

SSR based parental polymorphism survey for marker assisted backcross breeding in rice (*Oryza sativa* L.)

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ABSTRACT

The brown planthopper (BPH), *Nilaparvata lugens* (Stål), is a destructive and widespread pest in rice-growing regions across Asia and developing resistant varieties is considered to be the most effective solution. Marker assisted backcrossing (MABC) is a widely used approach for introgressing resistant genes using backcross breeding to the highly adapted varieties from donors with the help of molecular markers and the availability of polymorphic markers being a critical factor for its success. The present study was aimed to assess parental polymorphism per centage using SSR markers between the rice varieties BPT5204 and RP2068-18-3-5 (donor for BPH resistant gene). A total of 340 SSR markers covering 12 chromosomes were used for the survey and 96 markers were found to be polymorphic between the parents. The number of polymorphic markers per chromosome ranged from 6 to 11, with the highest number (11) observed on chromosome 3 showing the highest percentage. The average polymorphism rate per chromosome was 28.3%. The identified polymorphic markers will be useful for estimating the recurrent parent genome recovery per centage in marker-assisted background selection and for mapping QTLs associated with BPH resistance.

Key words: Parental survey, Polymorphism, Rice and SSR markers

Rice (*Oryza sativa* L.) is a staple food for more than 3.5 billion people worldwide. With a growing global population, rice production needs to be doubled by 2030 to meet the future demands. However, rice is highly susceptible to various diseases and pests throughout its growth and development, resulting in significant yield losses in many rice producing countries.

The brown planthopper (BPH) caused by *Nilaparvata lugens* (Stål), poses a significant threat to rice production globally. This pest causes substantial yield losses annually, making it a major concern for farmers and researchers. BPH inflicts damage on rice plants through direct feeding and by transmitting viral diseases. The pest's feeding behaviour involves sucking sap from the lower portions of rice plants, leading to a reduction in chlorophyll and protein content in leaves. This, in turn, decreases the rate of photosynthesis and results in leaf yellowing, reduced tiller number and the production of unfilled grains. In severe cases, BPH

infestation can cause complete drying and plant death, a condition known as 'hopper burn' (Muduli *et al.*, 2021).

Furthermore, BPH acts as a vector for various plant pathogens, transmitting viral diseases such as grassy stunt virus (RGSV) and ragged stunt virus (RRSV). These diseases indirectly harm rice crops, compounding the damage caused by direct feeding (Yan et al., 2023). In China, BPH outbreaks led to major yield losses, with about 3 million tons of rice destroyed during infestations from 2005 to 2008 (Hu et al., 2016). Comparable severe yield reductions occurred due to BPH invasions in Japan, Korea, Vietnam, Central Thailand and Indonesia in 2005, 2007, 2009 and 2011, respectively (Brar et al., 2009 and Catindig et al., 2009). The most severe outbreak of BPH in India occurred in Kerala at the end of 1973 and early 1974 (Koya, 1974 and Nalinakumari and Mammen, 1975). In 2007, severe BPH infestations were reported in parts of the

Cauvery command area in Karnataka, and similar infestations were observed in Haryana, Punjab, and Delhi states in 2008 (Gowda, 2009).

Developing resistant cultivars using BPH resistance genes is regarded as the most promising strategy (Iswanto et al., 2020), rather than relying on pesticides, which are costly and contribute to environmental issues. To date, researchers have identified 40 BPH resistance genes from indica and wild Oryza species (Tan et al., 2021). Markerassisted backcross breeding (MABB) is an efficient strategy for transferring a desired gene from a donor parent to a recurrent parent. This process involves selecting the target loci, minimizing the size of the introgressed fragment containing the target loci and maximizing the recovery of the recurrent parent genome through repeated backcrossing (Wang et al., 2019). A critical component of this approach is parental polymorphism survey, which is essential for marker-assisted background selection (MABS), a technique used to analyze the recovery of recurrent parent genome during gene introgression. Parental polymorphism refers to the genetic variation between parents used in breeding programs, and it is influenced by the specific combination of parents chosen. Among the molecular markers employed in polymorphism surveys, microsatellites (SSRs) are the most widely used due to their high polymorphism, co-dominance, wide genomic distribution and ease of amplification through polymerase chain reaction (PCR). SSR markers also enhance breeding efficiency by allowing precise transfer of specific genomic regions (Miah et al., 2013). In this context, the present investigation was aimed to assess parental polymorphism (%) between the rice varieties, BPT5204 and RP2068-18-3-5 (BPH donor parent) by using genome wide SSR markers.

MATERIAL AND METHODS

The present study was conducted at Agricultural Research Station, Bapatla, Andhra Pradesh, India during *rabi*, 2021-22. Parental polymorphism survey was performed at Central Instrumentation Cell, Agricultural College, Bapatla. The genotypes in the study were BPT5204 (recurrent parent) which is a high yielding but susceptible to brown planthopper, whereas RP2068-18-3-5 (donor parent) is a brown planthopper resistant variety and contains Bph33(t) gene on chromosome 1.

DNA extraction and Quality check

DNA was extracted from leaf samples collected from 20 to 25 days old seedling for parental polymorphism survey using the CTAB method described by Doyle and Doyle (1990). The finely chopped leaf samples were ground using mortar and pestle with 500 iL of CTAB extraction buffer (2% CTAB, 100 mM Tris, pH 8.0, EDTA pH 8, 1.4 M NaCl). An additional 300 iL of extraction buffer was added to each homogenized sample in an Eppendorf tube, followed by heating the samples in a water bath at 65°C for 45 minutes. The tubes were centrifuged at 13,000 rpm for 20 minutes at 4°C and collected the supernatant into fresh centrifuge tubes. After collecting the supernatant, an equal volume of Chloroform: Isoamyl alcohol (24:1) was added, and the tubes were vortexed for 10 minutes. The mixture was centrifuged at 13,000 rpm for 20 minutes at 4°C and the supernatant was transferred to a fresh sterile tube. An equal volume of cold isopropanol was added, and the tubes were stored overnight at -20°C. The next day, the samples were centrifuged at 10,000 rpm for 15 minutes at 4°C, and the supernatant was carefully discarded without disturbing the DNA pellet. The pellet was washed with 200 iL of 70% ethanol and centrifuged again at 10,000 rpm for 10 minutes at 24°C. The pellet was then air-dried at room temperature overnight. Depending on the pellet size, 100 µL molecular grade water was added to dissolve the DNA. The purity of the extracted DNA was assessed using the Nanodrop.

Polymerase chain reaction using SSR markers

In the present study, a set of 340 SSR markers were utilized to conduct parental polymorphism survey across all 12 chromosomes of rice. The polymerase chain reaction (PCR) was performed in a total volume of 10 iL, which included 2 iL of template DNA. Master mix was prepared by taking each 1 iL of 10 pmol marker (both forward and reverse markers), 0.5 iL of 2.5 mM deoxy ribonucleotides (dNTPs), 2 µL of 10 X Hi-buffer with 0.5 µL of 50 mM MgCl, and 0.5 U (0.1 iL) of 5U/iL Taq DNA polymerase and 3.9 iL of molecular grade water was added to make up the volume to 10 iL. After centrifuging the PCR mixture at 1000 rpm for one minute, it was placed in a 96-well PCR thermal cycler. The protocol began with a 5 minute denaturation step at 94°C, followed by 35 cycles

consisting of 45 seconds at 94°C of denaturation, 45 seconds at 56°C for primer annealing, 1 minute at 72°C for extension, and concluded with a final extension at 72°C for 10 minutes.

Agarose gel electrophoresis and gel image documentation

The PCR products were analyzed by electrophoresis using 3% agarose gel in a gel electrophoresis unit. 3.0 g of agarose was weighed and transferred to a conical flask, to which 100 ml of 1X TAE buffer was added and mixed thoroughly. The mixture was then boiled slowly while stirring intermittently in a microwave until the agarose was completely melted, resulting in a transparent solution. To clean the gel-casting tray, it was soaked in water and wiped down with ethanol. Once the agarose was cooled to room temperature, 2 iL of EBr (10 mg/ml) was added to the molten agarose, which was then poured into a gel casting tray fitted with the necessary gel combs and allowed to set for 20 to 30 minutes. The gel was then transferred to the electrophoresis unit containing 1X TAE buffer.

Before loading, the PCR-amplified products were mixed with 1/6th volume of gel loading dye (40% sucrose and 0.25% bromophenol blue) and loaded into the wells. A 100 bp DNA ladder was included in one well to determine the sizes of the amplified fragments. The DNA fragments were visualized under a gel documentation system.

Parental polymorphism per centage

Polymorphism (%)=

 $\frac{\text{Markers showing polymorphism}}{\text{Total number of markers used}} \times 100$

The polymorphism per centage was calculated using the above formula

where markers showing polymorphism is the molecular markers that showed different alleles between the two parents (donor and recurrent parents) total number of markers used is the total number of SSR markers that were analyzed between the two parents

Graphical genotyping

To visualize the marker data, the GGT 2.0 program was employed (Berloo, 2008). GGT 2.0

focuses on the visualization and analysis of molecular marker scores. It was used to map the distribution of polymorphic markers along the length of the chromosome based on their physical positions in megabases (Mb). The visualization was generated from the input of physical marker positions in a rowand-column data matrix.

RESULTS AND DISCUSSION

Parental polymorphism data is essential for marker-assisted breeding programs. In this study, genome-wide microsatellite (SSR) markers were used to evaluate parental polymorphism between two contrasting rice varieties, BPT5204 and RP2068-18-3-5 for identifying informative polymorphic SSR markers.

A total of 340 SSR markers were used for parental polymorphism survey across 12 chromosomes using PCR, following the standard rice microsatellite protocol. The survey revealed significant variation between the parental lines, with 96 markers being polymorphic and 244 monomorphic. Details on the number of markers tested, polymorphic markers identified and percentage of polymorphism per chromosome are presented in Table 1.

The number of SSR markers screened for polymorphism across the 12 chromosomes ranged from 21 to 36, with chromosome 10 having the highest markers screened (36). Chromosome 1 was screened with 31 markers, followed by chromosomes 2 and 3 with 30 each, chromosome 7 with 29, chromosomes 5 and 12 with 28, chromosomes 6, 8 and 11 with 27, chromosome 9 with 26 and chromosome 4 with 21 markers.

The results showed that the number of polymorphic markers ranged from 6 to 11, with the highest number (11) observed on chromosomes 1 and 3. Chromosome 2 showed 10 polymorphic markers, followed by chromosome 7 with 9, chromosomes 5 and 12 with 8, chromosomes 6, 8 and 11 with 7 and chromosomes 4, 9 and 10 with 6 polymorphic markers each. The lower levels of polymorphism on certain chromosomes may be due to genetic similarities between the parental lines (Marri *et al.*, 2005). The frequency distribution of polymorphic SSR markers across 12 chromosomes is presented in Fig.1 and the representative gel image of the marker, polymorphism survey is presented in Fig. 2.

S.No.	Chro.No.	Total no. of markers screened/ chromosome	No. of polymorphic markers/ chromosome	No. of monomorphic markers/ chromosome	Percentage of polymorphism per chromosome
1	1	31	11	20	35.5
2	2	30	10	20	33.3
3	3	30	11	19	36.7
4	4	21	6	15	28.6
5	5	28	8	20	28.6
6	6	27	7	20	25.9
7	7	29	9	20	31
8	8	27	7	20	25.9
9	9	26	6	20	23.1
10	10	36	6	30	16.7
11	11	27	7	20	25.9
12	12	28	8	20	28.6
	Total	340	96	244	
	Average p	bercent of polymorphism		28.3	

Table 1. Details of SSR Markers polymorphic between BPT5204 and RP2068-18-3-5





The percentage of polymorphism varied across the chromosomes, ranging from 16.7% to 36.7%, with chromosome 3 showing the highest per centage of polymorphism (36.7%) while the chromosome 10 recorded the lowest (16.7%).

Chromosome 1 exhibited 35.5% polymorphism, followed by chromosome 2 with 33.3%, chromosome 7 with 31%, chromosomes 4, 5 and 12 with 28.6% and chromosomes 6, 8 and 11 with 25.9% and chromosome 9 with 23.1%. The average per centage of polymorphism was 28.3%, indicating substantial genetic variability between the

parents BPT5204 and RP2068-18-3-5. In a parental polymorphism survey, a higher percentage of polymorphism on a chromosome indicates greater genetic diversity between the parents for that particular chromosome. This suggests that the parents possess more contrasting alleles or loci on that chromosome. In the present study, chromosome 3 showed the higher percentage of polymorphism.

These results are consistent with Jairin *et al.* (2009) who identified 75 polymorphic markers out of 120 SSR markers screened in a parental polymorphism survey between Rathu Heenathi and



L- 100 bp Ladder; 1- BPT5204; 2-RP2068-18-3-5 Polymorphic markers- RM490, RM3206, RM3252, RM254, RM3747, RM243 and RM184 Fig 2. Parental polymorphism survey between BPT5204 and RP2068-18-3-5 with SSR markers

KDML105 of rice. Similarly, Suh *et al.* (2011) used 260 SSR markers in a parental polymorphism survey and reported an average polymorphism rate of 84.4%. Lakshmi *et al.* (2021) detected 87 polymorphic markers (17.1%) out of 494 SSR markers exploited in a parental polymorphism survey between a BPH-resistant line (M-229) and a susceptible line (RNR 15048), while Bhargava *et al.* (2023) utilized 816 SSR markers in a parental polymorphic murvey and identified 97 as polymorphic with an average polymorphism rate of 12.5%.

Information regarding 96 SSR markers, such as chromosomal location, forward and reverse primer sequences and physical positions (start and end of the SSR), was curated from the Gramene Markers Database and the details of 96 polymorphic SSR markers are presented in Table 2 and the distribution of polymorphic SSR markers across all the 12 chromosomes, created using Graphical Genotyping 2.0 software are presented in Figure 3.

CONCLUSION

The 96 identified polymorphic SSR markers can be utilized in marker-assisted background selection to estimate the percentage of recurrent parent genome recovery. Identifying polymorphic markers between parents is crucial for mapping genomic regions that influence key traits, particularly BPH resistance. This study highlights the potential of polymorphic marker for effective quantitative trait loci (QTL) mapping and marker-assisted selection (MAS) in rice breeding. The identified polymorphic markers offer valuable tools for marker-assisted breeding strategies, though further research is needed to overcome limitations and broaden the application to other traits and diverse rice germplasm.

LITERATURE CITED

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	Mc						
	Couch	Position	Chro.			PCR	Annealing
S.No.	Locus	(cM)	No.	Forward sequence	Reverse sequence	product	$temn(^{0}C)$
	ID	(0112)	1.00			size	
1	RM009	19.4	1	GGTGCCATTGTCGTCCTC	ACGGCCCTCATCACCTTC	136	55
2	RM243	57.3	1	GATCTGCAGACTGCAGTTGC	AGCTGCAACGATGTTGTCC	116	55
3	RM246	115.2	1	GAGCTCCATCAGCCATTCAG	CTGAGTGCTGCTGCGACT	116	55
4	RM490	51	1			101	55
5	RM493	79.7	1	TAGCTCCAACAGGATCGACC	GTACGTAAACGCGGAAGGTG	211	55
6	RM580	68.2	1	GATGAACTCGAATTTGCATCC	CACTCCCATGTTTGGCTCC	211	55
7	RM583	43.2	1	AGATCCATCCCTGTGGAGAG	GCGAACTCGCGTTGTAATC	102	55
8	RM640	176.3	1			1/2	50
0	RM1207	121.6	1	GTGCCTTACAACTCAACGAC		145	55
10	DM1240	102.7	1			160	55
10	DM225	0.2	1	GETAACTTEETECCATECC	GGTCAATCATCCATCCAACC	172	55
12	DM262	127.5	1	CCCACCCTACCTCATCAACC	CCTACCTTTCACCTACCACC	1/2	55
12	RN1203	127.3	2		CCCTACCACTTAACCTCCCC	199	55
13	RIVI2/9	1/.3	2		GGUIAGGAGIIAACUICGCG	1/4	55
14	RIVI482	187.5	2			188	55
15	RM492	53	2		AAGACGIACAIGGGICAGGC	224	<u> </u>
16	RM497	150.8	2		GCCAGIGCIAGGAGAGIIGG	213	55
1/	RM530	158	2	GCACIGACCACGACIGIIIG	ACCGIAACCCGGAICIAICC	161	22
18	RM555	34.7	2			223	55
19	RM573	143.7	2		TCTTCTTCCCTGGACCACAC	201	55
20	RM5430	91.5	2	TAAAAACTGAGCCGTGAGCC	ACCATGGGGAGCTGCTTC	181	61
21	RM6933	123.9	2	TGTAGCAGAAACCAATGCTC	GICACICCACITCGCTTAIC	215	55
22	RM168	171.2	3	TGCTGCTTGCCTGCTTCCTTT	GAAACGAATCAATCCACGGC	116	55
23	RM251	79.3	3	GAATGGCAATGGCGCTAG	ATGCGGTTCAAGATTCGATC	147	55
24	RM338	108.4	3	CACAGGAGCAGGAGAAGAGC	GGCAAACCGATCACTCAGTC	183	55
25	RM347	131.5	3	CACCTCAAACTTTTAACCGCAC	TCCGGCAAGGGATACGGCGG	207	55
26	RM422	205.4	3	TTCAACCTGCATCCGCTC	CCATCCAAATCAGCAACAGC	385	55
27	RM442	224.2	3	CTTAAGCCGATGCATGAAGG	ATCCTATCGACGAATGCACC	257	55
28	RM520	191.6	3	AGGAGCAAGAAAAGTTCCCC	GCCAATGTGTGACGCAATAG	247	55
29	RM85	231	3	CCAAAGATGAAACCTGGATTG	GCACAAGGTGAGCAGTCC	107	55
30	RM3206	28.2	3	GCGCCTCTCTTCTTCCTCTC	GAAAATCGAATCACGGCGAC	112	55
31	RM5924	31.3	3	CTCCCAAGAAACTGAACCAG	AGGATTCGTCGTTGCTCAAC	209	55
32	RM6283	83.3	3	TGGAGACTGAGCTGATGCC	TCAGGTGGTCGGTTCCTTAC	93	55
33	RM131	148.8	4	TCCTCCCTCCCTTCGCCCACTG	CGATGTTCGCCATGGCTGCTCC	215	61
34	RM335	21.5	4	GTACACACCCACATCGAGAAG	GCTCTATGCGAGTATCCATGG	104	55
35	RM451	115.5	4	GATCCCCTCCGTCAAACAC	CCCTTCTCCTTTCCTCAACC	207	55
36	RM471	53.8	4	ACGCACAAGCAGATGATGAG	GGGAGAAGACGAATGTTTGC	106	55
37	RM5709	109.9	4	CTGAATTTATTATAGGACGGAAG	CATAGTATTGGATTGGACACG	163	55
38	RM8213	10.7	4	AGCCCAGTGATACAAAGATG	GCGAGGAGATACCAAGAAAG	177	55
39	RM163	78.7	5	ATCCATGTGCGCCTTTATGAGGA	CGCTACCTCCTTCACTTACTAGT	124	55
40	RM334	141.8	5	GTTCAGTGTTCAGTGCCACC	GACTTTGATCTTTGGTGGACG	182	55
41	RM465	68.3	5	GTGCCTCCATCATCATCATC	TAGGACAAGCGAAGAAACCG	212	55
42	RM480	130.6	5	GCTCAAGCATTCTGCAGTTG	GCGCTTCTGCTTATTGGAAG	225	55
43	RM574	41	5	GGCGAATTCTTTGCACTTGG	ACGGTTTGGTAGGGTGTCAC	155	55
44	RM2010	12	5	ATCTTCTAGGAAATCGAGGA	GTTGGCAACTTGTAGTCTTG	117	55
45	RM6024	67.5	5	ACATTCGTCCAGGGATTCAC	TTGTGGTTGCTCACCTCTTG	178	50
46	RM7446	103.9	5	TGAAGGCAGTTTCACTGACG	AGCCAAGAAGAAGAAAGGGG	188	55
47	RM340	133.5	6	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC	163	55
48	RM402	40.3	6	GAGCCATGGAAAGATGCATG	TCAGCTGGCCTATGACAATG	133	55
49	RM510	20.8	6	AACCGGATTAGTTTCTCGCC	TGAGGACGACGAGCAGATTC	122	55
50	RM527	61.2	6	GCTCGTACGGTGGGTGAATCC	GATGCGTCCTTCTTAGGTTGAAAG	273	55

Table 2. Details of 96 SSR markers polymorphic between BPT5204 and RP2068-18-3-5

31 Bible 32 16 ARTCRGUIGATE TARC Could Technologic 116 35 2 RMTI3 105.1 6 ARTCRGATEGGATTGGC ACCCAACCATTAGTGCACC 129 55 3 RMI8 105.2 6 CACTGACATAGCTAGCTAGGC ACCCAACCATTATTATAGTAGTCC 176 5 RM32 35.1 7 CACAGTGAGCAAGCAGCCCTGG CACGTGAGCAAGCAAGCAGGCG 180 55 5 RM32 35.1 7 CACAGTGAGCAAGCAGGCAGGG 180 55 5 RM32 35.1 7 CAAGCGTAATAGGAGGAAGAIC GAATTGGAGGAGGAGG 180 55 7 RM33 180.5 7 CAAGCCTATAATGGAG ACTATCCAAGTGGTGAGGAG 118 55 8 RM13 180.5 7 GACTGCATCATCTCAGG CTGTCCTCTCTCTCTCTCTCAG CGGAAGGAATAGGTCTAAGCAG 119 50 6 RM37 180.5 7 GACTGCATCATCTCTAG ACGGAAGCAATC 114 55 6 RM40 10.5 TCGCACACTACAGTGAACCATC CTGTTCTCCTCTCTCTCTCT	51	DM580	2.2	6		CACCTTCCAACCACACTC	186	55
20. BMIT2 102-1 127 127 127 125 20. BMIT2 102-1 126 127 125 125 21. BMIT2 102-1 126 125 125 125 125 125 125 126 126 125 125 125 125 126 126 126 125 125 125 126 126 126 125 125 125 126 126 126 126 125 125 126 <td< td=""><td>52</td><td>RM1309</td><td>105.1</td><td>6</td><td></td><td></td><td>120</td><td>55</td></td<>	52	RM1309	105.1	6			120	55
Jack 10 Sec. Construction Sec.	52	RM8101	8 2	6		TEGTTA ACTOCOLATIATIA A TEACTTCG	273	55
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Jack 102 Construction of the interval One of the interval of the inte	55	DM205	00.2	7		CATCTCCTCCACCCACC	130	55
30 IDAD 2014 7 CARCONTCATCONTRACT Distribution 37 RM342 78 7 CARCONTCATCONTRACT ANTITUTAGCARTGGTCACCC 141 55 38 RM104 708 7 CAAGCCTATAATGGAATIG ANTITUTAGCAGTGGTCACCC 141 55 39 RM33 105.7 7 GCATCCATCCATCATGGGG 168 55 40 RM550 81.05 7 GCACATCCATCCATCCATCCAT 145 55 61 RM550 81.05 7 GCCCATCCATCCATCCATCCATC CTITTCACATCCATCCATCCATCCATCCATCCATCCATCC	56	RM220	36.1	7		GATTIGCTIACCACAGCTC	167	55
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Jas Jas <td>50</td> <td>DM1042</td> <td>70.4</td> <td>7</td> <td></td> <td></td> <td>141</td> <td>55</td>	50	DM1042	70.4	7			141	55
39 RATIS 10.7 CACHORATOGATINATION ADATE CARACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	50	DM1224	105.7	7			150	55
100 NB373 8135 7 GAADAAC LAGAACACCC CHARIAGC CAADACACACC CHARIAGC CAADACACACC 119 50 61 RM503 810.5 7 GICCATGCATCCATCTAG TGGTCCTTCTTCCATCCAAG 177 50 62 RM571 242 7 GTCCATGCATCCATCTCTAG ACGGAAGAATACGTCCATCCC 172 55 63 RM407 5.7 8 GATTGAGGAGACCACCCATC CTTTTCAGATTCAGCCC 178 55 64 RM281 12.8 6 CCCAGACCGTGGAGTGTT CACCGGAGTCAGTAATGAGGAGAACA 218 55 67 RM251 69 8 GACCAGAGGAGAAAAATGC CATATCATTGATTCAGGCCAAG 176 55 68 RM311 69 8 GAACCAGAGGAGACAAAATGC CATATCATTGCATTCAGGCACA 176 55 68 RM312 69 8 GAACCAGAGGAGACACAGAGAC TGAGCAGCCCTCTCTGTGAGAGACA 236 55 70 RM105 32.1 9 GICCAACCAGAGGACACAAGAC TGAGCAGCCTCTCTTCTGTAGGTCAAGGAC 124 55	59	DM2751	<u>105.7</u> <u>91.05</u>	7			100	50
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18/10 128.6 8 GHORORE LACIOC CLACION 178 138 155 67 RM325 69 8 GACGATGAATCAGGAGAACG GTCCTCATACAGTCACATG 138 55 68 RM331 69 8 GAACCAGAGGACAAAATGC CATCATACAGTCACAGTGCACAG 176 55 69 RM404 60.9 8 CCAATCATTAACCCCTGAGC GCCTTCATACAGTCAGAGAAC 236 55 70 RM105 32.1 9 GTCGTCGACCCCATCGGAGCCAC TGGTCGAGCCCATCCATGGAGCAGCAAGAGC 134 55 71 RM215 9.4 9 CAAAATGGAGCAGAAAGGC TGGTCGAGCACCCTTCTGTAG 148 55 72 RM189 36 9 GGCCAACGTGTGATGTCTC TATATGCCAGAGGAGAGAC 125 55 74 RM242 72.3 9 GGCCAACGTGTGATGCC ACGTACGAGCGAGGAGGAGC 125 55 74 RM248 74.6 9 CCGGTCAGTTCAACGTCTG ACGTATCGAGCGAGCGAGGAGC 125 55 78 RM449 73.10	04	RIVI250	112.2	0			237	55
66 RM281 128.6 8 ACCAAUCATCAGIGACCAG GITCTTCATACAGIGACTAGG 138 53 67 RM325 69 8 GACGATGAATCAGGAGAACG GGCATGCATTGAGAATAGG 201 55 68 RM31 69 8 GACACAGAGACAAAAATGC CATCATACATTGACACCAG 166 55 69 RM404 60.9 8 CCAATCATTAACCCCTGAGC GGCATGGATCGAGCAGCAG 176 55 70 RM105 32.1 9 GTCGTCGACCCATCGGAGCCAC TGGGCATCGGATCCGGTC 134 55 71 RM128 9 GACAAGGATAAAGTGTTAGA CCTATGAGACTCAACCACCAC 108 55 72 RM189 36 9 GGCAACGTGTAAGTGACCAC 125 55 73 RM242 72.3 9 GCCAACGTGTGATCCTC TATATGCCAAGCAGCAC 125 55 74 RM288 74.6 9 CCAGTTGGACCATCGA ACGTATCGAACGACCA 125 55 75 RM184 8.3 10 TCCCCATTCGACAGTGA ACGAGTA	03	KIVI204	128.0	0			1/8	55
67 RM325 69 8 CACGATGAALCAGAGAAACG COCATGATIAGGACAA 231 351 69 84 04ACCAGAGGACAAAAAGC CATCATACATTTGCACCCAG 176 555 55 69 RM404 60.9 8 CCAATCATTAACCCCTGAGC CATCATACATTTGCAGCCAG 236 55 70 RM105 32.1 9 GTCGTCGACCCATCGAGCCAC TGGTCGAGGGGGGGGGGGTC 134 55 71 RM125 99.4 9 CAAAATGGACCACCACCTGTTCATGCTTCTCTTTCTTCTTGTAG 148 55 72 RM189 36 9 GGCAACGTGTGTATGTCTC TATATCCCAAGACGAGTAGAGC 108 55 73 RM242 72.3 9 GGCCAACGTGTGTATGTCTC TATCATCCAACATTCAGTCGAC 192 55 74 RM288 74.6 9 CCAGTTCGAGCGCGCATTCC CCCCCCGAATCCACCC 97 55 75 RM148 98.8 10 TACGGCTCGGCGCGCATTCC CCCCCGAATCACCCC 97 55 78 RM484 97.3 10 CTCCCTCTCACACTTGGCACGCGCC <td>00</td> <td>KM281</td> <td>128.0</td> <td>8</td> <td></td> <td></td> <td>138</td> <td>55</td>	00	KM281	128.0	8			138	55
68 RM331 69 8 GAACCAGAGGACAAAAAAGC CAICATACATTACCCCAG 176 55 69 RM404 60.9 8 CCAATCATTAACCCCTGAGC GCCTTCAGGGTCGAGACAGAGAC 236 55 70 RM105 32.1 9 GTCGTCGACCACTCGGACCAC GGCTTCAGGGTGGGGATCGGGTC 134 55 71 RM215 99.4 9 CAAAATGGAGCAGCAAGAGC TGAGCACCTCTTCTTCTGTAG 148 55 72 RM189 36 9 GGACAAGGTAAGTGTTAGA CCTAAGACCAGACGACAC 125 55 73 RM242 72.3 9 GGACAAGGTATAGATGTTC TATATGCCAAGACGACAC 125 55 74 RM288 74.6 9 CCGGTCAGTTCAAGCTCTG ACGTTATAGACGACAC 125 55 75 RM1416 1.8 9 CTAGTTGGCCATACGATGCC TGAGCCTCCATCGACACC 125 55 76 RM147 99.8 10 TACGGCTTCGGCGGCTGATTCC CCCCCCGAATCCAACC 176 CCCCCCGAATCCAACCCACTGGACGAGAGGAGGAGGGGGTGGG 124 55	6/	RM325	69	8	GAUGAIGAAICAGGAGAAAGG	GGCAIGCAICIGAGIAAIGG	201	55 55
69 RN404 60.9 8 CCAAICATTACCCCTGAGC GCUTTCATGCTGAGCCGGGTC 236 55 70 RM105 32.1 9 GTCGTCGACCCATCGGAGCCAC TGGTCGAGCGGGGTC 134 55 71 RN125 99.4 9 CAAAATGGAGCAGCAAGAGC TGGTCGACCTCTTCTCTGTGAG 148 55 71 RN128 74.6 9 GGCCAACGTGTGTATGTCT TATATGCCAAGAGCGGAGCAGC 125 55 74 RN288 74.6 9 CCAGTGTGGCATACGATGGC ACGTTACGACGGAGCAGCA 192 55 75 RN144 98.10 TACGGCTTCGGCGGCGATTCC CCCCCACAACCTGGAAACCCGGC 97 55 76 RN147 99.8 10 TACGGCTTCGGCCGACCGGCC TGGCCCATCAGAGCGGGGG 219 55 77 RN184 \$8.3 10 ATCCCATTCGCCAAACGGGC TGGTCGCCATCCATCGAAGCGGGG 219 55 77 RN144 99.3 10 CTCCCTCTCCCCACATGTGC TGGTGGACCAGCAGGGGG 219 55 78 RN444 9.3	68	RM331	69	8			1/6	<u> </u>
10 RM105 52.1 9 GIGICGACCALCUGACCAL IEGICGACGATOGGALCUGAL 134 55 71 RM215 99.4 9 CAAAATGGAGCAGCAGAGAGC TGAGCACCTCCTTCTCTGTAG 148 55 72 RN189 36 9 GGACAGGGTAAAGTGTTAGA CCTAAGACCTACAATCCAA 108 55 73 RN242 72.3 9 GGCCAACGTGTATGTCTC TATATGCCAAGACGAC 125 55 74 RM288 74.6 9 CCGGTCAGTCAACGATGGC ACGTTATGCAACACA 192 55 75 RM316 1.8 9 CTAGTTGGGCATACGATGGC ACGCTTATGAACACC 192 55 76 RM147 99.8 10 TACGGCTTCGCGCGGCTGATTCC CCCCCCGAATCCATCCACAC 192 55 77 RM184 53.3 10 GCTCGCGCAATCAATCCAC CTGGATCGGACGAGGAGGGGGGGC 124 55 79 RM110 55.3 10 GCGCGGGAATCAATCACCAC CTGGATCAGAGAGGAGGAGG 124 55 80 RM527 3.9	69	RM404	60.9	8			236	<u> </u>
71 RM215 99.4 9 CAAAAIGGACAGCAAGAAGAC H0AGCACCTCTCTCTCTAGG 148 55 72 RM189 36 9 GGACAGGGTAAAGTGTTAGA CCTAAGACCTATCAACTCCA 108 55 73 RM242 72.3 9 GGCCAACGTGTATGTCTC TATATGCCAAGACGGATGGG 225 55 74 RM288 74.6 9 CCGGTCAGTTCAACTCTG ACGTACGGACGGACAGCA 192 55 75 RM316 1.8 9 CTAGTTGGGCATACGATGGC ACGTATATGTACGTCAACC 192 55 76 RM147 99.8 10 TACCGGCTCGGCGCGCGATTCC CCCCCCGAATCCATCCAACC 97 55 77 RM184 58.3 10 ACCCATCGACACGGCC TGACACTTGGAGAGGGGTGGGG 219 55 78 RM444 97.3 10 TCTCCCTCTCCACACTTGGT TGCGGCTCTCTCTCTCTCTCTC 259 55 79 RM110 55.3 10 GCTGTGAGATTGTAGGTACA GTAGTTATGGTACAGGAGA 124 55 80 RM527 3.9 10 CGGTGTAGATGTGGGCCATCA GTAGAGACCAGAGAGGA 125 50	70	RM105	32.1	9	GICGICGACCCAICGGAGCCAC		134	55
72 RM189 36 9 GGACAGGGTGAAAGTGTTAGA CCTAAGACCTATCAACTCA 108 55 73 RM242 72.3 9 GGCCAACGTGTGTATGTCTC TATATGCCAAGCGAGGGG 225 55 74 RM288 74.6 9 CCGGTCAGTTCAAGCTCG ACGTACGGACGACGAC 125 55 75 RM147 9.8 10 TACGGCTTCGGCGATACGATGC CCCCCGAATCCCATCGAAACCC 97 55 76 RM147 9.8 10 TACGGCTTCGGCGATTCC CCCCCGAATCCATCGAACC 97 55 77 RM184 58.3 10 ATCCCATTCGCCAAAACCGGCC TGACACTTGGAAGGAGGAGGGGG 219 55 78 RM484 97.3 10 TCTCCCTCTCACCATTGTC TGCTGGCCTCTCTCTCTCTC 259 55 79 RM110 55.3 10 CGCTGGAATGAACCA GTAGTTTAGTTATGCGCAA GTAGTTTAGGACAGAGGAG 124 55 80 RM527 3.9 10 CGGTGTAGGTGCCATTCC CAAGATCAAAGGAGGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGGAGGAG 258	71	RM215	99.4	9		IGAGCACCICCTICICIGIAG	148	55
73 RM242 72.3 9 GCCCAACGTIGIATATCTC TATATAGCCAAGCGGATGGG 225 55 74 RM288 74.6 9 CCGGTCAGTTCAAGCTCTG ACGTAGGACGAGCGAC 125 55 75 RM316 1.8 9 CTAGTTGGGCATACGATGGC ACGCTTATATGTTACGTCAAC 192 55 76 RM147 99.8 10 TACGGCTTGGCGGGTGTGTTCC CCCCCGAATCCATGGAAACCC 97 55 77 RM184 58.3 10 ATCCCCATTCGCCAAACCGGCC TGGACCTTGGAGAGGGGGGGGG 219 55 78 RM484 97.3 10 TCTCCCTCTCACCATTGTC TGCTGCCCTCTCTCTCTC 259 55 79 RM110 55.3 10 GCTGGGAATCAATCCAC CTGGATCTGGACAGAGGAG 124 55 80 RM527 3.9 10 CGGTGTAGATTGTAGGTCAA GTAGTTTAGTTAGTAGAGGAG 125 50 81 RM535 71.4 10 GGAACTAAACATGGTGCCATC CAAGATCAAGGAGAGA 125 50 82 RM116 41.7 11 TCACGCACAGCGGCGCC CTGCAGAGAGAGAGGAG 258 55	72	RM1896	36	9	GGACAGGGIAAAGIGITAGA	CCTAAGACCTATCAACTCCA	108	55
74 RM288 74.6 9 CCGGTCAGTTCAAGCTCIG ACGTACGGACGTGACGAC 125 55 75 RM316 1.8 9 CTAGTTGGGCATACGATGGC ACGTCTATATGTTACGTCAAC 192 55 76 RM147 99.8 10 TACGGCTTCGGCGGCGATACC CCCCCGAATCCATGGAAACCC 97 55 77 RM184 58.3 10 ATCCCATTCGCCAAACCGGCC TGCACCTTGGAGAGGGGGGGG 219 55 78 RM484 97.3 10 TCTCCCTCCTCACCATTGTC TGCTGCCCCTCTCTCTCTC 259 55 79 RM110 55.3 10 GCTCGCGAATCAATCCAC CTGGATCATGAAGAGGACGAG 124 55 80 RM527 3.9 10 CGGTGTAGATTGAGGTACA GTAGTTAGTATGTGGGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCAATGAAGGAAGGAG 228 55 82 RM116 41.7 11 TCACGCACAGGGAGGGGCGC CTGCAGGAGAAGGGAGGGG 238 55 83 RM139 121.3 11 GGCACTGGCGCAATTGATC GCTGGAGAAGGAGGAGGGAGGCGGC CTGCAGGAGAAGGAGGAGGAGG	73	RM242	72.3	9	GGCCAACGIGIGIATGICIC	TATATGCCAAGACGGATGGG	225	55
75 RM316 1.8 9 CTAGTTGGGCGATACGATGGC ACGCTTATATGTTAGGTCAAC 192 55 76 RM147 99.8 10 TACGGCTTCGGCGGCGTGATTCC CCCCCGAATCCCATCGAAACCC 97 55 77 RM184 58.3 10 ATCCCATTCGCCAAAACCGGCC TGACACTTGGAGAGGGGGTGGG 219 55 78 RM484 97.3 10 TCTCCCTCCTCACCATTGTC TGCTGGCCTCTCTCTCTCTC 259 55 79 RM110 55.3 10 GCTCGCGAATCAATCCAC CTGGATCTGGACAGAGGAGGA 124 55 80 RM527 3.9 10 CGGTGTAGATTGTAGGTGCAAG GTAGTTTAGTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCAATGAAGCAGAGAGGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAATGAAGGAGGAGG 238 55 83 RM139 121.3 11 GAGAGGAGGAGGAGGCGC CTGCCATGGCAGAGAGGAGGCC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTGATCC GCTGGGAGGAGGAGGAGGCGGC 13	74	RM288	74.6	9	CCGGTCAGTTCAAGCTCTG	ACGTACGGACGTGACGAC	125	55
76 RMI47 99.8 10 TACGGCTTCGGCGGCTGATTCC CCCCCGAATCCATCGAAACCC 97 55 77 RMI84 58.3 10 ATCCCATTCGCCAAAACCGGCC TGACACTTGGAGAGCGGTGTGG 219 55 78 RM484 97.3 10 TCTCCCTCTCACCATTGTC TGCTGCCCTCTCTCTCTCC 259 55 79 RMI10 55.3 10 GCTCGCGAATCAATCCAC CTGGATCCTGGACAGAGAGGAG 124 55 80 RM527 3.9 10 CGGTGTAGATGTAGGGACA GTAGTTTAGTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCAATGGAAGAGAGGAG 258 55 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGACAAGGAGAGAGGGCGC 278 55 83 RM139 121.3 11 GAGAGGAGAGGAGGCGGC CTGCACAGGGAAGTGAGAGAGGAGGCGGC 237 55 84 RM144 123.2 11 TGCCCTGGCGAAATTCACCT CTGGAGGAGACGTAGGAGTGGCAGGC 165 55 84 RM144 123.2 11 GACACGAGAGAGAGGAGGC TGGCCAGAGGAGGCGGC 16	75	RM316	1.8	9	CTAGTTGGGCATACGATGGC	ACGCTTATATGTTACGTCAAC	192	55
77 RM184 58.3 10 ATCCCATTCGCCAAAACCGGCC TGACACTTGGAGAGGCGGTGTGG 219 55 78 RM484 97.3 10 TCTCCCTCCTCACCATTGTC TGCTGCCCTCTCTCTCTCTC 259 55 79 RM110 55.3 10 GCTCGCGAATCAATCCAC CTGGATCTGGACAGAGGAG 124 55 80 RM527 3.9 10 CGGTGTAGATTGTAGGTACA GTAGTTTAGTTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCAAGGAAGGAGGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGGAGAGGAGGAG 238 55 83 RM139 121.3 11 GAGAGGAGGAGGAGGGGC CTGCCATGGCAGAGAGAGGAGCAGCAGAGGC 386 55 84 RM144 123.2 11 TGCCCTGGCCAAATTGATC GTGAGGAGAGCAGAGAGAGAGAGAGAGGAGC 386 55 84 RM144 123.2 11 CAAAATGGAGCAGCAGAGAG TGAGGACACTCCTTGTCTGTGTGAG 148 55 86 RM254 110 11 AGCACGTGATGAGATAAGATCACTC CTGGAGAGCATTGCTGTCGC </td <td>76</td> <td>RM147</td> <td>99.8</td> <td>10</td> <td>TACGGCTTCGGCGGCTGATTCC</td> <td>CCCCCGAATCCCATCGAAACCC</td> <td>97</td> <td>55</td>	76	RM147	99.8	10	TACGGCTTCGGCGGCTGATTCC	CCCCCGAATCCCATCGAAACCC	97	55
78 RM484 97.3 10 TCTCCCTCCTCACCATTGTC TGCTGCCCTCTCTCTCTCCTC 259 55 79 RM110 55.3 10 GCTCGCGAATCAATCCAC CTGGATCCTGGACAGACGAG 124 55 80 RM527 3.9 10 CGGTGTAGATTGTAGGTACA GTAGTTTAGTTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCACATGAAGGAGAGGGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGGAAAGGGAGGGG 258 55 83 RM139 121.3 11 GAGAGGGAGGAGGAGGCGGC CTGCCATGGCAGAAAGGGAGGCGGC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTGATCC GCTAGAGGAGGAGGAGGCAGC 1763GGAGGAGGAGGCGGC 1763GGAGGAGGAGGCAGCAAGAGC 1763GGCGAATGGAGCAAGAGGC 1783 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGG TGAGCACCTCCTTCTGTGGAGGAGGAGGC 165 55 86 RM254 110 11 AGCCCGAATAAATCACCCT CTGGGAGGAGGCAGCTGTGCC 195 55 87 RM52	77	RM184	58.3	10	ATCCCATTCGCCAAAACCGGCC	TGACACTTGGAGAGCGGTGTGG	219	55
79 RM1101 55.3 10 GCTCGCGAATCAATCCAC CTGGATCCTGGACAGACGAG 124 55 80 RM527 3.9 10 CGGTGTAGATTGTAGGTACA GTAGTTTAGTTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCAAGGCATGAAAGGAGGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGCATGAAAGGAGGGG 258 55 83 RM139 121.3 11 GAGAGGGAGGAGGAGGCGGC CTGCCATGGCAGAGAAGGGGGCC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTGATCC GCTAGAGGAGAGAAGGGGGCC 386 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTGTAGG 148 55 86 RM254 110 11 AGCCAGTGTGGATTCAGTG TGCTCAACGTTGGAGCGC 165 55 87 RM552 40.6 11 CGCAGTGTGCATGACCCCTTGATC TGTCTCCTCTTGGTTGG 143 55 88 RM374 8.6 11 AGCAATGCACTGCCTGATGAACG TCACCTGGTCAGCCTCTTTC 124	78	RM484	97.3	10	TCTCCCTCCTCACCATTGTC	TGCTGCCCTCTCTCTCTCTC	259	55
80 RM527 3.9 10 CGGTGTAGATTGTAGGTACA GTAGTTTAGTTATTGCGCAC 184 55 81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCACATGAAGAGGAG 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGCCATGAAAGGAGGGG 258 55 83 RM139 121.3 11 GAGAGGGAGGAGGAGGCGC CTGCCATGGCAGAGAGAGGAGGCGC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTGATCC GCTAGAGGAGAAGGAGAGGAGGAGGCAGC 386 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTCTCTGTAG 148 55 86 RM254 110 11 AGCCCGAATAATCCACCT CTGGAGGAGCACTTGGTAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTCAGTG TGCTCACGTTGTGCTTTGG 143 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGCACTGGCCAACGCC 124 55 90	79	RM1108	55.3	10	GCTCGCGAATCAATCCAC	CTGGATCCTGGACAGACGAG	124	55
81 RM535 71.4 10 GGAACTAAACATGGTGCAAG ACCAGATCACATGAAGAGAGA 125 50 82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGCCATGAAAGGAGGGG 258 55 83 RM139 121.3 11 GAGAGGGAGGAGGAGGCGGC CTGCCATGGCAGAGAGGGAGGCC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTTGATCC GCTAGAGGAGAGTGGTGCATG 237 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTCTGTGAG 148 55 86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGGAGCATTTGGTAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCTAACGTTGACTGTCC 195 55 88 RM374 8.6 11 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTGACAACG 131 55 91 RM31 65.5 12 TGCTACAAGTGTTCTCAGGAC GCTCACCTTTTGTGTTCAC 111	80	RM5271	3.9	10	CGGTGTAGATTGTAGGTACA	GTAGTTTAGTTATTGCGCAC	184	55
82 RM116 41.7 11 TCACGCACAGCGTGCCGTTCTC CAAGATCAAGCCATGAAAGGAAGGGAGG 258 55 83 RM139 121.3 11 GAGAGGGAGGAAGGGAGGCGC CTGCCATGGCAGAGAAGGGAGGCC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTTGATCC GCTAGAGGAGATCAGATGGTAGTGCATG 237 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTGTGTAG 148 55 86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGCAGTTGGAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCTACACGTTTGGTTGGC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGCTCTCCTCTGGTTGGG 143 55 90 RM235 91.3 12 AGAAGCTAGGGCTAACGAC TCACCTGGTCAACGCC 111 55 90 RM247 32.3 12 TAGTGCCGATCGATGTACGAC GCTAACATTGATGATCAC 124 55 91 <t< td=""><td>81</td><td>RM5352</td><td>71.4</td><td>10</td><td>GGAACTAAACATGGTGCAAG</td><td>ACCAGATCACATGAAGAGGA</td><td>125</td><td>50</td></t<>	81	RM5352	71.4	10	GGAACTAAACATGGTGCAAG	ACCAGATCACATGAAGAGGA	125	50
83 RM139 121.3 11 GAGAGGGAGGAAGGGAGGCGC CTGCCATGGCAGAGAGGGAGGGCGC 386 55 84 RM144 123.2 11 TGCCCTGGCGCAAATTTGATCC GCTAGAGGAGATCAGATGGTAGTGCATG 237 55 85 RM215 85.7 11 CAAAATGGAGCAGCAGCAAGAGC TGAGCACCTCCTTCTCTGTAG 148 55 86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGGAGTTGGAGCAGCAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTCAGTG TGCTCAACGTTTGACTGTCC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTGAGCAC 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92	82	RM116	41.7	11	TCACGCACAGCGTGCCGTTCTC	CAAGATCAAGCCATGAAAGGAGGG	258	55
84 RM144 123.2 11 TGCCCTGGCGCAAATTTGATCC GCTAGAGGAGATCAGATGGTAGTGCAGTG 237 55 85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTCTCTGTAG 148 55 86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGCATTTGGTAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCAACGTTTGACTGTCC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGAGCA 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTACACTTTTGTGATACAC 128 55 92 RM188 9.4 12 ACCACTAAATAGCACATAC GGCATCATACATTACATTAAATAC 128 55 93 RM2	83	RM139	121.3	11	GAGAGGGAGGAAGGGAGGCGGC	CTGCCATGGCAGAGAAGGGGCC	386	55
85 RM215 85.7 11 CAAAATGGAGCAGCAAGAGC TGAGCACCTCCTTCTCTGTAG 148 55 86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGCATTTGGTAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCAACGTTTGACTGTCC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATGATGCTAC 159 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGATGCTAC 159	84	RM144	123.2	11	TGCCCTGGCGCAAATTTGATCC	GCTAGAGGAGATCAGATGGTAGTGCATG	237	55
86 RM254 110 11 AGCCCCGAATAAATCCACCT CTGGAGGAGCATTTGGTAGC 165 55 87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCAACGTTTGACTGTCC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAA 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCTAC 159 55 95 RM333	85	RM215	85.7	11	CAAAATGGAGCAGCAAGAGC	TGAGCACCTCCTTCTCTGTAG	148	55
87 RM552 40.6 11 CGCAGTTGTGGATTTCAGTG TGCTCAACGTTTGACTGTCC 195 55 88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAA 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTGGTTACTCG 169 55<	86	RM254	110	11	AGCCCCGAATAAATCCACCT	CTGGAGGAGCATTTGGTAGC	165	55
88 RM374 8.6 11 AGCAATGCACTCCCTTGATC TGTCTTCCTCCTTGGTTTGG 143 55 89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTCAGGAC GCTCACCTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	87	RM552	40.6	11	CGCAGTTGTGGATTTCAGTG	TGCTCAACGTTTGACTGTCC	195	55
89 RM235 91.3 12 AGAAGCTAGGGCTAACGAAC TCACCTGGTCAGCCTCTTTC 124 55 90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	88	RM3747	8.6	11	AGCAATGCACTCCCTTGATC	TGTCTTCCTCCTTGGTTTGG	143	55
90 RM247 32.3 12 TAGTGCCGATCGATGTAACG CATATGGTTTTGACAAAGCG 131 55 91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	89	RM235	91.3	12	AGAAGCTAGGGCTAACGAAC	TCACCTGGTCAGCCTCTTTC	124	55
91 RM313 65.5 12 TGCTACAAGTGTTCTTCAGGAC GCTCACCTTTTGTGTTCCAC 111 55 92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCG 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	90	RM247	32.3	12	TAGTGCCGATCGATGTAACG	CATATGGTTTTGACAAAGCG	131	55
92 RM188 9.4 12 ACCACTAAATAAGCACATAC GGCATCATACATTAAAATAAC 128 55 93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	91	RM313	65.5	12	TGCTACAAGTGTTCTTCAGGAC	GCTCACCTTTTGTGTTCCAC	111	55
93 RM252 79.1 12 CATTAAAATCAGTGGGACTG AGGCATTTCCTGATATGATC 134 55 94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	92	RM1880	9.4	12	ACCACTAAATAAGCACATAC	GGCATCATACATTAAAATAC	128	55
94 RM 297 65.3 12 GAGCCAATATGTTGTCTTGA GTTCAGATCATGATGCCTAC 159 55 95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	93	RM2529	79.1	12	CATTAAAATCAGTGGGACTG	AGGCATTTCCTGATATGATC	134	55
95 RM333 89.5 12 CCTCCTCCATGAGCTAATGC AGGAGGAGCGGATTTCTCTC 129 50 96 RM710 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	94	RM 297	65.3	12	GAGCCAATATGTTGTCTTGA	GTTCAGATCATGATGCCTAC	159	55
96 RM7102 71.85 12 TTGAGAGCGTTTTTAGGATG TCGGTTTACTTGGTTACTCG 169 55	95	RM3331	89.5	12	CCTCCTCCATGAGCTAATGC	AGGAGGAGCGGATTTCTCTC	129	50
	96	RM7102	71.85	12	TTGAGAGCGTTTTTAGGATG	TCGGTTTACTTGGTTACTCG	169	55

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