

NY

中华人民共和国农业行业标准

NY/T XXXXX—202X

金针菇品种及其实质性派生品种鉴定
MNP 标记法

Identification of *Flammulina filiformis* variety and its essentially derived varieties
—MNP marker method

（征求意见稿）

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前 言

本文件按照GB/T 1.1—2020《标准化工作导则 第1部分：标准化文件的结构和起草规则》的规定起草。

本文件的某些内容可能涉及专利，本文件的发布机构不承担识别专利的责任。

本文件由中华人民共和国农业农村部农产品质量安全监管司提出。

本文件由全国植物新品种测试标准化技术委员会（SAC/TC277）归口。

本文件起草单位：上海市农业科学院、江汉大学、上海雪榕生物科技股份有限公司、农业农村部植物新品种测试（上海）分中心、陆良爨乡绿圆菇业有限公司。

本文件主要起草人：王瑞娟、彭海、陆欢、李甜甜、尚晓冬、胡卫红、韩瑞玺、方治伟、刘建雨、周俊飞、徐珍、吴燕莎、陈海荣、王小艳。

金针菇品种及其实质性派生品种鉴定 MNP 标记法

1 范围

本文件规定了应用多核苷酸多态性（Multiple Nucleotide Polymorphism, MNP）标记法进行金针菇（*Flammulina filiformis*）品种及其实质性派生品种鉴定的术语和定义、原理、试剂和材料、仪器设备、操作程序、质量控制、数据分析和结果判定。

本文件适用于金针菇品种及其实质性派生品种的鉴定。

2 规范性引用文件

下列文件中的内容通过文中的规范性引用而构成本文件必不可少的条款。其中，注日期的引用文件，仅该日期对应的版本适用于本文件；不注日期的引用文件，其最新版本（包括所有的修改单）适用于本文件。

GB/T 6682 分析实验室用水规格和试验方法

GB/T 38551 植物品种鉴定 MNP 标记法

NY/T 2594 植物品种鉴定 DNA 分子标记法 总则

3 术语和定义

下列术语和定义适用于本文件。

3.1

多核苷酸多态性 multiple nucleotide polymorphism, MNP

在一段不超过 300 bp 的核苷酸序列中，由多个核苷酸引起的序列多态性。

[来源：GB/T 38551，3.1，有修改]

3.2

实质性派生品种 essential derived variety, EDV

指由原始品种实质性派生，或者由该原始品种的实质性派生品种派生出来的品种，与原始品种有明显区别，并且除派生引起的性状差异外，在表达由原始品种基因型或者基因型组合产生的基本性状方面与原始品种相同。

[来源：中华人民共和国种子法，第九十条第十款]

3.3

平均覆盖倍数 average coverage

在基因组上比对到所有标记位点上的所有测序片段的总数与标记位点总数的比值。

[来源：GB/T 38551，3.4，有修改]

3.4

检出标记位点 detected markers

至少有一个等位基因型且有 20 条及以上测序片段支持的标记位点。

[来源：GB/T 38551，3.5，有修改]

4 原理

利用多重聚合酶链式反应（PCR）、二代高通量测序以及生物信息学方法扩增、检测和分析品种 MNP 标记，获得 MNP 标记基因型及其在品种间的遗传差异，将遗传差异与判定阈值进行比较，获得品种鉴定结论和实质性派生品种鉴定结论。

5 试剂和材料

除非另有规定，仅使用分析纯试剂，实验用水符合 GB/T 6682 中规定的一级水的要求。

5.1 多重PCR扩增与文库构建试剂盒

应匹配MNP标记和标记检测引物，以及高通量测序试剂盒。

5.3 高通量测序试剂盒

应匹配高通量测序仪。

5.4 MNP标记和标记检测引物

应符合附录A的要求。

6 仪器设备

6.1 离心机

最大转速度不小于12,000 rpm。

6.2 电泳仪

6.3 基因扩增仪

6.4 高通量测序仪

测序读长不低于300 bp。

6.5 计算机服务器

7 操作程序

7.1 样品准备

送检样品宜为新鲜的菌丝体或子实体，供检菌种与对照菌种在相同条件下培养，培养量可共做3个平行试验。

从金针菇品种群体中抽取的个体数量宜满足NY/T 2594要求。

抽取的样本可以混合后检测。

7.2 DNA 提取

利用核酸提取试剂提取待测样品DNA。提取的DNA在260 nm与230 nm处的吸光度值的比值大于2.0，260 nm与280 nm吸光度比值介于1.7~1.9之间。

7.3 多重 PCR 扩增与文库构建

按多重 PCR 扩增与文库构建试剂盒的说明书进行 DNA 质控、多重 PCR 扩增、文库构建与纯化。其中，多重 PCR 的扩增循环数不高于 20 次。

7.4 高通量测序

按高通量测序试剂盒和高通量测序仪的操作说明，对7.3中获得的高通量测序文库进行高通量测序。高通量测序的平均覆盖倍数设置为700倍以上，测序长度不小于300 bp。

8 质量控制

8.1 环境

样品准备、DNA 提取、多重 PCR 扩增、文库构建和高通量测序宜在规定的区域或相互隔离的区域按单一方向进行操作，不同区域的仪器设备需专用。

8.2 测序数据

8.2.1 高通量测序原始数据质量应满足所采用的高通量测序仪的操作手册中所规定的测序质量要求。

8.2.2 将样品的测序数据比对到参考基因组的标记位点上，统计第一次检测的标记位点的平均覆盖倍数 C_1 。

8.2.3 当 C_1 小于 500 时，判定样品的测序数据量不足，从 7.4 或之前的步骤开始重新实验至第一次检测的标记位点的平均覆盖倍数 C_1 大于或等于 500。

8.2.4 当 C_1 大于或等于 500 时，进一步计算检出标记位点的比例 R_1 。

R_1 按式 (1) 计算

$$R_1 = \frac{T_1}{T} \times 100\% \dots \dots \dots (1)$$

式中：

R_1 ——样品检出标记位点的比例；

T_1 ——样品检出标记位点的数目；

T ——样品检测标记位点的数目。

8.2.5 当 R_1 大于或等于 95% 时，判定测序数据合格；否则，从 7.2 或之前的步骤重新实验至第二次检出的标记位点的平均覆盖倍数 C_2 大于或等于 500。

8.2.6 当 C_2 大于或等于 500 时，进一步计算第一次和第二次共同检出的标记位点的比例 R_2 。

R_2 按式 (2) 计算

$$R_2 = \frac{2T_{12}}{T_{11}+T_2} \times 100\% \dots \dots \dots (2)$$

式中：

R_2 ——第一次和第二次共同检出的标记位点的比例；

T_{12} ——第一次和第二次共同检出标记位点的数目；

T_{11} ——第一次检出标记位点的数目；

T_2 ——第二次检出标记位点的数目。

8.2.7 当 R_2 大于或等于 95% 时，判定测序数据合格。

注：附录 B 提供了一个操作案例，其他满足 DNA 提取、文库制备和高通量测序的试剂、仪器设备均可；样品不要求必须重复检测 2 次，但重复检测有助于减少样品编号、PCR 扩增、测序过程中的随机错误。

9 数据分析

9.1 测序数据比对与记录

9.1.1 将测序数据同源比对到参考基因组上的每个 MNP 标记位点上。

9.1.2 检出标记位点的基因型记录为该位点的所有检出等位基因型，其中，检出等位基因型指从该标记第一个到最后—个碱基构成的检出 DNA 片段，不同检出等位基因型用“/”隔开。检出标记位点的基因型记录实例附录 B.8。

9.2 遗传相似度计算

遗传相似度按式（3）计算

$$GS = \frac{n_{ij}}{N_{ij}} \times 100\% \dots\dots\dots (3)$$

式中：

- GS——待测品种与对照品种的遗传相似度；
- n_{ij} ——待测品种与对照品种中均检出的但基因型无任何差异的标记位点的数目；
- N_{ij} ——待测品种与对照品种中均检出标记位点的数目。

10 结果判定

10.1 品种鉴定判定规则

- 10.1.1 当待测品种与对照品种的遗传相似度（GS）小于 97%时，判定为“不同品种”；
- 10.1.2 当待测品种与对照品种的遗传相似度（GS）大于或等于 97%时，判定为“疑同品种”。

10.2 实质性派生关系判定规则

- 10.2.1 当待测品种与对照品种的遗传相似度（GS）小于 94%时，判定为“不存在实质性派生关系”；
- 10.2.2 当待测品种与对照品种的遗传相似度（GS）大于或等于 94%时，判定为“疑似存在实质性派生关系”；
- 10.2.3 对判定为疑似存在实质性派生关系的样品，可综合育种过程等其他信息进一步判定。

10.3 结果表述

待测品种__与对照品种__比较位点数为__，差异位点数为__，遗传相似度为__，判定为__。

示例1：待测品种A与对照品种B比较位点数为336，差异位点数为10，遗传相似度为98.51%，判定为疑同品种。

示例2：待测品种A与对照品种B比较位点数为333，差异位点数为100，遗传相似度为69.97%，判定为不存在实质性派生关系。

附录A
(规范性附录)
MNP标记

A.1 金针菇 MNP 标记见表 A.1。

表 A.1 金针菇 MNP 标记

位点 编号	染色体	正向引物 (5'→3')	反向引物 (5'→3')	变异碱基位置、类型与比例	参照品种	
					T011	JZ19
AMPL16 90001	scaffold3	CGTCAAT TTCTGAT TCCGAAG CTTC	TTTTGTTT CTCTCCC ACCATCT TTG	47(C-3%,T-99%);80(A-1%,G-99%);108(C-22%,G-94%);110(C-0%,T-100%);111(G-100%,T-0%);128(A-8%,G-100%);149(A-1%,T-99%);162(G-100%,T-0%);164(C-1%,T-99%);172(A-1%,G-99%);173(C-99%,T-1%);186(C-97%,T-15%);187(A-1%,G-99%);189(C-1%,T-100%);190(G-0%,A-100%);192(G-0%,A-99%,T-1%);193(G-1%,T-99%);205(C-1%,T-99%);	T;G;G;T ;G;G;T; G;T;G; C;C;G;T ;A;A;T; T	T;G;G;T ;G;G/A; T;G;T;G ;C;C;G; T;A;A;T ;T
AMPL16 90002	scaffold5	CAGCTGT ATTCCGA ATGCCAT G	ATGATGA AATTCGC TAAAGCT TCCG	37(C-2%,T-98%);43(C-98%,T-2%);44(G-100%,T-0%);45(C-0%,G-100%);52(C-2%,T-98%);54(C-100%,T-2%);55(A-1%,G-100%);61(G-98%,T-2%);76(A-29%,T-96%);79(A-2%,T-98%);82(C-2%,G-98%);85(A-4%,G-96%);88(A-2%,G-98%);94(C-98%,T-2%);96(C-100%,T-1%);98(C-0%,G-100%);103(G-4%,T-96%);104(C-100%,T-0%);106(A-4%,T-96%);109(G-2%,A-98%);110(C-79%,A-78%);112(G-0%,C-100%);114(A-2%,T-100%);115(C-80%,T-75%);116(A-1%,G-99%);118(C-0%,T-100%);121(G-96%,T-4%);127(A-2%,C-98%);129(G-81%,A-73%);133(C-4%,T-96%);139(G-100%,T-0%);140(C-2%,G-98%);145(C-2%,T-98%);151(G-100%,T-0%);155(C-2%,T-98%);161(C-3%,T-98%);166(G-2%,A-98%);183(A-100%,T-0%);184(C-96%,T-5%);187(G-70%,A-80%);	T;C;G; G;T;C; G;G;T;T ;G;G;G; C;C;G;T ;C;T;A; C/A;C;T ;T/C;G; T;G;C; G/A;T; G;G;T; G;T;T;A ;A;C;A/ G	T;C;G; G;T;C; G;G;A/ T;T;G;G ;G;C;C; G;T;C;T ;A;A/C; C;T;T/C ;G;T;G; C;G/A; T;G;G;T ;G;T;T; A;A;C; A
AMPL16 90003	scaffold5	CATTGCT AGAGACG CTCCATT TTAG	GCCGTAC CGTTCTA AATGAAT AGTG	49(C-1%,A-100%);82(A-2%,C-100%);86(G-1%,T-100%);87(A-1%,C-97%);97(C-99%,T-3%);98(G-3%,A-99%);154(A-1%,G-100%);158(C-1%,T-100%);182(A-3%,G-99%);193(C-3%,T-98%);198(G-3%,A-99%);215(C-99%,T-3%);	A;C;T;C ;C;A;G; T;G;T;A ;C	A;C;T;C ;C;A;G; T;G;T;A ;C
AMPL16 90004	scaffold5	ACATACC AGGACTC ATAAACT GCTT	ATTCTTA GCGGACA TTTCTAC CAGA	51(G-1%,A-100%);53(A-1%,G-99%);56(A-2%,G-98%);59(C-77%,G-0%,T-82%);68(C-100%,T-0%);80(A-0%,G-100%);93(C-100%,T-9%);95(C-100%,T-1%);104(C-95%,T-31%);110(A-2%,G-98%);116(G-100%,T-0%);122(G-2%,C-98%);125(A-0%,G-100%);128(C-98%,T-2%);143(G-2%,A-98%);146(G-0%,A-100%);149(A-1%,G-99%);152(G-0%,A-100%);155(A-54%,C-0%,G-91%);156(C-100%,T-0%);167(C-0%,T-100%);185(C-97%,T-18%);188(C-0%,A-100%);190(G-100%,T-1%);191(G-0%,A-100%);197(G-0%,A-100%);202(G-77%,T-79%);203(G-1%,A-99%);206(A-1%,G-92%,T-59%);	A;G;G; C/T;C;G ;C;C;C; G;G;C; G;C;A; A;G;A; G/A;C; T;C;A; G;A;A; G/T;A;T /G	A;G;G; T/C;C;G ;C;C;C/ T;G;G; C;G;C; A;A;G; A;G;C; T;T/C;A ;G;A;A; G/T;A; G

AMPL16 90005	scaffold6	CATTGGA TCTAGGC GCATTTA CTG	GATGTGT CGGTAAT AGGGTCA GG	38(C-0%,A-100%);40(G-1%,A-99%);41(A-2%,G-1%,C-98%);42(G-1%,A-100%);44(C-0%,T-100%);56(A-1%,T-99%);59(C-2%,G-98%);62(A-29%,T-91%);65(C-99%,T-1%);71(G-0%,A-100%);74(C-100%,T-0%);83(G-2%,C-97%,T-1%);87(C-1%,T-99%);88(C-15%,A-95%,T-1%);89(C-1%,T-99%);90(C-1%,G-1%,A-98%);91(C-99%,T-1%);93(C-3%,T-99%);94(A-3%,C-100%);97(A-1%,G-98%);98(A-1%,C-99%);99(C-32%,T-89%);100(C-8%,A-99%);101(C-99%,T-1%);102(C-97%,T-12%);104(G-1%,C-99%,T-1%);105(C-99%,T-1%);106(A-0%,G-100%);108(G-99%,T-10%);109(G-1%,C-97%,T-11%);111(C-98%,T-2%);114(C-99%,T-10%);116(C-1%,T-99%);117(A-9%,G-99%);118(C-0%,A-100%);119(A-0%,C-99%);120(C-1%,T-99%);122(C-0%,G-99%);126(A-23%,G-91%,T-0%);127(A-97%,T-1%);128(C-98%,T-1%);129(A-2%,T-96%);130(C-0%,T-98%);132(A-5%,G-95%,T-0%);135(A-0%,G-100%);138(A-97%,T-12%);141(C-33%,T-86%);144(A-1%,G-100%);145(C-100%,T-1%);153(A-9%,G-97%);159(C-11%,T-99%);162(A-0%,T-100%);164(C-0%,T-100%);183(C-100%,T-0%);198(A-2%,C-98%,T-1%);200(C-100%,T-1%);201(A-0%,T-100%);217(A-0%,G-100%);218(C-2%,T-98%);	A;A;C; A;T;T;G ;T;C;A; C;C;T;A ;T;A;C; T;C;G;C ;T;A;C; C;C;C; G;G;C; C;C;T;G ;A;C;T; G;G;A; C;T;T;G ;G;A;T; G;C;G; T;T;T;C ;C;C;T; G;T	A;A;C; A;T;T;G ;A/T;C; A;C;C;T ;A;T;A; C;T;C;G ;C;T/C; A;C;C; C;C;G; G;C;C; C;T;G; A;C;T; G;A;G; A;C;T;T ;G;G;A; C/T;G;C ;G;T;T; T;C;C;C ;T;G;T
AMPL16 90007	scaffold7	TAATCAT GGAGTTC GCGTTAA CATG	GATCAAG GCGTCGA ATACAAT GAAC	42(C-17%,A-89%);48(G-97%,T-4%);51(C-97%,T-4%);63(A-4%,G-97%);64(A-10%,G-93%);65(G-8%,A-97%);66(G-8%,A-97%);68(A-8%,G-92%);78(C-4%,T-93%);82(C-4%,G-93%);87(C-93%,T-10%);90(C-10%,T-93%);91(A-10%,T-93%);95(G-8%,C-97%);96(A-10%,G-93%);97(C-10%,T-93%);101(C-4%,G-14%,A-89%);105(C-2%,T-100%);109(A-11%,G-93%);111(C-17%,T-92%);112(C-100%,T-0%);113(C-100%,T-0%);122(G-14%,A-93%);132(G-18%,A-89%);134(G-2%,A-100%);143(C-4%,G-97%);156(G-93%,T-6%);157(G-8%,C-97%);171(C-12%,G-93%);211(C-100%,T-2%);213(C-100%,T-2%);215(C-89%,T-20%);221(C-97%,T-8%);233(C-4%,T-98%);	A;G;C; G;G;A; A;G;T; G;C;T;T ;C;G;T; A;T;G;T ;C;C;A; A;A;G; G;C;G; C;C;C;C ;T	A/C;G; C;G;G; A/G;G/ A;G/A; T;G;C;T ;T;C/G; G;T;A/ G;T;A/ G;C/T;C ;G;A; A/G;A; G;- /G;C/G; C/G;C; C;T/C;C /T;T
AMPL16 90008	scaffold1	CGCCTCT AAACAAG TACGTTT CATT	TTTTGAA GATAGGC CAGGACA TCTT	36(C-99%,T-1%);45(C-96%,T-4%);46(C-1%,T-99%);47(G-4%,A-100%);48(G-0%,A-100%);51(G-2%,A-99%,T-0%);52(C-4%,A-96%);53(A-0%,C-99%);59(C-0%,A-100%);60(C-43%,T-94%);64(C-47%,T-91%);67(C-98%,T-2%);70(G-80%,T-76%);73(C-96%,T-4%);115(C-100%,T-0%);118(C-0%,G-87%,T-42%);122(A-4%,G-96%);123(C-1%,T-99%);126(G-0%,C-100%);127(A-2%,C-98%);148(A-0%,C-100%);154(A-4%,G-96%);157(A-4%,G-96%);160(C-98%,T-2%);166(C-0%,G-100%);	C;C;T;A ;A;A;A; C;A;C/T ;T/C;C; T/G;C;C ;G;G;T; C;C;C; G;G;C; G	C;C;T;A ;A;A;A; C;A;T;T ;C;T/G; C;C;G/T ;G;T;C; C;C;G; G;C;G

AMPL16 90009	scaffold11	GCGAAGA GTTACCG TTGGATC A	CTAAACC GGCTCAT CCTCTTC TT	35(C-0%,T-100%);41(C-8%,T-99%);44(A-87%,C-6%,T-28%);45(G-0%,A-100%);51(A-0%,G-100%);53(A-0%,G-100%);55(A-0%,G-98%,T-2%);56(A-3%,G-99%);62(G-1%,C-98%,T-2%);63(A-1%,G-100%);65(C-100%,T-0%);70(C-0%,T-100%);71(G-1%,C-100%);74(A-8%,G-99%);77(A-95%,C-0%,G-18%);80(C-5%,T-95%);81(G-2%,A-98%);82(C-100%,T-0%);83(A-8%,G-2%,C-94%,T-2%);84(C-99%,T-1%);86(C-1%,G-98%,T-1%);107(A-2%,C-99%,T-0%);122(A-1%,G-100%);125(C-0%,T-100%);128(A-12%,G-93%);132(G-98%,A-20%);134(A-1%,C-100%);137(C-2%,G-3%,A-95%,T-0%);143(C-99%,T-1%);149(A-2%,G-98%);158(A-0%,G-100%);161(C-27%,T-93%);164(A-100%,T-0%);167(G-1%,T-100%);170(C-100%,T-0%);173(A-2%,C-2%,G-96%);176(C-98%,T-2%);188(G-24%,T-92%);190(C-98%,T-0%);191(G-98%,T-0%);197(C-0%,T-100%);200(C-0%,G-3%,A-97%);201(A-0%,C-100%);203(C-100%,T-0%);204(A-6%,G-100%);205(C-1%,A-100%);209(C-32%,T-88%);	T;T;A;A ;G;G;G; G;C;G; C;T;C;G ;A;T;A; C;C;C; G;C;G; T;G;G; C;A;C; G;G;T; A;T;C; G;C;T;C ;G;T;A; C;C;G; A;T	T;T;T/A ;A;G;G; G;G;C; G;C;T;C ;G;G/A; T;A;C;C ;C;G;C; G;T;G; A/G;C; A;C;G; G;T/C; A;T;C; G;C;G/ T;C;G;T ;A;C;C; G;A;C/ T
AMPL16 90010	scaffold3	GTTATCG TGCTCAC ATCGGTA AGAT	AGCGTAG GTTGTGT GGTAGC	36(C-4%,T-100%);42(C-100%,T-6%);48(A-25%,G-91%);49(G-0%,A-100%,T-0%);51(C-4%,T-96%);54(C-98%,T-2%);57(C-96%,T-4%);58(A-3%,G-100%);60(G-1%,C-99%,T-1%);61(A-13%,G-98%);63(A-100%,T-1%);69(G-2%,A-100%);74(A-0%,C-2%,T-98%);75(C-97%,T-13%);76(G-5%,C-94%,T-5%);77(G-4%,A-99%,T-0%);78(C-1%,T-100%);79(A-11%,C-2%,T-95%);80(C-3%,T-100%);81(A-0%,C-0%,G-96%,T-7%);83(C-0%,A-100%);85(A-0%,C-0%,G-100%,T-7%);86(A-1%,C-99%);87(C-0%,T-96%);88(G-1%,A-99%);89(A-99%,T-0%);91(A-97%,T-7%);93(C-1%,A-100%,T-0%);94(G-3%,T-96%);99(A-0%,C-100%);100(A-2%,G-0%,C-96%,T-2%);101(A-3%,C-28%,G-92%,T-0%);102(C-2%,T-100%);103(A-1%,G-99%,T-2%);106(C-3%,T-98%);107(A-1%,C-2%,G-97%);108(C-95%,T-4%);120(C-1%,G-86%,T-35%);121(C-0%,T-100%);123(C-100%,T-1%);129(A-0%,C-1%,G-100%);132(C-99%,T-7%);135(C-19%,T-93%);	T;C;G; A;T;C;C ;G;C;G; A;A;T; C;C;A;T ;T;T;G; A;G;C; T;A;A; A;A;T; C;C;G;T ;G;T;G; C;G;T;C ;G;C;T	T;C;G; A;T;C;C ;G;C;G; A;A;T; C/T;C;A ;T;A/T; T;G;A; G;C;T; A;A;A; A;T;C;C ;G/C;T; T;G;G; C;T/G;T ;C;G;C; C/T
AMPL16 90011	scaffold3	TTGATCC AGGAAAT GTCAAAA ACGT	TATCTGT CCATCAA CTGTCAG TACG	36(A-1%,G-100%);37(G-0%,A-100%);38(A-1%,G-100%);39(C-0%,T-100%);47(G-28%,A-90%);53(G-9%,T-99%);55(A-100%,T-2%);65(A-9%,G-99%);67(A-7%,C-100%);76(G-23%,A-95%);81(A-0%,T-100%);83(C-1%,T-100%);85(A-6%,C-98%,T-1%);102(A-99%,T-9%);105(A-0%,G-100%);109(A-0%,T-98%);113(A-0%,C-98%);114(C-0%,G-1%,A-99%);117(C-100%,T-0%);131(A-8%,G-99%);132(A-92%,T-21%);138(C-8%,T-100%);	G;A;G; T;A;T;A ;G;C;A; T;T;C;A ;G;T;C; A;C;G; A;T	G;A;G; T;G/A;T ;A;G;C; A/G;T;T ;C;A;G; T;C;A;C ;G;T/A; T
AMPL16 90012	scaffold3	GCAAGCC AAAGAAA TCCAAAA CG	CCTTCTT GGATTTT GGGGAAG ATTC	44(C-95%,T-21%);47(G-1%,C-100%);50(C-99%,T-2%);53(C-21%,T-95%);59(A-0%,C-100%);77(G-1%,A-100%);95(A-1%,G-100%);110(A-1%,G-100%);113(A-2%,G-98%);129(G-2%,A-98%);132(G-4%,A-100%);139(C-2%,A-98%);143(G-2%,A-99%);146(C-0%,T-100%);160(C-100%,T-	C;C;C;T ;C;A;G; G;G;A; A;A;A; T;C;G; G	C;C;C;T ;C;A;G; G;G;A; A;A;A; T;C;A/ G;G

				0%);161(A-18%,G-97%);176(G-98%,T-2%);		
AMPL16 90013	scaffold5	CGGATTG ATATCGC GAATGTC TTC	TTCTACA CCAATGA CCTATGT GTCC	36(G-2%,A-98%);37(G-1%,A-100%);49(A-0%,G-100%);52(C-100%,T-2%);64(C-0%,T-100%);68(G-4%,T-100%);70(G-6%,A-96%);73(C-1%,G-100%);82(G-1%,A-100%);85(A-0%,C-100%);88(C-38%,T-86%);91(A-23%,G-2%,C-94%,T-0%);94(C-99%,T-6%);97(G-27%,T-92%);106(C-2%,T-98%);112(A-2%,C-98%,T-2%);115(C-98%,T-2%);118(C-2%,T-100%);121(C-100%,T-0%);123(A-2%,G-98%);124(G-0%,A-100%);127(C-2%,G-22%,A-94%);130(G-4%,A-100%);136(C-0%,G-100%);141(G-2%,A-98%);144(G-2%,A-99%);146(G-98%,A-23%);148(C-0%,T-100%);151(C-1%,T-99%);161(C-100%,T-0%);164(G-2%,A-98%);165(C-98%,T-2%);167(G-0%,C-99%,T-0%);170(C-100%,T-0%);175(C-100%,T-0%);194(A-0%,G-100%);197(A-0%,G-100%);206(C-2%,T-98%);209(A-0%,G-100%);212(C-4%,T-96%);215(C-100%,T-1%);221(A-96%,C-0%,G-26%);230(A-1%,C-99%,T-0%);	A;A;G; C;T;T/G ;A;G;A; C;T;C;C ;T;T;C; C;T;C;G ;A;A;A; G;A;A; G;T;T;C ;A;C;C; C;C;G; G;T;G;T ;C;A;C	A;A;G; C;T;T/G ;A;G;A; C;C/T;C ;C;T;T; C;C;T;C ;G;A;A; A;G;A; A;A/G; T;T;C;A ;C;C;C; C;G;G; T;G;T;C ;A/G;C
AMPL16 90015	scaffold6	GTCACCT ATCCTCA CCTACCT GATT	CACCATC AACCTCA TCTTCAA ACAA	55(C-7%,T-96%);66(A-99%,T-3%);111(A-10%,T-95%);114(G-96%,T-7%);152(C-12%,T-94%);159(A-10%,G-95%);160(C-99%,T-3%);166(C-3%,T-99%);229(G-16%,T-93%);	T;A;T;G ;T;G;C; T;T	T;A;T;G ;T;G;C; T;T
AMPL16 90016	scaffold7	CCCATAC TCACTAT TCGTTCT CTCA	TGGTTCC AGGTAAG TTCTTTCT TGA	71(A-0%,T-100%);106(C-100%,T-1%);111(C-4%,G-99%);114(A-1%,G-100%);120(A-0%,G-100%);171(A-3%,G-100%);185(G-1%,A-100%);190(A-15%,G-96%);202(C-3%,T-100%);215(G-1%,A-100%);	T;C;G; G;G;G; A;G;T; A	T;C;G; G;G;G; A;A/G; T;A
AMPL16 90017	scaffold2	GAGACGC ATTTGAG CACCTTT TAG	AATATCT AAGGAAA CGAGGGA GACG	42(C-100%,T-0%);45(G-0%,A-100%);48(C-95%,T-12%);51(G-0%,T-100%);52(C-0%,T-100%);53(C-100%,T-0%);55(C-0%,T-100%);58(G-0%,A-100%);59(G-13%,T-94%);65(A-94%,G-13%);66(C-0%,A-100%);67(A-0%,G-100%);72(G-100%,T-0%);75(A-94%,C-13%);80(A-0%,G-100%);98(A-0%,G-100%);99(A-0%,G-100%);100(C-0%,T-100%);126(A-100%,T-0%);132(C-100%,T-0%);155(C-94%,G-15%);185(C-100%,T-0%);186(C-0%,G-100%);190(A-0%,G-100%);	C;A;C;T ;T;C;T; A;T;A; A;G;G; A;G;A; G;T;G; C;C;C; G;G	C;A;C/T ;T;T;C; T;A;G/T ;G/A;A; G;G;C/ A;G;G; G;T;A; C;G/C; C;G;G
AMPL16 90018	scaffold7	AAGGAAG ATCATTA TAGAGCG ACGG	GTTGGAG TACTAGA TCCCGAT GTTG	37(G-1%,C-100%);39(A-6%,C-99%);40(A-1%,C-4%,T-100%);48(C-98%,T-7%);55(C-99%,T-1%);57(G-0%,T-100%);59(G-12%,A-97%);60(A-0%,G-100%);65(C-1%,T-99%);66(C-11%,A-97%);91(C-23%,T-98%);92(A-13%,G-100%);93(A-1%,G-99%);97(A-3%,C-99%);99(A-13%,G-100%);102(A-2%,G-100%);103(A-1%,C-100%);106(A-1%,G-100%);107(C-0%,G-100%);109(G-0%,A-100%);110(G-0%,A-100%);111(C-11%,T-99%);112(G-0%,A-100%);121(A-9%,G-100%);122(C-100%,T-9%);123(A-87%,T-53%);125(C-100%,T-3%);126(C-100%,T-3%);128(A-2%,G-100%);129(C-0%,T-100%);130(A-4%,G-100%);136(C-37%,T-96%);139(C-100%,T-2%);144(C-53%,T-	C;C;T;C ;C;T;A; G;T;A;T ;G;G;C; G;G;C; G;G;A; A;T;A; G;C;A; C;C;G;T ;G;T;C; T;G;G;T ;T	C;C;T;C ;C;T;A; G;T;A; C/T;G; G;C;G; G;C;G; G;A;A; C/T;A; G;C;A/ T;C;C;G ;T;G;T; C;T/C;G ;G;T;T

				87%);145(A-1%,G-99%);149(G-100%,T-4%);150(C-1%,T-99%);153(C-37%,T-96%);		
AMPL16 90019	scaffold1	CACTACT TAACGAA CATACGA AGCC	GCATTCA CTTCTTTC TATCGCT TGA	51(C-14%,A-98%);55(C-100%,T-0%);61(G-2%,A-98%);62(C-100%,T-0%);65(C-98%,T-14%);76(A-1%,T-99%);82(G-2%,A-98%);84(C-85%,T-24%);86(G-14%,C-98%);124(C-0%,T-100%);128(G-1%,A-100%);129(A-3%,G-98%);130(A-2%,G-99%);138(C-98%,T-2%);145(G-14%,A-98%);148(C-100%,T-0%);154(C-100%,T-0%);155(A-94%,G-14%);159(C-14%,A-98%);169(C-100%,T-2%);171(A-0%,G-100%);182(C-100%,T-0%);189(C-1%,T-100%);214(C-100%,T-0%);220(C-99%,T-4%);222(C-2%,G-98%);223(A-0%,C-99%,T-2%);226(C-2%,A-99%);231(G-16%,C-97%);232(G-18%,C-93%,T-5%);236(C-2%,T-98%);237(G-100%,T-0%);	A;C;A; C;C;T;A ;C;C;T; A;G;G; C;A;C; C;A;A; C;G;C;T ;C;C;G; C;A;C; C;T;G	A;C;A; C;C;T;A ;T;C;T; A;G;G; C;A;C; C;G;A; C;G;C;T ;C;C;G; C;A;C; C;T;G
AMPL16 90020	scaffold1	CCTCTCT TACTTTT AAACGAT CCGC	CGCATAA CATCATA CTTTTCT GTGT	46(G-90%,A-56%);55(A-0%,G-100%);61(C-65%,T-87%);77(C-100%,T-0%);96(A-1%,G-100%);97(A-87%,C-0%,G-64%);98(C-0%,G-0%,A-100%);109(A-0%,T-100%);110(A-100%,T-0%);117(A-11%,C-99%);122(A-5%,C-99%);127(G-0%,A-59%);133(G-5%,T-99%);134(G-0%,A-100%);156(C-12%,T-98%);162(G-0%,A-100%);172(C-1%,A-100%);176(C-1%,T-100%);177(C-0%,G-0%,A-100%);179(C-100%,T-0%);187(G-0%,T-100%);216(G-59%,T-88%);230(A-1%,G-100%);	G/A;G; T/C;C;G ;G/C;C; T;A;C; ;A/-;T;A ;T;A;A; T;A;C;T ;G/T;G	A/G;G; T/C;C;G ;A/G;A; T;A;C; ;A/-;T;A ;T;A;A; T;A;C;T ;T/G;G
AMPL16 90022	scaffold1	GATCTTC TCAAGAA CCAGTCC TACC	GATGAGA GAGGCTG CTTGGTC	36(G-78%,C-75%);46(A-0%,G-100%);51(A-2%,C-98%);54(A-0%,G-100%);57(A-0%,G-100%);60(C-100%,T-0%);66(C-100%,T-1%);78(A-86%,G-66%,T-1%);81(C-88%,A-64%);84(G-2%,C-99%);93(C-51%,T-94%);102(A-1%,G-99%);105(C-2%,T-98%);108(C-91%,T-54%);113(C-2%,T-98%);114(C-15%,T-97%);117(C-2%,T-98%);120(C-5%,T-95%);123(C-100%,T-0%);132(C-38%,T-87%);138(A-1%,C-31%,T-91%);141(C-98%,T-3%);147(C-100%,T-1%);153(A-84%,G-68%);156(C-98%,T-2%);168(C-95%,T-26%);171(A-100%,T-0%);180(C-100%,T-1%);183(C-100%,T-0%);195(C-75%,T-78%);201(A-2%,G-98%);204(A-0%,G-100%);213(C-76%,T-77%);222(C-13%,T-99%);228(C-0%,T-100%);231(C-98%,T-2%);	C/G;G; C;G;G; C;C;A/ G;A/C; C;T/C;G ;T;T/C; T;T;T;T ;C;T;T; C;C;A/ G;C;C; A;C;C;T /C;G;G; C/T;T;T ;C	C/G;G; C;G;G; C;C;G/ A;A/C; C;T;G;T ;C;T;C/ T;T;T;C ;T/C;C/ T;C;C;A /G;C;T/ C;A;C; C;T/C;G ;G;T/C; T;T;C
AMPL16 90025	scaffold2	CATTGGT TCGATTC TGTTCTT ACCC	TCGCAAG AGGATAG TTTACCA CATA	44(C-5%,G-99%);47(C-100%,T-0%);80(C-99%,T-4%);92(C-0%,T-100%);105(C-0%,G-100%);119(G-85%,A-93%);138(A-0%,T-100%);143(C-100%,T-0%);	G;C;C;T ;G;G/A; T;C	G;C;C;T ;G;A/G; T;C
AMPL16 90026	scaffold3	GTAAACA TTGAGGC TATCATA CCGC	GGGTATA TCATTCG CTAGATG CAGA	48(A-1%,G-99%);51(A-1%,G-99%);69(C-99%,T-1%);76(C-100%,T-0%);81(G-1%,A-99%);82(G-1%,T-99%);83(C-0%,T-100%);84(G-1%,T-100%);86(G-16%,A-98%);91(A-1%,C-99%,T-0%);97(A-1%,G-99%);106(A-99%,T-1%);110(G-1%,T-98%);114(A-1%,C-99%);118(C-1%,T-99%);121(C-99%,T-1%);127(G-1%,A-99%);128(C-22%,A-87%);129(G-1%,A-96%);134(G-99%,T-1%);139(G-10%,A-96%);140(G-1%,T-99%);141(A-1%,C-99%,T-0%);142(G-1%,T-99%);145(G-0%,A-100%);148(A-0%,G-	G;G;C; C;A;T;T ;T;A;C; G;A;T; C;T;C;A ;A;A;G; A;T;C;T ;A;G;C; T;G;C; G;G;A; C;T	G;G;C; C;A;T;T ;T;A;C; G;A;T; C;T;C;A ;A;A;G; A;T;C;T ;A;G;C; T;G;C; G;G;A; C;T

				100%);157(C-99%,T-1%);161(C-1%,T-100%);162(A-1%,G-99%);167(C-99%,T-1%);174(A-1%,G-100%);177(A-1%,G-99%);181(G-2%,A-100%);198(A-5%,C-99%);225(A-1%,T-100%);		
AMPL16 90027	scaffold3	TAAAGAA GTACTGA GGCTGAC GAC	AATCAGC TTGTTGG ATTTTCG TAAG	51(A-0%,G-100%);74(G-0%,A-100%);104(G-0%,A-100%);106(C-7%,T-99%);154(A-0%,G-100%);160(A-1%,G-98%);178(G-15%,A-89%);179(A-15%,G-89%);	G;A;A; T;G;G; A;G	G;A;A; T;G;G; A;G
AMPL16 90028	scaffold3	GGAATTG CTCTTGC TACAGGA TTTT	TGAACGT GTATATG GGCTATG TGTA	73(A-9%,T-96%);77(C-0%,T-100%);143(A-0%,C-100%);187(A-98%,T-7%);206(C-100%,T-0%);207(C-100%,T-0%);209(C-1%,A-99%);218(G-0%,C-100%);	T;T;C;A ;C;C;A; C	A/T;T;C ;A/T;C; C;A;C
AMPL16 90029	scaffold3	TTGTTGA CTTTCTC CAGTTCC ATTG	GAAACAT CTCTTCA AAATGGC CAGG	45(C-99%,T-4%);60(A-100%,T-4%);63(G-1%,A-100%);71(G-0%,C-100%);72(G-0%,T-100%);84(A-1%,G-100%);99(C-17%,G-96%);107(A-0%,G-100%);112(C-100%,T-0%);114(G-22%,A-94%);129(G-0%,A-100%);141(A-0%,G-100%);161(C-100%,T-3%);181(A-0%,G-100%);198(C-1%,T-100%);201(A-0%,C-99%,T-4%);202(C-100%,T-0%);211(A-22%,C-93%);214(G-22%,A-93%);217(C-0%,T-100%);221(G-25%,A-92%);222(A-4%,T-100%);223(G-25%,A-92%);227(A-14%,C-20%,T-89%);240(A-25%,T-92%);	C;A;A; C;T;G; G;G;C; A;A;G; C;G;T;C ;C;C;A; T;A;T;A ;T;T	C;A;A; C;T;G; G;G;C; A;A;G; C;G;T;C ;C;C;A; T;A;T;A ;T/C;T
AMPL16 90030	scaffold3	AACTTTG ATGTGTA GCTTATT CGCT	CTTTAAC AGCCGCT TCGCTAC	36(C-3%,T-100%);45(G-0%,C-100%);51(C-0%,T-100%);54(A-2%,C-22%,T-92%);63(C-1%,T-99%);69(C-0%,G-100%);72(A-3%,G-99%);75(G-9%,T-98%);111(C-99%,T-4%);117(A-0%,G-100%);118(C-18%,T-97%);120(A-2%,C-7%,T-98%);123(G-99%,T-7%);127(C-1%,A-99%);130(C-24%,T-90%);131(A-24%,G-93%);132(G-2%,A-90%,T-24%);135(G-100%,T-0%);138(A-100%,T-2%);139(C-100%,T-0%);144(C-98%,T-2%);145(G-0%,A-100%);147(A-0%,C-100%);148(C-100%,T-0%);150(C-0%,A-100%);153(C-95%,T-20%);156(C-0%,T-99%);158(C-1%,T-100%);163(C-2%,T-100%);178(C-100%,T-0%);184(C-94%,T-21%);187(A-7%,C-2%,T-98%);190(C-100%,T-2%);205(G-25%,A-90%,T-0%);209(A-0%,G-100%);215(C-90%,T-25%);	T;C;T;T ;T;G;G; T;C;G;T ;T;G;A; T;G;A; G;A;C; C;A;C; C;A;C;T ;T;T;C; C;T;C;A ;G;C	T;C;T;C /T;T;G; G;T;C; G;C/T;T ;G;A;C/ T;A/G; A/T;G; A;C;C; A;C;C; A;C;T;T ;T;T;C; T/C;T;C ;A/G;G; C/T
AMPL16 90031	scaffold6	CCTCTTG TCATCCT TCAGAAG ATGA	AACTCCA GGCTTGA CAAATCC C	42(C-26%,T-90%);45(C-9%,A-96%);49(G-1%,A-100%);54(C-99%,T-1%);57(A-1%,G-100%);63(G-2%,A-100%);70(A-1%,G-100%);77(G-0%,T-100%);91(A-2%,G-99%);92(C-11%,G-94%);93(C-100%,T-0%);95(A-96%,T-8%);100(A-0%,C-6%,G-98%);103(A-0%,G-100%);106(A-17%,G-95%);132(A-1%,G-100%);133(C-98%,T-5%);144(G-1%,C-99%);148(A-3%,T-99%);149(G-0%,T-100%);150(C-0%,T-100%);155(C-100%,T-0%);158(A-8%,G-97%);159(G-1%,A-100%);164(C-100%,T-0%);169(C-100%,T-0%);180(G-5%,C-99%);183(C-0%,T-100%);184(A-0%,G-100%,T-1%);189(C-100%,T-0%);190(A-2%,G-99%);192(G-0%,A-100%);195(G-2%,A-99%);196(C-100%,T-0%);204(C-14%,T-95%);206(C-0%,G-5%,A-98%);	T;A;A; C;G;A; G;T;G; G;C;A; G;G;G; G;C;C;T ;T;T;C; G;A;C; C;C;T;G ;C;G;A; A;C;T; A	T/C;A; A;C;G; A;G;T; G;G;C; A;G;G; A/G;G; C;G;T;T ;T;C;G; A;C;C; C;T;G;C ;G;A;A; C;C/T;A

AMPL16 90032	scaffold6	ACAAAAG TGAATAC AGCATCC AACA	CTATCTC TGGGCTG CTATGGT TGAT	56(G-2%,T-99%);	T	T
AMPL16 90033	scaffold6	ATTGTAA ATTAGTT GAAGTGC GCCT	CACTGAC AGCTCTC AAGATTG AATT	37(G-17%,C-93%,T-2%);53(A-0%,G-100%);60(C-99%,T-8%);78(C-100%,T-0%);79(C-0%,T-100%);81(C-100%,T-0%);82(A-2%,G-99%);86(C-100%,T-0%);93(C-1%,A-100%);99(C-18%,T-92%);118(G-1%,A-99%);134(A-0%,G-100%);143(G-0%,C-100%);148(C-1%,T-100%);149(A-0%,G-100%);155(A-17%,G-93%);193(A-3%,G-100%);211(C-0%,A-100%);212(A-0%,G-100%);213(C-0%,A-100%);222(A-100%,T-0%);224(A-100%,T-3%);	C;G;C; C;T;C;G ;C;A;T; A;G;C; T;G;G; G;A;G; A;A;A	C;G;C; C;T;C;G ;C;A;T; A;G;C; T;G;G; G;A;G; A;A;A
AMPL16 90034	scaffold7	TCTCAAC GATATCA ATCTTCC CACA	GTCCTGA GACTTCT ACGAGTG AC	64(C-88%,T-45%);73(A-0%,C-100%);74(C-100%,T-0%);84(C-88%,T-43%);88(C-4%,A-100%);116(C-91%,T-35%);120(A-100%,T-0%);136(C-97%,T-7%);137(A-3%,G-99%);140(A-2%,G-100%);146(A-0%,G-100%);147(C-92%,T-35%);154(C-100%,T-0%);173(C-100%,T-1%);182(A-36%,G-1%,C-91%);183(C-100%,T-0%);202(C-100%,T-0%);203(G-41%,A-90%);208(C-0%,A-100%);211(G-0%,A-100%);213(C-100%,T-2%);214(G-100%,T-0%);221(A-38%,G-90%);224(C-87%,T-42%);237(C-40%,T-89%);	C;C;C;C ;A;C;A; C;G;G; G;C;C; C;C;C;C ;A;A;A; C;G;G; C;T	C;C;C;C ;A;C;A; C;G;G; G;C;C; C;C;C;C ;A;A;A; C;G;G; C;T
AMPL16 90035	scaffold7	TAAACTA GGCTCTT GCTCTTG CTAT	ATTTAGT AGTGGTA AAGCGCC GAAA	37(A-0%,C-100%);45(C-100%,T-0%);47(G-0%,A-100%);63(A-6%,G-97%);70(C-99%,T-1%);79(C-6%,T-97%);80(C-100%,T-0%);81(C-0%,T-100%);103(A-97%,T-6%);110(G-3%,A-99%);113(A-1%,C-100%);124(C-0%,T-100%);134(A-6%,C-98%);136(C-99%,T-1%);148(C-96%,T-8%);149(G-18%,A-91%);175(C-1%,T-99%);189(G-100%,T-1%);192(C-100%,T-1%);	C;C;A; G;C;T;C ;T;A;A; C;T;C;C ;C;A;T; G;C	C;C;A; G;C;T;C ;T;A;A; C;T;C;C ;C;A;T; G;C
AMPL16 90036	scaffold8	GTCAATC ATGAAGT GGCTGAA GTG	AGAATAC CTGGACA AGAAAGC TGTC	39(C-95%,T-22%);50(A-0%,G-100%);52(G-1%,A-100%);56(C-14%,T-96%);63(C-100%,T-0%);73(C-0%,A-100%);115(C-0%,T-100%);131(C-23%,T-82%);162(C-10%,T-100%);190(A-8%,C-99%);	C;G;A; T;C;A;T ;T;T;C	C;G;A; T;C;A;T ;-;T;C
AMPL16 90038	scaffold1	TATGACA GGATGCA AAGGAGG TAAT	TGGGTTT CATCACC AAAGTTT TCAA	73(A-0%,G-100%);77(A-13%,G-94%);116(A-14%,G-0%,C-93%);140(A-0%,G-100%);143(G-0%,A-100%);155(G-1%,C-99%);161(G-1%,A-99%);164(G-99%,T-1%);168(C-15%,T-92%);170(A-99%,T-1%);173(G-0%,A-100%);	G;G;C; G;A;C; A;G;T; A;A	G;G/A; A/C;G; A;C;A; G;C/T; A;A
AMPL16 90039	scaffold3	ATCCTAG ATAAATG TCTCCAG TGCC	TGTTATC CATCTGC ATCCTCA TCAT	46(C-14%,T-96%);50(G-4%,A-97%);51(A-14%,C-90%,T-14%);54(A-0%,C-10%,G-98%);60(A-0%,T-100%);61(G-10%,A-99%);83(A-6%,C-97%);99(G-7%,A-99%);141(C-7%,T-97%);165(A-7%,G-97%);167(C-2%,G-99%);176(A-0%,G-100%);	T;A;C; G;T;A; C;A;T; G;G;G	T;A;C/T ;G;T;A; C;G/A; T;G;G; G
AMPL16 90040	scaffold3	GGATTGT TTCCCAT TGTTTGG CT	CTCTTGG TGCGTGT CCTGAC	38(G-3%,C-98%);40(A-15%,G-96%);41(C-97%,T-4%);49(C-11%,T-98%);54(C-3%,T-98%);55(C-0%,T-100%);62(G-2%,A-98%);66(A-98%,T-11%);88(C-16%,T-97%);96(C-100%,T-0%);98(A-98%,T-3%);103(C-100%,T-0%);107(A-0%,G-100%);110(A-98%,T-3%);118(C-98%,T-3%);119(C-11%,A-97%);121(C-2%,G-98%);125(G-15%,A-94%);133(G-3%,T-98%);136(G-3%,T-98%);137(C-0%,T-	C;G;C;T ;T;T;A; A;T;C; A;C;G; A;C;A; G;A;T;T ;T;A;A; G;C;C; G;G;A; C;C;A	C;G;C;T ;T;T;A; A;T;C; A;C;G; A;C;A; G;A;T;T ;T;A;A; G;C;C; G;G;A; C;C;A

				100%);148(G-2%,A-98%);150(G-2%,A-98%);158(A-2%,G-100%);159(A-3%,C-98%);160(C-98%,T-2%);163(C-2%,G-98%);167(A-2%,G-100%);172(A-100%,T-0%);173(A-1%,C-100%);175(G-2%,C-98%);176(C-1%,A-100%);		
AMPL16 90041	scaffold4	AAGAGGA AGGAAAA ACGCGTG G	CCATTTC TGACCAA GCAAGAA ACAG	48(A-3%,G-100%);58(A-21%,C-89%);75(A-9%,G-3%,C-93%);80(C-5%,G-99%);83(C-22%,T-97%);85(G-18%,A-98%);88(G-0%,A-100%);90(C-28%,G-3%,A-89%,T-0%);97(G-0%,A-100%);98(G-0%,T-100%);101(C-99%,T-3%);102(A-8%,C-0%,G-98%);105(C-0%,G-100%);108(C-0%,T-100%);109(A-0%,C-100%);111(G-1%,C-99%);113(C-100%,T-0%);114(A-0%,T-100%);117(C-1%,G-4%,A-98%);125(G-0%,A-100%);128(G-100%,T-2%);140(G-1%,A-100%);141(G-1%,C-99%);143(G-1%,A-100%);144(A-14%,C-97%);145(A-0%,C-2%,G-99%,T-1%);148(C-100%,T-1%);149(G-23%,A-98%);155(C-100%,T-1%);164(C-99%,T-1%);166(A-26%,C-11%,T-83%);167(A-8%,G-100%);168(G-0%,A-100%);172(A-1%,G-97%);174(A-3%,C-89%,T-24%);176(G-0%,A-100%);177(A-0%,G-100%);178(C-100%,T-4%);179(G-99%,T-1%);181(G-0%,C-99%,T-1%);183(A-2%,G-99%,T-1%);193(G-100%,T-0%);198(C-100%,T-0%);199(C-100%,T-0%);	G;C;C; G;T;A; A;A;A; T;C;G; G;T;C;C ;C;T;A; A;G;A; C;A;C; G;C;A; C;C;T;G ;A;G;C; A;G;C; G;C;G; G;C;C	G;A;A; G;T;A; A;C;A; T;C;G; G;T;C;C ;C;T;A; A;G;A; C;A;C; G;C;A; C;C;A; G;A;G; T;A;G; C;G;C; G;G;C; C
AMPL16 90042	scaffold4	TATCAAC TCCAAAG AATATTG CGCC	GGCTGGA TTGGATA TGATTTT CTGG	36(C-96%,T-9%);40(C-0%,A-100%);41(A-0%,T-100%);44(C-0%,T-100%);45(A-4%,C-97%);46(A-2%,G-99%);47(A-1%,G-8%,C-92%,T-0%);48(G-17%,A-90%);51(A-1%,T-99%);52(C-100%,T-0%);57(A-10%,C-90%);58(A-1%,C-0%,G-1%,T-96%);60(A-2%,C-0%,G-0%,T-96%);61(C-93%,T-8%);63(G-0%,A-100%);65(C-4%,A-93%,T-1%);67(G-9%,A-92%);74(G-0%,A-100%);79(G-1%,A-99%);80(G-3%,A-99%);86(A-8%,G-94%);90(A-0%,T-100%);114(C-0%,G-100%);119(C-4%,T-99%);135(C-13%,T-92%);136(A-0%,G-100%);137(C-91%,T-14%);144(A-0%,G-100%);152(C-100%,T-0%);153(C-99%,T-3%);155(G-0%,C-99%);	C;A;T;T ;C;G;C; A;T;C;C ;T;T;C; A;A;A; A;A;A; G;T;G;T ;T;G;C; G;C;C; C	C;A;T;T ;C;G;C; A;T;C;C ;T;T;C; A;A;A; A;A;A; G;T;G;T ;T;G;C; G;C;C; C
AMPL16 90043	scaffold6	CACTCCA GCTTGTC TTATTCA CATC	AATATTG GCGAGGA GTTTGTG AATG	40(G-100%,T-1%);41(C-100%,T-1%);50(C-100%,T-0%);54(A-3%,G-99%);60(A-24%,G-90%);72(C-24%,T-90%);78(C-8%,T-100%);80(A-23%,T-90%);92(A-16%,G-96%);93(G-100%,T-0%);94(C-96%,T-16%);96(G-16%,A-96%);104(G-0%,A-100%);105(C-8%,A-100%);108(C-100%,T-0%);109(G-4%,A-99%);116(C-96%,T-9%);129(G-0%,A-100%);132(C-1%,T-100%);143(G-0%,T-100%);149(A-0%,C-100%);160(G-10%,C-98%);175(C-2%,A-100%);178(G-2%,A-100%);182(A-10%,G-98%);185(G-1%,A-100%);189(G-8%,A-100%);190(A-10%,G-98%);208(G-3%,A-99%);	G;C;C; G;G;T;T ;T;G;G; C;A;A; A;C;A; C;A;T;T ;C;C;A; A;G;A; A;G;A	G;C;C; G;A/G; T/C;T/C ;A/T;G/ A;G;T/ C;A/G; A;C/A; C;A;C; A;T;T;C ;C/G;A; A;A/G; A;A/G; G/A;A
AMPL16 90044	scaffold6	GCACAAT AAGAGCT TTCGATC GTTA	TATTGTT CTCTGCT CTCATTT CCGA	40(C-0%,T-100%);41(C-20%,T-97%);60(A-0%,G-100%);67(G-1%,A-100%);74(C-31%,T-88%);111(C-31%,T-88%);134(C-1%,T-99%);141(C-100%,T-1%);143(G-0%,A-100%);146(C-92%,T-25%);163(C-97%,T-	T;T;G;A ;T;T;T; C;A;C; C;C;T	T;T/C;G ;A;T/C; C/T;T;C ;A;C;C/ T;C;T

AMPL16 90045	scaffold6	TCCCAAG GATACGT AATATAC CGTG	ATAGTAC TTCACAT ACCGAGC AGAG	20%);164(A-16%,C-97%);169(C-25%,T-92%); 57(A-99%,T-1%);61(G-0%,A-100%);66(C- 1%,T-99%);83(C-0%,G-100%);93(C-99%,T- 4%);99(G-0%,A-100%);100(A-1%,C- 99%);109(A-0%,G-100%);117(G-4%,A- 99%);123(G-13%,A-94%,T-0%);134(A-0%,C- 100%);140(A-0%,G-100%);143(C-4%,A- 99%);149(C-100%,T-0%);152(C-100%,T- 0%);155(A-4%,T-99%);166(C-0%,T- 100%);168(C-100%,T-0%);205(A-0%,G- 100%);213(C-4%,G-99%);	A;A;T; G;C;A; C;G;A; A;C;C; A;C;C;T ;T;C;G; G	A;A;T; G;C;A; C;G;A; A;C;C; A;C;C;T ;T;C;G; G
AMPL16 90047	scaffold7	AAGGGAA TACATAT CAATACC GCCA	GACGGAC CATACAA TGTGTGT AAAT	39(A-4%,G-96%);53(G-5%,A-96%);66(C-4%,T- 97%);69(G-100%,T-1%);94(A-5%,C- 96%);114(C-41%,G-91%);145(G-2%,A- 99%);153(C-1%,T-99%);183(G-99%,T-2%);	G;A;T; G;C;G; A;T;G	G;A;T; G;C;G; A;T;G
AMPL16 90048	scaffold3	CTAGTCG ACAAGGT TCGAAGA GTAA	CTGGTGG GAAGAAG GAATTTT ATCG	47(C-2%,T-99%);53(A-1%,G-100%);55(C- 98%,T-14%);57(C-1%,T-100%);72(A-100%,T- 0%);97(G-100%,T-0%);109(C-93%,T- 23%);113(A-20%,T-94%);120(G-15%,A- 98%);124(C-2%,A-100%);129(C-0%,T- 100%);131(G-99%,T-3%);132(C-3%,T- 99%);144(C-21%,T-95%);149(G-1%,A- 100%);150(A-15%,C-98%);151(A-1%,G- 100%);152(C-99%,T-3%);158(G-1%,A- 100%);166(C-3%,T-100%);174(C-0%,T- 100%);178(C-100%,T-0%);180(G-20%,A- 93%);184(G-3%,A-100%);192(C-92%,T- 21%);196(A-21%,C-93%);200(A-1%,G- 100%);206(G-1%,C-100%);208(A-5%,G- 93%);209(A-97%,T-9%);212(C-1%,T-99%);	T;G;C;T ;A;G;C; T;A;A;T ;G;T;T; A;C;G; C;A;T;T ;C;A;A; C;C;G; C;G;A; T	T;G;C/T ;T;A;G; T/C;T/A ;A/G;A; T;G;T;T /C;A;A/ C;G;C; A;T;T;C ;A/G;A; T/C;C/A ;G;C;- /G;A;T
AMPL16 90049	scaffold3	GAAATAG ACACTGC CGTCAAC TTC	TCGATAA GCAAGTT GGTCTCC AA	40(C-100%,T-6%);42(A-100%,T-0%);43(G- 0%,T-100%);46(A-0%,G-100%);58(G-2%,A- 100%);61(A-0%,G-15%,T-93%);67(G-25%,A- 93%);73(A-0%,G-100%);76(G-1%,A- 99%);79(A-5%,G-98%);88(G-5%,A-95%);91(A- 3%,G-99%);92(C-100%,T-0%);94(C-2%,T- 98%);99(C-98%,T-2%);100(G-5%,T- 99%);109(G-0%,A-100%);124(C-0%,G- 100%);129(C-100%,T-0%);136(G-0%,A- 100%);147(A-0%,G-100%);148(G-100%,T- 0%);160(G-0%,A-100%);169(G-1%,A- 99%);171(C-7%,A-100%);175(G-2%,C-94%,T- 23%);181(A-1%,C-100%);184(A-12%,G- 99%);187(G-1%,A-100%);190(C-95%,T- 5%);196(G-2%,A-98%);199(A-0%,G- 100%);202(C-1%,T-100%);211(C-2%,T- 100%);214(G-0%,A-100%);222(A-100%,T-0%);	C;A;T; G;A;T; A;G;A; G;A;G; C;T;C;T ;A;G;C; A;G;G; A;A;A; C;C;G; A;C;A; G;T;T;A ;A	C;A;T; G;A;T; A;G;A; G;A;G; C;T;C;T ;A;G;C; A;G;G; A;A;A; T/C;C;A /G;A;C; A;G;T;T ;A;A
AMPL16 90050	scaffold3	GTATTTT GCTATAG TCTGAAG GGCC	CGATCCT AATACGG ACCAAAT GATG	38(A-2%,G-99%);39(A-4%,T-98%);41(C- 99%,T-1%);44(G-4%,A-99%);48(A-93%,T- 19%);50(A-1%,G-99%);51(C-100%,T-2%);52(C- 0%,T-100%);53(A-4%,G-97%);61(C-100%,T- 0%);63(G-32%,A-85%);64(A-1%,G-99%);73(A- 1%,C-99%,T-2%);74(A-0%,G-100%);76(G- 0%,A-100%);102(C-100%,T-6%);104(G-0%,C- 100%);107(C-13%,G-96%);108(C-100%,T- 0%);110(C-100%,T-0%);113(C-0%,G-0%,T- 99%);116(A-0%,C-0%,G-100%);117(A-100%,T- 0%);118(G-2%,C-98%,T-0%);122(A-0%,G- 100%);123(C-25%,T-93%);125(A-9%,G- 100%);136(G-2%,C-100%);140(C-2%,T- 98%);143(A-0%,G-97%,T-3%);149(C-100%,T- 0%);156(G-1%,T-99%);164(C-90%,T-	G;T;C; A;A;G; C;T;G;C ;A;G;C; G;A;C; C;G;C; C;T;G; A;C;G; T;G;C;T ;G;C;T; C;G;G; G;G;G; A;T;T	G;T;C; A;T/A; G;C;T; G;C;A/ G;G;C; G;A;C/ T;C;G;C ;C;T;G; A;C;G; C/T;G/ A;C;T; G;C;T;T /C;G;G; G;G;G; A;T/-;T

				25%);166(A-0%,G-100%);173(C-3%,G-100%);174(A-1%,G-99%);181(A-8%,G-97%);182(A-2%,G-98%);187(A-99%,T-0%);189(A-1%,T-92%);191(A-1%,T-95%);		
AMPL16 90051	scaffold3	GAATAGT TGAGCAC ATGAGCA TGAG	TATCACT ATCGTCT TCGGACT TGTC	49(C-98%,T-2%);50(C-100%,T-0%);53(C-100%,T-0%);55(C-7%,A-98%);56(C-100%,T-0%);58(A-100%,T-0%);59(A-4%,G-100%);61(G-0%,A-100%);67(C-0%,T-100%);69(C-24%,G-0%,A-91%,T-2%);70(C-0%,G-3%,A-98%);73(C-2%,G-98%,T-0%);74(G-0%,A-100%);77(C-1%,T-100%);84(C-1%,T-99%);94(C-0%,T-100%);102(C-3%,T-97%);105(A-3%,G-97%);111(C-2%,T-98%);112(G-1%,A-99%);117(G-3%,A-97%,T-4%);119(G-3%,T-97%);120(C-100%,T-0%);129(C-99%,T-2%);131(A-0%,T-100%);137(C-0%,T-100%);141(A-4%,C-100%);147(C-99%,T-7%);150(G-3%,A-97%);153(G-7%,A-99%);162(A-0%,G-100%);164(G-100%,T-0%);171(G-0%,A-100%);176(A-1%,G-100%);180(G-1%,A-100%);183(C-0%,A-100%);186(C-21%,T-94%);187(A-0%,G-100%);192(C-2%,T-100%);198(C-16%,T-97%);199(G-87%,T-32%);203(A-0%,T-100%);207(G-32%,A-87%);210(C-3%,T-98%);211(C-0%,T-100%);213(A-1%,G-99%);216(A-0%,C-0%,T-99%);217(C-100%,T-0%);225(A-3%,G-97%);228(A-100%,T-0%);236(C-0%,G-100%);237(A-0%,G-100%);	C;C;C; A;C;A; G;A;T; A;A;G; A;T;T;T ;T;G;T; A;A;T; C;C;T;T ;C;C;A; A;G;G; A;G;A; A;T;G;T ;T;G;T; A;T;T;G ;T;C;G; A;G;G	C;C;C; A;C;A; G;A;T; C/A;A; G;A;T;T ;T;T;G; T;A;A;T ;C;C;T; T;C;C;A ;A;G;G; A;G;A; A;T;G;T ;T/C;T/ G;T;G/ A;T;T;G ;T;C;G; A;G;G
AMPL16 90052	scaffold3	TCCTACG CTGCTTA TAGGTTT ATGT	CCAATGA CGGTACT ATGATTC ATGC	39(C-98%,T-2%);115(C-100%,T-0%);161(C-2%,T-98%);	C;C;T	C;C;T
AMPL16 90053	scaffold4	CAAAATG TCTGTTA CGCTCAG TCAT	TTTTTAG CTCTGCT CCCTTGA ATTC	39(C-99%,T-3%);96(A-88%,G-30%);	C;A	C;A/G
AMPL16 90054	scaffold6	CTCACAA TCCGACG TCGTTTT AG	GATAACC TCCCCAA CGTCTTC TC	34(A-11%,C-99%);37(C-10%,G-99%,T-5%);39(C-0%,T-100%);55(C-9%,G-96%);59(A-0%,G-100%);73(A-1%,G-99%);74(C-1%,T-99%);82(G-100%,T-1%);83(A-1%,G-99%);95(G-100%,T-4%);97(G-1%,C-100%);109(A-2%,G-99%);121(G-1%,A-99%);127(G-100%,T-0%);133(A-1%,T-99%);134(C-1%,T-100%);139(A-18%,G-9%,T-94%);142(C-25%,T-94%);145(G-15%,A-98%);154(C-21%,T-96%);160(A-1%,G-100%);166(C-23%,G-93%,T-0%);169(A-12%,G-99%);175(C-11%,T-98%);190(A-1%,G-99%);192(C-99%,T-1%);202(C-1%,T-100%);208(A-0%,G-100%);211(A-6%,G-99%);213(G-10%,A-99%);217(A-0%,T-100%);219(G-100%,T-0%);220(A-10%,G-99%);223(A-22%,G-95%);225(C-2%,T-100%);235(A-1%,G-99%);241(A-0%,C-100%);	C;G;T; G;G;G; T;G;G; G;C;G; A;G;T;T ;T;T;A; T;G;G; G;T;G; C;T;G; G;A;T; G;G;G; T;G;C	A/C;G/ C;T;G; G;G;T; G;G;G; C;G;A; G;T;T;T /A;T/C; G/A;C/ T;G;G/ C;A/G; T/C;G;C ;T;G;G; A/G;T; G;A/G; A/G;T; G;C

AMPL16 90055	scaffold6	ATGATCT ACGGTGT CTACGAA AACA	GGAAGTC GTCCAAC TTGAAGG TATC	39(C-97%,T-3%);45(A-2%,G-98%);51(A-2%,C-9%,G-99%);66(C-99%,T-10%);72(C-11%,T-96%);78(G-2%,T-98%);82(A-22%,G-94%);86(A-2%,T-98%);87(C-3%,T-99%);88(C-2%,T-98%);89(A-2%,G-98%);92(C-98%,T-4%);93(A-10%,G-99%,T-0%);99(C-98%,T-2%);100(A-5%,G-99%);103(G-10%,T-99%);104(C-1%,T-99%);107(A-100%,T-1%);108(A-0%,G-3%,T-96%);109(C-100%,T-0%);113(A-1%,C-97%,T-3%);115(G-4%,A-96%);116(G-0%,C-96%,T-4%);119(A-0%,T-100%);128(C-96%,T-13%);134(C-28%,A-90%);137(A-0%,G-100%);143(A-1%,G-100%);152(C-99%,T-1%);155(C-100%,T-0%);158(C-99%,T-1%);164(G-0%,A-100%);167(G-0%,T-100%);170(C-2%,T-98%);173(G-0%,C-100%);176(C-4%,T-96%);179(C-0%,T-100%);194(C-16%,G-94%,T-2%);196(G-4%,A-96%);200(C-1%,G-100%);	C;G;G; C;T;T;G ;T;T;T; G;C;G; C;G;T;T ;A;T;A; C;A;C;T ;C;A;G; G;C;C; C;A;T;T ;C;T;T; G;A;G	C;G;G/ C;C;T;T ;G/A;T; T;T;G;C ;G;C;G; T;T;A;T ;C;C;A; C;T;C;C /A;G;G; C;C;C; A;T;T;C ;T;T;G; A;G
AMPL16 90056	scaffold7	GCGTCGT TGATCCT CTTATAA GTTG	TTGAACG TTGAGCT GCTAGAG TAAA	53(C-98%,T-13%);60(C-100%,T-0%);73(A-0%,G-100%);77(C-100%,T-3%);92(C-98%,T-6%);113(G-99%,T-3%);116(G-0%,A-100%);118(G-0%,T-100%);130(C-100%,T-4%);133(C-18%,G-94%);146(C-0%,T-100%);155(A-100%,T-1%);167(C-6%,T-98%);173(G-24%,C-91%);176(A-0%,C-100%);184(A-0%,G-100%);191(C-6%,G-3%,A-99%);192(A-94%,T-18%);193(G-100%,T-4%);195(C-99%,T-9%);	C;C;G; C;C;G; A;T;C; G;T;A;T ;C;C;G; A;A;G; C	C/T;C;G ;C;C;G; A;T;C; G;T;A;T ;G/C;C; G;A;A; G;T/C
AMPL16 90057	scaffold7	GACTCCA TACCTAT CTCCTTC GAC	TCATCCA CAATGCA TATCCTA TGGT	58(C-99%,T-5%);90(G-10%,A-97%);93(C-10%,T-97%);105(A-4%,C-100%);123(C-0%,A-100%);146(G-10%,A-99%);151(A-4%,G-97%);153(C-3%,A-99%,T-4%);158(A-7%,G-98%);177(C-98%,T-6%);188(G-0%,A-100%);191(G-1%,C-100%);	C;A;T;C ;A;A;G; A;G;C; A;C	C;A;T;C ;A;A/G; G;A;G; C;A;C
AMPL16 90058	scaffold7	AATGCGA AGGCGTT AAAGATG AATC	ACAGCGC TTCTTCA AATTTCT CATT	43(A-1%,G-100%);45(A-0%,G-100%);46(A-3%,G-99%);51(A-4%,T-98%);61(C-6%,A-98%);62(G-2%,C-100%);64(C-0%,T-100%);67(G-9%,A-96%);75(A-93%,T-11%);79(C-1%,G-100%);86(A-11%,G-94%);89(C-100%,T-0%);92(A-4%,C-98%);100(C-2%,T-100%);110(G-3%,C-99%);111(G-97%,T-9%);113(C-3%,T-99%);116(G-0%,C-100%);123(C-97%,T-9%);127(A-3%,T-99%);137(C-9%,G-0%,A-96%);139(A-1%,G-100%);	G;G;G; T;A;C;T ;A;A;G; G;C;C;T ;C;G;T; C;C;T;A ;G	G;G;G; T;A;C;T ;A;A;G; G;C;C;T ;C;G;T; C;C;T;A ;G
AMPL16 90059	scaffold7	GTTCAAT TTGGTCA GTCTCAG AACT	CTACGAG TTGAGAG AAGATGG AACG	49(C-99%,T-15%);55(C-16%,T-99%);64(C-15%,T-99%);69(G-6%,A-100%);70(C-0%,G-100%);79(C-15%,A-99%);82(A-15%,G-99%);88(G-99%,T-15%);100(G-4%,A-100%);109(C-99%,T-15%);112(A-15%,G-99%);115(G-21%,A-93%);122(C-100%,T-6%);124(C-15%,G-0%,A-99%);127(A-15%,G-99%);133(C-15%,T-99%);139(A-19%,G-96%);145(C-15%,A-99%);148(G-15%,A-99%);157(C-99%,T-15%);166(G-99%,T-15%);178(C-15%,T-99%);193(G-15%,T-99%);202(C-99%,T-15%);226(C-15%,A-99%);232(G-0%,A-100%);235(C-15%,T-99%);	C;T;T;A ;G;A;G; G;A;C; G;A;G; A;G;T; G;A;A; C;G;T;T ;C;A;A; T	C/T;C/T ;C/T;A; G;A/C; G/A;G/ T;A;C/T ;A/G;A/ G;C;A/ C;A/G; T/C;A/ G;A/C; G/A;C/ T/G;T /C;G/T; T/C;A/C ;A;C/T

AMPL16 90060	scaffold1	TCTACTT TGGAGGA ATGAAGA ACCC	TACATTT GTTGAGA GCGAGAA GAGA	72(C-100%,T-0%);73(C-1%,G-100%);101(A-4%,T-96%);102(C-97%,T-14%);107(C-0%,A-100%);115(G-0%,A-100%);121(A-0%,T-98%);123(G-1%,A-98%);125(C-2%,A-98%);126(C-100%,T-0%);127(A-2%,C-98%);128(A-40%,C-29%,T-84%);130(C-92%,T-40%);141(A-2%,T-96%);142(A-2%,C-98%);161(C-100%,T-1%);168(C-2%,T-98%);178(C-98%,T-2%);180(A-2%,G-98%);181(C-98%,T-2%);183(A-1%,C-0%,G-99%);184(G-0%,A-100%);192(C-0%,T-100%);195(G-100%,T-0%);198(C-0%,T-100%);201(C-100%,T-1%);204(C-74%,T-79%);210(A-2%,C-98%);214(G-7%,A-100%);225(G-0%,T-100%);228(C-0%,T-100%);	C;G;T;C ;A;A;T; A;A;C; C;T/A;C /T;T;C; C;T;C;G ;C;G;A; T;G;T;C ;T/C;C; A;T;T	C;G;T;C ;A;A;T; A;A;C; C;C/T;C ;T;C;C; T;C;G;C ;G;A;T; G;T;C;C /T;C;A; T;T
AMPL16 90062	scaffold3	CTTTCTTT GTTGAGG ACATCAC AGG	ACTCACT TAATACC TTAGGAT GTGGA	44(C-9%,G-97%);47(A-0%,G-0%,C-97%);48(G-8%,A-98%);49(A-0%,G-3%,T-98%);50(A-12%,T-96%);53(A-9%,G-97%);56(C-6%,A-95%,T-8%);105(A-2%,G-98%);120(G-0%,A-100%);140(G-7%,T-99%);166(C-0%,T-100%);167(C-13%,G-6%,T-92%);169(C-3%,G-8%,A-97%);171(A-1%,G-100%);172(A-3%,T-98%);183(C-99%,T-1%);189(C-12%,T-96%);195(C-7%,T-99%);200(G-17%,A-93%);201(C-92%,T-18%);220(G-0%,T-100%);221(A-1%,T-99%);222(C-1%,T-99%);227(G-0%,A-100%);228(C-5%,T-97%);	G;C;A; T;T;G;A ;G;A;T; T;T;A;G ;T;C;T; T;A;C;T ;T;T;A; T	G;C;A; T;T;G;A ;G;A;T; T;T;A;G ;T;C;T; T;A;C;T ;T;T;A; T
AMPL16 90063	scaffold3	GGCCGTA CTCTTTTC TCAATAG GAT	CTTAGCC ATCTCCT CAGCCTT TTT	71(C-99%,T-1%);83(C-96%,T-5%);101(G-0%,T-100%);149(A-5%,T-96%);167(G-96%,T-5%);179(G-2%,A-99%);185(C-100%,T-0%);188(C-2%,T-99%);190(G-2%,A-99%);191(C-2%,A-99%);194(C-4%,T-96%);204(A-1%,G-100%);206(C-1%,T-100%);212(C-2%,G-97%,T-2%);214(G-2%,A-98%);215(A-1%,C-0%,T-99%);218(G-5%,A-96%);221(A-4%,T-97%);222(C-1%,G-99%);227(G-2%,A-98%);234(G-1%,A-99%);	C;C;T;T ;G;A;C; T;A;A;T ;G;T;G; A;T;A;T ;G;A;A	C;C;T;T ;G;A;C; T;A;A;T ;G;T;G; A;T;A;T ;G;A;A
AMPL16 90064	scaffold3	CTGTCTA ACGGTGT TGACTCA AAAT	CAGACCA CAGCTCG TAATGTA TAGA	37(C-4%,T-99%);63(C-100%,T-1%);69(C-1%,T-100%);75(C-100%,T-0%);90(G-1%,A-100%);96(C-2%,T-99%);99(A-1%,G-100%);102(C-19%,T-95%);108(G-2%,A-98%);114(C-100%,T-0%);132(C-0%,T-100%);137(A-5%,G-100%);140(A-98%,T-2%);144(G-4%,C-86%,T-29%);146(A-1%,G-99%);147(G-6%,C-98%);148(A-2%,G-98%);152(A-1%,G-100%);153(C-1%,G-99%);156(C-2%,T-98%);157(A-0%,G-100%);158(C-1%,T-100%);159(G-8%,A-100%,T-0%);162(A-0%,G-100%);164(A-20%,C-7%,G-1%,T-90%);166(A-5%,T-100%);167(C-0%,T-100%);168(C-1%,G-1%,A-99%,T-1%);170(C-4%,T-100%);171(C-1%,G-99%,T-1%);172(C-0%,G-2%,A-99%);173(C-15%,T-94%);183(C-97%,T-9%);189(A-0%,G-100%);195(A-0%,T-100%);201(A-0%,G-100%);220(G-0%,A-100%);228(C-0%,T-100%);	T;C;T;C ;A;T;G; T;A;C;T ;G;A;C; G;C;G; G;G;T; G;T;A; G;T;T;T ;A;T;G; A;T;C; G;T;G; A;T	T;C;T;C ;A;T;G; T;A;C;T ;G;A;T/ C;G;C; G;G;G; T;G;T;G /A;G;A/ T;T;T;A ;T;G;A; T;C;G;T ;G;A;T
AMPL16 90065	scaffold3	TAGTCAT TTCTGCT GATCCTT GTGT	TACTTCA TGCATAA TCTGAGG GGTC	43(A-1%,G-99%);48(C-99%,T-6%);50(A-14%,G-96%);57(G-6%,T-99%);67(G-21%,A-92%);69(C-99%,T-1%);70(A-1%,G-99%);76(A-1%,G-99%);84(A-0%,G-100%);94(A-1%,G-99%);103(C-99%,T-1%);109(A-0%,T-100%);111(C-10%,G-1%,T-98%);	G;C;G; T;A;C; G;G;G; G;C;T;T	G;C;G; T;A;C; G;G;G; G;C;T;T

AMPL16 90066	scaffold3	GAGAAGG AGAGAGA GATCGAG AAGG	AAACTGT AGTCTTA TGAATGC CTCG	36(C-0%,T-100%);37(A-1%,G-100%);38(A-0%,C-100%);40(G-0%,T-100%);42(A-0%,G-100%,T-0%);45(G-0%,A-100%);54(C-10%,G-99%);56(C-6%,G-99%);63(G-27%,C-91%);69(A-0%,G-100%);87(A-3%,C-0%,T-99%);91(A-0%,G-100%,T-0%);93(G-0%,C-100%);99(A-0%,G-100%);100(C-0%,T-100%);101(A-0%,C-100%);114(A-0%,T-100%);123(C-100%,T-0%);125(A-100%,T-0%);126(C-94%,T-26%);127(G-0%,T-100%);129(C-100%,T-1%);134(C-0%,G-100%);143(A-0%,G-100%);145(G-0%,A-100%);148(A-1%,G-100%);152(C-100%,T-0%);153(G-0%,A-100%);159(C-27%,T-92%);162(C-0%,T-100%);167(G-100%,T-0%);168(C-100%,T-0%);169(C-0%,A-100%);181(G-0%,A-100%);190(G-0%,A-100%);191(A-0%,T-100%);194(G-0%,A-100%);196(A-1%,G-100%);198(A-4%,C-100%);199(G-0%,C-100%);200(A-99%,T-3%);208(C-5%,T-90%);209(A-2%,T-94%);214(C-0%,T-94%);217(C-100%,T-0%);226(A-0%,T-100%);236(C-100%,T-0%);	T;G;C;T ;G;A;G; G;C;G; T;G;C; G;T;C;T ;C;A;C; T;C;G; G;A;G; C;A;T;T ;G;C;A; A;A;T; A;G;C; C;A;T;T ;T;C;T; C	T;G;C;T ;G;A;C/ G;G;C/ G;G;T; G;C;G; T;C;T;C ;A;T/C; T;C;G; G;A;G; C;A;T/C ;T;G;C; A;A;A; T;A;G; C;C;A;- /T;T/-; /T;C;T; C
AMPL16 90067	scaffold3	ATCCATA TCTACAC AAACAAC CCCA	CGAGATT ACAGCTC CTCACTT CTAA	36(A-3%,C-97%,T-0%);77(A-2%,G-98%);144(A-3%,C-97%);	C;G;C	C;G;C
AMPL16 90068	scaffold4	GATAATA CGTACAG GATCGTG CACG	AAGCTAC GAACAAA AAGAAAC AGGT	60(G-8%,A-98%);61(C-100%,T-0%);68(C-99%,T-4%);76(C-10%,T-95%);77(C-95%,T-10%);125(A-8%,G-99%);155(C-99%,T-4%);156(C-99%,T-3%);187(C-10%,T-95%);190(A-95%,T-10%);	A;C;C;T ;C;G;C; C;T;A	A;C;C;T ;C;G;C; C;T;A
AMPL16 90069	scaffold6	CTTTGGC TGCTGCA ATAGAAT CATA	CAACAAA AATCTGC CGAAGAA AAGG	43(A-7%,C-100%);52(A-10%,C-100%);53(C-100%,T-0%);59(A-3%,C-16%,T-96%);62(A-2%,T-100%);68(G-99%,T-4%);86(G-7%,A-100%);92(C-9%,T-100%);95(A-0%,C-100%);108(A-0%,G-100%);118(C-1%,G-100%);125(G-4%,A-100%);129(A-4%,G-100%);131(C-1%,T-100%);138(C-4%,A-100%);158(C-100%,T-3%);167(C-28%,T-95%);168(C-100%,T-0%);170(C-4%,A-100%);172(C-0%,T-100%);181(G-2%,C-100%);201(A-1%,G-100%);205(C-2%,T-100%);	C;C;C;T ;T;G;A; T;C;G; G;A;G; T;A;C;T ;C;A;T; C;G;T	C;C;C;T ;T;G;A; C/T;C;G ;G;A;G; T;A;C;T /C;C;A; T;C;G;T
AMPL16 90070	scaffold6	CATGACC ACGTTCC GGGATG	CGAGATG GCCAATA TCAAGAT TGTA	53(C-100%,T-0%);120(C-95%,T-5%);122(C-99%,T-2%);126(A-0%,G-100%);147(C-96%,T-5%);	C;C;C; G;C	C;C;C; G;C
AMPL16 90071	scaffold7	GCTAACG ATATCCA GTGTTTT TCCA	CTTTCCT ACTCGTC CGAACAG TTA	37(G-5%,A-97%);43(G-100%,T-0%);46(A-99%,T-1%);68(A-3%,G-98%);71(C-1%,T-100%);87(A-3%,G-98%);91(G-1%,C-100%);102(A-1%,C-100%);127(G-0%,T-100%);128(G-99%,T-1%);139(C-100%,T-0%);161(A-0%,G-100%);187(C-1%,T-100%);	A;G;A; G;T;G; C;C;T;G ;C;G;T	A;G;A; G;T;G; C;C;T;G ;C;G;T
AMPL16 90072	scaffold7	GGTGGAA GACGGAG ACAAGTA TTC	TGTCTTT CTCAAGT ATTCAAG CACA	57(C-100%,T-2%);58(A-2%,G-100%);62(G-100%,T-0%);76(A-0%,C-100%);78(C-0%,T-100%);106(C-100%,T-0%);115(G-2%,A-99%);147(A-0%,G-100%);152(C-0%,T-100%);165(C-0%,T-100%);168(A-100%,T-2%);170(A-2%,C-100%);173(A-0%,T-100%);	C;G;G; C;T;C;A ;G;T;T; A;C;T	C;G;G; C;T;C;A ;G;T;T; A;C;T
AMPL16 90073	scaffold8	CATTGAC AGGAACA GCAACAC	GAGAAAA AGTTCTA TGAACCA	49(G-0%,A-100%);56(A-89%,T-29%);74(G-11%,A-96%);85(A-26%,G-89%);86(A-26%,G-89%);136(C-20%,T-93%);137(A-1%,G-	A;A;A; G;G;T; G;A;A	A;T/A; A;G/A; A/G/T/

		C	GCCC	100%);155(A-100%,T-0%);197(G-10%,A-97%);		C;G;A; A
AMPL16 90074	scaffold10	CACGATG AAGACTA GACGACT GAG	CATCTTT TCCACGT AGCAGCG	40(G-93%,A-9%);47(C-91%,G-3%,T-9%);51(A-4%,G-96%);72(C-99%,T-1%);79(A-1%,G-96%);83(A-83%,T-15%);85(A-1%,G-99%);88(C-83%,T-20%);96(A-1%,G-99%);102(C-98%,T-2%);105(C-92%,T-11%);110(G-0%,A-100%);113(C-99%,T-3%);117(C-14%,T-91%);118(G-92%,A-12%);124(C-7%,T-94%);125(C-1%,G-99%);127(C-96%,T-5%);138(G-0%,A-100%);147(A-3%,G-98%);152(A-89%,C-0%,G-13%);153(G-0%,A-99%);155(G-99%,T-0%);161(A-0%,G-98%);178(C-99%,T-1%);187(C-98%,T-2%);189(A-90%,G-13%);194(A-0%,G-100%);200(C-11%,T-86%);213(C-95%,T-0%);216(C-0%,A-100%);217(A-0%,G-100%);227(A-83%,G-20%);228(A-98%,T-3%);236(A-92%,G-11%);	G;C;G; C;G;A; G;C;G; C;C;A; C;T;G;T ;G;C;A; G;A;A; G;G;C; C;A;G; T;C;A; G;A;A; A	A;T;G; C;G;T; G;T;G; C;T;A;C ;C;A;T; G;C;A; G;G;A; G;G;C; C;G;G; C;C;A; G;G;A; G
AMPL16 90075	scaffold19	CAAGTTG GACCTGT CGGGGAA ATAC	TCCCGTC CCTCCTC TCAAAG	37(A-2%,G-99%);40(G-100%,T-0%);42(A-0%,G-100%);43(G-22%,C-100%);49(C-3%,G-0%,T-99%);50(C-100%,T-10%);51(G-99%,T-2%);52(C-2%,T-99%);53(C-0%,G-100%);55(C-98%,T-13%);61(C-99%,T-11%);64(A-19%,G-96%);67(C-8%,G-99%);70(C-10%,G-22%,A-91%);76(C-12%,T-98%);79(A-6%,G-99%);102(G-10%,A-100%);103(A-13%,G-98%);104(G-100%,T-8%);106(G-7%,A-100%);111(C-100%,T-0%);112(A-3%,G-100%);115(C-4%,G-96%,T-13%);118(A-16%,G-27%,C-90%,T-0%);121(C-2%,G-98%,T-20%);122(A-22%,T-99%);124(C-22%,T-98%);127(A-6%,G-100%);130(A-6%,C-100%,T-0%);133(G-8%,A-99%);136(G-12%,A-99%);144(A-0%,G-100%);145(C-20%,G-4%,T-97%);151(A-1%,G-100%);159(C-0%,T-100%);163(A-1%,G-100%);166(A-10%,G-100%);169(A-10%,G-99%);175(A-0%,G-100%);181(A-3%,G-100%);184(A-8%,G-100%);190(A-10%,C-4%,G-98%,T-0%);193(G-21%,A-97%);196(A-4%,G-99%);199(G-100%,T-0%);202(A-15%,G-98%);211(A-11%,G-100%);214(A-21%,G-89%,T-18%);217(G-18%,A-93%);219(C-1%,T-100%);220(G-20%,A-93%);223(A-18%,G-99%);226(C-19%,G-97%);	G;G;G; C;T;C;G ;T;G;C; C;G;G; A;T;G; A;G;G; A;C;G; G;C;G; T;T;G;C ;A;A;G; T;G;T;G ;G;G;G; G;G;G; A;G;G; G;G;G; A;T;A; G;G	G;G;G; C;T;C;G ;T;G;C; C;G;G; A;T;G; A;G;G; A;C;G; G;C;G; T;T;G;C ;A;A;G; T;G;T;G ;G;G;G; G;G;G; A;G;G; G;G;G; A;T;A; G;G
AMPL16 90076	scaffold2	GAACCAT TTGTCAA GGTCAGG CTTC	AAGAAAA TTCTTGC CGTCTTC ACC	36(A-0%,G-100%);45(C-99%,T-1%);63(C-98%,T-2%);78(C-2%,T-98%);89(A-1%,C-99%);90(C-2%,T-98%);93(C-98%,T-2%);99(A-1%,C-99%);114(C-2%,T-98%);116(A-1%,G-99%);125(A-0%,T-100%);141(G-1%,C-99%);143(C-98%,T-2%);146(A-2%,G-0%,T-98%);153(G-2%,T-98%);158(G-2%,A-98%);159(A-2%,G-98%);165(A-1%,C-1%,G-98%);167(G-1%,A-99%);173(G-99%,T-1%);174(C-1%,T-99%);177(G-1%,A-99%);179(C-1%,T-99%);182(C-99%,T-1%);193(A-1%,G-99%);213(C-0%,A-100%);216(C-1%,G-99%);220(G-2%,C-98%);223(A-0%,G-100%);224(A-2%,G-98%);229(A-100%,T-0%);	G;C;C;T ;C;T;C; C;T;G;T ;C;C;T; T;A;G; G;A;G; T;A;T;C ;G;A;G; C;G;G; A	G;C;C;T ;C;T;C; C;T;G;T ;C;C;T; T;A;G; G;A;G; T;A;T;C ;G;A;G; C;G;G; A

AMPL16 90077	scaffold3	AGAAGAA AGGACCA AGGAATG ACTA	TCGATAG TCAGTGG GAATACG TTTT	47(C-99%,T-1%);68(A-99%,T-3%);74(G-100%,T-0%);81(C-99%,T-3%);105(G-3%,A-99%);107(C-10%,T-96%);108(C-99%,T-4%);112(C-0%,G-100%);117(C-13%,T-93%);120(G-13%,A-94%);124(A-13%,G-94%);125(C-12%,G-94%);127(G-1%,A-100%);129(C-94%,T-12%);133(G-0%,C-98%);139(C-0%,A-99%);142(C-5%,G-97%);148(G-1%,A-100%);153(G-0%,C-100%);155(C-100%,T-7%);160(A-0%,T-100%);166(C-1%,A-99%);179(A-0%,G-100%);186(G-1%,A-100%);191(G-9%,A-96%);197(C-100%,T-0%);206(C-98%,T-2%);208(G-20%,A-93%);209(A-6%,G-98%);213(C-100%,T-0%);215(C-0%,T-100%);	C;A;G; C;A;T;C ;G;T;A; G;G;A; C;C;A; G;A;C; C;T;A; G;A;A; C;C;A; G;C;T	C;A;G; C;A;T;C ;G;T;A; G;G;A; C;C;A; G;A;C; C;T;A; G;A;A; C;C;A; G;C;T
AMPL16 90079	scaffold3	TCTGTTG CAAAGAG ATTCAGT TGTC	TCTTTGC TGCCGTA GACATAT ATGT	60(G-0%,A-100%);138(C-99%,T-3%);143(C-0%,T-100%);147(A-0%,C-3%,T-99%);168(C-1%,T-99%);218(A-1%,G-100%);	A;C;T;T ;T;G	A;C;T;T ;T;G
AMPL16 90080	scaffold3	CTATGGT AGCTCGA ACACTAT CGTC	ATAACTG ACGATAC TCCCATG TGAG	41(C-10%,G-93%);45(A-3%,G-98%);55(C-90%,T-14%);56(C-93%,T-11%);59(A-0%,T-100%);64(G-97%,T-3%);71(C-90%,T-21%);82(A-1%,G-99%);89(A-1%,G-99%);91(A-0%,C-100%);95(A-11%,G-93%);104(A-1%,C-99%);106(G-1%,A-99%);113(G-1%,T-99%);134(A-1%,G-99%);135(C-9%,T-95%);144(G-1%,T-100%);145(G-18%,A-92%);152(C-1%,T-96%);155(A-3%,G-97%);156(G-1%,A-99%);158(C-1%,T-99%);164(A-7%,G-93%);169(A-3%,C-97%);171(A-0%,G-99%);172(G-17%,A-91%,T-0%);173(C-1%,T-98%);183(G-95%,T-9%);184(A-0%,G-100%);185(C-97%,T-3%);193(C-100%,T-6%);204(G-1%,A-100%);207(C-1%,G-99%);213(C-1%,T-99%);	G;G;C; C;T;G;C ;G;G;C; G;C;A; T;G;T;T ;A;T;G; A;T;G; C;G;A; T;G;G; C;C;A; G;T	G;G;C; C;T;G;C ;G;G;C; G;C;A; T;G;T;T ;A;T;G; A;T;G; C;G;A; T;G;G; C;C;A; G;T
AMPL16 90081	scaffold3	GTAGGAT TGGACGA AGAAGAC ATGA	CATGAAA CACATAC CAAGTGG GAAT	39(A-15%,G-93%);40(C-100%,T-0%);50(G-4%,T-96%);51(A-0%,G-100%);52(C-100%,T-0%);53(G-5%,A-96%);56(G-99%,T-1%);59(C-2%,A-96%);60(C-10%,T-95%);62(A-96%,T-4%);64(C-0%,T-100%);66(C-0%,A-100%);69(A-0%,T-100%);74(C-15%,T-93%);75(G-0%,A-100%);77(C-0%,T-100%);81(C-10%,T-98%);82(C-93%,T-15%);83(G-1%,A-98%,T-0%);85(A-2%,C-96%,T-2%);86(A-99%,T-1%);89(A-0%,G-100%);91(C-0%,T-100%);94(C-4%,G-96%);100(A-12%,G-96%);118(A-2%,T-98%);121(G-5%,A-94%,T-0%);122(A-1%,T-98%);124(G-10%,A-98%);125(C-100%,T-1%);126(A-4%,C-96%);127(C-1%,T-99%);128(C-0%,T-100%);129(A-98%,T-2%);137(C-3%,T-98%);138(G-15%,A-93%);140(C-1%,T-99%);143(C-100%,T-0%);145(A-0%,G-100%);148(G-10%,A-98%);149(A-10%,G-98%);152(G-99%,T-1%);153(C-0%,A-100%);155(A-0%,C-100%);156(C-11%,T-98%);159(C-0%,G-10%,T-97%);161(C-1%,T-99%);164(C-98%,T-2%);	G;C;T; G;C;A; G;A;T; A;T;A;T ;T;A;T; T;C;A;C ;A;G;T; G;G;T; A;T;A; C;C;T;T ;A;T;A; T;C;G; A;G;G; A;C;T;T ;T;C	G;C;T; G;C;A; G;A;T; A;T;A;T ;T;A;T; T;C;A;C ;A;G;T; G;G;T; A;T;A; C;C;T;T ;A;T;A; T;C;G; A;G;G; A;C;T;T ;T;C

AMPL16 90082	scaffold3	GATTTGT CTAACTT TACAAGC GGGC	TATGTTA CAGTGAC GTTGTGG GG	39(C-97%,T-3%);40(A-0%,C-100%);45(C-100%,T-1%);56(C-17%,T-93%);65(A-20%,C-90%);81(G-18%,T-92%);85(G-0%,T-100%);87(C-90%,T-20%);102(G-18%,A-92%);108(C-0%,T-100%);109(C-1%,T-99%);110(G-0%,A-100%);111(G-100%,T-0%);118(C-96%,T-14%);121(G-1%,A-99%);146(A-0%,G-100%);150(A-16%,C-94%);154(A-15%,G-95%);156(C-99%,T-1%);181(C-20%,T-90%);182(C-1%,T-99%);190(A-9%,C-90%);191(C-94%,T-9%);193(G-90%,T-16%);194(G-97%,T-7%);195(A-9%,G-93%);206(C-20%,T-90%);216(A-7%,G-100%);222(C-1%,T-99%);237(A-1%,G-99%);	C;C;C;T ;C;T;T; C;A;T;T ;A;G;C; A;G;C; G;C;T;T ;C;C;G; G;G;T; G;T;G	C;C;C;C /T;C/A; G/T;T;T /C;G/A; T;T;A;G ;T/C;A; G;A/C; A/G;C; C/T;T;A /C;C;T/ G;T/G; G;T/C; G/A;T; G
AMPL16 90083	scaffold3	GGTGTTA CCAAAAT ACCGGTC TAGA	TATTAAT TAACGCG TCACACT GTCG	39(C-9%,T-99%);40(G-92%,T-9%);41(A-9%,G-92%);42(C-92%,T-9%);43(C-1%,T-99%);44(C-100%,T-4%);47(A-1%,G-99%);53(A-1%,G-100%);63(C-1%,A-99%);64(G-4%,A-100%);69(C-1%,T-99%);78(A-8%,G-18%,C-92%);79(G-24%,A-92%);89(A-24%,G-93%);103(G-24%,A-92%);104(G-7%,A-99%);109(G-99%,T-1%);110(C-99%,T-1%);112(A-7%,G-99%);116(A-1%,G-99%);127(C-1%,T-99%);142(A-1%,G-99%);146(C-0%,T-100%);148(C-1%,G-99%);152(G-99%,T-1%);154(C-26%,T-91%);166(A-26%,T-91%);173(G-1%,A-100%);175(C-97%,T-16%);182(A-1%,C-99%);	T;G;G; C;T;C;G ;G;A;A; T;C;A; G;A;A; G;C;G; G;T;G;T ;G;G;T; T;A;C;C	T/C;G/T ;G/A;T/ C;T;C;G ;G;A;A; T/C/A; G/A;A/ G;A/G; A/G;G; C;A/G; G;T;G;T ;G;G;C/ T;A/T;A ;C;C
AMPL16 90084	scaffold3	GGTACCG ATGTTTT AGAAGAC ACTG	CGACGTT CCCTTGT CTTTCT AATC	39(G-7%,A-98%);40(G-100%,T-1%);48(A-2%,C-0%,G-100%);52(C-94%,T-13%);53(C-2%,T-99%);54(A-0%,C-12%,G-94%);56(A-1%,G-100%);60(A-0%,G-100%);69(G-2%,C-99%);76(A-2%,C-99%);78(A-1%,T-100%);80(A-2%,C-99%);87(C-2%,G-99%);92(C-100%,T-0%);98(A-8%,T-97%);100(G-100%,T-0%);101(A-0%,G-100%);105(A-0%,C-2%,T-99%);124(G-100%,T-1%);126(C-1%,G-100%);129(C-100%,T-1%);135(A-8%,G-95%);137(A-0%,C-99%);141(G-1%,A-100%);144(A-0%,G-100%);145(A-100%,T-0%);147(C-0%,T-100%);150(C-0%,A-100%);158(G-0%,A-100%);166(C-1%,G-100%);167(A-0%,G-100%,T-0%);169(A-0%,G-100%);177(A-2%,G-100%);180(A-0%,C-100%);184(G-2%,A-99%);187(A-1%,C-100%);199(A-0%,G-100%);200(A-5%,C-96%);204(C-0%,T-100%);206(C-100%,T-0%);	A;G;G; C;T;G; G;G;C; C;T;C;G ;C;T;G; G;T;G; G;C;G; C;A;G; A;T;A; A;G;G; G;G;C; A;C;G; C;T;C	A;G;G; C;T;G; G;G;C; C;T;C;G ;C;T;G; G;T;G; G;C;G; C;A;G; A;T;A; A;G;G; G;G;C; A;C;G; C;T;C
AMPL16 90085	scaffold3	CATTCTT TTGCGAG CAAACCA TATG	ATACTCT TATTTC CTTTGAA AGCC	36(C-99%,T-10%);37(G-1%,C-99%);38(G-1%,C-100%);39(G-20%,C-92%,T-1%);40(C-20%,G-94%);45(A-0%,G-100%);47(A-0%,G-100%);54(G-100%,T-0%);55(C-0%,G-0%,A-100%);56(C-6%,T-99%);57(C-99%,T-2%);63(A-21%,G-0%,C-91%);66(G-6%,A-99%,T-0%);68(C-2%,A-99%);69(A-4%,C-10%,T-95%);70(A-1%,G-99%);72(G-4%,A-98%,T-0%);76(G-1%,A-100%);81(G-2%,C-100%);84(A-19%,T-94%);88(A-0%,C-100%);90(A-16%,G-96%);94(A-6%,G-98%);99(A-24%,G-91%);102(G-1%,A-100%);108(G-12%,C-94%);111(C-2%,T-	C;C;C;C ;G;G;G; G;A;T; C;C;A; A;T;G; A;A;C; T;C;G; G;G;A; C;T;T;C ;C;T;G; G;A;C; A;T;C;C ;G;C;T;	C;C;C;C ;G;G;G; G;A;T; C;C;A; A;T;G; A;A;C; T;C;G; G;G;A; C;T;T;C ;C;T;G; G;A;C; A;T;C;C ;G;C;T;

				99%);114(A-1%,T-100%);115(A-1%,C-100%,T-0%);116(G-0%,C-100%);120(C-3%,T-99%);123(A-0%,G-100%);126(A-4%,G-99%);129(G-1%,A-100%);132(A-1%,C-100%);134(A-100%,T-0%);137(C-4%,T-98%);138(C-100%,T-2%);143(C-99%,T-3%);150(A-1%,G-100%);156(A-2%,C-98%,T-2%);159(A-0%,C-6%,T-98%);160(C-1%,T-100%);163(C-3%,T-99%);164(C-0%,G-14%,A-92%);165(C-0%,T-100%);168(C-0%,T-100%);171(A-0%,G-100%);176(C-1%,T-99%);179(G-1%,A-99%);181(A-0%,C-97%,T-10%);182(C-10%,A-96%);189(C-96%,T-9%);190(A-0%,G-2%,C-98%);195(C-96%,T-9%);	T;T;A;T ;T;G;T; A;C;A; C;C;C	T;T;A;T ;T;G;T; A;C;A; C;C;C
AMPL16 90086	scaffold6	TTTGGA TGTATGC GGTCAAA GAAC	GTTACAT TGAGGCA TTAGCGG AAG	39(A-1%,G-99%);44(C-99%,T-1%);46(G-1%,A-99%);48(A-1%,G-99%);54(G-1%,T-99%);65(C-1%,T-99%);69(C-99%,T-1%);132(A-0%,G-100%);140(G-1%,A-99%);154(A-1%,G-99%);171(A-99%,T-1%);197(C-99%,T-1%);200(C-99%,T-1%);224(A-1%,T-99%);225(C-99%,T-1%);230(C-1%,T-99%);	G;C;A; G;T;T;C ;G;A;G; A;C;C;T ;C;T	G;C;A; G;T;T;C ;G;A;G; A;C;C;T ;C;T
AMPL16 90087	scaffold6	GTTCCCG ACACAGA TGGAGTA G	ATCGTTA CTGAGGA ACGAGGT C	33(G-0%,A-100%);37(A-3%,G-99%);42(C-98%,T-3%);59(C-100%,T-0%);60(A-2%,G-99%);68(G-4%,A-97%);69(G-0%,A-97%,T-3%);90(C-2%,G-1%,T-99%);92(A-2%,G-99%);93(A-2%,G-99%);96(C-99%,T-2%);99(G-1%,A-100%);113(G-1%,T-100%);114(G-100%,T-1%);117(C-99%,T-2%);120(C-100%,T-1%);123(A-3%,G-99%);129(G-1%,A-100%);133(A-13%,G-90%);136(A-4%,G-98%);137(C-2%,G-6%,A-94%);139(C-100%,T-1%);140(A-7%,G-96%);141(C-91%,T-12%);142(A-3%,G-97%,T-2%);144(A-1%,G-99%);147(C-0%,A-100%);148(C-3%,T-99%);151(G-100%,T-0%);152(G-100%,T-1%);153(A-2%,T-98%);154(C-100%,T-0%);155(G-2%,A-99%);156(C-2%,G-6%,A-94%);158(C-98%,T-5%);159(G-1%,A-100%);162(C-7%,A-95%);163(A-12%,C-91%);165(C-1%,T-99%);168(G-2%,A-98%);169(C-1%,A-95%);170(G-6%,C-91%);171(G-1%,A-100%);173(A-0%,C-7%,G-96%);175(C-1%,A-100%);176(G-2%,A-94%);177(A-1%,G-95%);182(A-0%,G-100%);186(C-4%,T-98%);189(A-3%,G-98%);192(G-12%,A-91%);201(A-2%,C-1%,T-99%);204(C-0%,T-100%);207(G-0%,C-100%);211(A-3%,G-99%);212(C-2%,A-98%);215(C-100%,T-0%);216(A-3%,G-98%);219(A-1%,G-99%);224(C-98%,T-2%);225(C-100%,T-0%);	A;G;C; C;G;A; A;T;G; G;C;A; T;G;C;C ;G;A;G; G;A;C; G;C;G; G;A;T; G;G;T; C;A;A; C;A;A; C;T;A; A;C;A; G;A;A; G;G;T; G;A;T;T ;C;G;A; C;G;G; C;C	A;G;C; C;G;A; A;T;G; G;C;A; T;G;C;C ;G;A;G; G;A;C; G;C;G; G;A;T; G;G;T; C;A;A; C;A;A; C;T;A; G;A;A; G;G;T; G;A;T;T ;C;G;A; C;G;G; C;C
AMPL16 90088	scaffold6	TATGCAT ATGGCTC TGGTTAT CACT	CCACGCT CTATGAT AACTTTG ACTG	36(A-11%,G-95%);40(G-2%,A-99%);42(A-0%,G-100%);67(C-2%,G-99%);68(G-0%,C-100%);70(G-1%,T-99%);74(G-7%,A-98%);75(A-2%,G-99%);76(A-0%,C-100%);77(A-2%,G-99%);81(C-8%,T-97%);90(C-100%,T-0%);91(C-2%,G-99%);96(A-0%,G-100%);101(A-99%,T-2%);106(A-0%,C-100%);108(G-2%,A-99%);112(G-2%,A-99%);114(C-13%,T-93%);116(C-100%,T-0%);117(G-100%,T-0%);120(A-0%,G-	G;A;G; G;C;T; A;G;C; G;T;C; G;G;A; C;A;A; T;C;G; G;A;T;T ;C;C;A; A;T;A;	G;A;G; G;C;T; A;G;C; G;T;C; G;G;A; C;A;A; T;C;G; G;A;T;T ;C;C;A; A;T;A;

				100%);124(G-2%,A-100%);131(C-2%,T-99%);134(C-0%,T-100%);135(C-100%,T-0%);136(C-99%,T-2%);138(A-99%,T-2%);144(G-2%,A-99%);147(G-2%,T-99%);152(C-0%,A-100%);165(A-8%,G-97%);168(C-2%,A-99%);169(A-2%,G-99%);186(C-2%,A-99%);188(C-97%,T-9%);191(C-0%,A-100%);198(A-0%,G-100%);	G;A;G; A;C;A; G	G;A;G; A;C;A; G
AMPL16 90089	scaffold6	GATCTAG AATGAGC AAAAGTG GAGC	GAGTTGA GCACTCG GGTTTCT T	37(G-1%,C-95%,T-12%);39(C-100%,T-1%);40(A-1%,G-99%);44(C-95%,T-12%);47(A-0%,C-1%,G-99%);52(C-99%,T-1%);59(C-100%,T-0%);65(C-100%,T-0%);69(C-100%,T-1%);71(G-0%,A-99%,T-1%);74(C-100%,T-1%);75(G-4%,A-98%);76(C-100%,T-1%);77(A-1%,G-100%);81(A-100%,T-0%);83(G-1%,A-99%);86(C-100%,T-1%);88(G-14%,A-93%);89(G-0%,A-100%);90(C-0%,T-100%);97(C-100%,T-0%);98(C-100%,T-0%);102(G-0%,T-100%);107(G-0%,A-100%);110(C-0%,G-100%);113(G-1%,C-99%);119(G-0%,C-100%);120(C-100%,T-1%);124(C-100%,T-0%);125(A-2%,G-100%);135(G-1%,A-99%);140(C-99%,T-2%);145(C-100%,T-1%);	C;C;G; C;G;C; C;C;C; A;C;A; C;G;A; A;C;A; A;T;C;C ;T;A;G; C;C;C;C ;G;A;C; C	C/T;C;G ;T/C;G; C;C;C;C ;A;C;A; C;G;A; A;C;A/ G;A;T; C;C;T;A ;G;C;C; C;C;G; A;C;C
AMPL16 90090	scaffold6	TAAATCA CTCGATT CTCGGAT TCGT	GTCTTCG AGTCCTC ATCGAAG AG	57(A-0%,C-100%);72(G-0%,A-100%);75(C-0%,A-100%);77(C-100%,T-0%);84(C-1%,T-97%);85(C-99%,T-1%);88(C-31%,T-89%);89(A-2%,C-99%,T-2%);90(C-99%,T-4%);92(G-100%,T-2%);93(C-0%,T-100%);94(C-31%,T-87%);95(G-9%,A-97%);96(C-0%,T-100%);107(G-0%,T-100%);111(C-98%,T-2%);112(C-6%,T-86%);131(C-100%,T-0%);146(A-98%,T-2%);149(A-0%,C-26%,T-94%);161(C-0%,T-100%);164(C-1%,G-100%);169(C-100%,T-0%);170(A-1%,G-100%);182(A-0%,G-100%);190(G-0%,A-100%);197(C-0%,T-100%);206(A-0%,G-100%);209(A-0%,C-0%,T-100%);	C;A;A; C;T;C;T ;C;C;G; T;T;A;T ;T;C;T; C;A;T;T ;G;C;G; G;A;T; G;T	C;A;A; C;T;C;C /T;C;C; G;T;C/T ;A;T;T; C;- /T;C;A; T/C;T;G ;C;G;G; A;T;G;T
AMPL16 90091	scaffold6	TGTACAA CTTAACA TCGGACA CTCT	CGACCTT ATATATT TACACAG CGCG	46(G-0%,T-100%);47(C-1%,T-100%);48(A-1%,C-100%);52(A-8%,G-96%);53(A-0%,G-100%);54(G-1%,A-100%);60(G-0%,A-100%);61(C-1%,T-100%);62(A-0%,C-100%);64(C-2%,A-100%);71(A-0%,G-100%);72(C-5%,G-99%);84(A-10%,G-94%);88(G-10%,T-95%);95(A-5%,C-1%,T-99%);99(A-0%,G-100%);103(G-0%,C-100%);111(A-2%,G-100%);118(G-1%,T-100%);126(C-99%,T-5%);129(A-8%,G-98%);136(A-0%,G-100%);138(G-1%,C-99%,T-0%);151(C-100%,T-0%);155(C-99%,T-3%);156(C-100%,T-1%);160(G-0%,A-100%);177(C-100%,T-1%);184(A-2%,G-100%);196(C-1%,T-100%);200(C-1%,T-100%);202(A-1%,T-100%);210(G-1%,A-100%);212(G-1%,T-100%);	T;T;C;G ;G;A;A; T;C;A; G;G;G; T;T;G;C ;G;T;C; G;G;C; C;C;C; A;C;G; T;T;T;A ;T	T;T;C;G ;G;A;A; T;C;A; G;G;G; T;T;G;C ;G;T;C; G;G;C; C;C;C; A;C;G; T;T;T;A ;T
AMPL16 90092	scaffold6	CTCAGAT TTAATTC CTCATGC ACGG	TTCTTGA TATGGTC CGGATTG ATGG	42(G-1%,C-99%);47(C-100%,T-0%);83(C-99%,T-1%);121(A-1%,C-99%);143(A-0%,G-100%);159(A-1%,C-99%);173(C-1%,G-99%);183(C-0%,A-100%);194(C-100%,T-0%);195(A-1%,G-99%);197(C-0%,G-0%,T-99%);205(C-100%,T-0%);209(C-1%,T-99%);210(G-1%,A-99%,T-1%);212(C-100%,T-	C;C;C;C ;G;C;G; A;C;G; T;C;T;A ;C	C;C;C;C ;G;C;G; A;C;G; T;C;T;A ;C

				0%);		
AMPL16 90093	scaffold7	AAAAATT TGTCTTC CGACCTC CATC	TAGAAGC AGACTGG CATACCT CAT	38(A-0%,G-100%);40(G-1%,A-100%);43(G-1%,A-100%);44(C-1%,T-100%);67(A-7%,C-99%);69(A-5%,G-99%);76(G-0%,A-100%);79(G-12%,C-98%);81(A-1%,G-100%);84(C-18%,T-94%);98(A-100%,T-2%);116(C-96%,T-14%);125(C-1%,G-100%);129(G-0%,A-100%);133(C-18%,T-94%);141(G-25%,A-94%);149(A-1%,G-100%);153(A-1%,C-0%,G-99%);156(G-18%,A-94%);159(C-25%,T-93%);163(A-5%,C-16%,T-94%);164(G-99%,T-4%);166(C-4%,A-99%);171(C-99%,T-7%);172(G-18%,C-94%);180(G-0%,C-100%);186(C-4%,T-99%);190(G-100%,T-1%);192(C-3%,T-100%);194(G-18%,A-94%);206(A-0%,G-100%);213(G-91%,T-28%);214(C-15%,T-95%);215(A-0%,G-100%);	G;A;A; T;C;G; A;C;G; T;A;C; G;A;T; A;G;G; A;T;T;G ;A;C;C; C;T;G;T ;A;G;G; T;G	G;A;A; T;C;G; A;G/C; G;C/T; A;C/T; G;A;C/ T;G/A; G;G;A/ G;T/C;T /C;G;A; C;C/G; C;T;G;T ;G/A;G; G;T/C/T ;G
AMPL16 90094	scaffold7	AGAATAT ATAGAGG ATCGGAG GAGGT	ATGACGA TGGCAGA GATACAA AAAC	39(G-0%,C-100%);40(A-0%,C-100%);46(G-4%,A-97%);75(A-98%,T-4%);83(A-0%,G-100%);87(G-0%,T-100%);113(A-5%,G-96%);117(G-0%,A-100%);119(A-3%,T-98%);124(G-2%,A-99%);129(A-100%,T-0%);143(A-0%,G-100%);151(G-3%,A-98%);152(C-3%,T-98%);157(G-0%,A-100%);159(G-100%,T-0%);175(A-8%,G-94%);176(G-0%,C-100%);183(A-0%,G-100%);188(G-8%,A-94%);195(C-95%,T-7%);203(C-94%,T-8%);214(G-99%,T-1%);215(C-0%,T-100%);220(C-0%,T-100%);222(A-4%,G-97%);225(C-0%,T-100%);226(C-100%,T-0%);228(G-0%,A-100%);	C;C;A; A;G;T; G;A;T; A;A;G; A;T;A; G;G;C; G;A;C; C;G;T;T ;G;T;C; A	C;C;A; A;G;T; G;A;T; A;A;G; A;T;A; G;G;C; G;A;C; C;G;T;T ;G;T;C; A
AMPL16 90095	scaffold7	ATCGTTG GTGAATG TCTCGGA T	ATCATAT GAAGGGT TGGTCCA TGAT	33(C-3%,T-99%);37(C-0%,T-100%);52(G-1%,A-99%);53(G-5%,A-98%);54(A-98%,T-5%);63(C-99%,T-3%);65(C-14%,T-95%);100(A-0%,G-100%);103(G-92%,T-22%);109(A-3%,T-99%);111(G-2%,A-99%);116(A-0%,C-100%);122(A-4%,C-100%);124(G-0%,C-100%);131(G-1%,C-100%);132(G-100%,T-4%);133(C-98%,T-7%);134(A-1%,T-100%);137(C-100%,T-0%);138(C-0%,T-100%);140(G-0%,A-100%);145(A-4%,G-99%);147(C-5%,T-98%);159(A-22%,C-92%);180(G-100%,T-0%);182(C-3%,T-100%);194(A-1%,G-99%);206(G-5%,A-98%);217(C-1%,G-99%,T-0%);218(A-0%,G-100%);222(G-0%,A-100%);	T;T;A;A ;A;C;T; G;G;T; A;C;C; C;C;G; C;T;C;T ;A;G;T; C;G;T; G;A;G; G;A	T;T;A;A ;A;C;T; G;G;T;T ;A;C;C; C;C;G; C;T;C;T ;A;G;T; C/A;G; T;G;A; G;G;A
AMPL16 90096	scaffold2	GAAACCA CATTCTT GATGCCT GAAT	ATTAATC ACATGCT CCTGAGA TCGA	36(G-10%,T-99%);38(A-89%,T-31%);39(A-2%,G-99%);40(G-31%,A-89%);41(C-31%,T-89%);44(A-2%,C-100%);45(A-26%,G-94%);46(C-0%,G-31%,A-89%);47(C-100%,T-0%);49(A-1%,C-0%,T-100%);51(G-23%,A-96%);54(G-26%,A-93%);56(G-3%,C-95%,T-24%);57(C-0%,G-100%);62(C-94%,T-26%);63(G-26%,A-94%);69(A-0%,G-100%);72(A-0%,G-94%,T-26%);75(G-23%,A-96%);76(A-100%,T-0%);80(C-94%,T-26%);93(C-1%,T-100%);96(C-100%,T-1%);97(A-0%,G-100%);100(G-23%,T-96%);102(G-0%,A-100%);107(A-100%,T-	T;A;G; A;T;C; G;A;C; T;A;A; C;G;C; A;G;G; A;A;C; T;C;G;T ;A;A;T; G;A;G; T;G;G;T ;A;A;T; T;T;C;T	T;T/A;G ;A/G;T/ C;C/A/ G;A/G; C;T;G/ A;A/G; C/T;G;T /C;A/G; G;T/G; A/G;A; T/C;T;C ;G;G;T; A;A;T;

				0%);108(G-0%,T-100%);112(G-100%,T-0%);114(G-23%,A-96%);121(G-100%,T-2%);123(C-2%,T-100%);125(G-100%,T-1%);127(A-23%,G-96%);128(G-23%,T-96%);131(G-33%,A-88%);133(G-0%,A-100%);136(A-23%,G-96%);137(G-32%,T-89%);159(G-23%,T-96%);162(A-2%,C-98%);169(C-0%,T-100%);172(G-26%,A-94%);173(C-100%,T-0%);174(C-0%,G-100%);192(A-2%,C-100%);	;A;C;G; C	G;G/A; G;T;G; G/A;T/ G/A/G; A;A/G; G/T;T/G ;C;T;A/ G;C;G; C
AMPL16 90097	scaffold3	GCGTAAC AAGTTGA TAGGCAA TCTT	GCCACAC TGTGAAA ACATTTG TTAG	36(G-0%,A-100%);43(A-100%,T-0%);46(C-100%,T-0%);50(A-100%,T-1%);60(C-1%,G-99%);64(C-1%,T-100%);67(G-2%,T-99%);68(C-1%,A-99%);71(G-0%,A-100%);86(A-0%,G-100%);87(C-0%,A-100%);88(C-100%,T-0%);96(C-9%,G-94%);97(C-100%,T-0%);105(C-98%,T-4%);106(A-99%,T-4%);112(G-3%,A-99%);114(C-100%,T-0%);115(G-0%,C-99%,T-1%);121(A-3%,C-99%);135(C-96%,T-6%);137(C-0%,A-99%);141(G-0%,A-100%);143(G-0%,A-100%);148(C-1%,G-0%,T-99%);158(C-6%,G-96%);164(A-2%,G-99%);168(G-6%,A-97%);170(G-0%,A-100%);178(G-100%,T-1%);186(G-0%,A-100%);192(A-0%,G-100%);193(G-1%,A-99%);194(C-100%,T-0%);198(A-3%,C-99%);199(C-7%,T-95%);202(G-8%,A-94%);207(C-99%,T-1%);209(G-3%,C-99%,T-0%);211(G-1%,C-99%);215(C-95%,T-8%);216(C-3%,T-99%);217(G-1%,T-99%);218(G-11%,A-93%,T-2%);220(G-99%,T-2%);222(G-3%,A-98%,T-2%);225(G-2%,A-99%);226(G-0%,A-100%);	A;A;C; A;G;T;T ;A;A;G; A;C;G; C;C;A; A;C;C; C;C;A; A;A;T; G;G;A; A;G;A; G;A;C; C;T;A;C ;C;C;C; T;T;A;G ;A;A;A	A;A;C; A;G;T;T ;A;A;G; A;C;G; C;C;A; A;C;C; C;C;A; A;A;T; G;G;A; A;G;A; G;A;C; C;T;A;C ;C;C;C; T;T;A;G ;A;A;A
AMPL16 90098	scaffold3	TTTACGC TCCTTCC GCACC	TACGTCC TTGATGT ATACCGT TACC	31(C-91%,T-25%);37(C-100%,T-1%);58(C-4%,T-99%);61(A-4%,G-99%);67(A-16%,T-96%);76(C-10%,T-98%);85(C-100%,T-0%);94(G-100%,T-1%);103(C-100%,T-1%);113(A-19%,C-94%);115(G-19%,A-94%);136(C-100%,T-0%);141(A-100%,T-1%);145(C-26%,T-89%);146(G-12%,A-99%,T-2%);149(A-12%,C-99%,T-0%);152(A-12%,C-93%,T-12%);155(C-97%,T-4%);157(C-96%,T-0%);158(A-94%,T-12%);161(C-12%,G-94%);162(C-100%,T-1%);163(C-12%,A-98%,T-1%);169(A-2%,C-4%,G-92%,T-23%);171(A-100%,T-1%);175(G-2%,A-100%);176(A-1%,C-99%);177(A-1%,T-99%);178(C-96%,T-5%);182(C-1%,G-100%);187(A-2%,C-4%,T-92%);193(C-5%,T-95%);	C;C;T;G ;T;T;C; G;C;C; A;C;A; T;A;C;C ;C;C;A; G;C;A; G;A;A; C;T;C;G ;T;T	C/T;C;T ;G;T;T; C;G;C; C;A;C; A;C/T; G/A;C/ A;A/C; C;C;A/T ;G/C;C; C/A;T/ G;A;A; C;T;- /C;G;- /T;-/T
AMPL16 90099	scaffold3	TCAAGAA GAAGAAA CCATTGC CTTC	CACAAGG GTATGTG GATGAAT ATTCT	No_variant	No_vari ant	No_vari ant
AMPL16 90100	scaffold3	CCAATCC TCATCGA TCCATTT GAAG	TCGCAAG ACTAGAG AGGTATT TTCG	42(A-0%,G-100%);73(A-0%,T-100%);80(A-0%,T-100%);101(C-0%,G-100%);143(C-0%,T-100%);149(C-100%,T-0%);173(G-4%,A-97%);174(A-97%,T-4%);184(G-97%,T-4%);209(C-97%,T-4%);	G;T;T;G ;T;C;A; A;G;C	G;T;T;G ;T;C;A; A;G;C
AMPL16 90101	scaffold3	ACAGTAT AACATTC AGCACTC GTGA	CCGGGAT ATTCAAA AACTAGC ACAA	40(G-6%,A-97%);87(C-100%,T-1%);98(C-98%,T-4%);126(A-1%,G-99%);	A;C;C; G	A;C;C; G

AMPL16 90102	scaffold3	GAGGATC CTGCTAC GCTTCTT C	CAGACTT CGCTTAA AACCTTC AGAA	42(A-91%,T-26%);45(C-92%,T-24%);51(C-91%,T-26%);54(A-26%,G-91%);60(C-2%,T-100%);66(C-100%,T-0%);72(C-91%,T-26%);83(A-100%,T-0%);86(C-1%,T-100%);93(C-26%,A-92%);95(A-0%,C-100%);98(C-0%,T-91%);99(C-89%,T-4%);102(G-91%,T-0%);103(A-14%,G-90%);110(A-100%,T-0%);116(A-15%,T-91%);119(C-100%,T-1%);123(G-26%,T-91%);130(G-26%,T-91%);133(C-26%,T-91%);139(G-3%,A-99%,T-0%);142(C-26%,T-92%);148(C-26%,T-91%);157(C-26%,G-91%);160(A-26%,G-91%);163(C-100%,T-0%);166(G-26%,T-91%);172(G-26%,T-91%);178(C-26%,A-91%);181(C-26%,T-91%);182(A-26%,C-91%);188(A-100%,T-1%);190(C-26%,T-91%);196(G-26%,A-91%);202(C-100%,T-0%);205(C-92%,T-26%);209(A-26%,G-91%);217(G-0%,T-100%);220(A-26%,G-91%);221(G-0%,T-100%);229(C-2%,T-100%);	A;C;C; G;T;C; ;A;T;A; C;T;C;G ;G;A;T; C;T;T;T ;A;T;T; G;G;C; T;T;A;T ;C;A;T; A;C;C; G;T;G;T ;T	T/A;T/C ;T/C;A/ G;T;C;C /T;A;T; C/A;C;- /T;-C; /G;G;-; A;T;-C; G/T;G/T ;T/C;A; C/T;T/C ;G/C;A/ G;C;G/ T;T/G;A /C;T/C; A/C;A; T/C;G/ A;C;T/C ;G/A;T; G/A;T;T
AMPL16 90103	scaffold3	GTATGCA TTTTCGA AAGCCAT TGAC	GACCGCG AAGGAAG AGTTATA AAAT	No_variant	No_vari ant	No_vari ant
AMPL16 90104	scaffold3	TATGTCT TGTTTCG AACTGTG TGTA	TGGAGTG TAGGCGA TTGTAGA TATC	47(C-100%,T-1%);48(G-100%,T-0%);62(G-0%,T-100%);79(C-1%,T-100%);83(C-96%,T-4%);97(G-2%,A-98%);98(G-1%,C-100%,T-1%);106(G-4%,A-100%);108(C-16%,T-96%);112(C-1%,T-100%);114(G-5%,C-100%,T-0%);117(A-1%,T-98%);118(A-1%,G-100%);121(A-1%,G-91%);122(A-3%,T-96%);123(G-2%,T-96%);124(A-2%,C-96%);125(A-4%,C-6%,G-91%);126(A-2%,T-97%);127(C-97%,T-2%);128(A-2%,C-97%);129(G-3%,A-97%);130(G-0%,C-94%,T-5%);132(G-1%,A-95%);133(A-0%,G-0%,C-95%,T-2%);136(G-0%,C-98%);137(C-0%,A-95%,T-3%);138(C-4%,G-96%);139(G-3%,T-92%);140(C-2%,A-98%);141(C-5%,T-94%);142(C-5%,G-93%);143(A-1%,C-4%,G-93%);145(C-100%,T-1%);147(A-11%,G-91%);157(C-100%,T-5%);158(C-9%,A-100%);163(G-5%,A-99%,T-3%);166(C-98%,T-2%);173(A-23%,G-96%);176(C-2%,G-98%);185(A-0%,G-100%);190(G-0%,C-97%,T-2%);193(C-100%,T-1%);196(G-97%,T-16%);198(G-100%,T-0%);201(G-2%,A-98%);208(C-27%,T-91%);223(A-91%,T-27%);234(G-1%,A-100%);	C;G;T;T ;C;A;C; A;T;T;C ;T;G;G; T;T;C;G ;T;C;C; A;C;A; C;C;A; G;T;A;T ;G;G;C; G;C;A; A;C;G; G;G;C; C;G;G; A;T;A; A	C;G;T;T ;C;A;C; A;C/T;T ;C;T;G; G;T;T;C ;G;T;C; C;A;C; A;C;C; A;G;T; A;T;G; G;C;G; C;A/C; A;C;A/ G;G;G; C;C;T/G ;G;A;T/ C;A/T; A
AMPL16 90105	scaffold3	GTTCGAG ATACGTT CATTGCC TATT	GATACCG ACCAAGA GCATTGA CA	58(C-0%,T-100%);62(C-100%,T-0%);66(G-1%,T-99%);69(C-0%,T-100%);70(A-1%,C-99%);73(A-1%,G-99%);83(C-1%,T-98%);89(A-1%,G-99%);94(A-1%,G-99%);101(C-99%,T-1%);104(C-1%,T-99%);107(A-0%,G-100%);108(C-99%,T-1%);109(C-0%,T-100%);114(G-2%,C-98%);116(C-3%,T-98%);123(C-98%,T-2%);127(G-1%,A-99%);129(G-1%,A-99%);131(C-1%,T-99%);133(G-99%,T-1%);135(C-4%,T-97%);136(C-0%,T-100%);139(A-1%,G-7%,C-95%);142(A-0%,G-100%);145(G-96%,T-	T;C;T;T ;C;G;T; G;G;C; T;G;C;T ;C;T;C; A;A;T; G;T;T;C ;G;G;G; A;A;C; T;G;A;T ;A;T;A; G;C;T;	T;C;T;T ;C;G;T; G;G;C; T;G;C;T ;C;T;C; A;A;T; G;T;T;C ;G;G;G; A;A;C; T;G;A;T ;A;T;A; G;C;T;

				7%);149(A-1%,G-99%);150(C-1%,A-99%);151(G-0%,A-100%);153(C-99%,T-1%);155(C-0%,T-100%);159(A-10%,G-93%);160(G-1%,A-99%);162(C-0%,T-100%);163(G-1%,A-95%);164(C-7%,T-95%);166(C-0%,A-100%);168(A-1%,G-99%);175(C-100%,T-0%);177(G-10%,T-94%);179(C-1%,A-99%);180(G-0%,A-100%);184(C-0%,T-94%);188(C-100%,T-1%);189(A-7%,G-96%);195(C-94%,T-10%);201(G-1%,T-99%);202(A-1%,C-99%);211(C-100%,T-0%);212(C-1%,A-99%);222(A-1%,C-96%,T-1%);224(A-4%,G-6%,T-92%);226(C-2%,T-96%);238(A-1%,G-100%);	A;A;T; C;G;C;T ;C;C;A; C;T;T;G	A;A;T; C;G;C;T ;C;C;A; C;T;T;G
AMPL16 90106	scaffold6	ATTCATC ACGAAGA ACACGAA AACA	GGTTGAA AGGATGT TACATTG AGGG	37(C-1%,T-99%);39(A-0%,G-100%);41(A-1%,C-99%,T-6%);42(G-7%,A-98%);43(C-98%,T-4%);46(A-0%,C-100%,T-0%);47(G-1%,T-99%);52(G-13%,A-95%);53(A-1%,C-99%,T-1%);54(C-98%,T-6%);55(A-2%,G-0%,T-98%);57(A-6%,T-95%);58(C-3%,T-99%);59(A-16%,C-2%,T-93%);60(C-0%,T-100%);61(A-2%,C-97%,T-8%);62(A-6%,T-98%);63(C-0%,T-100%);64(G-2%,C-100%,T-0%);65(A-6%,T-98%);67(G-29%,A-90%);69(C-100%,T-1%);71(G-0%,A-100%);72(C-6%,G-1%,A-98%);73(C-99%,T-1%);74(C-9%,T-97%);76(C-93%,T-13%);77(C-5%,T-96%);78(A-0%,C-20%,T-97%);80(C-1%,T-100%);81(C-99%,T-4%);89(A-1%,G-99%,T-2%);90(C-2%,T-98%);101(C-0%,T-100%);107(A-1%,C-0%,G-99%);110(C-3%,T-99%);120(A-0%,T-100%);122(A-1%,C-100%);123(C-0%,T-100%);125(A-1%,G-100%);134(G-4%,A-99%);140(G-2%,A-99%);142(A-0%,C-0%,T-100%);146(A-3%,G-99%);147(C-1%,T-99%);148(C-0%,T-100%);149(A-1%,T-100%);150(C-100%,T-1%);152(C-100%,T-0%);157(G-13%,A-99%);159(A-1%,G-98%);161(G-0%,A-99%,T-2%);165(C-2%,T-99%);168(C-98%,T-2%);170(C-99%,T-3%);171(A-1%,G-99%);172(C-1%,T-100%);173(C-1%,T-100%);175(C-1%,G-100%);177(C-3%,G-1%,A-96%,T-6%);178(A-1%,G-99%,T-1%);181(C-0%,T-100%);182(A-1%,C-2%,G-98%);183(C-16%,T-98%);201(G-0%,A-100%);202(C-100%,T-0%);204(A-0%,G-100%);	T;G;C; A;C;C;T ;A;C;C; T;T;T;T ;T;C;T; T;C;T;A ;C;A;A; C;T;C;T ;T;T;C; G;T;T;G ;T;T;C; T;G;A; A;T;G;T ;T;T;C; C;A;G; A;T;C;C ;G;T;T; G;A;G; T;G;T;A ;C;G	T;G;C; A;C;C;T ;A;C;C; T;- /T;T;T; T;C;T;T ;C;T;A/ G;C;A; A;C/-;T; C;T/-;C/ T;T;C;G ;T;T;G; T;T;C;T ;G;A;A; T;G;T;T ;T;C;C; A/G;G; A;T;C;C ;G;T;T; G;A;G; T;G;T/C ;A;C;G
AMPL16 90107	scaffold6	CGTTTGG AAGAGAT TCTGCGT G	GTAGGAA TTCAAAC TGAGGCT GAAG	33(C-18%,G-93%);39(C-0%,G-100%);40(A-0%,G-100%);42(C-1%,A-99%,T-0%);45(C-19%,G-1%,A-91%);46(C-100%,T-1%);48(A-0%,G-19%,C-91%,T-1%);56(C-0%,G-100%);57(A-20%,C-91%);63(C-3%,T-98%);66(G-20%,A-91%);69(C-1%,T-100%);74(A-1%,G-100%);75(C-0%,A-100%);83(C-2%,T-99%);84(G-2%,T-99%);86(C-2%,A-99%);87(A-0%,T-100%);88(C-0%,T-100%);92(C-100%,T-1%);98(C-95%,T-14%);141(C-4%,G-16%,T-92%);145(C-1%,T-99%);150(C-99%,T-1%);153(A-0%,T-100%);158(G-0%,T-100%);165(C-0%,G-100%);186(G-2%,C-99%);195(C-100%,T-	G;G;G; A;A;C; C;G;C;T ;A;T;G; A;T;T;A ;T;T;C; C;T;T;C ;T;T;G; C;C;T;T ;G	G/C;G; G;A;A/ C;C;G/ C;G;C/ A;T;A/ G;T;G; A;T;T;A ;T;T;C; T/C;T/G ;T;C;T; T;G;C;C ;T;A/T; A/G

				1%);198(C-0%,T-100%);207(A-14%,T-95%);216(A-15%,G-93%);		
AMPL16 90108	scaffold6	CTCTCGA CGAAGAA CAGGAAG ATAT	AGTTCGC ACAATCT GTATTAC ATGC	37(C-99%,T-1%);39(G-0%,T-100%);40(G-100%,T-0%);45(A-0%,G-100%);64(C-7%,T-95%);74(G-100%,T-1%);78(G-0%,A-100%);79(G-2%,A-98%);82(G-1%,A-99%);83(A-0%,C-0%,G-100%);85(A-2%,G-98%);87(A-0%,C-16%,T-90%);91(A-7%,G-96%);94(G-1%,A-100%);98(C-0%,G-0%,T-100%);100(C-2%,A-98%,T-0%);101(A-7%,G-96%);102(A-0%,T-100%);105(C-3%,T-99%);109(A-2%,C-2%,T-98%);114(C-2%,T-98%);117(G-0%,A-100%);118(C-97%,T-4%);119(C-1%,T-100%);120(A-0%,G-100%);121(A-99%,T-1%);123(C-0%,T-100%);125(A-7%,G-96%);129(G-2%,A-99%);130(C-99%,T-3%);132(G-95%,T-5%);134(C-2%,T-98%);138(C-1%,T-100%);140(A-7%,T-96%);142(G-2%,T-98%);143(C-100%,T-0%);145(G-98%,T-2%);147(G-7%,T-96%);152(G-7%,T-96%);158(A-0%,G-100%);161(G-0%,A-99%);165(C-0%,G-99%);176(G-0%,A-100%);177(A-2%,T-99%);183(A-2%,T-98%);185(A-0%,C-0%,G-100%);186(G-0%,A-100%);190(C-99%,T-2%);191(A-99%,T-2%);192(A-1%,G-100%);201(A-0%,G-100%);206(A-7%,C-3%,T-96%);207(G-3%,A-97%);	C;T;G; G;T;G; A;A;A; G;G;T; G;A;T; A;G;T;T ;T;T;A; C;T;G; A;T;G; A;C;G; T;T;T;T ;C;G;T; T;G;A; G;A;T;T ;G;A;C; A;G;G; T;A	C;T;G; G;T;G; A;A;A; G;G;T; G;A;T; A;G;T;T ;T;T;A; C;T;G; A;T;G; A;C;G; T;T;T;T ;C;G;T; T;G;A; G;A;T;T ;G;A;C; A;G;G; T;A
AMPL16 90109	scaffold6	TAGACTG TTCTCAG ACATAGG TCCT	TTTATCG CTGTTGA GATAGCC TAGT	40(G-6%,C-98%);71(C-11%,T-95%);98(A-0%,G-100%);104(A-3%,G-100%);107(C-1%,A-100%);109(A-2%,G-99%);112(A-5%,T-97%);125(G-1%,A-100%);129(A-0%,G-100%);138(A-0%,G-100%);162(A-0%,G-100%);163(G-5%,C-97%);178(A-100%,T-0%);188(G-1%,A-100%);	C;T;G; G;A;G; T;A;G; G;G;C; A;A	C;T;G; G;A;G; T;A;G; G;G;C; A;A
AMPL16 90110	scaffold7	CATGATG GTGGTAG AAAGCAA AGAG	GTAAAGT TCGCGAT ACACGTT CAAG	43(A-0%,C-100%);122(C-99%,T-6%);129(C-100%,T-0%);139(G-9%,A-97%);140(C-0%,A-100%);147(A-1%,C-100%);151(C-1%,T-100%);156(C-12%,T-96%);174(C-0%,G-100%);197(C-5%,T-98%);212(C-17%,T-94%);219(C-0%,A-100%);	C;C;C; A;A;C; T;T;G;T ;T;A	C;C/T;C ;A;A;C; T;T;G;T ;T/C;A
AMPL16 90111	scaffold7	ACGGAGA AGATACA TCATCAC TCTG	AAGAAAT AACACGT GGGTAAA GGTG	37(G-1%,C-99%);41(A-99%,T-1%);46(C-99%,T-1%);50(C-0%,T-100%);72(A-0%,G-100%);78(C-1%,T-99%);90(C-1%,T-99%);103(C-0%,G-100%);118(G-99%,T-1%);128(A-1%,T-99%);132(C-1%,T-99%);137(G-1%,T-99%);139(G-1%,A-99%);162(A-99%,T-1%);163(A-99%,T-1%);166(A-1%,G-99%);167(A-1%,C-99%);173(C-1%,T-99%);178(C-1%,T-99%);181(G-99%,T-1%);182(A-1%,G-99%);184(C-1%,T-99%);205(A-1%,T-99%);232(G-1%,A-99%);	C;A;C;T ;G;T;T; G;G;T;T ;T;A;A; A;G;C; T;T;G;G ;T;T;A	C;A;C;T ;G;T;T; G;G;T;T ;T;A;A; A;G;C; T;T;G;G ;T;T;A
AMPL16 90112	scaffold7	GTAATAA TCAACGT CGGCGCA AATC	AGTCTTC CGTCTTG TATACAA CCAT	36(G-14%,A-90%);38(G-5%,T-100%);44(A-1%,G-100%);45(G-3%,A-99%);46(A-6%,G-96%);47(G-4%,C-99%);52(G-1%,A-100%);57(A-1%,C-98%);58(A-1%,G-99%);60(A-99%,T-2%);67(C-0%,G-97%,T-4%);75(G-1%,A-99%);121(A-8%,G-95%);132(G-1%,C-99%);145(A-12%,G-94%);	A;T;G; A;G;C; A;C;G; A;G;A; G;C;G	A;G/T; G;A;G; C;A;C; G;A;G; A;G;C; G

AMPL16 90113	scaffold7	ATGTTAG AACAGCT ATTCAAA GGCG	GAGACTG AATTCCC ACCTGAA CC	36(G-3%,C-99%);41(G-3%,A-99%);44(C-21%,T-93%);57(C-21%,T-94%);72(G-2%,C-99%);83(G-22%,A-93%);89(G-8%,A-98%);108(A-11%,T-96%);112(C-22%,T-93%);114(G-22%,C-93%);124(A-1%,C-99%);127(G-22%,A-93%);140(C-99%,T-2%);141(G-22%,A-93%);142(C-99%,T-2%);143(A-0%,C-100%);144(G-22%,A-93%);153(C-100%,T-0%);	C;A;T;T ;C;A;A; T;T;C;C ;A;C;A; C;C;A; C	C;A;C/T ;T/C;C; G/A;A; T/A;T/C ;G/C;C; G/A;C; G/A;C; C;A/G; C
AMPL16 90114	scaffold7	CGAACAC CATGATA TGCATCG TAGA	GCAGTCT GCGATCT CATCATT ACTA	47(C-100%,T-0%);50(C-15%,T-98%);53(G-2%,A-98%,T-1%);56(A-4%,G-6%,T-99%);59(C-100%,T-0%);62(G-2%,A-100%);65(C-4%,T-98%);70(C-0%,T-100%);71(A-6%,G-98%);82(A-1%,G-100%);86(G-100%,T-0%);89(C-10%,T-98%);92(C-99%,T-8%);102(C-20%,T-93%);104(A-18%,G-95%);113(A-6%,G-98%);116(A-0%,G-98%,T-3%);125(C-1%,G-94%,T-17%);128(A-18%,G-95%);134(C-99%,T-8%);142(C-100%,T-1%);161(C-1%,G-1%,A-99%);163(C-0%,A-100%);164(A-0%,C-1%,G-1%,T-99%);167(G-1%,C-100%);169(G-1%,A-99%);170(A-3%,T-99%);171(C-0%,T-100%);172(G-0%,T-100%);175(G-0%,C-100%);182(C-18%,G-0%,A-93%,T-1%);184(C-100%,T-1%);185(A-1%,G-100%);201(G-100%,T-0%);203(A-0%,G-100%);204(G-4%,C-92%,T-19%);205(G-5%,A-98%);211(G-18%,A-94%);214(A-0%,G-100%);	C;T;A;T ;C;A;T; T;G;G; G;T;C;T ;G;G;G; G;G;C; C;A;A; T;C;A;T ;T;T;C; A;C;G; G;G;C; A;A;G	C;T;A;T ;C;A;T; T;G;G; G;T;C;T ;G;G;G; G;G;C; C;A;A; T;C;A;T ;T;T;C; A;C;G; G;G;C; A;A;G
AMPL16 90115	scaffold7	CCTTTCTT TGCTTTC GAGAACT CTT	GTTCCGA AGATCCC AAATTCA AAGT	45(C-1%,G-99%);48(C-99%,T-1%);51(G-4%,A-98%);66(A-1%,G-100%);72(G-1%,A-99%);87(G-4%,A-100%);90(C-5%,G-1%,T-98%);93(C-100%,T-4%);96(C-1%,T-99%);105(C-5%,T-99%);107(A-2%,G-99%);108(A-1%,T-100%);113(C-1%,T-100%);117(C-94%,T-14%);120(G-99%,T-5%);123(A-99%,T-7%);124(A-7%,G-99%);126(G-3%,C-99%);129(G-9%,A-98%);134(G-3%,A-99%);135(A-8%,G-98%);143(C-7%,T-98%);144(G-6%,A-98%);145(C-99%,T-1%);159(A-1%,G-99%);165(G-99%,T-5%);169(G-99%,T-4%);170(G-14%,C-94%);172(G-1%,A-99%);176(A-14%,T-95%);178(C-2%,T-99%);180(G-12%,A-95%);181(A-98%,T-7%);183(C-3%,T-99%);184(C-4%,T-99%);187(A-4%,G-99%);188(G-1%,A-99%);189(C-99%,T-4%);191(G-6%,T-98%);192(A-4%,G-99%);193(G-5%,A-98%);204(G-99%,T-5%);205(A-6%,G-99%);209(C-1%,T-100%);210(G-7%,A-99%);212(G-1%,A-99%);219(G-1%,A-99%);222(A-4%,G-99%);225(A-1%,C-99%);229(G-100%,T-1%);233(C-100%,T-1%);	G;C;A; G;A;A; T;C;T;T ;G;T;T; C;G;A; G;C;A; A;G;T; A;C;G; G;G;C; A;T;T;A ;A;T;T; G;A;C; T;G;A; G;G;T; A;A;A; G;C;G; C	G;C;A; G;A;A; T;C;T;T ;G;T;T; C;G;A; G;C;A; A;G;T; A;C;G; G;G;C; A;T;T;A ;A;T;T; G;A;C; T;G;A; G;G;T; A;A;A; G;C;G; C
AMPL16 90116	scaffold8	CCCAGTG ACATCAA ACAGAAA ATCA	CCTCAGA TTATGTT GCGCTAT TGTT	56(C-5%,A-97%);60(C-98%,T-3%);67(G-2%,A-99%);75(G-0%,A-100%);79(C-99%,T-3%);81(C-99%,T-3%);94(C-100%,T-0%);96(G-1%,A-99%);98(C-6%,T-97%);103(C-98%,T-6%);104(A-2%,G-7%,T-95%);109(A-3%,C-99%);110(C-3%,T-99%);115(C-96%,T-7%);118(C-96%,T-7%);119(A-0%,G-100%);140(G-1%,T-99%);141(C-99%,T-1%);143(C-1%,T-99%);169(A-1%,C-4%,T-	A;C;A; A;C;C; C;A;T;C ;T;C;T; C;C;G;T ;C;T;T; G;C	A;C;A; A;C;C; C;A;T;C ;T;C;T; C;C;G;T ;C;T;T; G;C

				97%);175(C-0%,G-100%);178(C-98%,T-4%);		
AMPL16 90117	scaffold8	TGGACCC TGTC AAT CCTAAAT CAAT	TTTGTCTT GTTTGTC TACAGTC TGC	80(G-1%,A-99%);84(C-100%,T-0%);85(A-1%,G-99%);99(G-1%,A-99%);100(C-99%,T-2%);102(G-1%,A-99%);106(C-99%,T-1%);111(C-5%,A-96%);122(G-1%,A-99%);126(A-1%,G-99%);132(C-100%,T-0%);139(G-1%,C-99%);170(G-99%,T-1%);174(C-1%,T-99%);177(G-1%,A-99%);	A;C;G; A;C;A; C;A;A; G;C;C; G;T;A	A;C;G; A;C;A; C;A;A; G;C;C; G;T;A
AMPL16 90118	scaffold8	AGAAAAC CAAGTCA TCGAAAT GGTC	ATGTGGC GCAACAA TTATATC ACAT	118(C-98%,T-3%);149(C-3%,T-98%);	C;T	C;T
AMPL16 90119	scaffold8	CAAGATG GCATCTT CTTGGGA A	GATGAAT GGAGAAA GCCGTAT GTAC	33(C-89%,T-32%);34(C-32%,T-89%);40(A-11%,C-99%);46(C-100%,T-0%);47(A-32%,G-89%);49(G-1%,C-100%,T-0%);59(A-33%,T-89%);61(C-1%,G-100%);66(G-89%,T-33%);67(A-100%,T-1%);74(A-11%,G-100%);76(C-23%,G-95%);79(A-12%,C-2%,G-98%);84(C-33%,T-89%);86(A-100%,T-10%);95(G-1%,A-100%);102(A-3%,G-99%);115(G-10%,A-100%);117(C-10%,T-100%);118(A-10%,G-100%);122(C-100%,T-10%);123(G-33%,A-89%);130(C-99%,T-3%);133(G-13%,A-100%);147(G-3%,C-99%);149(C-100%,T-3%);151(C-99%,T-2%);160(C-99%,T-7%);172(A-3%,G-21%,C-95%);173(C-21%,T-95%);181(C-100%,T-13%);182(C-10%,T-100%);186(A-89%,T-30%);189(C-4%,T-99%);191(C-23%,T-92%);192(G-3%,C-92%,T-23%);195(C-21%,G-97%);198(A-3%,C-100%);201(C-89%,T-32%);203(C-1%,T-100%);206(C-100%,T-10%);209(C-32%,A-89%,T-4%);	C;T;C;C ;G;C;T; G;G;A; G;G;G; T;A;A; G;A;T; G;C;A; C;A;C; C;C;C;C ;T;C;T; A;T;T;C ;G;C;C; T;C;A	T/C;T/C ;A/C;C; A/G;C; T/A;G;T /G;A;G/ A;G;G; C/T;A; A;G;G/ A;T/C; A/G;C/ T;A/G; C;A/G; C;C;C;C ;C;T/C/ T;C/T;A /T;T;T; C;G;C; C/T;T;C /T;A/C
AMPL16 90120	scaffold5	AACTCAT CTACTTA GCTTCGC ACAA	GTAGCTG CGAAAGA AGAGTGA AC	37(G-14%,C-96%);40(C-99%,T-1%);49(C-99%,T-1%);61(A-12%,C-20%,G-89%);64(C-0%,A-100%);69(G-3%,T-99%);84(G-7%,A-99%);86(C-100%,T-0%);90(A-3%,C-99%);96(G-7%,A-99%);98(G-6%,T-99%);99(A-96%,T-9%);100(C-89%,T-27%);101(C-6%,T-99%);104(C-0%,T-100%);108(G-1%,T-99%);118(A-19%,C-95%);122(G-0%,T-100%);130(G-6%,C-97%,T-3%);133(C-17%,T-95%);135(A-100%,T-0%);143(A-100%,T-0%);154(C-17%,G-95%);155(C-0%,T-100%);168(G-0%,T-100%);170(C-1%,A-99%,T-6%);171(C-98%,T-8%);174(G-13%,A-94%);179(G-6%,T-99%);180(G-2%,A-98%);183(G-100%,T-0%);184(G-7%,A-99%);185(C-8%,T-99%);189(C-100%,T-0%);194(A-3%,G-99%);196(A-7%,G-100%);197(G-7%,A-100%);199(C-6%,T-99%);200(A-0%,G-100%);201(G-0%,A-100%);203(G-6%,C-99%);205(C-100%,T-0%);206(A-8%,G-97%);207(A-8%,C-98%);217(C-100%,T-0%);219(A-1%,G-99%);220(C-0%,T-100%);222(A-2%,T-99%);223(A-3%,G-97%,T-0%);224(A-5%,T-98%);	C;C;C; G;A;T; A;C;C; A;T;A; C;T;T; C;T;C; T;A;A; G;T;T;A ;C;A;T; A;G;A; T;C;G; G;A;T; G;A;C; C;G;C; C;G;T; ;G;T	G/C;C; C;G/C; A;T;A; C;C;A;T ;A;T/C; T;T;T;C ;T;C;T; A;A;G; T;T;A;C ;A;T;A; G;A;T; C;G;G; A;T;G; A;C;C; G;C;C; G;T;T;G ;T

AMPL16 90121	scaffold7	GAACTTG AAGTCGA TGCTCAA AGTG	TATATCA TCTCAAC TATGCCC CTGG	43(C-0%,A-99%);45(G-17%,A-90%);46(G-99%,T-3%);48(G-0%,C-96%);49(C-1%,T-95%);62(A-0%,G-100%);64(C-3%,T-99%);73(C-21%,G-89%,T-2%);74(A-20%,G-92%);75(A-98%,T-6%);77(G-6%,A-98%);87(A-23%,T-91%);92(C-23%,A-91%);108(G-8%,T-90%);113(A-21%,G-90%);120(A-22%,G-89%);125(A-8%,T-99%);140(G-0%,A-100%);196(A-3%,G-96%,T-5%);198(A-5%,C-97%);199(A-0%,G-100%);223(G-22%,A-91%);224(A-24%,G-90%);	A;A;G; C;T;G;T ;G;G;A; A;T;A;T ;G;G;T; A;G;C; G;A;G	A;G/A; G;C;T; G;T;G/ C;G/A; A;A;A/ T;C/A;- /T;A/G; G/A;A/ T;A;G; C;G;A/ G;A/G
AMPL16 90123	scaffold15	TGGTCTA TCCCGGT ATCTCTA CTC	ATCCAAC GAATGTA GAAAGCA GAAT	43(C-13%,T-97%);48(C-6%,G-100%);49(C-3%,T-99%);51(C-97%,T-13%);57(C-6%,T-100%);71(C-100%,T-0%);74(G-13%,A-97%);93(C-6%,T-99%);99(A-3%,G-99%);101(G-5%,T-99%);106(C-8%,A-97%);111(C-97%,T-13%);112(G-0%,A-100%);116(C-0%,T-100%);124(A-5%,G-100%);126(A-100%,T-0%);128(A-100%,T-0%);129(C-100%,T-5%);162(C-5%,T-100%);170(A-0%,G-100%);177(C-13%,T-97%);182(C-98%,T-4%);217(A-97%,T-8%);224(A-1%,C-1%,T-100%);	T;G;T;C ;T;C;A; T;G;T;A ;C;A;T; G;A;A; C;T;G;T ;C;A;T	T;G;T;C ;T;C;A; T;G;T;A ;C;A;T; G;A;A; C;T;G;T ;C;A;T
AMPL16 90124	scaffold2	TATTCCC CTTCCTT CACCAAA AGAT	GACCTAG GCAAAAA TGACAAG GAAA	48(C-97%,T-5%);57(A-3%,G-98%);65(C-7%,T-96%);81(C-3%,A-98%);84(G-0%,C-100%);	C;G;T; A;C	C;G;T; A;C
AMPL16 90125	scaffold2	CTTGAAC TACGACT TTTCAGC CTAC	ACTCGGA ACAAGTT CGTGATA AAAC	47(G-6%,C-96%,T-0%);56(C-0%,T-100%);71(C-6%,A-97%);74(C-6%,T-97%);102(C-100%,T-0%);103(C-96%,T-6%);119(C-0%,A-99%);123(C-96%,T-6%);125(C-0%,T-100%);126(A-6%,G-97%);140(C-96%,T-7%);143(C-6%,T-96%);151(C-7%,T-96%);	C;T;A;T ;C;C;A; C;T;G;C ;T;T	C;T;A;T ;C;C;A; C;T;G;C ;T;T
AMPL16 90126	scaffold3	GCAGATC AGTCAGT AGATCTC CAAG	TTGTTTG ATGGACT AGTCTGG TGAA	52(G-1%,C-97%,T-4%);63(A-1%,G-100%);69(A-100%,T-0%);71(G-8%,A-97%);78(C-9%,T-96%);94(C-99%,T-3%);143(A-2%,C-100%);144(A-12%,T-97%);147(C-1%,G-99%);158(A-0%,T-100%);159(C-100%,T-0%);162(C-1%,T-99%);165(G-1%,A-99%);177(C-1%,T-99%);179(A-16%,G-95%);185(A-1%,G-99%);197(C-1%,T-99%);	C;G;A; A;T;C;C ;T;G;T; C;T;A;T ;G;G;T	C;G;A; A;T;C;C ;T;G;T; C;T;A;T ;G;G;T
AMPL16 90127	scaffold3	CCGTCAA CTTCAAC ACCTTAT TCTT	TTTGTAG CTACGCC CAATTCC AAAT	38(A-1%,C-100%);40(A-10%,C-97%);41(C-19%,G-5%,A-92%,T-1%);43(A-0%,G-100%);47(G-4%,A-98%);54(G-4%,T-96%);55(C-100%,T-0%);59(A-99%,T-12%);62(A-0%,C-100%);71(G-0%,C-100%);74(G-0%,A-100%);77(G-2%,A-99%);80(G-0%,A-100%);86(G-33%,A-87%);89(C-100%,T-1%);91(A-1%,G-99%);95(A-4%,C-96%);104(G-18%,A-94%);105(C-1%,T-99%);110(A-6%,C-100%);113(G-7%,C-100%);116(C-99%,T-1%);119(C-8%,G-98%);121(G-98%,T-8%);125(G-19%,C-94%);134(A-4%,G-100%);137(A-1%,G-10%,C-100%);138(G-97%,T-3%);139(G-2%,T-98%);140(A-0%,G-0%,C-100%);143(C-6%,G-1%,T-97%);146(A-0%,G-100%);149(A-0%,G-3%,C-97%);150(G-97%,T-3%);158(G-0%,C-98%,T-11%);161(G-14%,C-94%,T-8%);163(A-0%,C-100%);164(C-2%,G-100%);170(C-7%,G-97%);173(C-2%,G-	C;C;A; G;A;T; C;A;C; C;A;A; A;A;C; G;C;A; T;C;C;C ;G;G;C; G;C;G; T;C;T;G ;C;G;C; C;C;G; G;A;T; G;G;G; G;T;G; G;G;T; G;T;A; C	C;C;C/ A;G;A; T;C;A;C ;C;A;A; A;A/G; C;G;C; A;T;A/ C;C/G; C;G;G; C;G;C/ G;G;T; C;T;G;C ;G;C/T; G/C;C; G;G;A; T;G;G; G;G;T; G;G;G; T;G;T;A ;C

				2%,A-97%);176(C-0%,G-2%,T-99%);185(A-0%,G-100%);188(C-1%,G-99%,T-0%);203(A-0%,C-1%,G-99%);209(A-0%,G-100%);212(G-14%,T-97%);214(A-2%,G-99%);215(A-2%,C-0%,G-97%,T-2%);218(A-3%,G-97%);221(C-0%,G-12%,T-96%);224(C-3%,G-98%);227(C-0%,T-100%);228(A-100%,T-0%);229(G-0%,C-100%);		
AMPL16 90128	scaffold3	ACAGTTA CAGTGTA TGAGGAA ACGA	AATAGTG GTCAGTT TGTTTTG CTGG	73(G-8%,A-97%);94(G-0%,A-100%);	A;A	A/G;A
AMPL16 90129	scaffold3	CTTCGCT TACACCG AGGCTTC ATC	CTAGGAG GAGGAGG AATGAGA CG	39(C-29%,T-91%);45(G-3%,A-98%,T-0%);48(C-29%,A-91%);51(A-2%,C-98%);62(A-98%,T-2%);68(A-3%,G-100%);70(A-3%,G-100%);72(A-2%,T-98%);90(A-98%,T-2%);91(A-1%,G-100%);92(C-100%,T-2%);93(A-4%,G-99%);96(C-18%,T-95%);99(C-98%,T-1%);102(A-1%,C-96%);105(C-5%,T-95%);106(A-0%,C-99%);108(C-100%,T-1%);109(A-3%,C-99%);118(A-98%,T-7%);156(C-7%,G-99%);157(C-99%,T-7%);164(C-3%,T-100%);168(C-97%,T-9%);170(G-8%,T-99%);171(C-23%,T-90%);172(C-98%,T-4%);174(C-94%,T-19%);176(C-98%,T-1%);182(C-97%,T-20%);183(C-1%,G-100%);185(C-100%,T-0%);188(A-99%,T-0%);189(C-4%,T-99%);190(C-89%,T-30%);192(C-0%,T-99%);194(A-14%,C-97%);196(C-8%,G-20%,T-92%);197(G-1%,A-98%);200(A-0%,T-94%);201(C-0%,T-94%);220(G-13%,C-97%);240(A-2%,C-98%);241(C-98%,T-2%);	T;A;A; C;A;G; G;T;A; G;C;G; T;C;C;T ;C;C;C; A;G;C; T;C;T;T ;C;C;C; C;G;C; A;T;C;T ;C;T;A; T;T;C;C ;C	T/C;A;C /A;C;A; G;G;T; A;G;C; G;C/T;C ;C/-;T;C /-;C;C;A ;G;C;T; C;T;C/T ;C;T/C; C;T/C;G ;C;A;T; T/C;T;C ;G/T;A;- /T;/-;C ;C;C
AMPL16 90130	scaffold3	TAGTGGT AAGTAGA AAGGGAG AGGA	TCCTAAC AGTGAGT CATTCTG TGAG	105(C-0%,T-100%);139(G-0%,A-100%);201(G-0%,A-100%);	T;A;A	T;A;A
AMPL16 90131	scaffold4	GCCTACC AATATTT TACGCTG TCTC	TATTCTA GGAAACG CGTACGA GTAC	36(G-0%,A-20%,T-94%);37(G-1%,A-100%);38(A-26%,T-89%);40(C-2%,A-98%);45(A-1%,T-100%);47(G-0%,A-100%);51(G-0%,A-100%);52(G-95%,T-47%);53(C-100%,T-0%);58(G-99%,A-16%);74(C-100%,T-1%);76(G-0%,A-100%);81(C-23%,T-91%);82(G-5%,C-95%,T-1%);85(A-89%,G-5%,C-20%);88(C-93%,T-20%);94(A-2%,C-98%,T-0%);97(A-0%,G-100%);100(C-98%,T-2%);102(G-93%,A-20%);106(G-0%,A-100%);109(A-4%,G-96%);115(G-0%,A-100%);124(A-0%,G-100%);127(G-2%,A-98%);130(G-93%,A-20%);136(A-0%,G-100%);	T;A;T;A ;T;A;A; G/T;C; G;C;A; T;C;A;C ;C;G;C; G;A;G; A;G;A; G;G	T/A;A; A/T;A;T ;A;A;G; C;A/G; C;A;C/T ;C;C/A; C/T;C;G ;C;G/A; A;G;A; G;A;G/ A;G
AMPL16 90132	scaffold6	ATATGAG AGTCCAA TTTGTCC AGGT	CAGAATG CCACGCA CTATATT TCAT	42(C-3%,T-99%);76(G-6%,T-97%);80(C-99%,T-3%);82(C-100%,T-1%);83(G-97%,T-6%);99(C-4%,T-99%);107(A-1%,G-100%);110(A-1%,C-99%);112(A-0%,G-100%);123(A-0%,C-100%);130(A-100%,T-1%);144(A-1%,G-99%);145(A-2%,G-98%);148(C-1%,G-99%);151(A-1%,G-100%);167(C-9%,A-96%);175(A-0%,T-100%);188(G-2%,A-98%);190(C-9%,T-96%);206(C-100%,T-0%);	T;T;C;C ;G;T;G; C;G;C; A;G;G; G;G;A; T;A;T;C	T;T;C;C ;G;T;G; C;G;C; A;G;G; G;G;A; T;A;T;C

AMPL16 90133	scaffold6	GATGGTA TAAGGGA AAGAACA GTGC	TTGGTGG CAATAAT GTGAGCT AAAG	53(G-10%,A-95%);57(G-0%,A-100%);68(A-17%,G-93%);81(A-17%,G-93%);94(G-17%,T-93%);101(A-17%,T-93%);102(A-17%,T-93%);117(A-17%,T-93%);120(A-17%,C-93%);122(A-1%,G-100%);123(C-17%,T-93%);130(C-93%,T-17%);131(C-93%,T-17%);152(A-0%,G-100%);154(C-93%,T-17%);164(G-17%,A-94%);219(A-17%,C-94%);	A;A;G; G;T;T; ;T;C;G; T;C;C;G ;C;A;C	A;A;G; G;T;T; ;T;C;G; T;C;C;G ;C;A;C
AMPL16 90134	scaffold6	TCAAGTA AGTACTC ACGACCA GATG	TCCACTC AGTATGT CTCTTGT ATGC	36(C-0%,T-100%);130(C-2%,T-99%);153(C-97%,T-3%);	T;T;C	T;T;C
AMPL16 90135	scaffold6	TGGTGAA AGACAAA GGGGTAG ATAT	GGGCATC TCAATTC GTGAAAT GTTA	174(G-11%,A-95%);	A	A
AMPL16 90138	scaffold6	CATTACG GTGCGTT CAAGGAT AAG	TTGACCT TCACTGT CTACTTT CTCG	39(C-8%,G-98%);42(A-3%,G-100%);45(C-100%,T-0%);62(C-13%,T-96%);65(A-100%,T-1%);66(A-13%,T-96%);67(A-9%,G-97%);68(G-1%,C-99%);71(G-3%,T-100%);75(C-2%,G-10%,A-95%);78(C-3%,T-99%);79(C-95%,T-15%);80(G-0%,A-100%);82(C-0%,G-100%);84(A-0%,T-100%);85(A-12%,G-97%);86(C-1%,T-100%);92(A-16%,G-94%);99(A-9%,G-97%);103(A-0%,G-1%,C-94%,T-12%);104(C-100%,T-1%);105(G-11%,A-95%);106(G-4%,T-100%);117(C-4%,G-100%);120(A-4%,G-100%);126(G-0%,C-100%);128(G-4%,A-97%);141(C-97%,T-9%);150(C-4%,T-100%);153(G-0%,A-100%);156(C-95%,T-15%);162(G-15%,A-95%);165(G-0%,A-100%);168(C-94%,T-16%);173(A-0%,G-100%);174(G-16%,A-94%);183(C-2%,T-99%);189(G-0%,T-100%);192(C-99%,T-2%);198(C-16%,T-93%);201(A-1%,G-99%);207(G-16%,T-93%);209(C-16%,T-93%);213(A-5%,G-96%);218(G-97%,T-12%);219(A-1%,T-99%);	G;G;C; T;A;T;G ;C;T;A; T;C;A; G;T;G;T ;G;G;C; C;A;T; G;G;C; A;C;T; A;C;A; A;C;G; A;T;T;C ;T;G;T; T;G;G;T	C/G;G; C;T/C;A ;T/A;A/ G;C;T; G/A;T; C/T;A; G;T;A/ G;T;A/ G;A/G; C/T;C;G /A;T;G; G;C;A; C/T;T;A ;T/C;A/ G;A;T/ C;G;G/ A;T;T;C ;T/C;G; G/T;C/T G;G/T; T
AMPL16 90139	scaffold7	TAATGTC TCCCTTG CTCCATC GAAT	TGATCAG TGGTACT GTTCAAG ATCG	38(G-100%,T-0%);47(G-34%,A-99%);62(A-0%,T-100%);76(G-1%,C-99%);83(C-100%,T-0%);88(G-35%,C-98%);89(C-35%,T-98%);92(A-98%,T-35%);93(C-35%,T-98%);97(A-98%,T-35%);105(G-35%,C-98%);117(C-34%,A-98%);118(C-98%,T-34%);127(C-34%,T-98%);129(C-35%,T-98%);139(C-98%,T-34%);141(C-34%,T-98%);145(C-34%,T-98%);149(G-35%,T-98%);157(G-0%,C-100%);160(C-34%,T-98%);173(C-34%,G-98%,T-0%);181(A-0%,G-100%);188(C-99%,T-34%);189(C-100%,T-0%);191(C-100%,T-0%);192(C-0%,T-100%);	G;A;T; C;C;C;T ;A;T;A; C;A;C;T ;T;C;T; T;T;C;T ;G;G;C; C;C;T	G;A;T; C;C;C;T ;A;T;A; C;A;C;T ;T;C;T; T;T;C;T ;G;G;C; C;C;T
AMPL16 90140	scaffold7	CTGAATT CAGCTAC AAGAAAA CGGT	CTATGAG TGTCGAT ATTACGG CTCA	36(C-99%,T-2%);41(C-7%,T-94%);48(G-1%,A-100%);59(A-2%,G-98%);60(A-3%,G-98%);61(G-6%,A-95%);65(G-97%,T-3%);66(C-1%,T-99%);85(C-99%,T-2%);91(C-99%,T-1%);100(C-2%,G-99%);111(C-100%,T-0%);120(C-100%,T-0%);133(G-98%,T-2%);142(A-2%,G-98%);160(A-99%,T-1%);169(C-99%,T-1%);172(A-2%,G-98%);174(G-0%,C-100%);175(G-6%,A-95%);182(G-6%,T-96%);191(G-4%,A-97%);196(G-0%,A-100%);201(G-6%,A-	C;T;A; G;G;A; G;T;C;C ;G;C;C; G;G;A; C;G;C; A;T;A; A;A;G; A;G;G; A	C;T;A; G;G;A; G;T;C;C ;G;C;C; G;G;A; C;G;C; A;T;A; A;A;G; A;G;G; A

				96%);210(A-0%,G-100%);213(C-0%,A-100%);214(A-0%,G-100%);217(A-0%,G-100%);220(G-0%,A-100%);		
AMPL16 90141	scaffold8	CATTCCC CGTACTA TTCAGAT ACGT	TCCTGTT ATCCTAG ACTTATT CGCG	47(C-99%,T-1%);59(G-2%,A-98%);62(G-0%,A-100%);74(C-100%,T-0%);75(A-0%,G-100%);95(C-3%,T-97%);104(G-1%,A-100%);107(A-1%,C-100%);110(A-0%,G-100%);122(G-1%,A-100%);127(A-0%,G-100%);128(G-0%,T-100%);137(C-0%,A-100%);152(G-0%,A-100%);	C;A;A; C;G;T; A;C;G; A;G;T; A;A	C;A;A; C;G;T; A;C;G; A;G;T; A;A
AMPL16 90142	scaffold8	TTTTCAA CCTGGAG ACGAAGA TTGA	AACAATA CGCAATC GATACCA AGAC	47(A-7%,G-97%);48(G-2%,C-99%);53(G-99%,T-2%);56(G-2%,A-98%);58(A-0%,C-100%);61(C-0%,T-100%);62(C-3%,T-99%);63(G-5%,A-99%);65(G-8%,T-96%);71(G-6%,A-98%);79(G-2%,A-100%);83(G-10%,T-95%);100(C-95%,T-8%);101(G-5%,A-97%);102(C-3%,A-99%);113(C-98%,T-6%);116(G-0%,A-100%);120(G-100%,T-0%);122(G-2%,C-100%);123(C-10%,T-95%);127(G-2%,C-99%);130(C-3%,G-99%);140(G-2%,T-99%);141(A-2%,C-98%);150(C-2%,G-98%);206(A-2%,G-99%);230(C-5%,T-97%);235(C-97%,T-0%);	G;C;G; A;C;T;T ;A;T;A; A;T;C; A;A;C; A;G;C; T;C;G;T ;C;G;G; T;C	G;C;G; A;C;T;T ;A;T;A; A;T;C; A;A;C; A;G;C; T;C;G;T ;C;G;G; T;C
AMPL16 90143	scaffold8	AAATCCA GGGCGCT GTGTTT	TATCACG AATGTGC CAATCCT CTTC	No_variant	No_vari ant	No_vari ant
AMPL16 90144	scaffold8	TAGCTCG ATGTTTG TATGGTT GGAT	TATAGCT CGATCGA ATCAGTC TGTC	37(C-0%,T-100%);39(A-0%,C-100%);43(C-100%,T-0%);44(C-98%,T-3%);61(A-1%,G-99%);70(A-1%,C-99%);135(C-0%,T-100%);149(C-1%,G-100%);153(C-1%,T-100%);163(A-0%,G-100%);167(C-1%,T-100%);176(A-11%,G-96%);198(G-0%,T-100%);229(A-1%,G-99%);232(A-12%,G-94%);	T;C;C;C ;G;C;T; G;T;G;T ;G;T;G; G	T;C;C;C ;G;C;T; G;T;G;T ;G/A;T; G;G/A
AMPL16 90145	scaffold8	GATTGAG TGTGTCA GCAGAAT CTTG	TGTTAGA CAGATAG GACACGA AGAC	36(C-1%,A-99%);42(A-0%,G-100%);53(A-99%,T-3%);65(A-0%,G-100%);69(A-1%,C-100%);77(A-10%,T-96%);80(G-3%,A-99%);92(A-0%,C-100%);99(A-10%,G-97%);100(C-100%,T-0%);113(C-2%,T-99%);117(G-7%,C-98%);136(C-97%,T-10%);144(C-100%,T-0%);146(G-11%,T-99%);147(C-98%,T-7%);149(C-7%,T-98%);	A;G;A; G;C;T; A;C;G; C;T;C;C ;C;T;C; T	A;G;A; G;C;T; A;C;G; C;T;C;C ;C;G/T; C;T
AMPL16 90150	scaffold10	CATCAAA GAATGCA GAGTCGT ACTC	ATGGTAC CAAAGGA AGACATG AAAC	44(C-100%,T-2%);47(A-13%,G-97%);59(G-91%,A-29%);71(G-0%,T-100%);80(A-1%,G-100%);92(C-29%,T-91%);93(A-0%,G-100%);101(G-4%,T-100%);104(C-97%,T-24%);116(G-97%,T-23%);119(C-23%,T-97%);131(A-97%,G-23%);134(C-100%,T-0%);138(A-11%,G-99%);140(A-23%,T-97%);145(G-2%,C-100%);157(A-0%,G-100%);158(C-100%,T-1%);	C;G;G; T;G;T;G ;T;C;G; T;A;C; G;T;C; G;C	C;G;A/ G;T;G;T /C;G;T; C/T;T/G ;T/C;G/ A;C;G; A/T;C; G;C
AMPL16 90151	scaffold2	CAGTTCT GTTTATA CACGGAA TGAA	AACTTTG CAAATCC GTCTATC AGTC	45(A-77%,G-97%);127(A-0%,G-100%);141(G-7%,C-100%);157(A-15%,T-85%);161(C-0%,T-100%);	G/A;G; C;T/-;T	A/G;G; C;T/A;T
AMPL16 90152	scaffold3	GACATAC ACAAAAC TCTACGC TCTG	GTAATGC AAAGTGG ATGATTG GGAA	50(C-98%,T-4%);58(G-100%,T-0%);67(C-4%,T-98%);68(G-1%,A-99%);108(G-0%,C-100%);117(C-94%,T-13%);121(C-0%,T-100%);122(G-13%,A-94%);131(G-100%,T-0%);133(C-13%,G-94%);134(C-100%,T-0%);135(G-99%,T-1%);136(C-94%,T-13%);152(A-1%,G-99%);162(C-12%,T-	C;G;T; A;C;C;T ;A;G;G; C;G;C; G;T;G;T ;G;C;C; T;T;T;G	C;G;T; A;C;C;T ;A;G;G; C;G;C; G;T;G;T ;G;C;C; T;T;T;G

				95%);184(A-0%,G-100%);195(G-1%,T-99%);201(A-4%,G-97%,T-1%);202(G-1%,C-99%);205(C-100%,T-0%);213(C-1%,T-99%);221(C-1%,T-99%);224(C-0%,T-100%);229(A-1%,G-99%);		
AMPL16 90154	scaffold6	CGTCAGA CACACCT GGTATAT TTTC	CCAAGCG GAAACAA ACAAATA TTCC	41(G-1%,C-99%);43(A-4%,C-2%,G-97%);61(A-4%,G-97%);70(A-0%,G-100%);71(G-1%,A-99%);77(C-98%,T-3%);78(A-5%,G-99%);90(A-0%,G-100%);98(A-3%,G-97%,T-2%);99(C-4%,T-98%);103(G-1%,T-99%);115(G-2%,C-99%);117(C-1%,T-100%);120(C-99%,T-2%);152(G-9%,A-95%);153(C-2%,T-99%);156(G-2%,C-99%);174(G-1%,A-99%);175(C-1%,T-99%);180(C-0%,G-100%);181(C-3%,T-99%);182(A-0%,G-99%);189(C-99%,T-1%);	C;G;G; G;A;C; G;G;G; T;T;C;T ;C;A;T; C;A;T; G;T;G; C	C;G;G; G;A;C; G;G;G; T;T;C;T ;C;A;T; C;A;T; G;T;G; C
AMPL16 90155	scaffold6	GAGCGTG ATTGTAG CTGTCTGA TAG	GACATAC CTTCCCA GCCTTGT AAG	57(A-3%,G-98%);67(C-3%,G-98%);68(G-3%,A-98%);71(C-98%,T-3%);90(C-98%,T-3%);103(C-98%,T-3%);168(C-3%,G-98%);169(G-98%,T-3%);170(C-3%,A-98%);172(G-3%,A-98%);176(A-3%,G-98%);180(G-98%,T-3%);194(A-3%,C-98%);195(C-98%,T-3%);	G;G;A; C;C;C; G;G;A; A;T;G; C;C	G;G;A; C;C;C; G;G;A; A;T;G; C;C
AMPL16 90156	scaffold8	GTATAAA GCCCCA GCCTTCT TACT	AACACGG ATGACAA GATCCAT ATCT	37(G-7%,A-97%);41(A-2%,G-99%);43(C-100%,T-1%);46(C-100%,T-1%);47(A-26%,G-89%);62(C-100%,T-1%);66(C-99%,T-7%);68(C-0%,T-100%);71(C-95%,T-15%);79(C-15%,G-95%);84(G-0%,A-100%);92(G-0%,A-100%);97(C-95%,T-1%);98(C-0%,T-95%);102(A-0%,C-95%,T-14%);105(C-19%,T-92%);108(A-0%,G-100%);110(C-100%,T-3%);128(G-0%,A-100%);129(G-95%,T-15%);130(C-17%,T-93%);133(C-95%,T-14%);134(C-14%,G-0%,T-95%);141(C-2%,T-99%);143(G-17%,A-94%);145(C-14%,A-95%);146(C-0%,T-100%);152(C-100%,T-0%);159(A-15%,C-0%,G-95%);161(G-0%,A-100%);164(G-100%,T-0%);168(A-2%,G-99%);169(A-2%,C-99%);179(A-3%,G-99%);185(G-14%,A-95%);	A;G;C; C;G;C; C;T;C;G ;A;A;C; T;C;T;G ;C;A;G; T;C;T;T ;A;A;T; C;G;A; G;G;C; G;A	A;G;C; C;A/G; C;C;T;C ;G;A;A; C;T;C;T ;G;C;A; G;T;C;T ;T;A;A; T;C;G; A;G;G; C;G;A
AMPL16 90157	scaffold1	AAATGGT GCATGGC GATAAAT ACAA	AATCAAA ATAACTG GGCTGCA GTAC	48(C-100%,T-0%);59(C-0%,A-100%);87(A-4%,G-98%);90(A-3%,G-98%);123(A-4%,G-98%);154(C-97%,T-4%);160(A-0%,G-100%);168(A-0%,C-100%);202(A-4%,G-97%);215(A-0%,G-100%);	C;A;G; G;G;C; G;C;G; G	C;A;G; G;G;C; G;C;G; G
AMPL16 90159	scaffold5	CTTTCGT CATACCC CGTACTT CTAT	ATAACTC CTCAACC ACCATGT CTTC	79(G-1%,C-99%);101(C-8%,A-100%);103(G-10%,A-99%);104(C-2%,A-99%);106(A-10%,G-99%);130(C-68%,A-82%);133(A-68%,G-82%);145(C-47%,A-82%,T-23%);152(C-91%,T-47%);161(G-47%,A-91%);167(C-1%,T-99%);177(A-76%,G-80%);203(G-91%,T-47%);217(C-0%,T-100%);220(C-98%,T-14%);224(G-100%,T-0%);	C;A;A; A;G;C/ A;G/A; C/A;T/C ;A/G;T; G/A;G/ T;T;C;G	C;A;A; A;G;C/ A;A/G; A/T;C; A;T;A/ G;G;T; C;G
AMPL16 90160	scaffold7	GCAGGGA TCTTGAG GATAGAT TCAA	GCCCAT ACATCAC GGTTATC AAAG	39(C-1%,T-100%);42(C-99%,T-3%);69(G-1%,A-100%);76(A-0%,G-100%);83(C-87%,T-45%);84(A-1%,G-99%);90(A-1%,G-100%);93(G-0%,A-100%);106(C-99%,T-1%);112(A-1%,G-99%);113(C-2%,T-99%);116(C-2%,T-100%);120(G-2%,A-99%);131(C-99%,T-1%);132(A-33%,G-97%);150(G-100%,T-0%);163(C-0%,G-98%,T-2%);165(G-34%,A-96%);171(C-99%,T-1%);172(A-1%,G-99%);185(C-2%,T-	T;C;A; G;C;G; G;A;C; G;T;T;A ;C;G;G; G;A;C; G;T;C; A	T;C;A; G;C;G; G;A;C; G;T;T;A ;C;G;G; G;A;C; G;T;C; A

				100%);192(A-15%,G-2%,C-93%,T-2%);195(G-51%,A-80%);		
AMPL16 90161	scaffold7	CGTTGGA AGGGAAA TATGAAG AAGG	GAGACTA ATTTTAG CACGTGA GTCG	41(C-52%,G-96%);68(G-1%,A-100%);77(C-100%,T-1%);91(C-100%,T-1%);95(A-1%,G-100%);108(A-2%,T-99%);109(G-100%,T-0%);110(G-1%,A-100%);115(C-16%,T-96%);120(C-3%,A-99%);134(A-23%,G-92%);145(A-11%,G-98%);147(C-2%,A-99%);158(A-3%,G-100%);160(C-100%,T-0%);174(C-1%,A-100%);181(A-2%,G-99%);187(A-0%,G-100%);202(G-2%,T-99%);203(G-1%,C-100%);207(C-22%,A-94%,T-1%);208(C-0%,T-100%);210(C-99%,T-2%);222(C-92%,T-21%);224(C-19%,G-94%,T-3%);229(A-0%,G-100%);	C/G;A; C;C;G;T ;G;A;T; A;G;G; A;G;C; A;G;G; T;C;A;T ;C;C;G; G	G;A;C; C;G;T; G;A;C/ T;A;A/ G;G;A; G;C;A; G;G;T; C;C/A;T ;C;T/C; G/C;G
AMPL16 90162	scaffold3	AATACAA CGGTGAT AGCTACG GATT	ACCTGGG ATATTTT TACAAGT AAACTGG	36(C-14%,T-96%);37(A-0%,G-100%);39(A-16%,C-92%);41(A-14%,G-96%);42(C-100%,T-0%);50(C-96%,T-14%);51(G-14%,C-96%);59(C-100%,T-0%);67(A-16%,G-92%);79(C-96%,T-13%);92(C-96%,T-14%);107(C-96%,T-14%);108(C-5%,G-26%,A-84%);110(C-96%,T-10%);128(A-13%,G-96%);132(A-14%,G-96%);138(A-14%,G-96%);154(C-96%,T-10%);162(C-96%,T-14%);167(A-14%,G-96%);171(G-3%,A-100%);180(C-99%,T-5%);181(C-92%,T-16%);206(G-1%,A-100%);210(A-14%,C-96%);213(A-14%,G-96%);214(C-100%,T-4%);216(C-100%,T-0%);222(A-10%,G-96%,T-4%);226(C-100%,T-0%);227(A-13%,G-96%);	T;G;C; G;C;C; C;C;G; C;C;C; A;C;G; G;G;C; C;G;A; C;C;A; C;G;C; C;G;C; G	T;G;C; G;C;C; C;C;G; C;C;C; A;C;G; G;G;C; C;G;A; C;C;A; C;G;C; C;G;C; G
AMPL16 90164	scaffold12	GAGGATC AGCATGG GTTTGC	AAACACC TTCCGCA TTAGACA AAAA	43(A-93%,T-12%);64(G-1%,A-100%);90(A-1%,T-99%);94(A-4%,C-99%);101(G-1%,A-100%);129(G-16%,T-92%);130(C-93%,T-14%);150(C-2%,T-99%);153(A-2%,G-99%,T-2%);158(A-2%,G-99%);159(G-2%,A-99%);168(G-2%,A-99%);184(G-2%,T-98%);194(C-99%,T-2%);198(G-93%,A-14%);200(C-2%,A-98%);202(G-16%,T-92%);204(A-93%,G-14%);217(C-100%,T-1%);225(C-1%,T-100%);227(A-1%,G-100%);233(G-100%,T-1%);	A;A;T; C;A;T;C ;T;G;G; A;A;T; C;G;A; T;A;C;T ;G;G	A/T;A;T ;C;A;T/ G;T/C;T ;G;G;A; A;T;C; G/A;A; G/T;G/ A;C;T; G;G
AMPL16 90168	scaffold5	CAGCATA TTGGCAC ATACGTA GTTT	ATCGTTC CAAGTTT TACGTAG GTCA	45(A-89%,T-65%);46(G-0%,A-100%);49(C-100%,T-3%);70(G-65%,A-89%);73(A-6%,G-100%);81(C-0%,A-100%);99(A-10%,G-100%);102(A-68%,G-83%);115(C-100%,T-3%);126(A-3%,G-100%);160(C-17%,T-99%);184(G-1%,A-100%);187(A-0%,G-100%);194(A-0%,T-100%);195(A-0%,G-100%);203(C-3%,T-100%);204(A-3%,G-100%);212(A-10%,C-100%);213(G-80%,T-73%);214(A-1%,C-100%);218(G-78%,T-79%);220(C-73%,T-81%);221(G-1%,A-100%,T-1%);222(C-100%,T-1%);223(A-31%,C-1%,G-48%,T-80%);225(G-69%,T-85%);226(C-73%,A-81%,T-0%);227(C-0%,T-100%);228(C-21%,T-97%);229(A-100%,T-2%);	A/T;A; C;G/A; G;A;G; A/G;C; G;T;A; G;T;G;T ;G;C;T/ G;C;G/ T;C/T;A ;C;T/G; T/G;A/ C;T;T;A	T/A;A; C;A/G; G;A;G; A/G;C; G;T;A; G;T;G;T ;G;C;T/ G;C;T/ G;T/C; A;C;A/ T;G/T;A /C;T/ C;A

AMPL16 90169	scaffold7	GACTGAC CTTAATC TCCACCT CG	CACATCG TACCCAA TGTTGTA CTTG	34(C-100%,T-3%);40(A-100%,T-0%);52(G-1%,A-99%,T-0%);58(C-98%,T-14%);61(G-2%,A-99%);64(G-0%,A-100%);65(C-1%,T-99%);67(C-96%,T-17%);70(A-3%,G-99%);71(C-1%,A-100%);73(A-2%,G-100%);76(G-0%,A-100%);79(G-1%,A-100%);82(C-100%,T-0%);85(C-100%,T-0%);88(C-4%,G-3%,T-98%);91(C-1%,T-100%);97(A-0%,C-100%);115(C-99%,T-3%);129(C-100%,T-0%);130(A-0%,G-100%);131(C-0%,G-100%);133(A-0%,G-100%);136(A-1%,G-100%);139(G-20%,A-95%);145(A-1%,C-6%,G-100%);148(A-1%,G-100%);151(G-12%,A-98%);154(A-6%,G-100%);157(G-100%,T-4%);160(A-0%,C-100%,T-2%);161(A-0%,C-100%);162(C-0%,G-100%);163(A-0%,G-100%);166(G-100%,T-0%);169(C-100%,T-1%);170(A-0%,G-100%);171(G-0%,C-100%);172(A-4%,C-1%,T-99%);178(C-0%,T-100%);180(A-0%,G-100%);181(A-9%,G-97%,T-0%);190(A-0%,C-100%,T-0%);192(A-1%,C-99%);193(C-1%,A-99%,T-0%);	C;A;A; C;A;A; T;C;G; A;G;A; A;C;C;T ;T;C;C; C;G;G; G;G;A; G;G;A; G;G;C; C;G;G; G;C;G; C;T;G; ;G;C;C; A	C;A;A; T/C;A; A;T/T/C ;G;A;G; A;A;C; C;T;T;C ;C;C;G; G;G;G; A/G;G; G;A;G; G;C;C; G;G;G; C;G;C;T ;T;G;G; C;C;A
AMPL16 90170	scaffold9	TCTATGT CACCACC AACATCT ACTC	CAACCAT AGTACCC AGAGGAT ACC	69(C-2%,T-98%);71(C-1%,G-62%,A-80%);80(C-100%,T-1%);104(A-2%,G-98%);105(C-100%,T-0%);108(C-100%,T-0%);110(G-2%,A-98%);111(A-0%,C-100%);114(A-0%,G-100%);119(G-100%,T-0%);120(C-2%,G-98%);121(G-1%,A-98%,T-2%);125(C-1%,T-100%);131(C-100%,T-0%);134(C-100%,T-0%);135(A-0%,G-100%);143(G-0%,T-100%);144(C-1%,T-100%);145(G-1%,C-100%);150(G-6%,A-99%);157(A-27%,G-90%);163(C-1%,T-99%);164(C-0%,G-100%);166(G-14%,A-97%);169(A-0%,G-1%,C-100%);175(C-100%,T-8%);178(C-7%,T-98%);193(G-100%,T-0%);200(A-0%,G-100%);202(C-2%,T-100%);	T;G/A; C;G;C; C;A;C; G;G;G; A;T;C;C ;G;T;T; C;A;G; T;G;A; C;C;T;G ;G;T	T;A;C; G;C;C; A;C;G; G;G;A; T;C;C;G ;T;T;C; A;G/A; T;G;G/ A;C;T/C ;T;G;G; T
AMPL16 90172	scaffold4	TATCTCT TCATCAT TCCACGT TCGT	AGATGGA GATGGGA AGTAGCT CTAT	74(C-100%,T-2%);84(A-93%,C-20%);89(G-3%,T-99%);167(C-95%,G-19%);198(C-49%,T-90%);	C;A;T;C ;T/C	C;A/C;T ;C/G;T
AMPL16 90173	scaffold1	TATATCT AACGCCT CCTAGAT TGGC	AAACCAC GACCTAA ATTTCGC C	41(C-57%,G-0%,A-88%,T-12%);62(A-6%,C-100%);68(C-0%,T-100%);88(C-100%,T-0%);89(A-0%,G-100%);92(A-100%,T-0%);95(A-0%,G-100%);113(G-0%,A-100%);115(G-1%,C-99%);116(A-3%,T-99%);126(G-1%,C-100%);128(C-1%,T-99%);129(G-0%,A-100%);130(G-0%,A-99%,T-0%);134(C-10%,T-99%);143(C-0%,T-100%);145(C-0%,A-100%);146(A-97%,T-19%);149(G-99%,T-1%);164(C-1%,T-99%);167(A-2%,C-100%);171(C-0%,T-100%);179(G-3%,T-100%);185(C-100%,T-0%);212(C-6%,T-100%);	C/A;C;T ;C;G;A; G;A;C; T;C;T;A ;A;T;T; A;A;G; T;C;T;T ;C;T	A;C;T;C ;G;A;G; A;C;T;C ;T;A;A; T;T;A;A ;G;T;C; T;T;C;T
AMPL16 90174	scaffold10	GAACGGC ACCATCA TCTTCGA	TGGCGCG AAGACTT GGAGT	34(C-100%,T-0%);40(C-100%,T-3%);43(C-18%,T-97%);44(C-9%,T-99%);48(G-88%,A-32%);58(C-98%,G-12%);61(C-12%,T-98%);67(C-4%,A-99%);70(C-98%,T-12%);73(A-0%,C-99%,T-3%);88(G-0%,A-100%);94(C-0%,A-12%,T-98%);113(C-100%,T-0%);115(C-0%,T-100%);118(A-0%,T-100%);119(C-97%,T-19%);120(C-100%,T-1%);122(A-2%,T-	C;C;T;T ;G;C;T; A;C;C; A;T;C;T ;T;C;C; T;G;T;T ;T;A;A; T;C;G;	C;C;C/T ;C/T;A/ G/G/C; T;C;A;T /C;C;A; T/A;C;T ;T;C/T; C;T;G;T

				100%);129(A-2%,G-100%);130(C-11%,T-98%);134(C-2%,T-100%);146(C-2%,G-0%,T-99%);147(C-3%,A-96%);149(A-89%,C-32%);150(A-9%,G-25%,T-89%);151(A-3%,G-0%,C-99%,T-1%);152(G-99%,T-3%);153(A-91%,C-30%);154(C-32%,T-89%);159(C-2%,T-100%);162(G-0%,A-100%);180(C-0%,T-100%);218(G-0%,A-100%);225(G-89%,T-31%);228(C-100%,T-0%);	A;T;T;A ;T;A;G; C	/C;T;T; A;A/C; T/G;C; G;A/C; C/T;T;A ;T;A;T/ G;C
AMPL16 90175	scaffold6	GAGTCCA GACCTAT CATAGTA AGCT	CTTGATC AGCATTG CCAACCTA TACG	59(C-1%,T-100%);73(A-61%,G-86%);169(G-13%,A-92%);	T;A/G; A	T;G;A
AMPL16 90176	scaffold8	TTCAGGT GATCCTT GGATTCC AATA	GACTAGG CTTCCTA TCTGTGG AAG	36(A-2%,G-98%);39(G-1%,A-100%);51(A-1%,T-100%);57(G-7%,C-100%);63(C-100%,T-0%);78(C-0%,A-100%);87(G-2%,A-98%);90(C-89%,T-25%);93(G-2%,A-98%);99(A-6%,G-96%);105(C-100%,T-0%);117(A-2%,G-99%);123(G-3%,C-98%);124(G-0%,C-100%);131(C-0%,T-100%);134(G-1%,A-100%);137(G-1%,T-100%);138(A-0%,G-100%);146(C-96%,T-4%);147(A-35%,G-81%);149(A-98%,T-4%);150(G-8%,C-92%,T-2%);153(C-100%,T-0%);157(G-1%,A-100%);161(G-12%,T-95%);162(C-100%,T-0%);163(G-0%,A-100%);167(A-0%,G-100%);176(A-0%,C-1%,G-100%,T-0%);179(A-5%,G-96%);185(A-0%,G-100%);190(C-7%,T-95%);202(C-0%,A-100%);208(C-2%,T-98%);209(A-100%,T-1%);210(A-36%,G-82%);213(G-0%,A-100%);215(A-1%,G-100%);218(C-100%,T-0%);219(A-1%,C-0%,G-100%);220(C-1%,T-100%);222(C-1%,A-100%);223(G-2%,A-99%);224(C-100%,T-0%);228(C-90%,T-20%);229(C-100%,T-2%);235(C-100%,T-0%);	G;A;T; C;C;A; A;C;A; G;C;G; C;C;T;A ;T;G;C; G;A;C; C;A;T;C ;A;G;G; G;G;T; A;T;A; G;A;G; C;G;T; A;A;C; C;C;C	G;A;T; G/C;C; A;A;T/ C;A;G; C;G;C; C;T;A;T ;G;C;G/ A;A;C; C;A;T;C ;A;G;G; G;G;T; A;T;A; G/A;A; G;C;G; T;A;A; C;C;C;C
AMPL16 90178	scaffold6	GAAGTAC AGCAGGC ATAGGAC TTAC	ATACATT TTGAACC GTTGCAA TCGA	183(A-100%,T-0%);206(A-0%,G-100%);213(G-21%,A-89%);	A;G;A	A;G;A
AMPL16 90180	scaffold1	GGTTTGA AGACAAT ATGAAAC CCGT	GTTTTTC GAAACGG GGTATAC AGTT	36(A-10%,G-100%);48(C-100%,T-0%);74(C-100%,T-0%);81(A-0%,G-100%);109(G-0%,T-100%);117(G-95%,A-27%);123(A-95%,G-27%);144(C-0%,T-100%);160(C-100%,T-0%);161(A-0%,G-100%);181(C-87%,G-39%);182(C-87%,A-39%);188(A-2%,C-87%,T-38%);189(A-0%,G-18%,C-98%);190(A-10%,T-100%);191(A-87%,C-39%);198(A-95%,T-27%);222(A-0%,T-100%);	G;C;C; G;T;G; A;T;C; G;C;C; C;C;T;A ;A;T	G;C;C; G;T;A/ G;G/A; T;C;G;C /G;A/C; T/C;C;T ;A/C;T/ A;T
AMPL16 90181	scaffold10	GACTTGA TACCACC ATGGGTA GAG	TTGAGGA GCAACAA GTGTGTC CTT	37(A-0%,G-100%);39(A-0%,G-100%);40(G-2%,A-99%);41(A-85%,G-35%);42(A-0%,C-84%,T-35%);44(G-100%,T-0%);46(C-1%,G-84%,A-19%,T-22%);48(A-1%,G-100%,T-0%);51(A-1%,G-100%);52(C-0%,A-100%);53(A-100%,T-0%);54(A-1%,G-99%);55(G-93%,T-23%);57(G-100%,T-0%);59(A-20%,G-96%);60(G-0%,A-100%);62(A-84%,C-13%,T-28%);67(G-1%,A-99%);73(C-2%,T-100%);82(G-1%,C-33%,T-87%);85(C-100%,T-1%);91(A-1%,C-1%,G-99%);94(A-1%,G-99%);118(A-2%,G-98%);121(A-1%,C-0%,G-99%);127(A-88%,G-	G;G;A; A;C;G; G;G;G; A;A;G; G;G;G; A;A;A; T;T;C;G ;G;G;G; A;C;G; T;C;C;G ;C;T;G; G;A;G; G;T;A;	G;G;A; G/A;C/ T;G;G/ A;G;G; A;A;G; G;G;G; A;A;T; A;T;T/C ;C;G;G; G;G;G/ A;C;G; T;C;C;G ;C;T;G;

				32%);130(C-99%,T-2%);133(A-2%,G-99%);139(C-23%,T-93%);145(C-96%,T-20%);148(C-100%,T-4%);151(A-1%,G-100%);160(C-100%,T-0%);163(C-13%,T-99%);166(A-4%,G-100%);184(A-2%,G-98%);187(A-86%,G-1%,T-33%);190(A-2%,G-98%);193(G-86%,A-34%);199(C-35%,T-85%);202(C-2%,A-98%);208(C-100%,T-0%);217(C-12%,T-98%);220(G-87%,A-33%,T-0%);226(C-98%,T-12%);228(G-0%,C-100%);235(A-0%,C-100%);	C;T;G;C ;C;C	G;T/A; G;G/A; C/T;A;C ;T/C;A/ G;T/C;C ;C
AMPL16 90184	scaffold5	GACCTCT CGCTACT CTCACAT TTAT	GCGTCTG ACTACGA TGAAATT TGTA	39(G-0%,A-100%);40(C-0%,T-100%);48(A-1%,T-100%);55(A-10%,C-98%);65(C-0%,T-100%);68(C-11%,T-99%);74(A-100%,T-0%);78(G-100%,T-0%);83(G-0%,T-100%);84(A-100%,T-0%);85(C-1%,T-99%);88(G-100%,T-0%);90(A-0%,G-100%);95(G-1%,T-100%);96(A-23%,G-93%);98(A-3%,G-100%);99(C-0%,T-100%);101(C-1%,T-100%);104(C-97%,T-9%);109(C-0%,G-100%);112(A-11%,C-97%);114(C-10%,T-98%);126(G-0%,A-100%);133(G-6%,T-97%);151(C-0%,G-100%);153(G-100%,T-0%);155(A-3%,T-99%);163(A-100%,T-1%);165(A-0%,C-0%,T-100%);179(G-1%,A-100%);183(G-3%,C-99%);192(C-0%,T-99%);196(C-80%,T-69%);202(G-60%,A-87%);205(G-0%,C-96%,T-14%);208(G-2%,C-99%);	A;T;T;C ;T;T;A; G;T;A;T ;G;G;T; G;G;T;T ;C;G;C; T;A;T;G ;G;T;A; T;A;C;T ;C/T;A/ G;C;C	A;T;T;C ;T;T;A; G;T;A;T ;G;G;T; A/G;G; T;T;C;G ;C;C/T; A;T;G; G;T;A;T ;A;C;T; C/T;A;C /T;C
AMPL16 90185	scaffold5	TCCATAA ACCTGGA TGCGAAG AG	AACACCC CAAAACA ATGAGAA AAA	42(G-0%,A-100%);47(A-0%,C-100%);48(A-2%,G-99%);53(C-68%,T-83%);54(A-77%,G-0%,T-76%);59(A-0%,G-100%);60(A-1%,C-100%);65(G-7%,A-100%);68(A-67%,G-83%);69(C-89%,T-51%);71(C-99%,T-13%);72(C-78%,T-76%);75(A-3%,G-100%);80(C-19%,T-96%);82(C-1%,T-90%);83(C-100%,T-3%);84(C-14%,T-97%);95(C-13%,G-98%);105(A-78%,C-76%);107(G-4%,A-99%);122(G-78%,T-76%);141(A-59%,G-86%);150(C-97%,T-16%);162(A-99%,T-4%);167(G-1%,A-100%);173(A-3%,G-100%);174(C-6%,T-100%);176(C-100%,T-0%);178(G-99%,T-1%);180(C-10%,A-99%);183(C-0%,T-100%);184(A-0%,T-100%);186(A-27%,C-94%);187(C-90%,T-48%);190(C-99%,T-0%);194(C-1%,T-98%);	A;C;G; T/C;T/A ;G;C;A; G/A;T/ C;C;C/T ;G;T;T/ ;C;T;G; C/A;A; G/T;G/ A;C;A; A;G;T; C;G;A; T;T;C;C /T;C;T	A;C;G; T;T/A;G ;C;A;G; C;C;C/T ;G;T/C; T;C;T/C ;C/G;A/ C;A;T/ G;G;T/ C;A;A; G;T;C; G;A/C; T;T;A/C ;C;C;T
AMPL16 90186	scaffold9	ATTCATC AAAGATG TGACACC CTTG	TAATTTT GCAAAAG ATTGTAT GCGC	57(C-94%,T-39%);58(A-0%,T-100%);61(C-0%,T-100%);64(C-2%,T-99%);82(A-0%,C-100%);102(C-100%,T-0%);131(G-2%,T-98%);133(C-0%,G-100%);143(G-1%,A-100%);147(C-13%,T-88%);148(C-13%,T-88%);164(C-0%,A-100%);	C/T;T;T ;T;C;C; T;G;A;T ;T;A	C;T;T;T ;C;C;T; G;A;T;T ;A
AMPL16 90187	scaffold7	CGATATC TGGGGAG GTTCGAT C	AAGACTT AGGGCTT AAATACA CCGT	42(G-100%,T-0%);43(C-99%,T-4%);47(C-100%,T-7%);50(A-1%,G-99%);52(C-26%,T-91%);55(A-24%,G-93%);56(C-99%,T-10%);59(C-0%,G-100%);60(G-0%,T-100%);61(C-100%,T-0%);63(C-99%,T-8%);70(G-53%,A-82%);73(C-100%,T-1%);75(A-100%,T-6%);83(C-0%,G-100%);86(A-0%,G-100%);100(A-99%,T-1%);103(C-53%,A-82%);104(A-1%,G-	G;C;C; G;T;G; C;G;T;C ;C;A;C; A;G;G; A;A;G; T;T;C;G ;T;T;C; C;T;T;T	G;C;C; G;C/T; A/G;C; G;T;C;T /C;G/A; C;A;G; G;A;A/ C;G;C/T ;T;A/C;

				100%);106(C-53%,T-82%);112(C-1%,T-98%);115(A-46%,G-4%,C-86%);116(A-4%,G-99%);118(A-2%,T-99%);121(A-0%,T-100%);128(G-0%,C-100%);129(C-100%,T-0%);130(C-4%,T-99%);131(C-1%,T-100%);138(A-0%,T-100%);		G;T;T;C ;C;T;T; T
AMPL16 90191	scaffold1	CGATTGA TAGCATT GGCCACA TAAT	TCCTTGT ACGATCT GTTTCCT TTGA	36(A-7%,G-100%);37(A-7%,T-100%);38(C-7%,T-100%);40(G-7%,T-100%);45(G-7%,A-100%);48(C-100%,T-7%);57(G-7%,A-100%);63(C-100%,T-0%);72(A-7%,G-100%);75(G-7%,A-100%);78(C-99%,T-7%);80(A-100%,T-0%);90(C-100%,T-0%);96(C-0%,T-100%);99(G-0%,A-100%);122(G-7%,A-100%);123(G-8%,T-99%);126(C-99%,T-8%);135(C-7%,G-42%,A-94%);141(C-7%,T-99%);144(G-7%,A-99%);150(G-7%,C-100%);162(A-7%,G-100%);168(G-100%,T-7%);171(C-100%,T-7%);175(A-7%,G-100%);183(A-7%,G-99%);188(C-94%,T-14%);189(G-69%,T-83%);196(G-0%,A-100%);201(G-7%,A-99%);206(A-7%,C-42%,T-94%);209(C-100%,T-0%);210(G-7%,A-100%);224(C-83%,T-69%);228(G-100%,T-0%);230(A-0%,C-100%);239(G-0%,A-100%);	G;T;T;T ;A;C;A; C;G;A; C;A;C;T ;A;A;T; C;G/A; T;A;C; G;G;C; G;G;C; G/T;A; A;T/C;C ;A;T/C; G;C;A	G;T;T;T ;A;C;A; C;G;A; C;A;C;T ;A;A;T; C;A;T; A;C;G; G;C;G; G;C/T; G/T;A; A;T;C; A;T/C; G;C;A
AMPL16 90192	scaffold4	CGCTGTG TTTCTAG TACCTAC ACTA	CATGTAA GTGATAT GTCCAAC GAGG	58(A-1%,G-99%);79(C-1%,T-99%);86(C-99%,T-1%);97(C-100%,T-1%);107(C-99%,T-4%);115(C-1%,T-99%);118(C-100%,T-1%);146(C-26%,T-87%);158(C-24%,T-90%);	G;T;C;C ;C;T;C; T;T	G;T;C;C ;C;T;C; T/C;T/C
AMPL16 90193	scaffold5	ACTCAGT TCCCGTT TACCATA AGAA	TATTTGG CGACGAC GGGGTAT A	37(G-96%,T-18%);41(G-98%,A-15%);75(C-0%,T-100%);76(C-0%,T-100%);81(A-3%,C-100%);83(G-38%,T-88%);86(G-1%,T-100%);87(C-1%,T-100%);88(C-1%,A-100%);89(C-98%,T-15%);90(C-0%,T-100%);93(C-19%,T-96%);99(G-1%,T-100%);109(A-7%,G-100%);110(C-100%,T-1%);117(C-98%,G-15%);118(A-3%,G-100%);128(G-6%,A-100%);129(A-0%,T-100%);133(C-3%,T-100%);147(G-98%,A-9%);148(A-97%,G-12%);175(C-38%,T-88%);176(C-7%,T-100%);184(A-88%,C-37%);	G;G;T;T ;C;T;T; T;A;C;T ;T;T;G; C;C;G; A;T;T;G ;A;T;T; A	G;A/G; T;T;C;T /G;T;T; A;C/T;T ;C/T;T; G;C;C/ G;G;A; T;T;G/A ;G/A;C/ T;T;A/C
AMPL16 90196	scaffold11	CTATGCC GATAATG CCAAAAA CCAT	ACACAGA CAGATAG TACTCTG GAAC	36(A-100%,T-0%);37(G-1%,A-99%);40(A-89%,G-32%);48(C-93%,T-30%);50(A-99%,T-0%);58(A-99%,G-13%);59(G-2%,C-100%);60(G-99%,A-13%);83(C-0%,G-99%);88(C-98%,T-4%);90(C-93%,T-30%);94(G-0%,A-99%);97(A-0%,T-100%);102(C-100%,T-0%);114(A-3%,C-16%,T-94%);117(A-2%,G-100%);122(G-99%,A-13%);123(C-100%,T-1%);134(C-0%,G-0%,A-100%);155(C-0%,T-100%);167(A-0%,C-0%,T-16%);168(C-13%,T-6%);170(C-1%,G-99%);171(A-0%,G-100%);180(C-100%,T-0%);193(A-0%,C-100%);209(A-0%,G-100%);210(C-99%,T-1%);	A;A;A; C;A;A; C;G;G; C;C;A;T ;C;T;G; G;C;A; T;-;-;G; G;C;C; G;C	A;A;G/ A;T/C; A;G/A; C;G/A; G;C;T/C ;A;T;C; C/T;G; A/G;C; A;T;- /T;C/-;G ;G;C;C; G;C
AMPL16 90199	scaffold8	TTGAGAT AAAAAGC AAAGCCA AGTG	AGAGGGG CTTTTAT ACATTCA CCAT	38(A-0%,G-100%);42(C-3%,T-100%);44(G-86%,T-30%);50(C-3%,G-99%);112(C-11%,T-97%);129(G-100%,T-0%);	G;T;G; G;T;G	G;T;G/T ;G;T/C; G
AMPL16 90200	scaffold3	TAAGCGA CAAAGTT GAGGTGT AGTA	AACAGGA AGATAGC ACTCCCC TAAT	41(A-1%,C-99%);103(C-1%,T-99%);137(G-1%,C-99%);140(C-99%,T-1%);149(G-28%,A-85%);168(C-99%,T-1%);	C;T;C;C ;A;C	C;T;C;C ;A;C

AMPL16 90201	scaffold1	TTCCATG CAAGTCC CATAGAG TTAT	AAAGAGA GAACATA GAGGAAG GAGG	38(A-2%,G-10%,T-96%);39(G-7%,A-97%);41(A-100%,T-0%);42(G-1%,A-100%);44(A-0%,T-100%);45(C-100%,T-1%);47(G-1%,A-100%);48(A-2%,G-98%);50(A-100%,T-1%);52(C-100%,T-1%);55(C-1%,G-100%);60(G-16%,A-95%);62(A-1%,T-100%);63(G-0%,C-100%,T-1%);64(G-0%,A-100%);68(C-100%,T-1%);72(C-100%,T-0%);85(A-2%,T-100%);87(A-2%,G-99%);88(C-2%,G-99%);91(C-100%,T-0%);92(A-0%,G-100%);95(G-1%,C-100%);98(C-100%,T-1%);103(C-100%,T-0%);105(C-100%,T-2%);106(G-2%,A-100%);113(A-8%,C-10%,T-95%);116(C-100%,T-1%);133(C-100%,T-0%);140(A-0%,G-100%);143(C-0%,T-100%);146(G-1%,A-100%);149(G-0%,C-100%);151(A-100%,T-0%);152(A-1%,G-100%);155(G-0%,C-100%);158(G-0%,A-100%);168(C-100%,T-6%);169(C-100%,T-2%);171(A-1%,C-1%,T-100%);172(G-1%,C-100%,T-1%);173(C-1%,A-100%);174(A-0%,T-100%);175(C-0%,G-75%,T-46%);	T;A;A; A;T;C; A;G;A; C;G;A; T;C;A;C ;C;T;G; G;C;G; C;C;C;C ;A;T;C; C;G;T; A;C;A; G;C;A; C;C;T;C ;A;T;G	T;A;A; A;T;C; A;G;A; C;G;A; T;C;A;C ;C;T;G; G;C;G; C;C;C;C ;A;T;C; C;G;T; A;C;A; G;C;A; C;C;T;C ;A;T;G/ T
AMPL16 90202	scaffold2	GGATGAT CAATCTA ACGGGAT GGTT	TCCAGCA TGAGCAG CATCTTA TC	44(C-1%,T-100%);46(G-0%,A-100%);51(G-3%,A-100%);55(G-0%,C-100%);62(C-100%,T-3%);64(A-1%,G-100%);66(A-2%,G-100%);74(G-3%,C-100%);75(A-7%,G-98%);78(A-0%,G-100%);81(G-7%,A-98%);90(C-100%,T-0%);91(G-3%,A-100%);93(C-100%,T-3%);94(C-100%,T-0%);97(C-100%,T-3%);121(C-100%,T-2%);123(A-0%,G-100%);124(C-100%,T-3%);132(G-0%,A-100%);136(C-100%,T-0%);138(C-100%,T-5%);141(A-5%,C-100%);144(A-0%,G-100%);147(A-3%,G-100%);151(A-4%,G-100%);152(G-0%,C-100%);156(A-2%,G-100%);157(A-2%,G-100%);158(A-2%,G-100%);159(A-98%,T-7%);163(C-100%,T-3%);171(A-2%,G-100%);174(A-6%,G-100%);185(G-3%,A-100%);186(C-2%,A-100%);189(C-0%,T-100%);198(C-100%,T-2%);202(G-3%,A-100%);205(C-100%,T-0%);206(A-0%,G-100%);207(C-100%,T-0%);213(G-82%,A-95%);216(C-0%,T-100%);219(C-0%,T-100%);228(G-98%,T-7%);	T;A;A; C;C;G; G;C;G; G;A;C; A;C;C; C;C;G; C;A;C; C;C;G; G;G;C; G;G;G; A;C;G; G;A;A; T;C;A;C ;G;C;G/ A;T;T;G	T;A;A; C;C;G; G;C;G; G;A;C; A;C;C; C;C;G; C;A;C; C;C;G; G;G;C; G;G;G; A;C;G; G;A;A; T;C;A;C ;G;C;G/ A;T;T;G
AMPL16 90203	scaffold2	ATACATC TGGTGGT ATCCGTC AAAA	TTGACAT TGCTGAA AGTGATA CCAC	36(A-2%,G-98%);41(A-97%,G-16%);47(C-0%,G-100%);56(G-0%,A-100%);63(A-95%,G-19%);64(C-100%,T-0%);68(G-2%,A-100%);74(G-98%,T-2%);78(C-2%,T-98%);79(A-2%,G-98%);80(A-2%,G-98%);108(C-0%,A-100%);112(G-2%,A-98%);121(C-14%,T-100%);	G;A;G; A;A;C; A;G;T; G;G;A; A;T	G;G/A; G;A;G/ A;C;A; G;T;G; G;A;A; C/T
AMPL16 90204	scaffold1	CTGTGGC TACGTCT ACTGAGG AG	GCTGAAG AAAATGA GCTGTGT GATA	41(C-98%,T-20%);44(C-2%,T-98%);50(C-98%,T-2%);65(C-72%,T-81%);71(C-2%,T-99%);74(A-3%,G-98%);97(C-0%,T-100%);99(C-3%,G-67%);100(C-98%,T-0%);101(A-0%,C-98%);102(C-81%,T-72%);104(C-5%,T-96%);108(A-20%,G-98%);110(G-0%,A-100%);113(G-0%,A-100%);114(C-0%,A-100%);115(C-85%,T-68%);118(G-2%,C-97%,T-6%);123(C-98%,T-0%);124(A-0%,G-98%,T-2%);125(C-81%,T-72%);131(A-5%,G-96%);135(C-5%,T-96%);138(A-5%,G-	C;T;C;C /T;T;G; T;- /G;C;C; T/C;T;G ;A;A;A; C/T;C;C ;G;C/T; G;T;G;T ;C/T;A; T;T;C;C	C;T;C;C /T;T;G; T;- /G;C;C; C/T;T;G ;A;A;A; T/C;C;C ;G;T/C; G;T;G;T ;C/T;A; T;T;C;C

				96%);140(G-2%,T-97%);142(C-81%,T-72%);153(A-98%,T-2%);166(C-4%,T-96%);172(C-1%,T-100%);181(A-2%,C-99%);184(C-97%,T-4%);193(C-96%,T-4%);198(C-0%,G-98%,T-2%);203(G-3%,A-98%);204(C-2%,G-98%);217(G-96%,T-5%);233(C-98%,T-2%);234(G-5%,A-96%);237(C-98%,T-2%);	;C;G;A; G;G;C; A;C	;C;G;A; G;G;C; A;C
AMPL16 90206	scaffold2	TGGAAAT GTATAAA TCACGAG GGGA	CTGGCTG GCTGTTA GGTATGT AAT	55(A-95%,G-18%);72(G-99%,T-7%);74(A-2%,C-99%);75(C-10%,T-18%);77(A-0%,G-24%);81(C-2%,G-23%);85(C-1%,T-24%);100(A-95%,G-18%);125(C-94%,T-20%);128(A-96%,G-18%);135(C-100%,T-0%);148(C-99%,T-1%);149(A-97%,G-15%);167(C-18%,T-96%);169(G-96%,A-18%,T-0%);173(G-0%,A-100%);174(C-0%,T-100%);176(G-3%,C-99%);194(G-0%,A-100%);202(C-96%,G-18%);209(C-96%,T-18%);	A;G;C;- ;-;-;-A; C;A;C; C;A;T; G;A;T; C;A;C; C	G/A;G; C;-/T;- /G;- /G;T;-G /A;C/T; A/G;C; C/G/A; T/C;G/ A;A;T; C;A;C/ G;T/C
AMPL16 90207	scaffold5	AGTCAGT TTCGATC GAAGTAC AAGA	ATCATGT GACTGTG AGTTCGT TCAA	37(C-1%,T-100%);63(G-89%,T-25%);64(A-0%,T-100%);89(A-99%,T-3%);91(C-0%,T-100%);175(G-25%,A-89%);	T;G;T;A ;T;A	T;T/G;T ;A;T;A/ G
AMPL16 90208	scaffold5	GAACAGT TCTTACA TGTCTTC TGCA	GATCTTT GAAGTCG GGTTAAG CG	39(C-35%,T-88%);40(A-1%,G-100%);48(A-13%,G-100%,T-0%);51(G-86%,A-38%);55(A-6%,C-100%);58(G-0%,C-99%,T-6%);61(C-7%,T-100%);63(C-100%,T-14%);64(A-3%,G-100%);65(C-100%,T-1%);66(A-20%,C-0%,G-98%);69(A-4%,G-100%);71(A-2%,T-100%);72(C-100%,T-13%);75(C-100%,T-2%);80(A-100%,T-1%);84(C-17%,T-98%);85(C-93%,T-26%);86(A-0%,G-100%);88(A-1%,G-100%);90(C-100%,T-9%);91(C-100%,T-6%);93(C-100%,T-9%);94(A-7%,G-100%);96(C-12%,T-96%);97(A-0%,G-100%);98(C-100%,T-1%);99(A-2%,G-100%);101(C-100%,T-1%);102(A-8%,G-99%);108(G-18%,A-96%);110(C-100%,T-0%);114(A-7%,C-100%);115(G-6%,T-100%);117(C-93%,T-17%);118(A-1%,G-100%);126(A-2%,C-100%,T-5%);135(C-100%,T-0%);136(C-100%,T-1%);142(C-100%,T-11%);143(A-3%,G-100%);	T;G;G; G;C;C;T ;C;G;C; G;G;T; C;C;A;T ;C;G;G; C;C;C; G;T;G; C;G;C; G;A;C; C;T;C;G ;C;C;C; C;G	C;G;G; A;C;C;T ;C;G;C; G;G;T; C;C;A;T ;T;G;G; C;C;C; G;T;G; C;G;C; G;A;C; C;T;T;G ;C;C;C; C;G
AMPL16 90209	scaffold2	CCGTGGA AGATGGT TTCGACT ATAT	TACTAGT CTTTCAC ACGTCGA AAGT	40(C-94%,T-6%);166(G-83%,A-26%);	C;G	C;G/A
AMPL16 90210	scaffold4	AATTATG TTCGTTTT TGGAGCA CCT	TCCAGGT TCCTATA TATGAAC GACG	39(G-84%,T-17%);42(G-1%,C-99%);44(C-2%,G-100%);46(C-2%,A-99%);48(A-56%,T-89%);49(C-5%,A-98%);52(C-87%,T-10%);54(G-12%,T-87%);56(A-1%,G-7%,T-91%);59(A-12%,G-87%);64(C-0%,T-100%);65(G-0%,T-100%);66(A-0%,G-100%);75(A-1%,T-99%);79(C-2%,G-98%);80(C-93%,T-49%);81(A-8%,G-96%);86(G-0%,A-100%);91(A-55%,G-88%);92(C-97%,T-6%);95(G-98%,T-6%);111(C-5%,T-98%);112(C-89%,T-53%);115(A-81%,G-69%);116(C-98%,T-2%);120(C-51%,T-91%);121(C-2%,A-98%,T-0%);124(C-81%,T-69%);129(G-7%,A-98%);131(A-5%,G-98%);143(C-94%,T-0%);145(A-94%,T-0%);152(G-47%,A-94%);154(C-4%,T-98%);155(A-0%,G-100%);163(G-2%,A-	G/-;C;G ;A;T/A; A;C/-;T/ ;- /T;G/-;T ;T;G;T; G;C/T; G;A;A/ G;C;G; T;T/C;A /G;C;C/ T;A;C/T ;A;G;- /C;A/-; A/G;T; G;A;A;	T/G;C; G;A;T; A;C;T;T ;G;T;T; G;T;G; C;G;A; G;C;G; T;C;G/ A;C;T; A;C/T; A;G;C; A;A;T; G;A;A; G;T;T;A /G;G;G; A;G;T;

				98%);170(G-2%,A-100%);174(G-89%,T-53%);181(A-0%,C-2%,T-98%);188(A-0%,T-100%);189(G-80%,A-70%);193(A-1%,G-99%);211(A-1%,G-99%);219(G-2%,A-100%);221(A-2%,G-100%);222(C-1%,T-100%);231(G-100%,T-0%);	G/T;T;T ;G/A;G; G;A;G; T;G	G
AMPL16 90211	scaffold5	GAAGCGA GAGTTCT TCGAGTT CAAA	CTGCTTG GATCTGT TTAAATA CGGC	41(G-12%,A-97%,T-0%);43(G-0%,A-100%);47(C-94%,T-14%);50(C-2%,T-99%);51(C-0%,T-100%);56(C-3%,T-100%);57(G-99%,T-12%);58(G-12%,C-99%,T-1%);71(G-100%,T-0%);82(G-1%,A-100%);83(G-21%,A-87%);86(C-100%,T-1%);90(C-0%,T-100%);103(G-10%,A-97%);107(A-98%,T-2%);121(A-0%,G-100%);128(A-12%,C-0%,G-99%);135(G-13%,A-97%);140(G-0%,A-100%);141(G-0%,A-100%);148(A-1%,G-99%);150(A-1%,G-100%);152(A-99%,T-1%);154(C-2%,G-1%,T-99%);155(C-3%,G-100%);156(C-99%,T-1%);158(A-13%,G-91%,T-10%);	A;A;C; T;T;T;G ;C;G;A; A;C;T; A;A;G; G;A;A; A;G;G; A;T;G; C;G	A;A;C; T;T;T;G ;C;G;A; A;C;T; A;A;G; G;A;A; A;G;G; A;T;G; C;G
AMPL16 90212	scaffold12	CGACAAG TTTACAG GAGGACT ATGT	AATCTTG GTTGTGG AGTAAGG ATGA	44(A-86%,T-71%);46(C-100%,T-0%);55(G-0%,A-100%);65(A-0%,G-100%);68(A-89%,G-63%);72(A-0%,G-100%);74(C-0%,A-100%);81(G-9%,A-64%,T-86%);84(A-86%,G-71%);93(A-72%,T-1%);94(C-1%,A-100%);95(G-72%,T-85%);98(C-72%,T-1%);100(A-1%,G-71%);101(C-0%,T-100%);106(A-86%,T-72%);107(C-1%,T-100%);140(G-0%,A-100%);	T/A;C; A;G;A/ G;G;A; A/T;G/ A;A/-;A ;T/G;- /C;G/-;T /T/A;T; A	T/A;C; A;G;A/ G;G;A; A/T;A/ G;A/-;A ;T/G;- /C;- /G;T/T/ A;T;A
AMPL16 90213	scaffold2	TAGAAGA CTTGATC ATAGGCG CTAC	TTCTATT AATTCAA ACGAGCC GAGC	44(G-7%,C-100%,T-0%);47(C-100%,T-0%);61(C-3%,T-97%);62(C-100%,T-0%);65(A-69%,G-0%,C-100%);66(C-0%,T-100%);67(C-1%,T-100%);69(A-0%,C-100%,T-0%);72(C-100%,T-3%);73(C-100%,T-4%);74(C-22%,T-92%);77(A-98%,T-6%);81(A-8%,C-100%,T-1%);82(C-3%,T-97%);85(C-1%,T-100%);87(A-79%,T-31%);88(C-100%,T-1%);92(G-3%,C-97%);95(C-2%,T-98%);100(C-2%,T-98%);103(C-100%,T-8%);106(C-82%,G-0%,T-87%);115(C-2%,A-100%);118(C-2%,T-98%);124(C-1%,G-2%,T-100%);127(A-0%,G-100%);130(C-70%,T-100%);134(C-2%,T-98%);151(C-3%,T-97%);169(G-0%,A-100%);175(C-99%,T-1%);178(C-0%,G-100%);181(C-98%,T-2%);	C;C;T;C ;A/C;T; T;C;C;C ;T;A;C; T;T;- /A;C;C; T;T;C;C /T;A;T; T;G;T/C ;T;T;A; C;G;C	C;C;T;C ;C/A;T; T;C;C;C ;C/T;A; C;T;T;T /-;C;C;T ;T;C;T; A;T;T;G ;T/C;T; T;A;C; G;C
AMPL16 90218	scaffold4	GGTTCGT AACTGGT CTATTTG CATT	CAGTACA ATGCATG TGTTCTGA GTAG	38(C-16%,T-93%);52(A-0%,G-100%);71(C-100%,T-0%);121(C-99%,T-1%);123(A-1%,C-99%);	T;G;C;C ;C	C/T;G;C ;C;C
AMPL16 90221	scaffold1	TTGAGAG AACACTC CTCGCTT AATC	GATGATG GCTCCCT CTAAAGA GATG	37(G-100%,T-6%);39(A-0%,C-100%);61(G-3%,A-99%);71(C-97%,T-10%);72(A-1%,G-99%);81(A-94%,G-21%);89(A-94%,G-21%);90(G-1%,A-100%);95(A-0%,G-100%);101(G-97%,T-11%);114(G-100%,T-0%);121(A-99%,T-13%);123(A-96%,T-17%);139(G-87%,C-34%);155(G-1%,A-100%);157(C-1%,A-100%);160(A-1%,G-99%);162(G-99%,T-12%);174(C-91%,T-23%);176(G-6%,A-100%);212(C-1%,T-100%);	G;C;A; C;G;A; A;A;G; G;G;A; A;G;A; A;G;G; C;A;T	G;C;A; C;G;G/ A;G/A; A;G;G; G;T/A; A/T;C/ G;A;A; G;T/G; C/T;A;T

AMPL16 90222	scaffold1	CAATGAT GCACATA TCAGTCG GTAC	GAGAACC ATGTTAT CCCCGCTT CTC	37(C-11%,G-1%,T-93%);39(C-98%,T-2%);41(A-0%,G-100%);48(C-19%,T-90%);52(A-1%,T-100%);57(C-100%,T-0%);59(C-0%,G-100%);62(A-0%,C-100%);65(C-99%,T-1%);73(A-1%,G-99%);84(C-0%,T-100%);86(A-0%,C-100%);87(A-0%,G-99%);92(C-100%,T-0%);95(A-1%,C-100%,T-0%);101(C-99%,T-1%);102(A-0%,G-100%);103(G-0%,T-100%);109(C-99%,T-1%);110(G-19%,A-91%);113(G-1%,T-99%);114(G-1%,A-99%);116(G-100%,T-0%);121(A-2%,T-99%);123(C-1%,G-99%);127(C-99%,T-3%);128(C-2%,A-98%);129(A-0%,C-100%);131(A-0%,G-1%,C-98%);137(C-0%,T-100%);145(C-99%,T-1%);148(C-100%,T-0%);155(G-99%,T-1%);160(C-1%,T-99%);162(G-3%,A-99%);168(G-0%,C-100%,T-0%);173(G-10%,A-95%);178(A-2%,T-98%);179(G-2%,T-98%);180(A-8%,G-97%);181(C-2%,A-98%);198(G-1%,A-98%);202(C-27%,T-83%);208(C-100%,T-0%);209(A-12%,G-96%);215(G-0%,C-100%);217(A-0%,G-100%);	T;C;G;T ;T;C;G; C;C;G;T ;C;G;C; C;C;G;T ;C;A;T; A;G;T; G;C;A; C;C;T;C ;C;G;T; A;C;A; T;T;G;A ;A;T;C; G;C;G	T;C;G;T ;T;C;G; C;C;G;T ;C;G;C; C;C;G;T ;C;A;T; A;G;T; G;C;A; C;C;T;C ;C;G;T; A;C;A; T;T;G;A ;C;C/T; C;G/A; C;G
AMPL16 90223	scaffold1	CTAGCTG CAGTGTC GATATTT TGG	TAGGTCG GAGGACT CTTGTCG	40(C-1%,G-99%);41(G-4%,A-98%);43(A-100%,T-2%);44(C-5%,A-97%);45(A-1%,T-99%);47(C-100%,T-0%);50(C-9%,T-99%);51(G-2%,A-100%);52(A-3%,C-99%,T-1%);53(A-0%,C-1%,G-100%);55(C-0%,T-100%);56(C-99%,T-2%);57(A-1%,G-100%);59(A-0%,C-0%,G-0%,T-100%);61(G-5%,A-100%);62(C-100%,T-0%);63(C-3%,G-98%,T-4%);64(C-100%,T-0%);66(C-1%,T-100%);69(C-94%,T-49%);70(G-3%,T-97%);71(C-7%,T-98%);73(A-2%,G-100%);75(C-1%,T-99%);76(G-99%,T-1%);78(A-0%,G-98%,T-1%);80(G-0%,A-100%);81(G-0%,A-100%);82(G-100%,T-0%);85(C-100%,T-0%);86(A-0%,G-100%);87(G-6%,A-100%);90(A-0%,C-0%,G-100%);91(C-47%,T-95%);94(C-0%,G-1%,T-99%);95(C-99%,T-1%);96(G-100%,T-0%);97(C-4%,A-98%);98(C-100%,T-1%);99(C-1%,T-99%);101(A-8%,G-97%);102(C-0%,G-100%);106(C-1%,T-99%);107(C-1%,T-99%);108(G-2%,A-98%,T-5%);109(C-97%,T-7%);110(A-0%,C-99%,T-4%);112(G-0%,A-100%);113(G-1%,A-99%);114(G-0%,C-100%);116(A-4%,G-99%);117(A-2%,G-100%);118(A-0%,T-100%);119(G-0%,T-99%);125(G-2%,C-100%);126(C-1%,G-99%);129(A-0%,G-97%,T-46%);130(A-0%,G-100%);131(A-0%,G-100%);132(G-2%,T-100%);134(G-41%,C-97%,T-1%);135(A-1%,G-98%,T-2%);136(A-1%,G-100%);137(A-2%,G-100%);143(A-0%,G-100%);148(A-48%,G-93%);149(G-1%,A-99%);153(G-96%,A-18%);154(C-2%,T-98%);156(G-46%,A-96%);157(C-5%,A-99%,T-0%);160(C-45%,G-23%,A-86%);162(G-1%,A-100%);167(G-1%,A-100%);168(G-0%,A-100%);169(A-0%,G-100%);170(A-48%,C-6%,G-93%);173(A-0%,T-100%);174(C-56%,T-93%);182(C-1%,T-100%);184(A-0%,T-100%);185(A-46%,G-	G;A;A; A;T;C;T ;A;C;G; T;C;G;T ;A;C;G; C;T;T/C ;T;T;G; T;G;G; A;A;G; C;G;A; G;T/C;T ;C;G;A; C;T;G; G;T;T;A ;C;C;A; A;C;G; G;T;T;C ;G;G/T; G;G;T; G/C;G; G;G;G; A/G;A; G;T;A/ G;A;A/ C;A;A; A;G;G/ A;T;T/C ;T;T;A/ G;C	G;A;A; A;T;C;T ;A;C;G; T;C;G;T ;A;C;G; C;T;C;T ;T;G;T; G;G;A; A;G;C; G;A;G; T;T;C;G ;A;C;T; G;G;T;T ;A;C;C; A;A;C; G;G;T;T ;C;G;G; G;G;T; C;G;G; G;G;G; A;G/A; T;A;A; A;A;A; A;G;G; T;T;T;T ;G;C

				95%);186(A-2%,C-99%);		
AMPL16 90225	scaffold5	TAGCTAT GGATGAG GATCTGC AAAT	GTGTTCA TAGGCTG GTCGAAA TTG	48(C-100%,T-2%);60(A-0%,G-100%);63(A-0%,G-100%);69(A-0%,G-100%);72(A-0%,T-100%);75(A-2%,G-99%);85(G-2%,A-100%);86(G-0%,A-100%);88(C-48%,A-94%,T-1%);94(G-3%,A-77%);97(C-77%,T-5%);105(G-0%,T-100%);108(G-12%,T-100%);115(G-80%,A-76%);116(G-0%,A-100%);120(G-0%,A-100%);122(C-0%,G-1%,A-99%);125(G-0%,T-100%);126(C-0%,G-0%,T-100%);127(G-9%,A-100%);128(G-0%,A-100%);133(A-0%,G-100%);136(A-0%,T-100%);137(A-0%,T-100%);160(A-4%,G-100%);165(C-100%,T-0%);166(A-10%,G-99%);171(C-0%,T-100%);181(A-100%,T-1%);183(C-0%,A-100%);195(C-0%,T-100%);196(A-0%,G-100%);202(G-36%,A-90%);217(G-0%,A-100%);224(C-100%,T-0%);225(C-100%,T-0%);226(C-100%,T-1%);229(A-0%,C-100%,T-2%);232(G-0%,C-100%);	C;G;G; G;T;G; A;A;C/ A;-/A;- /C;T;T; A/G;A; A;A;T;T ;A;A;G; T;T;G;C ;G;T;A; A;T;G; A;A;C; C;C;C;C	C;G;G; G;T;G; A;A;A;- /A;- /C;T;G/ T;A/G; A;A;A; T;T;A;A ;G;T;T; G;C;G; T;A;A;T ;G;A/G; A;C;C; C;C;C
AMPL16 90227	scaffold8	TTCAACT AGATGCC AAACTTT CTGA	AAGTTGA CGGTTGT AGCAGAA TATG	36(G-5%,C-99%,T-1%);41(C-7%,T-99%);57(A-10%,G-96%);66(C-99%,T-5%);67(C-4%,G-98%);74(C-100%,T-0%);78(C-99%,T-6%);79(A-1%,G-100%);82(C-17%,T-93%);99(C-96%,T-10%);100(A-0%,G-100%);102(A-99%,T-5%);106(C-99%,T-5%);115(G-1%,T-100%);124(A-5%,G-99%);127(C-98%,T-3%);132(C-25%,T-84%);133(A-6%,G-98%);142(C-7%,T-97%);144(A-5%,G-99%);151(C-100%,T-0%);160(C-100%,T-0%);162(C-8%,T-99%);	C;T;G;C ;G;C;C; ;G;C;C; G;A;C; T;G;C;T ;G;T;G; C;C;T	C;T;G;C ;G;C;C; ;G;T;C; G;A;C; T;G;C;T ;G;T;G; C;C;T
AMPL16 90228	scaffold8	AATCAGA TGCGAAA TCACAAG GTAC	TCTCTTC GAAGTTC ATCCTGT TGAA	40(C-1%,T-99%);42(A-0%,G-100%);47(G-4%,A-96%);50(A-1%,G-99%);54(C-25%,T-88%);55(A-1%,C-99%);56(A-0%,G-100%);58(C-4%,T-96%);62(G-0%,T-100%);63(C-0%,T-100%);67(C-0%,T-100%);70(G-2%,T-98%);71(C-21%,G-92%);72(C-85%,T-32%);73(C-98%,T-2%);75(C-98%,T-2%);77(G-0%,A-100%);80(A-20%,G-92%);82(A-20%,C-92%,T-0%);83(G-2%,A-98%);84(A-6%,C-0%,T-98%);85(G-0%,T-100%);86(C-100%,T-0%);88(A-0%,G-92%,T-20%);90(C-4%,A-100%);91(C-0%,A-100%);93(C-1%,T-100%);105(A-0%,G-100%);120(G-0%,C-100%);126(A-1%,G-100%);135(G-4%,A-96%);138(C-24%,T-89%);140(A-0%,G-100%);147(A-0%,G-	T;G;A; G;T;C; G;T;T;T ;T;T;G; C;C;C; A;G;C; A;T;T;C ;G;A;A; T;G;C; G;A;T; G;G;A; A;C;A; T;A;A;T ;C;C;A	T;G;A; G;T/C;C ;G;T;T; T;T;T;C /G;T/C; C;C;A; A/G;C/ A;A;T;T ;C;T/G; A;A;T; G;C;G; A;T/C; G;G;A; G/A;C; G/A;T; A;A;T;

				100%);156(G-4%,A-96%);157(G-32%,A-85%);158(C-100%,T-0%);162(G-25%,A-88%);164(C-0%,T-100%);172(G-0%,A-100%);183(A-100%,T-0%);192(C-0%,T-100%);198(G-2%,C-98%);203(C-100%,T-0%);207(G-0%,A-100%);		C;C;A
AMPL16 90229	scaffold5	CTCATCC AAATTCC AAGATGA TGCA	AGACACA AGAAAGA GATGCTA ACGA	41(C-3%,A-98%);61(G-97%,A-9%);79(A-0%,G-100%);93(A-1%,C-99%);110(G-0%,C-100%);115(C-98%,T-7%);149(A-83%,C-33%);154(G-97%,C-9%);162(C-96%,T-5%);166(A-1%,C-99%);	A;G;G; C;C;C; A;G;C; C	A;A/G; G;C;C; C;A/C; G/C;C; C
AMPL16 90230	scaffold1	GTATCAT GTCAAAG GAGGTGA AACG	CCAATGC CATCGGT TTGTAGA AATA	96(C-22%,T-80%);105(G-65%,A-90%);111(C-0%,T-100%);123(A-61%,T-93%);130(A-90%,T-64%);133(G-1%,A-100%);155(C-0%,G-100%);177(A-1%,G-100%);	T/-;G/A; T;A/T;A /T;A;G; G	- /T;G/A; T;A/T;A /T;A;G; G
AMPL16 90231	scaffold10	AAGGTCA AGATGAA ACACAGC AAAT	ATTGCCT TTAGGAA GCTGCCT ATTT	41(G-99%,T-1%);42(C-2%,T-98%);67(A-97%,T-1%);68(C-16%,T-92%);78(G-97%,T-1%);83(A-2%,G-98%);85(G-3%,A-97%);93(C-1%,T-100%);102(C-99%,T-1%);109(A-0%,G-29%);110(A-10%,C-0%,T-24%);112(A-10%,G-24%);115(G-29%,T-1%);117(A-0%,T-29%);119(C-29%,T-0%);122(C-29%,T-1%);124(C-29%,T-0%);128(A-0%,G-29%);136(A-0%,G-100%);137(G-1%,T-99%);146(C-99%,T-10%);147(A-0%,G-100%);148(C-100%,T-0%);149(C-3%,G-97%);154(A-98%,G-9%);157(A-0%,G-0%,T-97%);159(A-2%,G-98%);160(C-100%,T-0%);163(G-1%,A-100%);165(C-100%,T-0%);166(G-10%,A-99%);170(C-10%,T-99%);177(G-10%,A-99%);178(A-0%,G-1%,C-96%,T-12%);180(C-99%,T-0%);186(C-2%,G-98%);195(G-0%,C-100%);204(A-1%,C-10%,G-96%);206(C-0%,A-98%);208(A-17%,C-93%);210(C-0%,A-98%);211(C-0%,T-98%);	G;T;A;T ;G;G;A; T;C;-;-; ;-;-;-;-; ;-G;T;C; G;C;G; A;T;G; C;A;C; A;T;A; C;C;G; C;G;A; C;A;T	G;T;A;T ;G;G;A; T;C;- /G;T/-; /G;- /G;T/-; /C;- /C;C/-; /G;G;T; C;G;C; G;G/A; G;C; A;C;A; T;A;C;C ;G;C;G; A;C;A; T
AMPL16 90233	scaffold2	TTTGAGG ACGATAG GACTCCT TTTT	TCAATGT CTCATCG GTCAATC TCAT	46(A-6%,C-100%);47(C-59%,T-91%);62(G-100%,T-0%);68(C-1%,T-100%);69(A-100%,T-0%);77(A-96%,G-14%);80(C-100%,T-1%);89(G-0%,A-100%);90(C-99%,T-48%);91(G-1%,A-100%);96(A-48%,C-99%);102(A-0%,C-100%);103(G-96%,A-14%);122(A-3%,G-98%);158(G-91%,A-59%);183(C-3%,G-99%);185(G-96%,A-14%);197(G-6%,A-100%);212(C-3%,T-99%);213(G-48%,C-99%);	C;T;G;T ;A;A;C; A;C;A; C;C;G; G;G;G; G;A;T; C	C;C;G;T ;A;G/A; C;A;C/T ;A;A/C; C;A/G;- /G;A;G; A/G;A; T;C/G
AMPL16 90234	scaffold4	CTAGCAA CTGTGTA GTCGTAC TAGG	TTTACTA TCAAGGA GTTGGCA ATGG	39(C-0%,T-100%);53(G-93%,T-54%);61(C-79%,T-81%);66(C-8%,T-93%);84(C-95%,T-50%);116(C-54%,T-93%);127(A-54%,G-93%);128(G-54%,T-93%);140(C-100%,T-0%);169(G-4%,A-99%);189(G-8%,A-100%);198(C-100%,T-0%);	T;G/T;C /T;- /T;T/C; T/C;G/ A;G/T; C;A;A; C	T;G;T/C ;T;C;T; G;T;C; A;A;C

AMPL16 90235	scaffold7	AAGGGGA AAATGAA GAGGATA GTGT	CGACACT GTTCTTC CATCTTT GTTA	36(G-2%,T-98%);38(A-1%,G-100%);39(G-2%,C-98%);45(A-2%,G-98%);52(G-5%,T-98%);57(A-0%,G-100%);62(A-1%,G-100%);67(A-5%,G-98%);73(A-4%,C-2%,G-97%);80(G-99%,T-3%);84(A-0%,C-100%);91(C-2%,T-98%);95(A-2%,G-99%);100(A-1%,G-100%);101(A-2%,G-99%);103(G-35%,T-96%);111(A-7%,G-99%);117(G-2%,A-99%);139(C-100%,T-0%);143(C-100%,T-1%);145(A-0%,G-100%);146(C-98%,T-3%);147(A-0%,G-100%);152(C-100%,T-0%);153(A-3%,G-99%);154(A-0%,C-98%,T-2%);155(A-3%,G-99%);163(C-100%,T-0%);164(A-0%,G-100%);167(C-96%,T-0%);170(G-0%,C-96%);174(C-91%,T-5%);175(G-19%,A-82%);178(G-1%,C-100%);181(G-2%,A-99%);182(A-5%,G-97%);191(C-100%,T-1%);192(A-0%,G-100%);199(C-100%,T-0%);202(C-1%,T-100%);208(C-1%,T-100%);215(G-47%,A-88%,T-0%);218(C-0%,T-100%);220(C-97%,T-5%);223(A-4%,T-98%);224(A-1%,G-100%);225(C-0%,A-100%);	T;G;C; G;T;G; G;G;G; G;C;T; G;G;G; T;G;A; C;C;G; C;G;C; G;C;G; C;G;C; C;C;A; C;A;G; C;G;C;T ;T;A;T; C;T;G; A	T;G;C; G;T;G; G;G;G; G;C;T; G;G;G; T;G;A; C;C;G; C;G;C; G;C;G; C;G;C; C;C;A; C;A;G; C;G;C;T ;T;A;T; C;T;G; A
AMPL16 90238	scaffold8	TGGCAGA AAAACCTA TGCCAAT TTCT	CGCAACA CAACAAG GAAATAC ATTC	99(A-5%,G-98%);115(A-0%,G-100%);127(C-13%,A-94%);135(C-5%,T-98%);157(C-94%,T-12%);215(A-0%,G-100%);	G;G;A; T;C;G	G;G;A; T;C;G
AMPL16 90240	scaffold5	CAACAGT CAAGTTC AGTGGTA GTTC	TACTTCT TCATTCC TGAGACC AAGG	43(C-36%,T-83%);46(A-2%,T-100%);48(A-1%,C-100%);53(G-36%,C-83%);60(A-1%,G-83%);68(C-83%,T-36%);71(G-3%,A-98%);74(C-83%,T-36%);102(C-36%,T-83%);114(A-100%,T-0%);132(C-36%,T-83%);135(A-36%,G-83%);138(G-1%,A-100%);146(C-100%,T-0%);174(A-36%,G-83%);180(C-83%,T-36%);198(A-2%,G-100%);216(C-100%,T-1%);	T;T;C;C ;G;C;A; C;T;A;T ;G;A;C; G;C;G; C	T/C;T;C ;C/G;G/ -/C/T;A; T/C;T/C ;A;T/C; A/G;A; C/A/G; T/C;G;C
AMPL16 90241	scaffold5	GGAACAA TAATAAC TTCTGCG GGAA	TTCATTT ATAGGCG CGACAAA AGAC	55(C-34%,T-86%);56(G-9%,A-98%);57(A-9%,C-98%);69(A-100%,T-0%);82(G-3%,C-100%);91(G-12%,T-95%);92(C-95%,A-12%);93(C-95%,T-12%);146(G-0%,A-100%);169(C-34%,T-86%);193(A-1%,G-100%);209(C-99%,T-2%);221(A-34%,T-86%);	T;A;C; A;C;T;C ;C;A;T; G;C;T	C/T;A;C ;A;C;T/ G/A/C; T/C;A;C /T;G;C; A/T
AMPL16 90242	scaffold10	GAGAAGA CTCATCG GACACTT CTTC	CATACCT CCCTCTC TTCACAA GAC	36(A-18%,T-94%);42(A-1%,G-100%);46(G-3%,A-99%);49(G-3%,A-99%);59(C-2%,A-100%);64(C-100%,T-0%);66(G-1%,A-99%,T-2%);67(G-100%,T-0%);69(G-1%,A-100%);71(G-3%,A-99%);75(C-0%,T-100%);78(G-21%,T-92%);79(C-3%,T-99%);80(C-3%,T-99%);81(A-2%,G-100%);85(C-99%,T-3%);88(C-99%,T-3%);92(G-100%,T-3%);94(C-99%,T-3%);98(C-18%,T-92%);105(C-100%,T-2%);107(C-3%,T-99%);110(C-3%,A-99%);115(G-18%,T-92%);117(C-99%,T-3%);125(C-21%,T-92%);127(A-92%,G-17%);132(G-3%,A-99%);141(C-92%,T-18%);145(A-0%,G-5%,C-100%);156(C-100%,T-2%);157(C-1%,T-100%);160(A-100%,T-0%);165(A-1%,C-100%);168(G-5%,A-100%);172(C-95%,G-17%);174(C-1%,A-100%);180(A-0%,G-100%);181(C-95%,A-17%);182(C-95%,A-17%,T-1%);183(A-0%,G-100%);191(C-17%,T-95%);203(A-92%,G-20%);207(A-92%,G-20%);208(A-92%,G-	T;G;A; A;A;C; A;G;A; A;T;T;T ;T;G;C; C;G;C;T ;C;T;A; T;C;T;A ;A;C;C; C;T;A;C ;A;C;A; G;C;C; G;T;A; A;A;C; A;C	A/T;G; A;A;A; C;A;G; A;A;T;T /G;T;T; G;C;C; G;C;T/C ;C;T;A; T/G;C;C /T;A/G; A;T/C;C ;C;T;A; C;A;G/ C;A;G; C/A;A/ C;G;T/C ;G/A;G/ A;A/G; C;A;C

				20%);210(G-2%,C-100%);211(G-3%,A-98%);224(C-100%,T-0%);		
AMPL16 90243	scaffold1	AGTGTAT CGCCCAT CTCAATC TTTA	GTATGGA TGAAATC GCGCGG	47(A-2%,C-98%);61(G-4%,A-96%);63(G-0%,T-100%);65(G-6%,T-100%);66(C-2%,A-98%);68(C-4%,T-96%);70(A-2%,G-98%);71(A-2%,G-98%);72(C-0%,T-100%);73(C-0%,A-100%);75(G-3%,A-99%);76(C-1%,T-100%);77(A-2%,G-98%);79(A-2%,G-99%);83(A-0%,G-100%);90(C-100%,T-1%);92(C-0%,T-100%);93(C-70%,T-84%);100(C-98%,T-2%);101(A-0%,T-100%);107(A-0%,G-100%);113(G-86%,A-66%);117(C-100%,T-1%);129(C-100%,T-0%);130(C-0%,T-100%);131(A-86%,G-4%,C-62%);140(C-99%,T-1%);141(G-0%,C-100%);142(C-100%,T-0%);145(A-0%,G-99%);147(C-0%,G-1%,A-100%);149(G-9%,C-98%,T-2%);153(A-2%,G-2%,T-96%);155(G-1%,A-71%);163(C-69%,T-2%);165(G-0%,A-100%);170(C-100%,T-0%);171(G-2%,A-99%);172(C-0%,T-100%);176(C-84%,G-67%,T-4%);177(G-0%,A-100%);182(C-100%,T-1%);194(A-0%,C-100%);198(A-6%,G-100%);200(G-0%,A-100%);201(G-0%,T-100%);203(A-4%,C-96%);220(C-100%,T-1%);224(C-100%,T-0%);	C;A;T;T ;A;T;G; G;T;A; A;T;G; G;G;C; T;T/C;C ;T;G;A/ G;C;C;T ;C/A;C; C;C;G; A;C;T;- /A/C/-; A;C;A; T;C/G; A;C;C; G;A;T; C;C;C	C;A;T;T ;A;T;G; G;T;A; A;T;G; G;G;C; T;T/C;C ;T;G;A/ G;C;C;T ;A/C;C; C;C;G; A;C;T; A/-;C/-; A;C;A; T;G;C; A;C;C; G;A;T; C;C;C
AMPL16 90244	scaffold11	TTCCTGG ATAGAGA AATGGCA GAAT	GTCCATG TGTGTAT ACGGAAC TCT	48(A-88%,G-34%);51(G-2%,A-98%);54(C-97%,T-7%);57(C-98%,T-6%);60(A-6%,G-98%);63(G-0%,C-98%,T-16%);66(G-1%,T-99%);69(G-6%,C-98%);72(A-89%,G-32%);73(A-0%,C-100%);78(C-21%,T-93%);82(C-2%,T-99%);90(C-2%,T-98%);102(C-1%,T-100%);105(C-1%,T-99%);111(A-95%,G-19%);115(G-100%,T-1%);123(C-23%,T-91%);124(C-2%,G-98%);126(C-98%,T-2%);138(G-2%,A-98%);144(A-12%,G-94%,T-9%);147(G-0%,A-100%);148(C-100%,T-0%);150(G-1%,C-100%,T-0%);159(C-100%,T-0%);162(C-99%,T-3%);168(C-100%,T-0%);171(C-100%,T-0%);172(G-2%,A-98%);180(C-91%,A-21%,T-5%);189(A-0%,G-98%);192(C-98%,T-7%);198(C-98%,T-7%);199(C-5%,T-100%);201(G-1%,A-100%);210(C-1%,G-100%,A-9%);	A;A;C; C;G;C;T ;C;A;C; T;T;T;T ;T;A;G; T;G;C; A;G;A; C;C;C;C ;C;C;A; C;G;C; C;T;A; G	G/A;A; C;C;G; C;T;C;G /A;C;T; T;T;T;T ;G/A;G; C/T;G;C ;A;G/T; A;C;C; C;C;C;C ;A;A/C; G;C;C;T ;A;G/A

AMPL16 90245	scaffold12	GGGATCA TCTCTAT ACGGCTC TTC	GGTGAGC AGCCAGA CTATGAA G	37(C-100%,T-0%);43(C-100%,T-1%);44(C-100%,T-1%);46(G-0%,C-99%,T-2%);47(G-0%,T-100%);48(A-3%,G-99%);51(C-1%,G-1%,A-100%,T-0%);52(G-1%,C-100%);53(A-0%,C-0%,G-100%,T-0%);54(C-1%,G-100%);55(C-1%,G-46%,A-77%);56(A-0%,G-100%);57(A-1%,G-100%);59(A-0%,G-19%);62(G-2%,A-99%);63(A-47%,G-17%);68(A-0%,G-100%);70(G-70%,A-74%);72(C-100%,T-0%);80(C-1%,T-76%);82(A-0%,G-76%);85(G-0%,A-100%);91(A-100%,T-0%);100(G-69%,A-72%);101(C-100%,T-1%);118(A-49%,C-6%,G-76%);120(G-100%,T-3%);126(G-0%,C-100%);129(G-0%,C-100%);133(C-100%,T-0%);134(C-8%,T-99%);136(G-7%,C-76%,T-46%);139(C-100%,T-0%);144(C-100%,T-0%);145(C-66%,G-73%);148(C-66%,G-15%,T-66%);155(A-3%,G-99%);159(G-1%,A-100%);160(A-1%,C-0%,G-70%,T-68%);161(G-3%,A-100%);172(C-2%,A-100%);175(G-59%,A-74%);176(C-3%,T-99%);178(G-100%,T-1%);181(G-0%,A-100%);184(A-47%,T-77%);190(A-0%,G-100%);193(C-99%,T-9%);199(C-0%,T-100%);201(G-76%,T-52%);202(C-100%,T-0%);205(A-2%,G-100%);208(C-75%,T-67%);211(C-0%,T-100%);212(C-16%,T-97%);213(G-0%,T-100%);214(G-99%,A-9%);	C;C;C;C ;T;G;A; C;G;G; A/G;G; G;-;A;- /A;G;G/ A;C;- /T;G/-;A ;A;G/A; C;G/A; G;C;C; C;T;C/T ;C;C;C/ G;C/T; G;A;G/ T;A;A; A/G;T; G;A;A/ T;G;C;T ;T/G;C; G;C/T;T ;T;T;G	C;C;C;C ;T;G;A; C;G;G; A;G;G; G/-;A;G /-;G;G/ A;C;T; G;A;A; A/G;C; G;G;C; C;C;T;C ;C;C;G; C/G;G; C/G;T; A;A;A; T;G;A;T ;G;C;T; G;C;G; C/T;T;T ;T;G/A
AMPL16 90246	scaffold7	AGTGGGA ATAGTTG CATTGGA GG	AATAATG CGGCTAT AGACAAG GCTA	34(C-2%,T-99%);46(C-100%,T-0%);65(C-6%,G-97%);67(G-0%,T-100%);68(A-15%,G-89%);97(C-100%,T-0%);98(G-9%,A-94%);104(A-7%,G-96%);113(A-6%,G-96%);114(C-15%,T-90%);135(A-0%,C-100%);136(G-15%,A-90%);138(C-95%,T-7%);172(C-7%,G-95%);185(A-0%,C-100%);192(C-16%,G-89%);194(C-16%,T-89%);205(C-100%,T-0%);206(G-16%,A-89%);	T;C;G;T ;G;C;A; G;G;T; C;A;C; G;C;G; T;C;A	T;C;G;T ;G;C;A; G;G;T; C;A;C; G;C;G; T;C;A
AMPL16 90249	scaffold5	GAAGCTA AAGGACC TTACATC ATGC	CACTGTT ACTCAAT GTCATCT GCAC	42(A-3%,C-98%);46(A-5%,C-4%,G-94%);47(C-5%,G-97%);48(A-5%,G-93%);77(G-0%,A-100%);90(G-0%,A-100%);91(G-0%,A-100%);97(A-1%,T-99%);115(C-99%,T-2%);131(A-0%,G-100%);	C;G;G; G;A;A; A;T;C; G	C;G;G; G;A;A; A;T;C; G
AMPL16 90250	scaffold8	ATTCTTG TTTACGT CGTTGAA TCGA	GAGTATC AATCCTC TTCTCGA CGAG	52(A-14%,C-96%);83(G-8%,T-98%);101(C-1%,T-100%);112(C-99%,T-2%);131(C-0%,T-100%);138(G-8%,A-98%);139(A-100%,T-0%);141(C-8%,T-100%);146(A-97%,T-18%);147(C-100%,T-0%);178(A-0%,T-100%);194(G-7%,A-99%);195(C-100%,T-1%);196(G-21%,A-91%);198(A-2%,T-97%);199(G-13%,A-96%);206(C-9%,G-98%);213(G-0%,A-100%);214(C-100%,T-0%);224(C-2%,T-99%);	C;T;T;C ;T;A;A; T;A;C;T ;A;C;A; T;A;G; A;C;T	C;T;T;C ;T;A;A; T/C;T/A ;C;T;A; C;A/G; T;A;G; A;C;T
AMPL16 90251	scaffold8	ATGGTCA GAAGACG ATTCATG TAGA	TGGCAGT TACAAAG ACTTTGA CATC	38(G-5%,A-99%);40(C-8%,A-97%);50(G-3%,C-98%);56(G-3%,T-98%);62(G-7%,T-97%);74(C-3%,T-98%);77(C-98%,T-3%);83(G-3%,A-98%);87(A-0%,G-100%);94(A-0%,G-100%);95(G-91%,T-17%);104(C-9%,T-94%);131(A-7%,G-97%);152(G-3%,A-98%);155(A-99%,T-5%);157(C-100%,T-0%);170(A-5%,G-99%);171(A-5%,G-99%);173(C-99%,T-5%);174(C-97%,T-8%);175(C-97%,T-8%);	A;A;C; T;T;T;C ;A;G;G; G;T;G; A;A;C; G;C;C; C;C	A;A;C; T;T;T;C ;A;G;G; G;T;G; A;A;C; G;G;C; C;C

AMPL16 90252	scaffold8	ATTTCGT CAACAGA ACATTGG CATC	TTATTGA GTGCGGG GATCAAG AG	55(C-0%,A-100%);72(C-100%,T-0%);84(A-1%,T-99%);100(C-1%,G-99%);110(G-1%,A-99%);118(A-99%,T-1%);135(G-100%,T-0%);139(C-99%,T-1%);145(C-1%,A-99%);212(C-99%,T-1%);	A;C;T; G;A;A; G;C;A; C	A;C;T; G;A;A; G;C;A; C
AMPL16 90253	scaffold5	TTGCCAG GTACATC TCTAAAT CCTC	GAGACAC TCTATGG GCAACAA TTCT	44(G-7%,A-94%);55(C-100%,T-0%);101(C-91%,T-12%);110(G-12%,A-91%);128(C-4%,G-98%);146(A-12%,G-91%);183(C-12%,A-91%);201(C-4%,T-98%);214(C-98%,T-3%);230(G-9%,A-94%);	A;C;C; A;G;G; A;T;C; A	A;C;C; A;G;G; A;T;C; A
AMPL16 90254	scaffold8	CGTACGT CTTCATT ATTGGTG ACTG	CCAGATT CTCGACG TTGTCCA AG	44(A-7%,G-100%);50(A-33%,T-86%);55(G-0%,A-100%);80(C-26%,G-94%);81(G-98%,T-12%);96(G-23%,C-92%);102(G-9%,A-99%);112(G-24%,C-96%);114(C-99%,T-3%);115(A-7%,G-100%);119(C-100%,T-4%);125(C-0%,T-100%);130(A-3%,T-99%);145(C-33%,G-86%);153(G-9%,C-99%);154(C-8%,G-7%,T-97%);162(A-1%,G-100%);165(C-100%,T-7%);208(A-0%,C-100%);212(G-100%,T-0%);	G;T;A; G;G;C; A;C;C; G;C;T; G;C;T; G;C;C; G	G;A/T; A;G;T/ G;C/G; A/G;C/ G;C;G; C;T;T;C /G;G;C; T;G;C;C ;G
AMPL16 90258	scaffold1	GTCTGTA AAGCGCT TGAGATT CAAA	AAAACCT CATCGTT CTGTCCT TTTG	41(A-100%,T-0%);44(C-100%,T-1%);48(C-65%,T-84%);57(G-84%,A-65%);61(A-0%,G-100%);63(A-84%,G-65%);72(C-14%,T-99%);105(C-100%,T-0%);114(C-0%,G-84%,T-65%);121(A-0%,C-100%);169(C-3%,G-100%);227(C-100%,T-3%);233(A-0%,T-100%);	A;C;C/T ;G/A;G; A/G;T; C;T/G;C ;G;C;T	A;C;T/C ;A/G;G; G/A;C/ T;C;T/G ;C;G;C; T
AMPL16 90259	scaffold4	GTGTCGT CAGATCT ACACTGT TCTA	CCATGGG TCATACG ATAAGTA CGAA	36(C-21%,T-92%);40(G-96%,A-18%);90(A-1%,T-100%);91(A-92%,C-21%);92(A-1%,G-100%);93(C-1%,G-100%);94(A-1%,G-100%);114(G-92%,A-20%);115(C-92%,T-20%);116(A-92%,G-20%);153(C-95%,T-17%);181(A-92%,G-21%);189(A-0%,G-100%);192(A-0%,G-100%);	T;G;T;A ;G;G;G; G;C;A; C;A;G; G	T;G;T;A ;G;G;G; G;C;A; C;A;G; G
AMPL16 90260	scaffold5	AGATTCA TAGCTGC TAGGATG CTAG	CGTGAGA ACTGCTT TTCATGA TCTT	36(C-6%,G-0%,A-95%);38(A-5%,G-97%);49(G-0%,A-100%);55(C-97%,T-3%);57(G-1%,A-99%);59(G-0%,T-100%);65(C-17%,T-87%);68(C-5%,T-96%);80(A-0%,T-100%);91(G-93%,T-11%);113(G-10%,A-92%);116(G-2%,A-99%);117(C-2%,G-100%);124(A-1%,G-100%);147(G-1%,A-100%);148(G-100%,T-1%);154(G-100%,T-1%);158(A-1%,C-100%);159(G-1%,A-100%);165(A-7%,G-94%);178(A-3%,C-98%);181(G-17%,T-87%);186(G-3%,A-97%);188(C-1%,A-100%);200(C-100%,T-1%);205(C-0%,G-7%,T-94%);206(A-97%,T-3%);230(A-1%,G-100%);233(A-0%,G-100%);	A;G;A; C;A;T;T ;T;T;G; A;A;G; G;A;G; G;C;A; G;C;T; A;A;C; T;A;G; G	A;G;A; C;A;T;T ;T;T;G; A;A;G; G;A;G; G;C;A; G;C;T; A;A;C; T;A;G; G
AMPL16 90262	scaffold1	GCAATGG TTCTGTG AACACAA TGAG	GGACAGG ATAGGAT ACCGATT ATCG	36(G-6%,A-99%);37(A-76%,G-0%,C-59%,T-21%);38(C-0%,G-1%,A-100%);42(C-99%,T-1%);44(C-0%,G-100%);45(A-0%,G-100%);46(A-0%,C-1%,T-99%);50(G-2%,A-100%);53(A-100%,T-0%);60(C-99%,T-1%);66(G-2%,A-98%);78(A-7%,G-100%);99(A-4%,G-96%);105(A-0%,C-100%);116(C-84%,G-41%);119(C-27%,T-96%);121(G-0%,A-100%);123(A-0%,C-2%,G-98%);128(G-0%,T-100%);129(C-39%,A-95%);131(C-0%,A-100%);132(C-3%,T-97%);134(C-100%,T-0%);135(A-3%,G-97%);136(C-0%,T-100%);138(C-100%,T-0%);141(C-98%,T-2%);142(A-100%,T-0%);143(G-39%,A-95%);144(G-25%,A-95%);145(A-39%,G-	A;A/C; A;C;G; G;T;A; A;C;A; G;G;C; C;T;A; G;T;C/ A;A;T; C;G;T;C ;C;A;G/ A;A;G/ A;T;G;T ;G;C;T; C/T	A;C/A; A;C;G; G;T;A; A;C;A; G;G;C; G/C;C/T ;A;G;T; A;A;T; C;G;T;C ;C;A;A; A;G;T; T;G;G; C;T;C

				95%);147(A-1%,C-0%,T-100%);148(G-100%,T-0%);150(C-3%,T-97%);151(G-99%,T-1%);152(G-25%,C-95%);153(C-4%,T-96%);170(C-87%,T-62%);		
AMPL16 90263	scaffold11	TCAAATA TTTTCTG CGCCACA ATTG	AACACGA CTAGCTA TCTTACC TACT	40(G-16%,T-0%);47(G-1%,A-15%);53(C-1%,G-14%);55(C-0%,A-99%);56(C-100%,T-4%);58(G-97%,A-16%);62(G-0%,T-100%);88(C-0%,A-100%);90(G-0%,A-100%);93(A-97%,C-17%);95(A-12%,C-99%);97(C-100%,T-4%);98(C-17%,T-97%);104(A-4%,C-100%);106(C-0%,A-100%);107(G-0%,T-100%);115(G-98%,T-14%);116(G-0%,T-100%);119(C-90%,A-29%);128(C-0%,T-100%);132(A-100%,T-3%);139(C-100%,T-4%);151(C-100%,T-1%);154(A-94%,G-20%);155(A-0%,G-100%);167(A-0%,G-100%);171(G-4%,C-100%);175(A-0%,G-100%);184(G-98%,T-14%);	-;-;-;A;C ;G;T;A; A;A;C; C;T;C;A ;T;G;T; C;T;A;C ;C;A;G; G;C;G; G	G/-;A/-; - /G;A;C; G/A;T; A;A;A/ C;C;C;C /T;C;A; T;T/G;T ;C/A;T; A;C;C; A/G;G; G;C;G; G/T
AMPL16 90264	scaffold5	ATTCAGT GGCACTA ACGATAT CGAA	CCTACTC GAAGCAT AGTAAGC TTGA	41(G-1%,C-99%);44(C-99%,T-1%);51(G-0%,A-100%);70(C-0%,T-100%);73(C-51%,T-92%);78(C-99%,T-1%);92(C-27%,T-94%);99(G-1%,A-99%);137(G-1%,A-99%);138(A-0%,G-100%);142(C-1%,G-99%);144(G-1%,A-99%);151(G-1%,A-99%);156(C-4%,T-99%);	C;C;A;T ;T/C;C; T;A;A; G;G;A; A;T	C;C;A;T ;T;C;C/ T;A;A; G;G;A; A;T
AMPL16 90265	scaffold8	TGTACTA CTTGCTA CATAGAC ACGG	CTGTCCG GAATTCG TAGATTT TGTC	38(A-19%,C-87%);56(C-1%,G-88%);58(C-88%,T-1%);60(G-0%,A-94%);67(C-96%,T-8%);68(G-8%,A-96%);69(C-0%,A-100%);70(G-12%,C-93%);74(C-4%,T-97%);76(C-1%,T-100%);78(G-1%,C-100%);88(C-87%,T-19%);91(C-4%,A-97%);103(C-1%,A-100%);105(C-91%,T-16%);109(A-8%,G-96%);118(G-100%,T-1%);121(G-15%,A-92%);125(C-100%,T-0%);133(A-13%,G-94%);134(G-0%,T-100%);152(A-87%,T-19%);153(C-19%,A-87%);154(A-13%,G-94%);157(C-1%,T-100%);168(C-12%,T-93%);169(A-1%,G-100%);171(C-1%,T-100%);180(C-19%,T-87%);187(C-19%,T-87%);189(C-97%,T-7%);191(G-19%,A-87%);193(A-12%,G-92%);	C;G;C; A;C;A; A;C;T;T ;C;C;A; A;C;G; G;A;C; G;T;A; A;G;T;T ;G;T;T; T;C;A; G	C;G;C; A;C;A; A;C;T;T ;C;C;A; A;C;G; G;A;C; G;T;A; A;G;T;T ;G;T;T; T;C;A; G
AMPL16 90268	scaffold2	GTAGCGA TTAATGG GAGAGAT GGAT	GTCTTGA CATGTCA GAAATCG AAGG	36(C-94%,T-67%);37(G-1%,A-100%);38(A-0%,G-1%,T-98%);39(A-1%,G-100%);40(C-1%,T-100%);43(A-71%,C-85%);46(C-0%,T-100%);47(A-0%,G-100%,T-1%);48(A-94%,G-20%);49(A-0%,T-100%);50(C-0%,T-100%);51(C-72%,T-85%);52(G-0%,A-100%);53(A-72%,G-85%);54(A-85%,T-72%);57(A-1%,G-100%);60(A-1%,G-99%);61(A-1%,G-100%,T-0%);62(C-100%,T-0%);63(A-3%,C-99%);64(A-14%,G-95%);65(G-100%,T-0%);66(A-73%,G-83%);69(G-98%,T-2%);72(C-1%,G-99%);84(A-1%,G-100%);96(G-69%,A-88%);102(G-1%,A-100%);105(G-1%,T-99%);114(C-1%,T-99%);120(A-0%,C-71%,T-85%);126(G-69%,A-88%);132(G-99%,T-1%);134(C-1%,T-100%);141(C-96%,T-6%);149(A-100%,T-1%);150(A-2%,G-0%,C-97%);153(G-1%,A-99%);155(C-99%,T-3%);	C;A;T; G;T;C;T ;G;A;T; T;T;A;G ;A;G;G; G;C;C; G;G;G; G;G;G; A;A;T;T ;T;A;G; T;C;A;C ;A;C	C;A;T; G;T;C;T ;G;G/A; T;T;T;A ;G;A;G; G;G;C; C;G;G; G;G;G; G;A;A; T;T;T;A ;G;T;C; A;C;A; C

AMPL16 90269	scaffold2	TGTCGTA TTTGCAG GCTTCT TTTG	GTCAACG GAATGGA GGATCCT T	38(G-6%,A-98%);43(A-24%,T-95%);51(C-0%,G-100%);58(C-99%,T-8%);63(G-0%,T-96%);65(G-11%,A-99%);66(C-97%,T-11%);67(A-1%,G-100%);71(C-19%,T-94%);74(C-1%,T-100%);77(A-1%,G-100%);82(G-11%,C-97%,T-9%);83(A-1%,G-99%,T-0%);92(G-2%,T-100%);100(C-37%,T-89%);115(C-15%,T-96%);123(A-11%,G-99%);124(C-95%,T-16%);126(G-99%,T-5%);129(C-99%,T-11%);130(A-26%,T-94%);139(C-7%,T-97%);160(A-6%,G-98%);163(C-95%,G-3%,T-13%);166(C-37%,T-89%);168(C-37%,T-89%);172(G-0%,A-100%);178(G-0%,T-100%);183(G-6%,A-99%);184(A-6%,C-99%);187(A-99%,T-6%);191(A-0%,T-23%);199(C-99%,T-11%);202(C-13%,T-1%);205(G-13%,T-97%);209(C-2%,G-0%,A-100%);215(A-0%,C-31%,T-90%);216(G-94%,A-28%);217(G-11%,A-99%);218(C-90%,G-31%);	A;T;G; C;T;A;C ;G;T;T; G;C;G; T;T;T;G ;C;G;C; T;T;G;C ;T;T;A; T;A;C; A;-;C;-; T;A;T;G ;A;C	A;T;G; C;T;A;C ;G;T;C; T;G;C; G;T;C/T ;T/C;G; C;G;C;T ;T;G;T/ C;C/T;T /C;A;T; A;C;A; T/-;C;C/ -;G/T;A; T/C;A/ G;A;C/ G
AMPL16 90270	scaffold4	GAGAGCC ATTGCGA TATGTTA TGG	AGACGTG TACGATG TGGGAAT ATTT	35(A-0%,G-100%);37(A-0%,G-100%);38(C-34%,T-81%);49(C-100%,T-0%);52(C-100%,T-0%);53(A-0%,T-100%);54(C-0%,T-100%);55(C-0%,T-100%);65(A-100%,T-0%);68(G-0%,C-100%,T-0%);77(C-100%,T-1%);78(A-2%,G-100%);95(C-0%,A-100%);99(C-100%,T-1%);100(A-0%,G-100%);114(G-4%,T-98%);118(C-100%,T-0%);121(C-100%,T-0%);128(C-3%,T-100%);130(G-0%,T-100%);141(G-100%,T-0%);143(G-0%,C-100%);150(A-2%,G-100%);151(A-100%,T-0%);162(C-100%,T-0%);172(A-0%,C-100%);178(C-100%,T-0%);187(G-0%,T-100%);188(C-100%,T-0%);204(C-9%,T-97%);	G;G;T; C;C;T;T ;T;A;C; C;G;A; C;G;T;C ;C;T;T; G;C;G; A;C;C; C;T;C;T	G;G;T; C;C;T;T ;T;A;C; C;G;A; C;G;T;C ;C;T;T; G;C;G; A;C;C; C;T;C;T
AMPL16 90272	scaffold8	GAGCCCT AAAAATC CAATCAG TCAG	GCATGAT CCTCGTC AAGAAAT TCTT	37(C-99%,T-1%);70(C-99%,T-1%);72(A-0%,G-100%);75(G-0%,A-100%);81(G-5%,A-98%);87(G-9%,A-95%);96(A-0%,G-100%);98(C-100%,T-0%);105(C-100%,T-0%);108(C-1%,G-0%,A-98%,T-2%);123(C-0%,G-100%);125(C-98%,T-5%);129(A-9%,G-95%);132(C-8%,T-95%);134(C-9%,T-95%);135(C-0%,T-100%);141(G-9%,A-95%);143(A-5%,T-98%);150(C-0%,A-100%);162(G-4%,T-98%);168(G-2%,C-99%);173(C-9%,T-95%);174(G-1%,A-99%);176(A-5%,C-96%,T-2%);186(C-96%,T-6%);198(G-2%,A-98%);200(A-15%,G-95%);	C;C;G; A;A;A; G;C;C; A;G;C; G;T;T;T ;A;T;A; T;C;T;A ;C;C;A; G	C;C;G; A;A;A; G;C;C; A;G;C; G;T;T;T ;A;T;A; T;C;T;A ;C;C;A; G
AMPL16 90273	scaffold8	GTGGTGG GAAAATG TCAGAGA ATTT	TCATCAT GATTCAC ATTGAAA GCCC	41(C-3%,A-100%);49(C-100%,T-3%);60(A-5%,C-97%);64(C-3%,T-100%);65(G-96%,T-13%);88(G-3%,A-100%);105(A-5%,G-97%);111(C-100%,T-0%);117(G-3%,A-100%);121(C-0%,T-96%);133(G-3%,C-100%);141(G-5%,T-97%);143(C-100%,T-3%);147(A-3%,C-100%);153(A-3%,C-100%);167(C-0%,T-100%);189(C-6%,T-100%);194(C-3%,A-100%);207(A-3%,C-99%);216(A-13%,G-97%);	A;C;C;T ;G;A;G; C;A;T;C ;T;C;C; C;T;T;A ;C;G	A;C;C;T ;G;A;G; C;A;T;C ;T;C;C; C;T;T;A ;C;G

AMPL16 90274	scaffold1	ATTGGCA TAATACA TCTGATC GTGG	TTCCCGT TTCGAAG TAGTTTG ATGA	39(A-0%,G-100%);57(A-1%,G-99%,T-0%);61(G-85%,A-26%);62(A-85%,C-26%);64(A-85%,G-26%);65(C-24%,T-87%);66(G-0%,C-97%);69(A-94%,G-26%);71(A-39%,T-85%);75(G-20%,A-97%);76(G-91%,A-30%);82(A-100%,T-0%);84(A-2%,G-98%);85(C-100%,T-1%);87(A-0%,C-100%);88(G-0%,T-100%);91(G-98%,C-21%);99(C-0%,T-100%);103(G-5%,A-95%);104(A-0%,G-100%);105(G-100%,T-0%);119(A-100%,T-4%);121(C-1%,G-100%);130(A-5%,G-95%);133(C-2%,G-98%);145(C-100%,T-0%);148(C-98%,A-14%,T-2%);149(G-85%,A-39%);150(A-0%,C-100%);153(C-0%,G-94%,T-30%);154(G-1%,A-98%,T-2%);155(G-99%,T-1%);157(G-0%,C-100%);163(A-2%,G-98%);165(A-0%,C-100%);166(G-4%,A-96%);173(C-0%,G-100%);175(A-2%,G-98%);181(C-1%,T-99%);187(C-35%,T-88%);	G;G;G; A;A;T; C;A;T; A;G;A; G;C;C;T ;G;T;A; G;G;A; G;G;G; C;C;G; C;G;A; G;C;G; C;A;G; G;T;T	G;G;G/ A;A/C; A/G;T/ C;C;A/ G;T/A; A;A/G; A;G;C; C;T;C/G ;T;A;G; G;A;G; G;G;C; A/C;A/ G;A;G; C;G;C; A;G;G; T;T/C
AMPL16 90275	scaffold1	CTGGACG GATATCT GTTCTAT GTGT	GCACTTA ACAGAAG TTCTTCC CAAA	37(C-100%,T-0%);42(C-0%,G-100%);45(C-100%,T-0%);56(A-88%,G-36%);57(A-0%,C-100%);62(C-0%,T-100%);66(A-0%,G-100%);70(A-0%,G-100%);77(A-0%,G-100%);80(A-0%,G-100%);88(G-0%,A-100%);91(C-0%,G-95%,T-25%);93(G-0%,A-100%);96(A-1%,C-100%);97(A-1%,G-100%);105(C-1%,T-100%);113(G-100%,T-0%);123(A-100%,T-0%);126(G-0%,C-35%,T-90%);137(C-0%,G-0%,T-100%);152(G-0%,A-35%);153(G-0%,A-35%);154(A-0%,G-35%);162(G-99%,T-0%);163(A-14%,G-98%);167(G-14%,T-99%);168(C-100%,T-0%);188(A-7%,G-100%);200(G-0%,A-100%);204(C-0%,T-100%);215(G-1%,C-100%);	C;G;C; A;C;T; G;G;G; G;A;G; A;C;G; T;G;A;T ;T;-;-;-; G;G;T; C;G;A; T;C	C;G;C; A/G;C; T;G;G; G;G;A; T/G;A; C;G;T; G;A;C/ T;T;- /A;A/-; G/-;G;G ;T;C;G; A;T;C
AMPL16 90279	scaffold1	AACTTTT GACTGGC AATTGTC TGAA	CATGTGG CCTGAAC GAACATC	102(C-84%,G-41%);103(C-98%,T-5%);118(A-6%,T-100%);119(G-4%,A-96%);121(C-2%,T-99%);124(G-98%,T-2%);125(A-1%,G-2%,C-98%);126(C-1%,G-98%);132(A-0%,T-100%);133(G-4%,T-96%);137(G-3%,C-98%);138(C-3%,A-98%);139(A-4%,G-1%,T-96%);141(C-3%,T-98%);145(A-6%,C-100%);155(G-98%,T-3%);158(C-0%,T-100%);160(G-3%,T-98%);162(A-90%,T-34%);166(C-0%,T-100%);176(C-2%,T-98%);177(G-98%,T-3%);178(C-3%,A-96%,T-2%);180(C-4%,T-96%);184(C-96%,T-4%);187(C-4%,A-96%);190(C-0%,A-100%);191(G-3%,A-96%);192(A-3%,C-0%,T-97%);196(A-3%,C-91%,T-29%);199(C-3%,T-96%);209(G-2%,A-23%);211(C-2%,A-23%);212(G-23%,T-2%);216(G-3%,A-98%);233(C-1%,T-98%);234(A-4%,C-96%);236(A-78%,T-78%);240(G-3%,A-98%);	C;C;T;A ;T;G;C; G;T;T;C ;A;T;T; C;G;T;T ;A;T;T; G;A;T; C;A;A; A;T;C;T ;-;-;-A; T;C;A/T ;A	C/G;C;T ;A;T;G; C;G;T;T ;C;A;T; T;C;G;T ;T;A/T; T;T;G;A ;T;C;A; A;A;T;T /C;T;- /A;A/-;- /G;A;T; C;T/A; A
AMPL16 90280	scaffold11	GCCGAGA TGATGAA TCATTGA ATGT	CAAATTT GAGTTAC CCCAGAT CACC	60(A-2%,G-99%);61(A-2%,G-99%);98(A-7%,G-100%);140(A-100%,G-11%);145(A-96%,T-21%);146(A-96%,T-21%);	G;G;G; A;A;A	G;G;G; G/A;A/ T;A/T

AMPL16 90282	scaffold1	CTATGCC CACCGTT ATCATT GTAC	CATACAG CTCTCAA GGTTGTT TTCG	44(G-3%,C-99%);51(C-100%,T-0%);63(C-100%,T-0%);66(A-50%,G-93%);73(G-2%,A-100%);78(G-98%,C-12%);80(C-0%,T-90%);81(C-5%,T-90%);82(G-0%,A-100%);85(A-2%,G-100%);87(G-0%,A-100%);89(C-0%,T-100%);91(G-96%,A-12%);92(G-6%,T-99%);93(C-55%,T-90%);94(C-6%,G-100%);96(G-69%,T-84%);98(C-5%,A-100%);102(A-2%,T-100%);103(G-0%,C-100%,T-2%);104(G-100%,T-0%);106(C-0%,G-100%);113(A-0%,C-100%,T-0%);118(G-100%,T-0%);121(G-0%,A-100%);138(G-0%,T-100%);141(C-94%,T-42%);144(A-3%,G-99%);145(A-10%,C-84%,G-61%);150(G-6%,A-100%);156(A-7%,G-99%);167(A-0%,C-100%,T-0%);180(G-99%,T-11%);182(G-0%,A-100%);183(A-99%,T-5%);201(A-5%,G-1%,T-99%);202(C-99%,T-6%);203(C-100%,T-3%);204(G-99%,T-5%);205(C-99%,T-5%);208(C-100%,T-0%);209(G-1%,A-99%,T-5%);213(A-5%,T-99%);214(C-5%,G-99%);222(A-0%,G-100%);223(C-100%,T-0%);225(G-0%,A-100%);226(A-0%,T-100%);231(G-1%,A-100%);	C;C;C; A/G;A; G;T/-;T/ -;A;G;A ;T;G;T; T/C;G; G/T;A;T ;C;G;G; C;G;A; T;T/C;G ;G/C;A; G;C;G; A;A;T; C;C;G; C;C;A;T ;G;G;C; A;T;A	C;C;C; G;A;G/ C;T;T;A ;G;A;T; A/G;T;T ;G;G/T; A;T;C; G;G;C; G;A;T; C;G;G/ C;A;G; C;G;A; A;T;C;C ;G;C;C; A;T;G; G;C;A; T;A
AMPL16 90283	scaffold4	GGACTCG CTTGACA TAGAGAT ACAT	GATTTCA TCCCTAG GCATTGA TTCG	41(C-1%,T-99%);53(C-90%,T-13%);54(C-2%,T-98%);57(A-3%,C-97%);59(A-0%,G-100%);60(A-3%,G-98%);71(C-3%,G-3%,A-96%);72(C-99%,T-4%);73(C-100%,T-0%);92(G-100%,T-0%);96(G-0%,A-100%);97(A-0%,G-100%);98(G-0%,C-100%);103(C-15%,G-94%);104(C-95%,T-5%);110(C-0%,T-100%);111(A-14%,G-93%);113(C-0%,A-100%);116(A-0%,C-0%,G-100%);117(A-14%,G-93%);120(G-0%,A-100%);135(A-0%,C-19%,T-90%);136(G-20%,A-90%);144(A-1%,G-99%);152(C-0%,T-100%);155(C-3%,T-98%);159(C-13%,T-96%);171(C-1%,G-99%);	T;C;T;C ;G;G;A; C;C;G; A;G;C; G;C;T; G;A;G; G;A;T; A;G;T;T ;T;G	T;C;T;C ;G;G;A; C;C;G; A;G;C; G;C;T; G;A;G; G;A;T; A;G;T;T ;T;G
AMPL16 90285	scaffold1	TCATGAT TGTAATC AATGAAA CGCA	ATGTGTT CAACAAA TGTCGAC GAAA	41(G-1%,A-99%);48(C-85%,T-38%);60(A-0%,T-100%);66(C-94%,T-23%);81(C-100%,T-0%);99(A-4%,G-98%);104(A-92%,T-29%);108(A-0%,C-99%,T-0%);111(A-0%,G-100%);122(G-0%,C-100%);129(A-100%,T-5%);130(A-5%,C-100%);143(C-1%,T-99%);151(C-40%,A-86%);152(A-99%,T-1%);166(C-1%,A-99%);201(C-7%,G-99%);226(A-0%,T-100%);231(A-99%,T-3%);	A;C;T;C ;C;G;A; C;G;C; A;C;T; A;A;A; G;T;A	A;C/T;T ;T/C;C; G;T/A; C;G;C; A;C;T;C /A;A;A; G;T;A
AMPL16 90287	scaffold8	TCTGGTA TCCTGAA CCAGACA TTC	GCCATAG AGCATAA GGTGGTA AATC	56(C-4%,T-100%);80(C-26%,T-96%);87(A-100%,T-4%);89(G-29%,C-90%);90(A-0%,G-100%);131(A-6%,G-99%);179(A-3%,C-100%);206(G-1%,A-100%);210(A-0%,G-100%);230(C-100%,T-0%);	T;T;A;C ;G;G;C; A;G;C	T;T;A;C ;G;G;C; A;G;C
AMPL16 90288	scaffold1	ATGGGCT TCATATA CGTGATT GGTA	GAGAGGT GCGTAAA GTGGACT TC	41(A-77%,T-24%);42(C-77%,T-24%);43(C-77%,T-24%);44(A-3%,T-97%);45(G-97%,T-3%);47(G-0%,T-24%);51(C-0%,T-100%);53(C-25%,T-3%);57(G-77%,T-24%);65(A-77%,C-21%,T-3%);69(A-2%,G-100%);71(G-98%,T-3%);87(G-0%,A-100%);93(C-0%,T-100%);96(A-3%,G-97%);97(G-2%,C-98%);102(C-31%,T-75%);105(G-79%,A-25%);108(C-79%,T-26%);109(G-0%,A-100%);111(A-1%,G-99%);114(A-3%,G-100%);118(A-1%,G-100%);132(A-3%,G-	A;C;C;T ;G;-;T;-; G;A;G; G;A;T; G;C;T; G;C;A; G;G;G; G;G;T; G;T;G;T ;A;T;T; T;G;G;T	T;T;T;T ;G;T;T; C;T;C;G ;G;A;T; G;C;C; A;T;A; G;G;G; G;G;T; G;T;G;T ;A;T;T; T;G;G;T

				100%);135(A-3%,G-97%);153(C-3%,T-98%);160(G-99%,T-1%);163(G-1%,T-100%);164(C-0%,G-96%,T-9%);168(C-3%,T-100%);172(G-3%,A-98%);176(A-1%,C-7%,T-95%);177(A-1%,C-6%,G-1%,T-98%);178(A-6%,C-0%,G-1%,T-98%);179(A-0%,C-3%,G-98%);181(A-7%,G-98%);186(A-0%,C-4%,T-97%);187(C-3%,T-97%);188(G-0%,A-100%);189(A-3%,C-97%,T-1%);194(A-0%,G-100%);196(C-100%,T-0%);197(A-3%,C-0%,T-97%);198(C-3%,G-98%);201(A-1%,G-99%);202(G-100%,T-0%);205(C-100%,T-0%);211(C-1%,T-100%);	;T;A;C; G;C;T; G;G;G; C;T	;T;A;C; G;C;T; G;G;G; C;T
AMPL16 90289	scaffold12	ACATCAC GATAACT GACTCCA AGTA	CTCGATG GCTGTGA CCAGTAT C	44(G-0%,A-22%);47(C-0%,T-22%);48(G-95%,A-23%);49(C-0%,T-100%);65(G-0%,T-100%);68(C-100%,T-0%);69(A-95%,T-22%);73(G-100%,T-0%);75(C-0%,T-100%);80(A-0%,G-95%,T-22%);82(G-0%,T-100%);89(G-95%,A-22%);90(A-0%,T-100%);98(A-0%,G-100%);134(C-95%,T-22%);164(A-95%,G-22%);173(C-95%,A-22%);183(A-95%,G-23%);	-;G;T; T;C;A; G;T;G;T ;G;T;G; C;A;C; A	-/A;- /T;A/G; T;T;C;A /T;G;T; G/T;T;G /A;T;G; C/T;G/ A/A;C; A/G
AMPL16 90290	scaffold14	GTTTAAC GACGCTG TTGTAAG AGAT	TTTTGAA GGCGAGG ATATACT GGAA	36(C-98%,T-5%);51(A-1%,G-99%);55(C-96%,T-12%);67(C-100%,T-0%);68(A-3%,G-100%);99(C-100%,T-1%);146(C-13%,T-95%);155(A-3%,C-14%,T-95%);162(G-1%,T-99%);169(C-100%,T-3%);	C;G;C; C;G;C;T ;T;T;C	C;G;C/T ;C;G;C; T/C;C/T ;T;C
AMPL16 90291	scaffold11	AGAAACG CCGATGA TGATATA CAGA	TATACAT CTCAGGT GTGTGTT GTGA	39(G-3%,A-99%);41(G-0%,A-100%);43(G-0%,A-100%);46(A-0%,T-100%);50(G-99%,T-11%);51(G-0%,A-100%);52(A-2%,G-0%,T-99%);54(C-2%,T-99%);60(G-96%,A-22%);61(A-1%,T-100%);68(C-0%,T-100%);70(A-0%,G-100%);71(A-99%,T-3%);77(C-31%,T-90%);83(C-0%,T-100%);96(C-99%,T-5%);99(A-1%,G-100%);105(G-1%,A-100%);129(G-3%,A-99%);141(C-2%,T-99%);149(A-1%,T-100%);150(A-1%,G-1%,T-100%);151(A-10%,G-96%);154(C-0%,T-100%);155(C-100%,T-1%);163(C-95%,T-17%);165(C-0%,T-100%);166(C-8%,T-97%);168(G-99%,T-3%);170(G-8%,A-97%);173(C-99%,G-10%);176(C-10%,T-99%);177(G-0%,A-100%);	A;A;A; T;G;A;T ;T;G;T; T;G;A;T ;T;C;G; A;A;T;T ;T;G;T; C;C;T;T ;G;A;C; T;A	A;A;A; T;T/G;A ;T;T;G/ A;T;T;G ;A;C/T; T;C;G; A;A;T;T ;T;G;T; C;T/C;T ;T;G;A; G/C;T/C ;A
AMPL16 90292	scaffold11	ACGCAAT TCCTTCTT TTCGACA TAT	GATTCGG ACCATCG CACATTT TAC	57(A-16%,T-98%);71(A-0%,G-100%);79(A-90%,G-32%);92(G-13%,A-99%);114(C-100%,T-0%);120(C-100%,T-0%);122(C-100%,T-13%);125(C-100%,T-13%);143(C-100%,T-0%);149(A-100%,T-0%);155(C-95%,T-20%);158(C-0%,A-100%);159(A-0%,T-100%);175(G-0%,C-100%,T-0%);183(G-0%,A-100%);209(A-0%,G-100%);210(G-0%,A-100%);214(C-0%,G-0%,T-100%);216(G-0%,T-100%);223(G-90%,A-32%);226(G-0%,A-100%);	T;G;A; A;C;C; C;C;C; A;C;A; T;C;A; G;A;T;T ;G;A	T;G;A/ G;A;C; C;C;C;C ;A;C/T; A;T;C; A;G;A; T;T;G/A ;A
AMPL16 90294	scaffold2	GCCATGG GTTACAT TCTGATG TATG	GATTCCC AAGAGAT CTACAGC ATCT	58(A-1%,C-12%);60(G-100%,T-13%);101(A-0%,G-100%);102(G-100%,T-0%);	-;G;G;G	C/-;G/T; G;G

AMPL16 90297	scaffold1	GAAAGCA CGAAGGC AATCTAA TCTT	TTTAAAA CGGTGAT GATCCCG TAAC	38(C-2%,T-98%);39(C-98%,T-2%);41(G-2%,A-98%);48(C-100%,T-0%);53(A-0%,T-100%);63(A-0%,G-100%);72(A-2%,T-98%);77(G-89%,A-62%);89(A-82%,C-76%);91(C-100%,T-0%);92(G-100%,T-0%);97(G-99%,A-13%);98(A-0%,G-100%);99(C-98%,T-7%);102(G-85%,A-70%);115(A-2%,T-98%);116(A-2%,G-98%);117(G-2%,A-98%);120(G-81%,A-76%);129(A-1%,G-99%);130(C-8%,T-100%);135(G-88%,A-62%,T-1%);140(C-100%,T-0%);145(A-6%,G-99%);149(C-7%,T-98%);160(C-1%,T-100%);176(C-1%,T-99%);182(G-2%,A-98%);184(C-100%,T-0%);191(G-0%,C-100%);197(A-89%,C-0%,G-62%);200(A-7%,C-98%);219(G-2%,A-98%);226(C-89%,T-62%);227(A-0%,G-100%);236(A-2%,G-98%);	T;C;A;C ;T;G;T; A/G;A/ C;C;G; G;G;C; A/G;T; G;A;A/ G;G;T; A/G;C; G;T;T;T ;A;C;C; G/A;C; A/T;C; G;G	T;C;A;C ;T;G;T; G/A;C/ A;C;G; G/A;G; C;G/A; T;G;A; A/G;G; T;G/A; C;G;T;T ;T;A;C; C;G/A; C;A;T/C ;G;G
AMPL16 90298	scaffold10	GCCAGAA CGAGAGC CATTATA TGTA	CGCCGAA TAGCATG CTTATGA AC	37(A-0%,G-100%);38(G-3%,A-100%);39(G-24%,A-92%);43(G-98%,A-9%,T-0%);44(C-99%,T-4%);46(C-100%,T-2%);48(A-98%,G-0%,T-10%);53(G-3%,T-99%);57(C-3%,A-100%);70(A-98%,G-10%);73(C-1%,A-100%);74(A-14%,C-96%);81(A-100%,T-1%);83(C-33%,T-88%);89(G-0%,A-100%);98(G-1%,A-13%);100(A-91%,C-28%);101(A-0%,G-100%,T-1%);107(G-3%,A-99%);109(C-98%,A-14%);111(C-3%,T-100%);114(A-0%,C-100%);115(A-3%,C-1%,T-100%);117(G-98%,A-11%);118(A-100%,T-0%);119(A-4%,C-100%);123(G-1%,A-100%);128(C-12%,T-98%);130(C-0%,T-100%);132(A-0%,G-98%,T-10%);134(C-98%,T-10%);139(A-0%,G-100%);141(C-97%,G-1%,T-18%);155(A-0%,C-1%,G-10%);160(C-3%,G-4%,T-100%);169(A-100%,T-3%);170(G-98%,C-10%);175(A-2%,G-100%);178(G-3%,C-100%);179(C-20%,T-97%);182(G-100%,T-0%);183(C-99%,T-0%);187(C-0%,G-97%,T-16%);189(G-10%,C-99%);193(A-4%,G-100%);210(A-0%,G-100%);211(G-0%,A-100%);215(A-0%,G-100%);218(A-4%,C-100%);223(G-13%,T-97%);224(C-98%,T-10%);225(C-10%,T-98%);	G;A;A; G;C;C; A;T;A; A;A;C; A;T;A;-; A;G;A; C;T;C;T ;G;A;C; A;T;T;G ;C;G;C;- ;T;A;G; G;C;T; G;C;G; C;G;G; A;G;C; T;C;T	G;A;A; G/A;C; G/A;T;T ;A;G/A; A;C;A; T/C;A;- /A;A/C; G;A;C/ A;T;C;T ;G/A;A; C;A;T/C ;T;T/G; C/T;G;T /C;G/-;T ;A;G/C; G;C;C/T ;G;C;G/ T;C;G; G;A;G; C;G/T;C /T;C/T
AMPL16 90300	scaffold8	TGTGCAT CTGCCTA CATACCA TTAT	ACTTATA GCATGGT TAACGTT GACG	47(G-99%,T-1%);57(C-98%,T-2%);60(G-7%,C-94%);65(C-98%,T-2%);100(C-1%,G-99%);105(C-5%,T-95%);121(G-99%,T-1%);140(C-1%,T-99%);143(A-4%,C-96%);154(C-96%,T-4%);185(C-96%,T-4%);207(C-0%,T-100%);210(C-100%,T-0%);	G;C;C; C;G;T; G;T;C;C ;C;T;C	G;C;C; C;G;T; G;T;C;C ;C;T;C
AMPL16 90301	scaffold11	TGTTTTC CTTGCTA CTTCGTC TCTA	GCGAATC TGAAGAC ACCATTA TGAG	62(G-6%,A-99%);68(A-13%,C-99%,T-0%);83(A-0%,G-100%);112(G-90%,C-31%);121(G-0%,A-100%);124(C-100%,T-4%);146(G-3%,A-100%);164(C-0%,A-100%);167(C-99%,T-13%);175(G-1%,A-100%);179(G-3%,A-100%);190(G-91%,A-30%);196(C-0%,A-100%);200(C-0%,T-100%);201(G-91%,A-30%);203(C-30%,T-91%);238(C-99%,T-3%);	A;C;G; G;A;C; A;A;C; A;A;G; A;T;G;T ;C	A;C;G; G/C;A; C;A;A; C/T;A; A;G/A; A;T;A/ G;T/C;C
AMPL16 90303	scaffold11	CTTAGCT AAAGCAA TGGCCAT	CGTCCAT CTATTTA AACGGTC	58(G-1%,A-100%);73(C-24%,T-92%);76(A-0%,C-2%,G-100%);114(A-95%,T-18%);119(A-1%,T-100%);126(G-100%,T-1%);129(A-1%,G-	A;T;G; A;T;G; G;A;A;	A;T/C; G;A/T;T ;G;G;A;

		AGTC	ACTG	100%);132(G-1%,A-100%);146(G-2%,A-100%);148(C-96%,A-18%);150(G-96%,A-18%);151(C-1%,T-100%);158(C-2%,A-100%);159(C-99%,T-4%);161(A-0%,C-100%);	C;G;T; A;C;C	A;C/A; A/G;T; A;C;C
AMPL16 90304	scaffold11	CGCTAGG CTCTGAG TAAAAAT AGGA	GTTAATT TTCGGTG GTGAAGA GCTC	44(A-0%,G-100%);63(G-0%,T-19%);64(G-1%,A-100%);65(G-1%,A-100%);70(A-92%,T-17%);71(G-17%,T-92%);93(A-0%,G-100%);98(G-13%,T-95%);101(A-0%,G-100%);110(G-0%,T-100%);115(A-0%,G-99%);118(A-6%,C-91%,G-13%);119(G-7%,A-96%);126(G-0%,C-100%);127(C-95%,T-13%);133(C-18%,T-91%);140(A-2%,T-100%);141(C-100%,T-2%);160(C-0%,T-100%);184(A-97%,G-9%);193(A-0%,G-100%);200(C-6%,T-97%);204(C-96%,T-6%);208(A-0%,C-100%);	G;-;A;A ;A;T;G; T;G;T;G ;C;A;C; C;T;T;C ;T;A;G; T;C;C	G;T/-;A; A;A/T;T /G;G;G/ T;G;T;G ;G/C;A; C;T/C;T /C;T;C; T;A/G; G;T;C;C
AMPL16 90305	scaffold16	GCATCTA GCGTTCA TTACAAT CCC	GGTTCAA GACGTTG TTATCTC CTTC	35(C-100%,T-0%);37(C-3%,T-100%);43(C-0%,T-100%);44(A-100%,T-0%);52(A-95%,G-23%);64(A-100%,T-0%);67(A-90%,T-32%);71(C-98%,T-8%);73(A-0%,G-99%);75(G-2%,A-100%);81(C-98%,T-10%);82(G-0%,T-100%);102(G-0%,A-100%);117(A-0%,G-100%);144(C-99%,T-12%);145(G-1%,A-100%);153(G-2%,A-99%);157(A-0%,C-100%);165(G-100%,T-0%);177(G-9%,C-99%);185(C-0%,A-100%);187(G-100%,T-0%);189(A-91%,G-31%);195(A-1%,G-97%,T-7%);198(C-0%,G-100%);213(A-0%,C-100%);219(A-1%,G-100%);	C;T;T;A ;A;A;A; C;G;A; C;T;A; G;C;A; A;C;G; C;A;G; A;G;G; C;G	C;T;T;A ;G/A;A; T/A;C; G;A;C; T;A;G; C;A;A; C;G;C; A;G;G/ A;G;G; C;G
AMPL16 90306	scaffold10	TATCTAT CAAAGTG AGGTAGG TGCG	TGGAAGG TCGTCTT GTGGTTA TATT	42(A-0%,C-100%,T-0%);88(A-1%,C-100%);107(A-0%,G-100%);113(A-0%,G-100%);115(C-1%,T-100%);117(C-0%,T-28%);132(A-1%,G-100%);141(C-10%,T-96%);142(C-96%,G-10%);144(C-10%,T-96%);149(C-10%,T-96%);155(A-0%,G-100%);164(C-96%,T-10%);165(G-96%,C-9%);169(G-28%,T-88%);170(A-10%,G-97%);175(A-0%,G-96%,C-10%);	C;C;G; G;T;-;G; T;C;T;T ;G;C;G; T;G;G	C;C;G; G;T;- /T;G;T/ C;C/G;T /C;C/T; G;T/C; G/C;T/ G;G;G/ C
AMPL16 90311	scaffold5	TCGCATA CAATGTC CATAATT GCAA	GTGTATT ACGATGG GTATCTG ATGT	54(C-11%,T-98%);57(C-89%,T-32%);62(C-3%,T-100%);64(C-2%,T-100%);74(C-20%,T-94%);82(C-98%,T-7%);86(A-0%,C-100%);87(G-3%,T-100%);91(C-3%,A-100%);111(G-0%,A-100%);113(G-30%,T-90%);114(C-100%,T-0%);126(C-98%,T-7%);137(C-6%,A-98%);138(A-0%,G-100%);139(C-0%,T-100%);144(A-0%,G-100%);147(A-93%,G-26%);151(A-1%,C-100%);154(G-100%,T-1%);156(G-100%,T-0%);159(C-0%,A-26%);163(C-0%,T-100%);165(G-0%,A-100%);166(C-1%,T-100%);168(C-0%,G-100%);169(A-0%,T-100%);193(G-3%,T-100%);197(G-0%,C-100%);200(G-0%,C-100%);204(C-86%,T-34%);214(C-100%,T-0%);215(A-1%,C-100%);	T;C;T;T ;T;C;C; T;A;A;T ;C;C;A; G;T;G; A;C;G; G;-;T;A; T;G;T;T ;C;C;C; C;C	T;C/T;T ;T;T;C; C;T;A; A;T/G; C;C;A; G;T;G; A/G;C; G;G;- /A;T;A; T;G;T;T ;C;C;C/ T;C;C
AMPL16 90312	scaffold8	CATAGCA TAGGTGG ATAAAAT GCGG	GTCTTGA AGATGGC AACCAAT CTG	37(G-1%,A-100%);42(G-5%,A-99%);45(G-0%,A-100%);48(C-6%,A-98%);55(C-0%,A-100%);70(G-100%,T-0%);76(C-100%,T-0%);78(C-4%,T-99%);79(C-12%,G-91%);82(C-9%,A-96%);86(C-96%,T-9%);100(G-1%,A-99%);101(A-2%,G-98%,T-5%);105(A-4%,C-99%);114(A-92%,T-12%);119(C-4%,T-99%);120(C-6%,T-98%);122(G-6%,C-	A;A;A; A;A;G; C;T;G; A;C;A; G;C;A; T;T;C;A ;T;G;G; C;G;T;T	A;A;A; A;A;G; C;T;G; A;C;A; G;C;A; T;T;C;A ;T;G;G; C;G;T;T

				98%);126(G-4%,A-99%);134(A-1%,T-99%);137(A-12%,G-93%);149(A-5%,G-98%);167(C-95%,T-9%);169(G-100%,T-0%);171(C-4%,T-98%);174(C-0%,T-100%);176(G-13%,A-92%,T-0%);197(C-87%,T-17%);203(A-0%,G-100%);205(A-100%,T-0%);206(C-10%,T-93%);209(C-98%,T-2%);218(C-10%,T-95%);219(G-15%,T-91%);221(A-0%,C-100%);223(C-98%,T-2%);230(C-100%,T-0%);231(C-5%,T-96%);232(G-5%,T-96%);	;A;C;G; A;T;C;T ;T;C;C; C;T;T	;A;C;G; A;T;C;T ;T;C;C; C;T;T
AMPL16 90313	scaffold1	AAGTTCG TAACGAT ATATTCC CGGA	GTGAGTC AATTCAT TCCTCCG ATTC	44(C-83%,T-30%);47(C-0%,T-100%);58(C-90%,T-12%);65(A-83%,G-3%,T-29%);69(A-85%,G-29%);82(A-3%,C-99%);84(C-14%,T-98%);85(A-0%,G-28%);86(G-85%,T-29%);90(A-3%,G-99%);110(C-3%,T-100%);145(G-2%,C-98%,T-14%);156(A-100%,T-1%);164(C-32%,T-84%);168(C-99%,T-12%);195(C-90%,T-14%);199(G-88%,A-25%);202(G-1%,A-100%);203(G-100%,T-0%);206(A-0%,G-100%);208(A-25%,T-88%);214(C-98%,T-16%);	C;T;C;A ;A;C;T;- ;G;G;T; C;A;T;C ;C;G;A; G;G;T; C	T;T;T;T ;G;C;T; G;T;G;T ;C;A;C; C;T;A; A;G;G; A;C
AMPL16 90314	scaffold3	TTTTATA GGGCCCT TCCTTTA CACA	GAGGGTA GACGATA ATGCTGA CTG	36(C-0%,T-100%);41(C-3%,T-99%);42(A-1%,C-1%,T-97%);45(A-1%,C-93%);47(C-0%,G-13%,A-95%);49(G-0%,A-100%);52(C-1%,T-100%);53(A-1%,G-100%);57(A-13%,T-95%);68(G-0%,A-100%);71(C-100%,T-0%);72(C-0%,A-99%,T-1%);73(A-1%,C-100%);76(C-6%,T-96%);78(G-2%,C-99%);98(C-100%,T-1%);112(G-3%,C-96%);114(C-99%,T-2%);119(C-0%,A-96%,T-5%);120(C-7%,T-95%);123(A-6%,G-97%);154(C-93%,T-16%);156(C-1%,T-99%);159(C-12%,T-96%);160(C-0%,T-100%);163(C-100%,T-0%);173(G-13%,C-95%);177(C-96%,T-6%);181(G-100%,T-0%);187(C-100%,T-0%);192(G-100%,T-0%);196(C-17%,T-93%);208(C-100%,T-0%);215(A-0%,T-100%);217(G-95%,T-14%);218(A-0%,G-100%);	T;T;T;C ;A;A;T; G;T;A; C;A;C;T ;C;C;C; C;A;T; G;C;T;T ;T;C;C; C;G;C; G;T;C;T ;G;G	T;T;T;- /C;G/A; A;T;G; A/T;A; C;A;C;T ;C;C;C; C;A;T; G;C/T;T ;T/C;T; C;C/G; C;G;C; G;T;C;T ;T/G;G
AMPL16 90315	scaffold1	TATTTTT GTCACAT TTGTGCC GTTC	GCGAATG TACTTAG CACGGAA TTAT	39(G-1%,T-100%);41(C-100%,T-1%);70(A-68%,T-85%);77(A-4%,C-100%);78(C-99%,T-9%);82(A-55%,G-18%);90(G-4%,A-100%);97(C-98%,T-13%);115(G-94%,T-3%);117(C-95%,T-55%);122(C-95%,T-55%);130(A-3%,G-100%);132(C-99%,T-7%);144(A-98%,C-14%);148(C-0%,G-100%);161(A-97%,T-16%);191(C-82%,T-69%);213(A-1%,G-100%);	T;C;T/A ;C;C;A/- ;A;C;G/ -;T/C;T/ C;G;C; A;G;A; T/C;G	T;C;A/T ;C;C;G/- ;A;T/C; G;C;C; G;C;C/ A;G;T/ A;T/C; G
AMPL16 90316	scaffold11	ATTCCCT CAGGGTG ATGAAGA AC	ATCAAGG ACTTTAT GCTCCAA GGAG	41(C-0%,T-100%);50(A-3%,G-100%);52(G-0%,T-100%);86(G-13%,A-94%);89(G-0%,A-100%);92(A-0%,G-100%);98(C-99%,T-1%);106(G-0%,C-100%);113(C-0%,T-100%);119(A-0%,G-100%);122(G-100%,T-8%);134(G-3%,A-98%,T-2%);137(A-2%,G-98%);143(G-99%,A-9%);146(A-99%,G-10%);155(A-1%,G-100%);158(G-0%,A-100%);178(G-5%,A-96%);179(C-96%,G-2%,T-16%);181(G-1%,C-100%);183(A-100%,G-9%);184(C-0%,T-100%);186(C-6%,A-99%);187(C-100%,T-6%);188(C-94%,G-6%,A-17%,T-0%);189(A-0%,G-100%);191(G-94%,A-21%);197(A-100%,T-0%);199(G-100%,T-	T;G;T;A ;A;G;C; C;T;G; G;A;G; G;A;G; A;A;C; C;A;T; A;C;C; G;G;A; G;G	T;G;T;A ;A;G;C; C;T;G; G;A;G; G/A;G/ A;G;A; A;T/C;C ;A/G;T; A;C;C/ A;G;G/ A;A;G; G

				4%);200(C-5%,G-95%);		
AMPL16 90317	scaffold12	CGGACAT GATTTTG AGTTTTT GTCC	GAGCTTG TCATCGC AGAGGTC	48(C-94%,T-45%);53(G-0%,A-100%);54(C-92%,T-28%);63(G-0%,A-100%);75(C-0%,T-100%);80(A-5%,T-100%);81(A-0%,G-100%);82(C-100%,T-0%);104(C-93%,G-27%);105(G-0%,A-100%);106(G-1%,T-99%);109(C-3%,G-72%);110(G-11%,A-17%);130(G-93%,T-27%);131(A-1%,C-100%);135(C-93%,T-0%);138(C-98%,T-2%);140(G-98%,T-2%);141(C-83%,A-67%);144(C-44%,G-83%,A-27%);145(C-0%,G-98%);147(C-44%,T-28%);148(C-66%,T-0%);149(A-45%,C-27%);151(C-45%,G-94%);152(G-0%,C-100%);153(C-91%,T-47%);163(A-13%,C-99%);168(C-25%,T-95%);181(G-93%,A-27%);188(A-0%,G-100%);191(A-95%,G-25%);196(A-0%,G-100%);214(C-25%,T-95%);	C/T;A;C ;A;T;T; G;C;C; A;T;- /G;-;G; C;- /C;C;G; A/C;C/ G;G;C/- ;C/-;- /A;G/C; C;C/T;C ;T;G;G; A;G;T	C;A;C/T ;A;T;T; G;C;G/ C;A;T; G/-;A/-; T/G;C;C ;C;G;C/ A;A;G; G;T/-;C/ -;C/-;G; C;C;C;C /T;G/A; G;G/A; G;T/C
AMPL16 90319	scaffold5	CAGTAGT AAAAGAA AAGACCG TCAA	GCTTGAC GAGTCCT ATAACAA GT	40(G-0%,A-100%);43(C-100%,T-0%);44(G-99%,A-11%);47(C-100%,T-0%);52(G-7%,A-100%);53(G-0%,A-100%);60(A-3%,G-100%);62(G-3%,A-100%);90(A-23%,G-98%);91(G-0%,A-100%);93(A-2%,G-100%);102(A-0%,G-100%);106(G-0%,A-100%);108(A-0%,G-100%);127(A-6%,G-100%);137(A-0%,C-100%);143(A-86%,G-34%);146(C-100%,T-3%);147(A-10%,G-100%);155(G-6%,A-100%);161(C-99%,T-16%);171(A-1%,C-100%);177(C-6%,A-100%);184(G-6%,A-100%);185(A-11%,G-100%);187(A-99%,G-11%);189(A-10%,G-100%);202(A-3%,G-100%);237(A-0%,C-100%);238(A-1%,C-100%);240(G-6%,A-100%);242(G-96%,A-27%);	A;C;G; C;A;A; G;A;G; A;G;G; A;G;G; C;A;C; G;A;C; C;A;A; G;A;G; G;C;C; A;G	A;C;G/ A;C;A; A;G;A; A/G;A; G;G;A; G;G;C; G/A;C; G;A;C; C;A;A; A/G;G/ A;G;G; C;C;A; G/A
AMPL16 90320	scaffold4	AGAGTAG AGTGAGT AATGCGA TTCC	TAAACCC ATGGATC TGTAGTG CTG	45(A-20%,T-90%);49(C-4%,T-100%);55(G-0%,T-100%);68(G-3%,A-99%);79(A-0%,G-100%);92(C-6%,G-99%);101(C-11%,T-95%);124(A-0%,G-100%);128(C-99%,T-1%);136(A-8%,G-100%);140(C-99%,T-3%);148(C-2%,A-100%);149(G-100%,T-1%);151(G-1%,A-100%);154(C-99%,T-3%);164(G-1%,A-100%);166(G-16%,A-92%);172(C-100%,T-0%);	T;T;T;A ;G;G;T; G;C;G; C;A;G; A;C;A; A;C	T;T;T;A ;G;G;T; G;C;A/ G;C;A; G;A;C; A;A;C
AMPL16 90323	scaffold10	CCTTCTC ATTCGTC AAGAGAT ACATG	GACTACG AGGGTGC ATGCAAG	41(A-1%,C-100%);65(G-99%,T-2%);71(G-84%,T-34%);74(A-0%,C-100%,T-11%);77(C-100%,T-1%);80(G-21%,A-95%);85(C-0%,T-100%);86(G-0%,T-100%);89(A-1%,G-100%);92(C-100%,T-1%);98(G-4%,A-100%);101(A-4%,G-100%);110(A-9%,G-100%);119(A-0%,G-100%);122(A-1%,G-100%);131(G-93%,A-96%,T-0%);137(C-100%,T-0%);140(A-3%,G-99%);149(G-88%,A-100%);167(G-1%,A-100%);170(C-3%,A-97%);180(G-2%,A-100%);182(A-88%,G-100%);188(G-0%,A-100%);194(G-96%,A-94%);200(A-0%,G-100%);212(A-1%,C-100%);	C;G;G; C;C;A;T ;T;G;C; A;G;G; G;G;A/ G;C;G; G/A;A; A;A;G/ A;A;G/ A;G;C	C;G;G/ T;C;C;A ;T;T;G; C;A;G; G;G;G; G/A;C; G;G/A; A;A;A; A/G;A; G/A;G; C

AMPL16 90325	scaffold2	CGTATCA GTGTATG ACCGGAA TTAC	CTTCAAA CTGTGCT CGATCGA TC	37(C-95%,A-24%);55(C-3%,T-100%);58(A-98%,C-19%);76(C-0%,G-0%,T-24%);78(A-1%,G-24%);80(C-0%,T-100%);87(C-19%,T-98%);88(G-98%,A-19%);99(A-6%,C-100%);104(A-0%,T-100%);105(G-1%,A-100%);106(C-2%,G-1%,A-100%);109(G-94%,T-24%);114(C-98%,G-19%);118(A-95%,G-24%);122(G-7%,T-99%);127(A-98%,G-19%);129(C-100%,T-0%);134(C-100%,T-1%);142(C-19%,T-98%);147(C-3%,T-99%);160(A-95%,C-19%);163(G-1%,T-100%);165(A-98%,T-19%);167(C-19%,T-98%);174(G-4%,A-16%);175(G-16%,T-99%);	C;T;A;-; -;T;T;G; C;T;A; A;G;C; A;T;A; C;C;T;T ;A;T;A; T;-;T	A/C;T;C /A;T;-;G /-;T;T/C ;G/A;C; T;A;A;T /G;G/C; G/A;T; A/G;C; C;T/C;T ;C/A;T; A/T;C/T ;-A;T
AMPL16 90328	scaffold14	CATCGTC AGTGACC ATAACCT AAGA	CAGCGTC GTAGTAT ATGGGGA AC	55(C-27%,T-90%);74(G-1%,A-100%);110(A-10%,G-100%);113(C-97%,T-17%);125(G-1%,C-99%);133(C-0%,T-100%);161(G-96%,C-18%);163(G-99%,A-14%);167(G-6%,A-99%);172(A-0%,G-99%);176(A-96%,G-18%);179(A-6%,G-99%);180(A-4%,G-99%);187(G-95%,A-19%);188(G-95%,C-15%);212(A-0%,T-100%);	T;A;G; C;C;T;G ;G;A;G; A;G;G; G;G;T	C/T;A; G;C;C;T ;G/C;G/ A;A;G; A/G;G; G;G/A; C/G;T
AMPL16 90329	scaffold1	GAAATGT CCGGGAA GAACTAG ACAT	CTGGAGA AAGGTCA TATTCAG GTGA	51(C-100%,T-4%);52(A-95%,G-18%);174(C-99%,T-12%);	C;A;C	C;G/A; C/T
AMPL16 90330	scaffold8	ATAAAGC CCATTTT GAGTCAT TGCT	GTCGATG AAGACAA CGTAGAC TTTG	76(G-0%,T-100%);110(A-8%,G-96%);	T;G	T;G
AMPL16 90331	scaffold8	CCCAGAG TGTCTAG TATAGGG AGTA	CGTATTC TGAATGA AAGGTCC ACTC	40(G-0%,C-100%);67(G-2%,T-98%);71(G-100%,T-0%);78(G-3%,A-98%);91(A-2%,G-98%);95(A-2%,G-98%);110(C-9%,T-98%);122(G-0%,A-100%);138(C-15%,T-93%);174(A-5%,T-96%);181(C-0%,T-100%);188(A-0%,G-100%);199(A-1%,C-98%,T-2%);215(A-10%,G-97%);	C;T;G; A;G;G; T;A;T;T ;T;G;C; G	C;T;G; A;G;G; C/T;A;T /C;T;T; G;C;G/ A
AMPL16 90332	scaffold10	AAGAGTC ACATAAG CATACCC GAAG	GTAGCCG ATGGTCA CCTGGAT AAAC	43(A-0%,G-2%,T-98%);46(A-2%,G-98%);54(C-100%,T-1%);56(C-100%,T-1%);70(G-100%,T-2%);72(C-1%,T-99%);82(G-100%,T-0%);83(G-99%,T-11%);85(A-1%,G-99%);91(A-89%,G-35%);92(C-2%,T-100%);93(C-1%,T-100%);94(G-1%,C-100%,T-1%);96(C-99%,T-1%);108(A-0%,G-100%);109(A-2%,G-98%);112(A-2%,G-2%,T-98%);114(G-16%,A-97%);115(A-1%,G-99%);121(G-1%,T-100%);123(A-2%,T-99%);124(G-100%,T-0%);126(C-1%,T-100%);130(G-14%,A-99%);132(G-16%,A-96%);136(G-2%,A-99%);142(A-2%,G-99%);148(A-1%,C-0%,G-100%);154(G-7%,A-98%);160(G-100%,T-0%);163(C-2%,A-98%);166(C-2%,T-98%);170(A-0%,C-100%);171(C-100%,T-0%);175(A-1%,G-100%);187(A-0%,G-100%);193(A-79%,C-38%,T-0%);194(A-1%,G-100%);196(G-1%,A-100%);198(G-4%,A-100%);199(G-100%,T-1%);202(G-97%,T-16%);211(A-2%,C-98%);214(A-0%,T-100%);217(C-2%,T-99%);218(G-0%,T-100%);223(A-0%,G-100%);226(C-26%,T-93%);238(C-5%,G-93%,T-22%);	T;G;C;C ;G;T;G; G;G;A; T;T;C;C ;G;G;T; A;G;T;T ;G;T;A; A;A;G; G;A;G; A;T;C;C ;G;G;A; G;A;A; G;G;C; T;T;T;G ;T;G	T;G;C;C ;G;T;G; G;G;G/ A;T;T;C ;C;G;G; T;A;G;T ;T;G;T; A;A;A; G;G;A; G;A;T; C;C;G; G;C/A; G;A;A; G;T/G; C;T;T; ;G;C/T; T/G

AMPL16 90334	scaffold2	GTTCATC ATCCGTT TATGGAC ATCC	TTCATTA GGCCTAC GTCATCT CCTA	56(C-0%,G-2%,T-98%);59(A-2%,C-28%,T-2%);61(A-80%,C-0%,G-26%,T-1%);62(A-1%,G-1%,C-99%);64(A-0%,G-3%,T-98%);65(A-0%,T-99%);66(G-2%,A-100%);68(A-0%,C-100%);71(A-100%,T-0%);74(A-1%,G-99%);75(G-0%,C-99%,T-1%);80(C-29%,T-78%);81(G-2%,C-98%);85(C-11%,G-94%);87(A-1%,G-99%);88(A-1%,C-97%,T-3%);89(C-99%,T-2%);90(G-2%,T-100%);93(G-98%,T-0%);97(C-0%,A-19%,T-1%);98(G-25%,T-2%);99(A-1%,G-26%);100(G-0%,A-95%);103(G-1%,A-99%);106(A-28%,T-78%);107(G-1%,C-99%,T-1%);108(G-1%,A-99%);113(G-90%,A-17%);128(G-78%,A-29%);134(A-0%,G-100%);137(G-78%,A-28%);140(A-1%,G-100%);143(A-1%,C-100%);146(G-13%,A-94%);161(G-0%,T-100%);164(G-1%,A-99%);167(A-0%,C-100%);170(C-0%,A-100%);178(A-1%,G-29%);179(G-77%,A-29%);180(C-0%,G-100%,T-0%);181(A-31%,T-75%);182(A-1%,T-99%);183(C-77%,T-29%);185(A-1%,G-99%);187(C-1%,A-30%,T-75%);188(A-1%,T-99%);189(G-0%,C-100%);190(A-0%,C-0%,G-100%);193(C-29%,T-77%);197(C-31%,T-75%);199(C-100%,T-0%);200(A-1%,G-30%,T-75%);203(G-0%,A-29%,T-76%);204(A-99%,T-1%);205(C-98%,T-3%);206(A-0%,C-1%,G-100%);207(C-75%,G-1%,A-29%);208(C-76%,T-28%);209(A-1%,G-75%,T-28%);210(A-1%,C-1%,G-11%,T-92%);211(A-75%,C-1%,G-30%);213(G-0%,A-100%);215(C-1%,T-99%);216(G-0%,A-100%);220(A-0%,C-99%,T-1%);222(A-99%,T-1%);225(C-77%,G-29%);226(C-1%,T-99%);	T;-;A;C; T;T;A;C ;A;G;C; T;C;G; G;C;C;T ;G;-;-; A;A;T; C;A;G; G;G;G; G;C;A; T;A;C; A;-;G;G ;T;T;C; G;T;T;C ;G;T;T; C;T;T;A ;C;G;C; C;G;T; A;A;T; A;C;A; C;T	T;C;G;C ;T;T;A; C;A;G; C;C;C; G;G;C; C;T;G; A;G;G; A;A;A; C;A;A; A;G;A; G;C;A; T;A;C; A;G;A; G;A;T;T ;G;A;T; C;G;C; C;C;G; A;A;C; G;A;T;T ;T;G;A; T;A;C; A;G;T
AMPL16 90335	scaffold4	TAATGAA CCAAATG GCATTGA AGCT	TATTAGC ATCGTCG GTATCCT TTGT	36(A-3%,G-98%);37(A-1%,G-99%);56(C-28%,T-89%);65(G-0%,T-100%);73(C-0%,T-100%);75(G-0%,A-100%);80(G-0%,T-100%);84(A-4%,G-98%);85(A-4%,T-98%);90(C-0%,T-100%);91(A-4%,G-98%);94(C-0%,T-100%);96(A-0%,G-100%);97(C-100%,T-0%);107(G-0%,A-100%);156(G-89%,A-28%);	G;G;T;T ;T;A;T; G;T;T;G ;T;G;C; A;G	G;G;T/ C;T;T;A ;T;G;T; T;G;T;G ;C;A;A/ G
AMPL16 90336	scaffold1	AACAGTT TGTCAGC TACCATT CTTG	AATGGTG TTGGTGT CAAGATC G	39(C-99%,T-4%);54(G-8%,C-99%,T-0%);62(G-1%,A-100%);65(G-38%,T-42%);72(C-0%,G-100%);90(G-1%,A-100%);139(A-100%,T-0%);157(C-100%,T-0%);161(G-87%,T-73%);166(A-99%,T-14%);	C;C;A;- /T;G;A; A;C;G/ T;A	C;C;A; G/-;G;A ;A;C;T/ G;T/A
AMPL16 90339	scaffold2	TACATAG GACCAAT AGCACTC AGAC	GAGCTTC AAGCCTA CGCGA	44(A-0%,G-100%);46(A-1%,G-100%);52(C-87%,A-26%);59(G-8%,A-98%);75(A-4%,G-99%);77(C-91%,A-23%);83(A-98%,T-7%);84(G-13%,T-15%);85(G-6%,A-22%);103(C-100%,T-0%);112(C-100%,T-0%);113(A-6%,G-98%);121(A-0%,G-100%);128(G-1%,A-99%);132(A-0%,G-100%);134(G-99%,T-3%);147(A-0%,G-100%);149(G-88%,A-26%);154(A-1%,C-95%,T-12%);157(A-98%,T-6%);161(C-3%,T-96%);163(G-5%,A-95%);181(C-98%,T-4%);194(A-0%,T-100%);200(G-87%,A-26%);206(G-0%,A-25%);209(A-4%,G-22%);211(G-21%,T-6%);212(A-21%,T-6%);	G;G;C; A;G;C; A;-;-;C; C;G;G; A;G;G; G;G;C; A;T;A; C;T;G;-; -;-;-	G;G;C/ A;A;G; C/A;A;- /G;A/-; C;C;G; G;A;G; G;G;G/ A;C;A; T;A;C;T A/G;A/ -/G/-/G/ -/A

AMPL16 90340	scaffold2	TCATGGG CTCTGAT GGATCTT TTT	AGGTTCA GATCGAC GAGTGG	35(A-0%,G-100%);37(G-3%,A-99%);54(G-1%,A-19%,T-87%);55(G-6%,A-97%,T-2%);56(A-99%,T-2%);57(A-87%,T-18%);58(C-2%,T-98%);85(A-88%,G-3%,C-15%,T-2%);90(C-0%,T-100%);92(A-4%,C-98%);93(G-4%,A-20%);95(C-1%,T-100%);97(C-98%,T-4%);103(C-1%,G-100%);105(A-0%,C-100%);119(C-100%,T-2%);120(A-85%,T-20%);126(A-0%,G-100%);130(A-0%,G-100%);131(G-1%,A-100%);137(C-3%,T-99%);138(A-3%,C-99%);140(G-80%,A-26%);144(A-1%,T-100%);149(A-2%,T-99%);152(G-6%,T-95%);155(G-3%,T-97%);159(C-2%,T-99%);161(G-3%,C-98%);162(G-5%,A-98%,T-2%);164(G-2%,A-100%);167(A-5%,T-99%);170(G-3%,A-98%);172(A-5%,G-99%);177(C-3%,T-99%);179(G-2%,T-100%);181(C-6%,T-97%);183(C-98%,T-2%);184(G-3%,A-96%);187(C-0%,T-98%);190(C-18%,T-89%);192(G-2%,A-99%);194(G-2%,A-100%);196(A-2%,T-99%);199(C-0%,T-100%);205(G-99%,T-1%);206(C-100%,T-0%);208(C-79%,T-25%);209(A-79%,G-25%);211(C-0%,T-97%);226(C-1%,G-25%,T-78%);228(G-83%,T-21%);237(C-0%,T-100%);238(C-17%,T-89%);239(C-78%,T-27%);240(A-89%,T-17%);242(G-1%,T-99%);	G;A;T; A;A;A; T;A;T;C ;-;T;C;G ;C;C;A; G;G;A; T;C;G;T ;T;T;T; T;C;A; A;T;A; G;T;T;T ;C;A;T; T;A;A;T ;T;G;C; C;A;T;T ;G;T;T; C;A;T	G;A;A; A;A;T;T ;C;T;C; A;T;C; G;C;C;T ;G;G;A; T;C;A;T ;T;T;T; T;C;A; A;T;A; G;T;T;T ;C;A;T; C;A;A; T;T;G;C ;T;G;T; G;T;T;C ;T;T;T
AMPL16 90341	scaffold12	AATCCAG TATGCAC CATAAAG CAAG	ACCGCTT TTTACCC TTTTTGA ATCT	101(A-18%,G-83%);	G	G
AMPL16 90342	scaffold18	AGACATG AAGATTA TCCGCCT GTAA	GGTACCA TCTCCAT CTGTAAA ACCT	36(G-85%,T-16%);38(A-100%,T-0%);124(A-2%,C-98%);151(A-3%,G-97%);160(C-100%,T-0%);	G;A;C; G;C	G;A;C; G;C
AMPL16 90344	scaffold14	GAAGCAG ACGTACC CACTATC AA	CTTGATG TATGGGA CCAGTTT GTC	39(C-97%,T-7%);42(C-96%,T-4%);45(C-1%,T-100%);51(C-0%,T-100%);54(A-98%,T-10%);63(A-0%,G-100%);65(C-27%,T-3%);70(A-95%,G-0%,T-13%);71(A-2%,C-98%);72(C-100%,T-1%);76(G-0%,A-100%);79(C-99%,T-3%);80(C-97%,T-3%);81(A-2%,G-100%);82(G-2%,A-98%);85(G-7%,A-95%);87(C-3%,G-4%,A-95%);88(A-0%,T-100%);89(C-0%,T-100%);93(G-0%,A-100%);95(C-0%,T-100%);96(A-2%,G-98%);98(A-4%,G-96%);99(C-2%,T-100%);102(C-0%,T-100%);109(C-10%,T-99%);115(C-4%,A-96%,T-0%);118(A-2%,C-1%,G-98%);121(C-26%,T-87%);127(C-100%,T-0%);133(G-2%,A-98%);145(A-0%,G-100%);148(C-2%,T-98%);151(C-99%,T-1%);153(A-100%,T-0%);154(C-100%,T-0%);163(G-5%,C-23%,T-87%);165(A-89%,G-23%);166(C-16%,T-95%);169(C-100%,T-0%);175(G-2%,A-98%);178(A-5%,G-100%);	C;C;T;T ;A;G;-; A;C;C; A;C;C; G;A;A; A;T;T;A ;T;G;G; T;T;T;A ;G;T;C; A;G;T; C;A;C;T ;A;T;C; A;G	C;C;T;T ;A;G;- /C;A/T; C;C;A; C;C;G; A;A;A; T;T;A;T ;G;G;T; T;C/T;A ;G;T/C; C;A;G; T;C;A;C ;T/C;G/ A;T/C;C ;A;G

AMPL16 90349	scaffold12	AGAAAGA ACTGACG AGTATCA CCAA	CTTGACT TCCCTGG TATCCTC AC	36(G-3%,A-98%);39(C-98%,T-3%);45(G-11%,C-16%,T-90%);46(C-100%,T-1%);47(C-100%,T-0%);48(A-1%,G-27%,T-88%);49(G-0%,C-99%,T-0%);50(C-99%,T-1%);51(C-19%,G-89%,A-9%,T-0%);54(C-27%,T-89%);57(C-3%,T-98%);60(C-99%,T-1%);66(A-2%,C-97%,T-2%);75(A-2%,G-98%);78(C-96%,T-13%);81(G-2%,A-99%);84(G-1%,T-100%);99(C-6%,T-99%);102(A-1%,G-99%);105(G-0%,A-100%);108(G-97%,A-11%);111(A-2%,G-99%);114(A-2%,C-7%,G-97%);117(G-6%,A-99%);120(A-2%,G-99%);123(G-99%,T-2%);129(A-3%,G-98%);132(A-4%,C-96%);135(A-1%,G-99%);138(G-0%,C-100%,T-1%);141(A-3%,C-97%);144(A-4%,G-1%,C-92%,T-9%);147(A-2%,G-99%);150(G-1%,C-100%);153(A-1%,G-99%);156(A-1%,G-99%);165(C-99%,T-1%);	A;C;T;C ;C;T;C; C;G;T;T ;C;C;G; C;A;T;T ;G;A;G; G;G;A; G;G;G; C;G;C; C;C;G; C;G;G; C	A;C;C/T ;C;C;G/ T;C;C;G /A;C/T; T;C;C;G ;C/T;A; T;T;G;A ;G/A;G; G;A;G; G;G;C; G;C;C; C;G;C; G;G;C
AMPL16 90350	scaffold5	CTCAAGG ATGTTTT GGACAGC TG	GCATTTC AATTCTC CATCTAC GTGT	46(A-4%,C-96%);48(A-0%,G-100%);51(A-1%,G-100%);54(G-0%,T-100%);57(G-98%,A-14%);72(C-1%,A-99%);81(C-6%,T-100%);87(A-1%,C-100%);102(A-1%,G-99%,T-3%);103(C-1%,T-100%);105(A-1%,G-100%);126(A-0%,G-100%);132(C-30%,T-94%);135(C-2%,T-99%);137(A-0%,C-100%);138(C-100%,T-0%);141(A-0%,G-100%);144(C-23%,T-91%);147(C-100%,T-1%);150(C-2%,T-98%);156(C-18%,T-96%);163(A-0%,G-100%);166(C-93%,T-31%);168(C-98%,T-0%);170(G-1%,T-98%);171(A-5%,G-96%,T-0%);172(C-30%,T-3%);174(C-0%,G-1%,T-33%);175(A-0%,G-93%,T-28%);176(G-4%,A-98%);177(G-2%,A-98%);178(G-34%,T-0%);180(G-1%,A-100%);182(A-4%,G-100%);183(G-1%,C-96%,T-1%);184(C-34%,T-90%);185(A-0%,C-31%,T-93%);186(C-90%,T-34%);188(G-0%,C-100%);189(A-89%,T-31%);190(C-89%,T-34%);192(A-0%,G-100%);193(A-93%,G-29%);194(C-1%,T-100%);195(A-93%,G-31%);196(G-1%,A-100%);199(A-3%,G-98%);202(C-1%,T-100%);203(C-100%,T-2%);204(G-2%,T-98%);205(A-1%,C-37%,T-87%);206(C-89%,T-34%);208(C-1%,T-100%);209(C-96%,T-5%);214(C-100%,T-0%);217(A-0%,G-100%);232(A-85%,C-37%);238(A-1%,G-100%);	C;G;G; T;G;A;T ;C;G;T; G;G;T;T ;C;C;G; T;C;T;T ;G;C;C; T;G;-;-; G;A;A;- ;A;G;C; T;T;C;C ;A;C;G; A;T;A; A;G;T; C;T;T;C ;T;C;C; G;A;G	C;G;G; T;G/A; A;T;C; G;T;G; G;T/C;T ;C;C;G; T/C;C;T ;C/T;G; T/C;C;T ;G;-C; /T;T/G; A;A;G/- ;A;G;C; T/C;T/C ;C/T;C; A/T;C/T ;G;G/A; T;A/G; A;G;T; C;T;T/C ;C/T;T; C;C;G; A/C;G
AMPL16 90353	scaffold1	ATCGTTA GCTCAAG AAGGATA GCG	ATTTCCT TCATCAT TTACACA GGTG	36(G-1%,A-99%);41(C-70%,G-63%);43(C-100%,T-0%);44(A-35%,G-98%);47(G-100%,T-0%);97(A-73%,G-28%);102(C-71%,T-62%);103(A-34%,C-98%);108(C-100%,T-1%);116(C-98%,T-34%);124(G-100%,T-0%);130(A-0%,G-100%);131(C-71%,A-62%);132(C-100%,T-0%);136(A-0%,G-100%);139(G-34%,C-98%);148(A-71%,G-62%);159(C-2%,T-99%);176(C-71%,T-62%);183(G-100%,T-2%);191(A-71%,G-62%);194(A-71%,G-62%);202(C-73%,A-27%);213(C-100%,T-0%);217(C-100%,T-0%);218(C-0%,T-100%);226(C-71%,T-61%);233(A-0%,G-100%);	A;C;C; G;G;A; C;C;C;C ;G;G;C; C;G;C; A;T;C; G;A;A; C;C;C;T ;C;G	A;G;C; G;G;G; T;C;C;C ;G;G;A; C;G;C; G;T;T;G ;G;G;A; C;C;T;T ;G

AMPL16 90355	scaffold4	AACAGCT ATATACC TGTACCC GAAC	CAGCGCT TAGGCAT ATAGGTG G	51(A-7%,G-100%);54(G-100%,T-3%);55(C-25%,T-91%);59(A-1%,G-100%);75(C-3%,T-23%);76(A-2%,C-25%);80(G-7%,C-97%,T-5%);87(C-100%,T-1%);98(G-97%,A-18%);100(G-5%,A-99%);104(A-91%,C-25%);108(G-94%,C-23%);110(A-43%,G-96%);112(A-99%,T-4%);120(C-23%,T-94%);126(A-8%,G-98%);131(A-99%,T-4%);132(A-1%,T-100%);134(C-100%,T-1%);135(G-100%,T-1%);141(A-7%,G-100%);151(A-1%,C-100%,T-1%);174(C-99%,T-4%);175(C-99%,T-4%);185(A-100%,T-0%);191(C-100%,T-3%);195(A-100%,T-0%);196(C-99%,T-7%);197(A-0%,G-100%);215(G-81%,A-81%);	G;G;T; G;-;-C; C;G;A; A;G;A/ G;A;T; G;A;T; C;G;G; C;C;C; A;C;A; C;G;A/ G	G;G;T/ C;G;T/-; C/-;C;C; G/A;A; A/C;G/ C;G;A; C/T;G; A;T;C; G;G;C; C;C;A; C;A;C; G;G/A
AMPL16 90358	scaffold14	TTGCTTT GCTTACA ACTCTTG CTAT	AAGTAGA AGGGTAG CACGTCA GTTA	41(A-94%,T-13%);42(A-3%,T-98%);47(C-0%,T-98%);48(C-3%,A-98%);56(C-0%,T-100%);60(G-1%,A-100%);66(G-5%,A-99%);76(A-94%,G-13%);77(C-94%,G-13%);81(A-13%,T-94%);104(C-0%,T-100%);106(C-0%,T-100%);116(C-9%,T-95%);120(G-0%,C-21%,T-88%);122(A-96%,T-8%);128(A-89%,G-21%);131(G-2%,A-100%);136(C-100%,T-0%);143(G-87%,T-22%);150(G-86%,A-19%);177(G-1%,A-99%);180(C-23%,T-87%);198(A-3%,T-99%);201(C-1%,T-99%);	A;T;T;A ;T;A;A; A;C;T;T ;T;T;T; A;A;A; C;G;G; A;T;T;T	T;T;T;A ;T;A;A; G;G;A; T;T;C;C ;A;G;A; C;A;A; A;C;T;T
AMPL16 90359	scaffold2	TCTAGTT CGAAGAT ACCCTGT TTGG	ACTACCA GATAGCG ACGATAT CAAG	37(A-0%,G-100%);39(G-100%,T-1%);41(C-0%,G-0%,T-99%);42(G-1%,C-99%);59(C-1%,G-2%,A-99%);61(A-0%,T-100%);63(A-4%,G-100%);64(A-0%,C-0%,T-99%);65(G-99%,A-18%);69(C-0%,T-100%);91(C-100%,T-3%);100(C-1%,T-100%);114(G-1%,A-99%);115(C-0%,T-100%);117(G-0%,A-100%,T-4%);142(G-19%,T-98%);148(A-0%,C-1%,T-99%);150(C-100%,T-0%);152(C-0%,T-100%);156(A-1%,G-99%);161(G-6%,A-99%);162(G-0%,A-100%);165(A-99%,G-18%);168(A-1%,G-100%);174(A-0%,G-100%);177(G-1%,A-99%);186(G-0%,T-100%);192(A-0%,G-100%);195(G-17%,A-97%);201(G-92%,A-31%);204(C-99%,T-1%);213(G-100%,T-0%);216(C-0%,T-100%);219(C-100%,T-0%);228(A-1%,G-100%,T-0%);234(G-100%,T-0%);236(A-100%,T-0%);	G;G;T; C;A;T; G;T;G;T ;C;T;A; T;A;T;T ;C;T;G; A;A;A; G;G;A; T;G;A; G;C;G; T;C;G; G;A	G;G;T; C;A;T; G;T;A/ G;T;C;T ;A;T;A; G/T;T;C ;T;G;A; A;A/G; G;G;A; T;G;A; A/G;C; G;T;C; G;G;A
AMPL16 90362	scaffold5	CGACAAC ATGGACT ATCATCC TGAT	AGCTGTA AAATACA CTGGGGA TCTT	37(C-19%,T-97%);42(A-16%,T-97%);48(G-100%,T-0%);49(C-7%,G-99%);50(G-6%,A-100%);54(G-0%,A-100%);61(A-1%,G-99%);64(A-0%,G-100%);66(C-0%,A-100%);80(C-6%,T-100%);82(A-0%,C-36%,T-88%);91(A-1%,T-100%);95(A-32%,T-0%);96(A-0%,G-100%);100(C-0%,T-100%);105(G-99%,T-4%);107(A-1%,T-99%);108(A-12%,G-98%);110(A-86%,G-40%);117(C-99%,T-5%);120(A-1%,G-99%);121(G-0%,C-99%,T-1%);124(A-1%,G-99%);137(A-0%,G-99%);141(A-0%,T-99%);145(C-27%,T-93%);146(G-1%,C-27%,T-93%);152(C-27%,T-94%);154(C-3%,T-100%);155(G-88%,A-38%);158(C-0%,G-100%);160(C-3%,T-100%);161(G-1%,A-100%);163(G-11%,T-	T;T;G;G ;A;A;G; G;A;T;T ;T;-;G;T ;G;T;G; A;C;G; C;G;G; T;T;T;T ;T;G;G; T;A;T;G ;C;C;C; A;T;T;A ;G;A;T; G;A	T;T;G;G ;A;A;G; G;A;T;T /C;T;- /A;G;T; G;T;G; G/A;C; G;C;G; G;T;C/T ;T/C;C/ T;T;A/G ;G;T;A; T;G;C;C ;C;A;T; T;A;G; A;T;G/

				99%);164(A-0%,G-100%);181(C-99%,T-0%);183(C-99%,T-10%);187(C-99%,T-5%);188(C-14%,A-98%);191(A-2%,T-100%);192(A-10%,T-99%);196(C-0%,A-100%);197(A-0%,G-100%);201(C-7%,A-99%);202(G-1%,T-99%);205(G-88%,A-38%);206(G-0%,A-100%);		A;A
AMPL16 90363	scaffold1	TCTCGAT ACGATCC TCTTCAA CATG	TCCAAGT ACAAACT CGTATTC TCCA	36(C-100%,T-0%);38(G-88%,A-57%);42(A-0%,G-100%);44(C-0%,T-100%);50(C-2%,G-99%);60(A-0%,G-100%);68(A-0%,G-100%);74(A-0%,G-100%);77(G-91%,A-55%);83(C-100%,T-1%);89(A-0%,G-100%);96(A-99%,T-0%);104(G-87%,T-59%);106(C-2%,T-100%);112(C-1%,A-100%);119(C-55%,T-91%);120(G-0%,A-100%,T-0%);121(G-0%,A-100%);122(C-0%,A-98%);125(A-85%,G-5%,C-59%);127(C-0%,T-100%);128(G-0%,A-98%);134(A-3%,G-98%);139(A-2%,C-98%);140(G-0%,A-100%);141(G-1%,A-99%);142(C-2%,A-98%);151(G-87%,A-59%);160(A-1%,G-100%);169(G-0%,A-100%);175(C-57%,T-89%);181(A-4%,C-0%,G-96%);184(G-91%,T-54%);189(A-0%,G-100%);190(C-100%,T-0%);194(C-54%,T-91%);196(A-55%,T-91%);200(C-2%,A-98%);202(C-100%,T-1%);207(G-0%,C-100%);208(G-0%,A-100%);213(G-88%,A-59%);238(C-1%,T-100%);	C;G/A; G;T;G; G;G;G; A/G;C; G;A;G/ T;T;A;T /C;A;A; A;A/C; T;A;G; C;A;A; A;G/A; G;A;C/ T;G;T/G ;G;C;T/ C;T/A; A;C;C; A;G/A; T	C;G/A; G;T;G; G;G;G; G/A;C; G;A;G/ T;T;A;T /C;A;A; A;A/C; T;A;G; C;A;A; A;G/A; G;A;T/ C;G;G/ T;G;C;T /C;T/A; A;C;C; A;G/A; T
AMPL16 90364	scaffold18	ATTAAGT AAGTCAA TCTCTGC CTGC	AAAAGGT ATCTTTA GGTGTGT CGGG	42(A-100%,T-0%);43(G-0%,T-100%);44(C-0%,T-100%);51(C-92%,T-8%);52(C-0%,T-100%);58(C-0%,T-100%);60(A-0%,G-100%);61(G-83%,T-18%);66(C-0%,A-100%);76(A-2%,C-0%,G-98%);	A;T;T;C ;T;T;G; G;A;G	A;T;T;C ;T;T;G; G;A;G
AMPL16 90367	scaffold10	TAGCTAT CTGAGTC CTTTCGT CTTC	TTGAATG AATCGAT CTTGAAT GGGG	52(A-2%,G-100%);53(G-28%,T-89%);54(A-2%,C-98%);58(C-100%,T-0%);61(C-98%,T-11%);67(A-13%,G-3%,C-96%);73(G-0%,A-100%);88(A-1%,C-99%);94(C-100%,T-0%);98(C-100%,T-1%);105(C-99%,T-3%);112(C-3%,T-99%);113(G-90%,C-27%);114(C-18%,T-96%);115(C-15%,T-96%);116(A-3%,T-99%);120(A-12%,G-97%);122(C-2%,T-99%);123(C-90%,G-27%);128(C-25%,T-92%);151(C-99%,T-1%);	G;T;C;C ;C;C;A; C;C;C;C ;T;G;T; T;T;G;T ;C;T;C	G;G/T; C;C;C/T ;C;A;C; C;C;C;T ;G/C;C/ T;T;T;G ;T;C/G; T/C;C
AMPL16 90368	scaffold11	GAAGAAC AGTGCAA CCTGTTC G	CCCTGTT ATTCCGT CTATTCC CATTA	33(G-0%,A-100%);37(G-100%,T-0%);39(A-9%,G-100%);40(A-3%,G-100%);42(C-100%,T-1%);43(G-0%,A-100%);45(C-0%,T-100%);46(A-1%,G-100%);53(C-100%,T-1%);55(C-100%,T-2%);60(A-0%,G-100%);61(A-0%,G-100%);64(C-0%,T-100%);66(A-0%,G-100%);73(A-12%,G-100%);76(A-37%,C-0%,G-100%);78(A-0%,G-100%);79(C-100%,T-1%);91(G-0%,A-100%);93(A-7%,C-99%);94(A-0%,G-7%,T-99%);95(G-0%,C-99%,T-7%);96(C-99%,T-8%);97(A-7%,G-100%);99(A-0%,G-100%);100(A-85%,G-60%);102(C-100%,T-1%);103(G-10%,A-100%);104(C-100%,T-1%);106(A-3%,G-100%);111(G-0%,A-100%);112(C-100%,T-0%);117(C-100%,T-1%);118(A-1%,G-100%);124(A-7%,G-	A;G;G; G;C;A; T;G;C;C ;G;G;T; G;G;G; G;C;A; C;T;C;C ;G;G;A; C;A;C; G;A;C; C;G;G; C;G;A; G;G;A; C;G;G; G;C;T	A;G;G; G;C;A; T;G;C;C ;G;G;T; G;G;G; G;C;A; C;T;C;C ;G;G;G; C;A;C; G;A;C; C;G;G; C;A;A; G;G;A; C;G;G; G;C;T

				99%);126(C-100%,T-1%);127(G-96%,A-11%);130(G-56%,A-93%);132(A-0%,G-100%);136(A-6%,G-99%);139(A-99%,T-10%);145(A-4%,C-100%,T-1%);146(A-6%,G-100%);147(G-100%,T-1%);148(A-1%,C-1%,G-100%,T-1%);150(C-100%,T-0%);151(A-5%,T-100%);		
AMPL16 90369	scaffold4	GCCGCTT CAAGTAG AGAGTAA AGTA	CAGCAGA AAGAGGA GAATTAC CAGT	60(A-0%,G-100%);87(C-57%,T-95%);98(A-99%,G-19%);100(G-0%,A-100%);107(C-95%,G-1%,T-62%);108(G-1%,A-100%);123(C-96%,T-44%);125(G-0%,A-100%);129(G-100%,T-0%);136(G-92%,C-67%);140(C-0%,T-100%);152(A-99%,T-17%);153(C-100%,T-0%);161(G-98%,A-29%);	G;T/C; A;A;T/ C;A;T/C ;A;G;C/ G;T;A; C;G	G;T;G/ A;A;T/ C;A;C; A;G;C/ G;T;T/A ;C;A/G
AMPL16 90370	scaffold7	TACTACA AGACACG CAGGATG AC	AGAGAAA ACGCAGA ACATAGA AAGC	35(G-3%,A-100%);36(C-99%,T-5%);44(G-58%,C-94%,T-0%);45(A-2%,G-99%);50(A-1%,G-100%);53(C-0%,T-100%);55(G-1%,C-100%);56(C-1%,T-100%);66(A-2%,T-93%);69(C-2%,T-100%);74(A-0%,G-100%);81(C-1%,A-100%);85(C-1%,G-100%);89(A-10%,T-99%);95(A-0%,C-100%);98(C-68%,T-86%);99(C-1%,G-68%,A-86%);100(A-1%,T-99%);102(A-68%,G-86%);103(G-100%,T-0%);114(A-2%,G-100%);116(C-86%,T-66%);117(C-80%,T-79%);118(G-2%,T-100%);119(A-2%,C-100%);127(C-100%,T-1%);128(G-78%,C-84%);131(A-2%,G-100%);132(C-58%,T-95%);133(C-100%,T-2%);134(A-2%,G-100%);142(C-81%,G-77%);146(C-63%,T-92%);149(A-100%,T-0%);152(G-0%,C-100%);156(G-100%,T-1%);163(G-63%,A-92%);169(G-99%,T-8%);171(C-1%,T-99%);177(G-63%,C-92%,T-1%);181(G-93%,T-63%);183(C-63%,G-3%,A-92%);185(A-93%,T-63%);186(G-2%,A-100%);188(A-1%,G-99%);189(A-17%,G-99%);200(C-5%,G-63%,T-88%);202(C-63%,A-93%);205(A-18%,G-95%);209(C-63%,A-93%);217(C-4%,T-99%);219(G-93%,T-63%);	A;C;C; G;G;T; C;T;T;T ;G;A;G; T;C;T;A ;T;G;G; G;C;C;T ;C;C;C; G;T;C; G;G;T; A;C;G; A;G;T; C;G;A; A;A;G; G;T;A; G;A;T; G	A;C;C; G;G;T; C;T;T;- T;G;A; G;T;C;T ;A;T;G; G;G;C; C/T;T;C ;C;C/G; G;T;C; G;G/C; T;A;C; G;A;G; T;C;G; G;A;A; G;G/A; T;A;G/ A;A;T; G
AMPL16 90373	scaffold14	GATGAGA CGTTTAC TGATTG GCTT	ACAGCTT AGCCTTA ACAGTCT ACAA	58(C-91%,T-27%);60(A-91%,G-27%);66(C-27%,T-1%);71(C-0%,T-100%);72(A-91%,C-27%);133(C-100%,T-9%);136(C-0%,T-100%);157(C-0%,T-100%);166(C-100%,T-1%);207(G-4%,A-100%);210(G-100%,A-9%);	C;A;-;T; A;C;T;T ;C;A;G	T/C;G/ A;C/-;T; A/C;C/T ;T;T;C; A;G/A
AMPL16 90375	scaffold1	GTGTCGA ATTGAAC ATCACGA TAGG	CTTTCGA CTCGTAC TTGGCTT TATT	42(C-0%,T-100%);43(A-1%,G-100%);44(C-99%,T-2%);47(G-0%,C-100%);58(C-99%,T-1%);61(C-88%,A-35%);82(G-1%,A-99%);85(G-0%,T-100%);87(C-88%,A-35%);99(G-0%,A-100%);103(C-100%,T-0%);104(G-0%,A-100%);108(C-7%,T-99%);123(A-0%,T-100%);126(G-0%,A-100%);131(A-89%,G-35%);132(C-88%,A-35%);135(G-1%,A-99%);138(A-1%,G-100%);154(G-100%,T-0%);161(C-36%,T-88%);199(C-19%,T-20%);213(A-1%,G-99%);215(A-35%,T-88%);217(A-100%,T-1%);218(A-1%,G-100%);	T;G;C;C ;C;C;A; T;C;A;C ;A;T;T; A;A;C; A;G;G; T;-;G;T; A;G	T;G;C;C ;C;C/A; A;T;A/ C;A;C; A;T;T;A ;A/G;A/ C;A;G; G;C/T;- /C;G;T/ A;A;G

AMPL16 90376	scaffold1	TTGATGT CACCTTT GGATCGA ACTT	TGATACA TGACGAT TTGTAGC ACAC	48(A-8%,G-100%);50(G-0%,C-100%);55(G-100%,T-7%);59(A-93%,T-31%);60(C-94%,T-22%);61(A-94%,G-32%);74(C-32%,T-94%);76(A-32%,T-93%);79(C-93%,G-32%);80(A-1%,G-100%);82(G-11%,A-100%);83(C-93%,T-32%);91(A-0%,G-100%);105(C-0%,T-100%);111(C-32%,T-94%);130(A-0%,T-100%);137(G-93%,T-32%);148(G-0%,A-100%);150(C-32%,T-94%);182(C-100%,T-2%);195(A-0%,G-100%);202(A-8%,G-100%);215(C-3%,T-100%);222(C-0%,T-100%);228(A-3%,C-99%);	G;C;G; A;C;A; T;T;C;G ;A;C;G; T;T;T;G ;A;T;C; G;G;T;T ;C	G;C;G; A/T;C/T ;G/A;C/ T;A/T;G /C;G;A; C/T;G;T ;C/T;T; T/G;A; C/T;C;G ;G;T;T; C
AMPL16 90378	scaffold14	ACAATAA GAATATC TTTTTCG CGAAC	CCTTGAT TACCAAT ACGGAAC GAAG	38(A-6%,G-98%);42(C-96%,A-13%);55(A-100%,T-2%);62(G-0%,C-100%);69(G-100%,T-0%);75(A-0%,G-100%);76(G-92%,A-21%);78(G-91%,A-22%);79(A-0%,C-100%);82(A-0%,G-100%);89(C-91%,G-22%);94(A-2%,C-100%);101(A-100%,T-2%);103(C-100%,T-2%);104(A-0%,G-21%);115(C-6%,A-98%);135(A-2%,C-100%);137(C-97%,T-13%);142(C-2%,A-100%);146(A-2%,G-100%);149(A-100%,T-2%);158(C-100%,T-2%);161(C-100%,T-2%);	G;C;A; C;G;G; G;G;C; G;C;C; A;C;-A ;C;C;A; G;A;C; C	G;C/A; A;C;G; G;A/G; A/G;C; G;C/G; C;A;C;- /G;A;C; C/T;A; G;A;C; C
AMPL16 90380	scaffold2	ACAAGAC TAGGGCA CTTCGAA ATTA	GGCATAC TCCTAAC TATTTCG CAGA	50(C-100%,T-0%);53(C-97%,T-60%);55(C-0%,T-100%);64(A-59%,G-0%,C-97%);65(A-0%,T-100%);66(G-68%,C-96%);67(G-0%,A-100%);71(A-60%,T-97%);72(A-2%,G-100%);74(A-0%,C-100%);81(C-0%,A-100%);82(G-0%,A-100%);84(A-100%,T-3%);87(A-60%,G-98%);89(C-100%,T-0%);93(C-97%,T-60%);96(C-98%,T-59%);102(G-0%,A-100%);111(C-60%,T-97%);120(G-0%,A-100%);121(C-60%,T-97%);126(A-97%,T-60%);127(G-0%,T-100%);134(A-0%,G-100%);140(C-100%,T-1%);158(C-97%,T-60%);161(G-6%,T-100%);167(A-59%,G-98%);175(C-82%,T-79%);176(C-100%,T-0%);177(G-2%,A-100%);180(G-59%,T-98%);182(C-81%,T-80%);189(C-54%,T-98%);192(C-98%,T-54%);196(C-59%,T-98%);198(C-98%,T-59%);200(C-1%,T-100%);215(C-59%,T-97%);217(A-1%,G-100%);221(A-0%,C-100%);222(C-21%,T-91%);223(G-1%,A-100%);232(G-1%,A-100%);233(G-0%,T-100%);237(A-0%,T-100%);238(A-60%,G-97%);239(C-100%,T-0%);	C;T/C;T ;C/A;T; C/G;A; T/A;G; C;A;A; A;A/G; C;T/C;C /T;A;T/ C;A;T/C ;T/A;T; G;C;T/C ;T;A/G; C/T;C;A ;G/T;T/ C;T/C;T /C;T/C; T/C;T;C /T;G;C; T;A;A;T ;T;G/A; C	C;T/C;T ;C/A;T; C/G;A; T/A;G; C;A;A; A;A/G; C;T/C;T /C;A;T/ C;A;C/T ;T/A;T; G;C;C/T ;T;A/G; C;C;A;T /G;T;T/ C;C/T;T /C;C/T; T;T/C;G ;C;T/C; A;A;T;T ;A/G;C
AMPL16 90390	scaffold2	CACTTGA ACCATTC TACTTCG AACG	TATGTTC ATCGAGA CATCAGC CC	42(G-0%,T-100%);43(A-2%,C-98%);45(G-100%,T-0%);56(G-2%,T-98%);60(A-2%,G-98%);65(C-0%,T-100%);66(G-87%,A-83%);68(C-2%,T-99%);73(A-97%,G-19%);75(C-6%,T-99%);86(A-2%,T-100%);87(G-2%,A-98%);98(A-1%,T-100%);104(A-97%,G-20%);106(G-4%,A-100%,T-0%);107(C-87%,T-85%);113(G-97%,A-19%);117(C-100%,T-0%);118(G-1%,A-100%);121(A-0%,G-100%);126(A-4%,G-100%);127(A-98%,T-2%);128(G-2%,A-98%);129(G-98%,T-2%);132(G-2%,C-18%);136(C-2%,G-98%);141(C-0%,G-99%);142(A-98%,G-18%);143(G-68%,A-98%);158(G-0%,C-100%);165(C-2%,T-98%);167(A-0%,G-100%);182(C-100%,T-1%);184(C-19%,T-	T;C;G;T ;G;T;A/ G;T;A;T ;T;A;T; A;A;C/ T;G;C; A;G;G; A;A;G;- G;G;A; A/G;C; T;G;C;T ;G;G;G; G;G;T; C;C;G; A	T;C;G;T ;G;T;A; T;A/G;T ;T;A;T; A/G;A; T;G/A; C;A;G; G;A;A; G;- /C;G;G; A/G;G/ A;C;T; G;C;T/C ;T/G;G/ A;A/G; G/A;G;

				97%);186(A-2%,G-97%,T-18%);189(G-97%,A-19%);207(G-99%,A-18%);213(G-99%,A-18%);216(G-100%,T-3%);222(C-2%,T-98%);224(A-0%,C-100%);225(A-0%,C-99%,G-18%);236(G-100%,T-0%);237(A-97%,G-19%);		T;C;C/G ;G;A/G
AMPL16 90392	scaffold11	GATCACA CTTGCTT GCTCATG TTT	ATTCTCT CTCAGGT CCTTCTA TTGC	51(G-95%,A-21%);53(A-95%,T-21%);94(C-98%,T-0%);100(C-0%,T-20%);102(C-3%,G-100%);112(A-0%,G-100%);181(C-0%,A-100%);209(C-95%,T-21%);210(C-95%,T-21%);214(C-93%,T-28%);219(A-4%,G-100%);	G;A;C;- ;G;G;A; C;C;C; G	A/G;T/ A;C;T/-; G;G;A; T/C;C/T ;C/T;G
AMPL16 90395	scaffold4	TTCTACG CTGAATG TTGCTTA TAGC	AAGAAGC TTTATCG TGTTCCA GAGG	37(A-45%,G-95%);74(A-45%,C-95%);91(A-0%,G-100%);116(C-92%,T-56%);142(A-13%,C-98%);143(A-0%,G-100%);158(A-0%,G-100%);183(C-100%,T-0%);184(C-2%,A-100%);202(A-13%,G-98%);228(C-96%,T-44%);229(C-3%,G-100%);	A/G;A/ C;G;C/T ;C;G;G; C;A;G; T/C;G	G;C;G; C;C;G; G;C;A; G;C;G
AMPL16 90396	scaffold12	CCGGATA ACAAAAA CCTAACC AACA	AGCGTTT ACCCTCT TTTATTCT TCG	50(C-100%,T-0%);84(A-83%,G-28%);88(A-1%,G-100%);227(A-73%,G-35%);	C;A;G; A	C;G;G; G
AMPL16 90398	scaffold1	GATGCAT TTCATCG TCTCTGT AGAC	TGAGAAT GGGCCAA AGAGAAA GT	37(A-0%,C-100%);40(G-100%,T-0%);43(A-3%,G-98%,T-0%);44(C-0%,A-100%);46(A-0%,C-100%);48(A-3%,C-99%);49(A-0%,T-100%);50(C-0%,T-100%);55(A-86%,G-37%);60(A-84%,G-38%);61(C-37%,T-85%);63(G-0%,C-100%,T-0%);64(C-0%,T-100%);66(G-0%,A-100%);67(A-0%,G-100%);70(A-19%,T-22%);71(A-3%,G-99%,T-0%);73(C-0%,G-2%,A-97%);74(A-87%,G-3%,C-32%);77(G-1%,A-99%);78(C-100%,T-0%);83(C-3%,T-98%);84(A-0%,G-100%);85(G-100%,T-0%);86(G-89%,A-34%);88(G-100%,T-0%);89(C-100%,T-0%);106(G-2%,A-98%);109(A-0%,G-100%);115(A-2%,G-99%);127(C-99%,T-2%);136(A-0%,G-100%);139(G-1%,A-100%);146(G-2%,A-99%);147(C-2%,T-99%);157(A-3%,G-100%);163(G-98%,T-8%);166(C-0%,T-100%);169(A-5%,G-98%);174(A-0%,T-100%);177(C-100%,T-0%);178(C-2%,T-100%);179(A-0%,G-100%);183(C-97%,T-11%);185(C-0%,T-100%);190(G-3%,A-99%);203(C-100%,T-0%);208(C-1%,T-100%);	C;G;G; A;C;C;T ;T;A;A; T;C;T;A ;G;-;G; A;A;A; C;T;G; G;G;G; C;A;G; G;C;G; A;A;T; G;G;T; G;T;C;T ;G;C;T; A;C;T	C;G;G; A;C;C;T ;T;G/A; A/G;T/ C;C;T;A ;G;T/-;G ;A;C/A; A;C;T; G;G;G/ A;G;C; A;G;G; C;G;A; A;T;G; G;T;G;T ;C;T;G; C;T;A;C ;T
AMPL16 90400	scaffold5	CAGTGGG TCTCTCT ACGTCTC TAT	TTTTGAA GATACGG GAGTGGT GGAT	37(C-0%,T-100%);64(C-99%,T-7%);90(C-99%,T-11%);92(G-0%,A-100%);100(C-92%,A-26%);102(C-100%,T-0%);127(A-6%,T-99%);128(C-99%,T-6%);145(G-100%,T-0%);162(C-100%,T-0%);165(C-100%,T-2%);166(A-87%,G-43%);175(G-0%,A-100%);177(C-98%,T-14%);196(C-90%,T-32%);200(C-32%,T-90%);203(A-42%,T-87%);204(C-42%,T-87%);219(A-2%,G-99%);226(C-87%,A-41%);234(C-99%,T-6%);237(G-0%,A-100%);	T;C;C;A ;C;C;T; C;G;C; C;A;A; C;C;T; T;G;C; C;A	T;C;C;A ;C/A;C; T;C;G;C ;C;G/A; A;C/T;C /T;C/T; A/T;C/T ;G;A/C; C;A

AMPL16 90401	scaffold1	TCGCGTT CTCTCCT TATACCA ATAC	GGAACTA ATACCGG CCGGATT AC	37(A-1%,G-100%);49(A-1%,C-100%);52(C-1%,T-100%);62(G-18%,A-20%);66(G-87%,A-34%);70(A-18%,G-20%);77(A-93%,G-20%);86(C-9%,A-98%);91(A-18%,G-99%);92(A-18%,C-1%,T-98%);93(C-18%,T-99%);94(C-18%,A-99%);100(C-15%,T-99%);102(C-100%,T-0%);105(C-2%,A-100%);111(G-92%,A-26%);113(C-21%,T-92%);120(C-90%,T-24%);124(C-19%,G-99%);126(A-1%,G-100%);129(G-100%,T-3%);133(C-1%,A-100%);135(G-3%,T-99%);136(C-3%,A-100%);137(A-21%,G-97%);143(G-0%,T-100%);144(A-8%,C-100%);146(A-84%,C-37%);153(C-8%,G-100%);155(C-1%,A-100%);156(A-1%,T-100%);157(G-1%,A-99%);158(C-99%,T-0%);	G;C;T;-; G;-;A;A ;G;T;T; A;T;C; A;G;T; C;G;G; G;A;T; A;G;T; C;A;G; A;T;A; C	G;C;T;- /A;G/A; G/-;A/G ;A;G;T; T;A;T;C ;A;A/G; T/C;T/C ;G;G;G; A;T;A; G;T;C; A/C;G; A;T;A; C
AMPL16 90403	scaffold4	AAAGCAA TAATCTG TGCCAAC GAAA	CTAGTCA TAGCCAA CGCTTTC TTTG	36(C-100%,T-0%);37(A-0%,G-100%);45(A-0%,T-100%);51(C-0%,T-100%);54(C-0%,T-100%);55(A-0%,G-100%);62(A-0%,G-100%);63(A-3%,G-98%);66(G-0%,A-100%);68(C-100%,T-0%);72(A-1%,G-98%,T-3%);84(G-1%,A-99%,T-0%);99(C-100%,T-0%);105(A-0%,G-100%);111(C-100%,T-2%);112(A-0%,G-100%);120(A-0%,G-0%,T-100%);126(C-17%,T-97%);130(C-100%,T-1%);146(C-100%,T-0%);153(G-0%,A-100%);156(C-0%,A-100%);161(A-89%,G-26%);171(A-0%,C-100%,T-0%);	C;G;T;T ;T;G;G; G;A;C; G;A;C; G;C;G; T;T;C;C ;A;A;A; C	C;G;T;T ;T;G;G; G;A;C; G;A;C; G;C;G; T;T/C;C ;C;A;A; G/A;C
AMPL16 90404	scaffold1	CTCGCCA AACGGGT TAAACC	GTCAATT CCTGTGT ATACCAT GGTG	36(G-98%,A-12%);46(C-100%,T-0%);50(C-100%,T-0%);64(G-100%,T-3%);74(C-0%,G-0%,A-100%);76(C-100%,T-0%);89(C-97%,T-12%);102(C-100%,T-0%);103(C-100%,T-0%);105(C-99%,T-1%);106(C-100%,T-0%);109(G-1%,T-99%);113(A-0%,C-100%);115(C-98%,T-12%);117(A-89%,G-100%);122(C-100%,T-0%);127(C-0%,T-100%);137(G-100%,T-0%);142(A-0%,T-99%);143(A-2%,G-98%);147(A-0%,G-100%);148(G-99%,T-1%);149(G-0%,A-100%);150(C-0%,T-100%);151(A-0%,G-100%);153(G-0%,T-100%);156(A-97%,C-0%,G-92%);157(A-100%,T-0%);161(C-0%,A-100%);164(A-0%,G-100%);165(A-0%,C-3%,T-97%);166(A-2%,G-98%);167(G-90%,A-100%);169(G-0%,A-100%);184(G-0%,T-100%);185(G-0%,A-100%);186(C-3%,T-98%);187(C-3%,T-98%);190(G-1%,C-99%,T-2%);193(G-1%,A-99%);195(A-0%,T-100%);202(G-0%,A-99%,T-1%);208(C-98%,T-3%);209(A-1%,G-100%);210(C-1%,G-99%);214(G-0%,A-100%);218(C-0%,T-100%);219(A-1%,G-99%);222(C-99%,T-1%);225(C-85%,T-100%);233(C-0%,G-100%);	G;C;C; G;A;C; C;C;C;C ;C;T;C; C;G/A; C;T;G;T ;G;G;G; A;T;G;T ;A/G;A; A;G;T; G;A/G; A;T;A;T ;T;C;A; T;A;C; G;G;A; T;G;C;C /T;G	A/G;C; C;G;A; C;T/C;C ;C;C;C; T;C;T/C ;G/A;C; T;G;T;G ;G;G;A; T;G;T;G /A;A;A; G;T;G; A/G;A; T;A;T;T ;C;A;T; A;C;G; G;A;T; G;C;C/T ;G
AMPL16 90407	scaffold11	GCGAGGT GTATATA TGTAGAC GTGA	CGGAGTA TCATAGT TTACTGA CGCT	38(C-0%,T-100%);40(A-89%,G-33%);42(G-0%,A-100%);46(G-89%,T-33%);48(A-5%,G-100%);49(A-1%,T-100%);65(G-89%,A-33%);69(G-5%,C-100%);72(C-100%,T-5%);73(G-90%,A-33%);74(A-89%,G-32%,T-1%);75(C-100%,T-5%);77(C-2%,A-100%);84(C-100%,T-5%);86(C-100%,T-0%);87(C-2%,A-100%);90(C-1%,T-99%);107(C-1%,T-100%);114(C-100%,T-1%);117(C-96%,A-	T;A;A; G;G;T; G;C;C; G;A;C; A;C;C; A;T;T;C ;C;G;T; A;C;G; C;T;C;A	T;G/A; A;G/T; G;T;G/ A;C;C; A/G;A/ G;C;A; C;C;A;T ;T;C;C/ A;G;T;

				17%);122(G-99%,T-2%);126(G-2%,T-99%);128(G-1%,A-100%);132(G-0%,C-100%);133(G-89%,A-32%);137(G-2%,C-98%,T-7%);138(A-32%,T-89%);140(C-89%,G-1%,A-32%);149(G-11%,A-98%);168(C-100%,T-1%);173(C-3%,T-100%);196(A-0%,T-100%);209(C-33%,T-89%);	;C;T;T; T	A;C;A/ G;C;T/ A;C/A; A;C;T;T ;T/C
AMPL16 90408	scaffold5	ACGGTAT GGTGGTA CAAGAAA TAGA	ACATACA CAGGAGA GAAATGA ACGA	44(A-100%,T-0%);50(C-99%,T-4%);57(C-1%,A-100%);59(C-4%,A-99%);67(C-100%,T-1%);68(A-6%,G-98%);73(A-23%,C-12%);104(A-1%,C-100%);111(A-100%,T-0%);120(G-28%,T-89%);127(A-0%,G-100%);142(G-89%,C-28%);	A;C;A; A;C;G;- ;C;A;T; G;G	A;C;A; A;C;G; C/-;C;A; T/G;G; G/C
AMPL16 90409	scaffold2	TTGGATT TACGATT GAAGACA GCAG	GATAGGC AATTTCC ACCTTTC CTTC	39(C-6%,T-99%);40(A-9%,T-97%);44(C-2%,T-98%);54(C-100%,T-0%);56(C-100%,T-1%);64(C-0%,T-100%);65(A-4%,G-97%);68(G-4%,A-97%);71(G-2%,A-99%);78(A-3%,G-98%);80(C-78%,T-35%);89(A-1%,G-100%);93(A-3%,T-100%);95(C-2%,T-98%);96(A-2%,C-98%);97(G-97%,T-3%);99(C-98%,T-2%);101(C-90%,T-26%);102(C-3%,T-97%);104(G-1%,C-98%);106(C-97%,T-3%);109(A-1%,C-98%);112(C-1%,T-99%);114(A-100%,T-1%);116(C-97%,T-1%);119(A-98%,T-1%);123(G-1%,T-99%);126(C-100%,T-0%);128(C-2%,T-98%);129(C-3%,T-98%);132(C-100%,T-0%);133(C-3%,T-98%);134(A-0%,G-100%);135(C-0%,T-100%);136(G-100%,T-3%);141(A-3%,G-97%);142(C-100%,T-1%);148(A-1%,G-99%);156(C-0%,G-1%,T-99%);158(C-98%,T-3%);160(C-3%,T-98%);166(C-100%,T-1%);169(C-2%,G-98%);175(C-99%,T-1%);178(A-0%,G-100%);181(C-1%,T-100%);184(G-1%,A-99%);188(C-99%,T-1%);196(A-2%,G-98%);197(C-98%,T-2%);199(A-1%,G-2%,T-97%);205(C-28%,T-87%);208(C-1%,T-100%);211(C-89%,G-26%);214(C-100%,T-1%);223(G-1%,C-99%);224(A-1%,C-100%);226(A-1%,G-100%);231(G-0%,A-100%);	T;T;T;C ;C;T;G; A;A;G; C;G;T;T ;C;G;C; C;T;C;C ;C;T;A; C;A;T;C ;T;T;C; T;G;T;G ;G;C;G; T;C;T;C ;G;C;G; T;A;C; G;C;T;T ;T;C;C; C;C;G; A	T;T;T;C ;C;T;G; A;A;G; T;G;T;T ;C;G;C; T;T;C;C ;C;T;A; C;A;T;C ;T;T;C; T;G;T;G ;G;C;G; T;C;T;C ;G;C;G; T;A;C; G;C;T;C ;T;G;C; C;C;G; A
AMPL16 90410	scaffold2	GAGCACA GACGGCG AGATTAT T	CAACACA GCATCAT CGCCAAG	34(A-0%,G-100%);38(A-1%,G-100%);48(A-6%,G-100%);71(G-98%,C-16%);72(C-97%,T-82%);75(A-68%,G-99%);76(A-100%,T-1%);83(C-0%,A-100%);101(C-0%,T-100%);102(G-1%,C-100%);103(A-0%,C-82%,G-92%);106(G-68%,T-25%);107(C-99%,T-1%);109(C-0%,T-18%);111(C-3%,A-97%);112(C-15%,G-18%,T-68%);113(A-1%,C-80%,G-80%,T-15%);114(A-71%,T-98%);115(A-2%,C-92%,T-80%);117(A-80%,G-69%,T-31%);118(G-0%,A-100%);120(G-29%,T-69%);126(A-69%,G-19%,T-0%);127(A-69%,T-19%);131(A-3%,C-0%,G-18%);133(A-0%,C-80%);134(G-68%,T-18%);143(C-0%,G-88%,A-82%);145(C-0%,G-100%);148(A-0%,G-100%);154(G-3%,A-100%);166(C-100%,T-2%);167(A-8%,G-97%);169(A-1%,G-99%);172(A-0%,C-100%);174(A-1%,G-100%);179(C-98%,T-0%);180(C-0%,T-100%);182(A-0%,C-97%,T-1%);183(C-0%,A-18%,T-89%);184(G-99%,T-0%);187(C-85%,T-	G;G;G; G;T/C; G/A;A; A;T;C;C /G;- /G;C;-; A/-;T/-; G/C;T/ A;C/T; G/A;A; T/-;A/-; A/-;-;C/- ;G/-;G/ A;G;G; A;C;G/- ;- /G;C;G; - /C;T;C/- ;T/-;G/-; T/C;A/T	G;G;G; G/C;T/C ;G/A;A; A;T;C; G;G/T; C;-/T;- /A;T/G; G;T/A; C;T/G; A;T/G; A/G;A/ T;G/-;C; T/G;A; G;G;A; C;- /G;G/-; C;G;C/-; T;- /C;A/-;- /G;C;T/ A;T/C;

				83%);188(G-0%,A-95%,T-68%);189(C-95%,T-68%);192(C-1%,G-93%,A-20%);193(A-1%,G-68%,T-97%);194(C-2%,A-78%,T-80%);195(G-6%,A-98%,T-0%);196(A-6%,C-0%,G-2%,T-99%);198(A-0%,G-100%);203(A-0%,G-100%);218(C-1%,T-100%);	;C/T;G; T/G;A/T ;A;T;G; G;T	G/A;G/ T;A;A;T ;G;G;T
AMPL16 90416	scaffold5	CAAGTTC CAGAGAC GATGCTT TTAG	CTCTTAC TACCACC ACGACGA TG	52(C-99%,T-3%);55(G-100%,T-0%);82(A-0%,G-100%);83(A-2%,G-100%);86(A-3%,G-36%,T-86%);105(A-1%,C-99%);116(G-86%,T-38%);125(A-86%,G-39%);133(A-39%,T-86%);150(A-3%,C-99%);159(C-100%,T-0%);163(G-88%,A-39%);166(A-100%,T-0%);167(C-0%,T-100%);176(G-93%,T-27%);177(A-93%,T-27%);186(C-89%,A-39%);187(A-0%,C-100%);188(G-88%,A-39%);190(A-1%,G-100%);191(C-100%,T-1%);201(G-1%,C-99%,T-3%);203(C-88%,T-39%);204(A-1%,T-100%);209(G-100%,T-1%);211(G-39%,T-88%);221(G-93%,A-28%);232(A-2%,G-100%);	C;G;G; G;T;C; G;A;T; C;C;G; A;T;G; A;C;C; G;G;C; C;C;T;G ;T;G;G	C;G;G; G;G/T; C;T/G; G/A;A/ T;C;C;A /G;A;T; G/T;A/T ;C/A;C; G/A;G; C;C;T/C ;T;G;T/ G;G/A; G
AMPL16 90417	scaffold1	GCGTGAA AACTTGA GTACCCA C	ATGGTCT TATGAAC TCCCTTG GAAA	41(A-3%,G-98%);56(G-2%,A-98%);59(A-0%,G-100%);60(C-35%,T-81%);65(C-0%,G-2%,A-98%);67(A-35%,T-81%);71(C-40%,G-60%);75(G-2%,T-98%);80(C-1%,G-100%);84(G-2%,A-98%);86(C-98%,T-2%);93(A-0%,G-1%,T-99%);94(A-35%,G-79%,T-3%);95(A-1%,T-100%);96(C-1%,T-100%);98(A-2%,G-98%);99(G-2%,A-98%);101(A-1%,G-100%);105(A-1%,C-98%,T-0%);106(A-1%,G-100%);108(G-0%,A-100%);110(G-1%,T-60%);112(G-1%,T-99%);119(C-98%,T-18%);124(A-2%,G-98%);125(C-100%,T-0%);126(A-1%,G-100%);153(G-38%,A-63%);155(A-40%,C-61%);157(A-2%,G-98%);162(G-0%,A-100%);166(G-1%,T-99%);168(A-40%,G-60%);171(G-0%,T-99%);173(A-1%,G-98%);179(G-1%,T-98%);180(G-99%,T-1%);185(A-98%,T-1%);188(G-0%,A-63%,T-1%);190(C-1%,T-99%);191(G-0%,A-100%);194(C-2%,G-38%,T-61%);198(A-38%,G-63%);206(C-99%,T-1%);211(A-2%,G-98%);214(A-3%,G-100%);	G;A;G; T;A;T;G ;T;G;A; C;T;G;T ;T;G;A; G;C;G; A;T;T;C ;G;C;G; A;C;G; A;T;G;T ;G;T;G; A;A;T; A;T;G; C;G;G	G;A;G; T;A;T;G ;T;G;A; C;T;G;T ;T;G;A; G;C;G; A;T;T;C ;G;C;G; A;C;G; A;T;G;T ;G;T;G; A;A;T; A;T;G; C;G;G
AMPL16 90418	scaffold9	CAAAAGT CTGGTGG TATGGGA ATG	ATTGTTA AGCCTTA AAAGTCG TCGC	40(C-100%,T-0%);48(C-1%,T-100%);54(C-2%,T-98%);55(C-0%,T-100%);60(C-2%,G-98%);63(A-0%,T-100%);66(C-1%,T-100%);69(C-0%,T-100%);87(C-100%,T-1%);99(A-2%,G-100%);105(C-1%,G-0%,A-100%);108(A-3%,G-100%);111(C-98%,T-2%);121(A-0%,C-1%,G-99%);122(C-1%,T-100%);124(C-0%,T-100%);126(C-100%,T-0%);129(G-0%,A-100%);130(A-1%,C-0%,T-99%);131(C-13%,T-95%);132(C-99%,T-1%);136(C-47%,T-68%);137(C-0%,T-100%);138(C-100%,T-0%);139(C-2%,T-100%);140(C-100%,T-1%);141(A-5%,G-100%);142(G-0%,A-100%);143(G-8%,A-	C;T;T;T ;G;T;T; T;C;G; A;G;C; G;T;T;C ;A;T;T; C;T;T;C ;T;C;G; A;A;T; C;C;T;C ;G;T;A; T;G;T;C ;T;T;C; C;C;T	C;T;T;T ;G;T;T; T;C;G; A;G;C; G;T;T;C ;A;T;T; C;C/-;T; C;T;C;G ;A;A;C/ T;C;C;T ;C;G;C/ T;A;T;G ;T;C;T; T;C;C;C

				97%);146(C-19%,T-92%);148(C-100%,T-0%);152(G-0%,C-100%);153(C-0%,T-100%);156(C-99%,T-1%);157(G-100%,T-0%);159(C-27%,T-92%);160(G-0%,A-99%,T-2%);161(C-0%,T-100%);162(C-0%,G-100%);163(C-0%,T-100%);164(A-1%,C-100%);166(C-0%,T-100%);167(C-0%,T-100%);168(A-1%,C-98%,T-2%);169(C-100%,T-0%);182(C-100%,T-1%);185(A-18%,T-96%);		;A/T
AMPL16 90419	scaffold10	CTCGACG TGGTAGA TGAGCC	CCCGAGA GTAGCGC AGATTAT G	39(G-98%,T-2%);42(C-0%,G-100%);50(G-3%,A-98%);54(A-1%,G-100%);57(C-100%,T-0%);63(A-0%,T-100%);66(A-0%,G-100%);72(A-3%,T-100%);75(A-4%,G-96%);87(A-1%,G-99%);92(G-0%,A-100%);96(C-1%,T-99%);98(C-100%,T-0%);104(C-0%,T-100%);106(A-0%,G-100%);111(C-1%,G-99%);112(G-1%,C-99%,T-0%);114(G-1%,A-99%);117(G-26%,A-90%);128(G-18%,T-96%);132(A-22%,T-94%);141(A-0%,G-100%);153(G-100%,T-0%);156(A-1%,G-100%);165(G-1%,A-99%);168(A-0%,G-100%);171(C-99%,T-1%);177(A-0%,G-100%);183(G-0%,C-100%);186(A-93%,G-21%);197(C-2%,G-100%);200(A-1%,G-100%);201(A-90%,G-30%);204(G-9%,A-98%);210(A-1%,G-99%);211(C-100%,T-11%);234(C-94%,T-26%);	G;G;A; G;C;T; G;T;G; G;A;T; C;T;G; G;C;A; A;T;T;G ;G;G;A; G;C;G; C;A;G; G;A;A; G;C;C	G;G;A; G;C;T; G;T;G; G;A;T; C;T;G; G;C;A; A;G;T;T /A;G;G; G;A;G; C;G;C; G/A;G; G;A/G; A;G;C; C/T
AMPL16 90422	scaffold2	CTTGCTG TTGTTGT TCATGAA ATCG	AAATTGC TAAGACT GTGCTTG TACG	38(C-0%,T-100%);39(A-2%,G-100%);41(G-2%,A-98%);42(C-96%,T-4%);43(G-1%,A-100%);44(C-4%,A-99%);51(G-4%,A-98%);52(A-94%,C-1%,G-24%);53(C-9%,G-95%,T-6%);56(C-1%,T-100%);57(C-90%,T-27%);58(C-4%,T-99%);59(C-97%,T-2%);60(C-1%,G-4%,A-98%);61(G-1%,A-99%);62(C-87%,G-1%,A-30%);63(A-1%,G-99%);64(G-0%,A-98%,T-3%);65(G-2%,C-98%,T-1%);66(A-5%,G-89%,T-24%);67(A-5%,G-97%);68(G-2%,A-99%);69(G-2%,C-96%,T-1%);70(A-2%,C-23%,T-92%);71(A-1%,C-97%,T-4%);73(G-1%,A-99%);74(A-91%,C-26%);75(C-2%,A-29%,T-88%);78(C-29%,T-88%);82(G-88%,C-29%);96(G-7%,A-95%);99(C-29%,T-89%);102(C-100%,T-0%);108(A-2%,G-89%,C-26%,T-2%);114(A-0%,G-100%);117(G-0%,A-100%);120(A-0%,G-100%);132(A-2%,G-99%);135(A-0%,G-100%);147(C-98%,T-3%);150(G-1%,C-100%,T-5%);152(C-100%,T-1%);153(C-95%,T-10%);157(G-0%,C-100%);158(A-0%,C-100%);162(G-91%,A-22%);168(A-5%,G-97%,T-2%);174(A-3%,G-98%);176(A-3%,G-98%);177(C-99%,T-1%);179(C-2%,G-98%,T-4%);180(C-2%,G-3%,A-96%);181(A-0%,G-3%,C-98%);182(A-0%,G-100%);184(G-2%,C-98%,T-1%);185(G-1%,A-99%);189(C-100%,T-0%);191(A-1%,G-99%);193(G-94%,A-17%);200(G-5%,A-19%,T-91%);202(A-93%,C-2%,G-2%,T-18%);203(A-92%,G-2%,T-19%);207(G-2%,A-98%);	T;G;A; C;A;A; A;A;G; T;C;T;C ;A;A;C; G;A;C; G;G;A; C;T;C;A ;A;T;T; C;G;T; A;G;G; G;C;C; C;C;C;C ;G;G;G; G;C;G; A;C;G; C;A;G; G;G;T; A;A;A	T;G;A; C;A;A; A;G/A; G;T;T/C ;T;C;A; A;C/A; G;A;C; T/G;G; A;C;C/T ;C;A;C/ A;T/A;T /C;C/G; A;C/T;C ;C/G;G; A;G;G; G;C;C; C;C;C;C A;G;G; G;A;C; G;C;A; C;G;A/ G;T/A;T /A;A/T; A
AMPL16 90423	scaffold15	TTCAAGA CCAATGCT GTAAGTT TGTC	AATGCAC AGGATAG AGGAGAT AGAG	43(C-98%,T-2%);46(G-84%,T-20%);63(C-98%,T-5%);99(C-64%,T-83%);108(C-91%,T-14%);121(C-100%,T-0%);	C;G;C; C/T;C;C	C;T;C;C ;T;C

AMPL16 90424	scaffold2	CAGACAG GAAAAAC AGCAATA TGGA	GATAGCC TTTTCAA ACTTCGT TCGC	39(C-19%,T-93%);47(C-0%,T-100%);49(G-100%,T-0%);53(C-0%,T-100%);54(A-19%,G-93%);62(C-12%,A-97%);64(C-99%,T-4%);70(C-100%,T-0%);71(C-0%,G-12%,A-97%);73(C-1%,A-100%);96(C-60%,G-56%);111(C-99%,T-1%);112(C-1%,T-99%);114(G-19%,A-93%);120(A-10%,G-97%);162(A-16%,G-95%);178(G-16%,T-95%);181(C-3%,T-99%);182(A-95%,T-16%);185(C-16%,T-95%);186(G-16%,C-95%,T-1%);	T;T;G;T ;G;A;C; C;A;A; C;C;T;A ;G;G;T; T;A;T;C	T;T;G;T ;G;A;C; C;A;A; G;C;T; A;G;G; T;T;A;T ;C
AMPL16 90425	scaffold4	CAATTGT AAAGATA GTTGCGC AAGG	CGTCGTA ATACTCT GGATAGT CCTC	74(G-94%,A-25%);105(C-25%,T-94%);106(C-94%,T-25%);107(C-100%,T-1%);111(C-100%,T-7%);123(C-72%,T-85%);129(A-49%,G-95%);130(A-1%,C-24%,T-94%);141(A-94%,G-25%);159(C-1%,T-100%);186(G-94%,C-24%);	G;T;C;C ;C;T/C; A/G;T; A;T;G	G/A;T/ C;T/C;C ;C;C/T; G;T/C; A/G;T; C/G
AMPL16 90426	scaffold15	TAGGGCT ACGGAAA ATGCTGT GATA	CATAAAA CTCGAAA TGCTGGG AAGT	43(C-99%,T-1%);48(C-23%,T-94%);52(A-1%,G-99%);54(A-94%,C-92%);59(A-0%,G-100%);61(C-100%,T-83%);62(C-83%,A-100%);76(G-83%,T-100%);77(A-0%,G-100%);78(C-83%,T-100%);82(C-94%,T-43%);89(C-94%,T-23%);90(C-99%,T-1%);100(A-93%,G-93%);101(A-93%,T-93%);106(A-23%,T-94%);116(C-0%,G-100%);119(A-23%,T-94%);121(G-94%,A-23%);125(A-84%,G-99%);126(C-94%,T-23%);135(G-94%,A-22%);136(G-94%,A-22%);156(A-1%,G-99%);160(G-100%,T-0%);161(C-86%,G-100%);163(G-43%,T-94%);173(A-83%,G-100%);184(G-100%,T-0%);197(G-1%,T-99%);201(C-100%,T-0%);204(A-1%,G-100%);205(G-0%,C-100%);207(G-1%,A-92%,T-94%);214(G-1%,A-99%);215(A-0%,G-100%);217(A-22%,T-84%);218(C-2%,A-22%,T-83%);	C;T;G; A/C;G; T/C;C/A ;G/T;G; C/T;T/C ;C;C;A/ G;A/T;T ;G;T;G; A/G;C; G;G;G; G;C/G; T/G;G/ A;G;T; C;G;C;T /A;A;G; T/-;T/-	C;T/C;G ;A/C;G; C/T;C/A ;T/G;G; T/C;C;T /C;C;G/ A;T/A;T /A;G;A/ T;A/G; A/G;C/ T;G/A; G/A;G; G;C/G; T;A/G; G;T;C; G;C;A/ T;A;G; A/- /T;T/-A
AMPL16 90427	scaffold11	CAAGTCT TCAAGAG CTGTACG C	GTCCCTT GAAAGAT CCTTACC AGAA	46(C-100%,T-0%);52(A-90%,C-25%);76(C-25%,T-90%);81(G-0%,C-100%);85(A-2%,C-100%);97(C-25%,T-90%);105(A-0%,C-100%);117(A-3%,G-100%);122(A-91%,G-25%);124(C-90%,A-25%);133(G-0%,C-100%);138(C-100%,T-3%);148(G-0%,A-100%);149(C-100%,T-0%);156(G-90%,A-25%);158(A-0%,G-100%);	C;A;T;C ;C;T;C; G;A;C; C;C;A; C;G;G	C;A/C;T /C;C;C; T/C;C;G ;G/A;A/ C;C;C; A;C;A/ G;G
AMPL16 90428	scaffold4	ATGGCTG TTGAGGA AGTTAGA ATTT	CGAGGAA GATGAGT GTTACAT CGAT	54(C-99%,T-3%);58(C-100%,T-0%);60(C-0%,T-100%);61(A-0%,G-100%,T-42%);64(G-0%,A-100%);67(G-1%,A-100%);70(A-1%,G-99%);73(C-1%,T-100%);74(A-0%,G-100%);90(G-0%,A-100%,T-0%);95(G-98%,T-2%);97(A-2%,G-0%,T-98%);100(A-0%,G-2%,T-98%);103(G-93%,T-63%);104(C-5%,G-42%,T-97%);105(A-1%,C-100%);108(C-2%,T-99%);109(G-100%,T-1%);110(A-0%,G-100%);113(G-1%,A-99%);114(A-98%,T-2%);115(C-1%,T-100%);118(G-2%,T-98%);119(A-94%,G-61%,T-0%);120(C-0%,G-1%,A-99%);122(A-2%,G-99%);124(C-43%,T-100%);125(G-0%,A-100%);126(A-0%,G-100%);127(G-1%,A-100%);128(C-1%,A-100%);136(C-91%,T-61%);139(G-42%,A-100%);140(A-2%,G-100%);141(C-42%,T-100%);147(C-2%,G-98%);148(C-100%,T-1%);151(G-2%,C-98%);152(G-43%,A-	C;C;T;T /G;A;A; G;T;G; A;G;T;T ;G/T;T/ G;C;T; G;G;A; A;T;T;G /A;A;G; C/T;A; G;A;A; C/T;G/ A;G;C/ T;G;C;A ;G/A;A; G;T/C;C ;G;A/C; T;C;T;G ;A;G;C;	C;C;T;G ;A;A;G; T;G;A; G;T;T;T /G;T;C; T;G;G; A;A;T;T /A/G;A; G;T;A; G;A;A; C/T;A; G;T;G; C;C;A; A;G;T; C;G;C;T ;C;T;G; A;G;C; G;C;T;C ;A

				100%);160(G-6%,A-99%);164(A-6%,G-99%);165(C-55%,T-95%);167(C-98%,T-2%);169(A-3%,C-0%,G-98%);173(A-49%,G-0%,C-97%);178(C-5%,T-99%);180(C-99%,T-5%);187(C-0%,T-100%);188(A-4%,G-99%,T-0%);194(G-0%,A-100%);196(A-1%,G-100%);200(C-100%,T-1%);202(A-0%,G-99%,T-1%);204(G-0%,C-100%);208(G-2%,T-98%);210(A-2%,C-98%);211(G-6%,A-99%);	G;C;T;C; ;A	
AMPL16 90429	scaffold1	CCCTTCT TGAACAC TTTGAGA CGAA	CATCAAG ATCGAGG AATATAG CACG	36(G-97%,A-17%);38(C-1%,T-100%);41(C-94%,T-80%);45(A-78%,G-96%);49(C-16%,T-97%);54(A-1%,G-100%);69(G-14%,A-98%);77(A-89%,G-92%);78(A-99%,T-12%);92(C-1%,G-100%);95(C-100%,T-0%);102(C-99%,T-3%);110(C-100%,T-1%);115(A-40%,C-96%);129(G-46%,A-95%);196(A-0%,G-100%);198(A-2%,G-100%);199(G-1%,C-100%);201(A-1%,G-100%);212(G-2%,A-100%);215(A-2%,G-100%);	G;T;T/C; ;G/A;T; G;A;G/ A;A;G; C;C;C; A/C;G/ A;G;G; C;G;A; G	A/G;T; C/T;G/ A;C/T; G;A;G/ A;A;G; C;C;C;C ;A;G;G; C;G;A; G
AMPL16 90432	scaffold10	GGAGAAG GATTCGT TGGAGGA TAAC	AAGTAGT GAGTGAG AGGAATA GAGC	64(C-8%,A-96%);66(C-2%,T-100%);71(G-2%,C-100%);103(G-1%,A-100%);135(C-100%,T-0%);174(C-0%,G-16%);182(C-14%,T-2%);184(G-10%,A-9%);192(C-95%,T-12%);200(C-12%,T-95%);	A;T;C; A;C;-;-; ;C;T	A;T;C; A;C;-;-; ;C;T
AMPL16 90433	scaffold14	GACTTTG AATATGG TTGACGA GCAG	ACCCAAA GAGAAAC AACATAC ACTG	43(G-2%,T-100%);48(G-92%,T-21%);52(A-14%,T-95%);60(C-97%,T-9%);65(C-1%,T-99%);66(C-3%,A-100%);68(G-1%,A-99%);71(C-22%,T-92%);74(C-3%,T-100%);77(G-6%,A-96%);83(C-1%,G-99%);89(A-4%,C-100%);95(C-24%,T-91%);98(A-96%,G-10%);104(G-100%,T-0%);107(C-97%,T-10%);110(A-3%,C-100%);119(A-1%,T-100%);122(A-1%,G-0%,T-99%);125(C-100%,T-1%);131(C-0%,G-100%);137(C-0%,T-100%);143(C-0%,G-100%);147(C-98%,T-3%);149(G-95%,C-16%);170(C-96%,T-13%);176(C-1%,T-99%);194(C-0%,T-100%);203(A-1%,C-11%,T-95%);	T;G;T;C; ;T;A;A; T;T;A;G; ;C;T;A; G;C;C;T ;T;C;G; T;G;C; G;C;T;T ;T	T;G;T;C; ;T;A;A; T;T;A;G; ;C;T;A; G;C;C;T ;T;C;G; T;G;C; G;C;T;T ;T
AMPL16 90434	scaffold2	ATGGTTT TGTGTAG AGTTATT GCCG	CCTAGTG AACACCA GACAATG AGAT	39(G-0%,T-100%);42(C-3%,T-100%);51(C-99%,T-1%);58(A-1%,G-99%);59(G-99%,T-1%);61(C-0%,T-100%);64(C-99%,T-2%);67(A-1%,T-99%);68(G-99%,T-1%);70(A-0%,G-98%,T-1%);72(C-99%,T-3%);76(C-0%,G-91%,T-20%);81(A-0%,C-98%);82(G-1%,A-99%);83(C-91%,G-21%);89(C-5%,G-20%);92(C-0%,T-24%);93(C-24%,T-0%);98(C-1%,T-100%);99(A-3%,G-100%);100(G-2%,A-98%);103(G-93%,A-20%);107(G-100%,T-0%);110(C-89%,T-32%);112(C-0%,T-100%);116(C-1%,T-99%);131(C-100%,T-0%);137(A-0%,G-100%);140(C-100%,T-0%);164(A-0%,G-100%);173(C-1%,T-99%);176(C-1%,T-99%);183(A-1%,C-99%);194(G-24%,T-90%);196(C-0%,G-100%);198(A-1%,G-100%);200(A-1%,G-99%);201(C-0%,T-100%);204(C-1%,T-99%);205(A-1%,C-1%,G-99%);209(G-8%,T-97%);211(A-99%,T-1%);212(C-97%,T-	T;T;C;G; ;G;T;C; T;G;G; C;G;C; A;C;-;-; ;T;G;A; G;G;C; T;T;C;G; ;C;G;T; T;C;T;G; ;G;G;T; T;G;T;A; ;C;G	T;T;C;G; ;G;T;C; T;G;G; C;T/G;C ;A;C/G; -/G;T/-; /C;T;G; A;G/A; G;T/C;T ;T;C;G; C;G;T;T ;C;G/T; G;G;G; T;T;G;T ;A;C;G

				8%);213(A-1%,G-99%);		
AMPL16 90438	scaffold11	GGATCTT TAATGAC TGGGAGA CGC	GAGCCAC CACCATT CGAGAAT ATC	35(A-0%,G-100%);39(C-1%,A-100%);45(C-56%,T-100%);66(C-90%,T-26%);74(C-100%,T-0%);98(G-0%,T-100%);117(A-1%,G-99%,T-1%);123(A-1%,G-99%);126(A-3%,G-99%);129(G-3%,A-100%);132(C-6%,T-100%);156(A-93%,G-25%);159(A-0%,C-100%);161(A-1%,G-100%);165(C-100%,T-3%);171(C-100%,T-0%);173(G-0%,A-100%);180(A-1%,G-100%);189(A-0%,C-100%);195(C-90%,T-72%);	G;A;T; C;C;T;G ;G;G;A; T;A;C; G;C;C; A;G;C; C	G;A;T;T /C;C;T; G;G;G; A;T;G/ A;C;G; C;C;A; G;C;C/T
AMPL16 90440	scaffold1	ACCATTG AAGAAAG TAAAACT GCGT	GCTCGCA TGTAGTG TTATCAT AGTG	37(A-0%,G-97%);38(G-1%,C-70%,T-76%);39(C-70%,T-76%);57(A-96%,T-2%);60(A-44%,C-2%,G-91%);65(A-2%,G-99%);67(A-2%,G-99%);69(C-96%,T-7%);70(A-0%,G-100%);79(A-100%,T-0%);80(A-2%,G-98%);85(C-14%,T-99%);98(A-2%,G-98%);112(G-98%,T-2%);122(A-2%,C-98%);125(A-7%,C-100%,T-1%);131(G-1%,T-100%);	G;T/C;T /C;A;A/ G;G;G; C;G;A; G;T;G; G;C;C;T	G;C/T;T /C;A;G; G;G;C; G;A;G; T/C;G; G;C;C;T
AMPL16 90441	scaffold4	CACCTTG TTGGAGA CAGGTAG AG	GAATGAT ATACTCT TGACTTG CCGC	38(G-7%,A-100%);54(C-21%,T-93%);62(G-82%,C-75%);83(A-0%,T-100%);85(G-0%,T-100%);110(A-24%,T-91%);121(A-91%,G-24%);127(G-18%,T-97%);140(C-0%,G-91%,T-24%);148(G-24%,T-91%);149(G-91%,A-24%);150(C-3%,G-100%);151(C-91%,A-24%);153(G-97%,A-18%);179(G-0%,A-100%);180(A-0%,G-100%);183(G-91%,A-24%);186(A-91%,G-24%);187(C-1%,A-99%);188(A-91%,G-0%,T-24%);191(C-99%,T-4%);193(G-100%,T-0%);214(C-3%,T-24%);	A;T;C/ G;T;T;T ;A;T;G; T;G;G; C;G;A; G;G;A; A;A;C; G;-	A;C/T; G/C;T;T ;T/A;A/ G;G/T; G/T;G/T ;G/A;G; C/A;A/ G;A;G; A/G;G/ A;A;T/ A;C;G;- /T
AMPL16 90442	scaffold1	GGAGAAA GAACATT TGATCCT GCTT	GCCTGAA ATTTCAA CGTGGCT ATAT	48(A-0%,G-100%);57(G-0%,A-100%);62(C-87%,G-62%);65(G-0%,T-100%);73(A-0%,G-61%);74(G-0%,A-61%);75(C-0%,T-61%);81(G-0%,A-61%,T-0%);92(G-0%,C-100%);93(A-87%,G-62%);103(C-87%,G-62%);107(G-0%,C-100%);123(C-87%,T-14%);136(G-87%,T-62%);137(C-88%,G-61%,T-0%);145(A-0%,G-100%);155(G-0%,A-100%);	G;A;G/ C;T;- /G;- /A;T/-;A /-;C;G/ A;G/C; C;C/T;G /T;G/C; G;A	G;A;G/ C;T;G/-; A/-;-/T;- /A;C;A/ G;C/G; C;C/T;T /G;C/G; G;A
AMPL16 90443	scaffold11	GATGCTG GGAGTGG GATCAG	ACAATCT TGTGTCT ACCCATT TTGT	40(C-99%,T-9%);45(C-100%,T-0%);46(G-0%,A-100%);59(A-0%,G-98%);64(C-98%,T-1%);68(C-93%,T-18%);70(C-0%,T-96%);71(C-3%,A-96%);72(A-2%,T-98%);74(C-99%,T-0%);78(C-99%,T-14%);81(C-2%,G-94%,T-11%);83(C-98%,T-2%);87(A-0%,G-100%);88(A-2%,C-1%,G-98%);92(C-0%,G-100%);93(G-1%,T-100%);95(C-2%,T-96%);105(C-2%,T-98%);106(C-2%,T-100%);120(G-99%,T-1%);121(C-100%,T-0%);130(C-0%,T-100%);131(A-2%,G-98%);153(A-99%,T-5%);155(G-5%,T-96%);158(C-0%,T-100%);159(A-86%,G-34%);161(C-2%,A-14%,T-96%);162(C-2%,T-	C;C;A; G;C;C;T ;A;T;C; C;G;C; G;G;G; T;T;T;T ;G;C;T; G;A;T;T ;A;T;T;- C;T;C; A;C;G; T;G	T/C;C;A ;G;C;T/ C;T;A;T ;C;C;G; C;G;G; G;T;T;T ;T;G;C; T;G;A;T ;T;G/A; A/T;T;- /T;C;T; C;A;C; G;T;G

				99%);165(C-2%,T-16%);171(C-99%,T-1%);172(G-2%,T-98%);173(A-0%,C-100%);176(A-98%,T-2%);177(G-2%,C-96%,T-5%);178(A-0%,G-100%);181(C-0%,T-100%);183(A-3%,C-1%,G-97%);		
AMPL16 90446	scaffold3	CTTGACG GCTTCTT TGAATGT GAT	CAATTCT ATCATTA CCACACC GCAA	79(G-1%,A-100%);82(C-2%,A-98%);100(G-0%,A-100%);103(G-12%,A-98%);108(C-49%,T-66%);109(A-6%,G-99%);115(C-0%,T-100%);117(A-0%,G-100%);127(A-0%,G-100%);139(G-22%,A-97%);163(C-25%,T-94%);166(C-94%,T-25%);167(G-0%,A-100%);169(A-0%,G-100%);172(C-0%,A-100%);175(A-2%,G-98%);186(C-100%,T-0%);187(A-0%,G-100%);190(A-0%,G-100%);193(G-30%,A-89%);199(G-0%,C-100%,T-0%);207(A-0%,G-100%);	A;A;A; A;T;G;T ;G;G;A; T;C;A; G;A;G; C;G;G; A;C;G	A;A;A; A;C;G; T;G;G; A/G;T/ C;C/T;A ;G;A;G; C;G;G; G/A;C; G
AMPL16 90447	scaffold1	TCCTACA GTGGCGA ACTAAAT GTAA	CGAAGGG AGCTTTT GTCGTC	43(A-4%,G-100%);45(C-99%,T-1%);48(G-6%,C-100%);53(C-96%,T-85%);54(A-39%,G-99%);55(C-100%,T-4%);57(G-1%,A-100%);60(G-1%,A-99%);61(G-6%,A-100%);63(C-0%,T-100%);66(G-53%,A-99%);73(A-5%,G-100%);77(A-0%,G-100%);80(G-43%,A-100%);82(C-11%,T-100%);83(G-1%,A-99%);84(C-93%,T-91%);88(C-1%,G-100%);93(A-0%,G-100%);96(C-0%,G-50%,A-100%);103(C-100%,T-1%);104(G-91%,A-95%);117(G-96%,A-21%);124(A-5%,G-100%);126(A-6%,C-100%);127(A-97%,G-19%);129(C-22%,T-96%);132(A-1%,G-99%);136(A-100%,T-6%);141(C-100%,T-1%);148(A-44%,G-100%);149(G-0%,C-100%);156(G-99%,T-1%);160(G-95%,C-68%);162(A-93%,C-72%,T-0%);166(G-1%,A-99%);167(A-1%,C-99%);171(C-71%,T-94%);184(A-0%,G-100%);194(G-100%,T-1%);196(C-8%,T-99%);200(C-99%,T-1%);202(G-1%,A-99%);213(C-1%,T-100%);217(A-1%,G-99%);218(C-100%,T-43%);230(C-90%,T-95%);	G;C;C;T /C;G;C; A;A;A; T;A/G; G;G;A/ G;T;A;T /C;G;G; G/A;C; A/G;G; G;C;A; T;G;A; C;G/A; C;G;G/ C;A/C; A;C;T/C ;G;G;T; C;A;T; G;T/C;T /C	G;C;C;T /C;A/G; C;A;A; A;T;A; G;G;A; T;A;T/C ;G;G;A; C;A/G; G/A;G; C;A/G; T/C;G; A;C;G; C;G;G/ C;C/A; A;C;T/C ;G;G;T; C;A;T; G;C;T/C
AMPL16 90452	scaffold2	TAGAAGA TTAGGAC TCGGATG CTTG	TCAAGGC CAACGAG ATCAATA ACTT	39(C-97%,T-6%);48(C-80%,T-32%);51(C-23%,T-16%);52(C-0%,A-100%);53(C-0%,T-100%);66(G-6%,T-95%);80(G-1%,T-100%);86(C-100%,T-0%);87(C-0%,G-0%,A-99%,T-1%);92(C-0%,G-16%,T-94%);93(C-75%,T-35%);99(C-0%,T-100%);100(C-1%,T-99%);110(C-99%,T-3%);112(G-21%,T-89%);114(G-89%,T-17%);116(C-0%,A-100%);117(C-75%,T-35%);121(A-15%,G-90%);151(A-0%,G-35%);152(A-0%,G-85%);156(C-0%,A-100%);157(A-0%,C-94%,T-17%);161(G-0%,T-100%);164(C-35%,T-75%);186(A-1%,C-100%);191(A-0%,G-100%);196(C-1%,G-93%,A-16%);197(C-1%,T-99%);199(C-0%,T-100%);202(G-23%,A-84%);208(A-1%,C-100%);	C;C;-;A; T;T;T;C ;A;T;C; T;T;C;T ;G;A;C; G;-;G;A ;C;T;T; C;G;G; T;T;A;C	C;C/T;- /T;A;T; T;T;C;A ;G/T;T/ C;T;T;C ;T/G;T/ G;A;C/ T;G;- /G;G;A; T/C;T;T /C;C;G; A/G;T;T ;A;C

AMPL16 90457	scaffold5	CTTTCTG GATGATA TTGATGG CGAC	CTCGTGA ACTCTCC CAAATCG AG	36(C-100%,T-0%);59(G-1%,A-100%);77(C-1%,T-100%);84(G-90%,C-31%);85(G-100%,T-2%);87(A-100%,T-2%);95(G-0%,A-100%);96(C-100%,T-0%);103(C-93%,A-29%);105(C-29%,T-93%);111(A-9%,T-98%);119(G-2%,A-100%);121(C-100%,T-0%);122(C-100%,T-0%);129(C-4%,A-100%);138(C-0%,T-100%);142(A-93%,G-29%);149(A-100%,T-0%);156(C-29%,T-93%);160(G-93%,A-29%);165(C-29%,T-93%);166(G-93%,T-29%);170(A-0%,C-100%);174(G-93%,C-29%,T-0%);176(C-0%,T-100%);179(A-0%,C-29%);181(A-93%,G-29%);211(C-10%,T-100%);232(C-91%,T-29%);	C;A;T; G;G;A; A;C;C;T ;T;A;C; C;A;T; A;A;T; G;T;G; C;G;T;-; A;T;C	C;A;T;C /G;G;A; A;C;A/ C;C/T;T ;A;C;C; A;T;A/ G;A;T/ C;A/G; C/T;T/G ;G;C/C; T;C/-;G/ A;T;T/C
AMPL16 90460	scaffold1	CCTTGAT CATCTTG ACAAACC TGAG	CTTCTTT GTCGTAC GACTCGT GTAT	56(A-100%,T-0%);58(G-0%,T-100%);59(A-90%,G-60%);60(A-100%,T-0%);61(C-0%,T-100%);63(A-82%,G-73%);74(A-0%,C-100%);86(G-1%,A-99%);92(G-2%,A-98%);101(A-0%,C-100%);104(G-99%,A-12%);107(G-1%,A-100%);113(G-0%,A-100%);119(G-2%,A-98%);122(A-2%,G-98%);125(G-1%,A-99%);128(C-100%,T-2%);129(A-0%,G-100%);140(G-0%,T-100%);152(G-0%,A-100%);153(A-9%,T-100%);158(C-100%,T-2%);164(G-82%,C-72%,T-0%);173(G-100%,T-2%);176(C-70%,T-84%);181(A-1%,G-100%);190(C-73%,T-83%);196(A-2%,C-98%);201(G-0%,A-100%);204(A-1%,G-99%);209(G-0%,A-100%);211(A-85%,G-70%);212(A-100%,T-0%);213(A-100%,T-0%);216(A-0%,G-100%);218(C-0%,T-100%);220(A-98%,T-2%);224(A-2%,G-98%);226(C-0%,T-100%);	A;T;A/ G;A;T; G/A;C; A;A;C; G;A;A; A;G;A; C;G;T; A;T;C;C /G;G;T/ C;G;T/C ;C;A;G; A;A/G; A;A;G; T;A;G;T	A;T;G/ A;A;T; G/A;C; A;A;C; G/A;A; A;A;G; A;C;G; T;A;T;C ;G/C;G; C/T;G;C /T;C;A; G;A;A/ G;A;A; T;A;A; G;T
AMPL16 90462	scaffold4	GTCTTTC GAGGACA CGATAGC A	GATTCGT TGATAGA CCATGAT ACGC	33(G-90%,A-22%);35(C-22%,T-90%);73(A-44%,G-96%);96(C-20%,T-92%);132(C-17%,T-94%);135(A-4%,G-98%);150(C-21%,T-91%);177(C-1%,G-99%);	G;T;A/ G;T;T;G ;T;G	G/A;T/ C;G;T/C ;T/C;G; T/C;G
AMPL16 90464	scaffold4	AACTCGT TGGGCAT GAAGAAT TCTA	GGACGAC TTCTGTT GACTACA TCAA	36(A-43%,T-97%);38(G-2%,T-100%);45(A-3%,G-99%);62(A-0%,G-100%);70(C-1%,G-100%);73(A-100%,T-0%);75(A-1%,G-100%);76(C-100%,T-2%);81(A-0%,C-49%,G-20%);82(C-12%,T-58%);84(G-49%,A-20%);91(G-81%,T-65%);92(A-81%,G-65%);158(C-100%,T-0%);160(G-10%,A-99%);	T/A;T;G ;G;G;A; G;C;C/-; -T;- /G;T/G; G/A;C; A	T;T;G;G ;G;A;G; C;-;-;-G ;A;C;A
AMPL16 90467	scaffold5	TTGAAGC AGTCAAG AGTTGGT CAAG	GACGCTA GGGAAAT CTTACAG TTTG	39(C-22%,T-2%);41(G-1%,A-22%,T-2%);52(A-91%,G-22%);86(A-7%,T-13%);91(A-0%,G-30%);94(C-22%,T-2%);103(G-4%,A-100%);109(G-0%,C-100%);123(A-1%,C-90%,T-23%);124(A-1%,T-100%);125(C-90%,T-23%);126(C-23%,T-90%);131(C-30%,T-89%);132(A-7%,C-99%);137(A-90%,T-23%);145(A-89%,G-23%,T-7%);160(C-90%,T-23%);162(C-99%,T-7%);166(C-89%,T-30%);177(C-7%,G-99%);178(A-89%,G-30%);181(C-99%,T-7%);183(A-2%,C-99%);188(G-11%,T-97%);200(C-98%,T-11%);	-;-A;-;-; -;A;C;C; T;C;T;T ;C;A;A; C;C;C; G;A;C; C;T;C	C/-;A/-; G/A;T/-; - /G;C/-; A;C;C/T ;T;C/T; T/C;C/T ;C;T/A; A/G;C/ T;C;T/C ;G;G/A; C;C;G/T ;C

AMPL16 90468	scaffold11	TTGATTT CTGGTGC ATTCCTT ATGG	CAGCGGA ATGTCTT ATCAACG AAAT	49(C-0%,G-2%,A-99%);51(C-0%,G-100%);52(C-0%,A-99%,T-0%);55(G-2%,C-99%);56(A-5%,G-100%);57(A-1%,G-100%);60(A-0%,C-100%,T-0%);63(G-99%,T-1%);73(C-10%,T-97%);75(C-100%,T-0%);76(A-5%,C-1%,G-99%,T-0%);77(C-100%,T-0%);81(G-0%,A-100%);84(C-1%,T-99%);87(C-0%,T-100%);90(C-96%,T-23%);105(C-0%,T-100%);108(A-92%,G-28%,T-0%);120(C-99%,T-2%);134(C-100%,T-5%);137(A-1%,C-0%,G-99%);138(G-0%,A-100%);142(C-100%,T-0%);143(A-99%,T-0%);144(C-99%,T-2%);145(C-99%,T-2%);146(C-0%,G-89%,T-30%);147(G-1%,A-99%);151(C-94%,T-26%);152(A-0%,G-100%);154(C-0%,T-100%);155(C-13%,T-98%);157(C-0%,T-100%);158(C-99%,T-0%);	A;G;A; C;G;G; C;G;T;C ;G;C;A; T;T;C;T ;A;C;C; G;A;C; A;C;C; G;A;C; G;T;T;T ;C	A;G;A; C;G;G; C;G;T;C ;G;C;A; T;T;C/T ;T;G/A; C;C;G; A;C;A; C;C;G/T ;A;T/C; G;T;C/T ;T;C
AMPL16 90469	scaffold12	ACAAACA TACAGAG ACAAGAG GGAA	GCACGAA GATAATC AGAGGTA GGAT	39(C-64%,T-81%);57(C-64%,T-1%);61(G-65%,T-3%);67(A-1%,G-99%);77(A-4%,G-99%);88(C-48%,T-91%);89(A-4%,C-0%,G-97%);105(G-1%,A-99%);113(G-97%,A-9%);115(A-97%,G-9%);119(G-97%,T-9%);140(C-99%,T-2%);	C/T;- /C;G/-; G;G;C/ T;G;A; G;A;G; C	C/T;- /C;- /G;G;G; T;G;A; A/G;G/ A;G/T; C
AMPL16 90472	scaffold12	CTCTTCG TCGTCTG CATCATC ATC	ATCTCAA ACTATCG GATAGAC TCGC	48(A-0%,T-100%);81(G-0%,T-100%);82(G-0%,A-100%);84(G-0%,A-100%);85(C-0%,T-100%);90(C-100%,T-0%);95(C-51%,G-60%);96(A-1%,G-99%);98(C-99%,T-1%);104(G-1%,A-100%);105(C-96%,T-11%);107(A-1%,G-100%);108(C-0%,T-100%);109(C-100%,T-1%);111(A-0%,G-100%);115(C-100%,T-0%);116(C-0%,T-100%);121(A-100%,T-0%);126(G-1%,A-100%);127(C-1%,T-100%);136(C-3%,G-98%);137(C-99%,T-1%);147(G-1%,T-100%);156(A-1%,G-100%);163(A-0%,C-100%);166(G-28%,A-75%);167(C-100%,T-1%);168(C-0%,A-100%);170(C-0%,T-100%);172(A-1%,G-100%);174(C-100%,T-0%);175(G-91%,A-10%);190(G-0%,A-100%);	T;T;A;A ;T;C;G; G;C;A; C;G;T;C ;G;C;T; A;A;T; G;C;T; G;C;A; C;A;T; G;C;G; A	T;T;A;A ;T;C;G; G;C;A; C;G;T;C ;G;C;T; A;A;T; G;C;T; G;C;A; C;A;T; G;C;A; A
AMPL16 90473	scaffold12	TTAGCAT GCATACA AAGCATG GTAG	AAATTCT GAGTTCG AGCTTCT CTGG	36(A-1%,G-100%);37(G-0%,A-100%);51(G-4%,A-99%);56(G-100%,T-1%);59(G-0%,A-100%);65(G-1%,A-100%,T-0%);68(A-1%,G-29%);69(G-1%,T-30%);70(C-30%,T-1%);71(G-1%,C-30%);76(A-1%,G-28%);77(G-1%,A-29%);78(A-99%,T-0%);79(A-28%,T-89%);80(C-98%,T-1%);82(G-29%,T-90%);84(C-98%,T-2%);89(G-3%,T-99%);90(C-99%,T-1%);91(G-1%,A-100%);94(C-100%,T-0%);96(G-0%,A-100%);97(C-100%,T-3%);98(C-1%,G-99%);102(A-5%,G-100%);104(A-5%,T-100%);106(A-7%,T-98%);107(C-2%,T-98%);111(G-99%,T-1%);116(A-98%,T-7%);124(G-0%,A-100%);128(A-11%,G-100%);130(A-93%,C-26%);131(A-0%,G-100%,T-0%);133(G-1%,A-100%,T-7%);134(C-7%,T-100%);135(A-98%,T-7%);136(C-1%,T-100%);137(A-2%,G-98%);140(A-1%,G-100%);145(A-1%,C-1%,G-100%);149(C-3%,T-100%);150(G-8%,A-97%,T-0%);153(A-2%,C-98%);158(G-2%,A-98%);161(C-1%,T-100%);164(C-2%,G-0%,A-98%);165(C-100%,T-	G;A;A; G;A;A;- ;-;-;-; A;T;C;T ;C;T;C; A;C;A; C;G;G; T;T;T;G ;A;A;G; A;G;A; T;A;T;G ;G;G;T; A;C;A; T;A;C;C ;G;T;C; C;T;G; A;T;C;C ;C;G;G; G;G;G	G;A;A; G;A;A;- /G;-T;- /C;- /C;G/-; /A;A;A/ T;C;T/G ;C;T;C; A;C;A; C;G;G; T;T;T;G ;A;A;G; C/A;G; A;T;A;T ;G;G;G; T;A;C; A;T;A; C;C;G; G/T;C/T ;T/C;T/ G;G;A; T;C;C;C

				0%);172(C-100%,T-0%);173(A-2%,G-100%);176(G-27%,T-90%);178(C-97%,T-19%);182(C-89%,T-30%);183(C-15%,G-16%,T-91%);185(A-2%,G-98%);187(A-100%,T-0%);189(C-0%,G-5%,T-99%);197(G-0%,C-98%);198(C-100%,T-1%);199(A-2%,C-98%,T-2%);221(A-2%,G-100%);222(C-98%,T-2%);223(A-1%,G-98%,T-2%);225(A-5%,G-99%);232(A-0%,G-100%);		;G;C;G; G;G
AMPL16 90474	scaffold10	TTCTTCCT CTTGGTG ACCTTGT ATT	ACTTTCG ACTACAA CGTAGAT CGAT	36(A-0%,G-100%);38(C-100%,T-0%);42(G-6%,A-99%);45(C-1%,G-2%,A-97%);48(C-0%,G-100%);51(G-0%,A-100%);54(A-0%,C-100%);59(G-0%,C-100%,T-0%);61(C-1%,G-1%,A-99%);62(G-1%,A-99%);65(A-3%,G-100%);68(G-96%,A-12%);72(A-98%,T-4%);74(G-0%,A-100%);75(A-32%,T-86%);77(G-86%,A-31%);79(A-1%,C-4%,T-99%);80(G-0%,C-9%,T-23%);81(C-29%,T-89%);82(C-100%,T-0%);85(G-0%,A-100%,T-0%);86(C-100%,T-0%);87(A-3%,C-0%,G-100%);88(G-2%,A-100%);90(A-99%,T-4%);91(A-3%,G-100%);92(C-2%,G-3%,A-97%);93(G-10%,A-98%);95(C-1%,A-100%);96(C-9%,T-97%);98(G-0%,A-100%);99(C-100%,T-1%);100(A-0%,G-100%);101(C-1%,T-99%);105(A-1%,C-99%,T-0%);108(G-2%,A-99%);111(C-4%,G-0%,T-99%);120(G-1%,A-100%);123(G-2%,A-100%);126(G-4%,A-98%);129(C-97%,T-4%);132(A-4%,G-97%,T-1%);135(C-23%,T-90%);144(A-100%,T-1%);150(A-0%,G-100%);153(G-1%,A-99%);156(A-0%,G-100%);159(C-100%,T-1%);165(C-100%,T-0%);174(A-0%,G-100%);180(G-1%,A-99%);183(C-100%,T-0%);	G;C;A; A;G;A; C;C;A; A;G;G; A;A;T; G;T;-;T; C;A;C; G;A;A; G;A;A; A;T;A; C;G;T;C A;T;A; A;A;C; G;T;A; G;A;G; C;C;G; A;C	G;C;A; A;G;A; C;C;A; A;G;G/ A;A;A; T/A;G/ A;T;C/-; T/C;C;A ;C;G;A; A;G;A; A;A;T; A;C;G; T;C;A;T ;A;A;A; C;G;T; A;G;A; G;C;C; G;A;C
AMPL16 90475	scaffold4	TTGCTAT GCACTGT AATTTGT AGGC	GCATCTT CCAAATT ATACCAG TGCT	38(C-100%,T-2%);40(G-97%,C-16%);41(A-97%,G-16%);42(C-16%,T-97%);45(G-97%,A-16%);50(G-97%,C-16%);56(A-97%,T-16%);70(C-97%,T-13%);80(C-97%,G-16%);81(C-97%,T-16%);90(C-97%,T-16%);106(A-97%,G-16%);135(C-99%,A-15%);138(C-0%,G-100%);141(G-44%,A-96%);149(G-1%,A-100%);181(G-91%,A-27%);182(G-27%,T-91%);183(G-91%,A-27%);208(G-91%,A-27%);235(A-3%,G-100%);	C;G;A; T;G;G; A;C;C; C;C;A; C;G;G/ A;A;G; T;G;G; G	C;C/G; A/G;T/ C/A/G; G/C;A/ T;C;C/G ;T/C;T/ C;G/A; A/C;G; A;A;A/ G;G/T; A/G;G/ A;G
AMPL16 90476	scaffold5	CGAAGCA GAGATAA TGAACCT GGG	TCCAGAT TGCTCAC AATACCT ACAT	38(A-9%,G-99%,T-1%);42(G-2%,C-100%);56(G-99%,A-12%);65(G-0%,T-100%);69(A-2%,G-100%);95(A-89%,G-37%);96(A-0%,T-100%);97(C-95%,T-30%);109(C-90%,T-40%);121(G-98%,T-23%);122(A-96%,G-32%);123(C-99%,T-12%);145(C-100%,T-3%);156(G-91%,C-37%);172(C-97%,T-15%);174(G-97%,A-15%);212(G-15%,T-99%);225(G-5%,C-31%);226(C-0%,T-100%);227(C-97%,G-29%);228(A-100%,T-1%);229(A-87%,G-41%);	G;C;G; T;G;A;T ;C;C;G; A;C;C; G;C;G; T;-;T;C; A;A	G;C;A/ G;T;G; G/A;T; C/T;C/T ;G/T;A/ G;C/T;C ;C/G;C/ T;A/G;T /G;- /C;T;G/ C;A;G/

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AMPL16 90477	scaffold4	CATTGTC ATTCCTT CCTGGTC AAAG	CGTAATT GTCGGAC GTGTTGT G	41(A-0%,C-8%,T-95%);50(C-100%,T-2%);53(G-8%,A-95%);59(C-0%,T-100%);62(C-8%,G-95%,T-0%);68(C-92%,T-29%);71(A-0%,G-100%);74(C-6%,T-96%);83(A-0%,G-100%);89(C-100%,T-0%);92(C-0%,T-100%);96(A-0%,C-100%);98(C-91%,A-28%,T-2%);101(C-100%,T-0%);116(C-0%,T-100%);119(A-2%,C-100%);122(C-95%,T-25%);128(C-100%,T-0%);146(A-1%,G-100%);149(C-5%,T-96%);158(A-3%,G-99%,T-1%);161(A-0%,G-100%);164(C-2%,T-100%);178(C-2%,T-98%);179(A-100%,T-0%);184(C-31%,T-90%);186(C-0%,T-100%);189(A-96%,T-4%);190(A-77%,G-77%,T-0%);191(G-5%,T-98%);193(A-0%,G-100%);194(C-100%,T-0%);202(C-100%,T-2%);203(G-98%,T-2%);204(C-95%,T-8%);205(C-5%,G-98%);207(G-53%,A-28%);210(A-86%,G-35%);215(A-0%,C-98%,T-5%);216(A-0%,G-100%);218(C-41%,A-35%,T-80%);219(A-86%,C-8%,T-28%);229(C-25%,T-95%);232(C-100%,T-0%);235(C-96%,T-24%);	T;C;A;T ;G;C;G; T;G;C;T ;C;C;C; T;C;C;C ;G;T;G; G;T;T;A ;T;T;A; G/A;T; G;C;C; G;C;G; G/-;A;C ;G;T/C; A;T;C;C	T;C;A;T ;G;T/C; G;T;G; C;T;C;A /C;C;T; C;C/T;C ;G;T;G; G;T;T;A ;T/C;T; A;G/A; T;G;C;C ;G;C;G; A/-;A/G ;C;G;T/ A;T/A;T /C;C;C/ T
AMPL16 90478	scaffold5	GAGACGG GTTTATG TAGAAGG AAGA	GAATATT AGCTGGC GTCTGAA AGTG	80(A-1%,G-100%);87(A-90%,T-35%);89(G-98%,A-12%);111(C-90%,A-36%);112(A-1%,C-100%);113(C-95%,T-16%);116(A-100%,T-1%);117(G-1%,C-100%);125(G-1%,A-100%);127(C-1%,G-100%);130(A-2%,C-99%);134(A-1%,C-100%);141(C-100%,T-0%);153(G-92%,C-34%);154(C-0%,T-100%);165(G-1%,T-34%);167(A-0%,G-99%);171(C-22%,T-12%);175(G-34%,T-92%);177(C-92%,G-34%);182(A-1%,G-100%);186(A-98%,G-11%);187(A-15%,G-100%);194(C-0%,A-100%);226(A-100%,T-1%);227(C-0%,G-100%);	G;A;G; C;C;C; A;C;A; G;C;C; C;G;T;-; G;-;T;C; G;A;G; A;A;G	G;A/T; G/A;C/ A;C;C/T ;A;C;A; G;C;C; C;C;C;T ;-/T;G;- /C;T/G; G/C;G; A/G;G; A;A;G
AMPL16 90479	scaffold1	GGTCAAG GTGGAAG AGAAAGA CTTA	GAGGCTA CCATCAG TTTTTCAG AATG	44(A-60%,G-54%);108(C-15%,T-93%);124(C-24%,T-92%);130(C-0%,T-100%);132(G-100%,T-0%);144(A-93%,C-15%);	A;T;T;T ;G;A	G;C/T;C /T;T;G; A/C
AMPL16 90480	scaffold1	GCATCAT GATCTGA GCGTCTA TTTC	GGATGTT TCGCTTC TCCTGTT ATAC	36(G-1%,A-65%);37(A-1%,T-65%);39(C-0%,A-63%);40(C-1%,G-99%);41(C-1%,T-99%);42(A-0%,C-99%);43(C-7%,T-99%);49(A-1%,G-54%,T-14%);52(A-2%,G-99%);72(C-100%,T-2%);88(A-1%,G-99%);97(G-42%,A-96%);100(G-92%,A-27%);108(C-99%,T-10%);112(A-99%,T-4%);115(C-6%,G-10%,T-97%);120(A-2%,G-99%);124(G-10%,A-99%);125(A-84%,G-70%);133(G-7%,A-97%,T-4%);135(C-53%,A-94%);139(G-0%,A-100%);141(C-99%,A-12%);142(G-4%,A-99%);151(C-0%,T-100%);158(C-0%,T-100%);169(C-70%,T-84%);176(G-5%,C-100%);193(A-97%,G-21%);	A/-;T/-; A/-;G;T; C;T;G/-; G;C;G; A/G;G; C;A;T; G;A;G/ A;A;A/ C;A;C; A;T;T;C /T;C;A	A/-;- /T;A/-;G ;T;C;T;- /G;G;C; G;A;A/ G;C;A; T;G;A; G/A;A; A;A;A/ C;A;T;T ;C/T;C; G/A

AMPL16 90483	scaffold1	GCTGAGA CAAGTTC GTCGTGA	AGGACAA CCTCAGA CAACGAC	32(A-10%,C-2%,G-2%,T-94%);35(A-83%,C-33%);41(C-2%,T-98%);44(C-45%,T-91%);47(C-49%,T-91%);50(C-95%,T-11%);53(C-98%,T-3%);56(C-58%,T-88%);59(G-88%,A-24%,T-1%);62(G-1%,A-100%);65(C-100%,T-1%);71(G-1%,A-99%);74(A-91%,G-25%);77(G-2%,C-97%,T-1%);80(C-44%,G-6%,A-89%,T-2%);83(C-1%,T-100%);92(A-95%,T-5%);95(A-2%,G-98%);113(C-100%,T-0%);116(C-100%,T-0%);125(G-1%,A-99%);128(A-2%,G-98%);140(A-9%,G-95%);143(C-99%,T-1%);152(G-100%,T-0%);155(G-0%,A-100%);158(C-2%,T-98%);161(G-74%,A-74%);173(A-1%,G-100%);182(A-5%,G-96%);	T;A;T;C /T;C/T; C;C;T/C ;G;A;C; A;A;C; C/A;T; A;G;C; C;A;G; G;C;G; A;T;G/ A;G;G	T;A/C;T ;T;T;C; C;T/C;A /G;A;C; A;G/A; C;A;T; A;G;C; C;A;G; G;C;G; A;T;A/ G;G;G
AMPL16 90485	scaffold5	CATCACT ATTCAAC TTTCACT GCCA	CTGGAAG GTCCTGT AGATCAT TCAT	40(C-100%,T-0%);42(G-37%,T-81%);44(C-0%,T-100%);84(C-82%,A-35%);88(A-3%,G-99%);89(C-84%,A-33%);100(G-84%,A-33%);114(G-1%,A-100%);118(A-1%,C-100%);161(G-81%,C-36%);172(A-82%,C-35%);211(A-9%,G-97%);213(C-82%,T-30%);221(G-0%,T-100%);	C;T;T;C ;G;C;G; A;C;G; A;G;C; T	C;G;T; A;G;A; A;A;C; C;C;G;T ;T
AMPL16 90487	scaffold4	ATGATTG TGATGCG ACCTATG ACTA	TCATCCT GAACACT GATTACC CATT	41(A-33%,G-76%);42(C-33%,T-76%);63(A-0%,G-93%);65(C-62%,T-39%);73(C-99%,T-3%);83(G-0%,T-100%);103(A-0%,G-100%);111(G-7%,A-98%);112(C-75%,T-34%);121(C-7%,T-98%);124(C-93%,T-8%);133(C-0%,T-100%);135(C-100%,T-0%);138(G-100%,T-0%);149(A-0%,G-100%);151(G-38%,A-70%);157(C-100%,T-0%);170(G-38%,A-73%);188(C-99%,T-3%);208(A-0%,G-100%);214(A-80%,G-28%);215(C-1%,T-99%);	G;T;G; C;C;T;G ;A;C;T; C;T;C;G ;G;A;C; A;C;G; A;T	G;T;G; C;C;T;G ;A;C;T; C;T;C;G ;G;A;C; A;C;G; G;T
AMPL16 90488	scaffold4	GGGGTAA AGGAGTA TATCATG ACCC	AATATCA GAGGAAA AGCAGCC GATC	38(G-0%,A-100%);43(A-0%,G-100%);48(G-0%,A-100%);67(C-0%,T-100%);73(C-3%,T-100%);81(A-3%,G-100%);82(C-94%,G-16%);89(G-0%,T-99%);90(G-100%,T-0%);92(C-100%,T-0%);102(C-22%,T-0%);107(G-1%,T-22%);114(G-9%,A-97%);124(A-100%,T-0%);125(A-0%,T-100%);138(A-0%,T-100%);143(A-1%,G-100%);144(G-80%,A-71%);153(G-0%,A-100%);162(A-88%,G-21%);164(C-0%,G-100%);174(G-0%,T-100%);180(A-3%,C-98%);	A;G;A; T;T;G;C ;T;G;C; ;A;A;T ;T;G;G/ A;A;A; G;T;C	A;G;A; T;T;G;G /C;T;G; C;-C;- /T;A;A; T;T;G;G /A;A;A/ G;G;T; C
AMPL16 90492	scaffold11	GCCTCAA AATTTCC TGTTCTG ACTT	GTCAACT TTCTCTTC CCCAAAG ATG	36(A-99%,T-1%);38(A-1%,G-99%);59(G-1%,A-99%);60(A-99%,T-1%);62(G-2%,C-98%);63(G-2%,A-98%);64(C-99%,T-1%);70(C-100%,T-0%);72(C-100%,T-0%);78(A-1%,T-99%);84(C-100%,T-0%);91(G-99%,T-1%);95(C-1%,A-99%);97(C-99%,T-1%);98(G-95%,A-28%);102(A-1%,C-99%);104(G-95%,A-28%);112(C-100%,T-1%);113(G-93%,A-30%);114(G-93%,A-30%);116(A-0%,G-100%);123(C-1%,G-99%);125(C-93%,G-28%,T-2%);126(G-99%,T-1%);136(C-1%,T-99%);137(A-1%,G-99%);138(C-99%,T-1%);141(A-93%,G-30%);144(C-30%,T-93%);147(C-31%,T-89%);154(G-1%,A-30%,T-93%);157(G-1%,A-100%);159(A-1%,G-99%);163(G-1%,A-100%);164(G-1%,C-100%);165(A-95%,C-28%);166(C-93%,T-30%);167(G-1%,A-100%);168(G-99%,T-1%);172(C-1%,A-99%);179(C-93%,T-	A;G;A; A;C;A; C;C;C;T ;C;G;A; C;G;C; G;C;G; G;G;G; C;G;T; G;C;A; T;T;T;A ;G;A;C; A;C;A; G;A;C; T;T;A;G ;T;T;T; A;T;G;T ;G;C;T; T	A;G;A; A;C;A; C;C;C;T ;C;G;A; C;G/A; C;G/A; C;G/A; A/G;G; G;C/G; G;T;G; C;G/A; T/C;C/T ;A/T;A; G;A;C; C/A;T/C ;A;G;A; C/T;C/T ;C/T;A; G;T;T;C

				30%);182(C-30%,T-93%);184(C-28%,T-95%);189(C-0%,A-100%);191(G-100%,T-1%);193(C-1%,T-99%);199(G-0%,T-100%);200(C-30%,T-93%);203(A-95%,T-28%);204(C-28%,T-95%);205(A-1%,G-95%,C-26%);206(C-28%,T-95%);208(G-99%,T-1%);212(C-95%,G-28%);218(C-0%,T-100%);219(C-1%,G-1%,T-99%);		/T;A/T; T/C;G/C; ;T/C;G; G/C;T;T
AMPL16 90493	scaffold1	TCCTATT ATGTTTA CAAGGGG ATGGT	ACGCGTC TAGACTA ATCATCT TACC	39(A-97%,C-23%);40(C-0%,T-99%);43(C-1%,T-100%);44(A-0%,G-99%);47(C-86%,T-68%);83(A-67%,C-0%,G-90%);123(C-100%,T-0%);127(G-0%,A-100%);135(A-1%,G-100%);	A;T;T;G ;C/T;A/ G;C;A; G	C/A;T;T ;G;C/T; G;C;A; G
AMPL16 90494	scaffold7	CCATGTA TGTTTTT CATCTTC CTCG	TAGAGGA CTCATCA GTACACG ACTA	38(C-100%,T-1%);42(C-100%,T-0%);44(C-1%,G-100%);48(C-0%,T-100%);49(C-0%,T-100%);50(A-54%,C-54%);54(G-100%,T-1%);60(G-100%,T-2%);63(G-1%,T-100%);65(A-0%,C-100%);84(G-100%,T-0%);90(C-2%,A-99%);103(C-0%,G-100%);104(A-1%,G-100%);108(A-1%,G-100%);109(C-54%,T-54%);	C;C;G;T ;T;A;G; G;T;C; G;A;G; G;G;T	C;C;G;T ;T;C;G; G;T;C; G;A;G; G;G;C
AMPL16 90495	scaffold2	AATGTCT TCTTCCT CTTCTGA CAGG	CGAACGA AGTCCGA AATAACC TTG	37(A-6%,G-100%);39(C-100%,T-0%);42(C-100%,T-1%);48(G-99%,T-1%);49(A-98%,G-22%);57(C-0%,T-100%);61(A-6%,T-100%);67(G-0%,A-100%);73(C-97%,G-16%,T-10%);79(G-6%,C-100%,T-88%);82(A-1%,G-100%,T-10%);85(A-97%,G-96%);95(C-100%,T-90%);97(C-95%,T-97%);98(G-97%,A-95%);99(C-100%,T-8%);103(A-1%,G-100%);105(C-100%,T-8%);112(G-1%,A-100%);142(A-0%,G-100%);145(A-0%,G-100%);148(G-9%,A-100%);151(C-1%,G-97%,T-16%);154(A-0%,G-100%);158(G-0%,A-100%);163(A-3%,G-100%);172(G-2%,A-100%,T-0%);177(A-0%,T-100%);178(C-100%,T-88%);	G;C;C; G;A;T;T ;A;C;C/ T;G;A/ G;C/T;C /T;A;G; C;G;C; A;G;G; A;G;G; A;G;A; T;C/T	G;C;C; G;G/A; T;T;A;C /G;T/C; G;G/A; C/T;T/C ;G/A;C; G;C;A; G;G;A; G/T;G; A;G;A; T;C/T
AMPL16 90497	scaffold14	CGGCAAT GAAGGAT AAAGTTC TTGT	AACCGAC GATAACC TAAACAA AAGC	43(C-91%,T-27%);44(G-0%,C-100%,T-1%);49(C-100%,T-0%);50(C-100%,T-1%);51(A-11%,G-96%,T-1%);57(A-1%,G-100%);58(C-100%,T-1%);62(C-16%,T-97%);63(C-99%,T-17%);64(A-12%,C-0%,G-97%);67(C-100%,T-0%);71(C-1%,T-100%);89(C-1%,T-100%);90(G-100%,T-0%);101(C-99%,T-17%);116(C-100%,T-0%);117(C-98%,T-10%);119(A-1%,G-100%);179(C-100%,T-0%);200(C-98%,T-10%);213(C-91%,A-26%,T-1%);218(C-100%,T-0%);227(C-100%,T-1%);229(A-1%,T-100%);239(C-98%,T-10%);	C;C;C;C ;G;G;C; T;C;G;C ;T;T;G; C;C;C; G;C;C; C;C;C;T ;C	C/T;C;C ;C;G;G; C;T/C;C /T;G;C; T;T;G;T /C;C;C; G;C;C; A/C;C; C;T;C
AMPL16 90499	scaffold12	CTTGTTT GATGGTG ATGTGTC ATGG	TTTGAAG CATGGGT TTGGCAC	41(A-6%,G-99%);42(G-0%,T-100%);50(A-6%,G-99%);55(G-0%,A-100%);61(C-72%,T-66%);63(C-71%,T-66%);71(A-72%,C-66%);83(A-0%,G-100%);103(G-0%,T-100%);104(C-0%,G-100%);109(A-5%,T-100%);121(C-100%,T-5%);125(A-6%,G-99%);135(A-5%,G-100%);137(C-5%,G-100%);140(A-5%,C-100%);145(G-100%,T-0%);147(C-72%,T-66%);148(A-72%,G-66%);149(C-66%,T-71%);156(G-71%,T-66%);157(G-72%,T-66%);166(C-100%,T-5%);185(C-72%,A-66%);189(C-96%,T-	G;T;G; A;T;T;C ;G;T;G; T;C;G; G;G;C; G;T;G; C;T;T;C ;A;C;G; T;G;T;G ;C;T	G;T;G; A;C/T;C /T;A/C; G;T;G;T ;C;G;G; G;C;G; T/C;G/ A;C/T; G/T;G/T ;C;A/C; T/C;G/C ;C/T;G;

				11%);193(C-72%,G-66%);202(C-70%,T-69%);203(A-0%,G-100%);205(A-0%,C-70%,T-69%);209(A-0%,G-100%);238(C-69%,T-70%);241(C-0%,T-100%);		T/C;G;C /T;T
AMPL16 90503	scaffold4	CAACAAC TGACGTA CGTCTCT TG	CACAATT GCATCCA CTCGTTT AGTA	35(A-0%,G-100%);43(C-99%,T-3%);46(C-0%,G-78%,T-0%);47(G-0%,A-77%);48(C-0%,A-100%);49(G-0%,A-100%);53(G-86%,C-77%);54(A-86%,T-77%);57(A-3%,G-27%,T-0%);58(G-77%,T-86%);61(G-100%,T-0%);66(A-50%,G-30%);68(A-3%,G-99%);70(A-3%,G-99%);71(C-99%,T-9%);73(G-50%,A-30%);74(C-1%,A-100%);78(C-0%,T-100%);79(G-86%,A-77%);80(C-95%,T-27%);94(C-96%,T-50%);95(G-0%,A-100%);97(G-83%,A-78%);100(G-100%,T-4%);101(C-100%,T-4%);104(C-27%,T-95%);109(G-50%,A-96%);122(C-0%,T-99%);134(A-7%,T-100%);135(A-0%,G-100%);138(C-90%,T-69%);	G;C;- /G;- /A;A;A; G/C;A/ T;-T/G; G;- /A;G;G; C;- /G;A;T; G/A;C; T/C;A; G/A;G; C;T;G/ A;T;T;G ;T/C	G;C;- /G;A/-; A;A;G/ C;A/T; G/-;T/G; G;G/-;G ;G;C;- /A;A;T; G/A;T/ C;C;A; G/A;G; C;T/C;A ;T;T;G; C/T
AMPL16 90508	scaffold7	TAAAGAT GCAACGG GAGAGCT AG	TCTTCAG AAGTATC CTGAGCA ATGT	43(A-6%,G-98%);57(A-97%,T-7%);66(G-0%,C-52%,T-55%);77(C-100%,T-1%);90(A-6%,C-0%,G-97%);105(C-0%,T-100%);114(A-100%,T-0%);122(C-0%,G-100%);154(A-1%,G-100%);176(G-6%,T-98%);178(A-8%,C-99%);188(C-74%,T-40%);206(G-74%,A-40%);225(A-0%,G-100%);234(G-0%,A-100%);	G;A;T; C;G;T; A;G;G; T;C;C;G ;G;A	G;A;C; C;G;T; A;G;G; T;C/A;T /C;G/A; G;A
AMPL16 90509	scaffold12	GAGGAAG TGGCATA CGAACAT TAGG	AAACAGC CGTCACA ATCATCA AG	37(A-90%,G-31%,T-0%);42(G-100%,T-0%);46(G-1%,C-100%);48(C-100%,T-1%);49(A-1%,G-100%);52(C-100%,T-0%);53(A-0%,G-100%);55(C-99%,T-4%);56(A-0%,G-100%);58(G-100%,T-0%);64(G-0%,A-100%);67(C-100%,T-0%);68(G-95%,A-17%);69(C-100%,T-1%);70(A-0%,G-100%);73(G-1%,A-100%);74(G-2%,A-98%);76(G-100%,T-0%);79(C-54%,T-62%);81(G-2%,C-98%);82(G-0%,C-100%,T-0%);85(G-0%,A-100%);92(A-0%,G-100%);93(C-100%,T-1%);94(A-0%,G-100%);95(G-8%,C-99%,T-0%);102(G-2%,T-100%);110(C-100%,T-0%);115(C-99%,T-2%);120(C-100%,T-0%);130(A-60%,G-56%);131(A-1%,G-99%);132(C-48%,T-72%);133(A-3%,G-100%);139(A-0%,G-100%);142(C-42%,T-75%);145(C-2%,T-98%);147(G-1%,T-99%);151(A-1%,G-99%);157(A-1%,G-99%);160(G-0%,T-100%);163(C-100%,T-3%);171(C-1%,T-99%);174(A-2%,T-99%);175(A-0%,G-100%);176(A-1%,G-100%);178(G-1%,A-99%);181(C-99%,T-1%);183(A-1%,G-99%);184(A-4%,G-99%);188(A-0%,G-100%);190(A-1%,G-0%,C-98%,T-1%);193(C-99%,T-1%);196(G-1%,A-99%);199(G-0%,A-100%);205(C-2%,T-98%);213(C-100%,T-0%);214(A-1%,G-99%);215(C-1%,T-99%);216(A-1%,G-99%);217(C-0%,G-0%,A-99%,T-0%);219(C-100%,T-0%);220(A-1%,G-99%);221(C-29%,T-88%);222(G-1%,T-99%);223(A-1%,G-0%,C-98%,T-0%);224(A-	A;G;C; C;G;C; G;C;G; G;A;C; G;C;G; A;A;G; T;C;C;A ;G;C;G; C;T;C;C ;C;A;G; T;G;G;T ;T;T;G; G;T;C;T ;T;G;G; A;C;G; G;G;C; C;A;A; T;C;G;T ;G;A;C; G;T;T;C ;C;C;T; A;A;T; G;G	A/G;G; C;C;G; C;G;C; G;G;A; C;A/G; C;G;A; A;G;C; C;C;A; G;C;G; C;T;C;C ;C;G;G; T/C;G; G;C/T;T ;T;G;G; T;C;T;T ;G;G;A; C;G;G; G;C;C; A;A;T; C;G;T; G;A;C; G;C/T;T ;C;C;C; T;A;A;T ;G;G

				0%,C-99%);225(C-100%,T-0%);226(A-1%,G-7%,T-98%);228(G-8%,A-99%);229(A-99%,T-0%);232(A-1%,C-7%,T-98%);233(A-0%,G-100%);238(A-6%,G-100%);		
AMPL16 90510	scaffold1	GGGCAAC AGGGTTG ATGATTA GAAT	GAGAAAT GTGGCGC AATATTA GACA	43(A-0%,C-79%,G-73%);44(C-0%,T-100%);62(A-100%,T-0%);67(C-1%,A-99%);70(A-0%,G-100%);73(G-0%,A-100%);80(C-1%,T-100%);85(C-0%,T-100%);89(C-100%,T-0%);96(G-0%,T-100%);109(A-1%,G-100%);112(A-1%,G-100%);122(G-0%,A-100%);124(A-1%,G-100%);125(A-1%,G-99%);127(A-1%,T-100%);131(A-1%,G-100%);133(C-100%,T-1%);141(A-3%,C-99%,T-4%);146(A-81%,C-67%,T-8%);149(A-3%,T-72%);152(C-21%,T-96%);155(A-3%,C-100%);158(C-1%,G-100%,T-0%);163(A-100%,T-8%);167(C-100%,T-0%);169(G-81%,T-72%);170(G-0%,C-100%,T-0%);172(C-43%,T-93%);173(C-0%,A-100%);179(G-79%,A-73%);182(G-0%,A-100%);186(C-1%,T-99%);187(A-100%,T-1%);188(C-1%,T-100%);189(C-1%,A-100%);194(G-1%,A-100%);	C/G;T; A;A;G; A;T;T;C ;T;G;G; A;G;G; T;G;C;C ;C/A;T/- ;T;C;G; A;C;G/ T;C;C/T ;A;A/G; A;T;A;T ;A;A	G/C;T; A;A;G; A;T;T;C ;T;G;G; A;G;G; T;G;C;C ;A/C;T/- ;C/T;C; G;A;C; T/G;C;T ;A;G/A; A;T;A;T ;A;A
AMPL16 90513	scaffold7	GCCAATC TTTGTA AAGTTGC ACAA	GCATCCA GCGTCCT CAAAATA TAC	37(C-100%,T-0%);39(C-0%,T-100%);40(C-100%,T-0%);41(A-8%,G-99%);42(G-8%,A-100%);44(G-8%,A-99%);46(A-0%,T-100%);50(G-8%,A-100%);51(G-8%,A-100%);52(G-8%,A-100%);53(G-66%,C-50%);62(C-68%,G-0%,T-46%);64(C-0%,T-100%);89(C-100%,T-1%);98(A-0%,G-100%);101(C-100%,T-3%);110(C-100%,T-1%);119(G-100%,T-0%);123(C-0%,G-100%);126(G-0%,T-100%);127(G-100%,T-0%);137(C-2%,A-99%);140(C-3%,T-100%);143(A-54%,C-54%);144(C-2%,A-99%);146(C-100%,T-0%);147(G-2%,T-99%);149(C-3%,T-100%);152(G-2%,A-99%);155(A-2%,C-99%);156(G-99%,T-2%);160(A-1%,C-99%,T-1%);161(A-9%,G-99%,T-2%);163(G-9%,A-100%);165(A-0%,G-2%,C-99%);169(C-100%,T-0%);170(A-0%,G-100%);176(G-0%,A-100%);182(G-99%,T-8%);185(C-94%,T-20%);188(G-20%,A-94%);	C;T;C;G ;A;A;T; A;A;A; G;C;T;C ;G;C;C; G;G;T; G;A;T; A;A;C; T;T;A;C ;G;C;G; A;C;C; G;A;G; C;A	C;T;C;G ;A/G;A; T;A/G; G/A;G/ A;G/C; T;T;C;G ;C;C;G; G;T;G; A;T;C; A;C;T;T ;A;C;G; C;G/A; G/A;C; C;G;A; G;T/C; A/G
AMPL16 90514	scaffold4	TGAAATG TCCTGAC AATAGAT CGGT	GATTCGA GAAGACT GGGATGA GGAT	45(A-0%,T-100%);49(G-0%,A-98%);55(A-100%,T-0%);56(C-91%,G-62%);57(A-94%,G-19%);66(C-100%,T-0%);118(G-46%,T-20%);119(G-88%,T-64%);127(G-91%,A-62%);129(C-0%,T-100%);134(A-0%,G-100%);171(G-93%,A-19%);173(G-0%,A-100%);181(A-93%,G-19%);197(G-100%,T-0%);206(C-93%,T-19%);	T;- /A;A;G/ C;A;C;- /G;T/G; A/G;T; G;G;A; A;G;C	T;A;A; C/G;A/ G;C;- /T;T/G; A/G;T; G;A/G; A;G/A; G;C/T

AMPL16 90523	scaffold4	GATTCTC TCCCCTG TGACGAA TC	GAAAATT CCTTTGA CATGCTT GAGC	41(A-87%,T-65%);50(G-85%,A-67%);51(G-0%,A-100%);56(G-87%,C-65%);98(A-85%,G-67%);102(A-0%,G-67%,T-85%);105(C-67%,T-85%);110(A-85%,G-67%);115(C-85%,T-67%);137(G-91%,A-23%);143(G-85%,A-67%);149(C-87%,T-65%);166(C-3%,T-99%);187(G-3%,T-99%);195(C-65%,T-87%);196(A-85%,G-67%);	A/T;G/ A;A;C/ G;A/G; G/T;T/C ;A/G;T/ C;G;A/ G;T/C;T ;T;T/C; A/G	A/T;G/ A;A;G/ C;G/A; T/G;C/T ;A/G;T/ C;G/A; G/A;C/ T;T;T;T /C;G/A
注 1：本表 AMPL1690209 行中，“40（C-94%，T-6%）；166（G-83%，A-26%）”表示该标记第 40 位和第 166 位碱基位置（该标记在版本号 GCA_041682555.1 的参考基因上起始位置计为 1）存在等位变异，且在第 40 位碱基位置中，分别有 94%和 6%的品种（总数为 319 个）存在等位变异 C 和 T；未列出比例小于或等于 5%的等位变异。 注 2：本表 AMPL1690209 行中，“CG”表示金针菇品种“T011”在第五列所示的第 40 位和第 166 位等位变异的碱基分别为 C 和 G；当使用“T011”作为质控样本时，上述信息可作为鉴定结果的参考值。 注 3：参照注 1 和注 2，可以类推本表第五列、第六列和第七列中所有记录的含义。						

附录 B (资料性) 品种鉴定流程示例

品种鉴定参见以下流程。

B.1 样品准备

用PDA培养基培养待测样品与对照样品的菌丝，分别取3个培养皿或者3个摇瓶中的菌丝培养物，混合后冻干成粉末，取每个样品0.5-1g粉末，装入离心管中。

B.2 DNA 提取

采用某公司生产的新型植物基因组DNA提取试剂盒提取金针菇组织的DNA，具体步骤如下：

- a) 向装有金针菇组织的离心管中加入液氮充分碾磨后，加入 400 μL 缓冲液 LP1 和 6 μL RNase A(10 mg/mL)，漩涡振荡 1 min，室温放置 10 min。
- b) 加入 130 μL 缓冲液 LP2，充分混匀，漩涡振荡 1 min。
- c) 12,000 rpm 离心 5 min，将上清移至新的离心管中。
- d) 加入 1.5 倍体积的缓冲液 LP3（使用前请先检查是否已加入无水乙醇），立即充分振荡混匀 15 s，此时可能会出现絮状沉淀。
- e) 将上一步所得溶液和絮状沉淀加入一个吸附柱 CB3 中（吸附柱放入收集管中），12,000 rpm 离心 30 s，倒掉废液，吸附柱 CB3 放入收集管中。
- f) 向吸附柱 CB3 中加入 600 μL 漂洗液 PW（使用前请先检查是否已加入无水乙醇），12,000 rpm 离心 30 s，倒掉废液，将吸附柱 CB3 放入收集管中。
- g) 重复操作步骤 f)。
- h) 将吸附柱 CB3 放回收集管中，12,000 rpm 离心 2 min，倒掉废液。将吸附柱 CB3 室温放置数分钟，彻底晾干吸附柱中残余的漂洗液。
- i) 将吸附柱 CB3 转入一个干净的离心管中，向吸附膜的中间部分悬空滴加 50 μL 洗脱缓冲液 TE，室温放置 2 min~5 min，12,000 rpm 离心 2 min，将溶液收集到离心管中。产物放于-20℃冰箱，以防 DNA 降解。
- j) DNA 质检。用分光光度计测定并计算 JZG01 和 JZG02 的 DNA 溶液在 260 nm 与 280 nm 处的吸光度比值，分别为 1.96 和 1.97。在 260 nm 与 230 nm 处的吸光度比值分别为 1.84 和 1.76；取 4 μL DNA 在 1%的琼脂糖凝胶上电泳，检测 DNA 条带是否完整，结果如图 B.1 所示；取 1 μL DNA 用 Qubit 荧光定量仪测定 JZG01 和 JZG02 的 DNA 浓度，分别为 27.6 ng/ μL 和 20.8ng/ μL 。



图A.1 JZG01 和 JZG02 的 DNA 电泳图

注：最左边条带为某公司生产的分子量标准，其由下至上片段大小分别为100 bp，250 bp，500 bp，750 bp，1,000 bp和2,000 bp。

B.3 多重 PCR 扩增与文库构建

B.3.1 多重PCR扩增

采用某公司生产的多重扩增试剂盒进行多重PCR扩增与文库构建，该试剂盒匹配后序步骤中某公司的测序平台，需自备80%乙醇，其余试剂均为试剂盒提供。

由于JZG01与JZG02的多重PCR扩增与文库构建实验流程完全一样，因此，除特别说明，下面仅就JZG01的实验流程进行说明。

- 1) 配制多重 PCR 扩增体系。在 PCR 管中加入 4 μL 表 A.1 中的多重 PCR 引物混合物（每条引物浓度为 0.2 μM ）、4 μL 样品 JZG01 的基因组 DNA、10 μL GenoPlexs 3 $\times$ T Master Mix 和 12 μL 水，振荡混匀。
- 2) 多重 PCR 扩增反应。多重 PCR 扩增程序：95 $^{\circ}\text{C}$ ，3 min；（95 $^{\circ}\text{C}$ ，20 s，60 $^{\circ}\text{C}$ ，4 min） $\times$ 15 个循环；72 $^{\circ}\text{C}$ ，4 min。反应结束后，获得多重 PCR 扩增产物。

B.3.2 多重PCR扩增产物纯化

- 3) 向 B.3.1 中获得的多重 PCR 扩增产物中加入 12 μL (B.3.1 中获得的 30 μL 多重 PCR 扩增产物的 0.4 倍体积) GenoPrep DNA Clean Beads，振荡混匀后，室温静置 5 min。
- 4) 将 PCR 管置于磁力架上吸附磁珠，直至溶液澄清。
- 5) 用移液器吸取上清液至新的 1.5 mL 离心管中，避免吸到磁珠。
- 6) 向上清液中加入 18 μL (B.3.1 中获得的 30 μL 多重 PCR 扩增产物的 0.6 倍体积)的 GenoPrep DNA Clean Beads，振荡混匀后，室温静置 5 min。
- 7) 用磁力架吸附磁珠，直至溶液澄清。用移液器小心吸取上清液，弃上清，留磁珠。
- 8) 加入 40 μL GenoPlexs BW10 Buffer，悬浮磁珠，室温静置 5 min。用磁力架吸附磁珠，直至溶液澄清。用移液器小心吸取上清液，弃上清，留磁珠。
- 9) 加入 100 μL 80%乙醇（现配现用），用移液器小心去除上清液，避免吸到磁珠。
- 10) 室温放置，直至乙醇挥发干净，避免过干，获得纯化的多重 PCR 扩增产物。

B.3.3 高通量测序文库构建

- 11) 向 B.3.2 中获得的纯化的多重 PCR 扩增产物中，加入：10 μL GenoPlexs 3 $\times$ T Master Mix、2 μL 浓度为 5 μM 的 P5 primer、2 μL 浓度为 5 μM 的 P7 barcode primer（引物中包含样品条形码，样品 JZG01 的条形码序列为 GGTTGTCTAG）和 16 μL 水。
- 12) 将配制好的反应体系振荡混匀并短暂离心，按如下程序进行 PCR 反应：95 $^{\circ}\text{C}$ ，3 min；（95 $^{\circ}\text{C}$ ，15 s；58 $^{\circ}\text{C}$ ，15 s；70 $^{\circ}\text{C}$ ，30 s） $\times$ 8 个循环；72 $^{\circ}\text{C}$ ，5min。
- 13) 反应结束后，即构建好 30 μL 样品 JZG01 的高通量测序文库。

B.3.4 高通量测序文库纯化

- 14) 向 B.3.3 中获得的高通量测序文库中加 24 μL (B.3.3 中获得的 30 μL 高通量测序文库的 0.8 倍体积) GenoPrep DNA Clean Beads，振荡混匀，室温静置 5 min。
- 15) 用磁力架吸附磁珠，直至溶液澄清。用移液器小心吸取上清，弃上清，留磁珠。
- 16) 加入 40 μL GenoPlexs BW07 Buffer，涡旋均匀。
- 17) 用磁力架吸附磁珠，直至溶液澄清。用移液器小心去除上清，避免吸到磁珠。
- 18) 加入 100 μL 80%乙醇（现配现用），用移液器小心去除上清。室温放置，直至乙醇挥发干净。
- 19) 加入 35 μL 10 mM Tris-HCl (pH = 8.0)，充分悬浮磁珠，室温静置 5 min。将离心管置于磁力架上，吸附磁珠，将上清液转移至另一新的 1.5 mL 离心管，获得纯化的高通量测序文库。获得的纯化高通量测序文库直接用于后续实验或置于-20 $^{\circ}\text{C}$ 保存。
- 20) 高通量测序文库质检。取 1 μL 纯化的高通量测序文库用 Qubit 荧光定量仪检测获得 JZG01 和 JZG02 的浓度分别为 36.4 ng/ μL 和 32.3ng/ μL 。取 4 μL 纯化的高通量测序文库在 3%的琼脂糖

凝胶上电泳。本次构建的高通量测序文库条带集中在 400 bp 左右，无明显非特异扩增条带和引物二聚体残留（图 B.2），质量合格。

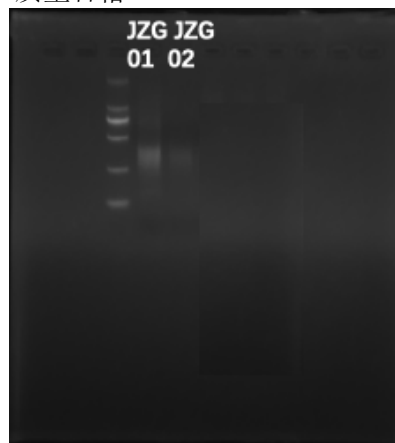


图 B.2 样品 JZG01 和样品 JZG02 的高通量测序文库电泳图

注：最左边条带为某公司生产的分子量标准，其由下至上分子量大小分别为100 bp，250 bp，500 bp，750 bp，1,000 bp和2,000 bp。

- 21) 高通量测序文库混合。分别取样品 JZG01 和样品 JZG02 各 100 ng，震荡混匀并离心，获得上机混合测序文库。

B.4 高通量测序

B.4.1 上机混合测序文库变性

采用某公司生产的高通量测序仪对B.3中获得的上机混合测序文库进行变性。

- 1) 采用 Qubit 荧光定量仪测定上机混合测序文库的浓度为 35.8 ng/μL。该试剂盒推荐文库投入量为 1 pmol，根据下面公式计算 1 pmol 上机混合测序文库对应的质量。1 pmol 上机混合测序文库的质量(ng)= $\frac{\text{DNA 主片段长度(bp)}}{1000 \text{ bp}} \times 660 \text{ ng}$ ，其中，DNA 主片段长度按 400 bp 计算，1 pmol 上机混合测序文库对应的质量为 264 ng，所需体积为 $264/35.8 = 7.4 \mu\text{L}$ 。
- 2) 取 7.4 μL 上机混合测序文库，用 TE Buffer 补充至总体积 48 μL 后于 PCR 扩增仪上 95°C 变性 3 min，获得文库变性产物。

B.4.2 文库变性产物单链环化

按某公司生产的环化试剂盒的操作手册对文库进行环化。

- 3) 在冰上配制 12.1 μL 的单链环化反应液，其中包含 11.6 μL 的 Splint Buffer 和 0.5 μL 的 DNA Rapid Ligase。
- 4) 向上述单链环化反应液中加入 B.4.1 中获得的文库变性产物，涡旋震荡 6 次，每次 3 s，瞬时离心将反应液收集至管底后，37°C 保温 30 min，获得单链环化产物。

B.4.3 酶切消化

对环化产物进行酶切，执行以下步骤。

- 5) 在冰上配制 4.0 μL 的酶切消化反应液，其中包含 1.4 μL 的 Digestion Buffer 和 2.6 μL 的 Digestion Enzyme。
- 6) 向酶切消化反应液中加入 B.4.2 中获得的单链环化产物后，涡旋震荡 6 次，每次 3 s，瞬时离心将反应液收集至管底，37°C 反应 30 min。
- 7) 反应结束后，加入 7.5 μL Digestion Stop Buffer，涡旋震荡 6 次，每次 3 s，瞬时离心将反应液收集至管底，获得酶切消化后的单链环化产物。
- 8) 将酶切消化后的单链环化产物转移到新的 1.5mL 离心管中。

B.4.4 单链环化产物纯化

对单链环化产物进行纯化，执行以下步骤。

- 9) 提前 30 min 取出 DNA Clean Beads 置于室温，使用前充分震荡混匀。
- 10) 吸取 170 μL DNA Clean Beads 至 B.4.3 获得的酶切消化后的单链环化产物中，用移液器轻轻吹打至少 10 次至完全混匀，最后一次应确保将吸头中所有液体及磁珠打入 1.5 mL 离心管中。
- 11) 室温孵育 10 min。
- 12) 瞬时离心，将 1.5 mL 离心管置于磁力架，静置 2 min~5 min 至液体澄清，用移液器小心吸取并丢弃上清。
- 13) 保持 1.5 mL 离心管置于磁力架上，加入 500 μL 新鲜配制的 80%乙醇漂洗磁珠及管壁，小心吸取并弃上清。
- 14) 重复步骤（13），尽量吸干管内液体。
- 15) 保持 1.5 mL 离心管置于磁力架上，打开 1.5 mL 离心管管盖，室温干燥，直至磁珠表面无反光、无开裂。
- 16) 将 1.5 mL 离心管从磁力架上取下，加入 22 μL TE Buffer 进行 DNA 洗脱，用移液器轻轻吹打至少 10 次至完全混匀。
- 17) 室温下溶解 10 min。
- 18) 瞬时离心，将 1.5 mL EP 管置于磁力架上，静置 2 min~5 min 至液体澄清，将 20 μL 上清液转移至新的 1.5 mL EP 管中，获得纯化的环化产物。纯化的环化产物可在-20℃冰箱储存一个月。
- 19) 环化产物质检。使用某公司生产的 Qubit® ssDNA Assay Kit 测定环化产物（为单链 DNA）浓度为 2.5 ng/ μL ，按如下公式进行换算环化产物的 fmol 浓度为 18.9 fmol/ μL 。
- 20) 环化产物浓度 C (fmol/ μL) = $\frac{3030 \times \text{环化产物质量浓度}}{400} = \frac{3030 \times 2.5}{400} = 18.9 \text{ fmol}/\mu\text{L}$

B.4.5 高通量测序

采用某公司生产的高通量测序试剂盒，对环化产物进行高通量测序。

- 21) 从某公司生产的高通量测序试剂盒中取出 DNB 制备缓冲液、DNB 聚合酶混合液 I、TE 缓冲液和 DNB 终止缓冲液，置于冰盒上约 0.5 h，待试剂融化后，使用漩涡振荡器震荡混匀 5 s 后，短暂离心置于冰盒上备用。
- 22) 取 0.2 mL PCR 管，在冰上配制 40 μL 的反应混合液体系，其中包括 2.1 μL 的环化文库 ssDNA（环化文库 ssDNA = $\frac{40 \text{ fmol}}{\text{环化产物浓度}} = \frac{40 \text{ fmol}}{18.9 \text{ fmol}/\mu\text{L}} = 2.1 \mu\text{L}$ ）、17.9 μL 的 TE 缓冲液和 20 μL 的 DNB 制备缓冲液。
- 23) 将（22）中获得的混合液体系漩涡振荡器震荡混匀，离心 5 s，置于 PCR 仪中 95℃，1 min；65℃，1 min、40℃，1 min 和 4℃，10 min。
- 24) 取出 DNB 聚合酶混合液 II (LC) 置于冰盒上，短暂离心 5 s，置于冰盒上备用（请勿将 DNB 聚合酶混合液 II (LC) 置于室温，请勿长时间触碰管壁）。
- 25) 当（23）中 PCR 仪达到 4℃后取出 PCR 管，离心 5 s；在冰上加入 40 μL DNB 聚合酶混合液 I 和 4 μL DNB 聚合酶混合液 II (LC)，震荡混匀，离心 5 s，立即置于 PCR 仪中，在 35℃热盖条件下 30℃，25 min 和 4℃，10 min；PCR 仪降温至 4℃后，立即加入 20 μL DNB 终止缓冲液，用阔口吸头缓慢地吹打混匀 5~8 次（切勿震荡或剧烈吹打），获得制备好的 DNA 纳米球（DNB）。
- 26) DNB 浓度测定。采用 Qubit® ssDNA Assay Kit 在 Qubit 荧光定量仪上检测制备好的 DNB 的浓度为 20.7 ng/ μL 。制备好的 DNB 可置于 4℃保存 48 小时。
- 27) DNB 加载。取出 DNB 加载缓冲液 I 和 DNB 加载缓冲液 II（如发现 DNB 加载缓冲液 II 中有结晶，使用漩涡振荡器持续剧烈振荡约 1~2 分钟至沉淀重新溶解，短暂离心后方可使用），置于冰盒上融化后，漩涡震荡 5 s 混匀，短暂离心后置于冰盒上备用。

- 28) 在 0.5 mL 冻存管中配制 DNB 加载体系：50 μ L 的 DNB 加载缓冲液 I、50 μ L 的 DNB 加载缓冲液 II、1 μ L 的 DNB 聚合酶混合液 II (LC) 和 100 μ L (浓度大于 8 ng/ μ L) 制备好的 DNA 纳米球 (DNB)；用阔口吸头缓慢混匀 5~8 次 (切勿离心、震荡及剧烈吹打)，4°C 保存备用。
- 29) 准备测序试剂槽。取出测序试剂槽，常温水浴解冻 3~4 小时 (或者提前一天将其置于 2°C~8°C 冰箱解冻) 后，置于 2°C~8°C 冰箱备用；使用前颠倒混匀试剂槽 3 次，然后将试剂槽置于正前方，前后左右剧烈晃动 10~20 次，直至试剂中无肉眼可见的分层，尤其是该测序试剂槽的 17 号试剂和 18 号试剂；打开试剂槽盖板，使用无尘纸擦净冷凝水。
- 30) 提前 1 h 取出 dNTPs 混合液 III 和 dNTPs 混合液 II，室温融化后置于冰上或 4°C 备用；加样前需使用漩涡振荡器震荡 5 s 混匀，短暂离心 (离心到底部即可) 后使用；使用前取出 DNA 聚合酶混合液，置于冰上或 4°C 备用，加样前需颠倒混匀 4~6 次。
- 31) 使用洁净的 1 mL 枪头在测序试剂槽的 1 号和 2 号孔边缘位置轻轻戳出一个直径约 2cm 的加样孔位；在 1 号孔位中加入 0.96 mL dNTPs 混合液 III 和 0.96 mL DNA 聚合酶混合液；在 2 号孔位中加入 2.04 mL dNTPs 混合液 II 和 1.02 mL DNA 聚合酶混合液；使用配套的透明封口膜将 1 号和 2 号加样孔封住 (切勿盖住孔位中心位置，避免影响试剂针下降)。
- 32) 测序试剂槽水平放置在桌面上，双手握住两侧，顺时针摇晃 10~20 次，再逆时针摇晃 10~20 次，期间要确保肉眼可见旋涡，直至该试剂槽中 1 号孔位中的试剂上下层颜色均匀一致，以保证试剂充分混匀。
- 33) 使用枪头戳破 15 号孔的封口膜；用 200 μ L 移液器移取 200 μ L MDA 聚合酶混合液加入到 MDA 试剂的试剂管中；颠倒混匀 4~6 次，使其充分混匀，再将混匀液加入 15 号孔中，加入时确保管底部无气泡，至此即完成测序试剂槽上机前的准备工作。
- 34) 上机测序。从 -20°C 冰箱中取出载片包装彩盒，将载片从中取出，拆开真空包装袋；打开载片舱门，一手压住水洗载片两侧，另一手按下载片吸附按钮，待真空释放后，将水洗载片从平台上取出；用空气罐吹净载片平台和载片背面的灰尘 (如果平台表面有可见结晶，需要用润湿的无尘纸轻轻擦拭)，按下载片吸附按钮，取出新的载片，两孔位置在左侧，一孔位置在右侧，标签位置靠右，双手握住载片两端；载片孔位对应定位柱放置，保持载片空位内壁与定位柱贴合，将载片边框左右两边同时按下，使载片吸附在平台上，确保载片可以牢固吸附，关闭载片舱门。
- 35) 打开试剂舱舱门，按照试剂槽盖板指示方向，把准备好的测序试剂槽轻轻推进试剂舱，直到推到底部并确认测序试剂槽完全放入；放入要加载的 DNB 冻存管，关闭试剂舱舱门。
- 36) 在电脑软件界面上点击“测序”，进入测序参数设置界面，输入 DNB 编号，选择测序方案“FCL PE150”，点击“下一步”，将光标放置在“试剂槽 ID”文本框，打开试剂舱舱门，使用条码扫描枪扫描测序试剂槽条码录入试剂槽信息，关闭试剂舱舱门；把光标移至“载片 ID”后面的文本框，打开载片舱舱门，扫描载片上的二维码录入载片信息；各项信息确认无误后，点击“开始”；待测序完成后，点击“完成”，并将测序数据拷贝至移动硬盘。

B.5 测序数据拆分

高通量测序仪根据样品条形码的序列，自动将测序数据拆分到样品 JZG220608001 和样品 JZG221224005。

由于采用双末端测序模式，因此，每个样品的每个测序片段均包括正向和反向测序序列。其中，样品 JZG220608001 的正向和反向测序序列存放文件的名称分别为 JZG220608001_1.fq.gz 和 JZG220608001_2.fq.gz；样品 JZG221224005 的正向和反向测序序列存放文件的名称分别为 JZG221224005_1.fq.gz 和 JZG221224005_2.fq.gz。

B.6 测序数据比对

金针菇参考基因组 Genbank 登录号为 GCA_041682555.1，文件名为 Dan3.fna。

数据比对软件为 Bowtie2 (版本号 2.1.0，下载地址：<https://bowtie-bio.sourceforge.net>)，需要该软件的索引构建模块 bowtie2-build 和序列比对模块 bowtie2。

在Linux窗口中输入以下命令行：bowtie2-build Dan3.fna Dan3.fna，构建金针菇参考基因组索引。

在Linux窗口中输入以下命令行：bowtie2 -q -p 2 -x Dan3.fna.fna -1 JZG220608001_1.fq.gz -2 JZG220608001_2.fq.gz -S JZG220608001.sam，将样品JZG220608001的测序数据比对到金针菇参考基因组上。其中，参数“-q”表示输入文件是fastq格式；参数“-p 2”表示采用2个线程做比对；参数“-x Dan3.fna.fna”指定比对参考基因组序列；参数“-1 JZG220608001_1.fq.gz -2 JZG220608001_2.fq.gz”指定样品JZG220608001的测序结果文件；参数“-S JZG220608001.sam”把比对结果输入到JZG220608001.sam文件中。

比对结果采用SAM（The Sequence Alignment / Map format，序列比对格式）格式保存。SAM文件格式详细说明见<http://samtools.github.io/hts-specs/SAMv1.pdf>。

按类似方法，将样品JZG221224005的测序数据比对到金针菇参考基因组上。

B.7 测序数据质量控制

若测序片段比对到参考基因组上的位置与标记位点在参考基因组上的位置重合，则判定该测序片段属于该标记位点。

统计每个标记位点的测序片段的数目，作为该标记位点的覆盖倍数。例如，样品JZG220608001的第1个标记位点覆盖倍数为791倍。

按上述方法，获得JZG220608001所有标记位点的覆盖倍数，计算JZG220608001标记位点的平均覆盖倍数 $C_1 = (791 + \text{第2个标记位点覆盖倍数} + \dots + \text{第350个标记位点的覆盖倍数}) / 350 = 3783.6$ 倍。

由于 $C_1 \geq 500$ 倍，判定样品JZG01的标记位点的平均覆盖倍数合格。

每个标记位点所有相同测序片段归为同一个等位基因型，统计该标记位点的每个等位基因型的测序片段的数目。例如，表B.1为样品JZG220608001在表A.1中的第2个MNP标记位点的所有等位基因型序列及其测序片段数目。

表B.1中第1个等位基因型的测序片段的数目为4737条 ≥ 20 条，判定样品JZG220608001的该标记位点为检出标记位点。依次判定样品JZG220608001的所有标记位点是否为检出标记位点。

统计样品JZG220608001的所有检出标记位点数量为350个，计算检出标记位点的比例 $R_1 = 350 / 350 = 100\%$ 。

由于 $R_1 \geq 95\%$ ，判定样品JZG220608001的检出标记位点的比例合格。

由于样品JZG220608001的标记位点的平均覆盖倍数和检出标记位点的比例均合格，判定样品JZG220608001的测序数据质量合格。

按同样方法，判定样品JZG221224005的测序数据质量合格。

表B.1 样品JZG220608001中第2个MNP标记位点测序片段统计结果

序号	测序片段数目	等位基因型
1	4737	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTACTCGTCGATGTG GGTTCCAGCGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGA AACAAGGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
2	3268	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTAAATCGTTGATGTG GGTTCCAACGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGA AACAAAGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
3	12	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTACTCGTCGATGTG GGTTCCAGCGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGA AACAAAGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
4	5	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTAAATCGTTGATGTG GGTTCCAACGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGA AACAAGGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
5	4	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTACTCGTCGATGTG GGTTCCAGCGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGGGA AACAAGGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
6	3	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGATGGTTCGAGCAC GGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTAAATCGTTGATGTG GGTTCCAACGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGA AACAAAGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT
7	2	CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGAGATCGGTGGTGGTTCGAGCA CGGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTACTCGTCGATG TGGGTTCCAGCGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCG AGAAACAAGGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT

注：以序号为1的等位基因型序列为参考，其他等位基因型中与之不相同的序列用灰色背景显示。

B.8 标记位点分型

将样品JZG220608001第2个标记位点的等位基因型的测序片段数目由高到低排列，其结果如表B.1所示。测序片段数目最多的等位基因型，即表B.1中序号为1的等位基因型称为主等位基因型，其他等位基因型称为次等位基因型。

计算表B.1中序号为2的次等位基因型的测序片段数目与主等位基因型测序片段数目的比值为 $3268/4737 = 0.69$ 。由于该比值大于0.2，不太可能由杂株或者测序错误等原因造成，因此保留该次等位基因型。

依次计算表B.1中其他次等位基因型的测序片段数目与主等位基因型测序片段数目的比值。由于获得的比值均小于等于0.2，因此均舍弃这些次等位基因型。

主等位基因型和所有保留的次等位基因组成样品JZG220608001第2个标记位点的基因型，记为：
CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCACGGTC
GGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCATCTCCTGTACTCGTCGATGTGGGTTCCAG
CGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGAAACAAGGTGGAA
ATAACGGAAGCTTTAGCGAATTTTCATCAT/CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGAT
CTGGGATCGGTGGTGGTTCGAGCACGGTCGGGTCGTAGGCTGCTGCGCCGGTGAATCCGCTGCA
TCTCCTGTAAATCGTTGATGTGGGTTCCAACGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACA
GTGGTGAAGGCGAGAAACAAGGTGGAAATAACGGAAGCTTTAGCGAATTTTCATCAT。

按类似的方法，获得样品JZG220608001和样品JZG221224005的所有标记位点的基因型。

B.9 计算遗传相似度

样品 JZG221224005 第 2 个标记位点的基因型为：
CAGCTGTATTCCGAATGCCATGGGCGGTAAAGGATCTGGGATCGGTGGTGGTTCGAGCACGGTC

GGGTCGTAGGCTGCTGCGCCGGTGTAATCCGCTGCATCTCCTGTAA**TCGT****T**GATGTGGGTTCCAA
CGCTTGCTGGGCGTATGTCGTGATTTCTCCATGAACAGTGGTGAAGGCGAGAAACAA**AGTGGAA**
ATAACGGAAGCTTTAGCGAATTTTCATCAT，判定其与样品 JZG220608001 第 2 个标记位点的基因型
不同（差异碱基用加粗字体和灰色背景显示）

依次判定样品JZG220608001与样品JZG221224005的 $N_{ij} = 349$ 个共同检出位点中，每个共同检出位点的基因型是否有差异。统计样品JZG220608001与样品JZG221224005中均检出的但基因型无任何差异的标记位点的数目 $n_{ij} = 267$ 个，差异位点数为82个。

计算样品 JZG220608001 与 样品 JZG221224005 的遗传相似度 $GS = \frac{n_{ij}}{N_{ij}} \times 100\% = \frac{267}{349} \times 100\% = 76.5\%$ 。

B. 10 结果表述

序号	待测品种		对照品种		比较 位点数	差异 位点数	遗传相似度 (GS)	结论
	样品编号	名称	样品编号	名称				
1	JZG220608001	T022	JZG221224005	1012	349	82	76.5%	不同品种