCAGGACCCAGAGAAATCGAATACAG	2986	TGCAGGACCCAGAGAAATCGAATACAT	3226	TGCAGGACCCAGAGAAATCGAATACAT	3466
CCCTCGTHNNCTAGCGTTAC		TTGACAANNHCTAGCGTTAC		TTATGTCHNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	2989	TGCAGGACCCAGAGAAATCGAATACAG	3229	TGCAGGACCCAGAGAAATCGAATACAT	3469
GGTGGACNNHCTAGCGTTAC		CGGCCATNNHCTAGCGTTAC		GGTAAACNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2990	TGCAGGACCCAGAGAAATCGAATACAT	3230	TGCAGGACCCAGAGAAATCGAATACAA	3470
AGCCAGGCHNNCTAGCGTTAC		TGCATAANNHCTAGCGTTAC		GCACATANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	2991	TGCAGGACCCAGAGAAATCGAATACAA	3231	TGCAGGACCCAGAGAAATCGAATACAA	3471
CTAATGTNNHCTAGCGTTAC		CAGAGCANNNHCTAGCGTTAC		TCCTCCANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2992	TGCAGGACCCAGAGAAATCGAATACAG	3232	TGCAGGACCCAGAGAAATCGAATACAT	3472
GTAAAGACNNHCTAGCGTTAC		GTACGTNNHCTAGCGTTAC		TTTGGACNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2993	TGCAGGACCCAGAGAAATCGAATACAG	3233	TGCAGGACCCAGAGAAATCGAATACAA	3473
CCGCCAGNNHCTAGCGTTAC		ATGCACGTNNHCTAGCGTTAC		TAGCCTGNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2994	TGCAGGACCCAGAGAAATCGAATACAA	3234	TGCAGGACCCAGAGAAATCGAATACAG	3474
TGCAGGACCCAGAGAAATCGAATACAG		TCTAAACNNHCTAGCGTTAC		GAGCTCTNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	2995	TGCAGGACCCAGAGAAATCGAATACAA	3235	TGCAGGACCCAGAGAAATCGAATACAA	3475
GTCCGGCCHNNHCTAGCGTTAC		CGAGAACNNHCTAGCGTTAC		CCCCACGNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2996	TGCAGGACCCAGAGAAATCGAATACAG	3236	TGCAGGACCCAGAGAAATCGAATACAG	3476
CTCTACANNHCTAGCGTTAC		CGCAGCCHNNHCTAGCGTTAC		GCGGCAANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	2997	TGCAGGACCCAGAGAAATCGAATACAA	3237	TGCAGGACCCAGAGAAATCGAATACAT	3477
GGCCACGNNHCTAGCGTTAC		CGCAGCCHNNHCTAGCGTTAC		CCAGACANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	2998	TGCAGGACCCAGAGAAATCGAATACAG	3238	TGCAGGACCCAGAGAAATCGAATACAA	3478
CGCATGCHNNHCTAGCGTTAC		GCGCATGCHNNHCTAGCGTTAC		AAAGCAANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	2999	TGCAGGACCCAGAGAAATCGAATACAA	3239	TGCAGGACCCAGAGAAATCGAATACAA	3479
GTTCGACNNHCTAGCGTTAC		ATCCAGCCHNNHCTAGCGTTAC		ACTCGGCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3000	TGCAGGACCCAGAGAAATCGAATACAA	3240	TGCAGGACCCAGAGAAATCGAATACAG	3480
GTAAAGACNNHCTAGCGTTAC		TTAATGTCHNNHCTAGCGTTAC		TGTCCTTNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3001	TGCAGGACCCAGAGAAATCGAATACAG	3241	TGCAGGACCCAGAGAAATCGAATACAG	3481
CCCTCGCHNNHCTAGCGTTAC		CGCTTCGCHNNHCTAGCGTTAC		ACGTAATNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	3002	TGCAGGACCCAGAGAAATCGAATACAT	3242	TGCAGGACCCAGAGAAATCGAATACAA	3482
AACACGCHNNHCTAGCGTTAC		ACATATGNNHCTAGCGTTAC		CCCATACNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3003	TGCAGGACCCAGAGAAATCGAATACAG	3243	TGCAGGACCCAGAGAAATCGAATACAA	3483
AAATATCANNHCTAGCGTTAC		TGGAACCHNNHCTAGCGTTAC		TGCCCCCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3004	TGCAGGACCCAGAGAAATCGAATACAG	3244	TGCAGGACCCAGAGAAATCGAATACAG	3484
GTATCTGCHNNHCTAGCGTTAC		TCTGTGTNNHCTAGCGTTAC		TCGCCGCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3005	TGCAGGACCCAGAGAAATCGAATACAT	3245	TGCAGGACCCAGAGAAATCGAATACAT	3485
GGCCACGCHNNHCTAGCGTTAC		GCAGTACNNHCTAGCGTTAC		CTACTTANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3006	TGCAGGACCCAGAGAAATCGAATACAG	3246	TGCAGGACCCAGAGAAATCGAATACAT	3486
CATTCTATNNHCTAGCGTTAC		ACAACCTNNHCTAGCGTTAC		ACCGGTANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	3007	TGCAGGACCCAGAGAAATCGAATACAG	3247	TGCAGGACCCAGAGAAATCGAATACAA	3487
TGATGTANNHCTAGCGTTAC		GAGAGGCHNNHCTAGCGTTAC		ACCTATANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3008	TGCAGGACCCAGAGAAATCGAATACAG	3248	TGCAGGACCCAGAGAAATCGAATACAG	3488
CACCTGCGHNNHCTAGCGTTAC		TAAATGTNNHCTAGCGTTAC		CGACTGCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	3009	TGCAGGACCCAGAGAAATCGAATACAG	3249	TGCAGGACCCAGAGAAATCGAATACAG	3489
CTCCCTANNHCTAGCGTTAC		GCTCACGNNHCTAGCGTTAC		GAGTCTANNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	3010	TGCAGGACCCAGAGAAATCGAATACAA	3250	TGCAGGACCCAGAGAAATCGAATACAT	3490
CAAACCAHNNHCTAGCGTTAC		CGTTTCCHNNHCTAGCGTTAC		ATGAAGCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3011	TGCAGGACCCAGAGAAATCGAATACAT	3251	TGCAGGACCCAGAGAAATCGAATACAA	3491
ATGTACANNHCTAGCGTTAC		GCCAGTANNHCTAGCGTTAC		CTGGCCCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3012	TGCAGGACCCAGAGAAATCGAATACAG	3252	TGCAGGACCCAGAGAAATCGAATACAG	3492
CGGCTCTNNHCTAGCGTTAC		TAAATGTNNHCTAGCGTTAC		AACCATGNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3013	TGCAGGACCCAGAGAAATCGAATACAG	3253	TGCAGGACCCAGAGAAATCGAATACAA	3493
CCATATTNNHCTAGCGTTAC		ACCTACTNNHCTAGCGTTAC		AGGTAGCCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAA	3014	TGCAGGACCCAGAGAAATCGAATACAG	3254	TGCAGGACCCAGAGAAATCGAATACAT	3494
CGACTCGHNNHCTAGCGTTAC		ATTGTATNNHCTAGCGTTAC		TCTCAGCCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3015	TGCAGGACCCAGAGAAATCGAATACAA	3255	TGCAGGACCCAGAGAAATCGAATACAT	3495
AATCTCTHNNHCTAGCGTTAC		ACTACATNNHCTAGCGTTAC		TCAGGTCHNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3016	TGCAGGACCCAGAGAAATCGAATACAG	3256	TGCAGGACCCAGAGAAATCGAATACAG	3496
AAATCTTNNHCTAGCGTTAC		CGTTGAHNNHCTAGCGTTAC		CAATCCCTNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3017	TGCAGGACCCAGAGAAATCGAATACAT	3257	TGCAGGACCCAGAGAAATCGAATACAG	3497
CACCTAGANNHCTAGCGTTAC		AATATTANNHCTAGCGTTAC		ACAGTTCTNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAT	3018	TGCAGGACCCAGAGAAATCGAATACAG	3258	TGCAGGACCCAGAGAAATCGAATACAA	3498
TTGCCACCHNNHCTAGCGTTAC		GTTTAATNNHCTAGCGTTAC		TCTTTACNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3019	TGCAGGACCCAGAGAAATCGAATACAG	3259	TGCAGGACCCAGAGAAATCGAATACAG	3499
AACTCTTNNHCTAGCGTTAC		CCACCTTNNHCTAGCGTTAC		CARTATTNNHCTAGCGTTAC	
TGCAGGACCCAGAGAAATCGAATACAG	3020	TGCAGGACCCAGAGAAATCGAATACAG	3260	TGCAGGACCCAGAGAAATCGAATACAG	3500
TGATGTCTNNHCTAGCGTTAC		TACTCTGNNHCTAGCGTTAC		TCTCCATNNHCTAGCGTTAC	

图16D

池 -13	SEQ ID NO:	池 -14	SEQ ID NO:	池 -15	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATACATCGATGTGNNNGATCGACATG	3021	TGCAGGACCCAGAGAATTGGAATACAAATCGGTCAANNNGATCGACATG	3261	TGCAGGACCCAGAGAATTGGAATACACAAACATANNNGATCGACATG	3501
TGCAGGACCCAGAGAATTGGAATACATGTACACGNNNGATCGACATG	3022	TGCAGGACCCAGAGAATTGGAATACAAACATGTNNNGATCGACATG	3262	TGCAGGACCCAGAGAATTGGAATACATCGTAGACNNNGATCGACATG	3502
TGCAGGACCCAGAGAATTGGAATACATCTTTAGTNNNGATCGACATG	3023	TGCAGGACCCAGAGAATTGGAATACACCTGTTGNNNGATCGACATG	3263	TGCAGGACCCAGAGAATTGGAATACAGTAGATAANNNGATCGACATG	3503
TGCAGGACCCAGAGAATTGGAATACAGGTAGGCGNNNGATCGACATG	3024	TGCAGGACCCAGAGAATTGGAATACACACAAGCTNNNGATCGACATG	3264	TGCAGGACCCAGAGAATTGGAATACAACAATACNNNGATCGACATG	3504
TGCAGGACCCAGAGAATTGGAATACAACTTTATNNNGATCGACATG	3025	TGCAGGACCCAGAGAATTGGAATACAGATAAGATNNNGATCGACATG	3265	TGCAGGACCCAGAGAATTGGAATACACACGACGCGNNNGATCGACATG	3505
TGCAGGACCCAGAGAATTGGAATACACGTCTATCANNNGATCGACATG	3026	TGCAGGACCCAGAGAATTGGAATACAAACACTCANNNGATCGACATG	3266	TGCAGGACCCAGAGAATTGGAATACACACAAANNNGATCGACATG	3506
TGCAGGACCCAGAGAATTGGAATACAGTAGAATNNNGATCGACATG	3027	TGCAGGACCCAGAGAATTGGAATACACGCCAGANNNGATCGACATG	3267	TGCAGGACCCAGAGAATTGGAATACACGTACCGGNNNGATCGACATG	3507
TGCAGGACCCAGAGAATTGGAATACACGTACCAANNNGATCGACATG	3028	TGCAGGACCCAGAGAATTGGAATACAGGTATTCGNNNGATCGACATG	3268	TGCAGGACCCAGAGAATTGGAATACACACCAATGNNNGATCGACATG	3508
TGCAGGACCCAGAGAATTGGAATACACACACCGNNNGATCGACATG	3029	TGCAGGACCCAGAGAATTGGAATACAACTCGGATNNNGATCGACATG	3269	TGCAGGACCCAGAGAATTGGAATACACGCTCTGCGNNNGATCGACATG	3509
TGCAGGACCCAGAGAATTGGAATACATGCGCGTNNNGATCGACATG	3030	TGCAGGACCCAGAGAATTGGAATACATATATCGANNNGATCGACATG	3270	TGCAGGACCCAGAGAATTGGAATACAGTCACGCTNNNGATCGACATG	3510
TGCAGGACCCAGAGAATTGGAATACAGCCCCCGNNNGATCGACATG	3031	TGCAGGACCCAGAGAATTGGAATACAACTCCATCANNNGATCGACATG	3271	TGCAGGACCCAGAGAATTGGAATACAACTCTTCGNNNGATCGACATG	3511
TGCAGGACCCAGAGAATTGGAATACATAGTAAGANNNGATCGACATG	3032	TGCAGGACCCAGAGAATTGGAATACAGAACTGGANNNGATCGACATG	3272	TGCAGGACCCAGAGAATTGGAATACAAACACGCGNNNGATCGACATG	3512
TGCAGGACCCAGAGAATTGGAATACATCTGPATANNNGATCGACATG	3033	TGCAGGACCCAGAGAATTGGAATACAGATCRAGGNNNGATCGACATG	3273	TGCAGGACCCAGAGAATTGGAATACAAACCGCGCANNNGATCGACATG	3513
TGCAGGACCCAGAGAATTGGAATACACTAATACANNNGATCGACATG	3034	TGCAGGACCCAGAGAATTGGAATACATGGAAGTANNNGATCGACATG	3274	TGCAGGACCCAGAGAATTGGAATACACACCTTTGNNNGATCGACATG	3514
TGCAGGACCCAGAGAATTGGAATACAAATGTCAGNNNGATCGACATG	3035	TGCAGGACCCAGAGAATTGGAATACAGCCAGCCGNNNGATCGACATG	3275	TGCAGGACCCAGAGAATTGGAATACATATGCGGNNNGATCGACATG	3515
TGCAGGACCCAGAGAATTGGAATACAAACAGAAATNNNGATCGACATG	3036	TGCAGGACCCAGAGAATTGGAATACATTTACTGTNNNGATCGACATG	3276	TGCAGGACCCAGAGAATTGGAATACAGACTCTTCNNNGATCGACATG	3516
TGCAGGACCCAGAGAATTGGAATACAGCCAGGTTNNNGATCGACATG	3037	TGCAGGACCCAGAGAATTGGAATACATGTCCAGGTTNNNGATCGACATG	3277	TGCAGGACCCAGAGAATTGGAATACAGAGCTTCGNNNGATCGACATG	3517
TGCAGGACCCAGAGAATTGGAATACAGTTCATGANNNGATCGACATG	3038	TGCAGGACCCAGAGAATTGGAATACACAGCGCTTANNNGATCGACATG	3278	TGCAGGACCCAGAGAATTGGAATACATAGCAATCTNNNGATCGACATG	3518
TGCAGGACCCAGAGAATTGGAATACACCGGTGCGANNNGATCGACATG	3039	TGCAGGACCCAGAGAATTGGAATACATGTGATCGNNNGATCGACATG	3279	TGCAGGACCCAGAGAATTGGAATACACGACCACGNNNGATCGACATG	3519
TGCAGGACCCAGAGAATTGGAATACAGAAATCCGNNNGATCGACATG	3040	TGCAGGACCCAGAGAATTGGAATACAGCTCGTAANNNGATCGACATG	3280	TGCAGGACCCAGAGAATTGGAATACATGGATTTCGNNNGATCGACATG	3520
TGCAGGACCCAGAGAATTGGAATACACAGGCGCANNNGATCGACATG	3041	TGCAGGACCCAGAGAATTGGAATACAACTTACTANNNGATCGACATG	3281	TGCAGGACCCAGAGAATTGGAATACACGACTAGTNNNGATCGACATG	3521
TGCAGGACCCAGAGAATTGGAATACACCTGCGGANNNGATCGACATG	3042	TGCAGGACCCAGAGAATTGGAATACAGATCAGTCNNNGATCGACATG	3282	TGCAGGACCCAGAGAATTGGAATACACCCCAACGNNNGATCGACATG	3522
TGCAGGACCCAGAGAATTGGAATACAGCTAAGGNNNGATCGACATG	3043	TGCAGGACCCAGAGAATTGGAATACAGGATTATTNNNGATCGACATG	3283	TGCAGGACCCAGAGAATTGGAATACATGACCCCGNNNGATCGACATG	3523
TGCAGGACCCAGAGAATTGGAATACATTTAAGGTNNNGATCGACATG	3044	TGCAGGACCCAGAGAATTGGAATACACATTTCGTNNNGATCGACATG	3284	TGCAGGACCCAGAGAATTGGAATACAGCATTAGCNNNGATCGACATG	3524
TGCAGGACCCAGAGAATTGGAATACAAACAGTAAANNNGATCGACATG	3045	TGCAGGACCCAGAGAATTGGAATACAGTACATGCGNNNGATCGACATG	3285	TGCAGGACCCAGAGAATTGGAATACAGCCAGATTNNNGATCGACATG	3525
TGCAGGACCCAGAGAATTGGAATACAAATTTGGTNNNGATCGACATG	3046	TGCAGGACCCAGAGAATTGGAATACAGGTCCAGNNNGATCGACATG	3286	TGCAGGACCCAGAGAATTGGAATACAAACAATAANNNGATCGACATG	3526
TGCAGGACCCAGAGAATTGGAATACAAAGTTAGCNNNGATCGACATG	3047	TGCAGGACCCAGAGAATTGGAATACATATTGTGTCNNNGATCGACATG	3287	TGCAGGACCCAGAGAATTGGAATACAGTAGGTCTNNNGATCGACATG	3527
TGCAGGACCCAGAGAATTGGAATACAAAGTTTGGNNNGATCGACATG	3048	TGCAGGACCCAGAGAATTGGAATACAAACAGTCCANNNGATCGACATG	3288	TGCAGGACCCAGAGAATTGGAATACAAATAAGGTNNNGATCGACATG	3528
TGCAGGACCCAGAGAATTGGAATACAAAGCTTCANNNGATCGACATG	3049	TGCAGGACCCAGAGAATTGGAATACAGCGATTGTNNNGATCGACATG	3289	TGCAGGACCCAGAGAATTGGAATACAAAGAGAAANNNGATCGACATG	3529
TGCAGGACCCAGAGAATTGGAATACAGGACTTGTNNNGATCGACATG	3050	TGCAGGACCCAGAGAATTGGAATACACCTGGATNNNGATCGACATG	3290	TGCAGGACCCAGAGAATTGGAATACATTTTGTGTNNNGATCGACATG	3530
TGCAGGACCCAGAGAATTGGAATACAGGTACGATNNNGATCGACATG	3051	TGCAGGACCCAGAGAATTGGAATACAAACGAGCAANNNGATCGACATG	3291	TGCAGGACCCAGAGAATTGGAATACAAAGCGTTTNNNGATCGACATG	3531
TGCAGGACCCAGAGAATTGGAATACACACAGAGANNNGATCGACATG	3052	TGCAGGACCCAGAGAATTGGAATACCAACCAACNNNGATCGACATG	3292	TGCAGGACCCAGAGAATTGGAATACCAAAAGGTANNNGATCGACATG	3532
TGCAGGACCCAGAGAATTGGAATACAGCGATCTANNNGATCGACATG	3053	TGCAGGACCCAGAGAATTGGAATACATTTAGTCTNNNGATCGACATG	3293	TGCAGGACCCAGAGAATTGGAATACCAACCGGATTNNNGATCGACATG	3533

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池-13	SEQ ID No.	池-14	SEQ ID No.	池-15	SEQ ID No.
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TCACCGANNNGATCGACATG	3054	GTAGCTGNNNGATCGACATG	3294	TCAAATANNNGATCGACATG	3534
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
CACTAATNNNGATCGACATG	3055	GCTTACANNNGATCGACATG	3295	CGAACANNNGATCGACATG	3535
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TATGAGANNNGATCGACATG	3056	GAACGACNNNGATCGACATG	3296	CCAGGACNNNGATCGACATG	3536
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GTAGCGNNNGATCGACATG	3057	CCAAAGNNNGATCGACATG	3297	CMGCTCANNNGATCGACATG	3537
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
AGCGTATNNNGATCGACATG	3058	GAGGTANNNGATCGACATG	3298	TATACATGNNNGATCGACATG	3538
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GACATGNNNGATCGACATG	3059	AGTCAAGNNNGATCGACATG	3299	ATAAGTGNNGATCGACATG	3539
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
CGCAACNNNGATCGACATG	3060	GAACACANNNGATCGACATG	3300	ATACTTANNNGATCGACATG	3540
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TTTTCGANNNGATCGACATG	3061	GAACACANNNGATCGACATG	3301	TCAATACNNNGATCGACATG	3541
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TACCCGNNNGATCGACATG	3062	AGTAATGNNNGATCGACATG	3302	GCTACGNNNGATCGACATG	3542
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TAACTGCTNNNGATCGACATG	3063	CCACGGTNNNGATCGACATG	3303	TAGCTTCNNNGATCGACATG	3543
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
AGCGTGNNGATCGACATG	3064	TGCGTTGNNNGATCGACATG	3304	CGGATANNNGATCGACATG	3544
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
CAACGTCANNNGATCGACATG	3065	AGCGGCANNNGATCGACATG	3305	AGCCGCANNNGATCGACATG	3545
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TAACTGNNNGATCGACATG	3066	GCGTGCANNNGATCGACATG	3306	ATCCTCTNNNGATCGACATG	3546
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACAPACNNNGATCGACATG	3067	GCTCAAGNNNGATCGACATG	3307	GTACCCANNNGATCGACATG	3547
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACATGGCANNNGATCGACATG	3068	GAACGCANNNGATCGACATG	3308	CCGGATANNNGATCGACATG	3548
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GTGTCANNNGATCGACATG	3069	CATGCGNNNGATCGACATG	3309	TAAAGTNNNGATCGACATG	3549
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TTTAACTNNNGATCGACATG	3070	GTCTAGNNNGATCGACATG	3310	AGGTTGNNNGATCGACATG	3550
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TAAAGTNNNGATCGACATG	3071	GCTGATNNNGATCGACATG	3311	TAGACGNNNGATCGACATG	3551
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
AATAGCGNNNGATCGACATG	3072	IAGTCCNNNGATCGACATG	3312	CTCGTTNNNGATCGACATG	3552
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
AATTAATNNNGATCGACATG	3073	GGCATGNNNGATCGACATG	3313	AATCTTNNNGATCGACATG	3553
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TCTTGTGNNNGATCGACATG	3074	ACGGTGGNNNGATCGACATG	3314	AGCAACTNNNGATCGACATG	3554
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GCCTGNNNGATCGACATG	3075	CGCTTTNNNGATCGACATG	3315	CACCTACNNNGATCGACATG	3555
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACGAAACNNNGATCGACATG	3076	GTGGACNNNGATCGACATG	3316	TAAATGNNNGATCGACATG	3556
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GTCTAGGNNNGATCGACATG	3077	TGCTTTNNNGATCGACATG	3317	TAATTTATNNNGATCGACATG	3557
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TAGCCTANNNGATCGACATG	3078	GAAGCGNNNGATCGACATG	3318	ACGAGACNNNGATCGACATG	3558
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TTCCCTGNNNGATCGACATG	3079	CGTGCGANNNGATCGACATG	3319	TCGGCATNNNGATCGACATG	3559
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACGAAATNNNGATCGACATG	3080	ACAACATNNNGATCGACATG	3320	CACACCGNNNGATCGACATG	3560
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACCCGCCNNNGATCGACATG	3081	TTACTCTNNNGATCGACATG	3321	GCCAGGANNNGATCGACATG	3561
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
TATGATANNNGATCGACATG	3082	TTCCCTANNNGATCGACATG	3322	AGGAGTTNNNGATCGACATG	3562
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACATGATNNNGATCGACATG	3083	ACACGGCNNNGATCGACATG	3323	CACCGCTNNNGATCGACATG	3563
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
GTACATANNNGATCGACATG	3084	AGAATTCNNNGATCGACATG	3324	CGATGAGNNNGATCGACATG	3564
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ACGAAANNNGATCGACATG	3085	TTCAGGNNNGATCGACATG	3325	TAGCATANNNGATCGACATG	3565
TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA		TGCAGGACCCAGAGAATTCGAATACAA	
ATACATANNNGATCGACATG	3086	TTACTTNNNGATCGACATG	3326	GTCCGANNNGATCGACATG	3566

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池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATACAG	3087	TGCAGGACCCAGAGAAATTCGAATACAA	3327	TGCAGGACCCAGAGAAATTCGAATACAA	3567
GAGAAATCCTGTTGCAATCAGGT		CTTACCTGTTGCAATCAGGT		GGCTGTTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3088	TGCAGGACCCAGAGAAATTCGAATACAG	3328	TGCAGGACCCAGAGAAATTCGAATACAT	3568
CTTGTGCTGTTGCAATCAGGT		AGTTCTGTTGTTGCAATCAGGT		CACTCATCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3089	TGCAGGACCCAGAGAAATTCGAATACAT	3329	TGCAGGACCCAGAGAAATTCGAATACAC	3569
AAGCGCTGTTGCAATCAGGT		TTCCAATGTTGTTGCAATCAGGT		TGCTTCATGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3090	TGCAGGACCCAGAGAAATTCGAATACAA	3330	TGCAGGACCCAGAGAAATTCGAATACAA	3570
CTTGAAGTTGTTGCAATCAGGT		TAAGTTGTTGTTGCAATCAGGT		CCGCGAAGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3091	TGCAGGACCCAGAGAAATTCGAATACAA	3331	TGCAGGACCCAGAGAAATTCGAATACAC	3571
TGCTTCTGTTGCAATCAGGT		ATCTATGTTGTTGCAATCAGGT		TCCGACGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3092	TGCAGGACCCAGAGAAATTCGAATACAG	3332	TGCAGGACCCAGAGAAATTCGAATACAT	3572
AGCGATGTTGCAATCAGGT		TCCAGGTTGTTGCAATCAGGT		ACGCGATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3093	TGCAGGACCCAGAGAAATTCGAATACAT	3333	TGCAGGACCCAGAGAAATTCGAATACAT	3573
AGGAGCTGTTGCAATCAGGT		CGACCAATGTTGCAATCAGGT		TTAGTAGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3094	TGCAGGACCCAGAGAAATTCGAATACAC	3334	TGCAGGACCCAGAGAAATTCGAATACAA	3574
ATCGCTTCTGTTGCAATCAGGT		TGCATAGTTGTTGCAATCAGGT		GGCAAGGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3095	TGCAGGACCCAGAGAAATTCGAATACAA	3335	TGCAGGACCCAGAGAAATTCGAATACAG	3575
CGCGTCTGTTGCAATCAGGT		CTTCCAGTTGTTGCAATCAGGT		CGCGCAATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAC	3096	TGCAGGACCCAGAGAAATTCGAATACAT	3336	TGCAGGACCCAGAGAAATTCGAATACAG	3576
TCAAGGTTGTTGCAATCAGGT		TAGATCTGTTGTTGCAATCAGGT		TGCTTGGCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3097	TGCAGGACCCAGAGAAATTCGAATACAC	3337	TGCAGGACCCAGAGAAATTCGAATACAA	3577
GTACGCTGTTGCAATCAGGT		ATTGCGAATGTTGCAATCAGGT		TACCTATGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3098	TGCAGGACCCAGAGAAATTCGAATACAC	3338	TGCAGGACCCAGAGAAATTCGAATACAC	3578
CTAGGCTGTTGCAATCAGGT		AGCAGATGTTGTTGCAATCAGGT		CACGCTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3099	TGCAGGACCCAGAGAAATTCGAATACAC	3339	TGCAGGACCCAGAGAAATTCGAATACAT	3579
GGCGTATGTTGCAATCAGGT		CCGCGAATGTTGCAATCAGGT		GAAGTGGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3100	TGCAGGACCCAGAGAAATTCGAATACAA	3340	TGCAGGACCCAGAGAAATTCGAATACAG	3580
AGATCTGTTGTTGCAATCAGGT		CAGATCTGTTGTTGCAATCAGGT		AGTTGTTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3101	TGCAGGACCCAGAGAAATTCGAATACAT	3341	TGCAGGACCCAGAGAAATTCGAATACAG	3581
GAUUAATGTTGCAATCAGGT		GGCTATGTTGTTGCAATCAGGT		CCGCGTTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3102	TGCAGGACCCAGAGAAATTCGAATACAA	3342	TGCAGGACCCAGAGAAATTCGAATACAC	3582
CCAGACCTGTTGCAATCAGGT		CRGGAGTTGTTGCAATCAGGT		AGATAGGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3103	TGCAGGACCCAGAGAAATTCGAATACAC	3343	TGCAGGACCCAGAGAAATTCGAATACAA	3583
CTGCACTGTTGCAATCAGGT		ATCCATGTTGTTGCAATCAGGT		AGTCCGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3104	TGCAGGACCCAGAGAAATTCGAATACAC	3344	TGCAGGACCCAGAGAAATTCGAATACAA	3584
TGCGACTGTTGCAATCAGGT		TACGCTGTTGTTGCAATCAGGT		ATCAGAAATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3105	TGCAGGACCCAGAGAAATTCGAATACAG	3345	TGCAGGACCCAGAGAAATTCGAATACAC	3585
TACGCAATGTTGCAATCAGGT		ACCTCAATGTTGCAATCAGGT		ACTCAGATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3106	TGCAGGACCCAGAGAAATTCGAATACAT	3346	TGCAGGACCCAGAGAAATTCGAATACAT	3586
AGCTATGTTGCAATCAGGT		CCCACGTTGTTGCAATCAGGT		TATTCGATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3107	TGCAGGACCCAGAGAAATTCGAATACAC	3347	TGCAGGACCCAGAGAAATTCGAATACAA	3587
GGCTATGTTGCAATCAGGT		ATTCGCTGTTGTTGCAATCAGGT		ACTAACATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3108	TGCAGGACCCAGAGAAATTCGAATACAG	3348	TGCAGGACCCAGAGAAATTCGAATACAT	3588
CGGAGTCTGTTGCAATCAGGT		ATCTGGTCTGTTGCAATCAGGT		TGTGCTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAC	3109	TGCAGGACCCAGAGAAATTCGAATACAT	3349	TGCAGGACCCAGAGAAATTCGAATACAA	3589
GGCTTCTGTTGCAATCAGGT		ATCGTTTCTGTTGCAATCAGGT		AGAGTCTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3110	TGCAGGACCCAGAGAAATTCGAATACAG	3350	TGCAGGACCCAGAGAAATTCGAATACAA	3590
CAGGTGTTGTTGCAATCAGGT		GATTCGTTGTTGCAATCAGGT		GGCTGTTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3111	TGCAGGACCCAGAGAAATTCGAATACAC	3351	TGCAGGACCCAGAGAAATTCGAATACAA	3591
GGCGCTGTTGCAATCAGGT		CGCATCTGTTGTTGCAATCAGGT		TATTCAGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3112	TGCAGGACCCAGAGAAATTCGAATACAG	3352	TGCAGGACCCAGAGAAATTCGAATACAA	3592
TGTGTCTGTTGCAATCAGGT		ACTAAATGTTGCAATCAGGT		TATATTTGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3113	TGCAGGACCCAGAGAAATTCGAATACAG	3353	TGCAGGACCCAGAGAAATTCGAATACAG	3593
TTTGGAGTTGTTGCAATCAGGT		TGGATGTTGTTGCAATCAGGT		TCAAGACCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3114	TGCAGGACCCAGAGAAATTCGAATACAC	3354	TGCAGGACCCAGAGAAATTCGAATACAA	3594
GGCCACTGTTGCAATCAGGT		CGTTTACGTTGTTGCAATCAGGT		GACGACCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAA	3115	TGCAGGACCCAGAGAAATTCGAATACAG	3355	TGCAGGACCCAGAGAAATTCGAATACAA	3595
ACACTGCTGTTGCAATCAGGT		ATTATCTGTTGTTGCAATCAGGT		GGCAGGCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3116	TGCAGGACCCAGAGAAATTCGAATACAC	3356	TGCAGGACCCAGAGAAATTCGAATACAA	3596
CGCGCTGTTGCAATCAGGT		ACTCGAATGTTGCAATCAGGT		CTTATAGTTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAG	3117	TGCAGGACCCAGAGAAATTCGAATACAG	3357	TGCAGGACCCAGAGAAATTCGAATACAC	3597
TAGCATCTGTTGCAATCAGGT		AACGTTCTGTTGCAATCAGGT		TACTAAATGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3118	TGCAGGACCCAGAGAAATTCGAATACAA	3358	TGCAGGACCCAGAGAAATTCGAATACAT	3598
GCAGCATGTTGCAATCAGGT		CCCGCAGTTGTTGCAATCAGGT		TTCAGTCTGTTGCAATCAGGT	
TGCAGGACCCAGAGAAATTCGAATACAT	3119	TGCAGGACCCAGAGAAATTCGAATACAG	3359	TGCAGGACCCAGAGAAATTCGAATACAC	3599
GCAGACTGTTGCAATCAGGT		TCTCTGTTGTTGCAATCAGGT		TGCTTCATGTTGCAATCAGGT	

图16G

池-13	SEQ ID NO:	池-14	SEQ ID NO:	池-15	SEQ ID NO:
TGCAGGACACAGAAATTCGAATACAA ACATGCGNNNTGCATCAGGT	3120	TGCAGGACACAGAAATTCGAATACAA TTGATCANNNTGCATCAGGT	3360	TGCAGGACACAGAAATTCGAATACAA GGTTGTGNNNTGCATCAGGT	3600
TGCAGGACACAGAAATTCGAATACAA ACATATCNNNTGCATCAGGT	3121	TGCAGGACACAGAAATTCGAATACAA AGTTTACHNNTGCATCAGGT	3361	TGCAGGACACAGAAATTCGAATACAA GTAGGTGNNNTGCATCAGGT	3601
TGCAGGACACAGAAATTCGAATACAA GGAAACGNNNTGCATCAGGT	3122	TGCAGGACACAGAAATTCGAATACAA GTTGTANNNTGCATCAGGT	3362	TGCAGGACACAGAAATTCGAATACAA CCGATAANNNTGCATCAGGT	3602
TGCAGGACACAGAAATTCGAATACAA GCTVTGNNNTGCATCAGGT	3123	TGCAGGACACAGAAATTCGAATACAA TCTCAACNNNTGCATCAGGT	3363	TGCAGGACACAGAAATTCGAATACAA AGAGTGNNNTGCATCAGGT	3603
TGCAGGACACAGAAATTCGAATACAA CTCCTGTNNNTGCATCAGGT	3124	TGCAGGACACAGAAATTCGAATACAA ACGGCCGNNNTGCATCAGGT	3364	TGCAGGACACAGAAATTCGAATACAA TTCGCTTNNNTGCATCAGGT	3604
TGCAGGACACAGAAATTCGAATACAA AACGTGNNNTGCATCAGGT	3125	TGCAGGACACAGAAATTCGAATACAA ATGGTAANNNTGCATCAGGT	3365	TGCAGGACACAGAAATTCGAATACAA TTATCANNNTGCATCAGGT	3605
TGCAGGACACAGAAATTCGAATACAA GTCCCTAANNNTGCATCAGGT	3126	TGCAGGACACAGAAATTCGAATACAA ACAACCGNNNTGCATCAGGT	3366	TGCAGGACACAGAAATTCGAATACAA CATGCTCHNNTGCATCAGGT	3606
TGCAGGACACAGAAATTCGAATACAA ATCGCTGNNNTGCATCAGGT	3127	TGCAGGACACAGAAATTCGAATACAA TACGCTCHNNTGCATCAGGT	3367	TGCAGGACACAGAAATTCGAATACAA ACGTAAANNNTGCATCAGGT	3607
TGCAGGACACAGAAATTCGAATACAA AAGCATGNNNTGCATCAGGT	3128	TGCAGGACACAGAAATTCGAATACAA GCGCTGNNNTGCATCAGGT	3368	TGCAGGACACAGAAATTCGAATACAA CATTTCCNNNTGCATCAGGT	3608

图16H

池-16	SEQ ID NO.	池-17	SEQ ID NO.	池-18	SEQ ID NO.
TGCAGGAC CAGAGAA TCGAATACAA	3809	TGCAGGAC CAGAGAA TCGAATACAA	3849	TGCAGGAC CAGAGAA TCGAATACAA	4089
GATTCAGNNNACGTATGCCA		TTCCGCGNNNACGTATGCCA		CCAGACANNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3810	TGCAGGAC CAGAGAA TCGAATACAA	3850	TGCAGGAC CAGAGAA TCGAATACAA	4090
CAAGTAANNNACGTATGCCA		CCCGAGANNNACGTATGCCA		GCTAATGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3811	TGCAGGAC CAGAGAA TCGAATACAA	3851	TGCAGGAC CAGAGAA TCGAATACAA	4091
TCAGTGTNNNACGTATGCCA		GCAGACGNNNACGTATGCCA		ACGTCGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3812	TGCAGGAC CAGAGAA TCGAATACAA	3852	TGCAGGAC CAGAGAA TCGAATACAA	4092
TTCCGTCNNNACGTATGCCA		GATACGTNNNACGTATGCCA		TTCCGTGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3813	TGCAGGAC CAGAGAA TCGAATACAA	3853	TGCAGGAC CAGAGAA TCGAATACAA	4093
GCACACANNNACGTATGCCA		CTCGCTANNNACGTATGCCA		TACAGGTCNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3814	TGCAGGAC CAGAGAA TCGAATACAA	3854	TGCAGGAC CAGAGAA TCGAATACAA	4094
GGCGCTNNNACGTATGCCA		ATTACAGNNNACGTATGCCA		CCCGTTGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3815	TGCAGGAC CAGAGAA TCGAATACAA	3855	TGCAGGAC CAGAGAA TCGAATACAA	4095
GCTTACGNNNACGTATGCCA		TTCCGACNNNACGTATGCCA		TAGGCTCNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3816	TGCAGGAC CAGAGAA TCGAATACAA	3856	TGCAGGAC CAGAGAA TCGAATACAA	4096
GCAGGACNNNACGTATGCCA		TTCCGCTNNNACGTATGCCA		CCAAATTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3817	TGCAGGAC CAGAGAA TCGAATACAA	3857	TGCAGGAC CAGAGAA TCGAATACAA	4097
AGGCTTNNNACGTATGCCA		CAATTGANNNACGTATGCCA		TCCGACGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3818	TGCAGGAC CAGAGAA TCGAATACAA	3858	TGCAGGAC CAGAGAA TCGAATACAA	4098
ATTGATTNNNACGTATGCCA		GCAGCGNNNACGTATGCCA		TGTAGTGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3819	TGCAGGAC CAGAGAA TCGAATACAA	3859	TGCAGGAC CAGAGAA TCGAATACAA	4099
AACTCAANNNACGTATGCCA		TTCCGATGNNNACGTATGCCA		ACGCTCANNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3820	TGCAGGAC CAGAGAA TCGAATACAA	3860	TGCAGGAC CAGAGAA TCGAATACAA	4100
TCAGGATGNNNACGTATGCCA		ACGACANNNACGTATGCCA		AGGCGTCNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3821	TGCAGGAC CAGAGAA TCGAATACAA	3861	TGCAGGAC CAGAGAA TCGAATACAA	4101
AGCTCAANNNACGTATGCCA		CAACCATNNNACGTATGCCA		TTGCTTANNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3822	TGCAGGAC CAGAGAA TCGAATACAA	3862	TGCAGGAC CAGAGAA TCGAATACAA	4102
TTGCTTANNNACGTATGCCA		AAAGTCCNNNACGTATGCCA		TTCCGTANNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3823	TGCAGGAC CAGAGAA TCGAATACAA	3863	TGCAGGAC CAGAGAA TCGAATACAA	4103
GAAGGAGNNNACGTATGCCA		CAGCTGTNNNACGTATGCCA		AGACGTCNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3824	TGCAGGAC CAGAGAA TCGAATACAA	3864	TGCAGGAC CAGAGAA TCGAATACAA	4104
TCACATGNNNACGTATGCCA		CCCACTGNNNACGTATGCCA		GGACCTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3825	TGCAGGAC CAGAGAA TCGAATACAA	3865	TGCAGGAC CAGAGAA TCGAATACAA	4105
CGCTCGANNNACGTATGCCA		TTCCGTAGNNNACGTATGCCA		TGCGTAGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3826	TGCAGGAC CAGAGAA TCGAATACAA	3866	TGCAGGAC CAGAGAA TCGAATACAA	4106
ACMAATTNNNACGTATGCCA		TTTCATGNNNACGTATGCCA		CCCGATGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3827	TGCAGGAC CAGAGAA TCGAATACAA	3867	TGCAGGAC CAGAGAA TCGAATACAA	4107
CGTGCAGNNNACGTATGCCA		AATCTAGNNNACGTATGCCA		ACCTCTGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3828	TGCAGGAC CAGAGAA TCGAATACAA	3868	TGCAGGAC CAGAGAA TCGAATACAA	4108
AATCTAGNNNACGTATGCCA		CCCGTAGNNNACGTATGCCA		CTACACNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3829	TGCAGGAC CAGAGAA TCGAATACAA	3869	TGCAGGAC CAGAGAA TCGAATACAA	4109
TCAGGAC CAGAGAA TCGAATACAA		GTGCTGNNNACGTATGCCA		CCCGCTGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3830	TGCAGGAC CAGAGAA TCGAATACAA	3870	TGCAGGAC CAGAGAA TCGAATACAA	4110
TCAGGAC CAGAGAA TCGAATACAA		GACAGCTNNNACGTATGCCA		ATCCAGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3831	TGCAGGAC CAGAGAA TCGAATACAA	3871	TGCAGGAC CAGAGAA TCGAATACAA	4111
ATTGAGCNNNACGTATGCCA		TCAGGAC CAGAGAA TCGAATACAA		AGTCGAGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3832	TGCAGGAC CAGAGAA TCGAATACAA	3872	TGCAGGAC CAGAGAA TCGAATACAA	4112
TCAGGAC CAGAGAA TCGAATACAA		AGTAAATTNNNACGTATGCCA		CCAGCCTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3833	TGCAGGAC CAGAGAA TCGAATACAA	3873	TGCAGGAC CAGAGAA TCGAATACAA	4113
TTCCGCGNNNACGTATGCCA		TGCAGGAC CAGAGAA TCGAATACAA		TATACAGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3834	TGCAGGAC CAGAGAA TCGAATACAA	3874	TGCAGGAC CAGAGAA TCGAATACAA	4114
TTGACGANNNACGTATGCCA		TTGACGANNNACGTATGCCA		CCGTCGTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3835	TGCAGGAC CAGAGAA TCGAATACAA	3875	TGCAGGAC CAGAGAA TCGAATACAA	4115
GGAGATGNNNACGTATGCCA		CTCTTTCNNNACGTATGCCA		BAATTAAANNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3836	TGCAGGAC CAGAGAA TCGAATACAA	3876	TGCAGGAC CAGAGAA TCGAATACAA	4116
CAACCCGNNNACGTATGCCA		CACAGGNNNACGTATGCCA		TCATCAINNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3837	TGCAGGAC CAGAGAA TCGAATACAA	3877	TGCAGGAC CAGAGAA TCGAATACAA	4117
TCAGGAC CAGAGAA TCGAATACAA		CCCCAGTNNNACGTATGCCA		ATGTAATTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3838	TGCAGGAC CAGAGAA TCGAATACAA	3878	TGCAGGAC CAGAGAA TCGAATACAA	4118
AGACCCGNNNACGTATGCCA		ATTGATTNNNACGTATGCCA		TTGTTATTNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3839	TGCAGGAC CAGAGAA TCGAATACAA	3879	TGCAGGAC CAGAGAA TCGAATACAA	4119
AGGATACTNNNACGTATGCCA		CTTCACTNNNACGTATGCCA		GTATCGGNNNACGTATGCCA	
TGCAGGAC CAGAGAA TCGAATACAA	3840	TGCAGGAC CAGAGAA TCGAATACAA	3880	TGCAGGAC CAGAGAA TCGAATACAA	4120
GGTAAATTNNNACGTATGCCA		TCGTTTANNNACGTATGCCA		GAGGTTGNNNACGTATGCCA	

图17A

池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATACAG	3641	TGCAGGACCCAGAGAATTGGAATACAT	3881	TGCAGGACCCAGAGAATTGGAATACAG	4121
CCCCAGGNNNACGTATGCCA		ACGTGACNNNACGTATGCCA		CACAGAGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3642	TGCAGGACCCAGAGAATTGGAATACAT	3882	TGCAGGACCCAGAGAATTGGAATACAA	4122
TGCTTGNNNACGTATGCCA		GTGGTGNNNACGTATGCCA		ACCCGCGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3643	TGCAGGACCCAGAGAATTGGAATACAG	3883	TGCAGGACCCAGAGAATTGGAATACAT	4123
CACGCGCNNNACGTATGCCA		ATCACAGNNNACGTATGCCA		GTGGCTANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3644	TGCAGGACCCAGAGAATTGGAATACAA	3884	TGCAGGACCCAGAGAATTGGAATACAG	4124
CGACCTANNNACGTATGCCA		AGCGCGNNNACGTATGCCA		TAGCTCANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3645	TGCAGGACCCAGAGAATTGGAATACAA	3885	TGCAGGACCCAGAGAATTGGAATACAG	4125
TTAGAAAGNNNACGTATGCCA		ATGTGAANNNACGTATGCCA		GCTGGCINNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3646	TGCAGGACCCAGAGAATTGGAATACAG	3886	TGCAGGACCCAGAGAATTGGAATACAT	4126
CCGTACGNNNACGTATGCCA		TAGCCGCGNNNACGTATGCCA		ACAGCTGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3647	TGCAGGACCCAGAGAATTGGAATACAT	3887	TGCAGGACCCAGAGAATTGGAATACAG	4127
AGAAAGCINNACGTATGCCA		GTGAATTNNNACGTATGCCA		TTGTGTNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3648	TGCAGGACCCAGAGAATTGGAATACAG	3888	TGCAGGACCCAGAGAATTGGAATACAA	4128
CACCTTAHNNNACGTATGCCA		GGTAAGANNNACGTATGCCA		GCATCGTNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3649	TGCAGGACCCAGAGAATTGGAATACAT	3889	TGCAGGACCCAGAGAATTGGAATACAA	4129
AGGATTANNNACGTATGCCA		CTGGTGANNNACGTATGCCA		ATAAAGCINNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3650	TGCAGGACCCAGAGAATTGGAATACAG	3890	TGCAGGACCCAGAGAATTGGAATACAG	4130
TCCGATTNNNACGTATGCCA		TCCGTTNNNACGTATGCCA		TATCGGANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3651	TGCAGGACCCAGAGAATTGGAATACAG	3891	TGCAGGACCCAGAGAATTGGAATACAG	4131
ACCTCGTNNNACGTATGCCA		CGTCGAGNNNACGTATGCCA		CGCCGCGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3652	TGCAGGACCCAGAGAATTGGAATACAT	3892	TGCAGGACCCAGAGAATTGGAATACAT	4132
TTGCTGCNNNACGTATGCCA		CGATCGTNNNACGTATGCCA		CGTTTCGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAT	3653	TGCAGGACCCAGAGAATTGGAATACAT	3893	TGCAGGACCCAGAGAATTGGAATACAG	4133
TCCTTGCGNNNACGTATGCCA		TTGCGTNNNACGTATGCCA		CTAGCAANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAT	3654	TGCAGGACCCAGAGAATTGGAATACAG	3894	TGCAGGACCCAGAGAATTGGAATACAT	4134
TGGCTCTNNNACGTATGCCA		TGGGCTCINNACGTATGCCA		GAACATTNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3655	TGCAGGACCCAGAGAATTGGAATACAT	3895	TGCAGGACCCAGAGAATTGGAATACAT	4135
GGAGCTAHNNNACGTATGCCA		CCACGCGCINNACGTATGCCA		GTACATNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3656	TGCAGGACCCAGAGAATTGGAATACAA	3896	TGCAGGACCCAGAGAATTGGAATACAG	4136
ATACITGNNNACGTATGCCA		CGTGCCGNNNACGTATGCCA		TCCGAJNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3657	TGCAGGACCCAGAGAATTGGAATACAT	3897	TGCAGGACCCAGAGAATTGGAATACAG	4137
CTCTTAGNNNACGTATGCCA		GTGGTACHNNNACGTATGCCA		TTGCGCGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3658	TGCAGGACCCAGAGAATTGGAATACAA	3898	TGCAGGACCCAGAGAATTGGAATACAG	4138
CAACCTGNNNACGTATGCCA		GCCGAANNNACGTATGCCA		CGATAGANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAT	3659	TGCAGGACCCAGAGAATTGGAATACAG	3899	TGCAGGACCCAGAGAATTGGAATACAT	4139
CGTGCGCINNACGTATGCCA		TGCTTAACHNNNACGTATGCCA		TACGTANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3660	TGCAGGACCCAGAGAATTGGAATACAG	3900	TGCAGGACCCAGAGAATTGGAATACAG	4140
ACCTCTHNNNACGTATGCCA		AAGCGCGCINNACGTATGCCA		CTTATANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAT	3661	TGCAGGACCCAGAGAATTGGAATACAG	3901	TGCAGGACCCAGAGAATTGGAATACAA	4141
ATAPACINNACGTATGCCA		GTTCACNNNACGTATGCCA		AACAGANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAT	3662	TGCAGGACCCAGAGAATTGGAATACAG	3902	TGCAGGACCCAGAGAATTGGAATACAT	4142
GACCCCTAHNNNACGTATGCCA		AGATGTGNNNACGTATGCCA		ACCCATCINNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3663	TGCAGGACCCAGAGAATTGGAATACAG	3903	TGCAGGACCCAGAGAATTGGAATACAA	4143
AGAUGAANNNACGTATGCCA		CTCACCTNNNACGTATGCCA		AAAGAGANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3664	TGCAGGACCCAGAGAATTGGAATACAG	3904	TGCAGGACCCAGAGAATTGGAATACAG	4144
GGAAATGANNNACGTATGCCA		GAAGCTINNACGTATGCCA		GTTCGANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3665	TGCAGGACCCAGAGAATTGGAATACAT	3905	TGCAGGACCCAGAGAATTGGAATACAA	4145
GTGATGANNNACGTATGCCA		ACTCGAGNNNACGTATGCCA		TGGATCINNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3666	TGCAGGACCCAGAGAATTGGAATACAT	3906	TGCAGGACCCAGAGAATTGGAATACAG	4146
ACCTCTAHNNNACGTATGCCA		TCCTTGANNNACGTATGCCA		CTCGATTANNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3667	TGCAGGACCCAGAGAATTGGAATACAG	3907	TGCAGGACCCAGAGAATTGGAATACAT	4147
CTGGCTACHNNNACGTATGCCA		AAGRAAGNNNACGTATGCCA		GTAAACGNNNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAG	3668	TGCAGGACCCAGAGAATTGGAATACAA	3908	TGCAGGACCCAGAGAATTGGAATACAA	4148
CAAATCCINNACGTATGCCA		GGCACGCGNNNACGTATGCCA		TGTACTINNACGTATGCCA	
TGCAGGACCCAGAGAATTGGAATACAA	3669	TGCAGGACCCAGAGAATTGGAATACAG	3909	TGCAGGACCCAGAGAATTGGAATACAG	4149
ATATAANNNNCTAGCGTTAC		LATACGGNNNCTAGCGTTAC		ATCGTACNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	3670	TGCAGGACCCAGAGAATTGGAATACAA	3910	TGCAGGACCCAGAGAATTGGAATACAT	4150
GGTTATANNNCTAGCGTTAC		GATCTTANNNCTAGCGTTAC		GAACGTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3671	TGCAGGACCCAGAGAATTGGAATACAA	3911	TGCAGGACCCAGAGAATTGGAATACAT	4151
CCCGCTCHNNNCTAGCGTTAC		CAACCCANNNCTAGCGTTAC		CCAACTCINNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAT	3672	TGCAGGACCCAGAGAATTGGAATACAT	3912	TGCAGGACCCAGAGAATTGGAATACAG	4152
GGCAAGNNNCTAGCGTTAC		GCTAACGNNNCTAGCGTTAC		CGGAGGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAG	3673	TGCAGGACCCAGAGAATTGGAATACAT	3913	TGCAGGACCCAGAGAATTGGAATACAT	4153
GTCTGCCNNNCTAGCGTTAC		GTAGTCGNNNCTAGCGTTAC		GCCCATNNNCTAGCGTTAC	

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATACAA	3674	TGCAGGACCCAGAGAATTGGAATACAA	3914	TGCAGGACCCAGAGAATTGGAATACAA	4154
GTGTATNNNNCTAGCGTTAC		TGGTGTNNNNCTAGCGTTAC		CGATCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3675	TGCAGGACCCAGAGAATTGGAATACAA	3915	TGCAGGACCCAGAGAATTGGAATACAA	4155
GTCTACTANNNNCTAGCGTTAC		GTAGGACNNNNCTAGCGTTAC		TAGGTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3676	TGCAGGACCCAGAGAATTGGAATACAA	3916	TGCAGGACCCAGAGAATTGGAATACAA	4156
CACCATANNNNCTAGCGTTAC		AAAAAANNNNCTAGCGTTAC		CCCTACGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3677	TGCAGGACCCAGAGAATTGGAATACAA	3917	TGCAGGACCCAGAGAATTGGAATACAA	4157
TTCAGGNNNNCTAGCGTTAC		GTTCATANNNNCTAGCGTTAC		ACACCAANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3678	TGCAGGACCCAGAGAATTGGAATACAA	3918	TGCAGGACCCAGAGAATTGGAATACAA	4158
TTTGTGNNNNCTAGCGTTAC		TAGGTGANNNNCTAGCGTTAC		GGTCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3679	TGCAGGACCCAGAGAATTGGAATACAA	3919	TGCAGGACCCAGAGAATTGGAATACAA	4159
TTTGGCANNNNCTAGCGTTAC		GNATGCCNNNNCTAGCGTTAC		TATCTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3680	TGCAGGACCCAGAGAATTGGAATACAA	3920	TGCAGGACCCAGAGAATTGGAATACAA	4160
AGAGGTTNNNNCTAGCGTTAC		CACCCGNNNNCTAGCGTTAC		CGAGCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3681	TGCAGGACCCAGAGAATTGGAATACAA	3921	TGCAGGACCCAGAGAATTGGAATACAA	4161
TTCCCGGNNNNCTAGCGTTAC		TAACCCANNNNCTAGCGTTAC		ACCGATGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3682	TGCAGGACCCAGAGAATTGGAATACAA	3922	TGCAGGACCCAGAGAATTGGAATACAA	4162
CCCTCATNNNNCTAGCGTTAC		CCOCTATNNNNCTAGCGTTAC		TACGGATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3683	TGCAGGACCCAGAGAATTGGAATACAA	3923	TGCAGGACCCAGAGAATTGGAATACAA	4163
AAAGGTTNNNNCTAGCGTTAC		GATAGATNNNNCTAGCGTTAC		TGTCTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3684	TGCAGGACCCAGAGAATTGGAATACAA	3924	TGCAGGACCCAGAGAATTGGAATACAA	4164
AAAGTCCNNNNCTAGCGTTAC		GAATGATNNNNCTAGCGTTAC		GGCTGCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3685	TGCAGGACCCAGAGAATTGGAATACAA	3925	TGCAGGACCCAGAGAATTGGAATACAA	4165
GGCGAAANNNNCTAGCGTTAC		TAGAGGCGNNNNCTAGCGTTAC		TGCTTCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3686	TGCAGGACCCAGAGAATTGGAATACAA	3926	TGCAGGACCCAGAGAATTGGAATACAA	4166
CTTCCGNNNNCTAGCGTTAC		CCCGCGNNNNCTAGCGTTAC		CAGGACNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3687	TGCAGGACCCAGAGAATTGGAATACAA	3927	TGCAGGACCCAGAGAATTGGAATACAA	4167
CCAGATGNNNNCTAGCGTTAC		CATACCTNNNNCTAGCGTTAC		ACACATANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3688	TGCAGGACCCAGAGAATTGGAATACAA	3928	TGCAGGACCCAGAGAATTGGAATACAA	4168
GAAGCCGNNNNCTAGCGTTAC		GAATTCGNNNNCTAGCGTTAC		CATCTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3689	TGCAGGACCCAGAGAATTGGAATACAA	3929	TGCAGGACCCAGAGAATTGGAATACAA	4169
GTGGCTGNNNNCTAGCGTTAC		GAACGGTNNNNCTAGCGTTAC		AAACCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3690	TGCAGGACCCAGAGAATTGGAATACAA	3930	TGCAGGACCCAGAGAATTGGAATACAA	4170
GGTACGANNNNCTAGCGTTAC		CTTCAAGNNNNCTAGCGTTAC		CTCCTCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3691	TGCAGGACCCAGAGAATTGGAATACAA	3931	TGCAGGACCCAGAGAATTGGAATACAA	4171
GGCGCAANNNNCTAGCGTTAC		AAATATCCNNNNCTAGCGTTAC		CGGATANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3692	TGCAGGACCCAGAGAATTGGAATACAA	3932	TGCAGGACCCAGAGAATTGGAATACAA	4172
GGCGCATNNNNCTAGCGTTAC		GTCCGCGNNNNCTAGCGTTAC		GGCAACANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3693	TGCAGGACCCAGAGAATTGGAATACAA	3933	TGCAGGACCCAGAGAATTGGAATACAA	4173
CATCTGNNNNCTAGCGTTAC		CTAATCANNNNCTAGCGTTAC		GAACACGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3694	TGCAGGACCCAGAGAATTGGAATACAA	3934	TGCAGGACCCAGAGAATTGGAATACAA	4174
GGCAGANNNNCTAGCGTTAC		GAACGCGNNNNCTAGCGTTAC		ACACTCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3695	TGCAGGACCCAGAGAATTGGAATACAA	3935	TGCAGGACCCAGAGAATTGGAATACAA	4175
GGCAGGNNNNCTAGCGTTAC		CGTSCCANNNNCTAGCGTTAC		GGACCTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3696	TGCAGGACCCAGAGAATTGGAATACAA	3936	TGCAGGACCCAGAGAATTGGAATACAA	4176
GTGACTGNNNNCTAGCGTTAC		AAATTGANNNNCTAGCGTTAC		TCTGAGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3697	TGCAGGACCCAGAGAATTGGAATACAA	3937	TGCAGGACCCAGAGAATTGGAATACAA	4177
CGTTGAGNNNNCTAGCGTTAC		GTTCACNNNNCTAGCGTTAC		CCCTCTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3698	TGCAGGACCCAGAGAATTGGAATACAA	3938	TGCAGGACCCAGAGAATTGGAATACAA	4178
TTAGTTNNNNCTAGCGTTAC		TCCGCGANNNNCTAGCGTTAC		GGTCAATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3699	TGCAGGACCCAGAGAATTGGAATACAA	3939	TGCAGGACCCAGAGAATTGGAATACAA	4179
CCAGGCGNNNNCTAGCGTTAC		CAGATANNNNCTAGCGTTAC		TGCTTGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3700	TGCAGGACCCAGAGAATTGGAATACAA	3940	TGCAGGACCCAGAGAATTGGAATACAA	4180
CGATGATNNNNCTAGCGTTAC		GGTAAGTNNNNCTAGCGTTAC		TTAAGTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3701	TGCAGGACCCAGAGAATTGGAATACAA	3941	TGCAGGACCCAGAGAATTGGAATACAA	4181
ATCTCGANNNNCTAGCGTTAC		ACACCTNNNNCTAGCGTTAC		CCAGATGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3702	TGCAGGACCCAGAGAATTGGAATACAA	3942	TGCAGGACCCAGAGAATTGGAATACAA	4182
GAGATGNNNNCTAGCGTTAC		AGCCTGTNNNNCTAGCGTTAC		CCCGCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3703	TGCAGGACCCAGAGAATTGGAATACAA	3943	TGCAGGACCCAGAGAATTGGAATACAA	4183
AGGTAAANNNNCTAGCGTTAC		GTCCAGCNNNNCTAGCGTTAC		CATAGCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3704	TGCAGGACCCAGAGAATTGGAATACAA	3944	TGCAGGACCCAGAGAATTGGAATACAA	4184
CTCAGGANNNNCTAGCGTTAC		GTGGGTTNNNNCTAGCGTTAC		GTGGGTTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3705	TGCAGGACCCAGAGAATTGGAATACAA	3945	TGCAGGACCCAGAGAATTGGAATACAA	4185
QATAGCNNNNCTAGCGTTAC		AAATTTGNNNNCTAGCGTTAC		CCAGATANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAATTGGAATACAA	3706	TGCAGGACCCAGAGAATTGGAATACAA	3946	TGCAGGACCCAGAGAATTGGAATACAA	4186
GAATTTGNNNNCTAGCGTTAC		AGGGGTGNNNNCTAGCGTTAC		TGCACGNNNNCTAGCGTTAC	

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
AGCAGGTNNNCTAGCGTTAC	3707	CGAGCCGNNNCTAGCGTTAC	3947	CGCGCGNNNCTAGCGTTAC	4187
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
ATACTCTNNNCTAGCGTTAC	3708	GATAAGNNNCTAGCGTTAC	3948	AAAGTGGNNNCTAGCGTTAC	4188
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
GGTCTCINNNTAGCGTTAC	3709	ATGGCTGNNNCTAGCGTTAC	3949	AAAGCANNNCTAGCGTTAC	4189
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
CGTAGTNNNCTAGCGTTAC	3710	CGCTCCTNNNCTAGCGTTAC	3950	TCGTGGNNNCTAGCGTTAC	4190
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
ATAGATTNNNCTAGCGTTAC	3711	CTTAGCGNNNCTAGCGTTAC	3951	GTATATANNNCTAGCGTTAC	4191
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CGCGAATNNNCTAGCGTTAC	3712	CAATCTGNNNCTAGCGTTAC	3952	GTATTGNNNCTAGCGTTAC	4192
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
GCATGCCNNNCTAGCGTTAC	3713	TAGCGCGNNNCTAGCGTTAC	3953	ACAPACTNNNCTAGCGTTAC	4193
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
ATATCCGNNNCTAGCGTTAC	3714	ACTCTGNNNCTAGCGTTAC	3954	TCCTAATNNNCTAGCGTTAC	4194
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
CTCAGCGNNNCTAGCGTTAC	3715	TGGCAGANNNCTAGCGTTAC	3955	GTCTGATNNNCTAGCGTTAC	4195
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TTCAAGGNNNCTAGCGTTAC	3716	GAGGTTNNNCTAGCGTTAC	3956	CAGGAAANNNCTAGCGTTAC	4196
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CAGTAATNNNCTAGCGTTAC	3717	CAGCTAANNNCTAGCGTTAC	3957	AGGCTTTNNNCTAGCGTTAC	4197
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
CGGCGAANNNCTAGCGTTAC	3718	GTGCGGNNNCTAGCGTTAC	3958	GCGGCAANNNCTAGCGTTAC	4198
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TGATCATNNNCTAGCGTTAC	3719	GCCTGTTNNNCTAGCGTTAC	3959	AAGTTGGNNNCTAGCGTTAC	4199
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GGCGGTTNNNCTAGCGTTAC	3720	TCCTGTCNNNCTAGCGTTAC	3960	CAGGTGGNNNCTAGCGTTAC	4200
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
GTCCGCGNNNCTAGCGTTAC	3721	CACAACTNNNCTAGCGTTAC	3961	GTAACTANNNCTAGCGTTAC	4201
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
ACTGGTANNNCTAGCGTTAC	3722	ATCGGTANNNCTAGCGTTAC	3962	TCACCAANNNCTAGCGTTAC	4202
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
TAAGACNNNCTAGCGTTAC	3723	AAGGTTGNNNCTAGCGTTAC	3963	AGCAACANNNCTAGCGTTAC	4203
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
CGCTACANNNCTAGCGTTAC	3724	AAAGGTCNNNCTAGCGTTAC	3964	CCGTCCGNNNCTAGCGTTAC	4204
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
CCAAAANNNCTAGCGTTAC	3725	GAAGGTCNNNCTAGCGTTAC	3965	AGGCGCANNNCTAGCGTTAC	4205
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
GAGTGCCNNNCTAGCGTTAC	3726	CATGCTTNNNCTAGCGTTAC	3966	AAGCAGTNNNCTAGCGTTAC	4206
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
ACCGGAANNNCTAGCGTTAC	3727	TCACCTTNNNCTAGCGTTAC	3967	TGGTATANNNCTAGCGTTAC	4207
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
AAAGCATNNNCTAGCGTTAC	3728	CTGSCAANNNCTAGCGTTAC	3968	MACTGTGNNNCTAGCGTTAC	4208
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CCCCGCGNNNCTAGCGTTAC	3729	TTTACAAANNNCTAGCGTTAC	3969	TGCTTTGNNNCTAGCGTTAC	4209
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
TGGTTTGGNNNCTAGCGTTAC	3730	CCCACAAANNNCTAGCGTTAC	3970	TTCCGCGNNNCTAGCGTTAC	4210
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CCACGTTNNNCTAGCGTTAC	3731	ECTCATANNNCTAGCGTTAC	3971	EAECTATGNNNCTAGCGTTAC	4211
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
TGAAGTANNNCTAGCGTTAC	3732	GCATTGNNNCTAGCGTTAC	3972	TGTAGCANNNCTAGCGTTAC	4212
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
CAATAAGNNNCTAGCGTTAC	3733	ACCCGATNNNCTAGCGTTAC	3973	GCGGTCANNNCTAGCGTTAC	4213
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
ATGTTTNNNCTAGCGTTAC	3734	GRCCAAACNNNCTAGCGTTAC	3974	CCATGAGNNNCTAGCGTTAC	4214
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
CGGTTCCNNNCTAGCGTTAC	3735	CCGAGGANNNCTAGCGTTAC	3975	GCTCCCTNNNCTAGCGTTAC	4215
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
TTACGTGNNNCTAGCGTTAC	3736	ATATGGANNNCTAGCGTTAC	3976	GCTTAACNNNCTAGCGTTAC	4216
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
GTCTTGGNNNCTAGCGTTAC	3737	TTCGGTCNNNCTAGCGTTAC	3977	GAGGAAANNNCTAGCGTTAC	4217
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TCTACAGNNNCTAGCGTTAC	3738	TAGGTTANNNCTAGCGTTAC	3978	CCGACGANNNCTAGCGTTAC	4218
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
ATAAGTTNNNCTAGCGTTAC	3739	ACCGGTTNNNCTAGCGTTAC	3979	ACATAACNNNCTAGCGTTAC	4219

图17D

池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAA	3740	TGCAGGACCAGAGAATTGGAATACAA	3980	TGCAGGACCAGAGAATTGGAATACAT	4220
AACTGCTANNNGATCGACATG		GGTAAGCANNNGATCGACATG		AACATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAC	3741	TGCAGGACCAGAGAATTGGAATACAA	3981	TGCAGGACCAGAGAATTGGAATACAG	4221
ATCATGSHNNNGATCGACATG		ATTGACTNNNGATCGACATG		TTGCGGCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3742	TGCAGGACCAGAGAATTGGAATACAT	3982	TGCAGGACCAGAGAATTGGAATACAA	4222
TCAGTGCNNNGATCGACATG		ACTGTAAANNNGATCGACATG		TCTGCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3743	TGCAGGACCAGAGAATTGGAATACAT	3983	TGCAGGACCAGAGAATTGGAATACAG	4223
TGCCGCCNNNGATCGACATG		TCTCTGGNNNGATCGACATG		GTTAGTGNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3744	TGCAGGACCAGAGAATTGGAATACAA	3984	TGCAGGACCAGAGAATTGGAATACAC	4224
GTCTGTNNNGATCGACATG		GAAGAAANNNGATCGACATG		TTAGATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3745	TGCAGGACCAGAGAATTGGAATACAA	3985	TGCAGGACCAGAGAATTGGAATACAC	4225
GGCGTCTNNNGATCGACATG		AATGAACNNNGATCGACATG		TCTTACANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3746	TGCAGGACCAGAGAATTGGAATACAA	3986	TGCAGGACCAGAGAATTGGAATACAG	4226
CCACGCGNNNGATCGACATG		ACACACNNNGATCGACATG		CTCAGTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3747	TGCAGGACCAGAGAATTGGAATACAT	3987	TGCAGGACCAGAGAATTGGAATACAG	4227
CGTTTAANNNGATCGACATG		AAATGCTNNNGATCGACATG		GTACTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3748	TGCAGGACCAGAGAATTGGAATACAA	3988	TGCAGGACCAGAGAATTGGAATACAT	4228
TACAACTNNNGATCGACATG		CCGGTTANNNGATCGACATG		AGTATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3749	TGCAGGACCAGAGAATTGGAATACAC	3989	TGCAGGACCAGAGAATTGGAATACAA	4229
CGAGGAANNNGATCGACATG		CGCGGTANNNGATCGACATG		AGCATCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3750	TGCAGGACCAGAGAATTGGAATACAC	3990	TGCAGGACCAGAGAATTGGAATACAA	4230
ACACTCANNNGATCGACATG		GTAGACTNNNGATCGACATG		CTAAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3751	TGCAGGACCAGAGAATTGGAATACAG	3991	TGCAGGACCAGAGAATTGGAATACAA	4231
CTCTAGNNNGATCGACATG		GAAGTCAANNNGATCGACATG		CTTTAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3752	TGCAGGACCAGAGAATTGGAATACAA	3992	TGCAGGACCAGAGAATTGGAATACAA	4232
CTTACTNNNGATCGACATG		GAATTGANNNGATCGACATG		CGAATAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3753	TGCAGGACCAGAGAATTGGAATACAA	3993	TGCAGGACCAGAGAATTGGAATACAT	4233
AAAGGAANNNGATCGACATG		CCCGTTANNNGATCGACATG		AGCGTCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3754	TGCAGGACCAGAGAATTGGAATACAT	3994	TGCAGGACCAGAGAATTGGAATACAA	4234
CAGCAANNNGATCGACATG		ACAGACNNNGATCGACATG		TCTATCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3755	TGCAGGACCAGAGAATTGGAATACAA	3995	TGCAGGACCAGAGAATTGGAATACAA	4235
GAGTACNNNGATCGACATG		TTAGACTNNNGATCGACATG		AAACAACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3756	TGCAGGACCAGAGAATTGGAATACAC	3996	TGCAGGACCAGAGAATTGGAATACAG	4236
ACTGTCAANNNGATCGACATG		ACTAGACNNNGATCGACATG		TATCAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3757	TGCAGGACCAGAGAATTGGAATACAG	3997	TGCAGGACCAGAGAATTGGAATACAT	4237
CGAGGCCNNNGATCGACATG		CCCTAAANNNGATCGACATG		ACTGTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3758	TGCAGGACCAGAGAATTGGAATACAA	3998	TGCAGGACCAGAGAATTGGAATACAA	4238
TGCATAGNNNGATCGACATG		GAAGTGTNNNGATCGACATG		GGACACANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3759	TGCAGGACCAGAGAATTGGAATACAA	3999	TGCAGGACCAGAGAATTGGAATACAG	4239
ACTGTGTNNNGATCGACATG		TCTGAATNNNGATCGACATG		TGACGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3760	TGCAGGACCAGAGAATTGGAATACAA	4000	TGCAGGACCAGAGAATTGGAATACAC	4240
CGACTGNNNGATCGACATG		GCATCAANNNGATCGACATG		TTGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3761	TGCAGGACCAGAGAATTGGAATACAA	4001	TGCAGGACCAGAGAATTGGAATACAG	4241
GGTGACANNNGATCGACATG		ACTGGAANNNGATCGACATG		CATSCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3762	TGCAGGACCAGAGAATTGGAATACAC	4002	TGCAGGACCAGAGAATTGGAATACAC	4242
AACTGANNNGATCGACATG		TAGCCCCNNNGATCGACATG		TGATTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3763	TGCAGGACCAGAGAATTGGAATACAT	4003	TGCAGGACCAGAGAATTGGAATACAG	4243
ATTTGTANNNGATCGACATG		CTTGTGNNNGATCGACATG		CAACTCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3764	TGCAGGACCAGAGAATTGGAATACAC	4004	TGCAGGACCAGAGAATTGGAATACAT	4244
CCCCGATNNNGATCGACATG		CGTCTGNNNGATCGACATG		ACCTCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAA	3765	TGCAGGACCAGAGAATTGGAATACAC	4005	TGCAGGACCAGAGAATTGGAATACAT	4245
GGAGCGNNNGATCGACATG		CTAACGANNNGATCGACATG		GCACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAC	3766	TGCAGGACCAGAGAATTGGAATACAA	4006	TGCAGGACCAGAGAATTGGAATACAG	4246
CCTCGAGNNNGATCGACATG		AAATAGCANNNGATCGACATG		TTCTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3767	TGCAGGACCAGAGAATTGGAATACAA	4007	TGCAGGACCAGAGAATTGGAATACAT	4247
GCACCTCANNNGATCGACATG		AGCACTCANNNGATCGACATG		ACTGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3768	TGCAGGACCAGAGAATTGGAATACAG	4008	TGCAGGACCAGAGAATTGGAATACAC	4248
AAGTCAGNNNGATCGACATG		TTCAACGNNNGATCGACATG		TTCATANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAG	3769	TGCAGGACCAGAGAATTGGAATACAG	4009	TGCAGGACCAGAGAATTGGAATACAT	4249
GGCTGCTNNNGATCGACATG		GTCTGTNNNGATCGACATG		CTGCTGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAC	3770	TGCAGGACCAGAGAATTGGAATACAG	4010	TGCAGGACCAGAGAATTGGAATACAT	4250
ATTGTCCNNNGATCGACATG		CACGGCTNNNGATCGACATG		GGTATTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3771	TGCAGGACCAGAGAATTGGAATACAA	4011	TGCAGGACCAGAGAATTGGAATACAA	4251
ACTTAATNNNGATCGACATG		CCCPAACNNNGATCGACATG		GAATGTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATACAT	3772	TGCAGGACCAGAGAATTGGAATACAC	4012	TGCAGGACCAGAGAATTGGAATACAG	4252
AGATGTTNNNGATCGACATG		ATAAATCANNNGATCGACATG		GGAGCAANNNGATCGACATG	

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
ATCGACGNNNGATCGACATG	3773	CGTAAAGCANNNGATCGACATG	4013	CCACAAATNNNGATCGACATG	4253
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
CTTGGGANNNGATCGACATG	3774	AGCTTGANNNGATCGACATG	4014	ATTCTCANNNGATCGACATG	4254
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
GGTACGNNNGATCGACATG	3775	TTTTGTNNNGATCGACATG	4015	AGACCTCANNNGATCGACATG	4255
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAC	
GTCAATNNNGATCGACATG	3776	SAGTAGGNNNGATCGACATG	4016	ACATATNNNGATCGACATG	4256
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA	
ACTTAANNNGATCGACATG	3777	SAGTCTGNNNGATCGACATG	4017	CCCTGAANNNGATCGACATG	4257
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
TTACCTANNNGATCGACATG	3778	GAAGCTGNNNGATCGACATG	4018	TAGACCTNNNGATCGACATG	4258
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAC	
GTTTGGCANNNGATCGACATG	3779	AGAGCGCANNNGATCGACATG	4019	CCCTCCGNNNGATCGACATG	4259
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
AGACATGNNNGATCGACATG	3780	CTTATGNNNGATCGACATG	4020	ATCCCACTNNNGATCGACATG	4260
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
AGGCATANNNGATCGACATG	3781	GCATATCANNNGATCGACATG	4021	GTCAATTANNNGATCGACATG	4261
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
CTCGCTCGNNNGATCGACATG	3782	CCGCTTANNNGATCGACATG	4022	GAACCAANNNGATCGACATG	4262
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA	
TGCTAGGNNNGATCGACATG	3783	TTATAGGNNNGATCGACATG	4023	TCCTCTGNNNGATCGACATG	4263
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAC	
CCCGACGNNNGATCGACATG	3784	TGCTTAANNNGATCGACATG	4024	TGTACCTNNNGATCGACATG	4264
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
ACGAATCANNNGATCGACATG	3785	SACGTACNNNGATCGACATG	4025	ATCCAGTNNNGATCGACATG	4265
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT	
CGTCTCGANNNGATCGACATG	3786	SAGRAAANNNGATCGACATG	4026	AAGTTCTANNNGATCGACATG	4266
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
ATCCATNNNGATCGACATG	3787	GTCTGTGNNNGATCGACATG	4027	CGTTAGANNNGATCGACATG	4267
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
CGCAACGNNNGATCGACATG	3788	GTATGNNNGATCGACATG	4028	AGAGACGNNNGATCGACATG	4268
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
ATTGATCANNNGATCGATCAGGT	3789	ATTGAGTNNNGATCGATCAGGT	4029	GCCCTACNNNGATCGATCAGGT	4269
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
TGGACANNNGATCGATCAGGT	3790	ATAGAGTNNNGATCGATCAGGT	4030	ACGGCTCANNNGATCGATCAGGT	4270
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TACGCTNNNGATCGATCAGGT	3791	AGACATCANNNGATCGATCAGGT	4031	CGCGAGANNNGATCGATCAGGT	4271
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TAGAGTTNNNGATCGATCAGGT	3792	AAGCCCAANNNGATCGATCAGGT	4032	CGATTAAGNNNGATCGATCAGGT	4272
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA	
GTGTGTNNNGATCGATCAGGT	3793	AGTCCCAANNNGATCGATCAGGT	4033	CGCTAGTNNNGATCGATCAGGT	4273
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
CAGAGCGNNNGATCGATCAGGT	3794	TCCGACTNNNGATCGATCAGGT	4034	TTGAATCANNNGATCGATCAGGT	4274
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT	
GTGGGCAANNNGATCGATCAGGT	3795	CAGTATNNNGATCGATCAGGT	4035	ATTAAATNNNGATCGATCAGGT	4275
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CTTCTCTNNNGATCGATCAGGT	3796	AGAATATNNNGATCGATCAGGT	4036	GTCTTGANNNGATCGATCAGGT	4276
TGCAGGACCCAGAGAATTGGAATACAC		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
AAAGATAANNNGATCGATCAGGT	3797	GTAAAGCANNNGATCGATCAGGT	4037	AGCTTTATNNNGATCGATCAGGT	4277
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG	
ACTACGNNNGATCGATCAGGT	3798	GGCTATCANNNGATCGATCAGGT	4038	CCCGACTNNNGATCGATCAGGT	4278
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG	
ACACAAGNNNGATCGATCAGGT	3799	ACGGTTGNNNGATCGATCAGGT	4039	TGCTCAANNNGATCGATCAGGT	4279
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAT	
TTAOCCTNNNGATCGATCAGGT	3800	AGGRAAGNNNGATCGATCAGGT	4040	ACATCGGNNNGATCGATCAGGT	4280
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CTACCACTNNNGATCGATCAGGT	3801	ATTGCAANNNGATCGATCAGGT	4041	ACTTTCCNNNGATCGATCAGGT	4281
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
AGTCTGTNNNGATCGATCAGGT	3802	AAGGCTCANNNGATCGATCAGGT	4042	GGCCTATNNNGATCGATCAGGT	4282
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
ATGCGAGNNNGATCGATCAGGT	3803	GAAGCGGNNNGATCGATCAGGT	4043	SACGGGAANNNGATCGATCAGGT	4283
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
ATGGACTNNNGATCGATCAGGT	3804	ACGATCTNNNGATCGATCAGGT	4044	CTGCCAGNNNGATCGATCAGGT	4284
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAT	
TGCGAGTNNNGATCGATCAGGT	3805	TGCAATCANNNGATCGATCAGGT	4045	CAATATAGNNNGATCGATCAGGT	4285

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAT	3806	TGCAGGACCAGAGAATTGGAATACAC	4046	TGCAGGACCAGAGAATTGGAATACAT	4286
TGCAGGACNNNTGCATCAGGT		ATCAATANNNTGCATCAGGT		GTCCGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAC	3807	TGCAGGACCAGAGAATTGGAATACAC	4047	TGCAGGACCAGAGAATTGGAATACAC	4287
CTCGGAGNNNTGCATCAGGT		ACACATGNNNTGCATCAGGT		ACGATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3808	TGCAGGACCAGAGAATTGGAATACAG	4048	TGCAGGACCAGAGAATTGGAATACAG	4288
ATCATGNNNTGCATCAGGT		CAGCGAGNNNTGCATCAGGT		ACTGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3809	TGCAGGACCAGAGAATTGGAATACAT	4049	TGCAGGACCAGAGAATTGGAATACAG	4289
AGGTAGNNNTGCATCAGGT		ACGGCTANNNTGCATCAGGT		TGGTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3810	TGCAGGACCAGAGAATTGGAATACAG	4050	TGCAGGACCAGAGAATTGGAATACAT	4290
GAACCTANNNTGCATCAGGT		AGCAGANNNTGCATCAGGT		GTAGGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3811	TGCAGGACCAGAGAATTGGAATACAA	4051	TGCAGGACCAGAGAATTGGAATACAA	4291
CCACCTANNNTGCATCAGGT		AGATTAGNNNTGCATCAGGT		ACCCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3812	TGCAGGACCAGAGAATTGGAATACAG	4052	TGCAGGACCAGAGAATTGGAATACAA	4292
CTTCTCANNNTGCATCAGGT		CAAGACNNNTGCATCAGGT		TTACAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3813	TGCAGGACCAGAGAATTGGAATACAA	4053	TGCAGGACCAGAGAATTGGAATACAG	4293
ACTCCGANNNTGCATCAGGT		TAACACNNNTGCATCAGGT		CAATAAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3814	TGCAGGACCAGAGAATTGGAATACAT	4054	TGCAGGACCAGAGAATTGGAATACAA	4294
ATTAGCTNNNTGCATCAGGT		TCCAAAANNNTGCATCAGGT		GGCTTAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3815	TGCAGGACCAGAGAATTGGAATACAT	4055	TGCAGGACCAGAGAATTGGAATACAT	4295
TAGTAGNNNTGCATCAGGT		GGTATCGNNNTGCATCAGGT		CATTGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3816	TGCAGGACCAGAGAATTGGAATACAA	4056	TGCAGGACCAGAGAATTGGAATACAC	4296
TTTTACTNNNTGCATCAGGT		ACACTTANNNTGCATCAGGT		ACTATAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3817	TGCAGGACCAGAGAATTGGAATACAA	4057	TGCAGGACCAGAGAATTGGAATACAG	4297
GGCAATGNNNTGCATCAGGT		CGGTGGCANNNTGCATCAGGT		TGCGTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3818	TGCAGGACCAGAGAATTGGAATACAA	4058	TGCAGGACCAGAGAATTGGAATACAC	4298
GAGGGCTNNNTGCATCAGGT		GTCTAGCANNNTGCATCAGGT		GATGAGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3819	TGCAGGACCAGAGAATTGGAATACAA	4059	TGCAGGACCAGAGAATTGGAATACAT	4299
TAACTGNNNTGCATCAGGT		GACTCCANNNTGCATCAGGT		AGARGGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3820	TGCAGGACCAGAGAATTGGAATACAC	4060	TGCAGGACCAGAGAATTGGAATACAA	4300
GTCAACGNNNTGCATCAGGT		CAGGATNNNTGCATCAGGT		TACCCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3821	TGCAGGACCAGAGAATTGGAATACAA	4061	TGCAGGACCAGAGAATTGGAATACAT	4301
GATTTTNNNTGCATCAGGT		GAATGATNNNTGCATCAGGT		CCAGCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3822	TGCAGGACCAGAGAATTGGAATACAA	4062	TGCAGGACCAGAGAATTGGAATACAG	4302
CGTATCANNNTGCATCAGGT		CCACATCANNNTGCATCAGGT		TCTTCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3823	TGCAGGACCAGAGAATTGGAATACAG	4063	TGCAGGACCAGAGAATTGGAATACAG	4303
CCGCGATNNNTGCATCAGGT		TAATAACNNNTGCATCAGGT		AAACGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3824	TGCAGGACCAGAGAATTGGAATACAA	4064	TGCAGGACCAGAGAATTGGAATACAG	4304
GGCCTAGNNNTGCATCAGGT		TTAACACNNNTGCATCAGGT		CGTCTAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3825	TGCAGGACCAGAGAATTGGAATACAA	4065	TGCAGGACCAGAGAATTGGAATACAA	4305
ACAGCCANNNTGCATCAGGT		CAAAATCANNNTGCATCAGGT		CCGAGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3826	TGCAGGACCAGAGAATTGGAATACAG	4066	TGCAGGACCAGAGAATTGGAATACAG	4306
CGTATGNNNTGCATCAGGT		GTCCATNNNTGCATCAGGT		CGCCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3827	TGCAGGACCAGAGAATTGGAATACAA	4067	TGCAGGACCAGAGAATTGGAATACAA	4307
GTGTGANNNTGCATCAGGT		GAAATCANNNTGCATCAGGT		PATAGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3828	TGCAGGACCAGAGAATTGGAATACAA	4068	TGCAGGACCAGAGAATTGGAATACAT	4308
TGGATTCNNNTGCATCAGGT		AATCACTNNNTGCATCAGGT		GACACTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3829	TGCAGGACCAGAGAATTGGAATACAG	4069	TGCAGGACCAGAGAATTGGAATACAA	4309
CGGACCGNNNTGCATCAGGT		TCCACGNNNTGCATCAGGT		CGCGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3830	TGCAGGACCAGAGAATTGGAATACAG	4070	TGCAGGACCAGAGAATTGGAATACAG	4310
ATCATAGNNNTGCATCAGGT		ATATATCANNNTGCATCAGGT		CAGAAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3831	TGCAGGACCAGAGAATTGGAATACAT	4071	TGCAGGACCAGAGAATTGGAATACAG	4311
GAAGCGTNNNTGCATCAGGT		GTAACANNNTGCATCAGGT		GCTGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3832	TGCAGGACCAGAGAATTGGAATACAT	4072	TGCAGGACCAGAGAATTGGAATACAG	4312
CGTCAAGNNNTGCATCAGGT		CGATTAAANNNTGCATCAGGT		TAGAAATANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3833	TGCAGGACCAGAGAATTGGAATACAG	4073	TGCAGGACCAGAGAATTGGAATACAG	4313
ACTGTGNNNTGCATCAGGT		GCCAAATNNNTGCATCAGGT		CATCGAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3834	TGCAGGACCAGAGAATTGGAATACAG	4074	TGCAGGACCAGAGAATTGGAATACAT	4314
CTTGGAGNNNTGCATCAGGT		TTGTAAANNNTGCATCAGGT		TGCTTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3835	TGCAGGACCAGAGAATTGGAATACAA	4075	TGCAGGACCAGAGAATTGGAATACAA	4315
TGAAATANNNTGCATCAGGT		ATTAGANNNTGCATCAGGT		CTCCCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAT	3836	TGCAGGACCAGAGAATTGGAATACAT	4076	TGCAGGACCAGAGAATTGGAATACAG	4316
GGCTTCGNNNTGCATCAGGT		AGCTTGGNNNTGCATCAGGT		TTTCCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAA	3837	TGCAGGACCAGAGAATTGGAATACAA	4077	TGCAGGACCAGAGAATTGGAATACAG	4317
GACTTCCNNNTGCATCAGGT		TAGGAGCANNNTGCATCAGGT		ACATTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATACAG	3838	TGCAGGACCAGAGAATTGGAATACAT	4078	TGCAGGACCAGAGAATTGGAATACAA	4318
CCCGTGGNNNTGCATCAGGT		TATATCANNNTGCATCAGGT		CTGAGGANNNTGCATCAGGT	

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池-16	SEQ ID NO:	池-17	SEQ ID NO:	池-18	SEQ ID NO:
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AGGAGATNNNTGCATCAGGT	3839	TGTTGCCNNNTGCATCAGGT	4079	TAGTGTNNNTGCATCAGGT	4319
TGCAGGACCAGAGAAATCGAATACAC		TGCAGGACCAGAGAAATCGAATACAT		TGCAGGACCAGAGAAATCGAATACAT	
AGGTATCNNNTGCATCAGGT	3840	TCCGAGANNNTGCATCAGGT	4080	TCAAAATCNNNTGCATCAGGT	4320
TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAA		TGCAGGACCAGAGAAATCGAATACAG	
TAGTATNNNTGCATCAGGT	3841	TCCCATCNNNTGCATCAGGT	4081	CATATCNNNTGCATCAGGT	4321
TGCAGGACCAGAGAAATCGAATACAA		TGCAGGACCAGAGAAATCGAATACAT		TGCAGGACCAGAGAAATCGAATACAA	
AGGAGGANNNTGCATCAGGT	3842	TTCGCACNNNTGCATCAGGT	4082	TTCGTAAANNNTGCATCAGGT	4322
TGCAGGACCAGAGAAATCGAATACAA		TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAA	
AGAGCCANNNTGCATCAGGT	3843	TGAGCGNNNTGCATCAGGT	4083	ATCCACNNNTGCATCAGGT	4323
TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAT		TGCAGGACCAGAGAAATCGAATACAG	
TCTCTCANNNTGCATCAGGT	3844	TGCATCTNNNTGCATCAGGT	4084	TGCCCGCANNNTGCATCAGGT	4324
TGCAGGACCAGAGAAATCGAATACAA		TGCAGGACCAGAGAAATCGAATACAT		TGCAGGACCAGAGAAATCGAATACAG	
CGGTGTNNNTGCATCAGGT	3845	TTCGAGANNNTGCATCAGGT	4085	GCTCGACNNNTGCATCAGGT	4325
TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAA	
GTACGATNNNTGCATCAGGT	3846	TCCAAAGNNNTGCATCAGGT	4086	TCCCGAGNNNTGCATCAGGT	4326
TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAT		TGCAGGACCAGAGAAATCGAATACAA	
AGGTGTANNNTGCATCAGGT	3847	TTCCTCGNNNTGCATCAGGT	4087	TTCAGCANNNTGCATCAGGT	4327
TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAG		TGCAGGACCAGAGAAATCGAATACAA	
ACCACAANNNTGCATCAGGT	3848	TCCACGNNNTGCATCAGGT	4088	AAATTCNNNTGCATCAGGT	4328

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池 -19	SEQ ID No:	池 -20	SEQ ID No:	池 -21	SEQ ID No:
TGCAGGACCAGAGAATTGGAATA	4329	TGCAGGACCAGAGAATTGGAATA	4569	TGCAGGACCAGAGAATTGGAATA	4809
CAGCGCTTCGNNNACGTATGCCA		CATGTTGTGNNNACGTATGCCA		CATGAACCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4330	TGCAGGACCAGAGAATTGGAATA	4570	TGCAGGACCAGAGAATTGGAATA	4810
CAGCAAGGCTNNNACGTATGCCA		CATAGCCAGCINNACGTATGCCA		CACCGTTGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4331	TGCAGGACCAGAGAATTGGAATA	4571	TGCAGGACCAGAGAATTGGAATA	4811
CATTTCTATGNNNACGTATGCCA		CATGCGCGACNNNACGTATGCCA		CAGCATTGGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4332	TGCAGGACCAGAGAATTGGAATA	4572	TGCAGGACCAGAGAATTGGAATA	4812
CAGCTGCCATTNNNACGTATGCCA		CAATCGTCTCINNACGTATGCCA		CATAGGCCATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4333	TGCAGGACCAGAGAATTGGAATA	4573	TGCAGGACCAGAGAATTGGAATA	4813
CAGTTTAGCGNNNACGTATGCCA		CATCGGCACNNNACGTATGCCA		CAACTCCTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4334	TGCAGGACCAGAGAATTGGAATA	4574	TGCAGGACCAGAGAATTGGAATA	4814
CAAPAAATGACNNNACGTATGCCA		CATTACTGAANNNACGTATGCCA		CACTAGGCCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4335	TGCAGGACCAGAGAATTGGAATA	4575	TGCAGGACCAGAGAATTGGAATA	4815
CACCTACTAGCINNACGTATGCCA		CAGAGTCCGCGNNNACGTATGCCA		CAGGTTTAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4336	TGCAGGACCAGAGAATTGGAATA	4576	TGCAGGACCAGAGAATTGGAATA	4816
CACACCCAGGNNNACGTATGCCA		CAGTGCCCTCINNACGTATGCCA		CATTGATACANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4337	TGCAGGACCAGAGAATTGGAATA	4577	TGCAGGACCAGAGAATTGGAATA	4817
CAGCCGCCCTNNNACGTATGCCA		CAGCGTAGCCNNNACGTATGCCA		CACCAATTACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4338	TGCAGGACCAGAGAATTGGAATA	4578	TGCAGGACCAGAGAATTGGAATA	4818
CACACCGTCANNNACGTATGCCA		CATAGCCACNNNACGTATGCCA		CAATACCGGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4339	TGCAGGACCAGAGAATTGGAATA	4579	TGCAGGACCAGAGAATTGGAATA	4819
CATCTCAGGNNNACGTATGCCA		CAATATACCANNNACGTATGCCA		CATGAAGCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4340	TGCAGGACCAGAGAATTGGAATA	4580	TGCAGGACCAGAGAATTGGAATA	4820
CATCATAAACNNNACGTATGCCA		CATAAAATCINNACGTATGCCA		CATTAGCTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4341	TGCAGGACCAGAGAATTGGAATA	4581	TGCAGGACCAGAGAATTGGAATA	4821
CATGCTCCCGNNNACGTATGCCA		CAGATGGTGANNNACGTATGCCA		CATATCAGATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4342	TGCAGGACCAGAGAATTGGAATA	4582	TGCAGGACCAGAGAATTGGAATA	4822
CAAGTAACCCNNNACGTATGCCA		CAGAACGTAGNNNACGTATGCCA		CAGAGAAATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4343	TGCAGGACCAGAGAATTGGAATA	4583	TGCAGGACCAGAGAATTGGAATA	4823
CAGTGACAGCINNACGTATGCCA		CAATATTARTNNNACGTATGCCA		CAGATCACGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4344	TGCAGGACCAGAGAATTGGAATA	4584	TGCAGGACCAGAGAATTGGAATA	4824
CAGCAATACGNNNACGTATGCCA		CATACCTGAATNNNACGTATGCCA		CAGGCTAGACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4345	TGCAGGACCAGAGAATTGGAATA	4585	TGCAGGACCAGAGAATTGGAATA	4825
CAATACGCTNNNACGTATGCCA		CAGTCCGAGCINNACGTATGCCA		CATTGACCGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4346	TGCAGGACCAGAGAATTGGAATA	4586	TGCAGGACCAGAGAATTGGAATA	4826
CACCATGTAGNNNACGTATGCCA		CACCTGGTANNNACGTATGCCA		CACCATGTGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4347	TGCAGGACCAGAGAATTGGAATA	4587	TGCAGGACCAGAGAATTGGAATA	4827
CACCCAGCCGNNNACGTATGCCA		CACCGTAGAANNNACGTATGCCA		CAGTCRGAAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4348	TGCAGGACCAGAGAATTGGAATA	4588	TGCAGGACCAGAGAATTGGAATA	4828
CAGCGGTTGCGNNNACGTATGCCA		CATTAAAGTCTNNNACGTATGCCA		CACCGACCTCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4349	TGCAGGACCAGAGAATTGGAATA	4589	TGCAGGACCAGAGAATTGGAATA	4829
CAGTGATCTGNNNACGTATGCCA		CAACGTGGCGNNNACGTATGCCA		CAATTAGTGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4350	TGCAGGACCAGAGAATTGGAATA	4590	TGCAGGACCAGAGAATTGGAATA	4830
CATAAGCGCTNNNACGTATGCCA		CAGCTATCCTNNNACGTATGCCA		CAGCATACCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4351	TGCAGGACCAGAGAATTGGAATA	4591	TGCAGGACCAGAGAATTGGAATA	4831
CATGTTGTGNNNACGTATGCCA		CAAGCGTTGTTNNNACGTATGCCA		CAAGTTTTCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4352	TGCAGGACCAGAGAATTGGAATA	4592	TGCAGGACCAGAGAATTGGAATA	4832
CAACGAGCGGNNNACGTATGCCA		CACCTCGCTANNNACGTATGCCA		CATTCGCGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4353	TGCAGGACCAGAGAATTGGAATA	4593	TGCAGGACCAGAGAATTGGAATA	4833
CATAGATCGCINNACGTATGCCA		CACATTTTTGNNNACGTATGCCA		CATGGACCCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4354	TGCAGGACCAGAGAATTGGAATA	4594	TGCAGGACCAGAGAATTGGAATA	4834
CATGATACGCGNNNACGTATGCCA		CAAACTTCGNNNACGTATGCCA		CACGTGGCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4355	TGCAGGACCAGAGAATTGGAATA	4595	TGCAGGACCAGAGAATTGGAATA	4835
CATAGTTACANNNACGTATGCCA		CATACCGTGANNNACGTATGCCA		CATCTTACTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4356	TGCAGGACCAGAGAATTGGAATA	4596	TGCAGGACCAGAGAATTGGAATA	4836
CACCTTGGTGANNNACGTATGCCA		CAAGCTTTTNNNACGTATGCCA		CAATCCGGTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4357	TGCAGGACCAGAGAATTGGAATA	4597	TGCAGGACCAGAGAATTGGAATA	4837
CATTAATCTCINNACGTATGCCA		CATGTTCTCGNNNACGTATGCCA		CAGACACCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4358	TGCAGGACCAGAGAATTGGAATA	4598	TGCAGGACCAGAGAATTGGAATA	4838
CATTAGACGCGNNNACGTATGCCA		CAARTCGGCTNNNACGTATGCCA		CATCCGCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4359	TGCAGGACCAGAGAATTGGAATA	4599	TGCAGGACCAGAGAATTGGAATA	4839
CAACACCGATTNNNACGTATGCCA		CATGAACCCANNNACGTATGCCA		CAAGATTACTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4360	TGCAGGACCAGAGAATTGGAATA	4600	TGCAGGACCAGAGAATTGGAATA	4840
CAACACGGAANNNACGTATGCCA		CAATTTTCATCINNACGTATGCCA		CAAGATTGAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4361	TGCAGGACCAGAGAATTGGAATA	4601	TGCAGGACCAGAGAATTGGAATA	4841
CAATGCAICGNNNACGTATGCCA		CACAGTCACANNNACGTATGCCA		CATTAAAGCINNACGTATGCCA	

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池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAAGAGAAATTCGAATA	4362	TGCAGGACCAAGAGAAATTCGAATA	4602	TGCAGGACCAAGAGAAATTCGAATA	4842
CATACACATANNNNACGTATGCCA		CACCCATAGANNNNACGTATGCCA		CAGAAATTCGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4363	TGCAGGACCAAGAGAAATTCGAATA	4603	TGCAGGACCAAGAGAAATTCGAATA	4843
CATCTTTCAANNNNACGTATGCCA		CACAGAAATGNNNNACGTATGCCA		CATTAAGCTCANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4364	TGCAGGACCAAGAGAAATTCGAATA	4604	TGCAGGACCAAGAGAAATTCGAATA	4844
CAGTATCGANNNNACGTATGCCA		CAGTATGAANNNNACGTATGCCA		CATAGAGGACNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4365	TGCAGGACCAAGAGAAATTCGAATA	4605	TGCAGGACCAAGAGAAATTCGAATA	4845
CATTAGCCAAANNNNACGTATGCCA		CAGTTTAAGTNNNNACGTATGCCA		CAATTGTTAGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4366	TGCAGGACCAAGAGAAATTCGAATA	4606	TGCAGGACCAAGAGAAATTCGAATA	4846
CAGCGGCGATNNNNACGTATGCCA		CAGCGTTATGNNNNACGTATGCCA		CAGCGTTGTAGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4367	TGCAGGACCAAGAGAAATTCGAATA	4607	TGCAGGACCAAGAGAAATTCGAATA	4847
CAGTTGTATANNNNACGTATGCCA		CATCCGTTACNNNNACGTATGCCA		CATTTGCTTGGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4368	TGCAGGACCAAGAGAAATTCGAATA	4608	TGCAGGACCAAGAGAAATTCGAATA	4848
CATTACCGCTNNNNACGTATGCCA		CACGAAACCTNNNNACGTATGCCA		CATAAGCGCTGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4369	TGCAGGACCAAGAGAAATTCGAATA	4609	TGCAGGACCAAGAGAAATTCGAATA	4849
CATGGCACTNNNNACGTATGCCA		CACCGGCTATGNNNNACGTATGCCA		CACCTACCAAGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4370	TGCAGGACCAAGAGAAATTCGAATA	4610	TGCAGGACCAAGAGAAATTCGAATA	4850
CAGATTTCAANNNNACGTATGCCA		CACGAAACCTNNNNACGTATGCCA		CAATCTATCAANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4371	TGCAGGACCAAGAGAAATTCGAATA	4611	TGCAGGACCAAGAGAAATTCGAATA	4851
CAGTATCTTNNNNACGTATGCCA		CAGGTTGTCTNNNNACGTATGCCA		CAGGTACACTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4372	TGCAGGACCAAGAGAAATTCGAATA	4612	TGCAGGACCAAGAGAAATTCGAATA	4852
CAGTACACAGANNNNACGTATGCCA		CACGGAAGGTTNNNNACGTATGCCA		CACCGGCTCAANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4373	TGCAGGACCAAGAGAAATTCGAATA	4613	TGCAGGACCAAGAGAAATTCGAATA	4853
CAGCGTTTCAANNNNACGTATGCCA		CATCCCGCGANNNNACGTATGCCA		CACAGAGACGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4374	TGCAGGACCAAGAGAAATTCGAATA	4614	TGCAGGACCAAGAGAAATTCGAATA	4854
CAGTATTTGGNNNNACGTATGCCA		CAGGCGATCTNNNNACGTATGCCA		CAATCATGGGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4375	TGCAGGACCAAGAGAAATTCGAATA	4615	TGCAGGACCAAGAGAAATTCGAATA	4855
CATCTCTATANNNNACGTATGCCA		CATCTATATGNNNNACGTATGCCA		CATATAGGTTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4376	TGCAGGACCAAGAGAAATTCGAATA	4616	TGCAGGACCAAGAGAAATTCGAATA	4856
CAGTCTGTACNNNNACGTATGCCA		CATTCGTCTGNNNNACGTATGCCA		CAGATTTACNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4377	TGCAGGACCAAGAGAAATTCGAATA	4617	TGCAGGACCAAGAGAAATTCGAATA	4857
CAGCTAGCAANNNNACGTATGCCA		CACCGGCTCTNNNNACGTATGCCA		CAATGGAACGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4378	TGCAGGACCAAGAGAAATTCGAATA	4618	TGCAGGACCAAGAGAAATTCGAATA	4858
CAATTTGGTCCNNNNACGTATGCCA		CACGCAATCAANNNNACGTATGCCA		CAGCTTTCAANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4379	TGCAGGACCAAGAGAAATTCGAATA	4619	TGCAGGACCAAGAGAAATTCGAATA	4859
CAGCTCAGCGNNNNACGTATGCCA		CAGTCTGCTCGNNNNACGTATGCCA		CAGTCTGCTGGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4380	TGCAGGACCAAGAGAAATTCGAATA	4620	TGCAGGACCAAGAGAAATTCGAATA	4860
CACACGAAACNNNNACGTATGCCA		CATAGCAGGANNNNACGTATGCCA		CATACTCCCAANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4381	TGCAGGACCAAGAGAAATTCGAATA	4621	TGCAGGACCAAGAGAAATTCGAATA	4861
CAGAAATTCATNNNNACGTATGCCA		CAGATGGAGTNNNNACGTATGCCA		CAGCGCGTCTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4382	TGCAGGACCAAGAGAAATTCGAATA	4622	TGCAGGACCAAGAGAAATTCGAATA	4862
CATTTCGCACTNNNNACGTATGCCA		CARAGCACTNNNNACGTATGCCA		CAGTCTACTGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4383	TGCAGGACCAAGAGAAATTCGAATA	4623	TGCAGGACCAAGAGAAATTCGAATA	4863
CAGCGTTAAGNNNNACGTATGCCA		CARAGCGGCTNNNNACGTATGCCA		CARAGCGAGGNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4384	TGCAGGACCAAGAGAAATTCGAATA	4624	TGCAGGACCAAGAGAAATTCGAATA	4864
CAGCGCTGCTNNNNACGTATGCCA		CAGGTTTGTNNNNACGTATGCCA		CAGCTACTATANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4385	TGCAGGACCAAGAGAAATTCGAATA	4625	TGCAGGACCAAGAGAAATTCGAATA	4865
CATTAACAGTNNNNACGTATGCCA		CACCTGTGATNNNNACGTATGCCA		CATCTCTCGANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4386	TGCAGGACCAAGAGAAATTCGAATA	4626	TGCAGGACCAAGAGAAATTCGAATA	4866
CAGAGATTTNNNNACGTATGCCA		CAATTGATCTNNNNACGTATGCCA		CACCATAGANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4387	TGCAGGACCAAGAGAAATTCGAATA	4627	TGCAGGACCAAGAGAAATTCGAATA	4867
CAATCCAGTTGNNNNACGTATGCCA		CATCCGTTGCCNNNNACGTATGCCA		CAGAGAGCATNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4388	TGCAGGACCAAGAGAAATTCGAATA	4628	TGCAGGACCAAGAGAAATTCGAATA	4868
CAGGTTTGCANNNNACGTATGCCA		CATCTCAGANNNNACGTATGCCA		CACGATATGCHNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4389	TGCAGGACCAAGAGAAATTCGAATA	4629	TGCAGGACCAAGAGAAATTCGAATA	4869
CAGATGACCTNNNNACGTATGCCA		CARAGCGGTTNNNNACGTATGCCA		CAGTTGCTCTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4390	TGCAGGACCAAGAGAAATTCGAATA	4630	TGCAGGACCAAGAGAAATTCGAATA	4870
CACAGCTATGNNNNACGTATGCCA		CACACCGCTGNNNNACGTATGCCA		CARACAGTTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4391	TGCAGGACCAAGAGAAATTCGAATA	4631	TGCAGGACCAAGAGAAATTCGAATA	4871
CATGTGGGCGNNNNACGTATGCCA		CAGCTAGTTGNNNNACGTATGCCA		CATGTGCACTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4392	TGCAGGACCAAGAGAAATTCGAATA	4632	TGCAGGACCAAGAGAAATTCGAATA	4872
CAGACCAAGGNNNNACGTATGCCA		CAGCGTTACTNNNNACGTATGCCA		CACCTCGCANNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4393	TGCAGGACCAAGAGAAATTCGAATA	4633	TGCAGGACCAAGAGAAATTCGAATA	4873
CAGTGTCTACTNNNNACGTATGCCA		CATAGCGCTGNNNNACGTATGCCA		CACCGTTTCTNNNNACGTATGCCA	
TGCAGGACCAAGAGAAATTCGAATA	4394	TGCAGGACCAAGAGAAATTCGAATA	4634	TGCAGGACCAAGAGAAATTCGAATA	4874
CATTCGAACCTNNNNACGTATGCCA		CAGGTAACGNNNNACGTATGCCA		CAACCTCGATNNNNACGTATGCCA	

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池 -19	SEQ ID NO.	池 -20	SEQ ID NO.	池 -21	SEQ ID NO.
TGCAGGACCAAGAAATTCGAATA	4395	TGCAGGACCAAGAAATTCGAATA	4625	TGCAGGACCAAGAAATTCGAATA	4875
CACAAATCCCTTNNNCTAGCGTTAC		CAGAAACCAAGNNNCTAGCGTTAC		CATTGGCTTCHNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4396	TGCAGGACCAAGAAATTCGAATA	4626	TGCAGGACCAAGAAATTCGAATA	4876
CATCGCTGCAANNCTAGCGTTAC		CAGGACTGTNNNCTAGCGTTAC		CATCGCAAGNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4397	TGCAGGACCAAGAAATTCGAATA	4627	TGCAGGACCAAGAAATTCGAATA	4877
CAAAAGCACTCHNNCTAGCGTTAC		CAATCGTGTGNNNCTAGCGTTAC		CATGCAAGAGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4398	TGCAGGACCAAGAAATTCGAATA	4628	TGCAGGACCAAGAAATTCGAATA	4878
CAATGAATCTNNNCTAGCGTTAC		CAGTCACGGCHNNCTAGCGTTAC		CAGAAATATGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4399	TGCAGGACCAAGAAATTCGAATA	4629	TGCAGGACCAAGAAATTCGAATA	4879
CATGGCCGCTNNNCTAGCGTTAC		CATCTCGTACHNNCTAGCGTTAC		CAACACATATNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4400	TGCAGGACCAAGAAATTCGAATA	4630	TGCAGGACCAAGAAATTCGAATA	4880
CATGGCAGGCHNNCTAGCGTTAC		CAATGCGCGCHNNCTAGCGTTAC		CAGTAGCACTHNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4401	TGCAGGACCAAGAAATTCGAATA	4631	TGCAGGACCAAGAAATTCGAATA	4881
CAGTCTTGGTNNNCTAGCGTTAC		CAGATAGTCGNNCTAGCGTTAC		CACGCGCGGCHNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4402	TGCAGGACCAAGAAATTCGAATA	4632	TGCAGGACCAAGAAATTCGAATA	4882
CAAAAGCTAGCHNNCTAGCGTTAC		CACATGTACGNNNCTAGCGTTAC		CATAGTGCACHNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4403	TGCAGGACCAAGAAATTCGAATA	4633	TGCAGGACCAAGAAATTCGAATA	4883
CAATGGACCAANNCTAGCGTTAC		CAGCGTATCANNNCTAGCGTTAC		CATCAATGCGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4404	TGCAGGACCAAGAAATTCGAATA	4634	TGCAGGACCAAGAAATTCGAATA	4884
CATGACGCGCTNNNCTAGCGTTAC		CACAATTTCTNNNCTAGCGTTAC		CAATGTAAAGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4405	TGCAGGACCAAGAAATTCGAATA	4635	TGCAGGACCAAGAAATTCGAATA	4885
CAATGCTAGCHNNCTAGCGTTAC		CAGACTCTATNNNCTAGCGTTAC		CAATAGTATGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4406	TGCAGGACCAAGAAATTCGAATA	4636	TGCAGGACCAAGAAATTCGAATA	4886
CAGACAGAGTNNNCTAGCGTTAC		CATCATCCGANNNCTAGCGTTAC		CATCAATCANNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4407	TGCAGGACCAAGAAATTCGAATA	4637	TGCAGGACCAAGAAATTCGAATA	4887
CAAAAGCTAGCHNNCTAGCGTTAC		CAGGCTTGGCHNNCTAGCGTTAC		CACACTTAGGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4408	TGCAGGACCAAGAAATTCGAATA	4638	TGCAGGACCAAGAAATTCGAATA	4888
CATACAAAAGNNCTAGCGTTAC		CAGTTCCTTGNNNCTAGCGTTAC		CATAGGATTAANNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4409	TGCAGGACCAAGAAATTCGAATA	4639	TGCAGGACCAAGAAATTCGAATA	4889
CATCTCCTGANNCTAGCGTTAC		CAATGAGATNNNCTAGCGTTAC		CAATCCCGTNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4410	TGCAGGACCAAGAAATTCGAATA	4640	TGCAGGACCAAGAAATTCGAATA	4890
CAAAAGCTAGCHNNCTAGCGTTAC		CAGTGTATCCNNNCTAGCGTTAC		CACCAATCCGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4411	TGCAGGACCAAGAAATTCGAATA	4641	TGCAGGACCAAGAAATTCGAATA	4891
CAAAATCAAGANNCTAGCGTTAC		CATACGCCCCGNNNCTAGCGTTAC		CACATTATAGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4412	TGCAGGACCAAGAAATTCGAATA	4642	TGCAGGACCAAGAAATTCGAATA	4892
CAAAAGCTAGCHNNCTAGCGTTAC		CATGGCCGCHNNNCTAGCGTTAC		CAGCGTATGTNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4413	TGCAGGACCAAGAAATTCGAATA	4643	TGCAGGACCAAGAAATTCGAATA	4893
CAGCTATATNNNCTAGCGTTAC		CAGGCTGTGNNNCTAGCGTTAC		CAATTTGGTATNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4414	TGCAGGACCAAGAAATTCGAATA	4644	TGCAGGACCAAGAAATTCGAATA	4894
CAGGACCCGCTNNNCTAGCGTTAC		CAGGTAGCCCHNNCTAGCGTTAC		CATTTCTGCHNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4415	TGCAGGACCAAGAAATTCGAATA	4645	TGCAGGACCAAGAAATTCGAATA	4895
CAGTCCCTATNNNCTAGCGTTAC		CATGACGTTGNNNCTAGCGTTAC		CAGAAATCCGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4416	TGCAGGACCAAGAAATTCGAATA	4646	TGCAGGACCAAGAAATTCGAATA	4896
CATTGCTGANNNCTAGCGTTAC		CAGCCACTATNNNCTAGCGTTAC		CACTTTCAAGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4417	TGCAGGACCAAGAAATTCGAATA	4647	TGCAGGACCAAGAAATTCGAATA	4897
CAATGGCTTNNNCTAGCGTTAC		CAAAAGCTAANNCTAGCGTTAC		CAGGATCAZNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4418	TGCAGGACCAAGAAATTCGAATA	4648	TGCAGGACCAAGAAATTCGAATA	4898
CAATCAATTCNNNCTAGCGTTAC		CAGGAGTATGNNNCTAGCGTTAC		CACAGTGTCHNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4419	TGCAGGACCAAGAAATTCGAATA	4649	TGCAGGACCAAGAAATTCGAATA	4899
CAGATGTATNNNCTAGCGTTAC		CAGTGTATANNNCTAGCGTTAC		CACCTAGTCCNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4420	TGCAGGACCAAGAAATTCGAATA	4650	TGCAGGACCAAGAAATTCGAATA	4900
CAGATCAATNNNCTAGCGTTAC		CATAATTCGANNNCTAGCGTTAC		CAAGTCCCGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4421	TGCAGGACCAAGAAATTCGAATA	4651	TGCAGGACCAAGAAATTCGAATA	4901
CAACCCGCTAANNCTAGCGTTAC		CAGGCTTGGNNNCTAGCGTTAC		CATGPAATCTNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4422	TGCAGGACCAAGAAATTCGAATA	4652	TGCAGGACCAAGAAATTCGAATA	4902
CAAAATTCGANNNCTAGCGTTAC		CAACATGTGNNNCTAGCGTTAC		CATCAATTAANNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4423	TGCAGGACCAAGAAATTCGAATA	4653	TGCAGGACCAAGAAATTCGAATA	4903
CAATGTACATNNNCTAGCGTTAC		CATCAGCGCGNNNCTAGCGTTAC		CAAAACCTGANNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4424	TGCAGGACCAAGAAATTCGAATA	4654	TGCAGGACCAAGAAATTCGAATA	4904
CAGCCATGTTNNNCTAGCGTTAC		CAGCCCGGTANNNCTAGCGTTAC		CATCATGATANNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4425	TGCAGGACCAAGAAATTCGAATA	4655	TGCAGGACCAAGAAATTCGAATA	4905
CAAAATTCGNNNCTAGCGTTAC		CAGCATTCACNNNCTAGCGTTAC		CAAAAGCTGNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4426	TGCAGGACCAAGAAATTCGAATA	4656	TGCAGGACCAAGAAATTCGAATA	4906
CACACGTCGNNNCTAGCGTTAC		CATTCCCTTNNNCTAGCGTTAC		CAAGCATACNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATA	4427	TGCAGGACCAAGAAATTCGAATA	4657	TGCAGGACCAAGAAATTCGAATA	4907
CACATATGCGNNNCTAGCGTTAC		CAACCGTCCGNNNCTAGCGTTAC		CAGGCAATGNNNCTAGCGTTAC	

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池 -19	SEQ ID No.	池 -20	SEQ ID No.	池 -21	SEQ ID No.
TGCAGGACCAGAGAAATTCGAATA	4428	TGCAGGACCAGAGAAATTCGAATA	4668	TGCAGGACCAGAGAAATTCGAATA	4908
CAGCTGTGGTANNHCTAGCGTTAC		CACACCTTACNNHCTAGCGTTAC		CAGCGAGTCCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4429	TGCAGGACCAGAGAAATTCGAATA	4669	TGCAGGACCAGAGAAATTCGAATA	4909
CAGTCAGTCTNNHCTAGCGTTAC		CAGGAGTTGANNHCTAGCGTTAC		CATTTTGAGANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4430	TGCAGGACCAGAGAAATTCGAATA	4670	TGCAGGACCAGAGAAATTCGAATA	4910
CAGTCCAGTTNNHCTAGCGTTAC		CAGACAGAGCHHCTAGCGTTAC		CATTCCTTANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4431	TGCAGGACCAGAGAAATTCGAATA	4671	TGCAGGACCAGAGAAATTCGAATA	4911
CAGATGAGCCHHCTAGCGTTAC		CAGCTTACGANNHCTAGCGTTAC		CATCGAAACANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4432	TGCAGGACCAGAGAAATTCGAATA	4672	TGCAGGACCAGAGAAATTCGAATA	4912
CAAAACCATNNHCTAGCGTTAC		CATCGCTCATNNHCTAGCGTTAC		CAGCTCCGTCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4433	TGCAGGACCAGAGAAATTCGAATA	4673	TGCAGGACCAGAGAAATTCGAATA	4913
CACCTGCGCTNNHCTAGCGTTAC		CACCAAGCCGNNHCTAGCGTTAC		CACCGAGTTCCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4434	TGCAGGACCAGAGAAATTCGAATA	4674	TGCAGGACCAGAGAAATTCGAATA	4914
CACACCGCGNNHCTAGCGTTAC		CACCCCTCGTNNHCTAGCGTTAC		CACCTTGGCTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4435	TGCAGGACCAGAGAAATTCGAATA	4675	TGCAGGACCAGAGAAATTCGAATA	4915
CATACTACANNHCTAGCGTTAC		CRAACTAGTNNHCTAGCGTTAC		CACCGCCATCCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4436	TGCAGGACCAGAGAAATTCGAATA	4676	TGCAGGACCAGAGAAATTCGAATA	4916
CATACCCGACNNHCTAGCGTTAC		CAGAGTGAGTNNHCTAGCGTTAC		CAGATCGATCCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4437	TGCAGGACCAGAGAAATTCGAATA	4677	TGCAGGACCAGAGAAATTCGAATA	4917
CATCTATAGANNHCTAGCGTTAC		CACAATACTANNHCTAGCGTTAC		CAACGCGCTCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4438	TGCAGGACCAGAGAAATTCGAATA	4678	TGCAGGACCAGAGAAATTCGAATA	4918
CAGGTGAGGCHHCTAGCGTTAC		CACCTTGGTNNHCTAGCGTTAC		CATCTCGAGANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4439	TGCAGGACCAGAGAAATTCGAATA	4679	TGCAGGACCAGAGAAATTCGAATA	4919
CACATACTCHHCTAGCGTTAC		CATTCRACCHHCTAGCGTTAC		CAATTGGCACCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4440	TGCAGGACCAGAGAAATTCGAATA	4680	TGCAGGACCAGAGAAATTCGAATA	4920
CATAGGAGTANNHCTAGCGTTAC		CAGTTATCCCHHCTAGCGTTAC		CACGCGCAGTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4441	TGCAGGACCAGAGAAATTCGAATA	4681	TGCAGGACCAGAGAAATTCGAATA	4921
CAGTGTGAGANNHCTAGCGTTAC		CAAAATTTGNNHCTAGCGTTAC		CACCTTACGTCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4442	TGCAGGACCAGAGAAATTCGAATA	4682	TGCAGGACCAGAGAAATTCGAATA	4922
CATTCGCGTNNHCTAGCGTTAC		CRCACCCCAANNHCTAGCGTTAC		CRAAACTAGCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4443	TGCAGGACCAGAGAAATTCGAATA	4683	TGCAGGACCAGAGAAATTCGAATA	4923
CAGCTACGAGNNHCTAGCGTTAC		CAGTTCCACANNHCTAGCGTTAC		CAGCGTAACTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4444	TGCAGGACCAGAGAAATTCGAATA	4684	TGCAGGACCAGAGAAATTCGAATA	4924
CAGGTGACANNHCTAGCGTTAC		CAGCTCTACTNNHCTAGCGTTAC		CAGATGTTCHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4445	TGCAGGACCAGAGAAATTCGAATA	4685	TGCAGGACCAGAGAAATTCGAATA	4925
CACACTAGCANNHCTAGCGTTAC		CATCAACAGCHHCTAGCGTTAC		CAAAACGAGTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4446	TGCAGGACCAGAGAAATTCGAATA	4686	TGCAGGACCAGAGAAATTCGAATA	4926
CAACGAGACCHHCTAGCGTTAC		CATTTGGTGGNNHCTAGCGTTAC		CAATAGACANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4447	TGCAGGACCAGAGAAATTCGAATA	4687	TGCAGGACCAGAGAAATTCGAATA	4927
CATTTTAAANNHCTAGCGTTAC		CAGCATCTGANNHCTAGCGTTAC		CATATTTGGANNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4448	TGCAGGACCAGAGAAATTCGAATA	4688	TGCAGGACCAGAGAAATTCGAATA	4928
CACITTCGAGANNHCTAGCGTTAC		CATGGCAGTNNHCTAGCGTTAC		CATCGGTGTHHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	4449	TGCAGGACCAGAGAAATTCGAATA	4689	TGCAGGACCAGAGAAATTCGAATA	4929
CATGCAATGCHHNGATCGACATG		CAGATCTCTCHHNGATCGACATG		CATGCTCGATHHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4450	TGCAGGACCAGAGAAATTCGAATA	4690	TGCAGGACCAGAGAAATTCGAATA	4930
CAGACGCGCCHHNGATCGACATG		CAGAGCCGCGANNHNGATCGACATG		CATTTGAGCHHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4451	TGCAGGACCAGAGAAATTCGAATA	4691	TGCAGGACCAGAGAAATTCGAATA	4931
CAGTITTTCAHNNHNGATCGACATG		CACCTCTCTAGHNNHNGATCGACATG		CACCTTCCAGHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4452	TGCAGGACCAGAGAAATTCGAATA	4692	TGCAGGACCAGAGAAATTCGAATA	4932
CAGTTTTATCHHNGATCGACATG		CACGTGCGCTNNHNGATCGACATG		CAAAATTTGCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4453	TGCAGGACCAGAGAAATTCGAATA	4693	TGCAGGACCAGAGAAATTCGAATA	4933
CAACACCCGCHHNGATCGACATG		CAAGCTAGTCHHNNHNGATCGACATG		CAAAATTTGATHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4454	TGCAGGACCAGAGAAATTCGAATA	4694	TGCAGGACCAGAGAAATTCGAATA	4934
CACGCTTTACHHNNHNGATCGACATG		CAGCTATGTTCHHNNHNGATCGACATG		CATCGACTTCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4455	TGCAGGACCAGAGAAATTCGAATA	4695	TGCAGGACCAGAGAAATTCGAATA	4935
CAGTAAATGANNHNGATCGACATG		CATCTGCTTCHHNNHNGATCGACATG		CATGCTTACCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4456	TGCAGGACCAGAGAAATTCGAATA	4696	TGCAGGACCAGAGAAATTCGAATA	4936
CATTTGAGTCHHNNHNGATCGACATG		CAGTACGCTACHHNNHNGATCGACATG		CAGTGTACCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4457	TGCAGGACCAGAGAAATTCGAATA	4697	TGCAGGACCAGAGAAATTCGAATA	4937
CACACCACTTNNHNGATCGACATG		CAGACCCGCTNNHNGATCGACATG		CATATTAGTCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4458	TGCAGGACCAGAGAAATTCGAATA	4698	TGCAGGACCAGAGAAATTCGAATA	4938
CATGTAGACANNHNGATCGACATG		CACCTCTGACCHHNNHNGATCGACATG		CATGCACTCHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4459	TGCAGGACCAGAGAAATTCGAATA	4699	TGCAGGACCAGAGAAATTCGAATA	4939
CACGCTGAACHHNNHNGATCGACATG		CACGCTAGACHHNNHNGATCGACATG		CACACCTTGGTHHNNHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	4460	TGCAGGACCAGAGAAATTCGAATA	4700	TGCAGGACCAGAGAAATTCGAATA	4940
CACCTIATGTHHNNHNGATCGACATG		CAGTAATGACHHNNHNGATCGACATG		CAGCGTGCACHHNNHNGATCGACATG	

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池-19	SEQ ID NO:	池-20	SEQ ID NO:	池-21	SEQ ID NO:
TGCAGGACCAAGAAATTCGAATA	4461	TGCAGGACCAAGAAATTCGAATA	4701	TGCAGGACCAAGAAATTCGAATA	4941
CACGTGACGANNNGATCGACATG		CATGGTATCTNNNGATCGACATG		CACGGCTTTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4462	TGCAGGACCAAGAAATTCGAATA	4702	TGCAGGACCAAGAAATTCGAATA	4942
CAACCGGCTGNNNGATCGACATG		CACACGTACANNNGATCGACATG		CAITGTAAACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4463	TGCAGGACCAAGAAATTCGAATA	4703	TGCAGGACCAAGAAATTCGAATA	4943
CACAAATCTNNNGATCGACATG		CATGACTAATNNNGATCGACATG		CARACGTAAGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4464	TGCAGGACCAAGAAATTCGAATA	4704	TGCAGGACCAAGAAATTCGAATA	4944
CAACTAAAGANNNGATCGACATG		CACCTACCGCANNNGATCGACATG		CAGTAATCTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4465	TGCAGGACCAAGAAATTCGAATA	4705	TGCAGGACCAAGAAATTCGAATA	4945
CATAGTCTCCNNNGATCGACATG		CAGGCGCTTANNNGATCGACATG		CAGTCTGCTTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4466	TGCAGGACCAAGAAATTCGAATA	4706	TGCAGGACCAAGAAATTCGAATA	4946
CACATAACATANNNGATCGACATG		CATGCTTAGCANNNGATCGACATG		CAGATGGTTCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4467	TGCAGGACCAAGAAATTCGAATA	4707	TGCAGGACCAAGAAATTCGAATA	4947
CATGCCCGCANNNGATCGACATG		CAGCTTAGCANNNGATCGACATG		CACCTGCCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4468	TGCAGGACCAAGAAATTCGAATA	4708	TGCAGGACCAAGAAATTCGAATA	4948
CACCTGGAGCANNNGATCGACATG		CARATCAACANNNGATCGACATG		CATACCGAACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4469	TGCAGGACCAAGAAATTCGAATA	4709	TGCAGGACCAAGAAATTCGAATA	4949
CACCAATCCANNNGATCGACATG		CAGTAGTAANNNGATCGACATG		CAGTAGCTGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4470	TGCAGGACCAAGAAATTCGAATA	4710	TGCAGGACCAAGAAATTCGAATA	4950
CAAACTCTANNNGATCGACATG		CATAGTTCGGNNNGATCGACATG		CACAGGTGAANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4471	TGCAGGACCAAGAAATTCGAATA	4711	TGCAGGACCAAGAAATTCGAATA	4951
CARAGCGCTANNNGATCGACATG		CAGTTGTGACNNNGATCGACATG		CAAGGTGAGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4472	TGCAGGACCAAGAAATTCGAATA	4712	TGCAGGACCAAGAAATTCGAATA	4952
CAGTCAGAGANNNGATCGACATG		CACGCGTAGCANNNGATCGACATG		CASAGCGTTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4473	TGCAGGACCAAGAAATTCGAATA	4713	TGCAGGACCAAGAAATTCGAATA	4953
CATCGGAGCTNNNGATCGACATG		CACATATGTGNNNGATCGACATG		CAGAAATGGCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4474	TGCAGGACCAAGAAATTCGAATA	4714	TGCAGGACCAAGAAATTCGAATA	4954
CATCGCGCTNNNGATCGACATG		CATTGCGCTANNNGATCGACATG		CAGAGTGCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4475	TGCAGGACCAAGAAATTCGAATA	4715	TGCAGGACCAAGAAATTCGAATA	4955
CATTAGGTGNNNGATCGACATG		CAATATCTCANNNGATCGACATG		CAAAACCTCTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4476	TGCAGGACCAAGAAATTCGAATA	4716	TGCAGGACCAAGAAATTCGAATA	4956
CATCCGCGCANNNGATCGACATG		CACCTTGAAANNNGATCGACATG		CATAACCTCTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4477	TGCAGGACCAAGAAATTCGAATA	4717	TGCAGGACCAAGAAATTCGAATA	4957
CAAAAGCAGCANNNGATCGACATG		CACCTAGTAGCANNNGATCGACATG		CATTAGTCCGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4478	TGCAGGACCAAGAAATTCGAATA	4718	TGCAGGACCAAGAAATTCGAATA	4958
CAGTGGCGCTNNNGATCGACATG		CATCCGACATNNNGATCGACATG		CAGTTCGCGCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4479	TGCAGGACCAAGAAATTCGAATA	4719	TGCAGGACCAAGAAATTCGAATA	4959
CAACGATATTNNNGATCGACATG		CAGTATCGACNNNGATCGACATG		CAGTGA-CCTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4480	TGCAGGACCAAGAAATTCGAATA	4720	TGCAGGACCAAGAAATTCGAATA	4960
CAACACAGGNNNGATCGACATG		CAGGCGCTCANNNGATCGACATG		CAGGACATGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4481	TGCAGGACCAAGAAATTCGAATA	4721	TGCAGGACCAAGAAATTCGAATA	4961
CAGTCCGAAANNNGATCGACATG		CAGGCGCTTANNNGATCGACATG		CATATGGAANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4482	TGCAGGACCAAGAAATTCGAATA	4722	TGCAGGACCAAGAAATTCGAATA	4962
CATCAAGCCANNNGATCGACATG		CACATAGCACNNNGATCGACATG		CACTAGCGGCHNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4483	TGCAGGACCAAGAAATTCGAATA	4723	TGCAGGACCAAGAAATTCGAATA	4963
CAGCTAATCANNNGATCGACATG		CACGACCTTGNNGATCGACATG		CAGCGTTTAGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4484	TGCAGGACCAAGAAATTCGAATA	4724	TGCAGGACCAAGAAATTCGAATA	4964
CAACACGAGNNNGATCGACATG		CATGTGACGCHNNNGATCGACATG		CACATATGCTCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4485	TGCAGGACCAAGAAATTCGAATA	4725	TGCAGGACCAAGAAATTCGAATA	4965
CATCCATCANNNGATCGACATG		CAATCGCTAGNNNGATCGACATG		CACATGTGACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4486	TGCAGGACCAAGAAATTCGAATA	4726	TGCAGGACCAAGAAATTCGAATA	4966
CAGTCCGACGNNNGATCGACATG		CAGAAATAGANNNGATCGACATG		CAATCAAAAGCHNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4487	TGCAGGACCAAGAAATTCGAATA	4727	TGCAGGACCAAGAAATTCGAATA	4967
CATGGCAGCCHNNNGATCGACATG		CAGGCGCTCANNNGATCGACATG		CAATAAACCTCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4488	TGCAGGACCAAGAAATTCGAATA	4728	TGCAGGACCAAGAAATTCGAATA	4968
CATTTCAGANNNGATCGACATG		CAPAATTGCATNNNGATCGACATG		CACCGGACCTCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4489	TGCAGGACCAAGAAATTCGAATA	4729	TGCAGGACCAAGAAATTCGAATA	4969
CATACGCTCTCANNNGATCGACATG		CATGGAACCTCANNNGATCGACATG		CACCGCGCTAGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4490	TGCAGGACCAAGAAATTCGAATA	4730	TGCAGGACCAAGAAATTCGAATA	4970
CACCGATCTTNNNGATCGACATG		CAAGCGCATNNNGATCGACATG		CACCTGTGGTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4491	TGCAGGACCAAGAAATTCGAATA	4731	TGCAGGACCAAGAAATTCGAATA	4971
CAATTAAGCTNNNGATCGACATG		CATTCCGCTCANNNGATCGACATG		CAGAACCTGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4492	TGCAGGACCAAGAAATTCGAATA	4732	TGCAGGACCAAGAAATTCGAATA	4972
CAAACTTCCNNNGATCGACATG		CMAATTCTCANNNGATCGACATG		CACGCGCTGACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATA	4493	TGCAGGACCAAGAAATTCGAATA	4733	TGCAGGACCAAGAAATTCGAATA	4973
CAGTCCGCTTNNNGATCGACATG		CATAATGCGCHNNNGATCGACATG		CAGGCGCTCANNNGATCGACATG	

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池-19	SEQ ID No:	池-20	SEQ ID No:	池-21	SEQ ID No:
TGCAGGACCAGAGAATTGGAATA	4494	TGCAGGACCAGAGAATTGGAATA	4734	TGCAGGACCAGAGAATTGGAATA	4974
CAGCCAGTATNNNGATCGACATG		CAACGCATTGNNNGATCGACATG		CACCGCAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4495	TGCAGGACCAGAGAATTGGAATA	4735	TGCAGGACCAGAGAATTGGAATA	4975
CAGAGAAANNNNGATCGACATG		CATGTCCGTANNNGATCGACATG		CATCCTACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4496	TGCAGGACCAGAGAATTGGAATA	4736	TGCAGGACCAGAGAATTGGAATA	4976
CAATAGCCANNNGATCGACATG		CATTTCAACNNNGATCGACATG		CATCCGACCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4497	TGCAGGACCAGAGAATTGGAATA	4737	TGCAGGACCAGAGAATTGGAATA	4977
CACACGTCCNNNGATCGACATG		CATAGTACTNNNGATCGACATG		CATGTAGGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4498	TGCAGGACCAGAGAATTGGAATA	4738	TGCAGGACCAGAGAATTGGAATA	4978
CAAGATTATCNNNGATCGACATG		CAAAATTAGTCNNNGATCGACATG		CACGGCGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4499	TGCAGGACCAGAGAATTGGAATA	4739	TGCAGGACCAGAGAATTGGAATA	4979
CACCTTTCCGNNNGATCGACATG		CAGGAATATNNNGATCGACATG		CACCTATTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4500	TGCAGGACCAGAGAATTGGAATA	4740	TGCAGGACCAGAGAATTGGAATA	4980
CACAACTCCGNNNGATCGACATG		CATTTTATAANNNGATCGACATG		CAGAACAAACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4501	TGCAGGACCAGAGAATTGGAATA	4741	TGCAGGACCAGAGAATTGGAATA	4981
CAGGACGTANNNGATCGACATG		CACACGTAAACNNNGATCGACATG		CATCCCTATTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4502	TGCAGGACCAGAGAATTGGAATA	4742	TGCAGGACCAGAGAATTGGAATA	4982
CACCCGACGNNNGATCGACATG		CAGTTTCCGTNNNGATCGACATG		CATACTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4503	TGCAGGACCAGAGAATTGGAATA	4743	TGCAGGACCAGAGAATTGGAATA	4983
CATCCGTATCNNNGATCGACATG		CAGGTATCTANNNGATCGACATG		CAGCGCTTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4504	TGCAGGACCAGAGAATTGGAATA	4744	TGCAGGACCAGAGAATTGGAATA	4984
CATTTCTTANNNGATCGACATG		CATCTAGTGGNNNGATCGACATG		CAGCTTCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4505	TGCAGGACCAGAGAATTGGAATA	4745	TGCAGGACCAGAGAATTGGAATA	4985
CATGCTACAGNNNGATCGACATG		CAGAGTACAGNNNGATCGACATG		CACACCATACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4506	TGCAGGACCAGAGAATTGGAATA	4746	TGCAGGACCAGAGAATTGGAATA	4986
CAGTTACTTNNNGATCGACATG		CAACTCCAGANNNGATCGACATG		CAGTGTCAACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4507	TGCAGGACCAGAGAATTGGAATA	4747	TGCAGGACCAGAGAATTGGAATA	4987
CAAAATGCCGNNNGATCGACATG		CAAAAACCAANNNGATCGACATG		CATACCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4508	TGCAGGACCAGAGAATTGGAATA	4748	TGCAGGACCAGAGAATTGGAATA	4988
CACCAGGACNNNGATCGACATG		CAGCCGCAACNNNGATCGACATG		CAAAATCCGACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4509	TGCAGGACCAGAGAATTGGAATA	4749	TGCAGGACCAGAGAATTGGAATA	4989
CATGGCCACNNNGATCGACATG		CAGATCTTANNNGATCGACATG		CAGCCGCGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4510	TGCAGGACCAGAGAATTGGAATA	4750	TGCAGGACCAGAGAATTGGAATA	4990
CAAAAGAGCTNNNGATCGACATG		CATAGAGCTNNNGATCGACATG		CACCTGCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4511	TGCAGGACCAGAGAATTGGAATA	4751	TGCAGGACCAGAGAATTGGAATA	4991
CATTAGCCACNNNGATCGACATG		CAGCAITCTCNNNGATCGACATG		CACGTTACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4512	TGCAGGACCAGAGAATTGGAATA	4752	TGCAGGACCAGAGAATTGGAATA	4992
CATGCGGATNNNGATCGACATG		CAGCAGGCCANNNGATCGACATG		CACGATTAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4513	TGCAGGACCAGAGAATTGGAATA	4753	TGCAGGACCAGAGAATTGGAATA	4993
CACAGGTGTNNNGATCGACATG		CAAGCTGCCGNNNGATCGACATG		CAAACTTAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4514	TGCAGGACCAGAGAATTGGAATA	4754	TGCAGGACCAGAGAATTGGAATA	4994
CAAAACATAGANNNGATCGACATG		CACCCGCTACNNNGATCGACATG		CAATCGGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4515	TGCAGGACCAGAGAATTGGAATA	4755	TGCAGGACCAGAGAATTGGAATA	4995
CAGAAATGATNNNGATCGACATG		CACAAAGCAANNNGATCGACATG		CAGGAACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4516	TGCAGGACCAGAGAATTGGAATA	4756	TGCAGGACCAGAGAATTGGAATA	4996
CATGCTGCTANNNGATCGACATG		CAGATGTATNNNGATCGACATG		CATCACACGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4517	TGCAGGACCAGAGAATTGGAATA	4757	TGCAGGACCAGAGAATTGGAATA	4997
CAAGGCGAGTNNNGATCGACATG		CACGGTATTGNNNGATCGACATG		CACATTGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4518	TGCAGGACCAGAGAATTGGAATA	4758	TGCAGGACCAGAGAATTGGAATA	4998
CATAGGTTATNNNGATCGACATG		CAGTATTTAGNNNGATCGACATG		CACCGGATATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4519	TGCAGGACCAGAGAATTGGAATA	4759	TGCAGGACCAGAGAATTGGAATA	4999
CATTTTCTGNNNGATCGACATG		CAGGATCAGANNNGATCGACATG		CACCTTATGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4520	TGCAGGACCAGAGAATTGGAATA	4760	TGCAGGACCAGAGAATTGGAATA	5000
CAAAACAGTNNNGATCGACATG		CAATCGAABANNNGATCGACATG		CAATTGGTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4521	TGCAGGACCAGAGAATTGGAATA	4761	TGCAGGACCAGAGAATTGGAATA	5001
CACGCGGTTANNNGATCGACATG		CAGCCATTTCNNNGATCGACATG		CAAGGCAACANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4522	TGCAGGACCAGAGAATTGGAATA	4762	TGCAGGACCAGAGAATTGGAATA	5002
CACITTTCGACNNNGATCGACATG		CATCAGACANNNGATCGACATG		CAGACCTTTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4523	TGCAGGACCAGAGAATTGGAATA	4763	TGCAGGACCAGAGAATTGGAATA	5003
CATAGACGTNNNGATCGACATG		CATTTGTCANNNGATCGACATG		CAGGACCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4524	TGCAGGACCAGAGAATTGGAATA	4764	TGCAGGACCAGAGAATTGGAATA	5004
CATCTAGTCCNNNGATCGACATG		CAACCTATCCNNNGATCGACATG		CACGTGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4525	TGCAGGACCAGAGAATTGGAATA	4765	TGCAGGACCAGAGAATTGGAATA	5005
CAAAACAGTNNNGATCGACATG		CAAAACCCGNNNGATCGACATG		CACAGATCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	4526	TGCAGGACCAGAGAATTGGAATA	4766	TGCAGGACCAGAGAATTGGAATA	5006
CATATGAGNNNGATCGACATG		CAGAGTCCGNNNGATCGACATG		CACACGACGNNNGATCGACATG	

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池 -19	SEQ ID NO.	池 -20	SEQ ID NO.	池 -21	SEQ ID NO.
TGCAGGACGAGAGAAATTCGAATA	4527	TGCAGGACGAGAGAAATTCGAATA	4767	TGCAGGACGAGAGAAATTCGAATA	5007
CATATTCGCCNNNTGCATCAGGT		CAATCATACANNNTGCATCAGGT		CAAGACTCCGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4528	TGCAGGACGAGAGAAATTCGAATA	4768	TGCAGGACGAGAGAAATTCGAATA	5008
CATTGCACGANNNTGCATCAGGT		CACAGATGAGNNNTGCATCAGGT		CAGTCCGAATCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4529	TGCAGGACGAGAGAAATTCGAATA	4769	TGCAGGACGAGAGAAATTCGAATA	5009
CAACTACTAANNNTGCATCAGGT		CACAGCTTAGNNNTGCATCAGGT		CAICCATPAANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4530	TGCAGGACGAGAGAAATTCGAATA	4770	TGCAGGACGAGAGAAATTCGAATA	5010
CAACTCATANNNTGCATCAGGT		CAACTTCTAANNNTGCATCAGGT		CAGTCCGACGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4531	TGCAGGACGAGAGAAATTCGAATA	4771	TGCAGGACGAGAGAAATTCGAATA	5011
CAAGGACTGANNNTGCATCAGGT		CACAACAGAGNNNTGCATCAGGT		CATGGTTGACNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4532	TGCAGGACGAGAGAAATTCGAATA	4772	TGCAGGACGAGAGAAATTCGAATA	5012
CACACATGCTNNNTGCATCAGGT		CACGTAGATCANNNTGCATCAGGT		CAAGACPAAGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4533	TGCAGGACGAGAGAAATTCGAATA	4773	TGCAGGACGAGAGAAATTCGAATA	5013
CAATAGCCAGNNNTGCATCAGGT		CACCTCCGANNNTGCATCAGGT		CAATATTCAGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4534	TGCAGGACGAGAGAAATTCGAATA	4774	TGCAGGACGAGAGAAATTCGAATA	5014
CAAGGAAGCTNNNTGCATCAGGT		CACAGCTTGNNNTGCATCAGGT		CACAGGAACTNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4535	TGCAGGACGAGAGAAATTCGAATA	4775	TGCAGGACGAGAGAAATTCGAATA	5015
CAACAGGCTTNNNTGCATCAGGT		CACAGACATCCNNNTGCATCAGGT		CACAGAGATCCNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4536	TGCAGGACGAGAGAAATTCGAATA	4776	TGCAGGACGAGAGAAATTCGAATA	5016
CACGCGCTTNNNTGCATCAGGT		CACAGCATCANNNTGCATCAGGT		CACGACACAGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4537	TGCAGGACGAGAGAAATTCGAATA	4777	TGCAGGACGAGAGAAATTCGAATA	5017
CAAGAAACGNNNTGCATCAGGT		CACCTTCTGACNNNTGCATCAGGT		CACATAACGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4538	TGCAGGACGAGAGAAATTCGAATA	4778	TGCAGGACGAGAGAAATTCGAATA	5018
CAGACATCTGNNNTGCATCAGGT		CACGCGCTAANNNTGCATCAGGT		CAGGAGGTGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4539	TGCAGGACGAGAGAAATTCGAATA	4779	TGCAGGACGAGAGAAATTCGAATA	5019
CAACGCGCTCANNNTGCATCAGGT		CATTTCATANNNTGCATCAGGT		CACGCGCTTANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4540	TGCAGGACGAGAGAAATTCGAATA	4780	TGCAGGACGAGAGAAATTCGAATA	5020
CAGTCACCGNNNTGCATCAGGT		CACGTGCGCANNNTGCATCAGGT		CACCGAGTGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4541	TGCAGGACGAGAGAAATTCGAATA	4781	TGCAGGACGAGAGAAATTCGAATA	5021
CAAGAGCGATNNNTGCATCAGGT		CAACGCTGGCANNNTGCATCAGGT		CACTTCAAGCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4542	TGCAGGACGAGAGAAATTCGAATA	4782	TGCAGGACGAGAGAAATTCGAATA	5022
CAATGCGCTTNNNTGCATCAGGT		CACAGATTCNNNTGCATCAGGT		CACAGCCGANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4543	TGCAGGACGAGAGAAATTCGAATA	4783	TGCAGGACGAGAGAAATTCGAATA	5023
CACCTGCAANNNTGCATCAGGT		CACAGGACTANNNTGCATCAGGT		CACCTTGACTNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4544	TGCAGGACGAGAGAAATTCGAATA	4784	TGCAGGACGAGAGAAATTCGAATA	5024
CAGTCGAACTNNNTGCATCAGGT		CATTGATTAGNNNTGCATCAGGT		CAGACCCAAANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4545	TGCAGGACGAGAGAAATTCGAATA	4785	TGCAGGACGAGAGAAATTCGAATA	5025
CATTGCGGANNNTGCATCAGGT		CACATGCATGNNNTGCATCAGGT		CATGATCTCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4546	TGCAGGACGAGAGAAATTCGAATA	4786	TGCAGGACGAGAGAAATTCGAATA	5026
CAAGCGTCTNNNTGCATCAGGT		CATTGACCTCANNNTGCATCAGGT		CAAGAAATGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4547	TGCAGGACGAGAGAAATTCGAATA	4787	TGCAGGACGAGAGAAATTCGAATA	5027
CAAGGATTGANNNTGCATCAGGT		CAGGCGACTGNNNTGCATCAGGT		CAGTGTGGCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4548	TGCAGGACGAGAGAAATTCGAATA	4788	TGCAGGACGAGAGAAATTCGAATA	5028
CAACGCTTANNNTGCATCAGGT		CATTCTCTCANNNTGCATCAGGT		CACATGTAGCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4549	TGCAGGACGAGAGAAATTCGAATA	4789	TGCAGGACGAGAGAAATTCGAATA	5029
CACCGCATANNNTGCATCAGGT		CAGCATTCAGNNNTGCATCAGGT		CATAGCCGCCNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4550	TGCAGGACGAGAGAAATTCGAATA	4790	TGCAGGACGAGAGAAATTCGAATA	5030
CACGATTTCCNNNTGCATCAGGT		CAGTAACTTANNNTGCATCAGGT		CAGTCTTCTNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4551	TGCAGGACGAGAGAAATTCGAATA	4791	TGCAGGACGAGAGAAATTCGAATA	5031
CAGTAAACANNNTGCATCAGGT		CAACTATGATNNNTGCATCAGGT		CATGTAAACNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4552	TGCAGGACGAGAGAAATTCGAATA	4792	TGCAGGACGAGAGAAATTCGAATA	5032
CAGGTGGCTCANNNTGCATCAGGT		CAACTAAGANNNTGCATCAGGT		CAACAGAGANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4553	TGCAGGACGAGAGAAATTCGAATA	4793	TGCAGGACGAGAGAAATTCGAATA	5033
CAATGCTCTGNNNTGCATCAGGT		CAATAGCTTANNNTGCATCAGGT		CAATGTCAGCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4554	TGCAGGACGAGAGAAATTCGAATA	4794	TGCAGGACGAGAGAAATTCGAATA	5034
CAGGTAATATNNNTGCATCAGGT		CACCTGCTGNNNTGCATCAGGT		CACCTGCTTANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4555	TGCAGGACGAGAGAAATTCGAATA	4795	TGCAGGACGAGAGAAATTCGAATA	5035
CAACTCGCTTNNNTGCATCAGGT		CAGGCTAGCCNNNTGCATCAGGT		CAACACCTCTNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4556	TGCAGGACGAGAGAAATTCGAATA	4796	TGCAGGACGAGAGAAATTCGAATA	5036
CACCAACGANNNTGCATCAGGT		CAGGTTGTACNNNTGCATCAGGT		CATAATTGACNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4557	TGCAGGACGAGAGAAATTCGAATA	4797	TGCAGGACGAGAGAAATTCGAATA	5037
CACGGAACAAANNNTGCATCAGGT		CATAAGCCGNNNTGCATCAGGT		CAGATTGCTCANNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4558	TGCAGGACGAGAGAAATTCGAATA	4798	TGCAGGACGAGAGAAATTCGAATA	5038
CACGCTGCTTNNNTGCATCAGGT		CAATCTTCTCANNNTGCATCAGGT		CAATAGAAAGNNNTGCATCAGGT	
TGCAGGACGAGAGAAATTCGAATA	4559	TGCAGGACGAGAGAAATTCGAATA	4799	TGCAGGACGAGAGAAATTCGAATA	5039
CACCTCCCTCANNNTGCATCAGGT		CACCAAGGANNNTGCATCAGGT		CATAAATAANNNTGCATCAGGT	

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池 -19	SEQ ID NO.	池 -20	SEQ ID NO.	池 -21	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATA CAGGCTTGCGNNHTGCATCAGGT	4560	TGCAGGACCAGAGAATTGGAATA CAACAAAGTNNHTGCATCAGGT	4800	TGCAGGACCAGAGAATTGGAATA CATGTCCAGANNHTGCATCAGGT	5040
TGCAGGACCAGAGAATTGGAATA CAAAATTTCGNNHTGCATCAGGT	4561	TGCAGGACCAGAGAATTGGAATA CAGGCCCCGNNHTGCATCAGGT	4801	TGCAGGACCAGAGAATTGGAATA CATTTGAGCCNNHTGCATCAGGT	5041
TGCAGGACCAGAGAATTGGAATA CATACCTAGGNNHTGCATCAGGT	4562	TGCAGGACCAGAGAATTGGAATA CAACATGCCNNHTGCATCAGGT	4802	TGCAGGACCAGAGAATTGGAATA CACCATCTNNHTGCATCAGGT	5042
TGCAGGACCAGAGAATTGGAATA CACACGCACGNNHTGCATCAGGT	4563	TGCAGGACCAGAGAATTGGAATA CATCGGAGTTNNHTGCATCAGGT	4803	TGCAGGACCAGAGAATTGGAATA CACTCCAGANNHTGCATCAGGT	5043
TGCAGGACCAGAGAATTGGAATA CACATTGCGNNHTGCATCAGGT	4564	TGCAGGACCAGAGAATTGGAATA CATAGCGGAANNHTGCATCAGGT	4804	TGCAGGACCAGAGAATTGGAATA CAGAGTCGANNHTGCATCAGGT	5044
TGCAGGACCAGAGAATTGGAATA CAGCATTAATNNHTGCATCAGGT	4565	TGCAGGACCAGAGAATTGGAATA CATCTACTCINNHTGCATCAGGT	4805	TGCAGGACCAGAGAATTGGAATA CATAACTCCCHNNHTGCATCAGGT	5045
TGCAGGACCAGAGAATTGGAATA CAAGACGGCCNNHTGCATCAGGT	4566	TGCAGGACCAGAGAATTGGAATA CATTTGACCCNNHTGCATCAGGT	4806	TGCAGGACCAGAGAATTGGAATA CAAGGCGCTCINNHTGCATCAGGT	5046
TGCAGGACCAGAGAATTGGAATA CACACACCATNNHTGCATCAGGT	4567	TGCAGGACCAGAGAATTGGAATA CAAGGCACGNNHTGCATCAGGT	4807	TGCAGGACCAGAGAATTGGAATA CAATTGTCANNHTGCATCAGGT	5047
TGCAGGACCAGAGAATTGGAATA CATGATTGANNHTGCATCAGGT	4568	TGCAGGACCAGAGAATTGGAATA CATTTGCCANNHTGCATCAGGT	4808	TGCAGGACCAGAGAATTGGAATA CACGCGTTAANNHTGCATCAGGT	5048

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池 -22	SEQ ID NO:	池 -23	SEQ ID NO:	池 -24	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA CATGTGTCGNNNACGTATGCCA	5049	TGCAGGACCAGAGAATTGGAATA CATAACTAACNNNACGTATGCCA	5289	TGCAGGACCAGAGAATTGGAATA CAGTTGCGCGNNNACGTATGCCA	5529
TGCAGGACCAGAGAATTGGAATA CACCCCTACGNNNACGTATGCCA	5050	TGCAGGACCAGAGAATTGGAATA CAAAAGCTCGNNNACGTATGCCA	5290	TGCAGGACCAGAGAATTGGAATA CAGGAGCACTGNNNACGTATGCCA	5530
TGCAGGACCAGAGAATTGGAATA CAGCGGCGAANNNACGTATGCCA	5051	TGCAGGACCAGAGAATTGGAATA CATGAGTTGNNNACGTATGCCA	5291	TGCAGGACCAGAGAATTGGAATA CACGGTAACNNNACGTATGCCA	5531
TGCAGGACCAGAGAATTGGAATA CATAGCGCGNNNACGTATGCCA	5052	TGCAGGACCAGAGAATTGGAATA CAACCAACAAANNNACGTATGCCA	5292	TGCAGGACCAGAGAATTGGAATA CAATGTGTGNNNACGTATGCCA	5532
TGCAGGACCAGAGAATTGGAATA CAGAGCGCTNNNACGTATGCCA	5053	TGCAGGACCAGAGAATTGGAATA CAGCCCTACGNNNACGTATGCCA	5293	TGCAGGACCAGAGAATTGGAATA CACGAGTTGNNNACGTATGCCA	5533
TGCAGGACCAGAGAATTGGAATA CAGACAGTGANNNACGTATGCCA	5054	TGCAGGACCAGAGAATTGGAATA CAGTTGAGAGNNNACGTATGCCA	5294	TGCAGGACCAGAGAATTGGAATA CATGAACCTGNNNACGTATGCCA	5534
TGCAGGACCAGAGAATTGGAATA CACTTTATCANNNACGTATGCCA	5055	TGCAGGACCAGAGAATTGGAATA CACAGTCACCTNNNACGTATGCCA	5295	TGCAGGACCAGAGAATTGGAATA CAACATCGCANNNACGTATGCCA	5535
TGCAGGACCAGAGAATTGGAATA CAGAGGAGTNNNACGTATGCCA	5056	TGCAGGACCAGAGAATTGGAATA CATGAAGACGNNNACGTATGCCA	5296	TGCAGGACCAGAGAATTGGAATA CAGAATTGCTNNNACGTATGCCA	5536
TGCAGGACCAGAGAATTGGAATA CAGTATTCGNNNACGTATGCCA	5057	TGCAGGACCAGAGAATTGGAATA CACCCCTATGNNNACGTATGCCA	5297	TGCAGGACCAGAGAATTGGAATA CAAAACACTTNNNACGTATGCCA	5537
TGCAGGACCAGAGAATTGGAATA CATCAGCGGNNNACGTATGCCA	5058	TGCAGGACCAGAGAATTGGAATA CATGGTTTGGNNNACGTATGCCA	5298	TGCAGGACCAGAGAATTGGAATA CATGTTTGGNNNACGTATGCCA	5538
TGCAGGACCAGAGAATTGGAATA CAAGCAGGTNNNACGTATGCCA	5059	TGCAGGACCAGAGAATTGGAATA CAGCACTCGNNNACGTATGCCA	5299	TGCAGGACCAGAGAATTGGAATA CACGGGTGCAANNNACGTATGCCA	5539
TGCAGGACCAGAGAATTGGAATA CAGTTAGTGNNNACGTATGCCA	5060	TGCAGGACCAGAGAATTGGAATA CAAAAGAGTTNNNACGTATGCCA	5300	TGCAGGACCAGAGAATTGGAATA CAGTATATGCGNNNACGTATGCCA	5540
TGCAGGACCAGAGAATTGGAATA CAATTTGAGTNNNACGTATGCCA	5061	TGCAGGACCAGAGAATTGGAATA CAGTTGCTGANNNACGTATGCCA	5301	TGCAGGACCAGAGAATTGGAATA CAGTTCAAGCANNNACGTATGCCA	5541
TGCAGGACCAGAGAATTGGAATA CAAGCAGCTTNNNACGTATGCCA	5062	TGCAGGACCAGAGAATTGGAATA CATCCCACTGNNNACGTATGCCA	5302	TGCAGGACCAGAGAATTGGAATA CATAATCAGTNNNACGTATGCCA	5542
TGCAGGACCAGAGAATTGGAATA CACCCGCTGNNNACGTATGCCA	5063	TGCAGGACCAGAGAATTGGAATA CAAAATTCGNNNACGTATGCCA	5303	TGCAGGACCAGAGAATTGGAATA CATTCCCAACNNNACGTATGCCA	5543
TGCAGGACCAGAGAATTGGAATA CAATATCTCTNNNACGTATGCCA	5064	TGCAGGACCAGAGAATTGGAATA CATCCACAGANNNACGTATGCCA	5304	TGCAGGACCAGAGAATTGGAATA CACTAGTAGCANNNACGTATGCCA	5544
TGCAGGACCAGAGAATTGGAATA CAATCTCTCATNNNACGTATGCCA	5065	TGCAGGACCAGAGAATTGGAATA CAAGAGTTTNNNACGTATGCCA	5305	TGCAGGACCAGAGAATTGGAATA CATTAATCGNNNACGTATGCCA	5545
TGCAGGACCAGAGAATTGGAATA CAGGTACTCANNNACGTATGCCA	5066	TGCAGGACCAGAGAATTGGAATA CATGGAGCGNNNACGTATGCCA	5306	TGCAGGACCAGAGAATTGGAATA CATACAGAGNNNACGTATGCCA	5546
TGCAGGACCAGAGAATTGGAATA CACCACTCTNNNACGTATGCCA	5067	TGCAGGACCAGAGAATTGGAATA CACTTTAATCANNNACGTATGCCA	5307	TGCAGGACCAGAGAATTGGAATA CACGGCACCAANNNACGTATGCCA	5547
TGCAGGACCAGAGAATTGGAATA CAATTAATTAANNNACGTATGCCA	5068	TGCAGGACCAGAGAATTGGAATA CAACGTCAGTNNNACGTATGCCA	5308	TGCAGGACCAGAGAATTGGAATA CATCTCCCAANNNACGTATGCCA	5548
TGCAGGACCAGAGAATTGGAATA CAACATAATCANNNACGTATGCCA	5069	TGCAGGACCAGAGAATTGGAATA CATGGAGCTTNNNACGTATGCCA	5309	TGCAGGACCAGAGAATTGGAATA CAGTAATGCAANNNACGTATGCCA	5549
TGCAGGACCAGAGAATTGGAATA CACCTTCGCTANNNACGTATGCCA	5070	TGCAGGACCAGAGAATTGGAATA CAGCACACGNNNACGTATGCCA	5310	TGCAGGACCAGAGAATTGGAATA CAGTAGTACNNNACGTATGCCA	5550
TGCAGGACCAGAGAATTGGAATA CAGGATCTTGNNNACGTATGCCA	5071	TGCAGGACCAGAGAATTGGAATA CATTTGCTGNNNACGTATGCCA	5311	TGCAGGACCAGAGAATTGGAATA CATAGCCGTGNNNACGTATGCCA	5551
TGCAGGACCAGAGAATTGGAATA CAGAGGCGGNNNACGTATGCCA	5072	TGCAGGACCAGAGAATTGGAATA CACAGCGAAANNNACGTATGCCA	5312	TGCAGGACCAGAGAATTGGAATA CACGGATAGANNNACGTATGCCA	5552
TGCAGGACCAGAGAATTGGAATA CACTCAAAATNNNACGTATGCCA	5073	TGCAGGACCAGAGAATTGGAATA CAACGATTGNNNACGTATGCCA	5313	TGCAGGACCAGAGAATTGGAATA CAGGAATAGCANNNACGTATGCCA	5553
TGCAGGACCAGAGAATTGGAATA CAGAACTGCAANNNACGTATGCCA	5074	TGCAGGACCAGAGAATTGGAATA CATAGCGTTGNNNACGTATGCCA	5314	TGCAGGACCAGAGAATTGGAATA CAGGAGTCAANNNACGTATGCCA	5554
TGCAGGACCAGAGAATTGGAATA CAGCGTTCCGNNNACGTATGCCA	5075	TGCAGGACCAGAGAATTGGAATA CAACGCTGCGNNNACGTATGCCA	5315	TGCAGGACCAGAGAATTGGAATA CAATTAGCTANNNACGTATGCCA	5555
TGCAGGACCAGAGAATTGGAATA CAGTGGTAGANNNACGTATGCCA	5076	TGCAGGACCAGAGAATTGGAATA CACTTTATGNNNACGTATGCCA	5316	TGCAGGACCAGAGAATTGGAATA CAAGACATTTNNNACGTATGCCA	5556
TGCAGGACCAGAGAATTGGAATA CATCTGAGTGNNNACGTATGCCA	5077	TGCAGGACCAGAGAATTGGAATA CAGCGAATGNNNACGTATGCCA	5317	TGCAGGACCAGAGAATTGGAATA CATCTACGCTNNNACGTATGCCA	5557
TGCAGGACCAGAGAATTGGAATA CAGAGGCGTTNNNACGTATGCCA	5078	TGCAGGACCAGAGAATTGGAATA CATTTATGNNNACGTATGCCA	5318	TGCAGGACCAGAGAATTGGAATA CATGCGCTCANNNACGTATGCCA	5558
TGCAGGACCAGAGAATTGGAATA CAGTGTGTTGNNNACGTATGCCA	5079	TGCAGGACCAGAGAATTGGAATA CATCCAGCGNNNACGTATGCCA	5319	TGCAGGACCAGAGAATTGGAATA CAAGATCAANNNACGTATGCCA	5559
TGCAGGACCAGAGAATTGGAATA CAATTTGTAANNNACGTATGCCA	5080	TGCAGGACCAGAGAATTGGAATA CACGCAATGCGNNNACGTATGCCA	5320	TGCAGGACCAGAGAATTGGAATA CAATCTCTTANNNACGTATGCCA	5560
TGCAGGACCAGAGAATTGGAATA CAAAAGTTCAANNNACGTATGCCA	5081	TGCAGGACCAGAGAATTGGAATA CAATGCTGTTNNNACGTATGCCA	5321	TGCAGGACCAGAGAATTGGAATA CAGTAGTTGNNNACGTATGCCA	5561

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池 -22	SEQ ID No.	池 -23	SEQ ID No.	池 -24	SEQ ID No.
TGCAGGACCCAGAGAAATTCGAATA	5082	TGCAGGACCCAGAGAAATTCGAATA	5322	TGCAGGACCCAGAGAAATTCGAATA	5562
CAAAATGCCCTNNNNACGTATGCCA		CAAAATGCCCTNNNNACGTATGCCA		CAAGCCCGGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5083	TGCAGGACCCAGAGAAATTCGAATA	5323	TGCAGGACCCAGAGAAATTCGAATA	5563
CAATATCCAGGNNNNACGTATGCCA		CAAGGTTTACGNNNNACGTATGCCA		CAAGCCCAAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5084	TGCAGGACCCAGAGAAATTCGAATA	5324	TGCAGGACCCAGAGAAATTCGAATA	5564
CAITTCGCCGNNNNACGTATGCCA		CAITTCGCCGNNNNACGTATGCCA		CAITTCGCCGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5085	TGCAGGACCCAGAGAAATTCGAATA	5325	TGCAGGACCCAGAGAAATTCGAATA	5565
CAATCTTGAAGNNNNACGTATGCCA		CAAGCGATGANNNNACGTATGCCA		CAAAATCTGTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5086	TGCAGGACCCAGAGAAATTCGAATA	5326	TGCAGGACCCAGAGAAATTCGAATA	5566
CAATACCGAGNNNNACGTATGCCA		CAACGGTTCAGNNNNACGTATGCCA		CAATATAATNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5087	TGCAGGACCCAGAGAAATTCGAATA	5327	TGCAGGACCCAGAGAAATTCGAATA	5567
CAATCTAGATNNNNACGTATGCCA		CAAGTATAGTNNNNACGTATGCCA		CAITGTCCAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5088	TGCAGGACCCAGAGAAATTCGAATA	5328	TGCAGGACCCAGAGAAATTCGAATA	5568
CAATCGGTANNNNACGTATGCCA		CAAGCTGAGANNNNACGTATGCCA		CAITCTCATGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5089	TGCAGGACCCAGAGAAATTCGAATA	5329	TGCAGGACCCAGAGAAATTCGAATA	5569
CAACCAAGCCANNNNACGTATGCCA		CAATCAGCTTNNNNACGTATGCCA		CAACACCCCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5090	TGCAGGACCCAGAGAAATTCGAATA	5330	TGCAGGACCCAGAGAAATTCGAATA	5570
CAATATCCATANNNNACGTATGCCA		CACTCACTACNNNNACGTATGCCA		CAITCTCAGCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5091	TGCAGGACCCAGAGAAATTCGAATA	5331	TGCAGGACCCAGAGAAATTCGAATA	5571
CAAGACTCTGNNNNACGTATGCCA		CAAGAGCAGAGNNNNACGTATGCCA		CAATATGCGANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5092	TGCAGGACCCAGAGAAATTCGAATA	5332	TGCAGGACCCAGAGAAATTCGAATA	5572
CAAGAGCAGANNNNACGTATGCCA		CAACCTTGCACNNNNACGTATGCCA		CACTCTCATGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5093	TGCAGGACCCAGAGAAATTCGAATA	5333	TGCAGGACCCAGAGAAATTCGAATA	5573
CAATACGCTAGNNNNACGTATGCCA		CAAGCAAGGAGNNNNACGTATGCCA		CAAGACGGTANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5094	TGCAGGACCCAGAGAAATTCGAATA	5334	TGCAGGACCCAGAGAAATTCGAATA	5574
CAAGAGGCTGNNNNACGTATGCCA		CAAGTACCTTNNNNACGTATGCCA		CAATATTTTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5095	TGCAGGACCCAGAGAAATTCGAATA	5335	TGCAGGACCCAGAGAAATTCGAATA	5575
CAITTCGACCAANNNNACGTATGCCA		CAACACCTTNNNNACGTATGCCA		CAITGCTTTCNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5096	TGCAGGACCCAGAGAAATTCGAATA	5336	TGCAGGACCCAGAGAAATTCGAATA	5576
CAACCAATCACNNNNACGTATGCCA		CACTGTATAANNNNACGTATGCCA		CAATATATCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5097	TGCAGGACCCAGAGAAATTCGAATA	5337	TGCAGGACCCAGAGAAATTCGAATA	5577
CAITTCGACGNNNNACGTATGCCA		CAATCTCCGANNNNACGTATGCCA		CAACCGGCTGANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5098	TGCAGGACCCAGAGAAATTCGAATA	5338	TGCAGGACCCAGAGAAATTCGAATA	5578
CAAGAGTCTGNNNNACGTATGCCA		CAATGTTGCGNNNNACGTATGCCA		CACAATCAGGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5099	TGCAGGACCCAGAGAAATTCGAATA	5339	TGCAGGACCCAGAGAAATTCGAATA	5579
CACTCTAATCANNNNACGTATGCCA		CAAGCACAGTNNNNACGTATGCCA		CAITCTTAGAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5100	TGCAGGACCCAGAGAAATTCGAATA	5340	TGCAGGACCCAGAGAAATTCGAATA	5580
CAAGAGAAATCANNNNACGTATGCCA		CAATCCGGTNNNNACGTATGCCA		CAACGGTCTGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5101	TGCAGGACCCAGAGAAATTCGAATA	5341	TGCAGGACCCAGAGAAATTCGAATA	5581
CACTCTAGATCANNNNACGTATGCCA		CACTATTTACNNNNACGTATGCCA		CAIAGGTTCTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5102	TGCAGGACCCAGAGAAATTCGAATA	5342	TGCAGGACCCAGAGAAATTCGAATA	5582
CAAGATAAGTANNNNACGTATGCCA		CACTGTGCCANNNNACGTATGCCA		CAAGATAACGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5103	TGCAGGACCCAGAGAAATTCGAATA	5343	TGCAGGACCCAGAGAAATTCGAATA	5583
CAAGGTTTCAGTNNNNACGTATGCCA		CAACGGTACGNNNNACGTATGCCA		CACTCGTACTNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5104	TGCAGGACCCAGAGAAATTCGAATA	5344	TGCAGGACCCAGAGAAATTCGAATA	5584
CAAGCTTGACGNNNNACGTATGCCA		CAAGCATATGNNNNACGTATGCCA		CAAGCACTTTCNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5105	TGCAGGACCCAGAGAAATTCGAATA	5345	TGCAGGACCCAGAGAAATTCGAATA	5585
CAITGGGCCAGNNNNACGTATGCCA		CAITGGTGGCNNNNACGTATGCCA		CAATTTCTGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5106	TGCAGGACCCAGAGAAATTCGAATA	5346	TGCAGGACCCAGAGAAATTCGAATA	5586
CAITGTCACTGNNNNACGTATGCCA		CAACACCTCAGNNNNACGTATGCCA		CACTTACCTCNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5107	TGCAGGACCCAGAGAAATTCGAATA	5347	TGCAGGACCCAGAGAAATTCGAATA	5587
CAAGATTCGTANNNNACGTATGCCA		CAACCAATTTNNNNACGTATGCCA		CAAGAGAGAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5108	TGCAGGACCCAGAGAAATTCGAATA	5348	TGCAGGACCCAGAGAAATTCGAATA	5588
CAACCCATGNNNNACGTATGCCA		CAAACTGAGNNNNACGTATGCCA		CAATAGGCTANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5109	TGCAGGACCCAGAGAAATTCGAATA	5349	TGCAGGACCCAGAGAAATTCGAATA	5589
CAACATTAGCGNNNNACGTATGCCA		CAAGGTAAGTNNNNACGTATGCCA		CAAGTACTAANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5110	TGCAGGACCCAGAGAAATTCGAATA	5350	TGCAGGACCCAGAGAAATTCGAATA	5590
CAATCCACCTGNNNNACGTATGCCA		CAAGCATGGCNNNNACGTATGCCA		CAACCGAATCANNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5111	TGCAGGACCCAGAGAAATTCGAATA	5351	TGCAGGACCCAGAGAAATTCGAATA	5591
CAACATCGGCTNNNNACGTATGCCA		CAAGTCAAGNNNNACGTATGCCA		CACTATTTGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5112	TGCAGGACCCAGAGAAATTCGAATA	5352	TGCAGGACCCAGAGAAATTCGAATA	5592
CAAGCTTACGNNNNACGTATGCCA		CAITGAATCTNNNNACGTATGCCA		CAACCGACAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5113	TGCAGGACCCAGAGAAATTCGAATA	5353	TGCAGGACCCAGAGAAATTCGAATA	5593
CAAACTCTGNNNNACGTATGCCA		CAATATGAGNNNNACGTATGCCA		CAACTTCGAGNNNNACGTATGCCA	
TGCAGGACCCAGAGAAATTCGAATA	5114	TGCAGGACCCAGAGAAATTCGAATA	5354	TGCAGGACCCAGAGAAATTCGAATA	5594
CACTTATATGNNNNACGTATGCCA		CAGACTTGTNNNNACGTATGCCA		CAITGATGCTGNNNNACGTATGCCA	

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池 ⁻²²	SEQ ID No.	池 ⁻²³	SEQ ID No.	池 ⁻²⁴	SEQ ID No.
TGCAGGACCAGAGAAATTCGAATA	5115	TGCAGGACCAGAGAAATTCGAATA	5155	TGCAGGACCAGAGAAATTCGAATA	5195
CAGTGGCTGNNHCTAGCGTTAC		CAAAATTAAGNNHCTAGCGTTAC		CAGCGCAGGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5116	TGCAGGACCAGAGAAATTCGAATA	5156	TGCAGGACCAGAGAAATTCGAATA	5196
CAATGATGCTNNHCTAGCGTTAC		CAGCGTTGTNNHCTAGCGTTAC		CAATTCACAAHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5117	TGCAGGACCAGAGAAATTCGAATA	5157	TGCAGGACCAGAGAAATTCGAATA	5197
CAGASTTGGNNHCTAGCGTTAC		CAGCTGTCCGNNHCTAGCGTTAC		CAATGCACTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5118	TGCAGGACCAGAGAAATTCGAATA	5158	TGCAGGACCAGAGAAATTCGAATA	5198
CAACAACCCGNNHCTAGCGTTAC		CAGTGACGCCNNHCTAGCGTTAC		CAGTTGCCCCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5119	TGCAGGACCAGAGAAATTCGAATA	5159	TGCAGGACCAGAGAAATTCGAATA	5199
CATACCGCAHNNHCTAGCGTTAC		CAGTGTTCGNNHCTAGCGTTAC		CAATTTCCGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5120	TGCAGGACCAGAGAAATTCGAATA	5160	TGCAGGACCAGAGAAATTCGAATA	5200
CAGGTTTAAHNNHCTAGCGTTAC		CACCCGATTTNNHCTAGCGTTAC		CACCGAGCGHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5121	TGCAGGACCAGAGAAATTCGAATA	5161	TGCAGGACCAGAGAAATTCGAATA	5201
CAGTGAAAGTNNHCTAGCGTTAC		CAATTTCCGNNHCTAGCGTTAC		CACCGACACGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5122	TGCAGGACCAGAGAAATTCGAATA	5162	TGCAGGACCAGAGAAATTCGAATA	5202
CAGTGGTCCGNNHCTAGCGTTAC		CAAAAGTCCGNNHCTAGCGTTAC		CATCTGCGTTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5123	TGCAGGACCAGAGAAATTCGAATA	5163	TGCAGGACCAGAGAAATTCGAATA	5203
CAGCTGTCCGNNHCTAGCGTTAC		CAGAGCCABNNHCTAGCGTTAC		CAATTTGCTATNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5124	TGCAGGACCAGAGAAATTCGAATA	5164	TGCAGGACCAGAGAAATTCGAATA	5204
CATCCGACCTNNHCTAGCGTTAC		CACCGTTCGNNHCTAGCGTTAC		CAATTTGCTTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5125	TGCAGGACCAGAGAAATTCGAATA	5165	TGCAGGACCAGAGAAATTCGAATA	5205
CATTCGCTCTNNHCTAGCGTTAC		CAGCGCGGTTNNHCTAGCGTTAC		CACGAGACTTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5126	TGCAGGACCAGAGAAATTCGAATA	5166	TGCAGGACCAGAGAAATTCGAATA	5206
CAACGAGGATNNHCTAGCGTTAC		CACCTCTAGNNHCTAGCGTTAC		CAAACTAGAHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5127	TGCAGGACCAGAGAAATTCGAATA	5167	TGCAGGACCAGAGAAATTCGAATA	5207
CAGTAGATGGNNHCTAGCGTTAC		CAGTGTAAGNNHCTAGCGTTAC		CACCTCGATTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5128	TGCAGGACCAGAGAAATTCGAATA	5168	TGCAGGACCAGAGAAATTCGAATA	5208
CACCAAGCTTNNHCTAGCGTTAC		CACCTATGCGNNHCTAGCGTTAC		CAGTGAAGAGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5129	TGCAGGACCAGAGAAATTCGAATA	5169	TGCAGGACCAGAGAAATTCGAATA	5209
CAGTTTGGCGNNHCTAGCGTTAC		CACGCCAGACNNHCTAGCGTTAC		CAACGTTACGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5130	TGCAGGACCAGAGAAATTCGAATA	5170	TGCAGGACCAGAGAAATTCGAATA	5210
CAACGGTATCNNHCTAGCGTTAC		CAATCAGTCCNNHCTAGCGTTAC		CAGCGTCCGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5131	TGCAGGACCAGAGAAATTCGAATA	5171	TGCAGGACCAGAGAAATTCGAATA	5211
CAATGATAGNNHCTAGCGTTAC		CAGTTCTAGCNNHCTAGCGTTAC		CAACTCCTACNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5132	TGCAGGACCAGAGAAATTCGAATA	5172	TGCAGGACCAGAGAAATTCGAATA	5212
CAGCAATACCTNNHCTAGCGTTAC		CACACCAATGNNHCTAGCGTTAC		CAGTTAGGCTCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5133	TGCAGGACCAGAGAAATTCGAATA	5173	TGCAGGACCAGAGAAATTCGAATA	5213
CAGATCCTAGNNHCTAGCGTTAC		CACAAGGATANNHCTAGCGTTAC		CACCTCTGAGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5134	TGCAGGACCAGAGAAATTCGAATA	5174	TGCAGGACCAGAGAAATTCGAATA	5214
CAATTTACCCGNNHCTAGCGTTAC		CACAAAGGCTNNHCTAGCGTTAC		CAATATTACGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5135	TGCAGGACCAGAGAAATTCGAATA	5175	TGCAGGACCAGAGAAATTCGAATA	5215
CAGTGTGCGNNHCTAGCGTTAC		CAGTGGTATGNNHCTAGCGTTAC		CAGCTTCAAGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5136	TGCAGGACCAGAGAAATTCGAATA	5176	TGCAGGACCAGAGAAATTCGAATA	5216
CATATGTCGNNHCTAGCGTTAC		CAAAAGTCCGNNHCTAGCGTTAC		CAGGACTAGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5137	TGCAGGACCAGAGAAATTCGAATA	5177	TGCAGGACCAGAGAAATTCGAATA	5217
CAGTGTCTTNNHCTAGCGTTAC		CAATGGCTGNNHCTAGCGTTAC		CAGTGGCAAHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5138	TGCAGGACCAGAGAAATTCGAATA	5178	TGCAGGACCAGAGAAATTCGAATA	5218
CAAAAGGCGCNNHCTAGCGTTAC		CAATTTCTATCNNHCTAGCGTTAC		CAATAAAGCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5139	TGCAGGACCAGAGAAATTCGAATA	5179	TGCAGGACCAGAGAAATTCGAATA	5219
CATCGTATATNNHCTAGCGTTAC		CAGGTATCCGNNHCTAGCGTTAC		CAGTATACCGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5140	TGCAGGACCAGAGAAATTCGAATA	5180	TGCAGGACCAGAGAAATTCGAATA	5220
CACATCAAGNNHCTAGCGTTAC		CATGGTGATNNHCTAGCGTTAC		CACCAATTAHNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5141	TGCAGGACCAGAGAAATTCGAATA	5181	TGCAGGACCAGAGAAATTCGAATA	5221
CAGTCAATCGNNHCTAGCGTTAC		CATGCTATTTNNHCTAGCGTTAC		CAATCTTTAGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5142	TGCAGGACCAGAGAAATTCGAATA	5182	TGCAGGACCAGAGAAATTCGAATA	5222
CAGTCCGATCNNHCTAGCGTTAC		CAGCCCGCGCNNHCTAGCGTTAC		CATGTTGCTCNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5143	TGCAGGACCAGAGAAATTCGAATA	5183	TGCAGGACCAGAGAAATTCGAATA	5223
CAAAAGGATGNNHCTAGCGTTAC		CACCCGCAAGNNHCTAGCGTTAC		CACCGGCTGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5144	TGCAGGACCAGAGAAATTCGAATA	5184	TGCAGGACCAGAGAAATTCGAATA	5224
CATGAAGATNNHCTAGCGTTAC		CATCGTGGCNNHCTAGCGTTAC		CACGAGTGTNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5145	TGCAGGACCAGAGAAATTCGAATA	5185	TGCAGGACCAGAGAAATTCGAATA	5225
CACAGGCTTNNHCTAGCGTTAC		CAGATCCCTNNHCTAGCGTTAC		CAGCGGTATNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5146	TGCAGGACCAGAGAAATTCGAATA	5186	TGCAGGACCAGAGAAATTCGAATA	5226
CACGATTCGNNHCTAGCGTTAC		CATAGATGNNHCTAGCGTTAC		CAAGTCTCGNNHCTAGCGTTAC	
TGCAGGACCAGAGAAATTCGAATA	5147	TGCAGGACCAGAGAAATTCGAATA	5187	TGCAGGACCAGAGAAATTCGAATA	5227
CATAACCAAGNNHCTAGCGTTAC		CAAGGCAAGTNNHCTAGCGTTAC		CAGTAGCAHNNHCTAGCGTTAC	

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池-22	SEQ ID NO.	池-23	SEQ ID NO.	池-24	SEQ ID NO.
TGCAGGACCAAGAGAAATTCGAATA	5148	TGCAGGACCAAGAGAAATTCGAATA	5388	TGCAGGACCAAGAGAAATTCGAATA	5628
CACGACGCTAAGNNCTAGCGTTAC		CATAATCTGANNCTAGCGTTAC		CACGGAGAGGNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5149	TGCAGGACCAAGAGAAATTCGAATA	5389	TGCAGGACCAAGAGAAATTCGAATA	5629
CACGACGCTAAGNNCTAGCGTTAC		CAGGCTCAAAANNCTAGCGTTAC		CAGCTTTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5150	TGCAGGACCAAGAGAAATTCGAATA	5390	TGCAGGACCAAGAGAAATTCGAATA	5630
CACGACGCTAAGNNCTAGCGTTAC		CAPAGCGCTNNNNCTAGCGTTAC		CATAATGATGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5151	TGCAGGACCAAGAGAAATTCGAATA	5391	TGCAGGACCAAGAGAAATTCGAATA	5631
CACGACGCTAAGNNCTAGCGTTAC		CACATGCGCGNNNNCTAGCGTTAC		CAATCTCTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5152	TGCAGGACCAAGAGAAATTCGAATA	5392	TGCAGGACCAAGAGAAATTCGAATA	5632
CACGACGCTAAGNNCTAGCGTTAC		CAGGAGATGNNNNCTAGCGTTAC		CAGTGTTTCCNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5153	TGCAGGACCAAGAGAAATTCGAATA	5393	TGCAGGACCAAGAGAAATTCGAATA	5633
CACGACGCTAAGNNCTAGCGTTAC		CATCAGCTAGNNNNCTAGCGTTAC		CACGTAGTACNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5154	TGCAGGACCAAGAGAAATTCGAATA	5394	TGCAGGACCAAGAGAAATTCGAATA	5634
CACGACGCTAAGNNCTAGCGTTAC		CAGTGTATGNNNNCTAGCGTTAC		CAGCGGAAATNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5155	TGCAGGACCAAGAGAAATTCGAATA	5395	TGCAGGACCAAGAGAAATTCGAATA	5635
CACGACGCTAAGNNCTAGCGTTAC		CACACTTGCANNNNCTAGCGTTAC		CATAATTACNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5156	TGCAGGACCAAGAGAAATTCGAATA	5396	TGCAGGACCAAGAGAAATTCGAATA	5636
CACGACGCTAAGNNCTAGCGTTAC		CACCTGAAATGNNNNCTAGCGTTAC		CACGCGCGGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5157	TGCAGGACCAAGAGAAATTCGAATA	5397	TGCAGGACCAAGAGAAATTCGAATA	5637
CACGACGCTAAGNNCTAGCGTTAC		CACGCTTAAGNNNNCTAGCGTTAC		CACGAGAGTNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5158	TGCAGGACCAAGAGAAATTCGAATA	5398	TGCAGGACCAAGAGAAATTCGAATA	5638
CATAGTGTGNNNNCTAGCGTTAC		CATATTTGTNNNNCTAGCGTTAC		CAAGGCTGTNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5159	TGCAGGACCAAGAGAAATTCGAATA	5399	TGCAGGACCAAGAGAAATTCGAATA	5639
CACGACGCTAAGNNCTAGCGTTAC		CATTTACGCGNNNNCTAGCGTTAC		CAUGAAGGANNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5160	TGCAGGACCAAGAGAAATTCGAATA	5400	TGCAGGACCAAGAGAAATTCGAATA	5640
CACGACGCTAAGNNCTAGCGTTAC		CATTCGCTGNNNNCTAGCGTTAC		CAGTCTACGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5161	TGCAGGACCAAGAGAAATTCGAATA	5401	TGCAGGACCAAGAGAAATTCGAATA	5641
CACGACGCTAAGNNCTAGCGTTAC		CAATGACCGNNNNCTAGCGTTAC		CACATGCGGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5162	TGCAGGACCAAGAGAAATTCGAATA	5402	TGCAGGACCAAGAGAAATTCGAATA	5642
CACGACGCTAAGNNCTAGCGTTAC		CAATGAGTGGNNNNCTAGCGTTAC		CATGACGCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5163	TGCAGGACCAAGAGAAATTCGAATA	5403	TGCAGGACCAAGAGAAATTCGAATA	5643
CACGACGCTAAGNNCTAGCGTTAC		CACGCTCAAGNNNNCTAGCGTTAC		CAAGCTTAGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5164	TGCAGGACCAAGAGAAATTCGAATA	5404	TGCAGGACCAAGAGAAATTCGAATA	5644
CACGACGCTAAGNNCTAGCGTTAC		CARAAGTGATNNNNCTAGCGTTAC		CARGCTCGGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5165	TGCAGGACCAAGAGAAATTCGAATA	5405	TGCAGGACCAAGAGAAATTCGAATA	5645
CACGACGCTAAGNNCTAGCGTTAC		CATCAACTCGNNNNCTAGCGTTAC		CAAGACCTCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5166	TGCAGGACCAAGAGAAATTCGAATA	5406	TGCAGGACCAAGAGAAATTCGAATA	5646
CACGACGCTAAGNNCTAGCGTTAC		CAGCTAATGNNNNCTAGCGTTAC		CAGTCTATGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5167	TGCAGGACCAAGAGAAATTCGAATA	5407	TGCAGGACCAAGAGAAATTCGAATA	5647
CACGACGCTAAGNNCTAGCGTTAC		CAGATTTGGCGNNNNCTAGCGTTAC		CATAATTCGCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5168	TGCAGGACCAAGAGAAATTCGAATA	5408	TGCAGGACCAAGAGAAATTCGAATA	5648
CACGACGCTAAGNNCTAGCGTTAC		CATACTACTGNNNNCTAGCGTTAC		CATTGACCTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5169	TGCAGGACCAAGAGAAATTCGAATA	5409	TGCAGGACCAAGAGAAATTCGAATA	5649
CACGACGCTAAGNNCTAGCGTTAC		CAGACTCGGCGNNNNCTAGCGTTAC		CACCTCTGTACNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5170	TGCAGGACCAAGAGAAATTCGAATA	5410	TGCAGGACCAAGAGAAATTCGAATA	5650
CACGACGCTAAGNNCTAGCGTTAC		CAGCTGTATGNNNNCTAGCGTTAC		CATTGATTTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5171	TGCAGGACCAAGAGAAATTCGAATA	5411	TGCAGGACCAAGAGAAATTCGAATA	5651
CACGACGCTAAGNNCTAGCGTTAC		CAAAATTTGCTNNNNCTAGCGTTAC		CAGCACATACNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5172	TGCAGGACCAAGAGAAATTCGAATA	5412	TGCAGGACCAAGAGAAATTCGAATA	5652
CACGACGCTAAGNNCTAGCGTTAC		CAACATGTTANNNNCTAGCGTTAC		CAGCTTTGTANNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5173	TGCAGGACCAAGAGAAATTCGAATA	5413	TGCAGGACCAAGAGAAATTCGAATA	5653
CACGACGCTAAGNNCTAGCGTTAC		CAAGATGGACNNNNCTAGCGTTAC		CATACGCTACNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5174	TGCAGGACCAAGAGAAATTCGAATA	5414	TGCAGGACCAAGAGAAATTCGAATA	5654
CACGACGCTAAGNNCTAGCGTTAC		CAGGTCTCCANNNNCTAGCGTTAC		CACACGCTCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5175	TGCAGGACCAAGAGAAATTCGAATA	5415	TGCAGGACCAAGAGAAATTCGAATA	5655
CACGACGCTAAGNNCTAGCGTTAC		CATTGGCTAGNNNNCTAGCGTTAC		CACCAAGGTTNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5176	TGCAGGACCAAGAGAAATTCGAATA	5416	TGCAGGACCAAGAGAAATTCGAATA	5656
CACGACGCTAAGNNCTAGCGTTAC		CATAATTTCCNNNNCTAGCGTTAC		CAGTTCCGCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5177	TGCAGGACCAAGAGAAATTCGAATA	5417	TGCAGGACCAAGAGAAATTCGAATA	5657
CACGACGCTAAGNNCTAGCGTTAC		CAGTGTATANNNNCTAGCGTTAC		CAACGCGCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5178	TGCAGGACCAAGAGAAATTCGAATA	5418	TGCAGGACCAAGAGAAATTCGAATA	5658
CACGACGCTAAGNNCTAGCGTTAC		CATGAGCAAGNNNNCTAGCGTTAC		CACGCCGAGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5179	TGCAGGACCAAGAGAAATTCGAATA	5419	TGCAGGACCAAGAGAAATTCGAATA	5659
CACGACGCTAAGNNCTAGCGTTAC		CACGCGCTTANNNNCTAGCGTTAC		CACCTCCATGNNNNCTAGCGTTAC	
TGCAGGACCAAGAGAAATTCGAATA	5180	TGCAGGACCAAGAGAAATTCGAATA	5420	TGCAGGACCAAGAGAAATTCGAATA	5660
CACGACGCTAAGNNCTAGCGTTAC		CAGTCCAGTNNNNCTAGCGTTAC		CATTTGCAACNNNNCTAGCGTTAC	

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
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CAAAATGGATTNNNGATCGACATG		CAGTTGGTGTNNNGATCGACATG		CAATTAGCAACHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5182	TGCAGGACAGAGAAATTCGAATA	5422	TGCAGGACAGAGAAATTCGAATA	5662
CACGCATGATNNNGATCGACATG		CACATTATTACNNNGATCGACATG		CATGCTCACCNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5183	TGCAGGACAGAGAAATTCGAATA	5423	TGCAGGACAGAGAAATTCGAATA	5663
CATACGATCTNNNGATCGACATG		CACTCGCAANNNGATCGACATG		CAGATTGAGANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5184	TGCAGGACAGAGAAATTCGAATA	5424	TGCAGGACAGAGAAATTCGAATA	5664
CAGGAAGCCNNNGATCGACATG		CACCTAGGTGNNNGATCGACATG		CA1CATACCCNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5185	TGCAGGACAGAGAAATTCGAATA	5425	TGCAGGACAGAGAAATTCGAATA	5665
CACCAAGCANNNGATCGACATG		CACACATATNNNGATCGACATG		CAGGTGGATANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5186	TGCAGGACAGAGAAATTCGAATA	5426	TGCAGGACAGAGAAATTCGAATA	5666
CAAGCCGACNNNGATCGACATG		CAADCGATACNNNGATCGACATG		CAGACATTCNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5187	TGCAGGACAGAGAAATTCGAATA	5427	TGCAGGACAGAGAAATTCGAATA	5667
CAGGAGTCCNNNGATCGACATG		CACCGGCTCGNNNGATCGACATG		CAATCTCCGANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5188	TGCAGGACAGAGAAATTCGAATA	5428	TGCAGGACAGAGAAATTCGAATA	5668
CACCTACGACNNNGATCGACATG		CACACGCGCTNNNGATCGACATG		CAGGCGCCGANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5189	TGCAGGACAGAGAAATTCGAATA	5429	TGCAGGACAGAGAAATTCGAATA	5669
CAACTCGCCNNNGATCGACATG		CATTTTAATTNNNGATCGACATG		CAAAATGTTGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5190	TGCAGGACAGAGAAATTCGAATA	5430	TGCAGGACAGAGAAATTCGAATA	5670
CACCTAAGCANNNGATCGACATG		CAAGTGTATTNNNGATCGACATG		CAACGTGGTANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5191	TGCAGGACAGAGAAATTCGAATA	5431	TGCAGGACAGAGAAATTCGAATA	5671
CAGGAGCACCNNNGATCGACATG		CAACTCTCAGNNNGATCGACATG		CAACTGAGGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5192	TGCAGGACAGAGAAATTCGAATA	5432	TGCAGGACAGAGAAATTCGAATA	5672
CAGGAGCGCANNNGATCGACATG		CAAAAGCCGCCNNNGATCGACATG		CAGAACTAAGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5193	TGCAGGACAGAGAAATTCGAATA	5433	TGCAGGACAGAGAAATTCGAATA	5673
CAGGAGCCTNNNGATCGACATG		CACACAGCGTNNNGATCGACATG		CAATTACGGCHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5194	TGCAGGACAGAGAAATTCGAATA	5434	TGCAGGACAGAGAAATTCGAATA	5674
CAGCGCTGCTNNNGATCGACATG		CAGGCTCTNNNGATCGACATG		CACAGCTCAGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5195	TGCAGGACAGAGAAATTCGAATA	5435	TGCAGGACAGAGAAATTCGAATA	5675
CAAGTATCTNNNGATCGACATG		CACCTTAGCCTNNNGATCGACATG		CAATCCCTTGHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5196	TGCAGGACAGAGAAATTCGAATA	5436	TGCAGGACAGAGAAATTCGAATA	5676
CACCTCGCANNNGATCGACATG		CAATTGCCATNNNGATCGACATG		CATGTCTCCATNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5197	TGCAGGACAGAGAAATTCGAATA	5437	TGCAGGACAGAGAAATTCGAATA	5677
CACCTCATCTNNNGATCGACATG		CAGCAGCCTAANNNGATCGACATG		CAGGTAGCCNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5198	TGCAGGACAGAGAAATTCGAATA	5438	TGCAGGACAGAGAAATTCGAATA	5678
CAGATTCGANNNGATCGACATG		CAAGATACGCHNNNGATCGACATG		CATGAGCAGANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5199	TGCAGGACAGAGAAATTCGAATA	5439	TGCAGGACAGAGAAATTCGAATA	5679
CACCTTATCTNNNGATCGACATG		CACCTGAAAGNNNGATCGACATG		CAGATCCGTANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5200	TGCAGGACAGAGAAATTCGAATA	5440	TGCAGGACAGAGAAATTCGAATA	5680
CAAGGCTACNNNGATCGACATG		CATCTCAGTNNNGATCGACATG		CATCCTAANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5201	TGCAGGACAGAGAAATTCGAATA	5441	TGCAGGACAGAGAAATTCGAATA	5681
CACCTGTAGANNNGATCGACATG		CACACGCTCCNNNGATCGACATG		CAAAATAGATNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5202	TGCAGGACAGAGAAATTCGAATA	5442	TGCAGGACAGAGAAATTCGAATA	5682
CATCGTGTANNNGATCGACATG		CACCGAGGCTCHNNNGATCGACATG		CATCGCGCTCHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5203	TGCAGGACAGAGAAATTCGAATA	5443	TGCAGGACAGAGAAATTCGAATA	5683
CACCTCGCCTNNNGATCGACATG		CACATTCAGNNNGATCGACATG		CAACCGACGCHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5204	TGCAGGACAGAGAAATTCGAATA	5444	TGCAGGACAGAGAAATTCGAATA	5684
CAACCATGANNNGATCGACATG		CATCCCTAGGNNNGATCGACATG		CACACGGACCHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5205	TGCAGGACAGAGAAATTCGAATA	5445	TGCAGGACAGAGAAATTCGAATA	5685
CAGGTGGACNNNGATCGACATG		CAATTACTCATNNNGATCGACATG		CAATATCGATNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5206	TGCAGGACAGAGAAATTCGAATA	5446	TGCAGGACAGAGAAATTCGAATA	5686
CAGGATAGANNNGATCGACATG		CAATCTGATANNNGATCGACATG		CATACCACGANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5207	TGCAGGACAGAGAAATTCGAATA	5447	TGCAGGACAGAGAAATTCGAATA	5687
CAGGATACGNNNGATCGACATG		CAGTCCACTNNNGATCGACATG		CAAGAGACGCHNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5208	TGCAGGACAGAGAAATTCGAATA	5448	TGCAGGACAGAGAAATTCGAATA	5688
CAAAACGGCTNNNGATCGACATG		CACAGGAACANNNGATCGACATG		CAAGTACCTGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5209	TGCAGGACAGAGAAATTCGAATA	5449	TGCAGGACAGAGAAATTCGAATA	5689
GAATATGCAANNNGATCGACATG		CACCTAGCTTCHNNNGATCGACATG		CAGTTTCAANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5210	TGCAGGACAGAGAAATTCGAATA	5450	TGCAGGACAGAGAAATTCGAATA	5690
CATCAATTGANNNGATCGACATG		CATTTGCCANNNGATCGACATG		CAGGATCTTANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5211	TGCAGGACAGAGAAATTCGAATA	5451	TGCAGGACAGAGAAATTCGAATA	5691
CAAGCATGNNNGATCGACATG		CACCGGAAGNNNGATCGACATG		CATAGTATCANNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5212	TGCAGGACAGAGAAATTCGAATA	5452	TGCAGGACAGAGAAATTCGAATA	5692
CAGTATGANNNGATCGACATG		CATCCCACTNNNGATCGACATG		CACGTATGGNNNGATCGACATG	
TGCAGGACAGAGAAATTCGAATA	5213	TGCAGGACAGAGAAATTCGAATA	5453	TGCAGGACAGAGAAATTCGAATA	5693
CACACTGCGNNNGATCGACATG		CATTCAGCGANNNGATCGACATG		CATCCCGCTNNNGATCGACATG	

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
TGCAGGACCAGAGAAATTCGAATA CAACCGCTCCNNNGATCGACATG	5214	TGCAGGACCAGAGAAATTCGAATA CAATTTTAAOCHNNGATCGACATG	5454	TGCAGGACCAGAGAAATTCGAATA CAGCGCTCTCHNNGATCGACATG	5694
TGCAGGACCAGAGAAATTCGAATA CACTAGGTTGNHNGATCGACATG	5215	TGCAGGACCAGAGAAATTCGAATA CATGGAGTCTNNNGATCGACATG	5455	TGCAGGACCAGAGAAATTCGAATA CAATTTCCCHNNGATCGACATG	5695
TGCAGGACCAGAGAAATTCGAATA CATAAATTAHNNHATCGACATG	5216	TGCAGGACCAGAGAAATTCGAATA CACGAGGACCHNNGATCGACATG	5456	TGCAGGACCAGAGAAATTCGAATA CATCGCCCHNNGATCGACATG	5696
TGCAGGACCAGAGAAATTCGAATA CAGTCACGTANNHNGATCGACATG	5217	TGCAGGACCAGAGAAATTCGAATA CATCCCATACNNHNGATCGACATG	5457	TGCAGGACCAGAGAAATTCGAATA CATGCATTGNHNGATCGACATG	5697
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TGCAGGACCAGAGAAATTCGAATA CACATGGAGHNGATCGACATG	5219	TGCAGGACCAGAGAAATTCGAATA CAGTCCCGCTHNGATCGACATG	5459	TGCAGGACCAGAGAAATTCGAATA CACTTTTATGNHNGATCGACATG	5699
TGCAGGACCAGAGAAATTCGAATA CAACGAGGCTNNHNGATCGACATG	5220	TGCAGGACCAGAGAAATTCGAATA CACGGCCCTTNNHNGATCGACATG	5460	TGCAGGACCAGAGAAATTCGAATA CAAAAGTCCGNNHNGATCGACATG	5700
TGCAGGACCAGAGAAATTCGAATA CACAAACGAGNNHNGATCGACATG	5221	TGCAGGACCAGAGAAATTCGAATA CATCAGCTTCNNHNGATCGACATG	5461	TGCAGGACCAGAGAAATTCGAATA CAACGAGTGANHNGATCGACATG	5701
TGCAGGACCAGAGAAATTCGAATA CAGATATGTTNNHNGATCGACATG	5222	TGCAGGACCAGAGAAATTCGAATA CAGGCTCGGTNNHNGATCGACATG	5462	TGCAGGACCAGAGAAATTCGAATA CAGAAATTAGNNHNGATCGACATG	5702
TGCAGGACCAGAGAAATTCGAATA CAGTTCTGTCHNNGATCGACATG	5223	TGCAGGACCAGAGAAATTCGAATA CARAGTTCCGNNHNGATCGACATG	5463	TGCAGGACCAGAGAAATTCGAATA CAATTATCTCHNNGATCGACATG	5703
TGCAGGACCAGAGAAATTCGAATA CATCTTTTCHNNGATCGACATG	5224	TGCAGGACCAGAGAAATTCGAATA CAAAAGGCGCHNNGATCGACATG	5464	TGCAGGACCAGAGAAATTCGAATA CAGTCTGGCHNNGATCGACATG	5704
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TGCAGGACCAGAGAAATTCGAATA CAACCGATGANHNGATCGACATG	5226	TGCAGGACCAGAGAAATTCGAATA CATTCAGATHNNHNGATCGACATG	5466	TGCAGGACCAGAGAAATTCGAATA CAACGAGTANNHNGATCGACATG	5706
TGCAGGACCAGAGAAATTCGAATA CATCTCTCACNNHNGATCGACATG	5227	TGCAGGACCAGAGAAATTCGAATA CACTCAGTCTNNHNGATCGACATG	5467	TGCAGGACCAGAGAAATTCGAATA CAGGAGTGCNNHNGATCGACATG	5707
TGCAGGACCAGAGAAATTCGAATA CATTTAGGCTCHNNGATCGACATG	5228	TGCAGGACCAGAGAAATTCGAATA CAAAAGATTGNHNGATCGACATG	5468	TGCAGGACCAGAGAAATTCGAATA CATCGATATANNHNGATCGACATG	5708
TGCAGGACCAGAGAAATTCGAATA CAGCGTACTANNHNGATCGACATG	5229	TGCAGGACCAGAGAAATTCGAATA CAGACTACANNHNGATCGACATG	5469	TGCAGGACCAGAGAAATTCGAATA CAGCGGTAGCHNNGATCGACATG	5709
TGCAGGACCAGAGAAATTCGAATA CAAGGTTAGCHNNGATCGACATG	5230	TGCAGGACCAGAGAAATTCGAATA CACACCGCTANNHNGATCGACATG	5470	TGCAGGACCAGAGAAATTCGAATA CACTGATTAHNNHNGATCGACATG	5710
TGCAGGACCAGAGAAATTCGAATA CACTTCACGCHNNGATCGACATG	5231	TGCAGGACCAGAGAAATTCGAATA CAAGTCAATANNHNGATCGACATG	5471	TGCAGGACCAGAGAAATTCGAATA CAGACTTCHNNGATCGACATG	5711
TGCAGGACCAGAGAAATTCGAATA CACATCTAGNNHNGATCGACATG	5232	TGCAGGACCAGAGAAATTCGAATA CATCTAGGACCHNNGATCGACATG	5472	TGCAGGACCAGAGAAATTCGAATA CATAGGCTTNNHNGATCGACATG	5712
TGCAGGACCAGAGAAATTCGAATA CATCGATATANNHNGATCGACATG	5233	TGCAGGACCAGAGAAATTCGAATA CAAGAGCTTNNHNGATCGACATG	5473	TGCAGGACCAGAGAAATTCGAATA CAATATGTANNHNGATCGACATG	5713
TGCAGGACCAGAGAAATTCGAATA CAACGAGGCHNNGATCGACATG	5234	TGCAGGACCAGAGAAATTCGAATA CAACGACTANNHNGATCGACATG	5474	TGCAGGACCAGAGAAATTCGAATA CAGTCGATTGNHNGATCGACATG	5714
TGCAGGACCAGAGAAATTCGAATA CAGTGGAAATGNHNGATCGACATG	5235	TGCAGGACCAGAGAAATTCGAATA CAACGAGCTCHNNGATCGACATG	5475	TGCAGGACCAGAGAAATTCGAATA CAATAGAGCHNNGATCGACATG	5715
TGCAGGACCAGAGAAATTCGAATA CAAAAAATGCHNNGATCGACATG	5236	TGCAGGACCAGAGAAATTCGAATA CAGTTACGAGNNHNGATCGACATG	5476	TGCAGGACCAGAGAAATTCGAATA CAGACTAAGNNHNGATCGACATG	5716
TGCAGGACCAGAGAAATTCGAATA CAGACTAGTCHNNGATCGACATG	5237	TGCAGGACCAGAGAAATTCGAATA CACGCTACCHNNGATCGACATG	5477	TGCAGGACCAGAGAAATTCGAATA CACCTACCTANNHNGATCGACATG	5717
TGCAGGACCAGAGAAATTCGAATA CACGTAGAGNNHNGATCGACATG	5238	TGCAGGACCAGAGAAATTCGAATA CAAGAGCTACNNHNGATCGACATG	5478	TGCAGGACCAGAGAAATTCGAATA CATAGGAGACNNHNGATCGACATG	5718
TGCAGGACCAGAGAAATTCGAATA CAGTTGAGAGNNHNGATCGACATG	5239	TGCAGGACCAGAGAAATTCGAATA CAATCTCTTNNHNGATCGACATG	5479	TGCAGGACCAGAGAAATTCGAATA CACCGCTATTNNHNGATCGACATG	5719
TGCAGGACCAGAGAAATTCGAATA CAAAAGTACTTNNHNGATCGACATG	5240	TGCAGGACCAGAGAAATTCGAATA CAATATTTANNHNGATCGACATG	5480	TGCAGGACCAGAGAAATTCGAATA CAGTGTTCAGNNHNGATCGACATG	5720
TGCAGGACCAGAGAAATTCGAATA CACGAAAGCTTNNHNGATCGACATG	5241	TGCAGGACCAGAGAAATTCGAATA CATATCGAATNNHNGATCGACATG	5481	TGCAGGACCAGAGAAATTCGAATA CAAGCGGTTNNHNGATCGACATG	5721
TGCAGGACCAGAGAAATTCGAATA CAATTGCTGCHNNGATCGACATG	5242	TGCAGGACCAGAGAAATTCGAATA CAGCTAATTTNNHNGATCGACATG	5482	TGCAGGACCAGAGAAATTCGAATA CAAACTCTTNNHNGATCGACATG	5722
TGCAGGACCAGAGAAATTCGAATA CATGTGTGCHNNGATCGACATG	5243	TGCAGGACCAGAGAAATTCGAATA CATTTGAGCCHNNGATCGACATG	5483	TGCAGGACCAGAGAAATTCGAATA CATAGCTATNNHNGATCGACATG	5723
TGCAGGACCAGAGAAATTCGAATA CACATCTTTNNHNGATCGACATG	5244	TGCAGGACCAGAGAAATTCGAATA CAGTTACAGNNHNGATCGACATG	5484	TGCAGGACCAGAGAAATTCGAATA CAAGAGACTGNHNGATCGACATG	5724
TGCAGGACCAGAGAAATTCGAATA CAGCATGCTANNHNGATCGACATG	5245	TGCAGGACCAGAGAAATTCGAATA CAGCATCTCTNNHNGATCGACATG	5485	TGCAGGACCAGAGAAATTCGAATA CAAGGAGAGNNHNGATCGACATG	5725
TGCAGGACCAGAGAAATTCGAATA CATATGTCAGNNHNGATCGACATG	5246	TGCAGGACCAGAGAAATTCGAATA CATTACACCHNNGATCGACATG	5486	TGCAGGACCAGAGAAATTCGAATA CATCGAACGNNHNGATCGACATG	5726

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池-22	SEQ ID NO:	池-23	SEQ ID NO:	池-24	SEQ ID NO:
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CACAGTAATTTNNNTGCATCAGGT		CATATTTTATNNNTGCATCAGGT		CACGGACATNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5248	TGCAGGACAGAGAAATTCGAATA	5488	TGCAGGACAGAGAAATTCGAATA	5728
CAAGGTTGNNNTGCATCAGGT		CATGTCCGCCNNNTGCATCAGGT		CATTCGCCATNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5249	TGCAGGACAGAGAAATTCGAATA	5489	TGCAGGACAGAGAAATTCGAATA	5729
CACGGTGGTNNNTGCATCAGGT		CAAAACCCGTTNNNTGCATCAGGT		CACGCCGCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5250	TGCAGGACAGAGAAATTCGAATA	5490	TGCAGGACAGAGAAATTCGAATA	5730
CAGTGGTTGNNNTGCATCAGGT		CAGTACCGATNNNTGCATCAGGT		CAGTTCCTGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5251	TGCAGGACAGAGAAATTCGAATA	5491	TGCAGGACAGAGAAATTCGAATA	5731
CATGTATTCTNNNTGCATCAGGT		CAGGGGTTCCNNNTGCATCAGGT		CAAGACAGCANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5252	TGCAGGACAGAGAAATTCGAATA	5492	TGCAGGACAGAGAAATTCGAATA	5732
CATAGTCCGNNNTGCATCAGGT		CACCTCCATCTNNNTGCATCAGGT		CAGAGCCCTCCNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5253	TGCAGGACAGAGAAATTCGAATA	5493	TGCAGGACAGAGAAATTCGAATA	5733
CATAGGACGANNNTGCATCAGGT		CACCGGACAGANNNTGCATCAGGT		CATACCTGCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5254	TGCAGGACAGAGAAATTCGAATA	5494	TGCAGGACAGAGAAATTCGAATA	5734
CACATAAATCNNNTGCATCAGGT		CACGCTTAGANNNTGCATCAGGT		CATTCGTATTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5255	TGCAGGACAGAGAAATTCGAATA	5495	TGCAGGACAGAGAAATTCGAATA	5735
CAGGCTGTGNNNTGCATCAGGT		CAGAAAGCCGNNNTGCATCAGGT		CATACCTTAGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5256	TGCAGGACAGAGAAATTCGAATA	5496	TGCAGGACAGAGAAATTCGAATA	5736
CATTGCGCTNNNTGCATCAGGT		CACCTCATCCANNNTGCATCAGGT		CAGACTACGTTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5257	TGCAGGACAGAGAAATTCGAATA	5497	TGCAGGACAGAGAAATTCGAATA	5737
CAGAGCGTTGNNNTGCATCAGGT		CAAGAGATCANNNTGCATCAGGT		CAACGAGCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5258	TGCAGGACAGAGAAATTCGAATA	5498	TGCAGGACAGAGAAATTCGAATA	5738
CAGTCTAGGTTNNNTGCATCAGGT		CAAAATTCGANNNTGCATCAGGT		CAGATCGTTGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5259	TGCAGGACAGAGAAATTCGAATA	5499	TGCAGGACAGAGAAATTCGAATA	5739
CATCCGTAAGNNNTGCATCAGGT		CAATTAATACNNNTGCATCAGGT		CAGATGGACANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5260	TGCAGGACAGAGAAATTCGAATA	5500	TGCAGGACAGAGAAATTCGAATA	5740
CATATCGGCAANNNTGCATCAGGT		CAAAATTTGNNNTGCATCAGGT		CATCGTAGTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5261	TGCAGGACAGAGAAATTCGAATA	5501	TGCAGGACAGAGAAATTCGAATA	5741
CAATCATCGNNNTGCATCAGGT		CACACAGTTNNNTGCATCAGGT		CACCCACATCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5262	TGCAGGACAGAGAAATTCGAATA	5502	TGCAGGACAGAGAAATTCGAATA	5742
CACGCTCTGANNNTGCATCAGGT		CATTAAACANNNTGCATCAGGT		CAGTGTCTACNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5263	TGCAGGACAGAGAAATTCGAATA	5503	TGCAGGACAGAGAAATTCGAATA	5743
CAACGCTACTNNNTGCATCAGGT		CAATGCAGACNNNTGCATCAGGT		CATTCTTCANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5264	TGCAGGACAGAGAAATTCGAATA	5504	TGCAGGACAGAGAAATTCGAATA	5744
CATCCGTAAGNNNTGCATCAGGT		CAAAAGACGNNNTGCATCAGGT		CATTACAGTANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5265	TGCAGGACAGAGAAATTCGAATA	5505	TGCAGGACAGAGAAATTCGAATA	5745
CAGAGCTCACNNNTGCATCAGGT		CAATCCGAAUINNNTGCATCAGGT		CAGAGCGCGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5266	TGCAGGACAGAGAAATTCGAATA	5506	TGCAGGACAGAGAAATTCGAATA	5746
CACATCAGCANNNTGCATCAGGT		CAGTTAGGAGNNNTGCATCAGGT		CAGGAGCTCCNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5267	TGCAGGACAGAGAAATTCGAATA	5507	TGCAGGACAGAGAAATTCGAATA	5747
CATGGCTGTANNNTGCATCAGGT		CATGGCCAGCINNNTGCATCAGGT		CAATTAACANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5268	TGCAGGACAGAGAAATTCGAATA	5508	TGCAGGACAGAGAAATTCGAATA	5748
CAGTTTACCNNNTGCATCAGGT		CAATGTGACNNNTGCATCAGGT		CAATCGAGCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5269	TGCAGGACAGAGAAATTCGAATA	5509	TGCAGGACAGAGAAATTCGAATA	5749
CACGCTCAGTANNNTGCATCAGGT		CAGTACAACNNNTGCATCAGGT		CAGGTAACGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5270	TGCAGGACAGAGAAATTCGAATA	5510	TGCAGGACAGAGAAATTCGAATA	5750
CACGAGCGGANNNTGCATCAGGT		CAGTGGCCGAGNNNTGCATCAGGT		CATGAAGAGCINNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5271	TGCAGGACAGAGAAATTCGAATA	5511	TGCAGGACAGAGAAATTCGAATA	5751
CAATATCGCANNNTGCATCAGGT		CAAGCTCTCTNNNTGCATCAGGT		CAATCCCGATNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5272	TGCAGGACAGAGAAATTCGAATA	5512	TGCAGGACAGAGAAATTCGAATA	5752
CAGCTTGGCCNNNTGCATCAGGT		CAACCTCTCTNNNTGCATCAGGT		CAGTGTCTCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5273	TGCAGGACAGAGAAATTCGAATA	5513	TGCAGGACAGAGAAATTCGAATA	5753
CACGGGCTCTNNNTGCATCAGGT		CATCAGCGTANNNTGCATCAGGT		CATGGATAGGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5274	TGCAGGACAGAGAAATTCGAATA	5514	TGCAGGACAGAGAAATTCGAATA	5754
CATTAAGTANNNTGCATCAGGT		CATCAGACGTTNNNTGCATCAGGT		CAAAACCCGNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5275	TGCAGGACAGAGAAATTCGAATA	5515	TGCAGGACAGAGAAATTCGAATA	5755
CAGACAGTCTNNNTGCATCAGGT		CATATAGATCINNNTGCATCAGGT		CACGGCGAATTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5276	TGCAGGACAGAGAAATTCGAATA	5516	TGCAGGACAGAGAAATTCGAATA	5756
CACGAGGTAANNNTGCATCAGGT		CAACCCGCTNNNTGCATCAGGT		CATTATCGCANNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5277	TGCAGGACAGAGAAATTCGAATA	5517	TGCAGGACAGAGAAATTCGAATA	5757
CACACGAACTNNNTGCATCAGGT		CACCGGATANNNTGCATCAGGT		CAGGCCACATNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5278	TGCAGGACAGAGAAATTCGAATA	5518	TGCAGGACAGAGAAATTCGAATA	5758
CATACACTGNNNTGCATCAGGT		CAAGAACTCGNNNTGCATCAGGT		CATGCTCATCTNNNTGCATCAGGT	
TGCAGGACAGAGAAATTCGAATA	5279	TGCAGGACAGAGAAATTCGAATA	5519	TGCAGGACAGAGAAATTCGAATA	5759
CATATTCTGTTNNNTGCATCAGGT		CAACATAGCTGNNNTGCATCAGGT		CAGCTGGGNNNTGCATCAGGT	

图19C

池 -22	SEQ ID NO.	池 -23	SEQ ID NO.	池 -24	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATA CATCTGCCGCCNNHTGCATCAGGT	5280	TGCAGGACCAGAGAATTGGAATA CAGTCCGCCANNHTGCATCAGGT	520	TGCAGGACCAGAGAATTGGAATA CRAAGGATGTNNHTGCATCAGGT	5760
TGCAGGACCAGAGAATTGGAATA CAGGAGCTATNNHTGCATCAGGT	5281	TGCAGGACCAGAGAATTGGAATA CAGCCCTGAGNNHTGCATCAGGT	521	TGCAGGACCAGAGAATTGGAATA CATCAGTAJANNHTGCATCAGGT	5761
TGCAGGACCAGAGAATTGGAATA CAACGCCATNNHTGCATCAGGT	5282	TGCAGGACCAGAGAATTGGAATA CAACTATGTNNHTGCATCAGGT	522	TGCAGGACCAGAGAATTGGAATA CAGTCCGTGANNHTGCATCAGGT	5762
TGCAGGACCAGAGAATTGGAATA CATCTCTGANNHTGCATCAGGT	5283	TGCAGGACCAGAGAATTGGAATA CATCTGATCCNNHTGCATCAGGT	523	TGCAGGACCAGAGAATTGGAATA CAGCTAGGCCNNHTGCATCAGGT	5763
TGCAGGACCAGAGAATTGGAATA CAAAATCTAGNNHTGCATCAGGT	5284	TGCAGGACCAGAGAATTGGAATA CATAAATAGANNHTGCATCAGGT	524	TGCAGGACCAGAGAATTGGAATA CACTCTGTANNHTGCATCAGGT	5764
TGCAGGACCAGAGAATTGGAATA CACCTCAGCCNNHTGCATCAGGT	5285	TGCAGGACCAGAGAATTGGAATA CAGGCCGTGTNNHTGCATCAGGT	525	TGCAGGACCAGAGAATTGGAATA CATTGATCAJNNHTGCATCAGGT	5765
TGCAGGACCAGAGAATTGGAATA CAGCCGCCGANNHTGCATCAGGT	5286	TGCAGGACCAGAGAATTGGAATA CAGCAACAGCCNNHTGCATCAGGT	526	TGCAGGACCAGAGAATTGGAATA CACTGTTCGTNNHTGCATCAGGT	5766
TGCAGGACCAGAGAATTGGAATA CAGTGTATAGNNHTGCATCAGGT	5287	TGCAGGACCAGAGAATTGGAATA CAGCCCTGAAANNHTGCATCAGGT	527	TGCAGGACCAGAGAATTGGAATA CATCTTATCAJNNHTGCATCAGGT	5767
TGCAGGACCAGAGAATTGGAATA CACTTGAAATGNNHTGCATCAGGT	5288	TGCAGGACCAGAGAATTGGAATA CACTGCTGTNNHTGCATCAGGT	528	TGCAGGACCAGAGAATTGGAATA CATACTGCCANNHTGCATCAGGT	5768

图19H

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
GCGACGTHNNACGTATGCCA	5769	TCTGCTANNHACGTATGCCA	6019	GTACGCAHHNACGTATGCCA	6249
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
CGATCAHHNNACGTATGCCA	5770	TACATGANNHACGTATGCCA	6010	ATGTGTNNHACGTATGCCA	6250
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
GCAATCTHNNACGTATGCCA	5771	GAGGATANNHACGTATGCCA	6011	TAGACTGNNHACGTATGCCA	6251
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
TAGGAGANNHACGTATGCCA	5772	GACATGTNNHACGTATGCCA	6012	ATCGTGTNNHACGTATGCCA	6252
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
TGATACCHNNACGTATGCCA	5773	CTTGAGHNNHACGTATGCCA	6013	TATCTCANNNHACGTATGCCA	6253
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
AGTACTCHNNACGTATGCCA	5774	AGCGATCHNNHACGTATGCCA	6014	ACCGTACNNHACGTATGCCA	6254
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
TGCCCGCHNNACGTATGCCA	5775	ACTAGAGHNNHACGTATGCCA	6015	ATCATAGHNNHACGTATGCCA	6255
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
ATGAGCANNNHACGTATGCCA	5776	TGCGATANNHACGTATGCCA	6016	GTTCGTNNHACGTATGCCA	6256
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
TGAGACCHNNHACGTATGCCA	5777	TGTGAGCHNNHACGTATGCCA	6017	TACAAACCHNNHACGTATGCCA	6257
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG	
TGCGCTCHNNHACGTATGCCA	5778	CGAATTTNNHACGTATGCCA	6018	TCCTCATNNHACGTATGCCA	6258
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
CTTTCCHNNHACGTATGCCA	5779	CTGTTTCHNNHACGTATGCCA	6019	GTAGCAHNNHACGTATGCCA	6259
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
RAATTCCHNNHACGTATGCCA	5780	CGCGTGANNHACGTATGCCA	6020	AAAPACANNHACGTATGCCA	6260
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
ATGTGCHNNHACGTATGCCA	5781	ACTCAAGHNNHACGTATGCCA	6021	TGCGCTANNHACGTATGCCA	6261
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
ACCTGCHNNHACGTATGCCA	5782	GCAATGCHNNHACGTATGCCA	6022	GAGTTGCHNNHACGTATGCCA	6262
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
ACCTGCGCHNNHACGTATGCCA	5783	GCATTATNNHACGTATGCCA	6023	AAATTTCHNNHACGTATGCCA	6263
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
CAAAATTHNNHACGTATGCCA	5784	ATTGCTANNHACGTATGCCA	6024	TAACCTGCHNNHACGTATGCCA	6264
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
TTGTTCCHNNHACGTATGCCA	5785	GATCCAAHNNHACGTATGCCA	6025	GTAAATCHNNHACGTATGCCA	6265
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
GTGAGCHNNHACGTATGCCA	5786	TGCGTGGHNNHACGTATGCCA	6026	ACTCTAHNNHACGTATGCCA	6266
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
CCCGCTCHNNHACGTATGCCA	5787	AGATTAAHNNHACGTATGCCA	6027	GGAAAAHNNHACGTATGCCA	6267
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT	
TGGACCTCHNNHACGTATGCCA	5788	TGCAAGCTHNNHACGTATGCCA	6028	GACTAGCHNNHACGTATGCCA	6268
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
TCTTACCHNNHACGTATGCCA	5789	CGGCGCHNNHACGTATGCCA	6029	ATCGTAGHNNHACGTATGCCA	6269
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
TCTTACTHNNHACGTATGCCA	5790	CTAATANNHACGTATGCCA	6030	GGTGTTCCHNNHACGTATGCCA	6270
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
GGATRAHNNHACGTATGCCA	5791	ATGGGCHNNHACGTATGCCA	6031	CCATTAGHNNHACGTATGCCA	6271
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
TCCCTTCHNNHACGTATGCCA	5792	CCGTTACHNNHACGTATGCCA	6032	CTTCTGTNNHACGTATGCCA	6272
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
GCATACCHNNHACGTATGCCA	5793	GCCTGGHNNHACGTATGCCA	6033	CCGCGTCHNNHACGTATGCCA	6273
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
CACCGATHNNHACGTATGCCA	5794	TCCCTGTNNHACGTATGCCA	6034	GTACACTHNNHACGTATGCCA	6274
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
TTGCTGCHNNHACGTATGCCA	5795	CGCGCTHNNHACGTATGCCA	6035	CAAGATTCNNHACGTATGCCA	6275
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
TCTTCTANNHACGTATGCCA	5796	CCGGCGHNNHACGTATGCCA	6036	GTGCTTCHNNHACGTATGCCA	6276
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG	
CGAAATTHNNHACGTATGCCA	5797	TTGCGCANNNHACGTATGCCA	6037	CATTATANNHACGTATGCCA	6277
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
AACTCACHNNHACGTATGCCA	5798	AAATGAHNNHACGTATGCCA	6038	TGGCATNNHACGTATGCCA	6278
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
GGCGCGHNNHACGTATGCCA	5799	AGGATGCHNNHACGTATGCCA	6039	ACGTCACHNNHACGTATGCCA	6279
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
GCTGCCCHNNHACGTATGCCA	5800	TGGACGCHNNHACGTATGCCA	6040	TTTACTHNNHACGTATGCCA	6280

图20A

池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT	
CACTCGTNNNACGTATGCCA	5801	CGTCAGTNNNACGTATGCCA	6041	AAAGATCINNACGTATGCCA	6281
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
TTACCGANNNACGTATGCCA	5802	GAAGTTCNNNACGTATGCCA	6042	ATTTCTTNNNACGTATGCCA	6282
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG	
TTACATANNNACGTATGCCA	5803	TGTGCCANNNACGTATGCCA	6043	GGCAAAANNNACGTATGCCA	6283
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
GGCTAGANNNACGTATGCCA	5804	CCGTGCCANNNACGTATGCCA	6044	CCGACANNNACGTATGCCA	6284
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
CACAGGTNNNACGTATGCCA	5805	TATTCGCNNNACGTATGCCA	6045	GGTTCGCCNNNACGTATGCCA	6285
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
ATATTTCNNNACGTATGCCA	5806	TAAGGTCNNNACGTATGCCA	6046	GAATTCGTNNNACGTATGCCA	6286
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
TGTGTTNNNACGTATGCCA	5807	GTAAACNNNACGTATGCCA	6047	GGCATTCNNNACGTATGCCA	6287
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
AAAGAGANNNACGTATGCCA	5808	TTGGTTCNNNACGTATGCCA	6048	CCACAAANNNACGTATGCCA	6288
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
GGATGTTNNNACGTATGCCA	5809	GTATATTNNNACGTATGCCA	6049	GTATATACNNNACGTATGCCA	6289
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT	
GCCTTTCNNNACGTATGCCA	5810	TTATTCAGNNNACGTATGCCA	6050	CTATCATNNNACGTATGCCA	6290
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
CTATACNNNACGTATGCCA	5811	GGGTTCNNNACGTATGCCA	6051	GGCTCTCINNACGTATGCCA	6291
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
TAGCCCGNNNACGTATGCCA	5812	GATCCAGNNNACGTATGCCA	6052	TGATTATNNNACGTATGCCA	6292
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
AAAGTCNNNACGTATGCCA	5813	AGTTTCAGNNNACGTATGCCA	6053	AGATTCNNNACGTATGCCA	6293
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
TTCAAGANNNACGTATGCCA	5814	GGCAGATNNNACGTATGCCA	6054	AGCTTTANNNACGTATGCCA	6294
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
ACAGAGANNNACGTATGCCA	5815	GGAGTAGNNNACGTATGCCA	6055	AGTAGTNNNACGTATGCCA	6295
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA	
CCGTTTANNNACGTATGCCA	5816	TAGTGATNNNACGTATGCCA	6056	TGTTAACNNNACGTATGCCA	6296
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
TTAGGANNNACGTATGCCA	5817	ACATTTAANNNACGTATGCCA	6057	AATCACANNNACGTATGCCA	6297
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAG	
AAAGCTACNNNACGTATGCCA	5818	GGTGGCCNNNACGTATGCCA	6058	ATGGCTCINNACGTATGCCA	6298
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
GGGACTTNNNACGTATGCCA	5819	CCGTGGCCNNNACGTATGCCA	6059	GGATTATNNNACGTATGCCA	6299
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
GGACTAANNNACGTATGCCA	5820	GGCGATCINNACGTATGCCA	6060	GGCATAGNNNACGTATGCCA	6300
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
GTGTTTCANNNACGTATGCCA	5821	AGACCTGNNNACGTATGCCA	6061	ATACGCANNNACGTATGCCA	6301
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
TTTTCANNNACGTATGCCA	5822	GAATACNNNACGTATGCCA	6062	GAACCCGNNNACGTATGCCA	6302
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
ATTTCATANNNACGTATGCCA	5823	TTAGCGNNNACGTATGCCA	6063	TCCCTAGNNNACGTATGCCA	6303
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAA	
TGACGACNNNACGTATGCCA	5824	GGCGGCCNNNACGTATGCCA	6064	GTGTGCTNNNACGTATGCCA	6304
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
CTTGTACNNNACGTATGCCA	5825	CCGATATNNNACGTATGCCA	6065	CTGTACTNNNACGTATGCCA	6305
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
GTGCGGANNNACGTATGCCA	5826	CCGGCCNNNACGTATGCCA	6066	ACACCCGNNNACGTATGCCA	6306
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
CATGAATNNNACGTATGCCA	5827	CTGGCTGNNNACGTATGCCA	6067	TTGGTGGNNNACGTATGCCA	6307
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
CGAAAGTNNNACGTATGCCA	5828	AGCCATANNNACGTATGCCA	6068	TTAGCCANNNACGTATGCCA	6308
TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA		TGCAGGACCCAGAGAAATTCGAATACAA	
AAATAATNNNCTAGCGTTAC	5829	ATGGAGCINNCTAGCGTTAC	6069	CGACACTNNNCTAGCGTTAC	6309
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAG	
TGGTGTNNNCTAGCGTTAC	5830	CACAGACNNNCTAGCGTTAC	6070	CATGACTNNNCTAGCGTTAC	6310
TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT		TGCAGGACCCAGAGAAATTCGAATACAT	
CGTCTTGNNNCTAGCGTTAC	5831	CCGTCCGNNNCTAGCGTTAC	6071	AGTGTANNNCTAGCGTTAC	6311
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG	
ACTGTGNNNCTAGCGTTAC	5832	AATGGACNNNCTAGCGTTAC	6072	CTGTTACNNNCTAGCGTTAC	6312
TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAG		TGCAGGACCCAGAGAAATTCGAATACAT	
CACTGGANNNCTAGCGTTAC	5833	TGCTCAANNNCTAGCGTTAC	6073	TGAGTCAANNNCTAGCGTTAC	6313

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池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCCAGAGAAATTCGAATACAC	5834	TGCAGGACCCAGAGAAATTCGAATACAT	6074	TGCAGGACCCAGAGAAATTCGAATACAT	6314
ACACCCNNNNCTAGCGTTAC		GTTCGGANNNNCTAGCGTTAC		CATCTTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5835	TGCAGGACCCAGAGAAATTCGAATACAC	6075	TGCAGGACCCAGAGAAATTCGAATACAC	6315
CCCCGCHNNNNCTAGCGTTAC		TGCGTGGNNNNCTAGCGTTAC		ACATTTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5836	TGCAGGACCCAGAGAAATTCGAATACAA	6076	TGCAGGACCCAGAGAAATTCGAATACAG	6316
CACCTTGNNNNNCTAGCGTTAC		CCGTCAANNNNCTAGCGTTAC		CCACATANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5837	TGCAGGACCCAGAGAAATTCGAATACAG	6077	TGCAGGACCCAGAGAAATTCGAATACAT	6317
GTACGACNNNNCTAGCGTTAC		GTACGANNNNCTAGCGTTAC		AAACAGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5838	TGCAGGACCCAGAGAAATTCGAATACAA	6078	TGCAGGACCCAGAGAAATTCGAATACAG	6318
CAAAAGANNNNCTAGCGTTAC		TGCGAGTNNNNCTAGCGTTAC		GTACCATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5839	TGCAGGACCCAGAGAAATTCGAATACAA	6079	TGCAGGACCCAGAGAAATTCGAATACAA	6319
TTGTTGANNNNCTAGCGTTAC		CCACGCGANNNNCTAGCGTTAC		GAAGAGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5840	TGCAGGACCCAGAGAAATTCGAATACAG	6080	TGCAGGACCCAGAGAAATTCGAATACAG	6320
CGGAAGCHNNNNCTAGCGTTAC		AGGATATNNNNCTAGCGTTAC		CTCTCATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5841	TGCAGGACCCAGAGAAATTCGAATACAT	6081	TGCAGGACCCAGAGAAATTCGAATACAA	6321
AGAAAGTNNNNCTAGCGTTAC		CCGATAGNNNNCTAGCGTTAC		GGCACAAANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5842	TGCAGGACCCAGAGAAATTCGAATACAT	6082	TGCAGGACCCAGAGAAATTCGAATACAG	6322
AGCATGNNNNCTAGCGTTAC		TAGTATGNNNNCTAGCGTTAC		CGATGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5843	TGCAGGACCCAGAGAAATTCGAATACAA	6083	TGCAGGACCCAGAGAAATTCGAATACAT	6323
AAAGCGNNNNCTAGCGTTAC		CAITTCANNNNCTAGCGTTAC		CACCTTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5844	TGCAGGACCCAGAGAAATTCGAATACAG	6084	TGCAGGACCCAGAGAAATTCGAATACAT	6324
AGTGAGGNNNNCTAGCGTTAC		TACTGACNNNNCTAGCGTTAC		AGGCGCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5845	TGCAGGACCCAGAGAAATTCGAATACAG	6085	TGCAGGACCCAGAGAAATTCGAATACAA	6325
GTGATACNNNNCTAGCGTTAC		GTGATTGNNNNCTAGCGTTAC		TTTAAATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5846	TGCAGGACCCAGAGAAATTCGAATACAA	6086	TGCAGGACCCAGAGAAATTCGAATACAT	6326
TGCGCTTNNNNCTAGCGTTAC		TGGCAGTNNNNCTAGCGTTAC		CTGCTTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5847	TGCAGGACCCAGAGAAATTCGAATACAG	6087	TGCAGGACCCAGAGAAATTCGAATACAA	6327
GACATANNNNCTAGCGTTAC		CCGACGTNNNNCTAGCGTTAC		GTGGAANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5848	TGCAGGACCCAGAGAAATTCGAATACAG	6088	TGCAGGACCCAGAGAAATTCGAATACAA	6328
TAGTATANNNNCTAGCGTTAC		AAAGCTGNNNNCTAGCGTTAC		TATGACTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5849	TGCAGGACCCAGAGAAATTCGAATACAG	6089	TGCAGGACCCAGAGAAATTCGAATACAG	6329
AACTTGNNNNNCTAGCGTTAC		GGCCAGTNNNNCTAGCGTTAC		AAAGACTNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5850	TGCAGGACCCAGAGAAATTCGAATACAG	6090	TGCAGGACCCAGAGAAATTCGAATACAG	6330
TGTTTTANNNNCTAGCGTTAC		ACAAAGCTNNNNCTAGCGTTAC		TGCGTGCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5851	TGCAGGACCCAGAGAAATTCGAATACAT	6091	TGCAGGACCCAGAGAAATTCGAATACAA	6331
ATAGGATNNNNCTAGCGTTAC		GGCACATNNNNCTAGCGTTAC		TGTCCGANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5852	TGCAGGACCCAGAGAAATTCGAATACAC	6092	TGCAGGACCCAGAGAAATTCGAATACAT	6332
GTCAAGTNNNNCTAGCGTTAC		CAAGTACNNNNCTAGCGTTAC		GTATATGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5853	TGCAGGACCCAGAGAAATTCGAATACAG	6093	TGCAGGACCCAGAGAAATTCGAATACAT	6333
CTGTTTCHNNNNCTAGCGTTAC		ACGACCGNNNNCTAGCGTTAC		GTCTGTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5854	TGCAGGACCCAGAGAAATTCGAATACAG	6094	TGCAGGACCCAGAGAAATTCGAATACAG	6334
CCGTGCGNNNNCTAGCGTTAC		CGGTATANNNNCTAGCGTTAC		ACGCTTANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5855	TGCAGGACCCAGAGAAATTCGAATACAG	6095	TGCAGGACCCAGAGAAATTCGAATACAG	6335
AGCTGCGNNNNCTAGCGTTAC		ATTGCGTNNNNCTAGCGTTAC		AAATTAATNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5856	TGCAGGACCCAGAGAAATTCGAATACAT	6096	TGCAGGACCCAGAGAAATTCGAATACAT	6336
CGTTACGNNNNCTAGCGTTAC		GTGTTTNNNNCTAGCGTTAC		CGACCCGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAA	5857	TGCAGGACCCAGAGAAATTCGAATACAT	6097	TGCAGGACCCAGAGAAATTCGAATACAG	6337
ACGAGCGNNNNCTAGCGTTAC		GTITTTGNNNNCTAGCGTTAC		CGTCCACNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5858	TGCAGGACCCAGAGAAATTCGAATACAG	6098	TGCAGGACCCAGAGAAATTCGAATACAC	6338
AAAGTTTTNNNNCTAGCGTTAC		GTGCTGNNNNCTAGCGTTAC		TGTATANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5859	TGCAGGACCCAGAGAAATTCGAATACAC	6099	TGCAGGACCCAGAGAAATTCGAATACAT	6339
CGGTTAANNNNCTAGCGTTAC		CACCTTGNNNNCTAGCGTTAC		TGAGTGNNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5860	TGCAGGACCCAGAGAAATTCGAATACAG	6100	TGCAGGACCCAGAGAAATTCGAATACAT	6340
GTGCCAANNNNCTAGCGTTAC		AGCGGTGNNNNCTAGCGTTAC		AAAGTGCCNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5861	TGCAGGACCCAGAGAAATTCGAATACAA	6101	TGCAGGACCCAGAGAAATTCGAATACAC	6341
CAAAACGNNNNCTAGCGTTAC		ACAAACGNNNNCTAGCGTTAC		AGATAAANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5862	TGCAGGACCCAGAGAAATTCGAATACAA	6102	TGCAGGACCCAGAGAAATTCGAATACAG	6342
GTAGAGNNNNCTAGCGTTAC		TTGCTTTNNNNCTAGCGTTAC		GAATCAGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5863	TGCAGGACCCAGAGAAATTCGAATACAG	6103	TGCAGGACCCAGAGAAATTCGAATACAG	6343
AGCTTCANNNNCTAGCGTTAC		CAGAGAAANNNNCTAGCGTTAC		AGCTTACNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAC	5864	TGCAGGACCCAGAGAAATTCGAATACAG	6104	TGCAGGACCCAGAGAAATTCGAATACAT	6344
ATCCCTAANNNNCTAGCGTTAC		ATACCTGNNNNCTAGCGTTAC		CATCTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAT	5865	TGCAGGACCCAGAGAAATTCGAATACAA	6105	TGCAGGACCCAGAGAAATTCGAATACAC	6345
ATTTCAGANNNNCTAGCGTTAC		CTTATTGNNNNCTAGCGTTAC		CACGTGNNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATACAG	5866	TGCAGGACCCAGAGAAATTCGAATACAA	6106	TGCAGGACCCAGAGAAATTCGAATACAC	6346
TGGAACNNNNCTAGCGTTAC		GTGTTANNNNCTAGCGTTAC		GTGTTATNNNNCTAGCGTTAC	

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池-25	SEQ ID NO:	池-26	SEQ ID NO:	池-27	SEQ ID NO:
TGCAGGACCAAGAAATTCGAATACAG	5847	TGCAGGACCAAGAAATTCGAATACAA	6107	TGCAGGACCAAGAAATTCGAATACAC	6347
ATCGCTNNNNCTAGCGTTAC		TGACTGNNNNCTAGCGTTAC		TCTCCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5868	TGCAGGACCAAGAAATTCGAATACAA	6108	TGCAGGACCAAGAAATTCGAATACAC	6348
ACTTCTGNNNNCTAGCGTTAC		GCAAAAGNNNNCTAGCGTTAC		AAGAGTNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAT	5869	TGCAGGACCAAGAAATTCGAATACAA	6109	TGCAGGACCAAGAAATTCGAATACAT	6349
AACTAGCNNNNCTAGCGTTAC		GACTATTNNNNCTAGCGTTAC		AGCTCTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5870	TGCAGGACCAAGAAATTCGAATACAG	6110	TGCAGGACCAAGAAATTCGAATACAG	6350
GTGTGCGNNNNCTAGCGTTAC		TGAAAGCNNNNCTAGCGTTAC		TGCCAGCNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5871	TGCAGGACCAAGAAATTCGAATACAA	6111	TGCAGGACCAAGAAATTCGAATACAT	6351
ACTCGATTNNNNCTAGCGTTAC		TGAAAGGNNNNCTAGCGTTAC		TGCACTCGANNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5872	TGCAGGACCAAGAAATTCGAATACAG	6112	TGCAGGACCAAGAAATTCGAATACAG	6352
GGATCGCNNNNCTAGCGTTAC		GCTAGTTNNNNCTAGCGTTAC		GGTCCGANNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAA	5873	TGCAGGACCAAGAAATTCGAATACAG	6113	TGCAGGACCAAGAAATTCGAATACAA	6353
CTCTACGNNNNCTAGCGTTAC		AAACCCACNNNNCTAGCGTTAC		AGCCACGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5874	TGCAGGACCAAGAAATTCGAATACAT	6114	TGCAGGACCAAGAAATTCGAATACAG	6354
GAAGGCGNNNNCTAGCGTTAC		TGTAGTANNNNCTAGCGTTAC		ATCTTTNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5875	TGCAGGACCAAGAAATTCGAATACAG	6115	TGCAGGACCAAGAAATTCGAATACAG	6355
ATATTAGNNNNCTAGCGTTAC		TACAGGTTNNNNCTAGCGTTAC		GCTCTAANNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5876	TGCAGGACCAAGAAATTCGAATACAA	6116	TGCAGGACCAAGAAATTCGAATACAT	6356
GGTGACGNNNNCTAGCGTTAC		GTGTACGNNNNCTAGCGTTAC		CTATGTTNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5877	TGCAGGACCAAGAAATTCGAATACAT	6117	TGCAGGACCAAGAAATTCGAATACAA	6357
TGCATGTTNNNNCTAGCGTTAC		TTTATGCGNNNNCTAGCGTTAC		CCCGCTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAT	5878	TGCAGGACCAAGAAATTCGAATACAA	6118	TGCAGGACCAAGAAATTCGAATACAG	6358
AACTGTTNNNNCTAGCGTTAC		ATCGGTGNNNNCTAGCGTTAC		TACTCTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAA	5879	TGCAGGACCAAGAAATTCGAATACAG	6119	TGCAGGACCAAGAAATTCGAATACAG	6359
CCCTTATTNNNNCTAGCGTTAC		GATCTGANNNNCTAGCGTTAC		GAGGCCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAA	5880	TGCAGGACCAAGAAATTCGAATACAG	6120	TGCAGGACCAAGAAATTCGAATACAT	6360
CTCCACTNNNNCTAGCGTTAC		ATAGTANNNNCTAGCGTTAC		ATCCGAGCNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5881	TGCAGGACCAAGAAATTCGAATACAG	6121	TGCAGGACCAAGAAATTCGAATACAG	6361
CAATATNNNNCTAGCGTTAC		AGTCCATTNNNNCTAGCGTTAC		CGTTGANNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5882	TGCAGGACCAAGAAATTCGAATACAG	6122	TGCAGGACCAAGAAATTCGAATACAG	6362
AAAGATGNNNNCTAGCGTTAC		ATGTGGTNNNNCTAGCGTTAC		GAAGATGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5883	TGCAGGACCAAGAAATTCGAATACAG	6123	TGCAGGACCAAGAAATTCGAATACAA	6363
CCAGAGCNNNNCTAGCGTTAC		ATCCCGCNNNNCTAGCGTTAC		GTGATCGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAT	5884	TGCAGGACCAAGAAATTCGAATACAA	6124	TGCAGGACCAAGAAATTCGAATACAG	6364
AAAGCGANNNNCTAGCGTTAC		CCAGATGNNNNCTAGCGTTAC		GTCACTNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5885	TGCAGGACCAAGAAATTCGAATACAT	6125	TGCAGGACCAAGAAATTCGAATACAT	6365
AGGCGCTNNNNCTAGCGTTAC		GCCGATANNNNCTAGCGTTAC		GAAGTGTNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5886	TGCAGGACCAAGAAATTCGAATACAG	6126	TGCAGGACCAAGAAATTCGAATACAT	6366
TTCCCTAGNNNNCTAGCGTTAC		AAAGCCTNNNNCTAGCGTTAC		TACAAACNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5887	TGCAGGACCAAGAAATTCGAATACAA	6127	TGCAGGACCAAGAAATTCGAATACAA	6367
GCAGAAANNNNCTAGCGTTAC		CTGACGJNNNNCTAGCGTTAC		AAATGTTGNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAT	5888	TGCAGGACCAAGAAATTCGAATACAA	6128	TGCAGGACCAAGAAATTCGAATACAT	6368
GTGCGTAGNNNNCTAGCGTTAC		AGCTGTGNNNNCTAGCGTTAC		TATAAGCNNNNCTAGCGTTAC	
TGCAGGACCAAGAAATTCGAATACAG	5889	TGCAGGACCAAGAAATTCGAATACAG	6129	TGCAGGACCAAGAAATTCGAATACAT	6369
GATCGAANNNGATCGACATG		GATCGAANNNGATCGACATG		CCGGATTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5890	TGCAGGACCAAGAAATTCGAATACAT	6130	TGCAGGACCAAGAAATTCGAATACAA	6370
CAATTANNNGATCGACATG		CCGACANNNGATCGACATG		GCCCTTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5891	TGCAGGACCAAGAAATTCGAATACAG	6131	TGCAGGACCAAGAAATTCGAATACAG	6371
ATAGGCTNNNGATCGACATG		CGACTAANNNGATCGACATG		TACACTGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5892	TGCAGGACCAAGAAATTCGAATACAG	6132	TGCAGGACCAAGAAATTCGAATACAG	6372
AAAAATTNNNGATCGACATG		ACCCTTANNNGATCGACATG		GTGTAGTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5893	TGCAGGACCAAGAAATTCGAATACAA	6133	TGCAGGACCAAGAAATTCGAATACAG	6373
ATAGACTNNNGATCGACATG		TGCCCTTNNNGATCGACATG		GAAGATGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5894	TGCAGGACCAAGAAATTCGAATACAT	6134	TGCAGGACCAAGAAATTCGAATACAT	6374
ATCGAAANNNGATCGACATG		CGAAAGCNNNGATCGACATG		TCTGGCTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAT	5895	TGCAGGACCAAGAAATTCGAATACAG	6135	TGCAGGACCAAGAAATTCGAATACAT	6375
CTATTACNNNGATCGACATG		ACCTTCTNNNGATCGACATG		ACTCGGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5896	TGCAGGACCAAGAAATTCGAATACAG	6136	TGCAGGACCAAGAAATTCGAATACAG	6376
CCCGATTANNNGATCGACATG		TACCTTANNNGATCGACATG		GTCCAAANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5897	TGCAGGACCAAGAAATTCGAATACAA	6137	TGCAGGACCAAGAAATTCGAATACAT	6377
AAAGCGANNNGATCGACATG		TGCGCTTNNNGATCGACATG		TGAACCGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5898	TGCAGGACCAAGAAATTCGAATACAG	6138	TGCAGGACCAAGAAATTCGAATACAG	6378
TGATCGTNNNGATCGACATG		CCACTANNNGATCGACATG		TCGCGCTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5899	TGCAGGACCAAGAAATTCGAATACAG	6139	TGCAGGACCAAGAAATTCGAATACAG	6379
GCAGCCANNNGATCGACATG		GCATTGANNNGATCGACATG		ATAAGTNNNGATCGACATG	

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池 -25	SEQ ID NO:	池 -26	SEQ ID NO:	池 -27	SEQ ID NO:
TGCAGGACCAAGAAATTCGAATACAT	5900	TGCAGGACCAAGAAATTCGAATACAG	6140	TGCAGGACCAAGAAATTCGAATACAA	6380
GCACATGNNNGATCGACATG		CTAGAGNNNGATCGACATG		TTACACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5901	TGCAGGACCAAGAAATTCGAATACAT	6141	TGCAGGACCAAGAAATTCGAATACAG	6381
GTCCACGNNNGATCGACATG		TTATAANNNGATCGACATG		TGTGCATNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5902	TGCAGGACCAAGAAATTCGAATACAT	6142	TGCAGGACCAAGAAATTCGAATACAG	6382
AGCATAANNNGATCGACATG		CCCTACANNNGATCGACATG		CCATAGTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5903	TGCAGGACCAAGAAATTCGAATACAA	6143	TGCAGGACCAAGAAATTCGAATACAC	6383
ACAGCGNNNGATCGACATG		CGTCTAGNNNGATCGACATG		TGATCTGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5904	TGCAGGACCAAGAAATTCGAATACAG	6144	TGCAGGACCAAGAAATTCGAATACAA	6384
CGGTAGANNNGATCGACATG		AGCCTTGNNNGATCGACATG		ACCGACINNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAT	5905	TGCAGGACCAAGAAATTCGAATACAA	6145	TGCAGGACCAAGAAATTCGAATACAC	6385
CATTACTNNNGATCGACATG		GAAGCGGNNNGATCGACATG		ATCGCCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5906	TGCAGGACCAAGAAATTCGAATACAC	6146	TGCAGGACCAAGAAATTCGAATACAT	6386
GAATAAANNNGATCGACATG		ATATACANNNGATCGACATG		AGGATCCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAT	5907	TGCAGGACCAAGAAATTCGAATACAA	6147	TGCAGGACCAAGAAATTCGAATACAA	6387
GGAAAGTNNNGATCGACATG		AGGCTAGNNNGATCGACATG		TGGCGTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5908	TGCAGGACCAAGAAATTCGAATACAT	6148	TGCAGGACCAAGAAATTCGAATACAC	6388
TGTTTAAHNNNGATCGACATG		ATCGACGNNNGATCGACATG		TAAATGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5909	TGCAGGACCAAGAAATTCGAATACAA	6149	TGCAGGACCAAGAAATTCGAATACAA	6389
GGATTGNNNGATCGACATG		GACGCTNNNGATCGACATG		CTACATANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5910	TGCAGGACCAAGAAATTCGAATACAT	6150	TGCAGGACCAAGAAATTCGAATACAC	6390
GTGGTGNNNGATCGACATG		GTATCCNNNGATCGACATG		ATCCCTCANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5911	TGCAGGACCAAGAAATTCGAATACAG	6151	TGCAGGACCAAGAAATTCGAATACAG	6391
TGCGCTHNNNGATCGACATG		CCTGCAGNNNGATCGACATG		ATGTGAGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5912	TGCAGGACCAAGAAATTCGAATACAC	6152	TGCAGGACCAAGAAATTCGAATACAA	6392
GAGAAGHNNNGATCGACATG		GTAAAGTNNNGATCGACATG		GGCCAAANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAT	5913	TGCAGGACCAAGAAATTCGAATACAA	6153	TGCAGGACCAAGAAATTCGAATACAC	6393
CATGGTNNNGATCGACATG		TCTTATCNNNGATCGACATG		CAAGCTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5914	TGCAGGACCAAGAAATTCGAATACAA	6154	TGCAGGACCAAGAAATTCGAATACAA	6394
TGCAGGACCAAGAAATTCGAATACAC	5915	TGCAGGACCAAGAAATTCGAATACAG	6155	TGCAGGACCAAGAAATTCGAATACAC	6395
TGTTAGHNNNGATCGACATG		ATTAAAGNNNGATCGACATG		CTCCGACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5916	TGCAGGACCAAGAAATTCGAATACAT	6156	TGCAGGACCAAGAAATTCGAATACAC	6396
TGCTGTHNNNGATCGACATG		TGCCAGANNNGATCGACATG		GCTGTGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5917	TGCAGGACCAAGAAATTCGAATACAC	6157	TGCAGGACCAAGAAATTCGAATACAT	6397
AAAGTCCNNNGATCGACATG		GGCATATHNNNGATCGACATG		ACCGCCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5918	TGCAGGACCAAGAAATTCGAATACAG	6158	TGCAGGACCAAGAAATTCGAATACAC	6398
GTAGCGNNNGATCGACATG		GTACGCCNNNGATCGACATG		GTCCGCTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5919	TGCAGGACCAAGAAATTCGAATACAC	6159	TGCAGGACCAAGAAATTCGAATACAC	6399
GGCTGAANNNGATCGACATG		TACCACTNNNGATCGACATG		CTCACCGNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5920	TGCAGGACCAAGAAATTCGAATACAC	6160	TGCAGGACCAAGAAATTCGAATACAG	6400
TAATCTHNNNGATCGACATG		GCACGGTNNNGATCGACATG		CCTGGACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5921	TGCAGGACCAAGAAATTCGAATACAT	6161	TGCAGGACCAAGAAATTCGAATACAA	6401
ACTTAAHNNNGATCGACATG		GCTTCGTNNNGATCGACATG		CTTGGACNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5922	TGCAGGACCAAGAAATTCGAATACAA	6162	TGCAGGACCAAGAAATTCGAATACAT	6402
TCACAATHNNNGATCGACATG		GCACGTGNNNGATCGACATG		GTTCGCTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5923	TGCAGGACCAAGAAATTCGAATACAC	6163	TGCAGGACCAAGAAATTCGAATACAC	6403
AGCCTGCHNNNGATCGACATG		TTACAAANNNGATCGACATG		GGCACGTNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5924	TGCAGGACCAAGAAATTCGAATACAG	6164	TGCAGGACCAAGAAATTCGAATACAA	6404
TCTAGGANNNGATCGACATG		GGTGGCCNNNGATCGACATG		GGTGTGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5925	TGCAGGACCAAGAAATTCGAATACAC	6165	TGCAGGACCAAGAAATTCGAATACAA	6405
GTAGATHNNNGATCGACATG		ACCGGCCANNNGATCGACATG		ACGACGANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5926	TGCAGGACCAAGAAATTCGAATACAG	6166	TGCAGGACCAAGAAATTCGAATACAC	6406
GGTTGCTHNNNGATCGACATG		CCATAACNNNGATCGACATG		ATCACTCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAG	5927	TGCAGGACCAAGAAATTCGAATACAT	6167	TGCAGGACCAAGAAATTCGAATACAT	6407
AGGTGCGNNNGATCGACATG		GAAGTCCNNNGATCGACATG		AATGCTANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5928	TGCAGGACCAAGAAATTCGAATACAG	6168	TGCAGGACCAAGAAATTCGAATACAC	6408
CTCAGACHNNNGATCGACATG		CAACACTHNNNGATCGACATG		GCCCTGCHNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5929	TGCAGGACCAAGAAATTCGAATACAA	6169	TGCAGGACCAAGAAATTCGAATACAT	6409
AAATGTATHNNNGATCGACATG		CGCTTCTNNNGATCGACATG		GATCAGCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAA	5930	TGCAGGACCAAGAAATTCGAATACAT	6170	TGCAGGACCAAGAAATTCGAATACAC	6410
ACCATTAAHNNNGATCGACATG		ACCGGCGNNNGATCGACATG		TTCCGAANNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAT	5931	TGCAGGACCAAGAAATTCGAATACAT	6171	TGCAGGACCAAGAAATTCGAATACAC	6411
GGCGCTHNNNGATCGACATG		GCTAAATANNNGATCGACATG		GCAAATCNNNGATCGACATG	
TGCAGGACCAAGAAATTCGAATACAC	5932	TGCAGGACCAAGAAATTCGAATACAT	6172	TGCAGGACCAAGAAATTCGAATACAA	6412
GCCCTGTHNNNGATCGACATG		AGGAGACNNNGATCGACATG		AGGACACNNNGATCGACATG	

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池 -25	SEQ ID NO:	池 -26	SEQ ID NO:	池 -27	SEQ ID NO:
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
AGCCCTANNNGATCGACATG	5933	AGCCCTANNNGATCGACATG	6173	AGCCCTANNNGATCGACATG	6413
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
GATAGTGNNNGATCGACATG	5934	GATAGTGNNNGATCGACATG	6174	GATAGTGNNNGATCGACATG	6414
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
AGGCGAGNNNGATCGACATG	5935	AGGCGAGNNNGATCGACATG	6175	AGGCGAGNNNGATCGACATG	6415
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
GGTCTGNNNGATCGACATG	5936	GGTCTGNNNGATCGACATG	6176	GGTCTGNNNGATCGACATG	6416
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
AGCTGGAGNNNGATCGACATG	5937	AGCTGGAGNNNGATCGACATG	6177	AGCTGGAGNNNGATCGACATG	6417
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
TTGTTGNNNGATCGACATG	5938	TTGTTGNNNGATCGACATG	6178	TTGTTGNNNGATCGACATG	6418
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CGAAGCGNNNGATCGACATG	5939	CGAAGCGNNNGATCGACATG	6179	CGAAGCGNNNGATCGACATG	6419
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
GATCCGTNNNGATCGACATG	5940	GATCCGTNNNGATCGACATG	6180	GATCCGTNNNGATCGACATG	6420
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
TACCGTGNNNGATCGACATG	5941	TACCGTGNNNGATCGACATG	6181	TACCGTGNNNGATCGACATG	6421
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
ATCATGTNNNGATCGACATG	5942	ATCATGTNNNGATCGACATG	6182	ATCATGTNNNGATCGACATG	6422
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
GTGTTGTNNNGATCGACATG	5943	GTGTTGTNNNGATCGACATG	6183	GTGTTGTNNNGATCGACATG	6423
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
GATACAGNNNGATCGACATG	5944	GATACAGNNNGATCGACATG	6184	GATACAGNNNGATCGACATG	6424
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TTCTGTGNNNGATCGACATG	5945	TTCTGTGNNNGATCGACATG	6185	TTCTGTGNNNGATCGACATG	6425
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
AGAGTCAANNNGATCGACATG	5946	AGAGTCAANNNGATCGACATG	6186	AGAGTCAANNNGATCGACATG	6426
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
TTTGTANNNGATCGACATG	5947	TTTGTANNNGATCGACATG	6187	TTTGTANNNGATCGACATG	6427
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TGAATCTNNNGATCGACATG	5948	TGAATCTNNNGATCGACATG	6188	TGAATCTNNNGATCGACATG	6428
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
CTACAGANNNTGCATCAGGT	5949	CTACAGANNNTGCATCAGGT	6189	CTACAGANNNTGCATCAGGT	6429
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CATCGATNNNTGCATCAGGT	5950	CATCGATNNNTGCATCAGGT	6190	CATCGATNNNTGCATCAGGT	6430
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
ACTGCTCANNNTGCATCAGGT	5951	ACTGCTCANNNTGCATCAGGT	6191	ACTGCTCANNNTGCATCAGGT	6431
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
CTGTTGTNNNTGCATCAGGT	5952	CTGTTGTNNNTGCATCAGGT	6192	CTGTTGTNNNTGCATCAGGT	6432
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
AGTCCGAANNNTGCATCAGGT	5953	AGTCCGAANNNTGCATCAGGT	6193	AGTCCGAANNNTGCATCAGGT	6433
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
TGACCAANNNTGCATCAGGT	5954	TGACCAANNNTGCATCAGGT	6194	TGACCAANNNTGCATCAGGT	6434
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
TGGTTATNNNTGCATCAGGT	5955	TGGTTATNNNTGCATCAGGT	6195	TGGTTATNNNTGCATCAGGT	6435
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CGCTCAGNNNTGCATCAGGT	5956	CGCTCAGNNNTGCATCAGGT	6196	CGCTCAGNNNTGCATCAGGT	6436
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
GGACCCGNNNTGCATCAGGT	5957	GGACCCGNNNTGCATCAGGT	6197	GGACCCGNNNTGCATCAGGT	6437
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
TACCAACNNNTGCATCAGGT	5958	TACCAACNNNTGCATCAGGT	6198	TACCAACNNNTGCATCAGGT	6438
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
TATAACTNNNTGCATCAGGT	5959	TATAACTNNNTGCATCAGGT	6199	TATAACTNNNTGCATCAGGT	6439
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CCGCTGANNNTGCATCAGGT	5960	CCGCTGANNNTGCATCAGGT	6200	CCGCTGANNNTGCATCAGGT	6440
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
TGATGACNNNTGCATCAGGT	5961	TGATGACNNNTGCATCAGGT	6201	TGATGACNNNTGCATCAGGT	6441
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
ATGGCATNNNTGCATCAGGT	5962	ATGGCATNNNTGCATCAGGT	6202	ATGGCATNNNTGCATCAGGT	6442
TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA		TGCAGGACCCAGAGAATTGGAATACAA	
TGATATCNNNTGCATCAGGT	5963	TGATATCNNNTGCATCAGGT	6203	TGATATCNNNTGCATCAGGT	6443
TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT		TGCAGGACCCAGAGAATTGGAATACAT	
GTAAAGNNNTGCATCAGGT	5964	GTAAAGNNNTGCATCAGGT	6204	GTAAAGNNNTGCATCAGGT	6444
TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG		TGCAGGACCCAGAGAATTGGAATACAG	
CTTGCCGNNNTGCATCAGGT	5965	CTTGCCGNNNTGCATCAGGT	6205	CTTGCCGNNNTGCATCAGGT	6445

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池 -25	SEQ ID NO:	池 -26	SEQ ID NO:	池 -27	SEQ ID NO:
TGCAGGACCAAGAAATTGGAATACAG	5966	TGCAGGACCAAGAAATTGGAATACAG	6206	TGCAGGACCAAGAAATTGGAATACAG	6446
AGGCACGNNNTGCATCAGGT		CCATGTTNNNTGCATCAGGT		CATGTCCNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5967	TGCAGGACCAAGAAATTGGAATACAG	6207	TGCAGGACCAAGAAATTGGAATACAG	6447
CTGAGCGNNNTGCATCAGGT		AGCAATGNNNTGCATCAGGT		AGGATCTNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5968	TGCAGGACCAAGAAATTGGAATACAG	6208	TGCAGGACCAAGAAATTGGAATACAG	6448
GTTCGCTANNNTGCATCAGGT		ATACCTANNNTGCATCAGGT		GTTCGCTNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5969	TGCAGGACCAAGAAATTGGAATACAG	6209	TGCAGGACCAAGAAATTGGAATACAG	6449
TGCAAGGNNNTGCATCAGGT		ATATTGNNNTGCATCAGGT		ATTCAGGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5970	TGCAGGACCAAGAAATTGGAATACAG	6210	TGCAGGACCAAGAAATTGGAATACAG	6450
CGTATGNNNTGCATCAGGT		ATCCATANNNTGCATCAGGT		CAACATANNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5971	TGCAGGACCAAGAAATTGGAATACAG	6211	TGCAGGACCAAGAAATTGGAATACAG	6451
AGGCACGNNNTGCATCAGGT		CCATTTANNNTGCATCAGGT		TGAAGGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5972	TGCAGGACCAAGAAATTGGAATACAG	6212	TGCAGGACCAAGAAATTGGAATACAG	6452
TTTGCNNNTGCATCAGGT		AGGTTCTNNNTGCATCAGGT		AGGTTGGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5973	TGCAGGACCAAGAAATTGGAATACAG	6213	TGCAGGACCAAGAAATTGGAATACAG	6453
AGTCTGNNNTGCATCAGGT		TGATACNNNTGCATCAGGT		GGAAAAINNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5974	TGCAGGACCAAGAAATTGGAATACAG	6214	TGCAGGACCAAGAAATTGGAATACAG	6454
TTCTCTNNNTGCATCAGGT		TGCGAGCCAGAGAAATTGGAATACAG		TGCAGGACCAAGAAATTGGAATACAG	
TGCAGGACCAAGAAATTGGAATACAG	5975	TGCAGGACCAAGAAATTGGAATACAG	6215	TGCAGGACCAAGAAATTGGAATACAG	6455
TGTGAANNNTGCATCAGGT		ATCAAGTNNNTGCATCAGGT		ACGCTTNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5976	TGCAGGACCAAGAAATTGGAATACAG	6216	TGCAGGACCAAGAAATTGGAATACAG	6456
CCCTCTNNNTGCATCAGGT		CTTAGGNNNTGCATCAGGT		GGCCTATNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5977	TGCAGGACCAAGAAATTGGAATACAG	6217	TGCAGGACCAAGAAATTGGAATACAG	6457
AGAGGCGNNNTGCATCAGGT		CTGTTCCNNNTGCATCAGGT		GTGATGGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5978	TGCAGGACCAAGAAATTGGAATACAG	6218	TGCAGGACCAAGAAATTGGAATACAG	6458
TTCATCTNNNTGCATCAGGT		GATCCATNNNTGCATCAGGT		GGATGAANNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5979	TGCAGGACCAAGAAATTGGAATACAG	6219	TGCAGGACCAAGAAATTGGAATACAG	6459
CCCTGACNNNTGCATCAGGT		CACTCCGNNNTGCATCAGGT		ACATAGCNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5980	TGCAGGACCAAGAAATTGGAATACAG	6220	TGCAGGACCAAGAAATTGGAATACAG	6460
GTATATANNNTGCATCAGGT		CAAGAGTNNNTGCATCAGGT		TTGCTGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5981	TGCAGGACCAAGAAATTGGAATACAG	6221	TGCAGGACCAAGAAATTGGAATACAG	6461
ATATATANNNTGCATCAGGT		CCGTCTNNNTGCATCAGGT		TGCAGGACCAAGAAATTGGAATACAG	
TGCAGGACCAAGAAATTGGAATACAG	5982	TGCAGGACCAAGAAATTGGAATACAG	6222	TGCAGGACCAAGAAATTGGAATACAG	6462
GGCCCTGNNNTGCATCAGGT		GCTTAGTNNNTGCATCAGGT		CGTCCGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5983	TGCAGGACCAAGAAATTGGAATACAG	6223	TGCAGGACCAAGAAATTGGAATACAG	6463
ATCAAGGNNNTGCATCAGGT		CTAAGCANNNTGCATCAGGT		AGCCCATNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5984	TGCAGGACCAAGAAATTGGAATACAG	6224	TGCAGGACCAAGAAATTGGAATACAG	6464
CGACATNNNTGCATCAGGT		CGCGAGNNNTGCATCAGGT		GAGGCGTNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5985	TGCAGGACCAAGAAATTGGAATACAG	6225	TGCAGGACCAAGAAATTGGAATACAG	6465
AGAGAGTNNNTGCATCAGGT		ATTCTTANNNTGCATCAGGT		CGTATCCNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5986	TGCAGGACCAAGAAATTGGAATACAG	6226	TGCAGGACCAAGAAATTGGAATACAG	6466
TTTACACNNNTGCATCAGGT		CTACGCTNNNTGCATCAGGT		GGCGAGCNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5987	TGCAGGACCAAGAAATTGGAATACAG	6227	TGCAGGACCAAGAAATTGGAATACAG	6467
TTAGCTANNNTGCATCAGGT		CGGAGCTNNNTGCATCAGGT		AGAGCTGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5988	TGCAGGACCAAGAAATTGGAATACAG	6228	TGCAGGACCAAGAAATTGGAATACAG	6468
TGACCGCNNNTGCATCAGGT		TACTTAANNNTGCATCAGGT		GGTGTGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5989	TGCAGGACCAAGAAATTGGAATACAG	6229	TGCAGGACCAAGAAATTGGAATACAG	6469
CGATATGNNNTGCATCAGGT		GGCGCTCNNNTGCATCAGGT		TAAATCANNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5990	TGCAGGACCAAGAAATTGGAATACAG	6230	TGCAGGACCAAGAAATTGGAATACAG	6470
AGCATATNNNTGCATCAGGT		CGACTTANNNTGCATCAGGT		TTTCCGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5991	TGCAGGACCAAGAAATTGGAATACAG	6231	TGCAGGACCAAGAAATTGGAATACAG	6471
TGCGCGNNNTGCATCAGGT		TGGCAAGNNNTGCATCAGGT		CTCCATANNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5992	TGCAGGACCAAGAAATTGGAATACAG	6232	TGCAGGACCAAGAAATTGGAATACAG	6472
TAGTAACTNNNTGCATCAGGT		GGAGGTGNNNTGCATCAGGT		TACTACTNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5993	TGCAGGACCAAGAAATTGGAATACAG	6233	TGCAGGACCAAGAAATTGGAATACAG	6473
ATCAGCGNNNTGCATCAGGT		CATTAACTNNNTGCATCAGGT		CGTTTATNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5994	TGCAGGACCAAGAAATTGGAATACAG	6234	TGCAGGACCAAGAAATTGGAATACAG	6474
GATCTCTNNNTGCATCAGGT		AGGAAATNNNTGCATCAGGT		TTCAATGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5995	TGCAGGACCAAGAAATTGGAATACAG	6235	TGCAGGACCAAGAAATTGGAATACAG	6475
AGGAGAGNNNTGCATCAGGT		CTAAGTNNNTGCATCAGGT		ACACACNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5996	TGCAGGACCAAGAAATTGGAATACAG	6236	TGCAGGACCAAGAAATTGGAATACAG	6476
GTCTGCTNNNTGCATCAGGT		AGAGGCTNNNTGCATCAGGT		ACCGCGNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5997	TGCAGGACCAAGAAATTGGAATACAG	6237	TGCAGGACCAAGAAATTGGAATACAG	6477
ACACTCANNNTGCATCAGGT		TGAGACANNNTGCATCAGGT		CATGGCNNNTGCATCAGGT	
TGCAGGACCAAGAAATTGGAATACAG	5998	TGCAGGACCAAGAAATTGGAATACAG	6238	TGCAGGACCAAGAAATTGGAATACAG	6478
AGTTCTGNNNTGCATCAGGT		GACGCGNNNTGCATCAGGT		CTGATANNNTGCATCAGGT	

图20G

池 -25	SEQ ID NO:	池 -26	SEQ ID NO:	池 -27	SEQ ID NO:
TGCAGGACAGAGAATTGGAATACAA	6239	TGCAGGACAGAGAATTGGAATACAT	6239	TGCAGGACAGAGAATTGGAATACAG	6479
ATTGCTANNNTGCATCAGGT		TTTACGTNNNTGCATCAGGT		ATGTGCTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAG	6000	TGCAGGACAGAGAATTGGAATACAG	6240	TGCAGGACAGAGAATTGGAATACAA	6480
CTGATTGNNNTGCATCAGGT		ATGATTNNNTGCATCAGGT		AGACCTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAT	6001	TGCAGGACAGAGAATTGGAATACAA	6241	TGCAGGACAGAGAATTGGAATACAG	6481
ATCCGAANNNTGCATCAGGT		CGGAA TGNNNTGCATCAGGT		TACTTGNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAA	6002	TGCAGGACAGAGAATTGGAATACAA	6242	TGCAGGACAGAGAATTGGAATACAT	6482
GGCCATTNNNTGCATCAGGT		ATGGCAGNNNTGCATCAGGT		CCCTCTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAG	6003	TGCAGGACAGAGAATTGGAATACAC	6243	TGCAGGACAGAGAATTGGAATACAT	6483
CTGCCANNNTGCATCAGGT		GACTGATNNNTGCATCAGGT		ACTTACTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAT	6004	TGCAGGACAGAGAATTGGAATACAA	6244	TGCAGGACAGAGAATTGGAATACAG	6484
GGACGCTNNNTGCATCAGGT		AGGTACNNNTGCATCAGGT		GTCTTCTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAC	6005	TGCAGGACAGAGAATTGGAATACAA	6245	TGCAGGACAGAGAATTGGAATACAG	6485
GAGGCAGNNNTGCATCAGGT		CGGCTTNNNTGCATCAGGT		GATCAGTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAG	6006	TGCAGGACAGAGAATTGGAATACAC	6246	TGCAGGACAGAGAATTGGAATACAT	6486
GTGCTATNNNTGCATCAGGT		CACGCTCNNNTGCATCAGGT		TGATGGCNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAA	6007	TGCAGGACAGAGAATTGGAATACAA	6247	TGCAGGACAGAGAATTGGAATACAC	6487
ATTGCCGNNNTGCATCAGGT		ACCAC TGNNNTGCATCAGGT		CACATTNNNTGCATCAGGT	
TGCAGGACAGAGAATTGGAATACAG	6008	TGCAGGACAGAGAATTGGAATACAG	6248	TGCAGGACAGAGAATTGGAATACAC	6488
GGCGACTNNNTGCATCAGGT		TCAGGTNNNTGCATCAGGT		AAAAAGTNNNTGCATCAGGT	

图20H

池 -28	SEQ ID NO:	池 -29	SEQ ID NO:	池 -30	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	6489	TGCAGGACCAGAGAATTGGAATA	6729	TGCAGGACCAGAGAATTGGAATA	6969
CACAGTATTANNACGTATGCCA		CAGCTGACCGNNACGTATGCCA		CATATTGCTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6490	TGCAGGACCAGAGAATTGGAATA	6730	TGCAGGACCAGAGAATTGGAATA	6970
CAGTACTTAATNNACGTATGCCA		CACGAGCATANNACGTATGCCA		CACCTAATAANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6491	TGCAGGACCAGAGAATTGGAATA	6731	TGCAGGACCAGAGAATTGGAATA	6971
CATTTAGCTNNACGTATGCCA		CACGAAGGATNNACGTATGCCA		CAGTTGGCGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6492	TGCAGGACCAGAGAATTGGAATA	6732	TGCAGGACCAGAGAATTGGAATA	6972
CAGTCATCTNNACGTATGCCA		CACGACGAGNNACGTATGCCA		CAGTGGCGTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6493	TGCAGGACCAGAGAATTGGAATA	6733	TGCAGGACCAGAGAATTGGAATA	6973
CACGAATTAANNACGTATGCCA		CATATTACCAANNACGTATGCCA		CAATATCCCGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6494	TGCAGGACCAGAGAATTGGAATA	6734	TGCAGGACCAGAGAATTGGAATA	6974
CAGACGTATCANNACGTATGCCA		CAGTGGTTTGNACGTATGCCA		CACACARACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6495	TGCAGGACCAGAGAATTGGAATA	6735	TGCAGGACCAGAGAATTGGAATA	6975
CAATTTACANNACGTATGCCA		CAGTTGGCATNNACGTATGCCA		CAATTAATANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6496	TGCAGGACCAGAGAATTGGAATA	6736	TGCAGGACCAGAGAATTGGAATA	6976
CAATTCGCAANNACGTATGCCA		CAATACCGCTCANNACGTATGCCA		CAGATTAGCGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6497	TGCAGGACCAGAGAATTGGAATA	6737	TGCAGGACCAGAGAATTGGAATA	6977
CAACCTATTNNACGTATGCCA		CACCTCGAAGTNNACGTATGCCA		CAGACAAATNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6498	TGCAGGACCAGAGAATTGGAATA	6738	TGCAGGACCAGAGAATTGGAATA	6978
CAGCTTACTCANNACGTATGCCA		CACAGCGCGTNNACGTATGCCA		CAATATTANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6499	TGCAGGACCAGAGAATTGGAATA	6739	TGCAGGACCAGAGAATTGGAATA	6979
CATTTGATGANNACGTATGCCA		CAATAGTCATNNACGTATGCCA		CAAAAAGTCAANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6500	TGCAGGACCAGAGAATTGGAATA	6740	TGCAGGACCAGAGAATTGGAATA	6980
CAGCGGACCAANNACGTATGCCA		CAGTCCGTCGNNACGTATGCCA		CAGTCTTAAANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6501	TGCAGGACCAGAGAATTGGAATA	6741	TGCAGGACCAGAGAATTGGAATA	6981
CAACAAGTTNNACGTATGCCA		CAGTGGCGTNNACGTATGCCA		CAAAAACGCTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6502	TGCAGGACCAGAGAATTGGAATA	6742	TGCAGGACCAGAGAATTGGAATA	6982
CATATTCTCATNNACGTATGCCA		CAAGTAAAGTNNACGTATGCCA		CATTTGCTCTGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6503	TGCAGGACCAGAGAATTGGAATA	6743	TGCAGGACCAGAGAATTGGAATA	6983
CAGCTTTGCTNNACGTATGCCA		CATATTGCAANNACGTATGCCA		CAATTAAGANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6504	TGCAGGACCAGAGAATTGGAATA	6744	TGCAGGACCAGAGAATTGGAATA	6984
CATAATTCTCANNACGTATGCCA		CAAGCCAGCGNNACGTATGCCA		CATCCGCTGTANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6505	TGCAGGACCAGAGAATTGGAATA	6745	TGCAGGACCAGAGAATTGGAATA	6985
CAACGCTCGTANNACGTATGCCA		CATGTCAATNNACGTATGCCA		CAACATCCGANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6506	TGCAGGACCAGAGAATTGGAATA	6746	TGCAGGACCAGAGAATTGGAATA	6986
CAGAGAGTAGNNACGTATGCCA		CAGTGAACGNNACGTATGCCA		CATTAGATCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6507	TGCAGGACCAGAGAATTGGAATA	6747	TGCAGGACCAGAGAATTGGAATA	6987
CAACGAATCANNACGTATGCCA		CAAGCGGATANNACGTATGCCA		CACGCTACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6508	TGCAGGACCAGAGAATTGGAATA	6748	TGCAGGACCAGAGAATTGGAATA	6988
CATTTTAACTNNACGTATGCCA		CAACGCGATTNNACGTATGCCA		CAGCTTAACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6509	TGCAGGACCAGAGAATTGGAATA	6749	TGCAGGACCAGAGAATTGGAATA	6989
CAGCTTTCTGNNACGTATGCCA		CATTAAGGATANNACGTATGCCA		CAGCTCATCTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6510	TGCAGGACCAGAGAATTGGAATA	6750	TGCAGGACCAGAGAATTGGAATA	6990
CATGCTGAGTNNACGTATGCCA		CATAGTGGAGNNACGTATGCCA		CACACCTATCANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6511	TGCAGGACCAGAGAATTGGAATA	6751	TGCAGGACCAGAGAATTGGAATA	6991
CACGTTGCAANNACGTATGCCA		CATGTGGAAGNNACGTATGCCA		CATCGGTATCANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6512	TGCAGGACCAGAGAATTGGAATA	6752	TGCAGGACCAGAGAATTGGAATA	6992
CACAGTACCTNNACGTATGCCA		CACCCAGCTCANNACGTATGCCA		CAGAAGCGCGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6513	TGCAGGACCAGAGAATTGGAATA	6753	TGCAGGACCAGAGAATTGGAATA	6993
CATGGATTTANNACGTATGCCA		CAGTAACCGAANNACGTATGCCA		CAGTTTTCGCANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6514	TGCAGGACCAGAGAATTGGAATA	6754	TGCAGGACCAGAGAATTGGAATA	6994
CAGGTGTACGNNACGTATGCCA		CATTTCTACATNNACGTATGCCA		CAAGTGGCCNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6515	TGCAGGACCAGAGAATTGGAATA	6755	TGCAGGACCAGAGAATTGGAATA	6995
CAGTTTATGANNACGTATGCCA		CATCAATGATNNACGTATGCCA		CAAGCCATACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6516	TGCAGGACCAGAGAATTGGAATA	6756	TGCAGGACCAGAGAATTGGAATA	6996
CAATATAGTANNACGTATGCCA		CATCGCGAATNNACGTATGCCA		CAATTCGAGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6517	TGCAGGACCAGAGAATTGGAATA	6757	TGCAGGACCAGAGAATTGGAATA	6997
CAGTAGAGCANNNACGTATGCCA		CATTAATGACTNNACGTATGCCA		CACAACCGCATNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6518	TGCAGGACCAGAGAATTGGAATA	6758	TGCAGGACCAGAGAATTGGAATA	6998
CATAAATACANNACGTATGCCA		CACAGGTTTGNACGTATGCCA		CAAGGTATGANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6519	TGCAGGACCAGAGAATTGGAATA	6759	TGCAGGACCAGAGAATTGGAATA	6999
CACAGGACANNACGTATGCCA		CATTCGGCTNNACGTATGCCA		CAATCGGCTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6520	TGCAGGACCAGAGAATTGGAATA	6760	TGCAGGACCAGAGAATTGGAATA	7000
CAATATCANNACGTATGCCA		CACCTTATTANNACGTATGCCA		CAGTCAATTANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6521	TGCAGGACCAGAGAATTGGAATA	6761	TGCAGGACCAGAGAATTGGAATA	7001
CATGAATCATNNACGTATGCCA		CATAGCATGNNACGTATGCCA		CATAAATCANNACGTATGCCA	

图21A

池 -28	SEQ ID NO:	池 -29	SEQ ID NO:	池 -30	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA CACTACGTAAGNNACGTATGCCA	6522	TGCAGGACCAGAGAATTGGAATA CAAAAAACGNNACGTATGCCA	6762	TGCAGGACCAGAGAATTGGAATA CAACGAGACNNACGTATGCCA	7002
TGCAGGACCAGAGAATTGGAATA CAGTACATCGNNACGTATGCCA	6523	TGCAGGACCAGAGAATTGGAATA CATAGCTGACNNACGTATGCCA	6763	TGCAGGACCAGAGAATTGGAATA CATCGGCCACNNACGTATGCCA	7003
TGCAGGACCAGAGAATTGGAATA CACGCGATGNNACGTATGCCA	6524	TGCAGGACCAGAGAATTGGAATA CACTACCCCGNNACGTATGCCA	6764	TGCAGGACCAGAGAATTGGAATA CAACGACTGNNACGTATGCCA	7004
TGCAGGACCAGAGAATTGGAATA CAACAAAGTNNACGTATGCCA	6525	TGCAGGACCAGAGAATTGGAATA CAAGCTGTANNACGTATGCCA	6765	TGCAGGACCAGAGAATTGGAATA CAGTTTAGCGNNACGTATGCCA	7005
TGCAGGACCAGAGAATTGGAATA CAAAACTTCNNACGTATGCCA	6526	TGCAGGACCAGAGAATTGGAATA CACCTTCAGNNACGTATGCCA	6766	TGCAGGACCAGAGAATTGGAATA CAGTTTCAANNACGTATGCCA	7006
TGCAGGACCAGAGAATTGGAATA CAAGGAGCCGNNACGTATGCCA	6527	TGCAGGACCAGAGAATTGGAATA CACACGTCTNNACGTATGCCA	6767	TGCAGGACCAGAGAATTGGAATA CAGAATGCCANNACGTATGCCA	7007
TGCAGGACCAGAGAATTGGAATA CACGTGACATNNACGTATGCCA	6528	TGCAGGACCAGAGAATTGGAATA CAACGGAACANNACGTATGCCA	6768	TGCAGGACCAGAGAATTGGAATA CAACCCGTAAANNACGTATGCCA	7008
TGCAGGACCAGAGAATTGGAATA CAATACATCANNACGTATGCCA	6529	TGCAGGACCAGAGAATTGGAATA CAGATCATANNACGTATGCCA	6769	TGCAGGACCAGAGAATTGGAATA CAGTCACCAANNACGTATGCCA	7009
TGCAGGACCAGAGAATTGGAATA CAATAACCTNNACGTATGCCA	6530	TGCAGGACCAGAGAATTGGAATA CACTAGAACNNACGTATGCCA	6770	TGCAGGACCAGAGAATTGGAATA CATTGAGCTGNNACGTATGCCA	7010
TGCAGGACCAGAGAATTGGAATA CACAGGCTTNNACGTATGCCA	6531	TGCAGGACCAGAGAATTGGAATA CATTTAGGTANNACGTATGCCA	6771	TGCAGGACCAGAGAATTGGAATA CAGAGCTTGNNACGTATGCCA	7011
TGCAGGACCAGAGAATTGGAATA CATCGCTTNNACGTATGCCA	6532	TGCAGGACCAGAGAATTGGAATA CATGATATTNNACGTATGCCA	6772	TGCAGGACCAGAGAATTGGAATA CATTAATTNNACGTATGCCA	7012
TGCAGGACCAGAGAATTGGAATA CACAGTCGCGNNACGTATGCCA	6533	TGCAGGACCAGAGAATTGGAATA CAGCGAAACNNACGTATGCCA	6773	TGCAGGACCAGAGAATTGGAATA CATACAAATGNNACGTATGCCA	7013
TGCAGGACCAGAGAATTGGAATA CATGATCGGTNNACGTATGCCA	6534	TGCAGGACCAGAGAATTGGAATA CAACTAACGNNACGTATGCCA	6774	TGCAGGACCAGAGAATTGGAATA CAAAAGTGGNNACGTATGCCA	7014
TGCAGGACCAGAGAATTGGAATA CAACACACACNNACGTATGCCA	6535	TGCAGGACCAGAGAATTGGAATA CATACTTGCGNNACGTATGCCA	6775	TGCAGGACCAGAGAATTGGAATA CAGCTGCGCGNNACGTATGCCA	7015
TGCAGGACCAGAGAATTGGAATA CATCAGCGTANNACGTATGCCA	6536	TGCAGGACCAGAGAATTGGAATA CACGTGCTAANNACGTATGCCA	6776	TGCAGGACCAGAGAATTGGAATA CAGCTGATACNNACGTATGCCA	7016
TGCAGGACCAGAGAATTGGAATA CATCGCTTNNACGTATGCCA	6537	TGCAGGACCAGAGAATTGGAATA CAAAACAGTANNACGTATGCCA	6777	TGCAGGACCAGAGAATTGGAATA CACTTTGATTNNACGTATGCCA	7017
TGCAGGACCAGAGAATTGGAATA CATTCAGACGNNACGTATGCCA	6538	TGCAGGACCAGAGAATTGGAATA CAGCATCATGNNACGTATGCCA	6778	TGCAGGACCAGAGAATTGGAATA CACTTTGCGNNACGTATGCCA	7018
TGCAGGACCAGAGAATTGGAATA CAGCGCAGGTNNACGTATGCCA	6539	TGCAGGACCAGAGAATTGGAATA CAACCTCGANNACGTATGCCA	6779	TGCAGGACCAGAGAATTGGAATA CAACTTCGTTNNACGTATGCCA	7019
TGCAGGACCAGAGAATTGGAATA CACCGACATNNACGTATGCCA	6540	TGCAGGACCAGAGAATTGGAATA CAACAGCTACNNACGTATGCCA	6780	TGCAGGACCAGAGAATTGGAATA CACAGATCGNNACGTATGCCA	7020
TGCAGGACCAGAGAATTGGAATA CATATTCAGGNNACGTATGCCA	6541	TGCAGGACCAGAGAATTGGAATA CACGTCAACANNACGTATGCCA	6781	TGCAGGACCAGAGAATTGGAATA CAGTCGCTCNNACGTATGCCA	7021
TGCAGGACCAGAGAATTGGAATA CACGAGATGNNACGTATGCCA	6542	TGCAGGACCAGAGAATTGGAATA CACCGGCCGNNACGTATGCCA	6782	TGCAGGACCAGAGAATTGGAATA CAGTGTGAANNACGTATGCCA	7022
TGCAGGACCAGAGAATTGGAATA CAATACGAAANNACGTATGCCA	6543	TGCAGGACCAGAGAATTGGAATA CATGCGCTGNNACGTATGCCA	6783	TGCAGGACCAGAGAATTGGAATA CAAGTAAGTANNACGTATGCCA	7023
TGCAGGACCAGAGAATTGGAATA CAGATGAGCANNACGTATGCCA	6544	TGCAGGACCAGAGAATTGGAATA CAAGAGCTGNNACGTATGCCA	6784	TGCAGGACCAGAGAATTGGAATA CAATTTATTNNACGTATGCCA	7024
TGCAGGACCAGAGAATTGGAATA CATACAATCANNACGTATGCCA	6545	TGCAGGACCAGAGAATTGGAATA CAGCAATGAGNNACGTATGCCA	6785	TGCAGGACCAGAGAATTGGAATA CAGGAATCGANNACGTATGCCA	7025
TGCAGGACCAGAGAATTGGAATA CATTTAATAANNACGTATGCCA	6546	TGCAGGACCAGAGAATTGGAATA CAAGGAGCTANNACGTATGCCA	6786	TGCAGGACCAGAGAATTGGAATA CAGCTGCTTNNACGTATGCCA	7026
TGCAGGACCAGAGAATTGGAATA CAGCGCGTCAANNACGTATGCCA	6547	TGCAGGACCAGAGAATTGGAATA CACCTGAGATTNNACGTATGCCA	6787	TGCAGGACCAGAGAATTGGAATA CAGTTAACTNNACGTATGCCA	7027
TGCAGGACCAGAGAATTGGAATA CACGATGATGNNACGTATGCCA	6548	TGCAGGACCAGAGAATTGGAATA CAACGGAGCGNNACGTATGCCA	6788	TGCAGGACCAGAGAATTGGAATA CAATCTTAAGNNACGTATGCCA	7028
TGCAGGACCAGAGAATTGGAATA CACCGAAGCGNNACGTATGCCA	6549	TGCAGGACCAGAGAATTGGAATA CAGATCGCGGNNACGTATGCCA	6789	TGCAGGACCAGAGAATTGGAATA CAAACTCAAGNNACGTATGCCA	7029
TGCAGGACCAGAGAATTGGAATA CACCGAAGCGNNACGTATGCCA	6550	TGCAGGACCAGAGAATTGGAATA CATGCTGCAANNACGTATGCCA	6790	TGCAGGACCAGAGAATTGGAATA CAACGAAGCGNNACGTATGCCA	7030
TGCAGGACCAGAGAATTGGAATA CAGGTCTTCNNACGTATGCCA	6551	TGCAGGACCAGAGAATTGGAATA CATCGGAATCANNACGTATGCCA	6791	TGCAGGACCAGAGAATTGGAATA CAGCGTAATCANNACGTATGCCA	7031
TGCAGGACCAGAGAATTGGAATA CACCTCGGTCNNACGTATGCCA	6552	TGCAGGACCAGAGAATTGGAATA CAGACGCGTCNNACGTATGCCA	6792	TGCAGGACCAGAGAATTGGAATA CAGGCTGCTANNACGTATGCCA	7032
TGCAGGACCAGAGAATTGGAATA CACCGCTGGAANNACGTATGCCA	6553	TGCAGGACCAGAGAATTGGAATA CAAGTGGAGNNACGTATGCCA	6793	TGCAGGACCAGAGAATTGGAATA CAGTTGAGTNNACGTATGCCA	7033
TGCAGGACCAGAGAATTGGAATA CAACACCTTNNACGTATGCCA	6554	TGCAGGACCAGAGAATTGGAATA CAAGTACGTCNNACGTATGCCA	6794	TGCAGGACCAGAGAATTGGAATA CACTGCGCTNNACGTATGCCA	7034

图21B

池 -28	SEQ ID NO.	池 -29	SEQ ID NO.	池 -30	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATA	6555	TGCAGGACCAGAGAATTGGAATA	6793	TGCAGGACCAGAGAATTGGAATA	7035
CATCTAAGTANNNNCTAGCGTTAC		CACGATTAAATNNNNCTAGCGTTAC		CAGGCGCTAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6556	TGCAGGACCAGAGAATTGGAATA	6796	TGCAGGACCAGAGAATTGGAATA	7036
CAATTAATAATNNNNCTAGCGTTAC		CATTACGCCCTNNNNCTAGCGTTAC		CAACCCCGCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6557	TGCAGGACCAGAGAATTGGAATA	6797	TGCAGGACCAGAGAATTGGAATA	7037
CATGGACCGCNNNNCTAGCGTTAC		CAGGAGGTGNNNNCTAGCGTTAC		CACCGTATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6558	TGCAGGACCAGAGAATTGGAATA	6798	TGCAGGACCAGAGAATTGGAATA	7038
CAGTTCACTANNNNCTAGCGTTAC		CAGTACACCANNNNCTAGCGTTAC		CATAGAACCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6559	TGCAGGACCAGAGAATTGGAATA	6799	TGCAGGACCAGAGAATTGGAATA	7039
CAACCGCACCANNNNCTAGCGTTAC		CAGGAAATTTNNNNCTAGCGTTAC		CACCGGAGGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6560	TGCAGGACCAGAGAATTGGAATA	6800	TGCAGGACCAGAGAATTGGAATA	7040
CATCATGGCANNNNCTAGCGTTAC		CACGGTTCTTNNNNCTAGCGTTAC		CAATGATCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6561	TGCAGGACCAGAGAATTGGAATA	6801	TGCAGGACCAGAGAATTGGAATA	7041
CAGGCTTTACNNNNCTAGCGTTAC		CAGGTCGACNNNNCTAGCGTTAC		CATTGGAACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6562	TGCAGGACCAGAGAATTGGAATA	6802	TGCAGGACCAGAGAATTGGAATA	7042
CAATCGTATTNNNNCTAGCGTTAC		CATTGCGCTCANNNNCTAGCGTTAC		CARAACACCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6563	TGCAGGACCAGAGAATTGGAATA	6803	TGCAGGACCAGAGAATTGGAATA	7043
CAGTATCGCTGNNNNCTAGCGTTAC		CACGCGCCGTTNNNNCTAGCGTTAC		CATCCTTTTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6564	TGCAGGACCAGAGAATTGGAATA	6804	TGCAGGACCAGAGAATTGGAATA	7044
CAATTCGTGGTNNNNCTAGCGTTAC		CAGCTGTGCGNNNNCTAGCGTTAC		CARAACCAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6565	TGCAGGACCAGAGAATTGGAATA	6805	TGCAGGACCAGAGAATTGGAATA	7045
CAGCTTAGGTTNNNNCTAGCGTTAC		CACACCAGTANNNNCTAGCGTTAC		CATCCAGTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6566	TGCAGGACCAGAGAATTGGAATA	6806	TGCAGGACCAGAGAATTGGAATA	7046
CATCTGTATTNNNNCTAGCGTTAC		CAATCATTTGANNNNCTAGCGTTAC		CACCTTCAAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6567	TGCAGGACCAGAGAATTGGAATA	6807	TGCAGGACCAGAGAATTGGAATA	7047
CAGGATAGCANNNNCTAGCGTTAC		CATAATCATGNNNNCTAGCGTTAC		CATATCTAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6568	TGCAGGACCAGAGAATTGGAATA	6808	TGCAGGACCAGAGAATTGGAATA	7048
CATTCACTCGNNNNCTAGCGTTAC		CAGTTGACCAANNNNCTAGCGTTAC		CACACCGCTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6569	TGCAGGACCAGAGAATTGGAATA	6809	TGCAGGACCAGAGAATTGGAATA	7049
CATTCTGCGANNNNCTAGCGTTAC		CAACTCATGNNNNCTAGCGTTAC		CACCTTTTTCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6570	TGCAGGACCAGAGAATTGGAATA	6810	TGCAGGACCAGAGAATTGGAATA	7050
CACGGTCGGTNNNNCTAGCGTTAC		CACCCAGTTTNNNNCTAGCGTTAC		CAAGTGCTTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6571	TGCAGGACCAGAGAATTGGAATA	6811	TGCAGGACCAGAGAATTGGAATA	7051
CAAGATCGCTNNNNCTAGCGTTAC		CATCAAGGAGNNNNCTAGCGTTAC		CAATGGTCCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6572	TGCAGGACCAGAGAATTGGAATA	6812	TGCAGGACCAGAGAATTGGAATA	7052
CAGCAITCGANNNNCTAGCGTTAC		CAAAACGCTTGGNNNNCTAGCGTTAC		CAGCCCGCTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6573	TGCAGGACCAGAGAATTGGAATA	6813	TGCAGGACCAGAGAATTGGAATA	7053
CACCGTGAATNNNNCTAGCGTTAC		CAGTTATATCANNNNCTAGCGTTAC		CAGTTGCTCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6574	TGCAGGACCAGAGAATTGGAATA	6814	TGCAGGACCAGAGAATTGGAATA	7054
CACGGTTACGNNNNCTAGCGTTAC		CAAGTGTCCANNNNCTAGCGTTAC		CAGCATATATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6575	TGCAGGACCAGAGAATTGGAATA	6815	TGCAGGACCAGAGAATTGGAATA	7055
CAAAATGTATNNNNCTAGCGTTAC		CAAGCGACCGNNNNCTAGCGTTAC		CAGGTCTTGGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6576	TGCAGGACCAGAGAATTGGAATA	6816	TGCAGGACCAGAGAATTGGAATA	7056
CACGCAAGACANNNNCTAGCGTTAC		CACGTGCTCCGNNNNCTAGCGTTAC		CAACTATTTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6577	TGCAGGACCAGAGAATTGGAATA	6817	TGCAGGACCAGAGAATTGGAATA	7057
CACCAGCGCTCANNNNCTAGCGTTAC		CAACTCAGCTNNNNCTAGCGTTAC		CAGCTTAAACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6578	TGCAGGACCAGAGAATTGGAATA	6818	TGCAGGACCAGAGAATTGGAATA	7058
CACITTTGTTGNNNNCTAGCGTTAC		CAAAATTTGANNNNCTAGCGTTAC		CATCGCAGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6579	TGCAGGACCAGAGAATTGGAATA	6819	TGCAGGACCAGAGAATTGGAATA	7059
CATATCGGCTGNNNNCTAGCGTTAC		CAGTAATATCANNNNCTAGCGTTAC		CAGATTCCGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6580	TGCAGGACCAGAGAATTGGAATA	6820	TGCAGGACCAGAGAATTGGAATA	7060
CAGTGGCATANNNNCTAGCGTTAC		CACAGAAATNNNNCTAGCGTTAC		CATGGCCGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6581	TGCAGGACCAGAGAATTGGAATA	6821	TGCAGGACCAGAGAATTGGAATA	7061
CATGACGGCCNNNNCTAGCGTTAC		CBATTTCCCAANNNNCTAGCGTTAC		CAAGAGCATGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6582	TGCAGGACCAGAGAATTGGAATA	6822	TGCAGGACCAGAGAATTGGAATA	7062
CATTCCTCTCANNNNCTAGCGTTAC		CAGTCTTAGCANNNNCTAGCGTTAC		CAATGATCTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6583	TGCAGGACCAGAGAATTGGAATA	6823	TGCAGGACCAGAGAATTGGAATA	7063
CATAACGGAGNNNNCTAGCGTTAC		CATACCGACANNNNCTAGCGTTAC		CATCGGCAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6584	TGCAGGACCAGAGAATTGGAATA	6824	TGCAGGACCAGAGAATTGGAATA	7064
CAGAGTGGATNNNNCTAGCGTTAC		CACACGCTCANNNNCTAGCGTTAC		CAATCGCGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6585	TGCAGGACCAGAGAATTGGAATA	6825	TGCAGGACCAGAGAATTGGAATA	7065
CATCGTAATNNNNCTAGCGTTAC		CAATTCGAGGNNNNCTAGCGTTAC		CAGAACTGGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6586	TGCAGGACCAGAGAATTGGAATA	6826	TGCAGGACCAGAGAATTGGAATA	7066
CACACGACTNNNNCTAGCGTTAC		CACATACAATNNNNCTAGCGTTAC		CAGGAACAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6587	TGCAGGACCAGAGAATTGGAATA	6827	TGCAGGACCAGAGAATTGGAATA	7067
CAGCACCGCTNNNNCTAGCGTTAC		CATTATGTTCTNNNNCTAGCGTTAC		CACATAACATNNNNCTAGCGTTAC	

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池 -28	SEQ ID NO.	池 -29	SEQ ID NO.	池 -30	SEQ ID NO.
TGCAGGACCCAGAGAAATTCGAATA	6588	TGCAGGACCCAGAGAAATTCGAATA	6628	TGCAGGACCCAGAGAAATTCGAATA	7068
CAGATTAATTCNNNCTAGCGTTAC		CAGTCTGTCTNNNCTAGCGTTAC		CAGAGGAGTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6589	TGCAGGACCCAGAGAAATTCGAATA	6629	TGCAGGACCCAGAGAAATTCGAATA	7069
CAGACTCATTNNNCTAGCGTTAC		CAGTCTGAACHNNCTAGCGTTAC		CATCCATGTCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6590	TGCAGGACCCAGAGAAATTCGAATA	6630	TGCAGGACCCAGAGAAATTCGAATA	7070
CATCAAACTNNNCTAGCGTTAC		CATGGTGGGNNNCTAGCGTTAC		CAGTACGAGANNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6591	TGCAGGACCCAGAGAAATTCGAATA	6631	TGCAGGACCCAGAGAAATTCGAATA	7071
CATTATTCNNNCTAGCGTTAC		CACAGAAACGNNNCTAGCGTTAC		CAGGCCACCTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6592	TGCAGGACCCAGAGAAATTCGAATA	6632	TGCAGGACCCAGAGAAATTCGAATA	7072
CATTTCCTGGNNNCTAGCGTTAC		CATCTGTTGNNNCTAGCGTTAC		CAGTCCGATANNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6593	TGCAGGACCCAGAGAAATTCGAATA	6633	TGCAGGACCCAGAGAAATTCGAATA	7073
CATAAGTAAGNNNCTAGCGTTAC		CACGATGGCTNNNCTAGCGTTAC		CATGTTACANNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6594	TGCAGGACCCAGAGAAATTCGAATA	6634	TGCAGGACCCAGAGAAATTCGAATA	7074
CATTAAAGCTNNNCTAGCGTTAC		CATTATATNNNCTAGCGTTAC		CATCTCCGACHNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6595	TGCAGGACCCAGAGAAATTCGAATA	6635	TGCAGGACCCAGAGAAATTCGAATA	7075
CATTAGGCTNNNCTAGCGTTAC		CATTCCAGCTNNNCTAGCGTTAC		CATGTTCAATNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6596	TGCAGGACCCAGAGAAATTCGAATA	6636	TGCAGGACCCAGAGAAATTCGAATA	7076
CAGAAGTAATNNNCTAGCGTTAC		CAGAGGAAGNNNCTAGCGTTAC		CAGAAGACGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6597	TGCAGGACCCAGAGAAATTCGAATA	6637	TGCAGGACCCAGAGAAATTCGAATA	7077
CATCAGCTAGNNNCTAGCGTTAC		CATTACACANNNCTAGCGTTAC		CATCCGACCCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6598	TGCAGGACCCAGAGAAATTCGAATA	6638	TGCAGGACCCAGAGAAATTCGAATA	7078
CATAACCATNNNCTAGCGTTAC		CAGGACCTGCHNNCTAGCGTTAC		CACACTAGTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6599	TGCAGGACCCAGAGAAATTCGAATA	6639	TGCAGGACCCAGAGAAATTCGAATA	7079
CAGACGAGTANNNCTAGCGTTAC		CACGCTAGAGNNNCTAGCGTTAC		CACCCGCGCTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6600	TGCAGGACCCAGAGAAATTCGAATA	6640	TGCAGGACCCAGAGAAATTCGAATA	7080
CATTAAATTCNNNCTAGCGTTAC		CACACCGCGTNNNCTAGCGTTAC		CACTTGCTACNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6601	TGCAGGACCCAGAGAAATTCGAATA	6641	TGCAGGACCCAGAGAAATTCGAATA	7081
CAGAGCTAAGNNNCTAGCGTTAC		CATTACGTAANNNCTAGCGTTAC		CATTGCACTGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6602	TGCAGGACCCAGAGAAATTCGAATA	6642	TGCAGGACCCAGAGAAATTCGAATA	7082
CACGCGTAGCHNNCTAGCGTTAC		CCTATGTTGANNNCTAGCGTTAC		CATAATCAAGTNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6603	TGCAGGACCCAGAGAAATTCGAATA	6643	TGCAGGACCCAGAGAAATTCGAATA	7083
CATTCTATGANNNCTAGCGTTAC		CACAGACTCANNNCTAGCGTTAC		CACTTGCCGCHNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6604	TGCAGGACCCAGAGAAATTCGAATA	6644	TGCAGGACCCAGAGAAATTCGAATA	7084
CATTAAAGCATNNNCTAGCGTTAC		CACGGATGCCNNNCTAGCGTTAC		CACTGGACCCNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6605	TGCAGGACCCAGAGAAATTCGAATA	6645	TGCAGGACCCAGAGAAATTCGAATA	7085
CATCGAGCCGCHNNCTAGCGTTAC		CACAGACTCTNNNCTAGCGTTAC		CACGACTCANNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6606	TGCAGGACCCAGAGAAATTCGAATA	6646	TGCAGGACCCAGAGAAATTCGAATA	7086
CATCGGACCCGNNNCTAGCGTTAC		CACTCTGCTNNNCTAGCGTTAC		CACACACTTANNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6607	TGCAGGACCCAGAGAAATTCGAATA	6647	TGCAGGACCCAGAGAAATTCGAATA	7087
CACCTTGGACANNNCTAGCGTTAC		CAGAACCGCGNNNCTAGCGTTAC		CATCTGCTAGNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6608	TGCAGGACCCAGAGAAATTCGAATA	6648	TGCAGGACCCAGAGAAATTCGAATA	7088
CATTCCAGCTCHNNCTAGCGTTAC		CATCGGATTGNNNCTAGCGTTAC		CACTATGGCANNNNCTAGCGTTAC	
TGCAGGACCCAGAGAAATTCGAATA	6609	TGCAGGACCCAGAGAAATTCGAATA	6649	TGCAGGACCCAGAGAAATTCGAATA	7089
CAGTTTTTACNNNGATCGACATG		CAGAGCAAAATNNNGATCGACATG		CAGCCCGCGANNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6610	TGCAGGACCCAGAGAAATTCGAATA	6650	TGCAGGACCCAGAGAAATTCGAATA	7090
CACACITTAGTNNNGATCGACATG		CACGAGTAGNNNGATCGACATG		CACGCGCTACNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6611	TGCAGGACCCAGAGAAATTCGAATA	6651	TGCAGGACCCAGAGAAATTCGAATA	7091
CACGCGCGGNNNGATCGACATG		CMAAGAGGCHNNNGATCGACATG		CACACATCAGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6612	TGCAGGACCCAGAGAAATTCGAATA	6652	TGCAGGACCCAGAGAAATTCGAATA	7092
CATAACTGTTANNNGATCGACATG		CATGAGTGGANNNGATCGACATG		CATAGACACCHNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6613	TGCAGGACCCAGAGAAATTCGAATA	6653	TGCAGGACCCAGAGAAATTCGAATA	7093
CAGTAAGTTTNNNGATCGACATG		CACGCTCCCANNNNGATCGACATG		CATTGTAAAGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6614	TGCAGGACCCAGAGAAATTCGAATA	6654	TGCAGGACCCAGAGAAATTCGAATA	7094
CACTTATGCGNNNGATCGACATG		CACACACTTCNNNGATCGACATG		CATTGCTCTGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6615	TGCAGGACCCAGAGAAATTCGAATA	6655	TGCAGGACCCAGAGAAATTCGAATA	7095
CACCTTTCCGNNNGATCGACATG		CAGCAGTCAATNNNGATCGACATG		CAGTGTCTCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6616	TGCAGGACCCAGAGAAATTCGAATA	6656	TGCAGGACCCAGAGAAATTCGAATA	7096
CACTGCTCTTNNNGATCGACATG		CACCATATGGNNNGATCGACATG		CAGCTTGCAHNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6617	TGCAGGACCCAGAGAAATTCGAATA	6657	TGCAGGACCCAGAGAAATTCGAATA	7097
CAGAATAATGNNNGATCGACATG		CATTGCGCGNNNGATCGACATG		CAGAGCGCTCHNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6618	TGCAGGACCCAGAGAAATTCGAATA	6658	TGCAGGACCCAGAGAAATTCGAATA	7098
CACAGCCCTCHNNNGATCGACATG		CAGTTGAAACCHNNNGATCGACATG		CATGCGCAGNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6619	TGCAGGACCCAGAGAAATTCGAATA	6659	TGCAGGACCCAGAGAAATTCGAATA	7099
CACGTAATGNNNGATCGACATG		CMAAGGTTGNNNGATCGACATG		CACGATGCCNNNGATCGACATG	
TGCAGGACCCAGAGAAATTCGAATA	6620	TGCAGGACCCAGAGAAATTCGAATA	6660	TGCAGGACCCAGAGAAATTCGAATA	7100
CAGTTGCTCTNNNGATCGACATG		CAGCAGCTGNNNGATCGACATG		CACCCGCGCHNNNGATCGACATG	

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池 -28	SEQ ID NO:	池 -29	SEQ ID NO:	池 -30	SEQ ID NO:
TGCAGGACCAGAGAAATTCGAATA	6621	TGCAGGACCAGAGAAATTCGAATA	6661	TGCAGGACCAGAGAAATTCGAATA	7101
CATTCCGTCANNNGATCGACATG		CAGCTCATAGNNNGATCGACATG		CATCATTTCAHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6622	TGCAGGACCAGAGAAATTCGAATA	6662	TGCAGGACCAGAGAAATTCGAATA	7102
CAACCGACGTTNNNGATCGACATG		CAACAGTCTGHHNGATCGACATG		CAICCGGCTGHHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6623	TGCAGGACCAGAGAAATTCGAATA	6663	TGCAGGACCAGAGAAATTCGAATA	7103
CAAAAGTAGCANNNGATCGACATG		CATTAAAGTGHNNGATCGACATG		CACGCAAGAGHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6624	TGCAGGACCAGAGAAATTCGAATA	6664	TGCAGGACCAGAGAAATTCGAATA	7104
CAAGTGAAGCANNNGATCGACATG		CAGATTAAATCANNNGATCGACATG		CAIAGACCACNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6625	TGCAGGACCAGAGAAATTCGAATA	6665	TGCAGGACCAGAGAAATTCGAATA	7105
CATCTCTCATANNNGATCGACATG		CAGAGAAAGGNNNGATCGACATG		CAACCGAAGANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6626	TGCAGGACCAGAGAAATTCGAATA	6666	TGCAGGACCAGAGAAATTCGAATA	7106
CAASTAGAGCANNNGATCGACATG		CAACATTCGGHNNGATCGACATG		CATCTCTGTANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6627	TGCAGGACCAGAGAAATTCGAATA	6667	TGCAGGACCAGAGAAATTCGAATA	7107
CATCCGGAATTNNNGATCGACATG		CATTGCCTCTNNNGATCGACATG		CACAGCTGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6628	TGCAGGACCAGAGAAATTCGAATA	6668	TGCAGGACCAGAGAAATTCGAATA	7108
CACAGAGCTCANNNGATCGACATG		CAGCTCACAHNNNGATCGACATG		CAGATCTGCANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6629	TGCAGGACCAGAGAAATTCGAATA	6669	TGCAGGACCAGAGAAATTCGAATA	7109
CAGAGTATCGNNNGATCGACATG		CACGTTAACCNNNGATCGACATG		CATCGAAGGANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6630	TGCAGGACCAGAGAAATTCGAATA	6670	TGCAGGACCAGAGAAATTCGAATA	7110
CACCGCAGTGNNGATCGACATG		CAGTACGTTGHHNGATCGACATG		CACGAGACGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6631	TGCAGGACCAGAGAAATTCGAATA	6671	TGCAGGACCAGAGAAATTCGAATA	7111
CAGAGAGCTCANNNGATCGACATG		CATGCTCAGANNNGATCGACATG		CACACCGGACNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6632	TGCAGGACCAGAGAAATTCGAATA	6672	TGCAGGACCAGAGAAATTCGAATA	7112
CAGTGCAGAGANNNGATCGACATG		CATACCAATNNNGATCGACATG		CATAAAGCTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6633	TGCAGGACCAGAGAAATTCGAATA	6673	TGCAGGACCAGAGAAATTCGAATA	7113
CAAAACGAGTANNNGATCGACATG		CACCATGATGHHNGATCGACATG		CATGCTCTGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6634	TGCAGGACCAGAGAAATTCGAATA	6674	TGCAGGACCAGAGAAATTCGAATA	7114
CACCTACACTCANNNGATCGACATG		CATATATGCAHNNGATCGACATG		CAJATGGAACNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6635	TGCAGGACCAGAGAAATTCGAATA	6675	TGCAGGACCAGAGAAATTCGAATA	7115
CACCCGACGACNNNGATCGACATG		CACCGCTTATHNNGATCGACATG		CACACACTTGHNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6636	TGCAGGACCAGAGAAATTCGAATA	6676	TGCAGGACCAGAGAAATTCGAATA	7116
CACCTACACTCANNNGATCGACATG		CACCGCTCACNNNGATCGACATG		CACAAATCCACNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6637	TGCAGGACCAGAGAAATTCGAATA	6677	TGCAGGACCAGAGAAATTCGAATA	7117
CACGCTAAGCANNNGATCGACATG		CAGGCATAGHNNNGATCGACATG		CAGCAAGCGGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6638	TGCAGGACCAGAGAAATTCGAATA	6678	TGCAGGACCAGAGAAATTCGAATA	7118
CAGAGTATCANNNGATCGACATG		CAGAAATTTGHHNGATCGACATG		CAGCCACGCGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6639	TGCAGGACCAGAGAAATTCGAATA	6679	TGCAGGACCAGAGAAATTCGAATA	7119
CATCCCTACACNNNGATCGACATG		CATCTTGACNNNGATCGACATG		CATCCTTAANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6640	TGCAGGACCAGAGAAATTCGAATA	6680	TGCAGGACCAGAGAAATTCGAATA	7120
CATTTTCTCANNNGATCGACATG		CACACGCTAGHHNGATCGACATG		CACTAGCGTANNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6641	TGCAGGACCAGAGAAATTCGAATA	6681	TGCAGGACCAGAGAAATTCGAATA	7121
CACGGATAGHNNNGATCGACATG		CAATCTCACNNNGATCGACATG		CACITGAGTTGHHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6642	TGCAGGACCAGAGAAATTCGAATA	6682	TGCAGGACCAGAGAAATTCGAATA	7122
CACAAATCGCANNNGATCGACATG		CATTGAGATTNNNGATCGACATG		CATGCGCGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6643	TGCAGGACCAGAGAAATTCGAATA	6683	TGCAGGACCAGAGAAATTCGAATA	7123
CAGTGTCCGCGNNNGATCGACATG		CATCAACGAGNNNGATCGACATG		CAGTGACTTGHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6644	TGCAGGACCAGAGAAATTCGAATA	6684	TGCAGGACCAGAGAAATTCGAATA	7124
CANVAGTATTNNNGATCGACATG		CATTTGACGHHNNGATCGACATG		CACTGCGAATNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6645	TGCAGGACCAGAGAAATTCGAATA	6685	TGCAGGACCAGAGAAATTCGAATA	7125
CAACCGGACGNNNGATCGACATG		CAGTTCAATTNNNGATCGACATG		CACATGACGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6646	TGCAGGACCAGAGAAATTCGAATA	6686	TGCAGGACCAGAGAAATTCGAATA	7126
CATTAAATCGCANNNGATCGACATG		CAGAGTGGTANNNGATCGACATG		CACCGAATTGHHNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6647	TGCAGGACCAGAGAAATTCGAATA	6687	TGCAGGACCAGAGAAATTCGAATA	7127
CACCTGCAAGTNNNGATCGACATG		CRAATTTGCTGHHNGATCGACATG		CPACTAGGAGHNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6648	TGCAGGACCAGAGAAATTCGAATA	6688	TGCAGGACCAGAGAAATTCGAATA	7128
CACCGTTTACNNNGATCGACATG		CAGATTTTAGHNNGATCGACATG		CAGCGGAGCTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6649	TGCAGGACCAGAGAAATTCGAATA	6689	TGCAGGACCAGAGAAATTCGAATA	7129
CAAGTGAAGCANNNGATCGACATG		CACCTAACAAHNNNGATCGACATG		CACACAGCCGHHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6650	TGCAGGACCAGAGAAATTCGAATA	6690	TGCAGGACCAGAGAAATTCGAATA	7130
CATATAGACNNNGATCGACATG		CAAGCTGATCANNNGATCGACATG		CAGCCTTGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6651	TGCAGGACCAGAGAAATTCGAATA	6691	TGCAGGACCAGAGAAATTCGAATA	7131
CAGTTGGCTANNNGATCGACATG		CACGACGCTGHHNGATCGACATG		CAAAATATCGTNNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6652	TGCAGGACCAGAGAAATTCGAATA	6692	TGCAGGACCAGAGAAATTCGAATA	7132
CATCGCTAAGHNNGATCGACATG		CACGCGCTACHHNGATCGACATG		CACCGAAGAGHNNGATCGACATG	
TGCAGGACCAGAGAAATTCGAATA	6653	TGCAGGACCAGAGAAATTCGAATA	6693	TGCAGGACCAGAGAAATTCGAATA	7133
CAAGCCCTCANNNGATCGACATG		CATTGCAGGTNNNGATCGACATG		CACAAAGGTGHHNNGATCGACATG	

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池 -28	SEQ ID NO.	池 -29	SEQ ID NO.	池 -30	SEQ ID NO.
TGCAGGACACAGAGAAATTCGAATA	6654	TGCAGGACACAGAGAAATTCGAATA	6654	TGCAGGACACAGAGAAATTCGAATA	7134
CATTACGAATNNINGATCGACATG		CATTAGCTGTNNINGATCGACATG		CAAAATCCATNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6655	TGCAGGACACAGAGAAATTCGAATA	6655	TGCAGGACACAGAGAAATTCGAATA	7135
CAGGCCACACNNINGATCGACATG		CAAGCTCTCAGNNINGATCGACATG		CAACCAATCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6656	TGCAGGACACAGAGAAATTCGAATA	6656	TGCAGGACACAGAGAAATTCGAATA	7136
CATCCTTATANNINGATCGACATG		CAATTCCTTANNINGATCGACATG		CACATTGGCAANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6657	TGCAGGACACAGAGAAATTCGAATA	6657	TGCAGGACACAGAGAAATTCGAATA	7137
CACATCTCTNNINGATCGACATG		CAGAGAGAGANNINGATCGACATG		CACATCAACGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6658	TGCAGGACACAGAGAAATTCGAATA	6658	TGCAGGACACAGAGAAATTCGAATA	7138
CACGACCTCTNNINGATCGACATG		CAGCAGAGCGNNINGATCGACATG		CAATCGAGAGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6659	TGCAGGACACAGAGAAATTCGAATA	6659	TGCAGGACACAGAGAAATTCGAATA	7139
CAAGGTAACGNNINGATCGACATG		CAGCGACTATNNINGATCGACATG		CACGCGCTCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6660	TGCAGGACACAGAGAAATTCGAATA	6660	TGCAGGACACAGAGAAATTCGAATA	7140
CACAGCACTCTNNINGATCGACATG		CAGACCTCTAANNINGATCGACATG		CATTACGCTTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6661	TGCAGGACACAGAGAAATTCGAATA	6661	TGCAGGACACAGAGAAATTCGAATA	7141
CAGCGCTTCGNNINGATCGACATG		CAATAAATCTNNINGATCGACATG		CAGTAGCTGTHNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6662	TGCAGGACACAGAGAAATTCGAATA	6662	TGCAGGACACAGAGAAATTCGAATA	7142
CATCATCTCGNNINGATCGACATG		CATCATATCTNNINGATCGACATG		CATGCTCTGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6663	TGCAGGACACAGAGAAATTCGAATA	6663	TGCAGGACACAGAGAAATTCGAATA	7143
CAGCGCTCTGNNINGATCGACATG		CAGATGGAATHNNINGATCGACATG		CAATACACTGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6664	TGCAGGACACAGAGAAATTCGAATA	6664	TGCAGGACACAGAGAAATTCGAATA	7144
CATCTCTGACNNINGATCGACATG		CACCTGGACGNNINGATCGACATG		CATATAAAGANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6665	TGCAGGACACAGAGAAATTCGAATA	6665	TGCAGGACACAGAGAAATTCGAATA	7145
CAGAGTAGTNNINGATCGACATG		CATAAGCCAGNNINGATCGACATG		CATACCTGCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6666	TGCAGGACACAGAGAAATTCGAATA	6666	TGCAGGACACAGAGAAATTCGAATA	7146
CAATTTTANNINGATCGACATG		CAGCAGCGCTNNINGATCGACATG		CATGAGAACGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6667	TGCAGGACACAGAGAAATTCGAATA	6667	TGCAGGACACAGAGAAATTCGAATA	7147
CAATTTCTANNINGATCGACATG		CACAGCCCGNNINGATCGACATG		CAGGAGCTGANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6668	TGCAGGACACAGAGAAATTCGAATA	6668	TGCAGGACACAGAGAAATTCGAATA	7148
CAACCGCTGNNINGATCGACATG		CATTAGAGAGNNINGATCGACATG		CAAGAGCCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6669	TGCAGGACACAGAGAAATTCGAATA	6669	TGCAGGACACAGAGAAATTCGAATA	7149
CAATCGACTGNNINGATCGACATG		CATTTCATAGNNINGATCGACATG		CAACCGCCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6670	TGCAGGACACAGAGAAATTCGAATA	6670	TGCAGGACACAGAGAAATTCGAATA	7150
CATAAGGATTTNNINGATCGACATG		CACCAAGCGNNINGATCGACATG		CATCCCTTAANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6671	TGCAGGACACAGAGAAATTCGAATA	6671	TGCAGGACACAGAGAAATTCGAATA	7151
CAGCCACAGANNINGATCGACATG		CACTCAGGCCGNNINGATCGACATG		CATCGGCATANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6672	TGCAGGACACAGAGAAATTCGAATA	6672	TGCAGGACACAGAGAAATTCGAATA	7152
CAACRAACGNNINGATCGACATG		CACTCGGCAGNNINGATCGACATG		CACGCGCTCCANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6673	TGCAGGACACAGAGAAATTCGAATA	6673	TGCAGGACACAGAGAAATTCGAATA	7153
CAAGAGTGCANNINGATCGACATG		CAIAGTCTGNNINGATCGACATG		CAAGGTGGCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6674	TGCAGGACACAGAGAAATTCGAATA	6674	TGCAGGACACAGAGAAATTCGAATA	7154
CACGGATCGNNINGATCGACATG		CACATTAATCTNNINGATCGACATG		CAAGAGTTCNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6675	TGCAGGACACAGAGAAATTCGAATA	6675	TGCAGGACACAGAGAAATTCGAATA	7155
CAGGATTCGNNINGATCGACATG		CAGAGACGANNINGATCGACATG		CACGGAAGCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6676	TGCAGGACACAGAGAAATTCGAATA	6676	TGCAGGACACAGAGAAATTCGAATA	7156
CAACCTAAGANNINGATCGACATG		CAATTCCTCTNNINGATCGACATG		CAAGGGACTCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6677	TGCAGGACACAGAGAAATTCGAATA	6677	TGCAGGACACAGAGAAATTCGAATA	7157
CAGCTATCGANNINGATCGACATG		CAGCGATCGGNNINGATCGACATG		CACACGAGCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6678	TGCAGGACACAGAGAAATTCGAATA	6678	TGCAGGACACAGAGAAATTCGAATA	7158
CATCAGATATNNINGATCGACATG		CATATAATANNINGATCGACATG		CAIATGCGTGHNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6679	TGCAGGACACAGAGAAATTCGAATA	6679	TGCAGGACACAGAGAAATTCGAATA	7159
CAGCGACCGTNNINGATCGACATG		CAACGACAGNNINGATCGACATG		CAGCATAGCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6680	TGCAGGACACAGAGAAATTCGAATA	6680	TGCAGGACACAGAGAAATTCGAATA	7160
CATCAGACTGNNINGATCGACATG		CAAGGCGCTGNNINGATCGACATG		CATGACTAGGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6681	TGCAGGACACAGAGAAATTCGAATA	6681	TGCAGGACACAGAGAAATTCGAATA	7161
CAATGCAAGTNNINGATCGACATG		CACAAAGAGCANNINGATCGACATG		CAGCGGAGCTNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6682	TGCAGGACACAGAGAAATTCGAATA	6682	TGCAGGACACAGAGAAATTCGAATA	7162
CATCTACTGNNINGATCGACATG		CATTCAGGACNNINGATCGACATG		CAACTGCAANNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6683	TGCAGGACACAGAGAAATTCGAATA	6683	TGCAGGACACAGAGAAATTCGAATA	7163
CATCTGTTGNNINGATCGACATG		CAAGCACGCGNNINGATCGACATG		CACCGACAATNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6684	TGCAGGACACAGAGAAATTCGAATA	6684	TGCAGGACACAGAGAAATTCGAATA	7164
CACTGTGTANNINGATCGACATG		CAGACACATCTNNINGATCGACATG		CACAGGCCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6685	TGCAGGACACAGAGAAATTCGAATA	6685	TGCAGGACACAGAGAAATTCGAATA	7165
CAGCTTGCTTNNINGATCGACATG		CACGAACACNNINGATCGACATG		CACAAACCCGNNINGATCGACATG	
TGCAGGACACAGAGAAATTCGAATA	6686	TGCAGGACACAGAGAAATTCGAATA	6686	TGCAGGACACAGAGAAATTCGAATA	7166
CACITTTCTNNINGATCGACATG		CAATACGCGTNNINGATCGACATG		CAAGAGCAGCANNINGATCGACATG	

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池 -28	SEQ ID NO:	池 -29	SEQ ID NO:	池 -30	SEQ ID NO:
TGCAGGACCAGAGAAATTCGAATA	6687	TGCAGGACCAGAGAAATTCGAATA	6927	TGCAGGACCAGAGAAATTCGAATA	7167
CATCAAGTCGNNNTGCATCAGGT		CATCAAGTCGNNNTGCATCAGGT		CATCAAGTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6688	TGCAGGACCAGAGAAATTCGAATA	6928	TGCAGGACCAGAGAAATTCGAATA	7168
CAATCCAGCANNNTGCATCAGGT		CACTCTCTCTNNNTGCATCAGGT		CAATAGCCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6689	TGCAGGACCAGAGAAATTCGAATA	6929	TGCAGGACCAGAGAAATTCGAATA	7169
CAAAACGCTANNNTGCATCAGGT		CACAATGAGGNNNTGCATCAGGT		CAITGGATATNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6690	TGCAGGACCAGAGAAATTCGAATA	6930	TGCAGGACCAGAGAAATTCGAATA	7170
CACGCTGTGNNNTGCATCAGGT		CACACAGTGTNNNTGCATCAGGT		CACATTCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6691	TGCAGGACCAGAGAAATTCGAATA	6931	TGCAGGACCAGAGAAATTCGAATA	7171
CATAGGCGCTNNNTGCATCAGGT		CAAACTACTNNNTGCATCAGGT		CACCTTGACNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6692	TGCAGGACCAGAGAAATTCGAATA	6932	TGCAGGACCAGAGAAATTCGAATA	7172
CATGTCTGNNNTGCATCAGGT		CACGGCATCGNNNTGCATCAGGT		CAAAATAGGANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6693	TGCAGGACCAGAGAAATTCGAATA	6933	TGCAGGACCAGAGAAATTCGAATA	7173
CATAGCAGTCNNNTGCATCAGGT		CAAGTGCATTNNNTGCATCAGGT		CACGTTGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6694	TGCAGGACCAGAGAAATTCGAATA	6934	TGCAGGACCAGAGAAATTCGAATA	7174
CACGCGCTGACNNNTGCATCAGGT		CAGCGATCCGNNNTGCATCAGGT		CAITTCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6695	TGCAGGACCAGAGAAATTCGAATA	6935	TGCAGGACCAGAGAAATTCGAATA	7175
CATATATCTNNNTGCATCAGGT		CAATTAAGTNNNTGCATCAGGT		CAACTACCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6696	TGCAGGACCAGAGAAATTCGAATA	6936	TGCAGGACCAGAGAAATTCGAATA	7176
CACACGAAGNNNTGCATCAGGT		CARGATTCTANNNTGCATCAGGT		CACCTCTGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6697	TGCAGGACCAGAGAAATTCGAATA	6937	TGCAGGACCAGAGAAATTCGAATA	7177
CAATAGATCTNNNTGCATCAGGT		CATCAGCTGTNNNTGCATCAGGT		CACTAGCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6698	TGCAGGACCAGAGAAATTCGAATA	6938	TGCAGGACCAGAGAAATTCGAATA	7178
CAGCTGTCCNNNTGCATCAGGT		CACAAATCTNNNTGCATCAGGT		CAACTGCTAGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6699	TGCAGGACCAGAGAAATTCGAATA	6939	TGCAGGACCAGAGAAATTCGAATA	7179
CAATGACCTGNNNTGCATCAGGT		CAITTAGCAANNNTGCATCAGGT		CACGCGCAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6700	TGCAGGACCAGAGAAATTCGAATA	6940	TGCAGGACCAGAGAAATTCGAATA	7180
CAATAGCCCTNNNTGCATCAGGT		CATCCTAGTCTNNNTGCATCAGGT		CAGGCTTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6701	TGCAGGACCAGAGAAATTCGAATA	6941	TGCAGGACCAGAGAAATTCGAATA	7181
CATGAGGTAGNNNTGCATCAGGT		CATAAAGAGTNNNTGCATCAGGT		CACCTGACTANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6702	TGCAGGACCAGAGAAATTCGAATA	6942	TGCAGGACCAGAGAAATTCGAATA	7182
CACCAATCTGNNNTGCATCAGGT		CACATGCACANNNTGCATCAGGT		CAACATCAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6703	TGCAGGACCAGAGAAATTCGAATA	6943	TGCAGGACCAGAGAAATTCGAATA	7183
CAGCCGACCTNNNTGCATCAGGT		CAITTCACCTNNNTGCATCAGGT		CATCAGTTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6704	TGCAGGACCAGAGAAATTCGAATA	6944	TGCAGGACCAGAGAAATTCGAATA	7184
CATTCAAACANNNTGCATCAGGT		CACCTGATCTGNNNTGCATCAGGT		CATCAGGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6705	TGCAGGACCAGAGAAATTCGAATA	6945	TGCAGGACCAGAGAAATTCGAATA	7185
CAAGGCTTACNNNTGCATCAGGT		CACCGCTTCGNNNTGCATCAGGT		CAGTATGCAANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6706	TGCAGGACCAGAGAAATTCGAATA	6946	TGCAGGACCAGAGAAATTCGAATA	7186
CAAAAGCGCANNNTGCATCAGGT		CACATAAGPANNNTGCATCAGGT		CATCAGGCGCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6707	TGCAGGACCAGAGAAATTCGAATA	6947	TGCAGGACCAGAGAAATTCGAATA	7187
CAGATAGGACNNNTGCATCAGGT		CAGATTACGNNNTGCATCAGGT		CAGTTTTCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6708	TGCAGGACCAGAGAAATTCGAATA	6948	TGCAGGACCAGAGAAATTCGAATA	7188
CAATGGCGANNNTGCATCAGGT		CACCTGACGATNNNTGCATCAGGT		CAGGTCGGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6709	TGCAGGACCAGAGAAATTCGAATA	6949	TGCAGGACCAGAGAAATTCGAATA	7189
CAACCAAGAGNNNTGCATCAGGT		CAAGTTTCTANNNTGCATCAGGT		CAATAGGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6710	TGCAGGACCAGAGAAATTCGAATA	6950	TGCAGGACCAGAGAAATTCGAATA	7190
CACAAACGCTNNNTGCATCAGGT		CACACATAGCANNNTGCATCAGGT		CAAGCCGACNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6711	TGCAGGACCAGAGAAATTCGAATA	6951	TGCAGGACCAGAGAAATTCGAATA	7191
CACGCTTTCANNNTGCATCAGGT		CAITAGTCTPANNNTGCATCAGGT		CACATGTCAANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6712	TGCAGGACCAGAGAAATTCGAATA	6952	TGCAGGACCAGAGAAATTCGAATA	7192
CATCCAGCGCANNNTGCATCAGGT		CATGGTCGCGNNNTGCATCAGGT		CATTTAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6713	TGCAGGACCAGAGAAATTCGAATA	6953	TGCAGGACCAGAGAAATTCGAATA	7193
CATTTGAATCINNNTGCATCAGGT		CCTTCCTGACNNNTGCATCAGGT		CCTCGAGTGGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6714	TGCAGGACCAGAGAAATTCGAATA	6954	TGCAGGACCAGAGAAATTCGAATA	7194
CACCTGCTGNNNTGCATCAGGT		CATAAAACCTNNNTGCATCAGGT		CAGCGACCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6715	TGCAGGACCAGAGAAATTCGAATA	6955	TGCAGGACCAGAGAAATTCGAATA	7195
CACGAATGAGNNNTGCATCAGGT		CAACTATAACNNNTGCATCAGGT		CATGTTGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6716	TGCAGGACCAGAGAAATTCGAATA	6956	TGCAGGACCAGAGAAATTCGAATA	7196
CATGTGTTANNNTGCATCAGGT		CATATGATGTNNNTGCATCAGGT		CAGTTGTGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6717	TGCAGGACCAGAGAAATTCGAATA	6957	TGCAGGACCAGAGAAATTCGAATA	7197
CATTCAAAACNNNTGCATCAGGT		CATCACCGCANNNTGCATCAGGT		CACGTGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6718	TGCAGGACCAGAGAAATTCGAATA	6958	TGCAGGACCAGAGAAATTCGAATA	7198
CACAGCCGANNNTGCATCAGGT		CAAGGTTATNNNTGCATCAGGT		CAAGGCTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAAATTCGAATA	6719	TGCAGGACCAGAGAAATTCGAATA	6959	TGCAGGACCAGAGAAATTCGAATA	7199
CAGACAGTAGNNNTGCATCAGGT		CAAGCAGCTNNNTGCATCAGGT		CATATCTCTGNNNTGCATCAGGT	

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池-28	SEQ ID NO.	池-29	SEQ ID NO.	池-30	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATA	6720	TGCAGGACCAGAGAATTGGAATA	6960	TGCAGGACCAGAGAATTGGAATA	7200
CACATTTCCTNNNTGCATCAGGT		CATCGAGACTNNNTGCATCAGGT		CACATTACTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6721	TGCAGGACCAGAGAATTGGAATA	6961	TGCAGGACCAGAGAATTGGAATA	7201
CATRATCCCAANNNTGCATCAGGT		CACACACTTCNNNTGCATCAGGT		CACCAAGACTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6722	TGCAGGACCAGAGAATTGGAATA	6962	TGCAGGACCAGAGAATTGGAATA	7202
CACGTACACNNNTGCATCAGGT		CAAAAAACNNNTGCATCAGGT		CAGGTTCCAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6723	TGCAGGACCAGAGAATTGGAATA	6963	TGCAGGACCAGAGAATTGGAATA	7203
CAATATCCGANNNTGCATCAGGT		CATACAGCCANNNTGCATCAGGT		CAAAACCGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6724	TGCAGGACCAGAGAATTGGAATA	6964	TGCAGGACCAGAGAATTGGAATA	7204
CATAATTCCTNNNTGCATCAGGT		CAATGAAACNNNTGCATCAGGT		CATGCTCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6725	TGCAGGACCAGAGAATTGGAATA	6965	TGCAGGACCAGAGAATTGGAATA	7205
CAGATGCAGANNNTGCATCAGGT		CAGTGAATGCTNNNTGCATCAGGT		CATCTTTATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6726	TGCAGGACCAGAGAATTGGAATA	6966	TGCAGGACCAGAGAATTGGAATA	7206
CAGGAGCCAGNNNTGCATCAGGT		CATTACAGTNNNTGCATCAGGT		CAGGTGACTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6727	TGCAGGACCAGAGAATTGGAATA	6967	TGCAGGACCAGAGAATTGGAATA	7207
CAGCGAGTTNNNTGCATCAGGT		CACACCCGNNNTGCATCAGGT		CATCCTAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6728	TGCAGGACCAGAGAATTGGAATA	6968	TGCAGGACCAGAGAATTGGAATA	7208
CAAACTGACGNNNTGCATCAGGT		CATGTGCCNNNTGCATCAGGT		CACCGTAAGNNNTGCATCAGGT	

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池 -31	SEQ ID NO:	池 -32	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATAC	7209	TGCAGGACCAGAGAATTGGAATA	7449
ATGCTCCANNNNACCTATGCCA		CATTCCAAATNNNNACCTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7210	TGCAGGACCAGAGAATTGGAATA	7450
AGTACTCAGNNNACGTATGCCA		CATGTACAGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7211	TGCAGGACCAGAGAATTGGAATA	7451
AGAAGCCCCNNNACGTATGCCA		CACAGGAGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7212	TGCAGGACCAGAGAATTGGAATA	7452
ATTAAACCGNNNACGTATGCCA		CAATGCGTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7213	TGCAGGACCAGAGAATTGGAATA	7453
ATAACCTGGNNNACGTATGCCA		CATATTTTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7214	TGCAGGACCAGAGAATTGGAATA	7454
AGTCGACTANNNACGTATGCCA		CAAAATGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7215	TGCAGGACCAGAGAATTGGAATA	7455
ACCAACCGTNNNACGTATGCCA		CATCTGACGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7216	TGCAGGACCAGAGAATTGGAATA	7456
AACGTATCGNNNACGTATGCCA		CACCGCGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7217	TGCAGGACCAGAGAATTGGAATA	7457
ACACGGCCANNNACGTATGCCA		CAAAACACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7218	TGCAGGACCAGAGAATTGGAATA	7458
AAGGTITTCNNNACGTATGCCA		CAGGTTCGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7219	TGCAGGACCAGAGAATTGGAATA	7459
ACGACGCGTNNNACGTATGCCA		CAACTAACCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7220	TGCAGGACCAGAGAATTGGAATA	7460
ACCGACGTGNNNACGTATGCCA		CATCAGGAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7221	TGCAGGACCAGAGAATTGGAATA	7461
ACAGTITTTNNNACGTATGCCA		CAGTCTCGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7222	TGCAGGACCAGAGAATTGGAATA	7462
ATGCGCGGANNNACGTATGCCA		CAACTGGCGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7223	TGCAGGACCAGAGAATTGGAATA	7463
AGCCACTCCNNNACGTATGCCA		CACGACTCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7224	TGCAGGACCAGAGAATTGGAATA	7464
AGACGAAGTNNNACGTATGCCA		CACCGAAGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7225	TGCAGGACCAGAGAATTGGAATA	7465
AGGTTCTTNNNACGTATGCCA		CAGGCGCGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7226	TGCAGGACCAGAGAATTGGAATA	7466
ACCGGAATTNNNACGTATGCCA		CACAGGACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7227	TGCAGGACCAGAGAATTGGAATA	7467
ATCGGCAGCANNNACGTATGCCA		CACCCAAAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7228	TGCAGGACCAGAGAATTGGAATA	7468
AGCTAGAGANNNACGTATGCCA		CACGGAATAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7229	TGCAGGACCAGAGAATTGGAATA	7469
ACCACTTACNNNACGTATGCCA		CAAGTAAGATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7230	TGCAGGACCAGAGAATTGGAATA	7470
AACCACCGNNNACGTATGCCA		CATCTCACACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7231	TGCAGGACCAGAGAATTGGAATA	7471
AGAAACATANNNACGTATGCCA		CAGGCCCCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7232	TGCAGGACCAGAGAATTGGAATA	7472
AGCTGAAGNNNACGTATGCCA		CAGGATTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7233	TGCAGGACCAGAGAATTGGAATA	7473
ATAACCACTNNNACCTATGCCA		CAAAATGACANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7234	TGCAGGACCAGAGAATTGGAATA	7474
ACCTCACTANNNACGTATGCCA		CATAAAPATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7235	TGCAGGACCAGAGAATTGGAATA	7475
ATTAGATCANNNACGTATGCCA		CATATGCGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7236	TGCAGGACCAGAGAATTGGAATA	7476
ATGGATCANNNACGTATGCCA		CAGTTGCTTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7237	TGCAGGACCAGAGAATTGGAATA	7477
ACCGAGCTGNNNACGTATGCCA		CACGTTTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7238	TGCAGGACCAGAGAATTGGAATA	7478
ACTCATAAANNNACGTATGCCA		CAGAACAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7239	TGCAGGACCAGAGAATTGGAATA	7479
ACTCTACTGNNNACGTATGCCA		CAATAGAAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7240	TGCAGGACCAGAGAATTGGAATA	7480
AASGTGAGTNNNACGTATGCCA		CAGTAAGGCCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7241	TGCAGGACCAGAGAATTGGAATA	7481
AGAACACTCANNNACGTATGCCA		CAGAGATGCANNNACGTATGCCA	

图22A

池 -31	SEQ ID NO:	池 -32	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATAC	7242	TGCAGGACCAGAGAATTGGAATA	7482
AGGCAGAGCANNACGTATGCCA		CACACCATCTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7243	TGCAGGACCAGAGAATTGGAATA	7483
ATTTCAGCANNACGTATGCCA		CAGATACACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7244	TGCAGGACCAGAGAATTGGAATA	7484
ACCCATCATNNACGTATGCCA		CAGATACTGCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7245	TGCAGGACCAGAGAATTGGAATA	7485
AATCAGCGTNNACGTATGCCA		CACGTAACTGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7246	TGCAGGACCAGAGAATTGGAATA	7486
ATGAAAAACNNACGTATGCCA		CATCCTCTTCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7247	TGCAGGACCAGAGAATTGGAATA	7487
AATGCGGAANNACGTATGCCA		CATGCGGTGCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7248	TGCAGGACCAGAGAATTGGAATA	7488
ACGCATTCAANNACGTATGCCA		CAACACCAACHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7249	TGCAGGACCAGAGAATTGGAATA	7489
ACTCATACGNNACGTATGCCA		CAAAAATTTTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7250	TGCAGGACCAGAGAATTGGAATA	7490
AACCTGCTTNNACGTATGCCA		CAAAGTCACNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7251	TGCAGGACCAGAGAATTGGAATA	7491
AGTTGTGCAANNACGTATGCCA		CATCTACGAGHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7252	TGCAGGACCAGAGAATTGGAATA	7492
AGAAATCGGNNACGTATGCCA		CAGATCTTCCNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7253	TGCAGGACCAGAGAATTGGAATA	7493
AAAGTTAGANNACGTATGCCA		CAGGACACCCNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7254	TGCAGGACCAGAGAATTGGAATA	7494
ATGTAACGCGNNACGTATGCCA		CAATAGGTGGNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7255	TGCAGGACCAGAGAATTGGAATA	7495
AGTTTGTGAANNACGTATGCCA		CACCATCGCCNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7256	TGCAGGACCAGAGAATTGGAATA	7496
ACAAACTGCHNNACGTATGCCA		CATGATCTCCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7257	TGCAGGACCAGAGAATTGGAATA	7497
AGCCTGAGCCHNNACGTATGCCA		CACGCCAATTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7258	TGCAGGACCAGAGAATTGGAATA	7498
ATCTTCCAGNNACGTATGCCA		CATATATAATHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7259	TGCAGGACCAGAGAATTGGAATA	7499
ATACCTTACNNACGTATGCCA		CATATCCCTTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7260	TGCAGGACCAGAGAATTGGAATA	7500
ATCATAGATNNACGTATGCCA		CATTACGAGCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7261	TGCAGGACCAGAGAATTGGAATA	7501
AGTATAGANNACGTATGCCA		CAGGTTTCTCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7262	TGCAGGACCAGAGAATTGGAATA	7502
ACCCTAAGHNNACGTATGCCA		CACCTTGCAHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7263	TGCAGGACCAGAGAATTGGAATA	7503
AGCGGTTTANNACGTATGCCA		CAGACATTANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7264	TGCAGGACCAGAGAATTGGAATA	7504
ATAGCTCAGNNACGTATGCCA		CAACACGAGANNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7265	TGCAGGACCAGAGAATTGGAATA	7505
ACCGTCCCHNNACGTATGCCA		CATGCGCCGCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7266	TGCAGGACCAGAGAATTGGAATA	7506
AACTGCCAANNACGTATGCCA		CACAGTCCTTNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7267	TGCAGGACCAGAGAATTGGAATA	7507
ATGAGCTTCHNNACGTATGCCA		CAGCATTTCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7268	TGCAGGACCAGAGAATTGGAATA	7508
ATATCGTGGNNACGTATGCCA		CAAGATATCCHNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATAC	7269	TGCAGGACCAGAGAATTGGAATA	7509
ATCAGACACNNCTAGCGTTAC		CACCAGGAGGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7270	TGCAGGACCAGAGAATTGGAATA	7510
ATACCTTGNNNCTAGCGTTAC		CATCGCCTTANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7271	TGCAGGACCAGAGAATTGGAATA	7511
ACATCGAGTNNCTAGCGTTAC		CATTACCGGTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7272	TGCAGGACCAGAGAATTGGAATA	7512
ATGAATCTANNCTAGCGTTAC		CAATCAGCTCHNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7273	TGCAGGACCAGAGAATTGGAATA	7513
AAATGGAGTNNCTAGCGTTAC		CACCAATTCCHNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7274	TGCAGGACCAGAGAATTGGAATA	7514
ACTGAAGGANNCTAGCGTTAC		CATGCGTGATNNCTAGCGTTAC	

图22B

池 -31	SEQ ID No:	池 -32	SEQ ID No:
TGCAGGACCAGAGAATTGGAATAC	7275	TGCAGGACCAGAGAATTGGAATA	7515
AAATGAGTTNNCTAGCGTTAC		CAGTCGGCGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7276	TGCAGGACCAGAGAATTGGAATA	7516
ACCGAGGCTNNNCTAGCGTTAC		CAAGGAATTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7277	TGCAGGACCAGAGAATTGGAATA	7517
ACCGTGCACNNNCTAGCGTTAC		CACCCCTACATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7278	TGCAGGACCAGAGAATTGGAATA	7518
ACGTATCAGNNNCTAGCGTTAC		CACGGTTTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7279	TGCAGGACCAGAGAATTGGAATA	7519
ATAACGCTGNNNCTAGCGTTAC		CATCGTATAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7280	TGCAGGACCAGAGAATTGGAATA	7520
AACCGTACANNNCTAGCGTTAC		CATAAGCAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7281	TGCAGGACCAGAGAATTGGAATA	7521
AGCTTACTGNNNCTAGCGTTAC		CACCGCTCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7282	TGCAGGACCAGAGAATTGGAATA	7522
ACCAACCGCNNNCTAGCGTTAC		CACCACTACTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7283	TGCAGGACCAGAGAATTGGAATA	7523
AGTATCGTGNNNCTAGCGTTAC		CACCCACTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7284	TGCAGGACCAGAGAATTGGAATA	7524
ATACAAATCNNNCTAGCGTTAC		CACGCCAATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7285	TGCAGGACCAGAGAATTGGAATA	7525
ACGTGCTTANNNCTAGCGTTAC		CACCTTCAACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7286	TGCAGGACCAGAGAATTGGAATA	7526
AAGACCACTNNNCTAGCGTTAC		CAGAGAGGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7287	TGCAGGACCAGAGAATTGGAATA	7527
AACAAGGTGNNNCTAGCGTTAC		CAATAATTGGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7288	TGCAGGACCAGAGAATTGGAATA	7528
AATACCTTGANNNCTAGCGTTAC		CACATAATGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7289	TGCAGGACCAGAGAATTGGAATA	7529
ACTTCCGATNNNCTAGCGTTAC		CAATCTTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7290	TGCAGGACCAGAGAATTGGAATA	7530
ACGTCTTGTNNNCTAGCGTTAC		CATAAAGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7291	TGCAGGACCAGAGAATTGGAATA	7531
AAAGTGGTGNNNCTAGCGTTAC		CACCATTGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7292	TGCAGGACCAGAGAATTGGAATA	7532
ATCGTGGCNNNCTAGCGTTAC		CATACCCCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7293	TGCAGGACCAGAGAATTGGAATA	7533
AAAAATCAGNNNCTAGCGTTAC		CAAGAACCGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7294	TGCAGGACCAGAGAATTGGAATA	7534
ATCCCGCGTNNNCTAGCGTTAC		CAACGATAGCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7295	TGCAGGACCAGAGAATTGGAATA	7535
AGGGACCGCTNNNCTAGCGTTAC		CAGGCGCCATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7296	TGCAGGACCAGAGAATTGGAATA	7536
AGCTGTCTTNNNCTAGCGTTAC		CAAAAAATCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7297	TGCAGGACCAGAGAATTGGAATA	7537
AAGCATAAANNNCTAGCGTTAC		CAGACTAGCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7298	TGCAGGACCAGAGAATTGGAATA	7538
ATCCGAATCANNNCTAGCGTTAC		CACCTGAGTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7299	TGCAGGACCAGAGAATTGGAATA	7539
ACGTTTCGTNNNCTAGCGTTAC		CACCCGCTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7300	TGCAGGACCAGAGAATTGGAATA	7540
AGCACTCTTNNNCTAGCGTTAC		CFAAAACTTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7301	TGCAGGACCAGAGAATTGGAATA	7541
ACTGCTGCGNNNCTAGCGTTAC		CAAGTAACCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7302	TGCAGGACCAGAGAATTGGAATA	7542
ACATACAGCINNCTAGCGTTAC		CAATCAACATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7303	TGCAGGACCAGAGAATTGGAATA	7543
AGAGCAAAACNNNCTAGCGTTAC		CACITTTGATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7304	TGCAGGACCAGAGAATTGGAATA	7544
AGCTTCCATNNNCTAGCGTTAC		CAGTGTACGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7305	TGCAGGACCAGAGAATTGGAATA	7545
ACCTAATTNNNCTAGCGTTAC		CATGCACACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7306	TGCAGGACCAGAGAATTGGAATA	7546
AAGCCCGACNNNCTAGCGTTAC		CATATACTTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7307	TGCAGGACCAGAGAATTGGAATA	7547
ATGGTGAAGNNNCTAGCGTTAC		CAGAAACTAANNNCTAGCGTTAC	

图22C

池 -31	SEQ ID NO.	池 -32	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATAC	7308	TGCAGGACCAGAGAATTGGAATA	7548
AATCGCTGANNNNCTAGCGTTAC		CAATCTCGAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7309	TGCAGGACCAGAGAATTGGAATA	7549
ATTAGTGTCCNNNNCTAGCGTTAC		CAATGTGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7310	TGCAGGACCAGAGAATTGGAATA	7550
AGGAGGCCANNNNCTAGCGTTAC		CAAGACATGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7311	TGCAGGACCAGAGAATTGGAATA	7551
ATACCTGTCCNNNNCTAGCGTTAC		CACGGCAATTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7312	TGCAGGACCAGAGAATTGGAATA	7552
AATATGCTANNNNCTAGCGTTAC		CATAATGTGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7313	TGCAGGACCAGAGAATTGGAATA	7553
AGATCAGCCANNNNCTAGCGTTAC		CAGCGAGGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7314	TGCAGGACCAGAGAATTGGAATA	7554
AGCGGAACGNNNNCTAGCGTTAC		CACGAACATCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7315	TGCAGGACCAGAGAATTGGAATA	7555
AAATCCTTTNNNNCTAGCGTTAC		CAGCATGTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7316	TGCAGGACCAGAGAATTGGAATA	7556
ATACTATACNNNNCTAGCGTTAC		CAGCAACTCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7317	TGCAGGACCAGAGAATTGGAATA	7557
AGTCTGTAGNNNNCTAGCGTTAC		CAGTACTCTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7318	TGCAGGACCAGAGAATTGGAATA	7558
AGACTATCGNNNNCTAGCGTTAC		CAGGCTAAAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7319	TGCAGGACCAGAGAATTGGAATA	7559
AAGGATTAAANNNNCTAGCGTTAC		CACCCCTTTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7320	TGCAGGACCAGAGAATTGGAATA	7560
ATTACATCTNNNNCTAGCGTTAC		CACGCGAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7321	TGCAGGACCAGAGAATTGGAATA	7561
ATTTGSCAGNNNNCTAGCGTTAC		CAGTAAGAATTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7322	TGCAGGACCAGAGAATTGGAATA	7562
ACAGTATGCGNNNNCTAGCGTTAC		CATGATTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7323	TGCAGGACCAGAGAATTGGAATA	7563
ATTCCATCCNNNNCTAGCGTTAC		CACAAAAATCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7324	TGCAGGACCAGAGAATTGGAATA	7564
AAATCCCTNNNNCTAGCGTTAC		CACCGTCCCTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7325	TGCAGGACCAGAGAATTGGAATA	7565
ACTCTCCCCNNNNCTAGCGTTAC		CAAACTTTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7326	TGCAGGACCAGAGAATTGGAATA	7566
ACAATTAAACNNNNCTAGCGTTAC		CAGCTTGCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7327	TGCAGGACCAGAGAATTGGAATA	7567
AAATTITGCTNNNNCTAGCGTTAC		CATTAGTCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7328	TGCAGGACCAGAGAATTGGAATA	7568
AATAAATCCNNNNCTAGCGTTAC		CAAACGGCCCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATAC	7329	TGCAGGACCAGAGAATTGGAATA	7569
ATACTCGTCNNNNCTAGCGTTAC		CAGCGTGAAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7330	TGCAGGACCAGAGAATTGGAATA	7570
AATGCGAAGNNNGATCGACATG		CATGCTGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7331	TGCAGGACCAGAGAATTGGAATA	7571
ATGCGCAGCNNNGATCGACATG		CATCGACGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7332	TGCAGGACCAGAGAATTGGAATA	7572
ATGCTAAANNNGATCGACATG		CATCATCCTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7333	TGCAGGACCAGAGAATTGGAATA	7573
ACACTCCATNNNGATCGACATG		CAGTCACTCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7334	TGCAGGACCAGAGAATTGGAATA	7574
ACCTATGGAANNNGATCGACATG		CACCGGTGACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7335	TGCAGGACCAGAGAATTGGAATA	7575
AATGCTCCTNNNGATCGACATG		CATATCGCGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7336	TGCAGGACCAGAGAATTGGAATA	7576
AGATTGPAANNNGATCGACATG		CAGACGCGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7337	TGCAGGACCAGAGAATTGGAATA	7577
AACACCCAAANNNGATCGACATG		CAGAACAGACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7338	TGCAGGACCAGAGAATTGGAATA	7578
ACCGCATGNNNGATCGACATG		CAGTGTGTGTHNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7339	TGCAGGACCAGAGAATTGGAATA	7579
ATCCGATTCNNNGATCGACATG		CAGATTGCGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7340	TGCAGGACCAGAGAATTGGAATA	7580
AGAAATCTGNNNGATCGACATG		CAGTAGATTNNNGATCGACATG	

图22D

池 -31	SEQ ID No.	池 -32	SEQ ID No.
TGCAGGACCAGAGAATTGGAATAC	7341	TGCAGGACCAGAGAATTGGAATA	7581
ATTTCGTGCGNNNGATCGACATG		CAGCTTGAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7342	TGCAGGACCAGAGAATTGGAATA	7582
ACTTCACTGNNNGATCGACATG		CACGCCACGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7343	TGCAGGACCAGAGAATTGGAATA	7583
ACCCATATTGNNNGATCGACATG		CACCTAATTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7344	TGCAGGACCAGAGAATTGGAATA	7584
AAGTAGTAANNNGATCGACATG		CAGACAGGATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7345	TGCAGGACCAGAGAATTGGAATA	7585
ACACCGTAANNNGATCGACATG		CACTTCCCTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7346	TGCAGGACCAGAGAATTGGAATA	7586
ATGTTTCCGNNNGATCGACATG		CATAGAGATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7347	TGCAGGACCAGAGAATTGGAATA	7587
AGCTGGACCGNNNGATCGACATG		CAACCGGAATCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7348	TGCAGGACCAGAGAATTGGAATA	7588
AGTAATTCTNNNGATCGACATG		CAGCCACACTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7349	TGCAGGACCAGAGAATTGGAATA	7589
AACCTTATANNNGATCGACATG		CATGCTTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7350	TGCAGGACCAGAGAATTGGAATA	7590
AGCTACCAANNNGATCGACATG		CATCGTTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7351	TGCAGGACCAGAGAATTGGAATA	7591
AGATAATGANNNGATCGACATG		CACAGTTGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7352	TGCAGGACCAGAGAATTGGAATA	7592
AAAATCATGNNNGATCGACATG		CAACTAGCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7353	TGCAGGACCAGAGAATTGGAATA	7593
AAATAGCCCCNNNGATCGACATG		CAAAACTAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7354	TGCAGGACCAGAGAATTGGAATA	7594
ATGCTGCTTNNNGATCGACATG		CAGTTTCGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7355	TGCAGGACCAGAGAATTGGAATA	7595
ATTACGCGNNNGATCGACATG		CACTCATAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7356	TGCAGGACCAGAGAATTGGAATA	7596
ACCCAGCCTTNNNGATCGACATG		CAGCAGTATCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7357	TGCAGGACCAGAGAATTGGAATA	7597
ACCATTTATNNNGATCGACATG		CATATAGTCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7358	TGCAGGACCAGAGAATTGGAATA	7598
AGTGCATCNNNGATCGACATG		CAGGTGTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7359	TGCAGGACCAGAGAATTGGAATA	7599
ACATCAGGTNNNGATCGACATG		CAAGTGAAATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7360	TGCAGGACCAGAGAATTGGAATA	7600
AGGCCACGANNNGATCGACATG		CAGGTGCTTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7361	TGCAGGACCAGAGAATTGGAATA	7601
AAAGCACGANNNGATCGACATG		CATCGCGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7362	TGCAGGACCAGAGAATTGGAATA	7602
ACACAGGAANNNGATCGACATG		CAAAAGAACTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7363	TGCAGGACCAGAGAATTGGAATA	7603
AGCAGCCTGNNNGATCGACATG		CATCCTTTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7364	TGCAGGACCAGAGAATTGGAATA	7604
AGGCTGCGTNNNGATCGACATG		CATGCGCTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7365	TGCAGGACCAGAGAATTGGAATA	7605
ACTCTAGCTNNNGATCGACATG		CAGGCTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7366	TGCAGGACCAGAGAATTGGAATA	7606
AGAAGGCTANNNGATCGACATG		CATGTCCATCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7367	TGCAGGACCAGAGAATTGGAATA	7607
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TGCAGGACCAGAGAATTGGAATAC	7368	TGCAGGACCAGAGAATTGGAATA	7608
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TGCAGGACCAGAGAATTGGAATAC	7369	TGCAGGACCAGAGAATTGGAATA	7609
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TGCAGGACCAGAGAATTGGAATAC	7372	TGCAGGACCAGAGAATTGGAATA	7612
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TGCAGGACCAGAGAATTGGAATAC	7373	TGCAGGACCAGAGAATTGGAATA	7613
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图22E

池 -31	SEQ ID NO:	池 -32	SEQ ID NO:
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TGCAGGACCAGAGAATTGGAATAC	7375	TGCAGGACCAGAGAATTGGAATA	7615
ATTTCGTGNNNGATCGACATG		CATGAGGCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7376	TGCAGGACCAGAGAATTGGAATA	7616
AGTGACCATNNNGATCGACATG		CATGAGTTATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7377	TGCAGGACCAGAGAATTGGAATA	7617
ACCCATATACNNNGATCGACATG		CAATTGGTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7378	TGCAGGACCAGAGAATTGGAATA	7618
ACCCATATACNNNGATCGACATG		CAGGCGTTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7379	TGCAGGACCAGAGAATTGGAATA	7619
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TGCAGGACCAGAGAATTGGAATAC	7380	TGCAGGACCAGAGAATTGGAATA	7620
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TGCAGGACCAGAGAATTGGAATAC	7381	TGCAGGACCAGAGAATTGGAATA	7621
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TGCAGGACCAGAGAATTGGAATAC	7382	TGCAGGACCAGAGAATTGGAATA	7622
AGTGGACTTNNNGATCGACATG		CAGATTGCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7383	TGCAGGACCAGAGAATTGGAATA	7623
AGTTACTGNNNGATCGACATG		CAGTTCCAGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7384	TGCAGGACCAGAGAATTGGAATA	7624
ATCCTAGGANNNGATCGACATG		CAAAACCGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7385	TGCAGGACCAGAGAATTGGAATA	7625
AAAACCTACNNNGATCGACATG		CACGCGTTGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7386	TGCAGGACCAGAGAATTGGAATA	7626
AAAGTGCCTNNNGATCGACATG		CAAAATCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATAC	7387	TGCAGGACCAGAGAATTGGAATA	7627
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TGCAGGACCAGAGAATTGGAATAC	7388	TGCAGGACCAGAGAATTGGAATA	7628
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TGCAGGACCAGAGAATTGGAATAC	7390	TGCAGGACCAGAGAATTGGAATA	7630
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TGCAGGACCAGAGAATTGGAATAC	7391	TGCAGGACCAGAGAATTGGAATA	7631
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TGCAGGACCAGAGAATTGGAATAC	7392	TGCAGGACCAGAGAATTGGAATA	7632
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TGCAGGACCAGAGAATTGGAATAC	7395	TGCAGGACCAGAGAATTGGAATA	7635
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TGCAGGACCAGAGAATTGGAATAC	7396	TGCAGGACCAGAGAATTGGAATA	7636
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TGCAGGACCAGAGAATTGGAATAC	7397	TGCAGGACCAGAGAATTGGAATA	7637
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TGCAGGACCAGAGAATTGGAATAC	7398	TGCAGGACCAGAGAATTGGAATA	7638
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TGCAGGACCAGAGAATTGGAATAC	7402	TGCAGGACCAGAGAATTGGAATA	7642
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TGCAGGACCAGAGAATTGGAATAC	7403	TGCAGGACCAGAGAATTGGAATA	7643
AGTTGCGTANNNTGCATCAGGT		CAGGAATAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7404	TGCAGGACCAGAGAATTGGAATA	7644
ACCAAAATCCNNNTGCATCAGGT		CAATTATACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7405	TGCAGGACCAGAGAATTGGAATA	7645
AGCTTTGTCNNNTGCATCAGGT		CACAAAGCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7406	TGCAGGACCAGAGAATTGGAATA	7646
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图22F

池 -31	SEQ ID No:	池 -32	SEQ ID No:
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TGCAGGACCAGAGAATTGGAATAC	7408	TGCAGGACCAGAGAATTGGAATA	7648
ACCAGGACCNNTGCATCAGGT		CACATTTTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7409	TGCAGGACCAGAGAATTGGAATA	7649
AAGAGCATGNNNTGCATCAGGT		CAGCAGAGGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7410	TGCAGGACCAGAGAATTGGAATA	7650
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TGCAGGACCAGAGAATTGGAATAC	7411	TGCAGGACCAGAGAATTGGAATA	7651
ACCTAAGCGNNNTGCATCAGGT		CAGGAGTCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7412	TGCAGGACCAGAGAATTGGAATA	7652
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TGCAGGACCAGAGAATTGGAATAC	7413	TGCAGGACCAGAGAATTGGAATA	7653
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TGCAGGACCAGAGAATTGGAATAC	7414	TGCAGGACCAGAGAATTGGAATA	7654
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TGCAGGACCAGAGAATTGGAATAC	7415	TGCAGGACCAGAGAATTGGAATA	7655
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TGCAGGACCAGAGAATTGGAATAC	7416	TGCAGGACCAGAGAATTGGAATA	7656
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TGCAGGACCAGAGAATTGGAATAC	7418	TGCAGGACCAGAGAATTGGAATA	7658
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TGCAGGACCAGAGAATTGGAATAC	7419	TGCAGGACCAGAGAATTGGAATA	7659
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TGCAGGACCAGAGAATTGGAATAC	7422	TGCAGGACCAGAGAATTGGAATA	7662
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TGCAGGACCAGAGAATTGGAATAC	7423	TGCAGGACCAGAGAATTGGAATA	7663
ATCCTATTANNNTGCATCAGGT		CAGCTTCTTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATAC	7424	TGCAGGACCAGAGAATTGGAATA	7664
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TGCAGGACCAGAGAATTGGAATAC	7425	TGCAGGACCAGAGAATTGGAATA	7665
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TGCAGGACCAGAGAATTGGAATAC	7426	TGCAGGACCAGAGAATTGGAATA	7666
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TGCAGGACCAGAGAATTGGAATAC	7427	TGCAGGACCAGAGAATTGGAATA	7667
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TGCAGGACCAGAGAATTGGAATAC	7429	TGCAGGACCAGAGAATTGGAATA	7669
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TGCAGGACCAGAGAATTGGAATAC	7430	TGCAGGACCAGAGAATTGGAATA	7670
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TGCAGGACCAGAGAATTGGAATAC	7431	TGCAGGACCAGAGAATTGGAATA	7671
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TGCAGGACCAGAGAATTGGAATAC	7437	TGCAGGACCAGAGAATTGGAATA	7677
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TGCAGGACCAGAGAATTGGAATAC	7438	TGCAGGACCAGAGAATTGGAATA	7678
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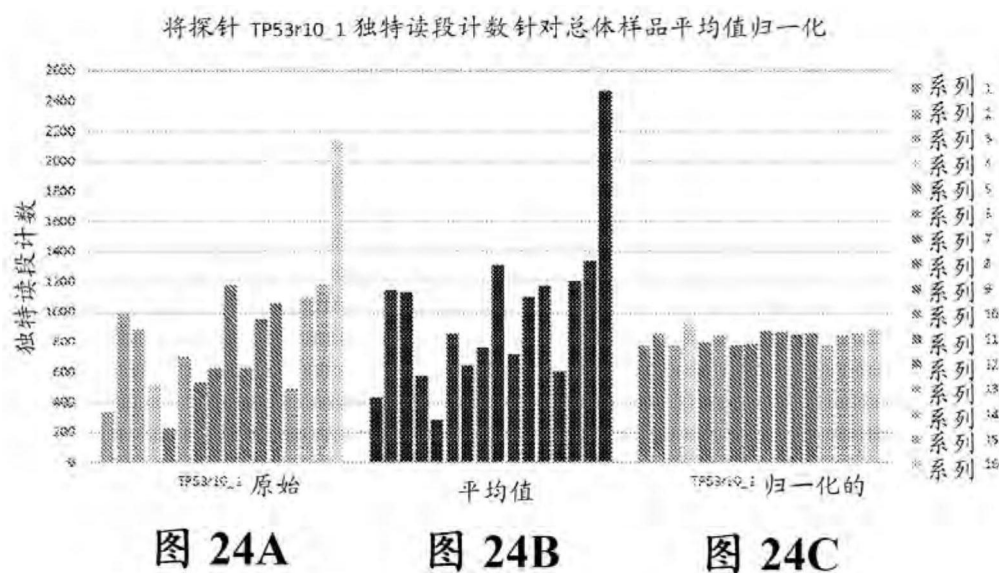
图22G

池 -31	SEQ ID NO:	池 -32	SEQ ID NO:
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TGCAGGACCAGAGAATTGGAATAC AATATCGTANNNTGCATCAGGT	7441	TGCAGGACCAGAGAATTGGAATA CAGACCATGNNNTGCATCAGGT	7681
TGCAGGACCAGAGAATTGGAATAC AACCTCTCANNNTGCATCAGGT	7442	TGCAGGACCAGAGAATTGGAATA CACCGCTAGNNNTGCATCAGGT	7682
TGCAGGACCAGAGAATTGGAATAC AGTTCGGTCNNNTGCATCAGGT	7443	TGCAGGACCAGAGAATTGGAATA CATTAGCTGNNNTGCATCAGGT	7683
TGCAGGACCAGAGAATTGGAATAC ATTGCCCGNNNTGCATCAGGT	7444	TGCAGGACCAGAGAATTGGAATA CATCTGATTNNNTGCATCAGGT	7684
TGCAGGACCAGAGAATTGGAATAC ACAGGCTGCNNNTGCATCAGGT	7445	TGCAGGACCAGAGAATTGGAATA CATCATAGGNNNTGCATCAGGT	7685
TGCAGGACCAGAGAATTGGAATAC ATCGCTTACNNNTGCATCAGGT	7446	TGCAGGACCAGAGAATTGGAATA CATGGAGGTANNNTGCATCAGGT	7686
TGCAGGACCAGAGAATTGGAATAC ACGGATTGTNNNTGCATCAGGT	7447	TGCAGGACCAGAGAATTGGAATA CAGTCTCTACNNNTGCATCAGGT	7687
TGCAGGACCAGAGAATTGGAATAC ACAAGCTGTNNNTGCATCAGGT	7448	TGCAGGACCAGAGAATTGGAATA CAGCCTGCTGNNNTGCATCAGGT	7688

图22H



图23



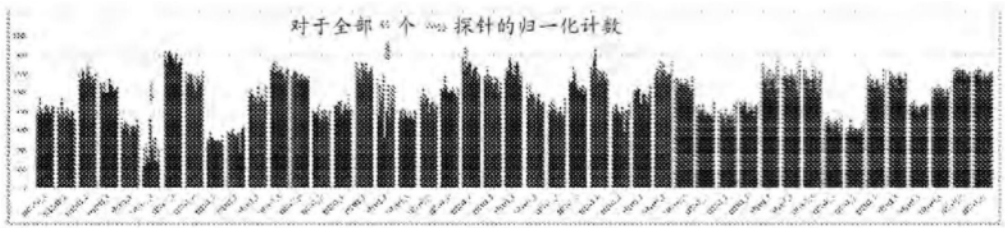


图25

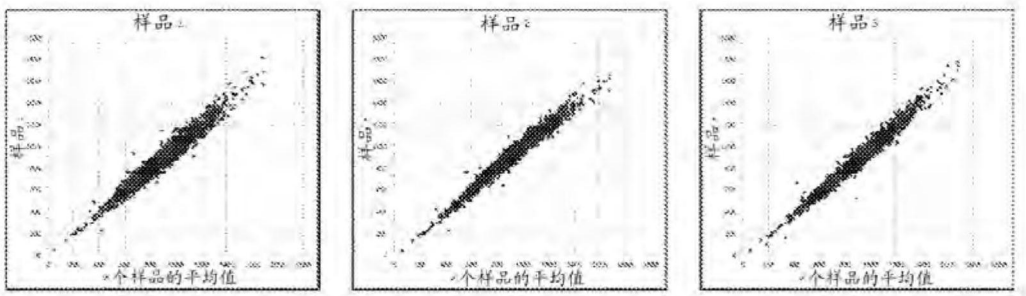


图26

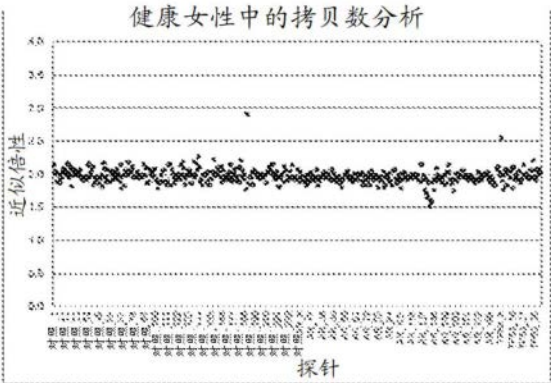


图27A

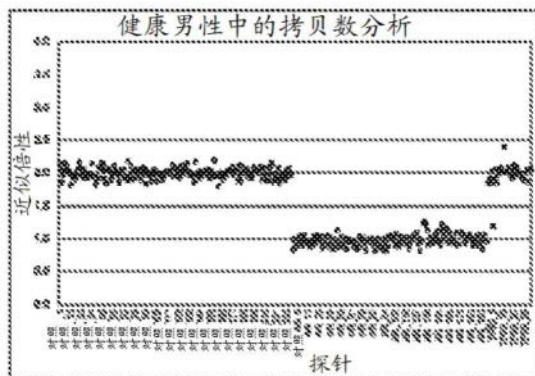


图27B

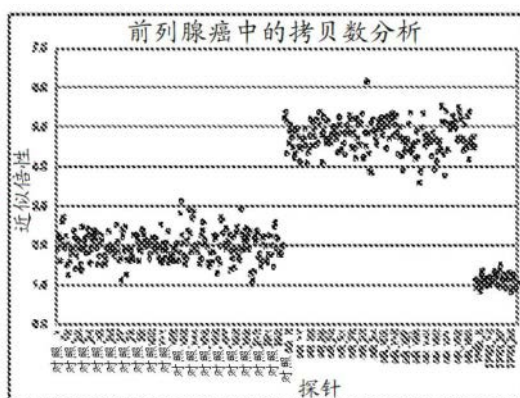


图27C

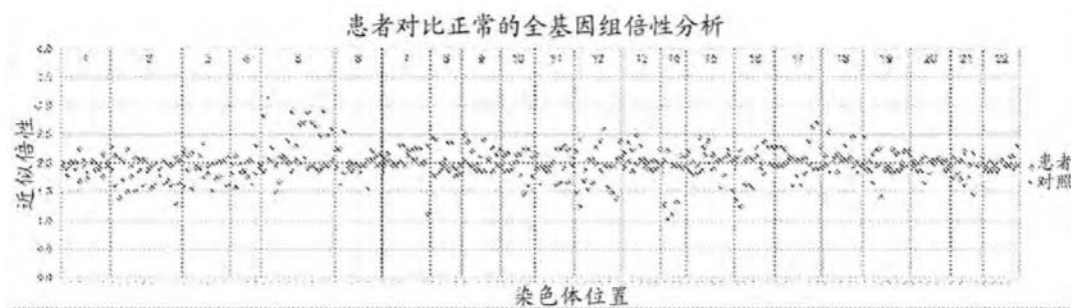


图28

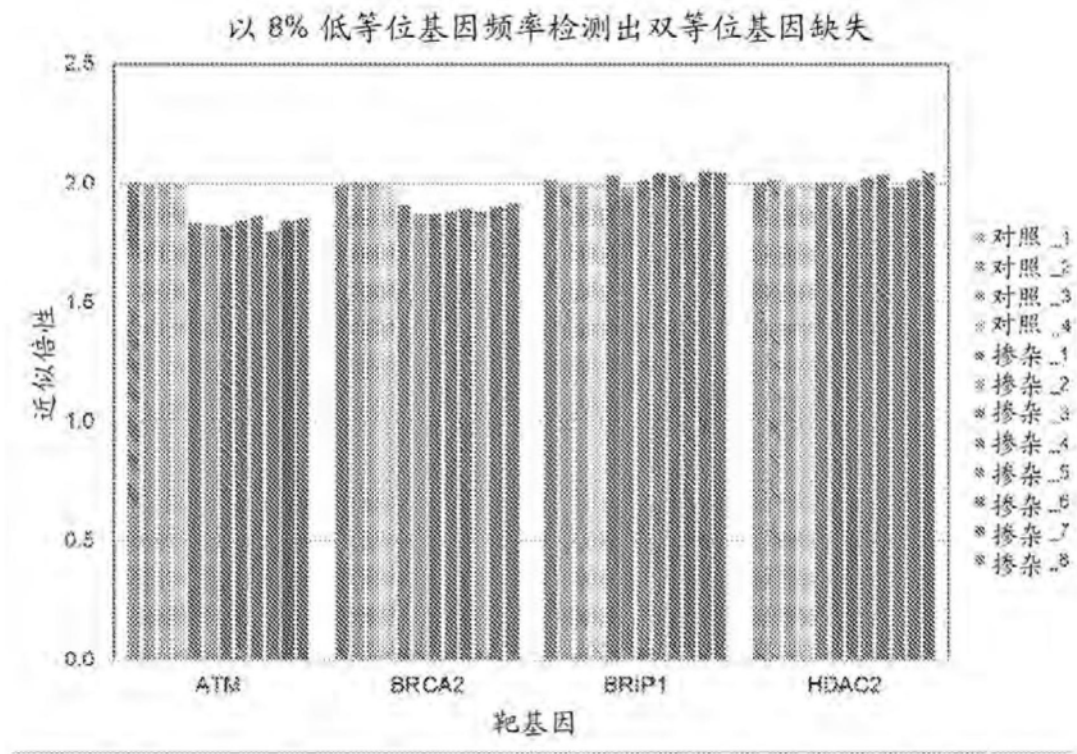


图29