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Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig



# Short communication

# Flanking region variation of ForenSeq<sup>TM</sup> DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans



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## ARTICLE INFO

Article history: Received 16 December 2016 Received in revised form 1 February 2017 Accepted 24 February 2017 Available online 27 February 2017

Keywords: Sequence variation STR SNP Flanking region ForenSeq<sup>™</sup> DNA Signature Prep Kit Massively parallel sequencing STRait Razor v2s

## ABSTRACT

Massively parallel sequencing (MPS) offers advantages over current capillary electrophoresis-based analysis of short tandem repeat (STR) loci for human identification testing. In particular STR repeat motif sequence information can be obtained, thereby increasing the discrimination power of some loci. While sequence variation within the repeat region is observed relatively frequently in some of the commonly used STRs, there is an additional degree of variation found in the flanking regions adjacent to the repeat motif. Repeat motif and flanking region sequence variation have been described for major population groups, however, not for more isolated populations. Flanking region sequence variation in STR and single nucleotide polymorphism (SNP) loci in the Yavapai population was analyzed using the ForenSeq<sup>™</sup> DNA Signature Prep Kit and STRait Razor v2s. Seven and 14 autosomal STRs and identity-informative single nucleotide polymorphisms (iiSNPs), respectively, had some degree of flanking region variation. Three and four of these identity-informative loci, respectively, showed  $\geq 5\%$  increase in expected heterozygosity. The combined length- and sequence-based random match probabilities (RMPs) for 27 autosomal STRs were  $6.11 \times 10^{-26}$  and  $2.79 \times 10^{-29}$ , respectively. When combined with 94 iiSNPs (a subset of which became microhaplotypes) the combined RMP was  $5.49 \times 10^{-63}$ . Analysis of length-based and sequencebased autosomal STRs in STRUCTURE indicated that the Yavapai are most similar to the Hispanic population. While producing minimal increase in X- and Y-STR discrimination potential, access to flanking region data enabled identification of one novel X-STR and three Y-STR alleles relative to previous reports. Five ancestry-informative SNPs (aiSNPs) and two phenotype-informative SNPs (piSNPs) exhibited notable flanking region variation.

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# 1. Introduction

Forensic DNA typing currently utilizes length-based separation of polymerase chain reaction (PCR)-amplified short tandem repeats (STRs) for routine casework. Massively parallel sequencing (MPS) elucidates an additional level of STR motif variation at the sequence level, increasing diversity [1–3]. Sequence-based STR information may add value in kinship analyses and complex

http://dx.doi.org/10.1016/j.fsigen.2017.02.014 1872-4973/© 2017 Elsevier B.V. All rights reserved. mixture de-convolution efforts. While some commonly used STR loci lack STR-motif sequence variation, they may harbor variation in the flanking regions of the amplicon [3,4]. The same concept for single nucleotide polymorphisms (SNPs) also may apply [5,6]. That is, the current SNPs in MPS kits may indeed be microhaplotypes and their amplicons may contain additional information. While Novroski, et al. [3] described STR flanking region variation in major populations, such variation in Native Americans has yet to be described. Potential genetic variation in flanking regions adjacent to 59 STRs and 172 SNPs in the ForenSeq<sup>™</sup> DNA Signature Prep Kit's primer panel was investigated in the Yavapai Native American population. The results show a moderate degree of STR and SNP flanking region genetic variation in the Yavapai population.

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## 2. Material and methods

MPS data for 27 autosomal, 7 X-chromosomal, and 25 Ychromosomal STRs, Amelogenin, and 94 identity-informative SNPs (iiSNPs), 56 ancestry-informative SNPs (aiSNPs), and 22 phenotype-informative SNPs (piSNPs) were generated from DNA samples from 62 Yavapai Native Americans [7–9]. The samples and typing methods were described previously by Wendt, et al. [10]. Fastq files were used as standard input for STRait Razor v2s [3,11] to identify flanking region sequence variation.

5X depth of coverage (DoC) and 0.20 allele coverage ratio (ACR) thresholds were applied to the data. In-house Excel-based workbooks and Genetic Data Analysis (GDA) [12] were used to compile length-based and sequence-based allele frequencies, calculate observed and expected heterozygosities ( $H_o$  and  $H_e$ , respectively), perform tests for departures from Hardy-Weinberg Equilibrium (HWE) and detection of pairwise linkage disequilibrium (LD), compare previously published observed allele frequencies to the Yavapai data using the Chi-Squared Goodness of Fit Test, and generate random match probabilities (RMPs). STRUCTURE v2.3.4 (July 2012) [13–15] was used to assess the genetic structure of the Yavapai relative to the major populations described by Novroski, et al. [3] using length-based and sequence-based autosomal STRs.

A length-based STR allele is defined as only the capillary electrophoresis (CE)-based allele call and a sequence-based STR allele as the repeat motif plus flanking region sequence information, presented herein as full string sequence and condensed nomenclature consistent with the recommendations of Parson et al., 2016 [16]. SNPs do not have a length-based allele call. Here we use the term "SNP" to describe the target SNP marker only or the MPS-based marker with invariable flanking sequences and "microhaplotype" to describe an entire string sequence that includes the target SNP plus adjacent flanking region sequence variation. All SNP and microhaplotype string sequences also are paired with a condensed nomenclature consistent with recommendations by Parson et al. [16].

#### 3. Results and discussion

The total number of loci analyzed herein includes 27 autosomal, 7 X-chromosomal, and 25 Y-chromosomal STRs, Amelogenin, and 94 iiSNPs, 56 aiSNPs, and 15 piSNPs (or piSNP-containing microhaplotypes) [3,11].

# 3.1. Sequencing performance

Analysis of MiSeq FGx Forensic Genomics System sequence data (with the ForenSeq<sup>TM</sup> DNA Signature Prep Kit) using STRait Razor v2s and the previously reported ForenSeq<sup>TM</sup> Universal Analysis Software (UAS) [6] produced slightly different DoCs due to the length differences of the analyzed string sequences. The average DoC and ACR using STRait Razor v2s were 1,600X  $\pm$  1730 and 0.782  $\pm$  0.147, respectively, for 59 STRs and Amelogenin (data not shown), and 1,310X  $\pm$  911 and 0.830  $\pm$  0.132, respectively, for 165 target SNPs and SNP microhaplotypes (data not shown).

#### 3.2. Flanking region variation

A full discussion of length-based and repeat motif variation for ForenSeq<sup>TM</sup> DNA Signature Prep Kit STR loci in the Yavapai population can be found in Wendt, et al. [6]. It should be noted that the string sequences analyzed by STRait Razor v2s are operationally defined, based on primer placement, to maximize data recovery from the ForenSeq<sup>TM</sup> DNA Signature Prep Kit amplicon for each marker [11]. As primer sequences of commercially available MPS library preparation kits are refined or modified, the

genomic coordinates of each amplicon may change, influencing the flanking region variation that can be observed for each target marker.

# 3.2.1. STRs

Relative to major population groups, few loci in the Yavapai population had flanking region sequence variation. Seven autosomal STRs (D13S317, D16S539, D18S51, D20S482, D2S441, D5S818, and D7S820) exhibited flanking region variation (Tables 1 and 2 and Supplemental Table 1). HWE and pairwise LD *p*-values for autosomal STRs and all other marker types, where appropriate, are listed in Supplemental Tables 2 and 3. Under the assumption of independence, the combined length-based and sequence-based RMPs for six autosomal STRs with flanking region variation were  $1.80 \times 10^{-5}$  and  $7.80 \times 10^{-8}$ , respectively.

Founder effects and population isolation of Native American populations suggest that these groups may exhibit lower genetic diversity than major population groups. Relative to Novroski, et al. [3], the Yavapai exhibited more loci with repeat region variation only and flanking region variation only than major United States populations but substantially less loci with variation in both regions (Fig. 1). Assuming the populations in Novroski, et al. [3] represent K = 4 (AFA, CHI, CAU, and HIS), STRUCTURE analysis of length-based and sequence-based autosomal STRs indicate that the Yavapai are most similar to the HIS population (data not shown).

Little flanking region variation was observed in the seven ForenSeq<sup>TM</sup> DNA Signature Prep Kit X-STR loci (Tables 1 and 2 and Supplemental Table 4). The allele, DXS10074 [CE 15]-GRCh38-ChrX:67757300-67757464 (AAGA)12 AAGG (AAGA)2 67757338-A, was observed once at the DXS100074 locus in the Yavapai. After Bonferroni correction (p < 0.00238), two significant pairwise LDs containing DXS10074 (DXS10074/DXS10135 and DXS10074/ DXS7132) were observed (p = 0.0015 and 0.0021, respectively). While not observed with length-based X-STR alleles [10], significant LD between DXS10074/DXS7132 is not surprising as they are part of a linkage block [18,19].

Minimal variation was observed in the Y-STR flanking regions. Two Y-STRs (DYS389I and DYS389II) exhibited flanking region sequence variation (Tables 1 and 2 and Supplemental Table 5).

One X- and three Y-STR alleles with flanking region variation in the Yavapai population were not reported by Novroski, et al. [3] ( Table 2). These novel observations may be the result of sampling error within the populations studied to date; however, given their relatively high frequencies, these alleles may be common variants within Yavapai (or other Native Americans). Future studies of larger Native American cohorts would better characterize the distribution of these alleles within and between Native American groups.

#### 3.2.2. SNPs

To our knowledge, string sequences for target SNPs and microhaplotypes captured by the ForenSeq<sup>TM</sup> DNA Signature Prep Kit have not been published previously (Supplemental Table 6). Twenty two target iiSNPs had flanking region variation adjacent to the target SNP (Table 1). Eight (8/22) provided no increase in the number of alleles at their respective loci. For example, an iiSNP microhaplotype contains the target SNP rs1015250 (G/C) and a flanking SNP rs6475200 (A/G) (Supplemental Table 6). In this population, the target SNP G allele is always observed with the flanking SNP A allele and the target SNP C allele is always observed with the flanking SNP G allele. Four iiSNP microhaplotypes, containing the target SNPs: rs10776839, rs1109037, rs2830795, and rs876724, substantially increased in diversity compared to the target iiSNPs alone. These markers exhibited an average H<sub>0</sub> increase of 0.318  $\pm$  0.190, with a range of 0.0645–0.500. Assuming

# Table 1

Average allele or haplotype frequencies for autosomal, X-chromosomal, and Y-chromosomal short tandem repeat (STR) and identity-informative (iiSNP), ancestryinformative (aiSNP), and phenotype-informative (piSNP) single nucleotide polymorphism (SNP) loci with flanking region sequence variation and their resulting impact on observed ( $H_o$ ) and expected heterozygosities ( $H_e$ ), single-locus random match probabilities (RMPs), and haplotype diversity relative to typing length-based STRs or target SNPs only. A comparison of sequence based allele frequencies from Novroski, et al. [3] was performed; *p*-values for significantly different allele frequencies are <0.05.

-	Marker Type	Number of Loci with Flanking Region Variation	Average Frequency	Average H <sub>o</sub> Increase	Average H <sub>e</sub> Increase	Average Single Locus RMP Decrease	Haplotype Frequency Decrease	Haplotype Diversity Increase	Comparison to Novroski, et al. [3] populations data	Additional Comments
-	Autosomal STR	7	$0.0704 \pm 0.0967$	$0.0553 \pm 0.0500$	$0.0516 \pm 0.0483$	$0.0400 \pm 0.0409$	-	-	<ul> <li>26 significantly differed from all four populations</li> <li>D12S391 differed from AFA, CHI, and CAU, but not HIS</li> </ul>	• Greatest RMP de- crease for D2S441 (0.13)
	X-STR	1	0.0139	0	0.03	-	-	-	<ul> <li>DXS10103, DXS10135, DXS7423, HPRTB differed from all four populations</li> <li>DXS7132 similar to all four popula- tions</li> <li>DXS10074 similar to HIS</li> <li>DXS8378 similar to CHI and HIS</li> </ul>	One novel allele observed (Table 2)
	Y-STR	2	0.136±0.0273	_	_	_	0	0	<ul> <li>DYF38751, DYS19, DYS385ab, DYS437, DYS438, DYS481, DYS570, and DYS635 dif- fered from AFA, CHI, CAU, and HIS</li> <li>DYS389II, DYS505, DYS533, and DYS549 differed from three popu- lations</li> <li>DYS391, DYS392, DYS448, DYS576, DYS643, and Y- GATA-H4 differed from two popula- tions</li> <li>DYS389I, DYS390, DYS480, and DYS522 differed from one popula- tion</li> <li>DYS439 was simi- lar to all four</li> </ul>	• Three novel alleles observed at DYS3891 and DYS3891I in the same three indi- viduals (Table 2)
	iiSNP	22	$0.121\pm0.150^{*}$	$0.109 \pm 0.166^{^{*}}$	$0.0865 \pm 0.123^{^\circ}$	$0.0900 \pm 0.115^{*}$	-	-	-	<ul> <li>14/22 provided in- creased heterozy- gosity and allele spread</li> </ul>
	aiSNP	6	$0.191 \pm 0.215^{^{*}}$	$0.116 \pm 0.144^{^{*}}$	$0.130 \pm 0.171^{*}$	-	-	-	-	• 5/6 provided in- creased heterozy- gosity and allele spread, two are previously reported [17,18]
	piSNP	2	$0.0524 \pm 0.0627$	0.161	$\textbf{0.0895} \pm \textbf{0.122}$	_	-	-	-	-

 $^{*}$  Reported values are based on the indicated subset of loci showing increase in allele spread.

independence, the combined 14-locus RMPs for iiSNPs and their corresponding iiSNP microhaplotypes were  $1.06\times 10^{-5}$  and  $1.67\times 10^{-7}$ , respectively. The flanking region variation of 14 iiSNP

microhaplotypes supports that a relatively small panel of microhaplotypes might be as informative as some low performing STR markers. Many iiSNPs lacked flanking region variation in the

# Table 2

Allele frequencies, observed (H<sub>o</sub>) and expected (H<sub>e</sub>) heterozygosities, and Hardy-Weinberg Equilibrium (HWE) *p*-values for length-based (LB) short tandem repeats (STRs), sequence-based (SB) STRs, single nucleotide polymorphisms (SNPs), and SNP-containing microhaplotypes which exhibited an increase in number of alleles due to sequence variation in the flanking regions adjacent to the target motif. Bolded and underlined regions indicate target repeat motif and flanking sequence variation, respectively; bolded and italicized HWE *p*-values are significant after Bonferroni correction for that specific marker type.

DT33311 (u=154)	2.10			and the	20 W	
18 Allele	Count	Frequency	String Sequence TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	SB Nomenclature	Count	Frequency
0	100 - 100 - 200	0.0505	TCTGTCTTTTTGGG TCTGACECATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	013331/ Icc el-aucilia: 13-0514/300-0514020/ (14)/Cb	10	0.0505
9	42	0.339	TETETETETETTTTTG66	0135317 [CE 9]-GRCh38-Chr13-82147986-82148107 (TATC)9	42	0.339
10	4	0.0323	ATCHTECTGTCTGTCTTTTGGG	82148069-T	7	0.323
- 			TETGACECATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	D13S317 [CE 11]-GRCh38-Chr13-82147986-82148107 (TATC)11 82148069-T	11	0.0887
11	39	0.315	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	0135317 [CE 11]-GRCh38-Chr13-82147986-82148107 (TATC]11	28	0.226
			TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	0135317 [CE 12]-GRCh38-Chr13-82147986-82148107 (TATC)12	11	0.0887
12	22	0.177	ATCTATCTATCTTTCTGTCTGTCTTTTTGGG TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC	82148069-T		0.0067
	201	0.553	ATCTATCTATCTATCTATCTATCTATCTATCTATCTATC	D13531/ [CE 12]-GRCh38-Chr13-8214/986-8214810/ [TATC]12	11	1380.0
13	9	0.0726	AATCATCTATCTATCTTTCTGTCTGTCTTTTTGGG	D135317 [CE 13]-GRCh38-Chr13-82147985-82148107 (TATC)13	9	0.0726
14	1	0.00806	TETGACCCATCTAACGCCTATCTGTATTTACAAATACATTACTATCTAT	D13S317 [CE 14]-GRCh38-Chr13-82147985-82148107 (TATC)14	1	0.00806
18 H, 0.751			SB H. 0.808 SB H. 0.742			
LB HWE p-value: 0	0.221		58 HWE p-value: 0.0253			
D165539 (n=124)						
LB Allele	Count	Frequency	String Sequence	SB Nomenclature	Count	Frequency
9	15	0.121	CAGAGATGGATGGATGGATAGATAG	86352761-C	12	0.0968
8	1.5	0.121	TECTETTECETAGATCAATACAGACAGACAGACAGGACAG	D16S539 [CE 9]-GRCh38-Chr16-86352664-86352781 (GATA)9	3	0.0242
			TCCTCTTCCCCTAGATCAATACAGACAGACAGACAGACAG	0165539 [CE 10]-GRCh38-Chr16-86352664-86352781 (GATA)10	20	0.161
10	26	0.210	AAAQLOKONGATIGGATIGGATIGATIAG. TECTCTTECCTAGATCAATACAGACAGACAGACAGACAGGTG <b>GATAGATAGATAGATAGATAGATAGATAGATAGA</b>	80332701-C 0165539 [CE 10].GBCb38.Cbr16.86352664.86352781 (GATA)10	6	0.0484
			AAAACAGAGATGGATGATAGATAC TECTETTECETAGATCAATACAGACAGACAGACAGGTGGATAGATAGATA	D165539 [CF 11]-GRCh38-Cbr16-86352664-86352781 (GATA)11		0.0-10-1
11	30	0.242	AGACAAAQCAGAGATGGATGGATAGATAG	86352761-C	9	0.0726
		200203	TECTETTECETAGATEAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGA	D165539 [CE 11]-GRCh38-Chr16-86352664-86352781 (GATA)11	21	0.169
12	46	0.371	TECTETTECETAGATCAATACAGACAGACAGACAGACAGGTG <b>GATAGATAGATAGATAGATAGATAGATAGATAGA</b>	0165539 [CE 12]-GRCh38-Chr16-86352664-86352781 (GATA)12	46	0.371
18	5	0.0403	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATA	0165539 [CE 13]-68Cb38-Cbr16-86352664-86352781 (6ATA)13	5	0.0403
	-	0.0403	ATCATTGAAAGACAAAAACAGAGATGGATGGATGGATAGATA	oressa fer tal dicito cinto oparación desarror (anin)ta	-	0.0405
14	2	0.0161	AGATATCATTGAAAGACAAAACAGAGATGGATGATAGATA	D165539 [CE 14]-GRCh38-Chr16-86352664-86352781 (GATA)14	2	0.0161
LB H <sub>e</sub> 0.749 LB H <sub>e</sub> 0.790			S8 H <sub>6</sub> 0.795 S8 H <sub>9</sub> 0.790			
LB HWE p-value: 0	0.354		58 HWE p-value: 0.347			
D18551 (n=124)	_				_	
US Anele	Lount	hrequency:	String Sequence GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	SIG Nomendature	Count	Prequency 0.00806
	A.	0.00000	AGTAGCAACTGTTATTGTAAGA	019331 [Ct 11]-040139-01119-03191005-03191130 [MOWH]11		0.00606
12	10	0.0806	GICICABAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 12]-GRCh38-Chr18-63281662-63281796 (AGAA)12	10	0.0806
13	22	0.177	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 ICE 13I-GRCh38-Chr18-63281662-63281796 (AGAA)13	22	0.177
			AAAGAAATAGTAGCAACTGTTATTGTAAGA GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA			
14	12	0.0968	AAAGAAAAGAAATAGTAGCAACTGTTATTGTAAGA	D18221 [ct 14]-ORCU28-CULIS-03181007-03181/30 [HOMA]14		0.0968
	0.842		CITTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			
15	9	0.0726	GTCTC <b>AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG</b>	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15	9	0.0726
15	9 24	0.0726 0.193	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16	9	0.0726
15 16	9 24	0.0726	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 (CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 (CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 (CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17	9 24 30	0.0726
15 16 17	9 24 31	0.0726 0.193 0.250	GTCTCAGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17	9 24 30	0.0726 0.194 0.242
15 16 17	9 24 31	0.0726 0.193 0.250	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 63281740-6	9 24 30 1	0.0726 0.194 0.242 0.00806
15 16 17 18	9 24 31 2	0.0726 0.193 0.250 0.0161	GTCTCAGAAGAAAGAAGAAGAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 E3281740-G D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18	9 24 30 1 2	0.0726 0.194 0.242 0.00806 0.0161
15 16 17 18 19	9 24 31 2 2 2	0.0726 0.193 0.250 0.0161 0.0161	GTCTCAGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19	9 24 30 1 2 2	0.0726 0.194 0.242 0.0806 0.0161 0.0161
15 16 17 18 19 20	9 24 31 2 2 2 5	0.0726 0.193 0.250 0.0161 0.0161 0.0403	GTCTCAGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)20	9 24 30 1 2 2 2 5	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0403
15 16 17 18 19 20	9 24 31 2 2 2 5	0.0726 0.193 0.250 0.0161 0.0161 0.0403	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 B3281710-6 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)20	9 24 30 1 2 2 5	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0403
15 16 17 18 19 20 22 18 H 0 950	9 24 31 2 2 2 5 5 6	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 29]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22	9 24 30 1 2 2 5 5 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0403 0.0484
15 16 17 18 19 20 22 18 H; 0.850 18 H; 0.850 18 H; 0.855	9 24 31 2 2 5 5 6	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22	9 24 30 1 2 2 5 5 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0403 0.0484
15 16 17 18 19 20 22 18 H <sub>2</sub> 0.850 18 H <sub>2</sub> 0.855 18 HWE p-value	9 24 31 2 2 5 5 6	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22	9 24 30 1 2 2 5 5 5	0.0726 0.194 0.242 0.00806 0.0161 0.0463 0.0463
15 16 17 18 19 20 22 18 He 0.850 18 Ho 0.850 18 HWE p-value P203422 (m12) 18 AMME p-value	9 24 31 2 2 5 5 5 6 ***************************	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22	9 24 30 1 2 2 5 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0463
15 16 17 18 19 20 22 18 H+, 0.850 18 H, 0.855 18 H/W, Pavaluu D203482 (n=12 18 Allele	9 24 31 2 2 5 5 6 8 8 24) Cou	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 0 0 0 0.0484	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CF 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22	9 24 30 1 2 2 5 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0463 0.0484
15 16 17 18 19 20 22 LB H <sub>2</sub> 0.850 LB H <sub>2</sub>	9 24 31 2 5 5 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0.0726 0.193 0.250 0.0161 0.0161 0.0163 0.0403 0.0484 0 0 Frequency 0.0484	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 63281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 S8 Nonvenclature D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12	9 24 30 1 2 2 5 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0484
15 16 17 18 19 20 22 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> P.valut <b>D205482</b> (n=12 LB Allele 12 13	9 24 31 2 2 5 6 e: 0.0087 24) Cou 6 28	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 e3281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13	9 24 30 1 2 2 5 5 5 5 5 5 27	0.0726 0.194 0.242 0.08806 0.0161 0.0161 0.0463 0.0484 Fréquency 0.0484 0.218
15 16 17 18 19 20 22 18 He 0.850 18 He 0.850 18 He 0.850 18 He 0.855 18 He 0.850 18 He 0.850 18 He 0.850 18 He 0.850 18 He 0.850 19 He 0.850 19 He 0.850 10 He 0.850 11 He 0.850 12	9 24 31 2 2 5 6 5 6 6 224 224 224 224 224 228	0.0726 0.193 0.250 0.0161 0.0161 0.0463 0.0484 0 0 Frequency 0.0484	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13	9 24 30 1 2 2 5 6 6 2 7 1	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0464 5Fequency 0.0484 0.218 0.00807
15 16 17 18 19 20 22 18 H, 0.850 18 H, 0.855 18 H, 0.855 19 H, 0.855 10 H, 0.855 11 H, 0.855 11 H, 0.855 11 H, 0.855 11 H, 0.855 11 H, 0.855 11 H, 0.855 12 H, 0.855 13 H, 0.855 14 H, 0.855 15 H, 0.855 15 H, 0.855 15 H, 0.855 16 H, 0.855 17 H, 0.855 17 H, 0.855 18	9 24 31 2 2 5 6 6 6 6 28	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 Frequency 0.0484	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 14]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 23]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr28-6328771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14	9 24 30 1 2 2 5 6 6	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0464 Fréquency 0.0484 0.218 0.0287 0.2540
15 16 17 18 19 20 22 18 H, 0.850 18 H, 0.850 18 H, 0.850 18 H, 0.850 18 H, 0.850 18 H, 0.850 18 H, 0.850 19 H, 0.850 19 H, 0.850 19 H, 0.850 19 H, 0.850 10	9 24 31 2 2 5 6 6 6 6 28 28 73	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 tr Frequency 0.0484 0.226 0.589	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGAAAG	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 53281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 14]-GRCh38-Chr20-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525774 (A525771 (AGAT)14	9 24 30 1 2 2 5 6 6 7 6 27 1 6 6 27	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0403 0.0440 0.0484 0.0484 0.0484 0.0484 0.01867 0.0484
15 16 17 18 19 20 22 18 H+0.0800 18 H+0.0805 18 H+0.0855 18 H+0.0855 18 H+0.0855 18 H+0.0855 18 H+0.0855 18 H+0.0850 18 H+0.0850 19 H+0.0850 18 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 19 H+0.0850 10 H+0.0850 10 H+0.0850 10 H+0.0850 10 H+0.0850 11 H+0.0855 11 H+0.0850 12	9 24 31 2 2 5 6 6 6 6 24 6 24 26 73	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 tt Frequency 0.0484 0.226 0.589	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGAAAG	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 53281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T	9 24 30 1 2 2 5 5 5 5 5 5 7 5 7 1 67 57 5	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0464 0.0464 0.218 0.00607 0.546 0.546
15 16 17 18 19 20 22 LB H <sub>2</sub> 0.850 LB H <sub>2</sub> 0.850 12 12 13 14	9 24 31 2 2 2 5 6 6 6 2 8 2 8 73 14	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0403 0.0484 0.0484 0.226 0.589 0.113	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 53281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 23]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 4525680-T D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 9205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14	9 24 30 1 2 2 5 5 5 5 5 6 27 1 5 6 11	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0484 0.0484 0.218 0.0484 0.218 0.00807 0.546 0.546
15 16 17 18 19 20 22 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> 0.850 LB H <sub>0</sub> 0.850 11 12 13 14	9 24 31 2 2 2 5 6 6 6 24 20 6 28 73 73 14	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0.0484 0.0484 0.226 0.589 0.113	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGAAAG	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14	9 24 30 1 2 2 5 5 5 5 5 5 5 7 1 67 6 11 3	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0484 0.0484 0.218 0.0484 0.218 0.00807 0.540 0.0484 0.0887 0.0241
15 16 17 18 19 20 22 18 He 0.850 18 Ho 0.850 18 Ho 0.850 19 Hove P value 12 13 14 15 16	9 24 31 2 2 2 5 6 6 24) 6 24) 6 28 73 73 14	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0.0484 0.0484 0.226 0.589 0.113 0.0242	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 d575603-	9 24 30 1 2 5 5 6 7 6 27 1 6 7 6 11 3 3	0.0726 0.194 0.242 0.08806 0.0161 0.0161 0.0484 0.0484 0.218 0.0484 0.218 0.0887 0.540 0.0887 0.0241
15 16 17 18 19 20 22 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 19 H <sub>0</sub> 0.255 10 H <sub>0</sub> 0.255 10 H <sub>0</sub> 0.255 11 H <sub>0</sub> 0.255 12 H <sub>0</sub> 0.255 13 H <sub>0</sub> 0.255 14 H <sub>0</sub> 0.255 16 H <sub>0</sub> 0.2592	9 24 31 2 2 5 6 6 6 6 28 73 73 14 3	0.0726 0.193 0.250 0.0161 0.0161 0.0463 0.0484 0 0 0 Frequency 0.0484 0.226 0.589 0.113 0.0242	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 14]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 e3281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 e3281740-6 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)15	9 24 30 1 2 5 5 6 7 6 7 6 7 6 11 3 3	0.0726 0.194 0.242 0.00806 0.0161 0.0463 0.0463 0.0464 0.0484 0.218 0.0287 0.0540 0.0887 0.0241
15 16 17 18 19 20 22 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.855 18 H <sub>0</sub> 0.855 10 H <sub>0</sub> 0.955 10 H <sub>0</sub>	9 24 31 2 2 5 6 6 6 6 6 28 73 14 3 3	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 0 7 7 7 7 9 0.0484 0.226 0.589 0.113 0.0242	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T	9 24 30 1 2 5 5 6 7 6 7 6 7 6 11 3 3	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0461 0.0484 0.0484 0.0484 0.0887 0.0484 0.0887 0.0242
15 16 17 18 19 20 22 18 H+0.055 18 H+0.055 18 H+0.055 18 H+0.055 18 H+0.055 13 Allele 12 13 14 15 16 16 18 H, 0.592 18 H, 0.645 18 H, 0.645 16 H, 0.645 18 H, 0.655 18 H, 0.655	9 24 31 2 2 5 6 6 28 6 28 73 14 14 3	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 tr Frequency 0.0484 0.226 0.589 0.113 0.0242	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T	9 24 30 1 2 2 5 6 6 7 1 6 7 6 7 6 7 6 7 1 3 3	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0484 0.0484 0.0484 0.218 0.00807 0.540 0.0484 0.0388 0.00807 0.540 0.0484 0.0388
15 16 17 18 19 20 22 18 H <sub>4</sub> 0.850 18 H <sub>4</sub> 0.850 18 H <sub>4</sub> 0.855 18 H <sub>4</sub> 0.855 18 H <sub>4</sub> 0.855 13 H <sub>4</sub> 0.855 14 H <sub>4</sub> 0.855 13 H <sub>4</sub> 0.855 16 H <sub>4</sub> 0.552 18 H <sub>4</sub>	9 24 31 2 2 5 6 6 28 6 28 73 14 3 	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0.0484 0.0484 0.226 0.0484 0.226 0.589 0.113 0.013	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 53281740-6 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 12]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGA7)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGA7)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGA7)14 4525680-7 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGA7)14 4525680-7 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGA7)15 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGA7)15 4525680-7	9 24 30 1 2 2 5 5 5 5 5 7 7 1 6 7 6 7 6 11 3 3 3	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0464 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484
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15 16 17 18 19 20 22 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 19 P.valut 12 13 14 15 16 18 H <sub>0</sub> 0.852 18 H <sub>0</sub>	9 24 31 2 5 5 6 6 26 28 28 28 28 28 28 28 28 28 28 28 28 28	0.0726 0.193 0.250 0.0161 0.0403 0.0403 0.0484 0.0484 0.226 0.589 0.113 0.0242 nt Frequency 0.589	GTCTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 d525680-T D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14 G255680-T	9 24 30 1 2 5 5 5 5 5 5 5 5 5 5 5 7 1 6 7 5 1 1 3 3 3 1 2 7 1 3 3 2 7 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0484 0.0484 0.218 0.0484 0.218 0.00807 0.540 0.0484 0.0287 0.0242 0.0242
15 16 17 18 19 20 22 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.850 19 P.valut 12 13 14 15 16 18 H <sub>0</sub> 0.892 18 H <sub>0</sub> 0.992 18 H <sub>0</sub> 0.992 19 H <sub>0</sub>	9 24 31 2 5 5 6 6 28 28 28 28 28 73 14 14 3 	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0.0484 0.226 0.589 0.113 0.0242 nt Frequency 0.259	GTCTCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	D18551 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 14]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 16]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 16]-GRCh38-Chr20-60011918-60012017 (TCTA)0 D25441 [CE 10]-GRCh38-Chr20-60011918-60012017 (TCTA)0 D25441 [CE 10]-GRCh38-Chr20-60011918-60012017 (TCTA)0 D25441 [CE 10]-GRCh38-Chr20-60011918-60012017 (TCTA)0	9 24 30 1 2 5 5 5 5 5 5 5 5 7 1 6 7 6 7 6 11 3 3 3 1 27 1 67 6 5 11 3 27 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0.0726 0.194 0.242 0.00806 0.0161 0.0403 0.0403 0.0404 0.0404 0.0484 0.0241 0.0241 0.0241 0.0241 0.0241 0.0241 0.0241
15 16 17 18 19 20 22 18 H <sub>0</sub> 0.850 18 H <sub>0</sub> 0.855 18 HWE p-value 12 13 14 15 16 18 H <sub>0</sub> 0.852 18 H <sub>0</sub> 0.855 18 HWE p-value 12 13 14 15 16 16 18 H <sub>0</sub> 0.852 18 H <sub>0</sub> 0.852 18 H <sub>0</sub> 0.852 18 H <sub>0</sub> 0.852 19 HWE p-value 10 10	9 24 31 2 5 6 6 28 73 24 6 28 73 14 3 :::::::::::::::::::::::::::::::::	0.0726 0.193 0.250 0.0161 0.0161 0.0463 0.0484 0 0 0 0 0 0 0 0 0.0484 0.226 0.589 0.113 0.0242 0.589 0.113	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D18551 [CE 22]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 13]-GRCh38-Chr28-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 16]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 16]-GRCh38-Chr20-8011918-68012017 (TCTA)10 D25441 [CE 10]-GRCh38-Chr2-68011918-68012017 (TCTA)10 D25441 [CE 10]-GRCh38-Chr20-6011918-68012017 (TCTA)10 D25441 [CE 10]-GRCh38-Chr20-68011918-68012017 (TCTA)10 D25441 [CE 10]-GRCh38-Chr20-6801191	9 24 30 1 2 5 6 5 6 7 6 7 1 6 7 6 7 1 6 7 6 7 1 3 3 3 20 1 20 1 20 1 22 35	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0463 0.0484 0.0484 0.0484 0.0484 0.0484 0.0887 0.540 0.0484 0.0242 0.0241 0.0242 0.0241 0.0242
15 16 17 18 19 20 22 18 H <sub>4</sub> 0.850 18 H <sub>4</sub> 0.855 18 H <sub>4</sub> 0.855 18 H <sub>4</sub> 0.855 18 H <sub>4</sub> 0.855 13 Jan 14 15 16 16 16 16 16 18 H <sub>4</sub> 0.592 18 H <sub>4</sub> 0.645 18 H <sub>4</sub> 0.652 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 10 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 10 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 10 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.592 19 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.555 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.555 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.555 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.655 18 H <sub>4</sub> 0.555 18	9 24 31 2 2 5 6 6 28 6 6 28 73 28 73 14 3 8 28 73 28 28 73 28 73 28 73 73 36	0.0726 0.193 0.250 0.0161 0.0161 0.0403 0.0484 0 0 0 0 0 0 0 0 0.589 0.113 0.0242 0.589 0.113 0.0242	GTCTCAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAA	D18551 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17 D18551 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)20 D18551 [CE 22]-GRCh38-Chr18-63281662-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr28-63281796 (AGAA)22 D205482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)14 d525680-T D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)15 D205482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)16 d525680-T	9 24 30 1 2 5 5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 1 1 3 3 3 2 7 1 1 5 2 7 1 1 5 7 6 7 6 7 6 7 6 7 6 7 6 7 1 1 2 2 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.0726 0.194 0.242 0.00806 0.0161 0.0161 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0484 0.0282 0.0494 0.0242 0.0241 0.0242

12	4	0.0323	CCAG <u>G</u> AACTGTGGGCTCATCTATGAAAACT <b>TCTATCTATCTATCTATCTATCTATCTATCTAT</b>	D25441 [CE 12]-GRCh38-Chr2-68011918-68012017 (TCTA)12	4	0.0323
13	1	0.00806	CCAG <u>G</u> AACTGTGGCTCATCTATGAAAACT <b>TCTATCTATCTATCTATCTATCTATCTATCTAT</b>	D2S441 [CE 13]-GRCh38-Chr2-68011918-68012017 [TCTA]10 TTTA (TCTA)2	1	0.00805
14	10	0.0806	CCAG <u>G</u> AACTGTGGCTCATCTATGAAAACT <b>TCTATCTATCTATCTATCTATCTATCTATCTAT</b>	D25441 [CE 14]-GRCh38-Chr2-68011918-68012017 [TCTA]11 TTTA (TCTA)2	10	0.0806
LB H <sub>e</sub> 0.566 LB H <sub>o</sub> 0.597 LB HWE p-value: (	0.686		58 H, 0.716 58 H, 0.742 58 HWE p-value: 0.472	59/5/2000 -		
D55818 (n=124)	Count	Freezensen	Elatina Canadana	18 Mexical datas	Count	Community
2	10	0.152	- Smill Sequence TATIT ATA//Y ATATATATATATATATATATATATATATATATATATAT	55 Manielicatore 555219 [CE 7].CBC529.Cbr5.122775542.122775606 (ATCT)7	10	0.152
8	7	0.0565	TATTIVATACCCCTATCTATCTATCTATCTATCTATCTATCTTCCAAAAT	D55818 [CE 8]-G8Ch38-Chr5-123775543-123775606 (ATCT)8	7	0.0565
9	2	0.0161	татттатасатстатстатстатстатстатстатстат	D55818 [CE 9]-GRCh38-Chr5-123775543-123775606 (ATCT)9 12377553-a	2	0.0161
			TATITATACCTCIAICIAICIAICIAICIAICIAICIAIC	D55818 [CE 10]-GRCh38-Ch/5-123775543-123775606 (ATCT)10	6	0.0484
10	7	0.0565	TATTTATACATCTATCTATCTATCTATCTATCTATCTAT	D55818 [CE 10]-GRCh38-Chr5-123775543-123775606 (ATCT)10 123775552-A	1	0.00806
			TATITATACCTCIATCIATCIATCIATCIATCIATCIATC	D55818 [CE 11]-GRCh38-Chr5-123775543-123775606 [ATCT]11	74	0.597
11	75	0.605	TATTTATACATCTATCTATCTATCTATCTATCTATCTAT	D55818 [CE 11]-GRCh38-Chr5-123775543-123775606 (ATCT)11 123775552-A	1	0.00806
			TATTTATAGCTCTATCTATCTATCTATCTATCTATCTATC	D55818 [CE 12]-GRCh38-Chr5-123775543-123775606 [ATCT]12	10	0.0806
12	13	0.105		D55818 [CE 12]-GRCh38-Chr5-123775543-123775606 (ATCT)12 123775552-A	3	0.0242
13	1	0.00806	ТАТТТАТАС <u>А</u> ТСТ <b>АТСТАТСТАТСТАТСТАТСТАТСТАТСТАТСТАТСТ</b>	D55818 [CE 13]-GRCh38-Chr5-123775543-123775606 (ATCT)13 123775552-A	1	0.00806
LB H <sub>e</sub> 0.598 LB H <sub>e</sub> 0.532 LB HWE p-value: (	0.263		58 H-0.612 58 H-0.6301 58 HWE p-value: 0.445			
B30030 (- 331)						
LB Allele	Count	Frequency	String Sequence	SB Nomenclature	Count	Frequency
7	1	0.00806	TATTTAGTGAGATAAAAAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCG</b> TTAGTTCAATCTAT	D75820 [CE 7]-GRCh38-Chr7-84160191-84160297 (TATC)7 84160204-A; 84160286-A	1	0.00806
i l	7	0.0565	TATTTAGTGAGATAAAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTG</b> TTAGTTCAATCTAT	D75820 [CE 8]-GRCh38-Chr7-84160191-84160297 (TATC)8 84160204-A; 84160286-A	1	0.00806
0	0.00	0.0505	TATTTAGTGAGATAAAAAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATC</b> GTTAGTTC <u>G</u> TTCTAAACTAT	D75820 [CE 8]-GRCh38-Chr7-84160191-84160297 (TATC)8 84160204-A	6	0.0484
9	5	0.0403	ŦĂŦŦŦĂġŦĠĂĠĂŦ <u>ġ</u> ĂĂĂĂĂĂĂĂĂĂĊĨĂŦĊſĂŦĊĨ <mark>ŦĬĊŢĂŦĊŢĂŦĊŢĂŦĊŢĂŦĊŢĂŦĊŢĂŢĊŢ</mark> ĂŢĠŢŦĸĠŢŦĿĊ <u>Ğ</u> ŦŢĊŢĂĂĂĊŢĂŢ	D75820 [CE 9]-GRCh38-Chr7-84160191-84160297 (TATC)9 84160204-A	5	0.0403
10	15	0.121	TATTTAGTGAGAT <u>A</u> AAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D75820 [CE 10]-GRCh38-Chr7-84160191-84160297 [TATC]10 84160204-A	15	0.121
83	1922	N 273227	TATTTAGTGAGAT <u>A</u> AAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D75820 [CE 11]-GRCh38-Chr7-84160191-84160297 [TATC]11 84160204-A	52	0.419
11	53	0.427	TATTTAGTGAGAT <u>I</u> AAAAAAAACTATCAATCIGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D75820 [CE 11]-GRCh38-Chr7-84160191-84160297 (TATC)11	1	0.00806
			TATTTAGTGAGATAAAAAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D7S820 [CE 12]-GRCh38-Chr7-84160191-84160297 [TATC]12 84160204-A	35	0.283
12	40	0.323	TATTTAGTGAGATT <u>A</u> AAAAAAACTATCAATCIGYC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCTA</b>	D75820 [CE 12]-GRCh38-Chr7-84160191-84160297 [TATC]12	5	0.0403
13	1	0.00806	TATTTAGTGAGATAAAAAAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D75820 [CE 13]-GRCh38-Chr7-84160191-84160297  TATC)13 84160204-A	1	0.00805
14	2	0.0161	TATTTAGTGAGAT <u>A</u> AAAAAAAAACTATCAATCTGTC <b>TATCTATCTATCTATCTATCTATCTATCTATCTATCT</b>	D7S820 [CE 14]-GRCh38-Chr7-84160191-84160297  TATC]14 84160204-A	2	0.0161
LB H <sub>e</sub> 0.699 LB H <sub>o</sub> 0.726 LB HWE p-value: (	0.456		58 H, 0.730 58 H, 0.774 58 HWE p-value: 0.613			

DXS10074 (n=72, LB Allele	,n <sub>m</sub> =26) Count (f(m)	Frequency (f m)	String Sequence	\$8 Nomenclature	Count (f]m)	Frequency (f)m)
14	5 1	0.0694 0.0385	TGTGTGTGCATGCATACACACACAGAGAGAGAGAGAGAGA	DX\$10074 [CE 14]-GRCh38-ChrX-67757300-67757464 (AAGA)11 AAGG (AAGA)2	5 1	0.06940 0.0 385
			TGTGTGTGCAT6CATACACACACAGAGAGAGAGAGAGAGAGAAAAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA GAAAGAAAGGAAGAA	DXS10074 [CE 15]-GRCh38-chrX-67757300-67757464 (AAGA)12 AAGG (AAGA)2	16 3	0.222 0.115
15	2014	0.278 0.154	TGTGTGTGCATGCATACACACACAGAGAGAGAGAGAGAGA	DXS10074 [CE 15]-GRCh38-ChrX-67757300-67757464 (AAGA)15	3 1	0.0417 0.03 85
			TGTGTGTGCATGCATACACACAGAGAGAGAGAGAGAGAAAAAAAA	DXS10074 [CE 15]-GRCh38-ChrX:67757300-67757464 (AAGA)12 AAGG (AAGA)2 67757338-A	1 0	0.0139 0
16	13  9	0.181 0.346	TeTETETETECTECATACACACCACEGAGAGAGAGAGAGAGAAAAAAGAACGAAAGAAA	DXS10074 (CE 16)-GRCh38-ChrX:67757300-67757464 (AAGA)13 AAGG AGGA AAGA DXS10074 (CE 16)-GRCh38-ChrX:67757300-67757464 (AAGA)13 AAGG (AbGA)2	0 2 13 7	0 0.0769
17	2217	0.30610.269	TGTGTGGCATGCATACACACACAGAGAGAGAGAGAGAGAG	DXS10074 [CE 17]-GRCh38-ChrX-67757300-67757464 (AAGA)14 AAGG (AAGA)2	22 7	0.306 0.269
18	9 3	0.125 0.115	TGTGTGTGCATGCATACACACACAGAGAGAGAGAGAGAGA	DXS10074 [CE 18]-GRCh38-ChrX-67757300-67757464 (AAGA)15 AAGG (AAGA)2	9[3	0.125 0.115
19	3 2	0.0417 0.0769	TGTGTGTGCATGCATACACACACACAGAGAGAGAGAGAGA	DXS10074 [CE 19]-GRCh38-ChrX-67757300-67757464 (AAGA)16 AAGG (AAGA)2	312	0.0417 0.07 69
LB H <sub>e</sub> * 0.786 LB H <sub>6</sub> * 0.805 LB HWE p-value: (	0.337		SB H," 0.812 SB H," 0.806 SB HWE p-value: 0.486			
"Does not include	male X-STE	R data due to hemizve	nsity of the male say chromosome.			
DYS389I (n=26)						
LB Allele	Count	Frequency	String Sequence	SB Nomenclature	Count	Frequency
12	6	0.231	TAGATAGATAGATAGATAGATAGATAGATAGATAGACAGAC	DYS389! [CE 12]-GRCh38-ChrY-12500448-12500513 (TAGA)9 [CAGA]3	6	0.231
13	18	0.692	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DY5389I [CE 13]-GRCh38-ChrY-12500448-12500513 [TAGA)10 [CAGA]3	15	0.577
~			TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389I [CE 13]-GRCh38-ChrY:12500448-12500513 (TAGA)10 [CAGA]3 12500506-G	3	0.115
14	2	0.0769	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389I [CE 14]-GRCh38-ChrY-12500448-12500513 (TAGA)11 [CAGA]3	2	0.0769
DVS389(1* (n=24)						
LB Allele	Count	Frequency	String Sequence	SB Nomenclature	Count	Frequency
28	1	0.0417	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389II [CE 28]-GRCh38-Chry:12500448-12500633 (TAGA)9 [CAGA]3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)11 (CAGA)5	1	0.0417
			TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS3898 [CE 29]-GRCh38-ChrY:12500448-12500533 (TAGA)9 [CAGA]3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)12 (CAGA)5	3	0.125
29	9	0.375	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389II [CE 29]-GRCh38-ChrY:12500448-12500533 (TAGA)10 (CAGA)3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)11 (CAGA)5	3	0.125
			TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389II [CE 29]-GRCh38-ChrY:12500448-12500533 (TAGA)10 [CAGA]3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)12 (CAGA)4	2	0.0833
			TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389H [CE 30]-GRCh38-Chry:12500448-12500533 [TAGA}10 [CAGA]3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)12 (CAGA)5	7	0.292
30	12	0.500	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	DYS389II [CE 30]-GRCh38-ChrY:12500448-12500533 (TAGA)10 [CAGA]3 TACA TAGA TAGT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)12 (CAGA)5 12500506-G	3	0.125

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31	2	0.0833	ТАĞАТАĞАТАĞАТАĞАТАĞАТАĞАТАĞАТАĞАТАĞАТАĞ	DYS389II (CE 31)-GRCh38-ChrY12500448-12500533 (TAGA)10 (CAGA)3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)3 (CAGA)5 DYS389II (CE 31)-GRCh38-ChrY12500448-12500533 (TAGA)1.1 (CAGA)3 TACA TAGA TAAT ACAG ATGA GAGT TGGA TACA GAAG TAGG TATA ATGA (TAGA)12 (CAGA)5	1	0.0417
*Hanking region rs10776839 (n=12	variation ob: 24)	served within the DYS	389II locus is the same as that observed within the DYS389I locus due to use of the same forward primer.			
Target Allele	Count	Frequency	String Sequence	Microhaplotype Nomenclature rs10776839 (CE TI-GRCh38-chr9:134525445-134525507 rs7037930-	Count	Frequency
т	61	0.492	CAGETGAGGAGECCEGAGITIGCCGTCAGATEAGAGECCECAGTIGCCEGGTCTGCCGCAGETCT	6; rs10776839-T	61	0.492
	63	0.508	CAGCTGAGGAGCCCGAGGTTGCCGTCAGATCAGAGCCCCAGTTGCCCGGTCTGCCGCAGCTCT	rs10776839 [CE G]-GRCh38-chr9:134525445-134525507 rs7037930-G; rs10776839-G	42	0.339
9	03	0.500	CAGCTGAGGAGCCCAAGGTTGCCGTCAGATCAGAGCCCCAGTTGCCCGGTCTGCCGCAGCTCT	rs10776839 [CE G]-GRCh38-chr9:134525445-134525507 rs10776839-G	21	0.169
Target SNP He 0.5	504		Microhaplotype H <sub>2</sub> 0.620			
Target SNP HWE	p-value: 0.61	19	Microhaplotype Houssa Microhaplotype HWE p-value: 0.172			
rs1109037 (n=124	4)					
Target Allele	Count	Frequency	String Sequence	Microhaplotype Nomendature	Count	Frequency
A	29	0.234	CCAGTTTCTCCAGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG	rs1109038-A	19	0.153
			CCAGTTICTCCAGAGTGGAAAGACTTICATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGGG	rs1109037 [CE A]-GRCh38-chr2:9945582-9945659 rs1109037-A rs1109037 [CE G]-GRCh38-chr2:9945582-9945659 rs1109037-G;	10	0.0806
G	95	0.766	CLAGTTICTCCGGAGTGGAAAGACTTICATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAGCGGGGGG	rs1109038-A rs11090371CE GLG8Ch38-chr2-9945582-9945659 rs1109037-G	49	0.395
Target SNP He 0.3	361		Microhaplotype H <sub>c</sub> 0.682	interest fee of diverse energy some syneary interest.		0.071
Target SNP H <sub>0</sub> 0.4 Target SNP HWE	\$03 p-value: 0.48	86	Microhaplotype H& 0.694 Microhaplotype HWE p-value: 0.728			
m12007452 (n-12	243					
Target Allele	Count	Frequency	String Sequence	Microhaplotype Nomenclature	Count	Frequency
G	88	0.709677	TTTTATGCTTTA4AGATACAGGTTATCTGTATTACATTGGGTTTTTACCTACC	rs12997453 [CE G]-GRCh38-chr2:181548493-181548547 rs12997453-G	88	0.710
10	900		TITTATGCTTTAAAGATATAGGTTATCTGTATTACATTGAGTTTTTACCTACC	rs12997453 [CE A]-GRCh38-chr2:181548493-181548547	27	0.218
A	36	0.290323	TITTATGCTITAAAGATACAGGTTATCTGTATTACATTGAGTTTTTACCTACC	rs12997453 [CE A] GRCh38-chr2:181548493-181548547	9	0.0726
Target SNP He 0.4	415		Microhaplotype H <sub>c</sub> 0.447	ts1299/453-A		
Target SNP H <sub>o</sub> 0.3 Target SNP HWF	387 p-value: 0.74	55	Microhaplotype H <sub>0</sub> 0.468 Microhaplotype HWE p-value: 0.0922			
			unitatelearly is core in press.			
rs13218440 (n=12 Target Allele	24) Count	Frequency	String Sequence	Microhaplotype Nomenclature	Count	Frequency
A	60	0.484	CCTCTGAGCAGCCTCCTGGAATACTCAGCTGGGATGGGGTTGGGGCTGCTTGAGGTACAGCTCCCACTGCCTCTGAGTGGCCCTCCATGAAA	rs13218440 [CE A]-GRCh38-chr6:12059715-12059838 rs13218440- A	60	0.483871
			CCTCTGGGCAGCCTCCTGGAATACTCAGCTGGGATGGGTTGGGGCTGCTTGAGGTACAGCTCCCACTGCCTCTGAGTGGCCCTCCATGAAA	rs13218440 [CE G]-GRCh38-chr6:12059715-12059838 rs13218440-	63	0.508065
G	64	0.516	ATGCCTCATGTCTCTGTGTCCCTAAACTGTAGG CCTCTGGGCAGCCTCCTGGAATACTCAGCTGGGATGGGTTGGGGCTGCTTGAGGTACAGCTCCCACT <u>A</u> CCTCTGAGTGGCCCTCCATGAAA	6 rs13218440 [CE G]-GRCh38-chr6:12059715-12059838 rs13218440-		0.00000153
Tarent SNP H. 0.5	104		ATGCCTCATGTCTCTGTGTCCCTAAACTGTAGG Microbackware H. 0.512	6;12059782-A	÷.	0.00806452
Target SNP H <sub>o</sub> 0.5	516	200	Microhaplotype H <sub>0</sub> 0.532			
Target SNP HWE	p-value: 1.00	0	Microhaplotype HWE p-value: 0,797			
rs1360288 (n=124	4)	Provide and		Ministerie New Maria	Count	
Target Anexe	100	0.806	String Sequence	rs1360288 [CE C]-GRCh38-chr9:126205735-126205813 rs1360288-	99	0 798
26	100	0.000		c		0.750
			GGGTAGAGGCTCCTTCCASCCTCTGGGGAGTAGGAGGAGACTTGGGAAGAACTGGCTGCATCCCTTAACAGATGCCCC	rs1360288 [CE C]-GRCh38-chr9:126205735-126205813	1	0.00805
T	24	0.194	GGG_JAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC	rs1360288 [CE C]-GR(h38-chr9:126205735-126205813 rs136412791-1; rs1380288-C rs1360281CF1-GRCH38-chr9:126205735-126205813 rs1360288-T	1	0.00806
T Target SNP H <sub>e</sub> 0.3	24	0.194	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaglotype H, 0 328 Microhaglotype H, 0 328	rs1360288 [CE C]-GR(h38-chr9:126205735-126205813 rs136412791-1; rs1360288-C rs1360288 [CE T]-GR(h38-chr9:126205735-126205813 rs1360288-T	1 24	0.00806 0.194
T Target SNP H <sub>o</sub> 0.3 Target SNP H <sub>0</sub> 0.3 Target SNP HWE	24 315 322 p-value: 1.0	0.194	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.329 Microhaplotype HWE p-value: 1.00	rs1360288 [CE C]-GR(h38-chr9:126205735-126205813 rs116412791-1; rs1360288-C rs1360288 [CE T]-GR(h38-chr9:126205735-126205813 rs1360288-T	1 24	0.00806
T Target SNP H <sub>e</sub> 0.3 Target SNP H <sub>0</sub> 0.0 Target SNP HWE rs2830795 (n=12	24 315 322 p-value: 1.0	0.194	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaglotype H, 0.329 Microhaglotype HWE p-value: 1.00	rs1360288 [CE C]-GR(h38-chr9:126205735-126205813 rs116412791-1; rs1360288-C rs1360288 [CE T]-GR(h38-chr9:126205735-126205813 rs1360288-T	1 24	0.00806 0.194
T Target SNP H <sub>0</sub> 0.3 Target SNP H <sub>0</sub> 0.3 Target SNP HWE rs2830795 (n=12) Target Allele	24 315 322 p-value: 1.0 (4) Count	0.194 0 Frequency 0.226	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.329 Microhaplotype HWE p-value: 1.00 String Sequence	rs1360288 [CE C]-GR(h38-chr9:126205735-126205813 rs136412791-1; rs1360288-C rs1360288 [CE T]-GR(h38-chr9:126205735-126205813 rs1360288-T Microhapletype Nomendature	1 24 Count	0.00806 0.194 Frequency
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.3 Target SNP HWE rs2830795 (n=12 Target Allele G	24 315 322 p-value: 1.0 (4) Count 29	0.194 0 Frequency 0.234	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplorype H, 0.328 Microhaplorype H, 0.239 Microhaplorype HWE p-value: 1.00 String Sequence GGAGCTGGGTTCACTTCTATAGACATAGGACAACCCATTTATTGTCTAAAGGCCAAAGAAGTCCTATTA GGAGCTGGGTTCACTTCTATAGACATAGGACAACCCATTTATTGTCTAAAGGCCAAAGAAGTCCTATTA	n 1360288 [Cf C]-GRCh36-chr9126205735-126205813 n118412791-1; n1360288-C n1360288 [Cf T]-GRCh38-chr9126205735-126205813 n1360288-T Microhapletype Nomendature n2830795 [Cf G]-GRCh38-chr21:27235792-27235861 n2830795-G n2830795 [Cf G]-GRCh38-chr21:27235792-27235861 n2830795-A	1 24 Count 29 49	0.00806 0.194 Frequency 0.234 0.395
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.3 Target SNP HWE rs2830795 (n=12 Target Alfele G	24 315 322 p-value: 1.0 (4) Count 29 95	0.194 0 Frequency 0.234 0.766	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.339 Microhaplotype HWE p-value: 1.00 String Sequence GGAGCTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGACAAGAGTCCTATTA	n 1360288 [Cf C]-GRCh38-chr9126205735-126205813 n136412791-1; n1360288-C n1360288 [Cf T]-GRCh38-chr9126205735-126205813 n1366288-T Microhapletype Nomendature n2830795 [Cf G]-GRCh8-chr21.27235792-27235861 n2830795-G n2830795 [Cf A]-GRCh8-chr21.27235792-27235861 n2830795-A n28830795 [Cf A]-GRCh8-chr21.27235792-27235861 n2830795-A	1 24 Count 29 49 42	0.00806 0.194 Frequency 0.234 0.395 0.339
T Target SNP H <sub>6</sub> ,0. Target SNP H <sub>6</sub> 0. Target SNP H <sub>6</sub> 0. <b>rs2830795</b> [n=12 Target Allele G	24 315 322 p-value: 1.0 (4) 29 95	0.194 0 0.214 0.766	GGGIAGAGGCTCCCTCCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype HWE p-value: 1.00 String Sequence GGAGCTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCCAAAGAGAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAGCCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAGCCCTATTA	rs1360288 [Cf C]-GRCh38-chr9-126205735-126205813 rs116412791-7; rs1360288-C rs1160288 [Cf C]-GRCh38-chr9-126205735-126205813 rs1360288-7 rs1360288 [Cf T]-GRCh38-chr9-126205735-126205813 rs1360288-7 microhaplotype Nomenclature rs2830795 [Cf G]-GRCh38-chr21-27235792-27235861 rs2830795-6 rs2830795 [Cf A]-GRCh38-chr21-27235792-27235861 rs2830795-6 rs2830795 [Cf A]-GRCh38-chr21-27235792-27235861 rs12626695- rs2830795 [Cf A]-GRCh38-chr21-27235792-27235861 rs12626695- rs2840784075 [Cf A]-GRCh38-chr21-27235792-27235861 rs12626695- rs284075 [Cf A]-GRCh38-chr21-27235792-27235861 rs126075755757575757575757575757575757575757	1 24 Count 29 49 42 4	0.00806 0.194 Frequency 0.234 0.395 0.339 0.0323
T Target SNP H <sub>4</sub> , 0. Target SNP H <sub>4</sub> , 0. Target SNP H <sub>4</sub> 0. <b>rs2830795</b> (n=12 Target Allele G A Target SNP H <sub>4</sub> , 0.3	24 315 322 p-value: 1.00 44] Count 29 95 95	0.194 0 5 7 7 7 6 7 6 6 7 6	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.329 String Sequence GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGACATAGGACACCCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA	n:1360288 [Cf C]-GRCh38-chr9:126205735-126205813 n:116412791-1; n:1360288-C n:1160288 [Cf T]-GRCh38-chr9:126205735-126205813 n:1360288-T Microhapletype Nomendature n:2830795 [Cf G]-GRCh38-chr21:27235792-37235861 n:2830795-G n:2830795 [Cf A]-GRCh38-chr21:27235792-27235861 n:12626695- C; n:2830795 [Cf A]-GRCh38-chr21:27235792-27235861 n:12626695- C; n:2830795 [Cf A]-GRCh38-chr21:27235792-27235861 n:12626695- C; n:2830795 [Cf A]-GRCh38-chr21:27235792-27235861 n:12626695- C; n:2830795 [Cf A]-GRCh38-chr21:27235792-27235861 n:12626695- C; 27235845-1; rs2830795-A	1 24 29 49 42 4	0.00806 0.194 7.0234 0.335 0.339 0.0323
T Target SNP He 0.1 Target SNP He 0.2 Target SNP HWE 1 Target SNP HWE 1 G A Target SNP He 0.2 Target SNP He 0.2 Target SNP He 0.2	24 315 222 p-value: 1.00 44 29 95 95 361 274 p-value: 0.0	0.194 0 <u>Frequency</u> 0.234 0.766	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGCTAGAGGAGACCTGGGAAGACTGGCTGCCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.329 Microhaplotype H, 0.329 String Sequence GGGGTCAC_TCTATAGACATAGGACAACACATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACACATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCAC_TCTATAGACATAGGACAACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA Microhaplotype H, 0.579 Microhaplotype H, 0.594 Microhaplotype HWE p-value: 0.101	rs1360288 [CE C]-GRCh38-chr9:126205735-126205813 rs116412791-1; rs1360288-C rs1360288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T Microhapletype Nomendature rs2803795 [CE G]-GRCh38-chr21:27235792-37235861 rs2803795-G rs2803795 [CE A]-GRCh38-chr21:27235792-27235861 rs2803795-G C; rs2803795 [CE A]-GRCh38-chr21:27233792-27235861 rs2803795-G C; rs2803795 [CE A]-GRCh38-chr21:27233792-27235861 rs2803795-A C; rs2803795 [CE A]-GRCh38-chr21:27233792-27235861 rs2803795-A	1 24 29 49 42 4	0.00806 0.194 Frequency 0.234 0.395 0.399 0.0323
T Target SNP He 0.3 Target SNP He 0.3 Target SNP HWE 1 Target SNP HWE 6 G A Target SNP He 0.3 Target	24 315 322 p-value: 1.00 41 Count 29 95 95 95 95 95 95	0.194 0 5.7requency 0.214 0.766 749	GGGIAGAGGCTCCCTCCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCCTCAGCGCTCTGGGGAGCTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.329 String Sequence GAGACTGGGTTCACTTCTATAGACATAGGACACCCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGACATAGGACACCCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGACATAGGACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACCCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTTGTGTAAGGACACCCCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA	n1360288 [CE C]-GRCh38-chr9:126205735-126205813 n116412791-1; n1360288-C rs1360288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T mcrohapletype Nomenclature rs2830795 [CE G]-GRCh38-chr21:27235792-27235861 rs2830795-G rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs12626695- C; 27235845-T; rs2830795-A	1 24 29 49 42 4	0.00806 0.194 7.194 0.234 0.395 0.339 0.0323
T Target SNP H <sub>6</sub> 0. Target SNP H <sub>6</sub> 0.	24 315 322 p-value: 1.00 41 29 95 95 95 361 274 p-value: 0.0 9 9 0 Count	0.194 0 5 Frequency 0.214 0.766 749 Frequency	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC GGGGAGAGGCTCCCGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGAACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype H, 0.328 Microhaplotype H, 0.329 String Sequence GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTTATTGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTATGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTATGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTATGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCCATTTATGTCTAAAGGCAAAGAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACACCATTTATGTCTAAAGGCAAAGAGTCCTATTA GAGACTGGGTTCACTCTATAGGACACCCCATTTGTCTAAAGGCAAAGAGTCCTATTA GAGACTGGGTTCACTCTATGGACACCCCATTTATGTCTAAAGGCAAAGAAGTCCTATTA GAGACTGGGTTGCTCTATAGGACACCCCATTTGTCTAAAGGCAAAGAGTCCTATTA GAGACTGGGTTGCC	n1360288 [CE C]-GRCh38-chr9:126205735-126205813 n116412791-1; n1360288-C rs1360288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T m2830795 [CE G]-GRCh38-chr9:126205735-126205813 rs1360288-T n2830795 [CE G]-GRCh38-chr9:127235792-27235861 rs2830795-G rs2830795 [CA J-GRCh38-chr9:1:27235792-27235861 rs2830795-G rs2830795 [CA J-GRCh38-chr9:1:27235792-27235861 rs2830795-G rs2830795 [CA J-GRCh38-chr9:1:27235792-27235861 rs2830795-A rs2830795 [CA J-GRCh38-chr9:1:27235792-27235861 rs12626635- C; p:2830795 [CA J-GRCh38-chr9:1:27235792-27235861 rs12626635- C; p:27235845-T; rs2830795-A Microhapletype Nomendature	1 24 29 49 42 4 4 Count	0.00806 0.194 7.234 0.335 0.339 0.0323
7 Target SNP H4, 0.3 Target SNP H4, 0.3 Tar	24 315 322 p-value: 1.0 44 Count 29 95 95 361 274 p-value: 0.0 9 Count	0.194 0 Frequency 0.234 0.766 749 Frequency	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGGGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGGAGCCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplorype H, 0.328         Microhaplorype H, 0.339         Microhaplorype HWE p-value: 1.00         String Sequence         GGAGCTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGACAAAGACCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGACAAAGACCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGACAAAGACCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGACAAGAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.594         Microhaplotype HWE p-value: 0.101	rs1360288 [CE C]-GRCh38-chr9:126205735-126205813 rs116412791-1; rs1360288-C rs1360288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T microhapletype Komendature rs2830795 [CE G]-GRCh38-chr21:27235792-27235861 rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs12626695- C; rs2830795-A rs2830795 [CE A]-GRCh38-chr21:27235792-27235861 rs12626695- C; 27235845-T]; rs2830795-A microhapletype Komendature rs354439 [CE A]-GRCh38-chr13:105285966-106286115 rs354439-A	1 24 29 49 42 4 4 Count 103	0.00806 0.194 7.24 0.395 0.339 0.0323 Frequency 0.831
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.2 Target	24 315 322 322 23 44) Count 29 95 361 274 9 y-value: 0.0 9 Count 104	0.194 0 5requency 0.234 0.766 749 Frequency 0.839	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAAGGAGAGGAG	n 1360288 [Cf C]-GRCh38-chr9126205735-126205813 n116412791-1; n1360288-C n1360288 [Cf T]-GRCh38-chr9126205735-126205813 n1360288-T n1860288 [Cf T]-GRCh38-chr9126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr21:27235792-27215861 n2820795-A n2820795 [Cf A]-GRCh38-chr21:27235792-27215861 n1262665- c; n2820795-A n282079-A n2820795-A n2820795-A n2820795-A n2820795-A n282079-A	1 24 29 49 42 4 4 20 103 1	0.00806 0.194 7.24 0.395 0.395 0.339 0.0323 7.74 0.831 0.00806
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.2 Target	24 315 322 p-value 1.00 44) Count 29 95 361 274 p-value: 0.0 0 Count 104 20	0.194 0 Frequency 0.234 0.766 749 Frequency 0.839 0.161	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGGAGAGGAGGAGCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.330         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.330         String Sequence         GGAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATTGTCTAAAGGACAAGAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACAACAGTGAACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.679         Microhaplotype H, 0.670         Microhaplotype H, 0.671         Mi	n 1360288 [Cf C]-GRCh38-chr9126205735-126205813 n116412791-1; n1360288-C n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr2127235792-27235861 n2820795-A n2820795 [Cf A]-GRCh38-chr2127235792-27235861 n2820795-A n2820795 [Cf A]-GRCh38-chr2127235792-27235861 n12626695- c; n2820795-A n2820795 [Cf A]-GRCh38-chr2127235792-27235861 n12626695- c; n2820795-A n2820795 [Cf A]-GRCh38-chr2127235792-27235861 n12626695- c; n2820795-A n2820795 [Cf A]-GRCh38-chr2127235792-27235861 n12626695- c; n2820795-A n3554439 [Cf A]-GRCh38-chr13106285996-106286115 n3554439-A n3554439 [Cf A]-GRCh38-chr13106285996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106285996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106286996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106285996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106285996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106285996-106286115 106286013- 1; n356439 [Cf T]-GRCh38-chr13106285996-106286115 106286013-	1 24 29 49 42 4 4 20	0.00806 0.194 Frequency 0.234 0.339 0.0323 0.0323 Frequency 0.831 0.00806 0.00806
T Target SNP He, 0.3 Target SNP He, 0.2 Target SNP HWE rs2830795 (n=32) Target Allele G A Target SNP He, 0.2 Target SNP He, 0.2 Target Allele A Target SNP He, 0.2 Target Allele	24 315 322 p-value: 1.00 44 Count 29 95 3661 274 p-value: 0.0 0 Count 104 20 273	0.194 0 57equency 0.234 0.766 749 749 0.839 0.161	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC           GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGGAGAGGAGGAGCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC           Microhaplotype H, 0.328           Microhaplotype H, 0.339           Microhaplotype HWE p-value: 1.00           String Sequence           GGAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA           GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA           GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAAGTCCTATTA           GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA           Microhaplotype H, 0.679           Microhaplotype H, 0.679           Microhaplotype H, 0.679           Microhaplotype H, 0.679           Microhaplotype H, 0.670           Microhaplotype H, 0.671           Microhaplotype H, 0.672           Microhaplotype H, 0.673           Microhaplotype H, 0.674           Microhaplotype H, 0.674           Microhaplotype H, 0.675           Microhaplotype H, 0.675           Microhaplotype H, 0.674           Microhaplotype H, 0.674           Microhaplotype H, 0.765	n 1360288 [Cf C]-GRCh38-chr9126205735-126205813 n116412791-T; n1360288-C n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1366288-T n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1366288-T n2820795 [Cf G]-GRCh38-chr9127235792-77235861 n2820795-G n2820795 [Cf G]-GRCh38-chr9127235792-77235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr9127235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr913.106285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr913.106285996-106286115 n354439-T	1 24 29 49 42 4 4 20	0.00806 0.194 7Fequency 0.234 0.395 0.335 0.0323 7Fraquency 0.831 0.00806 0.161
T         Target SNP He 0.3           Target SNP He 0.4         Target SNP He 0.4           Target SNP He 0.4         Target SNP He 0.4           Target SNP He 0.3         Target SNP He 0.3           Target SNP He 0.4         Target SNP He 0.4	24 315 322 p-value: 1.00 41 Count 29 95 361 274 p-value: 0.07 36 Count 104 20 273 258	0.194 0 5 749 749 749 749 749 0.839 0.161	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGAGAGGAGCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         String Sequence         GAGACTGGGTTCACTCTCTATAGACATAGGACACACCATTTATTGTCTAAGGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.593         Microhaplotype H, 0.593         Microhaplotype H, 0.594         TTCTTACTCTCAATTGCAGTGCGATAGAAAACAGTGAAACAGTGAATATTGTGCTTAAAGGAATGTGATACATGAGAGAGGACACAGAGT         ACTAAAGGGAAAGAGAAGACCACGAAAACAGTGAAACAGTGAATATTATGGCTTAAAAGGAATGTGATACATGAGAGAGA	n 1360288 [Cf C] GRCh38-chr9126205735-126205813 n116412791-7; n1360288-C n1160288 [Cf C] GRCh38-chr9126205735-126205813 rs1366288-7 Microhapletype Nomendature n2880795 [Cf G] GRCh38-chr2127235792-77235861 n2880795-G n2880795 [Cf A] -GRCh38-chr2127235792-77235861 n2880795-A n2880795 [Cf A] -GRCh38-chr2127235792-77235861 n2880795-A n2880795 [Cf A] -GRCh38-chr2127235792-77235861 n2820795-A n2880795 [Cf A] -GRCh38-chr2127235792-77235861 n12626695- C; n280795 [Cf A] -GRCh38-chr21:27235792-77235861 n12626695- C; n280795 [Cf A] -GRCh38-chr21:106285996-106286115 n354439-A n354439 [Cf A] -GRCh38-chr13:106285996-106286115 n354439-A n354439 [Cf T] -GRCh38-chr13:106285996-106286115 n354439-T	1 24 29 49 42 4 4 20 103 1 20	0.00806 0.194 7requency 0.234 0.339 0.0323 0.0323 7requency 0.831 0.00806 0.161
T         Target SNP He 0.1           Target SNP He 0.2         Target SNP He 0.2	24 315 322 p-value: 1.00 41 Count 29 95 361 274 p-value: 0.0 9 Count 104 20 273 258 p-value: 0.6	0.194 0 5 749 749 749 0.839 0.161	GGGIAGAGGCTCCCTGCAGCCTCTGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         String Sequence         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATGTCTAAAGGCCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.593         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.593         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.276         String Sequence         TICTTAACTCAAATTGCGCTGCGATAGAAAACAGTGAATGTGATATTCAGAATATTGTGCTTAAAAGGAATGTGATACATGAGAGAGA	n 1360288 [CI C] (-GRCh38-chr9:126205735-126205813 n116412791-T; n1360288-C n1160288 [CI T]-GRCh38-chr9:126205735-126205813 rs1360288-T Microhapletype Nomendature n2839795 [CI G]-GRCh38-chr21:27235792-37235861 n:12626695- c; n2830795 [CI A]-GRCh38-chr21:27235792-37235861 n:12626695- c; n2830795 [CI A]-GRCh38-chr21:106285996-106286115 n:354439-A n:354439 [CI A]-GRCh38-chr13:106285996-106286115 n:354439-A n:354439 [CI T]-GRCh38-chr13:106285996-106286115 n:354439-T	1 24 29 49 42 4 4 2 4 2 103 1 20	0.00806 0.194 0.234 0.339 0.0323 Frequency 0.831 0.00806 0.161
T Target SNP He 0.1 Target SNP He 0.2 Target SNP	24 315 322 p-value: 1.00 Count 29 95 361 274 95 361 274 104 20 273 28 p-value: 0.60 41 Count 104	0.194 0	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         String Sequence         GAGACTGGGTTCACTCTCATAGACATAGGACACCCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACCCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACGTCTAGGACACACCACATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACGTCCATAGGACACACCATTTATTGTCTAAAGAGCAAAGAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.694         Microhaplotype H, 0.591         Microhaplotype H, 0.592         Microhaplotype H, 0.573         Microhaplotype H, 0.574         Microhaplotype H, 0.573         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.278	rs1360288 [CI C]-GRCh38-chr9:126205735-126205813 rs116012791-1; rs1360288-C rs1360288 [CI C]-GRCh38-chr9:126205735-126205813 rs1360288-T microhapletype Nomendature rs2830795 [CI G]-GRCh38-chr21:27235792-37235861 rs2830795-G rs2830795 [CI G]-GRCh38-chr21:27235792-37235861 rs1262665- C; rs2830795 [CI G]-GRCh38-chr21:27235792-27235861 rs1262665- C; rs2830795 [CI G]-GRCh38-chr21:27235792-27235861 rs1262665- C; rs2830795 [CI G]-GRCh38-chr21:27235792-37235861 rs1554439-A rs354439 [CI G]-GRCh38-chr13:106285996-106286115 rs354439-T rs354439 [CI T]-GRCh38-chr13:106285996-106286115 rs354439-T	1 24 29 49 42 4 4 20 5 20 5 20 5 5 5 5 5 5 5 5 5 5 5 5 5	0.00806 0.194 Frequency 0.234 0.395 0.339 0.0323 Frequency 0.831 0.00806 0.161 Frequency
T Target SNP He 0.1 Target SNP He 0.2 Target SNP	24 315 322 p-value: 1.0 Count 29 95 351 274 97 20 20 273 20 273 20 20 20 4) Count 104 20 4) Count 104 20 20 21 29 29 29 29 29 29 29 29 29 29	0.194 0 0 0.234 0.234 0.766 749 0.839 0.151 44 Frequency	GGGIAGAGGCTCCCTGCAGCCTCTGGGAGTAGAGGAGACCTGGGAAGAACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGAATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.379         GGAGACTGGGTTCAC_TCTATAGACATAGGACACCCATTTATGCTCAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCAC_TCTATAGACATAGGACACCCATTTATGCTCAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCAC_TCTATAGACATAGGACACCCATTTATGCTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCAC_TCTATAGACATAGGACACCCATTTATGCTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCAC_TCTATAGACATAGGACACCCATTTATGCTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCAC_GCTCTATAGACAACGACACCATTTATGCTCTAAAGAGCAAAGGAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.593         Microhaplotype H, 0.593         Microhaplotype H, 0.594         Microhaplotype H, 0.593         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.278         Microhaplot	rs1360288 [CE C]-GRCh38-chr9:126205735-126205813 rs116012791-1; rs1360288-C rs1600288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T million288 [CE T]-GRCh38-chr9:126205735-126205813 rs1360288-T rs2830795 [CE G]-GRCh38-chr9:122235792-37235861 rs2830795-G rs2830795 [CE G]-GRCh38-chr21:27235792-37235861 rs284079- rs28409 [CE A]-GRCh38-chr21:06285996-106286115 rs354439-A rs354439 [CE T]-GRCh38-chr13:106285996-106286115 rs354439-T rs354439 [CE T]-GRCh38-chr13:106285996-106286115 rs354439-T	1 24 29 49 42 4 103 1 20 Count 1	0.00806 0.194 Frequency 0.234 0.395 0.339 0.0323 Frequency 0.831 0.00806 0.161 Frequency 0.00806
7         Target SNP He, 0.3           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.2           Target SNP He, 0.2         Target Allele           7         Target SNP He, 0.2           Target SNP He, 0.2         Target Allele           7         Target Allele           7         Target Allele           7         Target Allele	24 315 22 p-value 1.00 29 95 361 29 95 361 29 95 361 20 20 273 258 p-value 0.6 41 Count 104 20 20 21 22 23 25 29 29 20 29 20 20 20 20 20 20 20 20 20 20	0.194 0 Frequency 0.234 0.766 749 Frequency 0.839 0.161 44 Frequency 0.274	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGGAGAGGAGGAGCTGGGAGGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplorype H, 0.328         Microhaplorype H, 0.339         Microhaplorype H, 0.339         Microhaplorype H, 0.338         Microhaplorype H, 0.39         Microhaplorype H, 0.39         String Sequence         GGAGACTGGCTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.579         Microhaplotype HWE P-value: 0.101         String Sequence         TTCTTAACTCCAAATGCAGTGCGATAGAAAACAGTGAATGATATTCAGAATATTGTGCTTAAAAGGAATGTGATACATGAGAGAGA	n 1360288 [CE C]-GRCh38-chr9126205735-126205813 n116412791-1; n1360288-C n1360288 [CE T]-GRCh38-chr9126205735-126205813 n1360288-T n2820755 [CE T]-GRCh38-chr9126205735-126205813 n1360288-T n2820755 [CE G]-GRCh38-chr9127235792-27215861 n2820795-A n2820755 [CE A]-GRCh38-chr91272735792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr9127235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr9127235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr9127235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr91207235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr91207235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr91207235792-27215861 n1262665- c; n2820795 [CE A]-GRCh38-chr91207235792-27215861 n12626651- n2854439 [CE A]-GRCh38-chr91207235792-27215861 n12626651- n354439 [CE A]-GRCh38-chr91207235792-106286115 n354439-A n354439 [CE A]-GRCh38-chr91206285996-106286115 n354439-A n354439 [CE T]-GRCh38-chr91206285996-106286115 n354439-T n354439 [CE T]-GRCh38-chr91207235792-1435746699-n4606077- T; n354439-T	1 24 29 49 42 4 20 Count 1 20 Count 1 20	0.00806 0.194 Frequency 0.234 0.395 0.339 0.0323 Frequency 0.831 0.00806 0.161 Frequency 0.00606 0.366
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.2 Target	24 315 322 p-value: 1.0( 29 95 361 29 95 361 29 95 361 104 20 277 20 273 258 p-value: 0.6 41) Count 104 20 21 20 21 29 20 21 29 20 20 20 20 20 20 20 20 20 20	0.194 0 Frequency 0.234 0.766 749 0.839 0.161 44 Frequency 0.274	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplorype H, 0.339         Microhaplorype H, 0.579         Microhaplorype H, 0.384         Microhaplorype H, 0.354         Microhaplorype H, 0.355         Microhaplorype H, 0.355         Microhaplorype H, 0.356         Microhaplorype H, 0.357	n 1360288 [Cf C]-GRCh38-chr9126205735-126205813 n116412791-1; n1360288-C n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr9127235792-27235861 n2820795-A n2820795 [Cf A]-GRCh38-chr9127235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr9127235792-27235861 n12626695- n2830795 [Cf A]-GRCh38-chr912707235792-27235861 n12626695- n2830795 [Cf A]-GRCh38-chr912707235792-27235861 n12626695- n2854439 [Cf A]-GRCh38-chr912706285996-106286115 n354439-A n3554439 [Cf A]-GRCh38-chr913106285996-106286115 n354439-T n3554439 [Cf T]-GRCh38-chr913106285996-106286115 n354439-T n4606077 [Cf T]-GRCh38-chr9143574552-143574669 rs4606077- T; n58774512-T n4606077 [Cf T]-GRCh38-chr9143574552-143574669 rs4606077- T; n58774512-T	1 24 29 49 42 4 103 1 20 Count 1 33	0.00806 0.194 7/2000 0.234 0.339 0.0323 0.0325 0.0320 0.0325 0.0000 0.0325 0.00000 0.000000000000000000000000000
T Target SNP He, 0.3 Target SNP He, 0.2 Target SNP HWE rs280795 (n=32) Target SNP He, 0.2 Target SNP	24 315 312 p-value: 1.0( 4) Count 29 95 361 774 p-value: 0.0 9 Count 104 20 273 258 p-value: 0.6 4) Count 34 State	0.194 0 Frequency 0.234 0.766 749 0.769 0.339 0.161 44 Frequency 0.274 0.274 0.726	GGGIAGAGGCTCCCTGCAGCCTCTGGGAGTAGAGGAGCTGGGAACCTGGGAGCACTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.39         Microhaplotype H, 0.319         Microhaplotype HWE p-value: 1.00         String Sequence         GGAGCTGGGTTCACTCTTATAGACATAGGACACACCATTTATGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.284         Microhaplotype H, 0.285         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.274         Microhaplotype H, 0.275         String Sequence	n 1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n13601289 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-7 n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-7 n2820795 [Cf G]-GRCh38-chr9 127235792-77235861 n2820795-6 n2820795 [Cf G]-GRCh38-chr9 127235792-77235861 n2820795-6 n2820795 [Cf A]-GRCh38-chr9 127235792-77235861 n2820795-6 n2820795 [Cf A]-GRCh38-chr9 127235792-77235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr9 127235792-77235861 n12626695- n3554399 [Cf A]-GRCh38-chr9 12705285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr9 12705285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr9 12705285996-106286115 n354439-T n3554399 [Cf T]-GRCh38-chr9 143574562-143574669 ns4606077- T; n560777 [Cf T]-GRCh38-chr8 143574562-143574669 ns4606077- T; n560777 [Cf T]-GRCh38-chr8 143574562-143574669 ns4606077- T; n56077 [Cf T]-GRCh38-chr8 143574562-143574669 ns4606077- C; n186414-A	1 24 29 49 42 4 2 4 2 20 1 20 20 20 1 33 33 90	0.00806 0.194 0.294 0.395 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.161 0.00806 0.2661 0.726
T         Target SNP He, 0.3           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP HWE         Target SNP HWE           G         A           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.4           Target SNP He, 0.4         Target SNP He, 0.3	24 315 312 p-value: 1.0( 4) Count 29 95 361 2774 p-value: 0.0 9 Count 104 20 273 258 p-value: 0.6 4) Count 34 90 40 20	0.194 0 Frequency 0.234 0.766 749 0.769 0.151 44 Frequency 0.274 0.274 0.726	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype HWE p-value: 1.00         String Sequence         GGAGACTGGGTTCACTCTCATAGACATAGGACACCCATTTATGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.284         Microhaplotype H, 0.274         Microhaplotype H, 0.284         Microhaplotype H, 0.274         Microhaplotype H, 0.275         String Sequence <td>n 1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n136012791-T; n1360288-C n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr21.27235792-27235861 n12620795-G n2820795 [Cf G]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.37235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.3106285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr13.106285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr13.106285996-106286115 n354439-T ns554439 [Cf T]-GRCh38-chr13.106285996-106286115 n354439-T ns554439 [Cf T]-GRCh38-chr13.106285996-106286115 n354439-T nr4606077 [Cf T]-GRCh38-chr13.105255962-143574669 ns4606077- T; n56077 [Cf T]-GRCh38-chr8.143574562-143574669 ns4606077- T; n5807431-T</td> <td>1 24 29 49 42 4 20 1 20 Count 1 20 Count 1 33 90</td> <td>0.00806 0.194 0.294 0.395 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.161 0.00806 0.2661 0.726</td>	n 1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n136012791-T; n1360288-C n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr21.27235792-27235861 n12620795-G n2820795 [Cf G]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.27235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.37235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr21.3106285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr13.106285996-106286115 n354439-A n354439 [Cf A]-GRCh38-chr13.106285996-106286115 n354439-T ns554439 [Cf T]-GRCh38-chr13.106285996-106286115 n354439-T ns554439 [Cf T]-GRCh38-chr13.106285996-106286115 n354439-T nr4606077 [Cf T]-GRCh38-chr13.105255962-143574669 ns4606077- T; n56077 [Cf T]-GRCh38-chr8.143574562-143574669 ns4606077- T; n5807431-T	1 24 29 49 42 4 20 1 20 Count 1 20 Count 1 33 90	0.00806 0.194 0.294 0.395 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.161 0.00806 0.2661 0.726
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3	24 315 312 p-value: 1.0 Count 29 95 361 274 p-value: 0.0 Count 104 20 20 20 20 20 20 20 20 20 20	0.194 0	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.330         String Sequence         GGAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGAGTCCTATTA         Microhaplotype H, 0.89         Microhaplotype H, 0.699         Microhaplotype H, 0.694         Microhaplotype H, 0.694         Microhaplotype H, 0.894         Microhaplotype H, 0.894         Microhaplotype H, 0.894         Microhaplotype H, 0.894         Microhaplotype H, 0.395         Microhaplotype H, 0.374         Microhaplotype H, 0.328         Microhaplotype H, 0.328         Microhaplotype H, 0.328         Microhaplotype H, 0.328         Microhaplotype H, 0.327         Microhaplotype H, 0.328         Microhaplotype H, 0.328         Microhaplotype H, 0.328 <td>m1360288 [Cf C] GRCh38-chr9126205735-126205813         m116012791-7; m1360288-C         m1160288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1160288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1260288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1260288 [Cf C] GRCh38-chr9126205792-77235861 m280795-G         m2830795 [Cf G] GRCh38-chr9127235792-77235861 m280795-G         m2830795 [Cf A]-GRCh38-chr91272735792-77235861 m12626695-C         m2830795 [Cf A]-GRCh38-chr9127235792-77235861 m12626695-C         m1260289 [Cf A]-GRCh38-chr9127235792-77235861 m12626695-C         m1260289 [Cf A]-GRCh38-chr9127275792-77235861 m12626695-C         m127235792-77235861 m12626695-C         m12830795 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-T         m400077 [Cf T]-GRCh38-chr9143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-C</td> <td>1 24 29 49 42 4 4 103 1 20 Count 1 33 90</td> <td>0.00806 0.194 7requency 0.234 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.161 7requency 0.00806 0.161</td>	m1360288 [Cf C] GRCh38-chr9126205735-126205813         m116012791-7; m1360288-C         m1160288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1160288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1260288 [Cf C] GRCh38-chr9126205735-126205813 m1360288-T         m1260288 [Cf C] GRCh38-chr9126205792-77235861 m280795-G         m2830795 [Cf G] GRCh38-chr9127235792-77235861 m280795-G         m2830795 [Cf A]-GRCh38-chr91272735792-77235861 m12626695-C         m2830795 [Cf A]-GRCh38-chr9127235792-77235861 m12626695-C         m1260289 [Cf A]-GRCh38-chr9127235792-77235861 m12626695-C         m1260289 [Cf A]-GRCh38-chr9127275792-77235861 m12626695-C         m127235792-77235861 m12626695-C         m12830795 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf A]-GRCh38-chr913106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-A         m354439 [Cf T]-GRCh38-chr9143106285996-106286115 m354439-T         m400077 [Cf T]-GRCh38-chr9143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-T         m4606077 [Cf T]-GRCh38-chr8.143574562-143574669 m4608077-C	1 24 29 49 42 4 4 103 1 20 Count 1 33 90	0.00806 0.194 7requency 0.234 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.161 7requency 0.00806 0.161
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.4	24 315 312 p-value: 1.0 20 27 29 95 361 274 274 274 274 20 20 273 225 p-value: 0.5 40 Count 104 20 20 27 34 90 40 20 20 20 20 20 20 20 20 20 2	0.194 0 5 5 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype HWE p-value: 1.00         String Sequence         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAGGGCAAAGAGACCCATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGCCATATA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGACCCTATTA         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGACAAGAGCCATATA         Microhaplotype H, 0.579         Microhaplotype HWE p-value: 0.101         String Sequence         TTCTTACTCTCAATTGCAGTGCGATAGAAAACAGTGAATATTGTGATTAATGGCTTAAAGGAATGTGATACATGAGAGAGA	n:1360288 [CI C] GRCh38-chr9:126205735-126205813 n:1160288 [CI C] GRCh38-chr9:126205735-126205813 rs1360288-T n:1360288 [CI C] GRCh38-chr9:126205735-126205813 rs1360288-T n:2820795 [CI G] GRCh38-chr9:122723792-77235861 rs280795-G rs2830795 [CI G] GRCh38-chr21:27235792-77235861 rs280795-G rs2830795 [CI A] -GRCh38-chr21:27235792-77235861 rs280795-G rs2830795 [CI A] -GRCh38-chr21:3106285996-106286115 rs354439-A rs354439 [CI A] -GRCh38-chr13:106285996-106286115 rs354439-A rs354439 [CI T] -GRCh38-chr13:106285996-106286115 rs354439-T rs4606077 [CI T] -GRCh38-chr13:106285996-106286115 rs354439-T rs4606077 [CI T] -GRCh38-chr13:10528596-105286115 rs354459-T rs4606077 [CI T] -GRCh38-chr13:13574562-143574669 rs4606077-T rs4606077 [CI T] -GRCh38-chr8:143574562-143574669 rs4606077-T rs4606077 [CI T] -GRCh38-chr8:143574562-143574669 rs4606077-T	1 24 29 49 42 4 4 20 103 1 20 20 20 20 20 20 20 20 20 20 20 20 20	0.00806 0.194 0.234 0.395 0.339 0.0323
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.4           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.4           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.4           Target SNP He, 0.4         Target SNP He, 0.5           Target SNP He, 0.4         Target SNP He, 0.5           Target SNP He, 0.5         Ta	24 315 312 p-value: 1.00 41 Count 29 95 361 274 29 95 361 274 20 20 20 20 20 20 20 20 20 20	0.194 0  Frequency 0.234 0.766 749 749 0.839 0.161 44 Frequency 0.274 0.726 64 Frequency 0.274 0.726	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGJAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         String Sequence         GAGACTGGGTTCACTCTCATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGACACACCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         Microhaplotype H, 0.579         Microhaplotype H, 0.593         Microhaplotype H, 0.274         Microhaplotype H, 0.275         String Sequence         TICTTACTCAAATTGCAGTTGCCATAGAAACAGTGAAACAGTGATATTCAGAATATTGTGCTTAAAAGGAAATGTGATACATGAGAGAGA	n 1360288 [CI C] GRCh38-chr9126205735-126205813 n116412791-7; n1360288-C n1160288 [CI C] GRCh38-chr9126205735-126205813 n1360288-T Microhaplotype Nomenclature n2839795 [CI G] GRCh38-chr2127235792-77235651 n2820795-G n2839795 [CI A] GRCh38-chr2127235792-77235651 n2820795-G n2839795 [CI A] GRCh38-chr21:27235792-77235651 n2820795-G n2839795 [CI A] GRCh38-chr21:27235792-77235651 n12626695- C, n2830795 [CI A] GRCh38-chr21:27235792-77235861 n12626695- C, n2830795 [CI A] GRCh38-chr13.106285996-106286115 n354439-A n354439 [CI A] GRCh38-chr13.106285996-106286115 n354439-A n354439 [CI T] GRCh38-chr13.106285996-106286115 n354439-T n354439 [CI T] GRCh38-chr13.106285996-106286115 n354439-T n354439 [CI T] GRCh38-chr13.106285996-106286115 n354439-T n4606077 [CI T] GRCh38-chr13.106285996-106286115 n354439-T n4606077 [CI T] GRCh38-chr13.10628596-106286115 n354439-T n4606077 [CI T] GRCh38-chr13.10574562-143574669 ns4606077- C, n18608077 [CI T] GRCh38-chr13.13574562-143574669 ns4606077- C, n18608414-A	1 24 29 49 42 4 4 20 103 1 20 20 20 20 20 20 20 20 20 20 20 20 20	0.00806 0.194 0.234 0.339 0.0323
T Target SNP H4, 0.3 Target SNP H4, 0.3 Tar	24 315 312 p-value: 1.00 29 95 361 274 95 361 274 104 20 273 28 p-value: 0.6 41 104 20 273 28 p-value: 0.6 41 20 20 20 20 20 20 20 20 20 20	0.194 0 5 5 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGGTAGAGGGAAGAGCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplorype H, 0.328         Microhaplorype H, 0.339         Microhaplorype H, 0.339         Microhaplorype H, 0.339         Microhaplorype HWE p-value: 1.00         String Sequence         GGAGACTGGGTTCACTCTCTAGACATAGGACACCCATTTATTGTCTAAAGGCAAAGAGTCCTATTA         GAGACTGGGTTCACTCTCTAGACATAGGACACCCATTTATTGTCTAAAGGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCTAGACATAGGACACCCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCTAGAGACTAGGACACCCATTTATTGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCTAGAGACTAGGACACCCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCTAGAGACTAGGACACCCATTTTATGTCTAAAGAGCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTCTAGAGACACCCCGTTTGGATAGAAACAGTGAATGTATTGTGCTTAAAAGGAATGTGATACATGAGAGAGA	n 1360288 [CI C]-GRCh38-chr9:126205735-126205813 n116412791-T; n1360288-C n1160288 [CI C]-GRCh38-chr9:126205735-126205813 rs1360288-T m2820795 [CI G]-GRCh38-chr9:126205735-125205813 rs1360288-T n2820795 [CI G]-GRCh38-chr9:1272735792-77235861 rs12620595- c, n2820795 [CI G]-GRCh38-chr21:27235792-37235861 rs12626685- C; n2820795 [CI A]-GRCh38-chr21:27235792-37235861 rs12626685- C; n2820795 [CI A]-GRCh38-chr21:27235792-37235861 rs12626685- C; n2820795 [CI A]-GRCh38-chr21:27235792-37235861 rs12626685- C; n2820795-A m856489 [CI A]-GRCh38-chr21:27235792-37235861 rs12626685- C; 27235845-1; rs2820795-A m856489 [CI A]-GRCh38-chr21:06285996-106286115 rs354439-A rs354439 [CI A]-GRCh38-chr13:106285996-106286115 rs354439-A rs354439 [CI T]-GRCh38-chr13:106285996-106286115 rs354439-T rs4606077 [CI T]-GRCh38-chr13:106285996-106286115 rs354439-T rs4606077 [CI T]-GRCh38-chr13:10628596-106286115 rs354439-T rs4606077 [CI T]-GRCh38-chr13:10528596-106286115 rs354439-T rs4606077 [CI T]-GRCh38-chr13:10528596-106286115 rs35449-T rs4606077 [CI T]-GRCh38-chr13:10528596-106286115 rs35449-T rs4606077 [CI T]-GRCh38-chr13:10528596-106286115 rs35449-T rs4606077 [CI T]-GRCh38-chr13:10528596-105286115 rs35449-T rs4606077 [CI T]-GRCh38-chr13:10574562-143574669 rs4606077- C; rs1869414-A	1 24 29 49 42 4 29 103 1 20 Count 1 33 90 Count 90	0.00806 0.194 0.234 0.395 0.339 0.0323 0.0323 Frequency 0.831 0.00806 0.161 Frequency 0.00806 0.2661 0.726 0.726
T T Target SNP He, 0.3 Target SN	24 315 222 p-value: 1.00 41 Count 29 95 361 274 p-value: 0.0 41 Count 104 20 273 258 p-value: 0.6 41 Count 34 90 40 Count 34 90 40 Count 20 27 27 20 27 20 27 20 27 20 27 20 27 20 20 20 20 20 20 20 20 20 20	0.194 0 Frequency 0.234 0.766 749 Frequency 0.839 0.161 44 Frequency 0.274 0.726 64 Frequency 0.782 0.218	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC           GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC           Microhaplorype H, 0.328           Microhaplorype H, 0.329           Microhaplorype H, 0.579           Microhaplorype H, 0.350           Microhaplorype H, 0.351           Microhaplorype H, 0.351           Microhaplorype H, 0.352           Microhaplorype H, 0.353           Microhaplorype H, 0.328           Microhaplorype H, 0.329           Microhaplorype H, 0.329           Microhaplorype H, 0.329	n 1360288 [CE C]-GRCh38-chr9126205735-126205813 n11641291-1; n1360288-C n1360288 [CE T]-GRCh38-chr9126205735-126205813 n1360288-T n1360288 [CE T]-GRCh38-chr9126205735-126205813 n1360288-T n2820795 [CE G]-GRCh38-chr9127235792-27215861 n2820795-A n2820795 [CE A]-GRCh38-thr1127235792-27215861 n1262665- C; n2820795 [CE A]-GRCh38-thr1127235792-27215861 n1262665- C; n2820795 [CE A]-GRCh38-thr1127235792-27215861 n1262665- C; n2820795 [CE A]-GRCh38-thr1127235792-27215861 n1262665- C; n2820795 [CE A]-GRCh38-thr11217235792-27215861 n1262665- C; n2820795 [CE A]-GRCh38-thr11106285996-106286115 n354439-A n354439 [CE A]-GRCh38-thr11106285996-106286115 n354439-A n354439 [CE A]-GRCh38-thr11106285996-106286115 n354439-A n354439 [CE T]-GRCh38-thr11106285996-106286115 n354439-T n4606077 [CE T]-GRCh38-thr11106285996-106286115 n354409 rs4606077-T r, rs58774512-T n4606077 [CE T]-GRCh38-thr11106285996-106286115 n354409 rs4606077-C r, rs1864414-A	1 24 29 49 42 4 20 1 20 1 20 Count 1 33 90 Count 97 2	0.00806 0.194 0.234 0.395 0.339 0.0323 0.0325 0.0323 0.0325 0.0355 0.035
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.2 Target	24 315 312 22 p-value: 1.0( Count 29 95 361 29 95 361 774 p-value: 0.0 0 Count 104 20 27 20 27 40 Count 104 20 20 27 40 Count 29 95 361 Count 29 95 361 Count 29 95 361 Count 29 95 361 Count 20 20 20 20 20 20 20 20 20 20	0.194 0  Frequency 0.234 0.766 749 0.839 0.161 44  Frequency 0.274 0.274 64  Frequency 0.274 0.726 64	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC           GGGGAAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC           Microhaplotype H, 0.339           Microhaplotype H, 0.539           Microhaplotype H, 0.579           Microhaplotype H, 0.385           Microhaplotype H, 0.355           Microhaplotype H, 0.325           Microhaplotype H, 0.325           Microhaplotype H, 0.325           Microhaplotype H, 0.325	n 1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n116412791-1; n1360288-C n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n2820795 [Cf G]-GRCh38-chr9 127235792-27235861 n2820795-6 n2820795 [Cf A]-GRCh38-chr9 127235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr9 127235792-27235861 n12626695- c; n2820795 [Cf A]-GRCh38-chr9 1272735792-27235861 n12626695- n3554439 [Cf A]-GRCh38-chr9 1206285996-106286115 n354439-A n3554439 [Cf A]-GRCh38-chr9 1306285996-106286115 n354439-A n3554439 [Cf T]-GRCh38-chr9 145574562-143574669 rs4606077- T; n5867457 [Cf T]-GRCh38-chr9 145574562-143574669 rs4606077- T; n58674577 [Cf T]-GRCh38-chr9 145574562-143574669 rs4606077- C; r1886414-A	1 24 29 49 42 4 103 1 20 Count 1 33 90 Count 97 2 25	0.00806 0.194 Frequency 0.234 0.339 0.0323 0.0325 0.00805 0.0265 0.0265 0.0265 0.0265 0.0325 0.0161 0.0202
T Target SNP H <sub>6</sub> 0.3 Target SNP H <sub>6</sub> 0.2 Target	24 315 315 22 p-value: 1.0( 4) Count 29 95 361 774 p-value: 0.0 0 Count 104 20 27 20 27 43 58 90 401 34 90 401 587 97 27 27 27	0.194 0  Frequency 0.234 0.766 749 749 0.339 0.161 44 Frequency 0.274 0.274 0.726 64 Frequency 0.782 0.782	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTGCATCCCCTCAACAGATGCCCC         GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.39         Microhaplotype H, 0.59         Microhaplotype H, 0.57         Microhaplotype H, 0.58         Microhaplotype H, 0.59         Microhaplotype H, 0.57         Microhaplotype H, 0.28         Microhaplotype H	n 1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n116412791-1; n1360288-C n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n1360288 [Cf C]-GRCh38-chr9 126205735-126205813 n1360288-T n2830795 [Cf G]-GRCh38-chr127235792-77235861 n12620695- c; n280795 [Cf A]-GRCh38-chr127235792-77235861 n12626695- c; n280795 [Cf A]-GRCh38-chr127235792-77235861 n12626695- c; n280795 [Cf A]-GRCh38-chr127235792-77235861 n12626695- c; n280795 [Cf A]-GRCh38-chr12 n27235792-77235861 n12626695- c; n280795 [Cf A]-GRCh38-chr13 106285996-106286115 n354439-A n3554439 [Cf A]-GRCh38-chr13 106285996-106286115 n354439-A n3554439 [Cf A]-GRCh38-chr13 106285996-106286115 n354439-A n3554439 [Cf A]-GRCh38-chr13 106285996-106286115 n354439-T n556439 [Cf T]-GRCh38-chr13 106285996-106286115 n354439-T ns554439 [Cf T]-GRCh38-chr13 106285996-106286115 n354439-T ns56439 [Cf T]-GRCh38-chr13 106285996-106286115 n354439-T ns606077 [Cf T]-GRCh38-chr13 106285996-106286115 n354469 ns4606077- T ns4606077 [Cf T]-GRCh38-chr13 106285996-106286115 n3574669 ns4606077- C; n1369434-A	1 24 29 49 49 42 4 20 1 1 20	0.00806 0.194 0.234 0.339 0.0323 0.00006 0.0261 0.0726 0.0726 0.0726 0.0726 0.0726
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP HWE         Target SNP HWE           Target SNP HWE         Target SNP HWE           G         A           Target SNP HWE, 0.3         Target SNP HWE           rstaget SNP HWE         Target SNP HWE           rarget SNP HWE         Target SNP HWE           Target SNP HWE         Target SNP HWE           Target SNP HWE         Target SNP HWE           Target SNP HWE         Target SNP HWE           G         Target SNP HWE           G         Target SNP HWE, 0.3           Target SNP HWE, 0.4         Target SNP HWE	24 315 312 22 24 20 29 95 361 29 95 361 29 95 361 29 95 361 29 95 361 29 95 361 29 95 361 104 20 20 27 20 20 20 20 20 20 20 20 20 20	0.194 0  Frequency 0.234 0.766 749 749 749 0.839 0.161 44  Frequency 0.274 0.274 0.274 0.274 0.276 64  Frequency 0.382 0.181	GGGIAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGCTGGGAAGACCTGGCTAGCATCCCCTCAACAGATGCCCC           GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC           Microhaplotype H, 0.328           Microhaplotype H, 0.329           Microhaplotype H, 0.339           Microhaplotype H, 0.537           Microhaplotype H, 0.579           Microhaplotype H, 0.384           Microhaplotype H, 0.384           Microhaplotype H, 0.328           Microhaplotype H, 0.328           Microhaplotype H, 0.328           Microhaplotype H, 0.328	n 1360288 [Cf C] GRCh38-chr9 126205735-126205813 n116012791-T; n1360288-C n1360288 [Cf C] GRCh38-chr9 126205735-126205813 n1360288-T n1360288 [Cf C] GRCh38-chr9 126205735-126205813 n1360288-T n2830795 [Cf G] GRCh38-chr12.27235792-77235861 n2820795-G n2830795 [Cf A] GRCh38-chr12.72735792-77235861 n12626695- c; n2830795 [Cf A] GRCh38-chr13.105285996-1052861 n12626695- c; n2830795 [Cf A] GRCh38-chr13.105285996-1052861 n12626695- c; n2830795 [Cf A] GRCh38-chr13.105285996-1052861 n12626695- c; n2830795 [Cf A] GRCh38-chr13.105285996-105286115 n354439-A n354439 [Cf A] GRCh38-chr13.105285996-105286115 n354439-A n354439 [Cf A] GRCh38-chr13.105285996-105286115 n354439-A n354439 [Cf A] GRCh38-chr13.105285996-105286115 n354439-T n4606077 [Cf T] GRCh38-chr13.105285986-105286115 n354439-T n4606077 [Cf T] GRCh38-chr13.2775757298-27972517 n5719366-A n5719386 [Cf G] GRCh38-chr19.27972398-27972517 n5719386-G; n219397-A n5719386 [Cf G] GRCh38-chr19.27972398-27972517 n5719366-G; n219397-A	1 24 24 29 49 42 4 103 1 20 Count 1 33 90 Count 90 2 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5	0.00806 0.194 0.234 0.335 0.335 0.0323 0.00006 0.0261 0.0261 0.0726 0.0726 0.0726
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.2           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3	24 315 315 312 p-value: 1.0( Count 29 95 361 274 97 361 104 20 273 288 p-value: 0.5( 4) Count 34 90 401 34 90 401 Count 97 27 27 27 27 34 30 27 27 27 27 27 27 27 27 27 27	0.194 0  Frequency 0.234 0.766 749 0.766 749 0.339 0.161 44 Frequency 0.274 0.726 64  Frequency 0.726 0.726 0.726 0.782 0.782 0.218 350	GGGLAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACCTGGCTAGCATCCCCTCAACAGATGCCCC         GGGGLAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC         Microhaplotype H, 0.328         Microhaplotype H, 0.339         Microhaplotype H, 0.339         Microhaplotype H, 0.339         GGAGACTGGCTTCACTCTATAGACATAGGAACACCACTTTATTGTCTAAGGGCAAGAGACTCCTATTA         GGAGACTGGGTTCACTCTATAGACATAGGAACACCACTTTATTGTCTAAGGGCAAAGAAGTCCTATTA         GGAGACTGGGTTCACTCTATAGACATAGGAACACCCATTTATTGTCTAAAGGLCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCCATTTATTGTCTAAAGGLCAAAGAAGTCCTATTA         GAGACTGGGTTCACTCTATAGACATAGGAACACCCATTTATTGTCTAAAGGLCAAAGAAGTCCTATTA         Microhaplotype H, 0.694         Microhaplotype H, 0.694         Microhaplotype H, 0.694         Microhaplotype H, 0.694         Microhaplotype H, 0.705         String Sequence         TTCTTACTCCAATTGCAGTTGCCATAGAAACAGTGAATGATATTCAGAATATTGTCCTTAAAAGGAATGTGATACATGAGAGAGGAGAAGAGCAACAGAA         TCTTAACTCCAATTGCAGTTGCCATAGAAAACAGTGAATGATATTCAGAATATTGTCCTTAAAGGAATGTGATACATGAGAGAGA	n 1360288 [CI C] GRCh38-chr9 126205735-126205813 n1160288 [CI C] GRCh38-chr9 126205735-126205813 n1360288-7 n1360288 [CI C] GRCh38-chr9 126205735-126205813 n1360288-7 n2820795 [CI G] GRCh38-chr21.27235792-77235861 n2820795-6 n2820795 [CI G] GRCh38-chr21.27235792-77235861 n2820795-6 n2820795 [CI A] GRCh38-chr21.27235792-77235861 n2820795-6 n2820795 [CI A] GRCh38-chr21.27235792-77235861 n2820795-6 n2820795 [CI A] GRCh38-chr21.27235792-77235861 n2820795-6 n2820795 [CI A] GRCh38-chr21.27235792-77235861 n2820695- c; 72820795 A n2820795 [CI A] GRCh38-chr21.27235792-77235861 n12626695- c; 72820795 A n356439 [CI A] GRCh38-chr21.37235792-17235861 n12626695- c; 72820795 A n356439 [CI A] GRCh38-chr21.3106285996-106286115 n356439-A n356439 [CI A] GRCh38-chr21.3106285996-106286115 n354439-A n356439 [CI C] GRCh38-chr21.3106285996-106286115 n354439-T n356439 [CI C] GRCh38-chr21.3106285996-106286115 n354439-T n4606077 [CI T] GRCh38-chr21.3106285996-106286115 n354439-T n74806077 [CI T] GRCh38-chr21.32774562-143574669 n4606077- C, r1866434-A n719386 [CI A] GRCh38-chr19.27972398-27972517 rs719386-A n719386 [CI G] GRCh38-chr19.27972398-27972517 rs719386-G n719386 [CI G] GRCh38-chr19.27972398-27972517 rs719386-G	1 24 29 49 42 4 103 1 20 Count 1 33 90 Count 1 33 90 Count 1 33 90 Count 1 33 90 Count 1 2 2 2 2 2 2 2 2 2 2 2 2 2	0.00806 0.194 0.234 0.395 0.339 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.0323 0.00806 0.2661 0.726 0.726 0.726 0.782 0.0161 0.202
T         Target SNP He, 0.3           Target SNP He, 0.1         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.2         Target SNP He, 0.2           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.3         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Target SNP He, 0.3           Target SNP He, 0.4         Ta	24 315 315 312 p-value: 1.0( Count 29 95 361 274 97 361 104 20 20 20 20 20 20 20 20 20 20	0.194 0  Frequency 0.234 0.766 743 0.766 743 0.339 0.161 744 0.274 0.274 0.274 0.726 64  Frequency 0.782 0.218 350 Frequency	GGGTAGAGGCTCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGAACCTGGCTGCATCCCCTCAACAGATGCCCC GGGGAAAGGCTCCCTGCAGCCTCTGGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC Microhaplotype HV 0.328 Microhaplotype HV 0.328 Microhaplotype HV 0.329 Microhaplotype HV 0.328 Microhaplotype HV 0.338 Microhaplotype HV 0.348 Microhaplotype	n 1360288 [CI C] GRCh38-chr9 126205735-126205813 n1160288 [CI C] GRCh38-chr9 126205735-126205813 n1360288-7 n1360288 [CI C] GRCh38-chr9 126205735-126205813 n1360288-7 n2820795 [CI G] GRCh38-chr9 122723792-77235861 n2820795-6 n72830795 [CI G] GRCh38-chr9 1272735792-77235861 n2820795-6 n72830795 [CI A] GRCh38-chr9 1272735792-77235861 n12626695- c; n2830795 [CI A] GRCh38-chr9 1277255792-77235861 n12626695- c; n2830795 [CI A] GRCh38-chr9 1207255792-77235861 n12626695- c; n2830795 [CI A] GRCh38-chr9 1207255792-106286115 n354439-A n354439 [CI A] GRCh38-chr9 13106285996-106286115 n354439-A n354439 [CI T] GRCh38-chr9 13106285996-106286115 n354439-T n4606077 [CI T] GRCh38-chr9 134574562-143574669 rs4606077- rs4606077 [CI T] GRCh38-chr9 12797298-27972517 rs71986-G rs71986 [CI G] GRCh38-chr9 2797298-27972517 rs71986-G	1 24 29 49 42 4 103 1 20 Count 1 33 90 Count 1 33 90 Count 25 Count 57 25 Count 25 Count 29 25 25 25 25 25 25 25 25 25 25	0.00806 0.194 Prequency 0.234 0.395 0.339 0.0323 Prequency 0.831 0.00806 0.161 0.726 Prequency 0.726 0.782 0.0161 0.202 Prequency 0.782 0.0161

c	94	0.758	AGTACATTTTTTGTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTAGATG	rs876724 [CE C]-GRCh38-chr2:114970-115036 rs876724-C; rs300773-T rs276724 [CE CLGRCh38-chr2-114970-115036 rs876724-C	39	0.314516
Target SNP H <sub>a</sub> ( Target SNP H <sub>0</sub> ( Target SNP HW	0.370 0.258 'E p-value: 0.0	0263	Microhapistype H, 0,651 Microhapistype H, 0,653 Microhapistype H, 0,758	instanta (colonolisioniti tapia tipos tovova c	33	0.113310
rr902100 /a=12	241					
Target Allele	Count	Frequency	String Sequence	Microhaplotype Nomendature	Count	Frequency
- 19 C		- 19 Mar - 1	TGATGCCCTGGCATCAAAGAAGGCTCCAACTGGGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	rs907100 [CE C]-GRCh38-chr2:238654924-238654989 rs907100-C	35	0.282
<b>C</b>	40	0.323	TGATGCCCTGGCATCAAAGAAGGCTCCAACTGAGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	rs907100 [CE C]-GRCh38-chr2:238654924-238654989 rs907100-C; rs11689319-A	5	0.0403
G	84	0.677	TGATGCCCTGGCATGAAAGAAGGCTCCAACTGGGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	rs907100 [CE G]-GRCh38-chr2:238654924-238654989 rs907100-G	84	0.677
Target SNP H <sub>e</sub> C Target SNP H <sub>e</sub> C Target SNP HW	0.441 0.484 'E p-value: 0.5	561	Microhapiotype He, 0.664 Microhapiotype HWE p-value: 0.589 Microhapiotype HWE p-value: 0.589			
rs987640 (n=12	24)	10		and a second		
Target Allele	Count	Frequency	String Sequence	Microhaplotype Nomenclature	Count	Frequency
	6.23		ACAGGTACATTCACTTAACAGGETCTCTTTCCACCCATGTAGAAATACAAAAATAAGACTTAATACAGACGATGG	rs987640 [CE A]-GRCh38-chr22:33163486-33163560 rs987640-A	50	0.403
A	51	0.411	ACCGGTACATTCACTTAACAGGCTCTCTTTCCACCCATGTAGAAAYACAAAAATAAGACTTAATACAGACGATGG	rs987640 [CE A]-GRCh38-chr22:33163486-33163560 rs17793354-C; rs987640-A	1	0.00806
т	73	0.589	ACAGGTACATTCACTTAACAGGCTCTCTTTCCACCCTTGTAGAAATACAAAAATAAGACTTAATACAGACGATGG	rs987640 [CE T]-GRCh38-chr22:33163486-33163560 rs987640-T	73	0.589
Target SNP H <sub>0</sub> C Target SNP H <sub>0</sub> C Target SNP HW	0.488 0.468 'E p-value: 0.1	800	Microhapiotype Hu. 0.495 Microhapiotype Hu. 0.495 Microhapiotype HWE p-value: 0.660			
rs9905977 (n=1	124)	Freedom		Martin Barrison Martin Alaria	Count	Francisco
Target Miles	count	Prequency	T6G1S1CCAAGGA6G6CT6G6T6ACTCGT6GCTCA6TCAGCATCAAGATTCCTTTCGTCTTTCCCCTCT6CCCTCCCTGSCTT6TCAGCTTT6		count	requercy
A	48	0.387	TCCCTCAGGCTTGGCCCCCTCGTGGCC	1233072311 [CE V]-OKCU38-SULTI:301E028-301E11/E 123302311-V	48	0.387
			TGGTGTCAAGGAGGGTGGGTGACTCGTGGCTCAGTCAGCGTCAAGATTCCTTTCGTCTTTCCCCTCGCCCTCCCT	rs9905977 [CE G]-GRCh38-chr17:3016058-3016176 rs9905977-G; rs28582109-A	3	0.0242
6	75	0.613	TectricAdectridected for the second s	rs9905977 [CE G]-GRCh38-chr17:3016058-3016176 rs9905977-G rs9905977 [CE G]-GRCh38-chr17:3016058-3016176 rs9905977-G; r 72309903.7	71 2	0.573
Target SNP H <sub>e</sub> C Target SNP H <sub>o</sub> C Target SNP HW	0.478 0.516 E p-value: 0.5	593	Nicrohapistype Hu, 0.565 Microhapistype Hu, 0.565 Microhapistype HU D-solue: 0.361	1373630326-1		
r=993934 /m=12	24)					
Target Allolo	Count	Frequency	String Sequence	Microhapletype Nomenclature	Count	Frequency
	1082	- 24 K (24)	TITGCTITGTAAGGCAATAGAGCAAAGTATTGTGATAACAGTCTCCAGAGTATATTAGCTTAGTTCATAA	rs993934 [CE A]-GRCh38-chr2:123351571-123351640 rs993934-A	83	0.669
A	85	0.685	TITIGCTITIGTAAGGCAATAGAGCAAAGTATTGCGATAACAGTCTCCAGAGTATATTAGCTTAGTTCATAA	rs993934 [CE A]-GRCh38-chr2:123351571-123351640 123351603- C: rs993934-A	2	0.0161
G	39	0.315	TTTGCTTTGTAAGGCAATAGAGCAAAGTATTGTGATAACAGTCTCCAGAGTATATTAGCTTAGTTCGTAA	rs993934 [CE G]-GRCh38-chr2:123351571-123351640 rs993934-G	39	0.315
Target SNP H <sub>e</sub> ( Target SNP H <sub>o</sub> ( Target SNP HW	0.435 0.565 E p-value: 0.0	)184	Microhapiotype Hu, 0.456 Microhapiotype Hu, 0.597 Microhapiotype HWE p-value: 0.0250			
rs200354 (n=12	24)	Second States				
Target Allele	Count	Frequency	String Sequence CAAGCTGCCTTGGAACTGGGCTGCCCCCATGCACCATGGCCATTTGGAACTGGGTAGTGAGAGGCTGCCCTGTCCATTGTAGAATGTTTAG	Microhaplotype Nomenclature	Count	Frequency
G	12	0.0968	CAGCATCCTCTGGGAGTAGCAAACTCCCCTC	rs200354 [CE 6]-GRCh38-chr14:98908931-98909052 rs200354-G	12	0.0968
т	112	0.903	CAAGCTGCCTTGGAACTGGGCTGCCCCCATGCACCATGGCCATTIGGAACTGGTTAGTGAGAGGCTGCCCTGTCC <u>G</u> TTGTAGAATGTTTAG CAGCATCCTCTGGGAGTAGCCAAACTCC <u>C</u> TC CAAGCTGCTTGGAACTGGGTGCCCCCCCCCCCCCCCC	rs200354 [CE T]-GRCh38-chr14-98908931-98909052 rs200354-T; rs200353-G	72	0.581
			CAGCATECTETGGGAGTAGECAAACTECCCTE	rs200354 [CE T]-GRCh38-chr14-98908931-98909052 rs200354-T	23	0.185

Yavapai population, however, access to these sequence data may reveal additional variation on a case-by-case basis or in other population groups, defining additional microhaplotypes.

Six aiSNPs had sequence variation adjacent to the target locus with an average frequency of 0.191  $\pm$ 0.215 (Table 1 and Supplemental Table 5). Two of the aiSNP microhaplotypes (rs1079597-rs1079598 or "mh11KK-090"; rs870347-870348 or "mh11KK-062" or "PAPD7") have been described previously [17,18]. One aiSNP microhaplotype (rs1079597-rs1079598; mh11KK-090) provided no increase in the number of alleles at the target rs1079597 locus. The average H<sub>o</sub> and H<sub>e</sub> were 0.319  $\pm$  0.237 and 0.343  $\pm$  0.209 for 5/6 aiSNPs, respectively, and 0.435  $\pm$  0.215 and 0.431  $\pm$ 0.217 for 5/6 aiSNP microhaplotypes, respectively. Prior to Bonferroni correction, no aiSNP microhaplotypes significantly deviated from HWE expectations. Before and after Bonferroni correction (p < 3.25 × 10<sup>-5</sup>), 381 and 22 aiSNP pairwise LDs were observed, respectively. No significant Bonferroni corrected LDs were observed between aiSNPs or aiSNP microhaplotypes on the same chromosome.

A minor increase in variation was observed for two piSNPs when considering flanking region sequences (Table 1 and Supplemental Table 6). Two piSNP microhaplotypes were defined as: mh16-MCR1B and mh16-MCR1C [5]. The average piSNP microhaplotype H<sub>o</sub> and H<sub>e</sub> were 0.198  $\pm$  0.213 and 0.190  $\pm$  0.196, respectively. After Bonferroni correction (p < 0.000549), one (rs1805009/mh-16-MCR1B) significant pairwise LD was observed. It is not surprising to observe significant LD between rs1805009 and mh16-MCR1B due to their close physical proximity (~325 basepairs) within the MCR1 gene.

## 3.3. Bioinformatic concordance

Consistent with the ForenSeq<sup>TM</sup> UAS and STRbase [10,20], Wendt, et al. [10] did not include the DYS612 [CCT]<sub>a</sub> [CTT]<sub>b</sub> motif in length-based alleles. Based on Parson, et al. [16] recommendations and Novroski, et al. [3] population data, this region is now included for the length-based alleles at the DYS612 locus.

Compared to frequency data previously published by Wendt, et al. [10], the piSNP N29insA is discordant. The locus was reported as having no observed heterozygosity and yet the allele frequencies are 0.516 and 0.484 for the null and insertion alleles, respectively. By using STRait Razor v2s, a bioinformatic error was discovered. Manual confirmation of the locus in the ForenSeq<sup>TM</sup> UAS indicated that the error occurred when the "ForenSeqRunStatistics" XML files were offline. Thus, the values reported herein are a discordant due to an operation issue independent of analyses performed with the UAS. The N29insA frequencies reported here (1.00 null and 0.00 insertion) are correct.

# 4. Conclusion

Twenty-one human-identity markers have been identified in this study of the Yavapai population which contain some degree of flanking region variation, with a wide range of relative frequencies. A small portion of target autosomal STRs and iiSNPs exhibited flanking region variation at relatively high frequencies. The human identification marker set captured by the ForenSeq<sup>TM</sup> DNA Signature Prep Kit produced combined RMPs of  $7.66 \times 10^{-58}$  and



Fig. 1. Sequence variation of autosomal identity-informative markers. (A) Number of short tandem repeat (STR) loci in the Yavapai population and the Novroski, et al. [3] study exhibiting sequence variation; (B) Observed and expected heterozygosity increase of autosomal STR loci with flanking region variation; an asterisk indicates the locus with flanking region and repeat region variation; (C) Observed and expected heterozygosity increase of identity-informative single nucleotide polymorphism containing microhaplotypes.

 $5.49 \times 10^{-63}$ , respectively, for a panel of 121 human identification markers (94 iiSNPs or MPS-based iiSNPs/iiSNP microhaplotypes plus 27 length-based or sequence-based autosomal STRs). With such low MPS-based RMPs, additional variation may not seem necessary, however, these results highlight that increased information can be obtained from the full amplicon.

# **Conflict of interest**

The authors report no conflict of interest.

#### Acknowledgements

This study was partly supported by a National Institute of Justice grant 2014-DN-BX-K024 to Sreetharan Kanthaswamy and David Glenn Smith and a research grant to Kelly L McCulloh from the UC Davis Forensic Science Graduate Program. Additionally, the authors would like to thank Illumina for kindly providing library preparation and sequencing reagents.

# Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j. fsigen.2017.02.014.

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