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Massively parallel sequencing of autosomal STRs and identity-informative SNPs highlights consanguinity in Saudi Arabia

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Running head: Sequencing Saudi Arabian autosomal STRs and identity SNPs

Highlights

• Sequences of 27 autosomal STRs and 91 identity-informative SNPs (iiSNPs) generated in 89 Saudi Arabian males
• STR repeat region variants and both STR and iiSNP flanking region variants observed
• Combined random match probability (RMP) across STRs and SNPs of 2.39E-73
• 23 STRs and 63 iiSNPs showed heterozygote deficiency, reflecting consanguinity
• Comparison of Saudi Arabians with HGDP panel for STRs and iiSNPs highlights effects of consanguinity in Middle Eastern populations generally

Abstract

While many studies have been undertaken of Middle Eastern populations using autosomal STR profiling by capillary electrophoresis, little has so far been published from this region on the forensic use of massively parallel sequencing (MPS). Here, we carried out MPS of 27 autosomal STRs and 91 identity-informative SNPs (iiSNPs) with the Verogen ForenSeq™ DNA Signature Prep Kit on a representative sample of 89 Saudi Arabian males, and analysed the resulting sequence data using Verogen's ForenSeq Universal Analysis Software (UAS) v1.3 and STRait Razor v3.0. This revealed sequence variation in the composition of complex STR arrays, and SNPs in their flanking regions, which raised the number of STR alleles from 238 distinct length variants to 357 sequence sub-variants. Similarly, between one and three additional polymorphic sites positions were observed within the amplicons of 37 of the 91 iiSNPs, forming up to six microhaplotypes per locus. These further enhance discrimination compared to the biallelic target SNP data presented by the primary UAS interface. In total, we observed twenty-two STR alleles previously unrecognised in the STRait Razor v3.0 default allele list, along with nine SNPs flanking target iiSNPs that were not highlighted by the UAS. Sequencing reduced the STR-based random match probability (RMP) from 2.62E-30 to 3.49E-34, and analysis of the iiSNP microhaplotypes reduced RMP from 9.97E-37 to 6.83E-40. The lack of significant linkage disequilibrium between STRs and target iiSNPs allowed the two marker types to be combined using the product rule, yielding a RMP of 2.39E-73. Evidence of consanguinity was apparent from both marker types. While TPOX was the only locus displaying a significant deviation from Hardy-Weinberg equilibrium, 23 out of 27 STRs and 63 out of 91 iiSNPs showed fewer than expected heterozygotes, demonstrating an overall homozygote excess probably reflecting the high frequency of first-cousin marriages in Saudi Arabia. We placed our data in a global context by considering the same markers in the Human Genome Diversity Panel (HGDP), revealing that the Saudi sample was typical of Middle Eastern populations, with a higher level of inbreeding than is seen in most European, African and Central/South Asian populations, correlating with known patterns of endogamy. Given reduced levels of diversity within endogamous groups, the ability to combine the discrimination power of both STRs and SNPs offers significant benefits in the analysis of forensic evidence in Saudi Arabia and the Middle East region more generally.

Introduction

Traditionally, forensic analysis of short tandem repeat (STR) diversity has been performed via capillary electrophoresis (CE), which considers only amplicon length and overlooks potentially informative sequence variation. Additional polymorphisms could include different numbers of diverged repeat units, together with indels and SNPs in both repeat arrays themselves and flanking regions: such variation can be accessed through massively parallel sequencing (MPS). MPS approaches not only provide increased (sequence-level) resolution of individual loci, but can also simultaneously analyse many diverse loci in a single test, thus simplifying analysis of different marker types and making the best use of limited amounts of casework material [1].

The ForenSeq™ DNA Signature Prep Kit (Verogen), formally released in 2015, exemplifies the advantages of an MPS approach by allowing the simultaneous amplification of either >150 loci including the standard autosomal and Y-STRs plus X-STRs and identity-informative SNPs (iiSNPs), or >230 loci which also include biogeographical ancestry- and phenotypically-informative SNPs; the choice of which to use depends on local legislation, sample type and/or application considerations. The kit has been extensively validated through a wide range of performance tests, including robustness, reproducibility, concordance with CE and sensitivity of detection [2-11]. Furthermore, the DNA Signature Prep Kit has been used on challenging samples to evaluate its applicability to real forensic cases [10, 12, 13]: in these tests, the kit as a whole compared favourably with CE, for example on formalin-fixed paraffin-embedded tissue, as well as on bone samples dating from the 7th to 18th centuries, detecting a greater number of informative markers in seven out of ten cases [2]. While optimised mini-STR multiplexes for CE and MPS SNP typing kits may perform better in detecting each type of marker on their own, the DNA Signature Prep Kit provided greater resolution in challenging samples as the simultaneous amplification of both STR and SNP markers allows the most discriminating markers to be detected from limited samples, despite the level of DNA degradation [14].

Although the primary interface with the manufacturer's ForenSeq™ Universal

Analysis Software (UAS) currently focuses on only a single iiSNP within each amplicon, additional variation exists in the flanking regions of many target SNPs [15], which could be useful in further increasing discriminating power and interpreting mixed stains. For several of the targeted SNPs the additional variant sites result in multiple alleles that will tend to be co-inherited as a microhaplotype, giving some iiSNP amplicons a resolving power approaching those of traditional simple-sequence STR loci. The DNA Signature Prep Kit has also improved resolution of both male/male and male/female mixtures involving minor contributors as low as 1:20 [2, 6, 8, 10] and this capability has proved useful in the first sexual assault court case using MPS in the Netherlands. The kit has also been implemented in casework by the INPS (Institut National de Police Scientifique) laboratory in Lyon, with MPS profiles uploaded to the French national DNA database, and the FBI has approved the kit itself, the MiSeq FGx System and the UAS for the US National DNA Index System within the terms of newly published SWGDAM guidelines for MPS [16].

The advantages conferred by MPS approaches could be particularly relevant to forensic science in the Middle East, where high average annual temperatures favour the use of forensic markers such as short-amplicon STRs and iiSNPs that provide robust discrimination from degraded DNA. In addition, populations in the region tend to exhibit endogamy and population structure [17], leading to clusters of individuals that share a common heritage and reducing the discrimination of forensic multiplexes relative to more diverse and exogamous societies. We have previously shown by conventional CE typing of both Y- [18] and autosomal STRs [19] that the indigenous population of Saudi Arabia is highly structured. This is apparent between the five regions of the country (North, South, East, West and Central), which have different tribal compositions and historical exposures to immigration.

Here we apply the DNA Signature Prep Kit typing to a sample dataset of Saudi males currently residing in the UK, to determine whether they reflect both the genetic composition of their home nation and the expected high rates of consanguinity, which could impact on the observed homozygosity of the autosomal markers. We ask whether analysing sequence variation of autosomal

markers (aSTRs and iiSNPs) within the DNA Signature Prep Kit significantly enhances resolution, and report novel variants within this population of the Middle East, a region from which little MPS data has so far been published [20].

Materials and Methods

DNA sampling, extraction and quantification

Samples were collected from 89 indigenous Arab males residing in the United Kingdom whose continuous paternal line ancestry can be traced back to a great-grandfather within one of the five geographical subdivisions of Saudi Arabia [18] (Central N = 19, Northern N = 9, Southern N = 26, Eastern N = 16, and Western N = 19). Ethical review for recruitment, sampling and analysis was provided by the University of Leicester Research Ethics Committee. Informed consent was provided by all participants, and using genealogical data obtained from the donors we confirmed that all paternal lineages are unconnected within the last three generations.

DNA was extracted either from buccal swabs [21], or from saliva samples using the Oragene DNA (OG-500) kit (DNA Genotek), and quantified as previously described [18].

Library preparation and sequencing

Sequencing libraries were prepared using the ForenSeq™ DNA Signature Prep Kit according to the manufacturer's recommendations (Verogen Inc., San Diego, CA, USA). Primer Mix A was used to amplify 58 STRs (27 autosomal STRs discussed in this paper, as well as 7 X-STRs and 24 Y-STRs which will be reported separately) and 94 identity-informative SNPs (iiSNPs) from 1 ng of template DNA. Steps for library preparation include target-specific amplification, target enrichment including incorporation of indexed adapters, purification, bead-normalisation and pooling, prior to sequencing on a Verogen MiSeq FGx device, all of which were performed in accordance with the manufacturer's recommended protocols. Either 96 or 32 libraries were analysed in each sequencing run, which included one positive and one negative control.

Calling of iiSNPs from HGDP sequence data

The iiSNPs were jointly called from the cram files of whole-genome sequenced (mean coverage 35 ×) Human Genome Diversity Project (HGDP) – CEPH (Centre d'Etude du Polymorphisme Humain) samples [22], mapped to GRCh38 using BCFtools (v1.8)[23] with minimum base quality 20 and mapping quality 20.

Data analysis

Sequence data were analysed using Verogen's default settings for the Analytical Threshold (AT), Interpretation Threshold (IT), Stutter Filter and Intra-Locus Balance in the ForenSeq™ Universal Analysis Software (UAS). Any sequence detected above the analytical threshold of 10 reads is reported to the user for their consideration, while above the 30-read interpretation threshold the UAS automatically reports the presence of an allele if the overall read depth for the locus is <650. When ≥650 reads are collected for a locus, the AT and IT defaults are set at 1.5% and 4.5% of reads respectively. Between the AT and IT, the result is flagged by the UAS and the user can determine whether the sequence is a true variant. User interpretation is also required when the Intra-locus Balance (equivalent to heterozygote balance) falls below 60%, or the level of stutter exceeds the default Stutter Filter value, which varies between STR loci. As all of our samples were good quality single-source reference DNAs, as demonstrated by earlier Yfiler Plus profiling [18], the interpretation was relatively straightforward.

The UAS provides a visual interface which displays each STR locus for an individual as a histogram arranged according to conventional CE allele length, with isometric heterozygotes (alleles of the same length but different sequence) shown as stacked bars. For STRs, the visual UAS interface displays only repeat region sequence variants, and for each of the iiSNP amplicons, only the target SNP. However, it is also possible to view "Flanking Region Reports" that show the flanking regions of both aSTR and iiSNP amplicons (which for Penta E is limited to a maximum of 197 bp to ensure sequencing data integrity). These files highlight variation at some, but not all, additional polymorphic sites within the amplicons. We used STRait Razor v3.0 [24] to check bioinformatic concordance of allele calls and to clarify appropriate nomenclature in line with ISFG considerations [25]. In the following sections we describe STR sequence

variation at three levels: length - a measure solely of allele length for compatibility with conventional CE methods; repeat region sequence - sequence variation within the repeat array as reported by UAS; and repeat plus flanking sequence, including all polymorphisms within the reported region of the amplicon, as obtained from the additional Flanking Region Reports.

Population, forensic and statistical analysis

Arlequin v 3.5 [26] was used to test Hardy-Weinberg equilibrium, and to calculate expected heterozygosity and pairwise linkage disequilibrium (LD). It was also used for performing AMOVA to investigate genetic diversity, to calculate fixation indices (F_{IS}) and to undertake population differentiation tests. STRAF [27] was used to calculate forensic statistics including: genotype count (N), allele count based on sequence (N_{all}), genetic diversity (GD), polymorphism information content (PIC), random match probability (PM), power of discrimination (PD), observed and expected heterozygosity (H_{obs} and H_{exp}), power of exclusion (PE), and typical paternity index (TPI). Allele frequencies were calculated in Excel (allele count/total).

Results

DNA profiles of 89 Saudi males generated with the ForenSeq DNA Signature Prep Kit Primer Mix A gave a mean total read count per sample of 34,821 reads for the complete complement of autosomal STR alleles, and 41,650 for the set of iiSNPs. Following visual checks of individual loci flagged by the default settings of the ForenSeq™ UAS, we called genotypes for all 27 autosomal STRs and 91 of the 94 iiSNPs. The three lowest-performing iiSNPs (rs1736442, rs2920816 and rs719366) were dropped from the analysis due to increased observations of sub-threshold calls (15, 9 and 5 respectively). The SNP rs1031825 was retained in the analysis but was below threshold in three individuals. In addition, two individuals had sub-threshold calls at the STR locus Penta E. Average read depths for the analysed autosomal STRs ranged from 3979 at TH01 to 285 at vWA, and for the iiSNPs from 1710 at rs1109037 to 64 at rs1031825.

Autosomal STR sequence variation and impact on discrimination

Among the 4804 STR alleles typed in the 89 individuals, there were 238 distinct length variants and 340 repeat sequence sub-variants identified by the UAS across the 27 loci (Table S1; Figure 1a). The loci D17S1301 and D4S2408 presented the lowest diversity, with five alleles each; together with ten other STRs, these showed only length variation when visualised solely with the UAS, thus providing the same discrimination power as a conventional CE approach. The UAS highlighted additional sequence variation within the repeat regions of the remaining 15 loci, contributing between one extra variant (at D19S433, TH01 and CSF1PO) up to 25 additional alleles at D12S391 (Figure 1a). Examination of the Flanking Region Report revealed a further 17 distinct variants including one, three, four and six additional alleles at D22S1045, D20S482, D16S539 and D7S820 respectively, whereas the visual interface of the UAS displayed only length variation. Two loci, D1S1656 and D2S441, each showed a total of six extra alleles as a result of sequence variation both within and flanking the repeat region, with SNPs in the flanking region contributing one and two of these extra alleles respectively. The sequences and frequencies of all autosomal STR alleles are shown in Table S1.

The number of additional alleles created by detection of sequence variation either within the repeat or flanking regions differs considerably between loci, but a more important parameter is how this affects the power of discrimination (PD). Figure 1b shows PD for each of the autosomal STRs, subdividing this into the proportions due to repeat number (length), repeat region sequence and flanking region variation.

Twenty-three 'novel' alleles, summarised in Table 1 (and more fully described in Table S1), were absent from the STRait Razor v3.0 default allele list. However, fifteen had been reported previously either in ForenSeq DNA Signature Prep Kit-related literature [20] or in the STRSeq database [28] (accessed via GenBank, July 2019); of these, seven sequences were previously seen in the Middle East, with two of them not yet reported outside of the region. Of the 23 'novel' alleles, two are rare short simple repeat-number variants; fifteen are compound STR alleles with novel numerical combinations of repeat blocks; three have single-base insertions within a repeat array producing intermediate alleles; and the remaining three have SNP variants in their flanking regions. Of the six SNP variants, only two have existing entries in dbSNP (rs563997442, rs554502154).

In terms of simple repeat number nomenclature for comparison with CE data, we did not observe any unusual genotypes. However, some loci displayed read counts at stutter positions above the stutter threshold that could represent potential somatic triallelic patterns. The allele counts that exceeded the stutter threshold by the greatest margin were at D8S1179, where three alleles were called by the UAS at 12,15,16 with read depths of 247, 86 and 295 respectively. The lowest of these contributions was at a stutter position and would equate to a stutter proportion of 0.29 of allele 16, whereas the next strongest stutter observed at this locus in this study was 0.26, only fractionally higher than the recommended UAS default permissible stutter ratio of 0.25 for the locus. Similar triallelic patterns generated by CE have been reported previously at this locus [https://strbase.nist.gov and [29].While imbalanced "triallelic" patterns can result from somatic mutations it is also possible that they are simply the result of unusually prominent stutter. It is unclear which explanation is appropriate in these two instances as the profiles are otherwise of good quality and do not show

excessive stutter at other loci, which might have been indicative of overamplification.

Sequence variation at autosomal iiSNPs and in their flanking regions

Fifty-four of the 91 iiSNP amplicons included in the analysis showed no additional variation within the regions covered by the Flanking Region Report while 27 have a second polymorphic site, eight have a third and two amplicons show variation at four positions (see Table S2). Combinations of alleles at two pairs and one trio of linked SNPs showed perfect associations (AT & TA at rs279844 & rs279845, AT & GC at rs6950322 & rs6955448, ATT & CCC at rs409820, rs430044 & rs430046 [target iiSNP underlined]) resulting in just two distinct microhaplotypes per amplicon in our population sample. The lack of perfect association between polymorphic sites within the remaining 34 amplicons added to the diversity with 25, six, two and one amplicons displaying three, four, five and six microhaplotypes respectively. As with the autosomal STRs, we compare the number of additional alleles we observe through sequencing (Figure 2a) with the increase in power of discrimination that they confer (Figure 2b).

The UAS highlights the target SNP in each amplicon, and also some - though not all - additional variants in the flanking regions, in its Flanking Region Report. Some of these additional variants are already described in the online database dbSNP (build 151), while others are novel. Here, eight amplicons displayed variation at positions not highlighted by the UAS. Two of these additional SNPs were associated with the rs1109037 amplicon, namely rs999755320, a rare C>T variant 1 bp upstream (at GRCh37 chr2:10085721 with a frequency of 2/30,976 in GnomAD) and a previously unrecorded T>C variant 4 bp downstream (@ 10085726). The other loci each displayed one additional rare or previously unrecorded variant site - six base substitutions and one indel; for these, dbSNP provides some information about previous observations within large genome-wide sequencing datasets. These studies include **TOPMed** - comprising participants in US National Heart, Lung, and Blood Institute studies (http://dx.doi.org/10.1101/563866), **GnomAD** - the Genome Aggregation Database led by the Broad Institute (http://gnomad-

old.broadinstitute.org/about), and an Estonian dataset comprising genetic variation from a pharmacogenomics study of adverse drug effects using electronic health records (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA489787).

- rs1015250 (+ rs1307278892 G/C, 9 bp downstream @ 1823783, TOPMed freq 5/125,568);
- rs1294331 (+ rs92280418 A/G, 4 bp upstream @ 233448409 [UAS reports reverse strand], GnomAD freq 1/30,950);
- rs13182883 (+ novel A/G SNP, 21 bp upstream @ 136633317),
- rs338882 (+ rs527589535 G/A SNP, 100 bp upstream @ 178890625 [UAS reports reverse strand], no frequency data available);
- rs354439 (+ novel A/C SNP, 30 bp upstream @ 106938381 [UAS reports reverse strand]);
- rs729172 (+ rs556717752 G/A, 32 bp upstream @ 233448409 [UAS reports reverse strand], GnomAD freq 2/30,984);
- rs891700 (+ rs543563536, T insertion in run of 10 Ts, 8 bp downstream @ chr1:239881909-239881918, freq 8/4480 among Estonians, also reported in https://doi.org/10.1016/j.fsigen.2017.09.003).

All of these were confirmed as true alleles displaying heterozygote balance between 52-98%. The sequences and frequencies of all iiSNP alleles are shown in Table S2, and those instances described above where the UAS flanking sequence report does not draw attention to nine additional polymorphic sites are included.

Possible recombination and recurrent mutation within SNP microhaplotypes

All four possible combinations of variants at co-amplified pairs of biallelic SNPs were observed within four amplicons (target iiSNP underlined): rs2830795 & rs12626695 (separated by 43 bp), rs2399332 & rs2399334 (separated by 100 bp), rs1109037 & rs1109038 (separated by 63 bp) and rs2076848 & rs7947725 (separated by 21 bp). Although recombination could explain these, the alternative explanation of recurrent mutation at a hypermutable CpG site is applicable in the last two cases and would seem most probable given the close proximity of two SNPs. The likely product of a CpG to CpA transformation at rs7947725 was seen in one and five individuals linked to the minor (A) and

major (T) allele at rs2076848, respectively. At rs1109037it is possible that the target SNP itself may have experienced recurrent mutation also resulting in a change from CpG to CpA, as a result of methylcytosine conversion to thymine on the opposing strand (see Table S1 for frequencies and sequence context).

Effect of combining autosomal STR and SNP sequence variants

One of the major potential benefits of typing with the DNA Signature Prep Kit is the increase in discrimination power when genotype data from independently inherited autosomal SNPs and STRs are combined. As there was no significant deviation from LD either among or between STRs and SNPs following Bonferroni correction, it is possible to combine the two marker types using the product rule. Forensic statistics for the autosomal STRs and SNPs are presented in Tables S3 and S4. In our dataset, we found that the RMP decreased by three orders of magnitude due to sequence variation within the STR repeat region itself compared to length variation alone, whilst sequence polymorphisms in the flanking regions of the STRs resulted in less than one order of magnitude further reduction (Figure 3). We compared the Saudi Arabian data with data from four comparator populations from the USA [15, 30]: the increases in resolution offered by sequencing in the Saudi Arabian sample are comparable with the other four groups. Notably, the difference between STR-based and iiSNP-based resolution is smaller in the African-Americans than in the other groups, suggesting that iiSNPs may be underestimating diversity in this particular population.

Evidence of consanguinity from patterns of STR and SNP diversity

Previously, we provided evidence from CE-based autosomal STR genotype data of the impact of consanguinity in the Saudi Arabian population [19]. Here, we ask if the sequence-based analysis of both STRs and SNPs showed a similar impact.

Among STRs, testing for fit to Hardy-Weinberg expectations revealed significant heterozygote deficiency only at TPOX ($P<0.005$ after Bonferroni correction). TPOX shows no internal sequence variation, simply mirroring the observed CE length variability, and was completely concordant with the results obtained from these individuals (data not shown) with the AmpFLSTR® GlobalFiler Kit (Thermo

Fisher Scientific). At the CE length level of comparison, 23 out of the 27 STR loci showed an excess of homozygotes (P=0.0002, binomial distribution, http://onlinestatbook.com/2/calculators/binomial_dist.html; see Table S5). This is consistent with 20 out of 21 GlobalFiler Kit loci displaying heterozygote deficiency (P<0.0001, binomial distribution) in our CE dataset of 523 indigenous males resident in Saudi Arabia (designated KSA) [19]. F_{ST} between the UK-based Saudi and KSA datasets at both regional (N, E, S, W and Central) and combined levels showed no evidence of significant differences between corresponding samples, and thus we consider our UK-based Saudi Arabian individuals to be a representative sample of autosomal variation within the indigenous population of the country as a whole (F_{ST} = 0.00086; P-value 0.09791). Heterozygote deficiency was also evident from AMOVA analysis, with an inbreeding coefficient (F_{IS}) of 0.04131 representing 4.13% of variation among our UK donors at the CE level, very close to the value we obtained with GlobalFiler from our KSA dataset (F_{IS}=0.0476; [19]. None of the iiSNPs showed a significant deviation from Hardy-Weinberg equilibrium after Bonferroni correction, but 63 of the 91 iiSNPs included in the analysis showed a deficiency of heterozygotes (P=0.0002, binomial distribution) mirroring the effect seen with autosomal STRs (see Table S6).

Comparing Saudi Arabian STR and SNP sequence diversity patterns with a set of global population samples

In order to set the observed Saudi Arabian population diversity and apparent effects of consanguinity in a broader context, we extracted data from the well-characterised HGDP samples [22]: STR sequence data were available from Phillips et al. (2018) [20] and iiSNP data were extracted from publicly available whole-genome sequences (see Table S7). Here we considered only the target iiSNPs rather than including flanking variants, as these are most likely to be reported in casework, and analysed only the 27 HGDP populations that contain 15 or more individuals. In Figure 4a we compare F_{IS} values between our Saudi dataset and these HGDP populations. European, African and East Asian populations generally show wide variation in F_{IS}, with a tendency to low values; a particularly broad range is seen in central South Asian populations. However, the

five populations from the Middle East, including the Saudi Arabians studied here, show consistently raised and highly similar levels indicative of widespread and frequent endogamy. In Figure 4b we also show, for the HGDP samples only, the proportion of specific mating types (unrelated, first cousin, second cousin, avuncular) estimated by a maximum-likelihood method from the distribution of homozygous-by-descent segments from high-density genome-wide SNP data by Leutenegger et al. (2011) [31]. This illustrates the high levels of consanguineous mating types in the Middle Eastern samples, though it also shows that some Central and South Asian samples exceed these levels.

For the full set of HGDP populations we also compared the level of homozygosity observed from the iiSNPs with an estimate based on haplotype homozygosity along chromosome 16 from genome-wide SNP data previously published by Li et al. (2008) [32] (Figure S1). Again, the iiSNP-based estimates are similar for all Middle Eastern populations (including our Saudi sample), and this is also true for the haplotype homozygosity estimates for the HGDP Middle Eastern samples. The haplotype homozygosity shows a trend to increase from Africa to the rest of the Old World and to the New World, previously noted both from genome-wide SNP [32]and STR data [33]. However, it is striking that the iiSNP-based homozygosity values do not follow this trend, with marked underestimation of both African and Middle Eastern diversity (Figure S1b), probably reflecting ascertainment bias in the original choice of SNPs for individual identification.

Discussion

A global survey of consanguinity has shown that the Middle East, North and sub-Saharan Africa and Western, Central and South Asia have consanguineous marriage levels between 20% and 50% [34]. Arabic-speaking countries showed the highest rates in the Middle East [35]. Indeed first-cousin marriages are particularly common and preferred in many regional communities, including the socially conservative regions of Saudi Arabia [36] where they comprise up to 33% of marriages. Saudi Arabia is also remarkable for its very rapid expansion in population size from 3.9 million in 1950 prior to the oil boom, to 20.8 million indigenous Saudi citizens in 2018, largely as a result of decreased child mortality and increasing life expectancy. Consequently, it is expected that clusters of closely related and genetically similar individuals will be commonplace, requiring more discriminating tests to generate the same confidence of individual resolution. Here, we used the high (sequence-based) resolution of MPS analysis, and the large number of independent autosomal loci (27 STRs and 91 iiSNPs) to analyse a sample of Saudi Arabians in order to address this question.

The lack of significant differentiation between the UK-based sample of Saudi Arabians analysed here and our previously reported [19] combined KSA dataset (F_{ST}=0.00072), suggests that our autosomal STR sequence dataset is representative of autosomal variation in the indigenous Saudi population as a whole. This study also replicates previous findings of heterozygote deficiency in Saudi populations [19, 37] likely due to high levels of endogamy (F_{IS}=0.04131 for autosomal STRs based on CE length and 0.04201 for iiSNPs) although the loci showing significant deviations differ between studies. Our earlier observation of an apparent significant deficiency of heterozygotes in the KSA population at D2S1338, thought to be partly due to a null allele, was not replicated in this study. However, this is unsurprising as the primer positions differ between the GlobalFiler and DNA Signature Prep kits, the latter of which has an amplicon approximately 180 bp shorter. In contrast the apparent homozygous excess seen at TPOX in this study was clearly not due to null heterozygotes caused specifically by the DNA Signature Prep Kit primers, as all homozygous

individuals were also scored as homozygotes with GlobalFiler, and we did not see a significant excess of such “homozygotes” in a much larger KSA dataset typed with the GlobalFiler kit (Khubrani et al. 2019). It seems likely that TPOX by chance showed the greatest excess of homozygosity due to consanguinity. Significant homozygous excess has been detected in many populations in the Middle East affecting a variety of loci: Iraq - D21S11 , FGA [38], Qatar - D13S317, D19S433 and vWA [39], Kuwait - vWA [40] and Tunisia - CSF1PO, Penta D and TPOX [41]. The lack of consistency across loci suggests that null alleles are not the general cause, and that demographic and stochastic factors are more likely.

The detection of sequence variation within autosomal STR amplicons enhances resolution by distinguishing among isoalleles that appear identical in CE analysis. Previous surveys of diverse ethnic groups have revealed differences of several orders of magnitude in random match probability (RMP) between length- and sequence-based estimates. Novroski et al. (2016) [30] obtained the following length- and sequence-RMP estimates for African-Americans (8.54E-34, 1.31E-39), Asians (6.37E-32, 8.66E-36), Caucasians (6.28E-32, 3.63E-36) and Hispanics (1.51E-31, 1.23E-35), whilst the levels of resolution were lower within our Saudi population (2.61E-30- length, 2.07E-33 - repeat region sequence & 3.49E-34 - including both repeat and flanking sequence). This reflects their more restricted geographic origins and therefore expected lower levels of diversity.

In previous studies, although sequencing of some STRs provided up to two-fold increased resolution per locus, other loci such as D10S1248, Penta D, Penta E and TPOX showed no improvement, as we observe in this dataset [2, 7, 42]. This is heavily influenced by the complexity of the STR repeat structure, but novel variants can arise in other STRs with a typically simple repeat structure as demonstrated by CSF1PO and TH01, both of which were invariant in previous studies but here displayed rare or regionally restricted variants that may be seen more frequently as datasets of Middle Eastern populations grow. Nine of the STR loci showed no improvement with sequencing, but six showed a greater than two-fold increase within the Saudi population. These include D12S391, where 13 length variants increased to 38 sequence variants, accompanied by a two-fold improvement in RMP from 0.0357 to 0.0173; and D3S1358, which saw a three-

fold improvement linked to an increase from 7 length variants to 13 sequence variants. Whereas most gains were due to novel arrangements of repeat variants in compound STRs, a greater than two-fold improvement resulted at D20S482 due solely to the presence of SNPs flanking the repeat array.

As with the STRs, sequencing of the iiSNP amplicons revealed additional sequence variants within the regions flanking the target SNP. Notably, not all of these variants were highlighted in the UAS Flanking Region Report, so care is needed in analysing data to ensure that all variation is recorded. Of the 91 iiSNPs analysed here, 34 showed additional sequence variation. This led to the RMP of 9.97E-37 for the target iiSNPs alone decreasing to 8.88E-40 when the flanking sequence variants were included. Most additional variants create novel rare microhaplotypes within our sample. The microhaplotypes created by the flanking sequence variation deserve further investigation in larger and more diverse samples.

It has been reported that the iiSNPs alone in the DNA Signature Prep Kit provide greater discrimination power than do available commercial STR kits [15], and this was certainly true within our Saudi dataset: taking sequence variation into account, the RMP of the autosomal STRs was 3.49E-34 compared with 8.88E-40 for the iiSNP amplicons. Overall, our study demonstrates that, while the additional alleles revealed by MPS substantially improve discrimination, the greatest contribution comes from the ability to analyse many independent loci simultaneously. The added power offered by combining STRs and SNPs will be beneficial in challenging cases, such as mixture analysis, complex kinship cases and where degradation results in partial profiles.

Conclusion

MPS analysis of autosomal loci in a representative sample of Saudi males demonstrated that profiling can significantly increase the discrimination power of forensic DNA testing through the simultaneous amplification of both STRs and identity-informative SNPs. This small-scale survey has uncovered a number of previously unobserved and rare alleles that may be present at significant frequencies within the Arabian Peninsula, supporting the value of larger-scale

surveys of this region. A striking feature of the data was a general deficiency of heterozygosity, and comparison with HGDP samples supports the idea that this reflects the practice of consanguinity in Saudi Arabia and in other Middle Eastern populations.

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Conflicts of interest

None

Figure legends

Figure 1: Counts of distinguishable alleles by STR locus, and per-locus increment of discriminatory power due to sequence variants.

a) The observed number of length variants among the 89 Saudi males is shown in grey below the x-axis, and the number of additional alleles resulting from sequence variation within and flanking the repeat array are shown above in white and black respectively. b) The power of discrimination resulting from length variation alone (equivalent to CE typing) is shown in grey and the additional contributions made by sequence variation within and flanking the repeat array are shown in white and black respectively (see also Table S3).

Figure 2: Counts of distinguishable haplotypes by SNP locus, and increment of discriminatory power due to sequence variants.

a) The observed number of haplotypes defined by the targeted SNP base alone among the 89 Saudi males is shown in white below the x-axis, and the number of additional haplotypes resulting from sequence variation due to flanking SNPs is shown above the axis in black. b) The probability of discrimination resulting from target SNP variation alone is shown in white and the additional contributions made by flanking SNPs are shown in black (also Table S4).

Figure 3: Increase in random match probability (RMP) offered by flanking sequence variation for both STRs and iiSNPs.

Data are shown for the Saudi Arabians studied here, and for four comparator populations from the literature [30].

Figure 4. F_{IS} for autosomal iiSNPs in Saudi Arabian and HGDP populations, compared with consanguineous mating type frequencies.

a) Mean F_{IS} is shown (target iiSNPs only) for HGDP populations with n≥15 and for Saudi Arabian data, clustered by continental origins; b) The coloured bars show genome-wide estimates of parental mating types for the HGDP samples, taken from Leutenegger et al. (2011) [31]. Different mating types are shown in the inset key.

Tables

Nomenclature	Type	Observations	HGDP occurrence
CSF1PO [CE 12]-GRCh38-Chr5-150076318-150076389 ATCT ACCT (ATCT)10	RS	3	MEA
D10S1248 [CE 9]-GRCh38-Chr10 129294226-129294318 (GGAA)9	RL	2	MEA/AFR
D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)11	RS	1	EUR/OCE/SAS
D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)10 AGAT	RS	1	EUR
D12S391 [CE 26]-GRCh38-Chr12-12296981-12297168 (AGAT)17 (AGAC)8 AGAT	RS	1	EAS
D13S317 [CE 9]-GRCh38-Chr13-82147986-82148107 (TATC)8 AATC	RS	1	not observed
D16S539 [CE 8]-GRCh38-Chr16-86352664-86352781 (GATA)8 86352692-G (rs563997442)	FS	1	n/a
D1S1656 [CE 17]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)16 230769682-G (rs NA)	FS	1	n/a
D21S11 [CE 36]-GRCh38-Chr21-19181939-19182111 (TCTA)11 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11	RS	1	not observed
D22S1045 [CE 15]-GRCh38-Chr22-37140181-37140357 (ATT)12 ACT (ATT)2 37140182-A (rs554502154)	FS	1	n/a
D2S1338 [CE 15]-GRCh38-Chr2-218014856-218014964 (GGAA)9 (GGCA)6	RS	1	EUR
D2S441 [CE 9]-GRCh38-Chr2-68011918-68012017 (TCTA)9	RL	1	MEA/EUR/AFR/EAS
D3S1358 [CE 13]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)9	RS	1	not observed
D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)13	RS	2	MEA/SAS
D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)14	RS	1	not observed
D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)13	RS	1	MEA/SAS
D3S1358 [CE 19]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)14	RS	1	MEA
D6S1043 [CE 25]-GRCh38-Chr6-91740160-91740292 (ATCT)6 ATGT (ATCT)4 ATGT (ATCT)13	RS	1	not observed
D8S1179 [CE 17.1]-GRCh38-Chr8-124894867-124894921 (TCTA)2 (TCTG)2 (TCTA)12 TCTTA	RS	1	not observed
D9S1122 [CE 13]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)8 CAGA (TAGA)2	RS	1	not observed
FGA [CE 16.1]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)3 A (AAAG)5 AGAA AAAA (GAAA)3 154587760-A	RS	1	not observed
PentaE [CE 16.4]-GRCh38-Chr15-96830996-96831114 (TCTTT)16 TCTT	RS	2	MEA/SAS
TH01 [CE 6]-GRCh38-Chr11-2171056-2171127 (AATG)3 AATA (AATG)2	RS	1	not observed

Table 1. Novel STR alleles found in this study.

Twenty-two STR alleles not previously recorded in the STRait Razor v3.0 default allele database are summarised here together with the allele structure as suggested by Parson et al. 2016 [25] the nature of its novelty (repeat length [RL], repeat region sequence [RS] or flanking sequence [FS]), its occurrence within the Saudi dataset (Obs.) and the geographical distribution of matching alleles in HGDP metapopulations [20]. AFR: African; EUR: European; MEA: Middle East; OCE: Oceanian; EAS: East Asian; SAS: South Asian; n/a: not available for search, since flanking variants are not listed in the literature [20].

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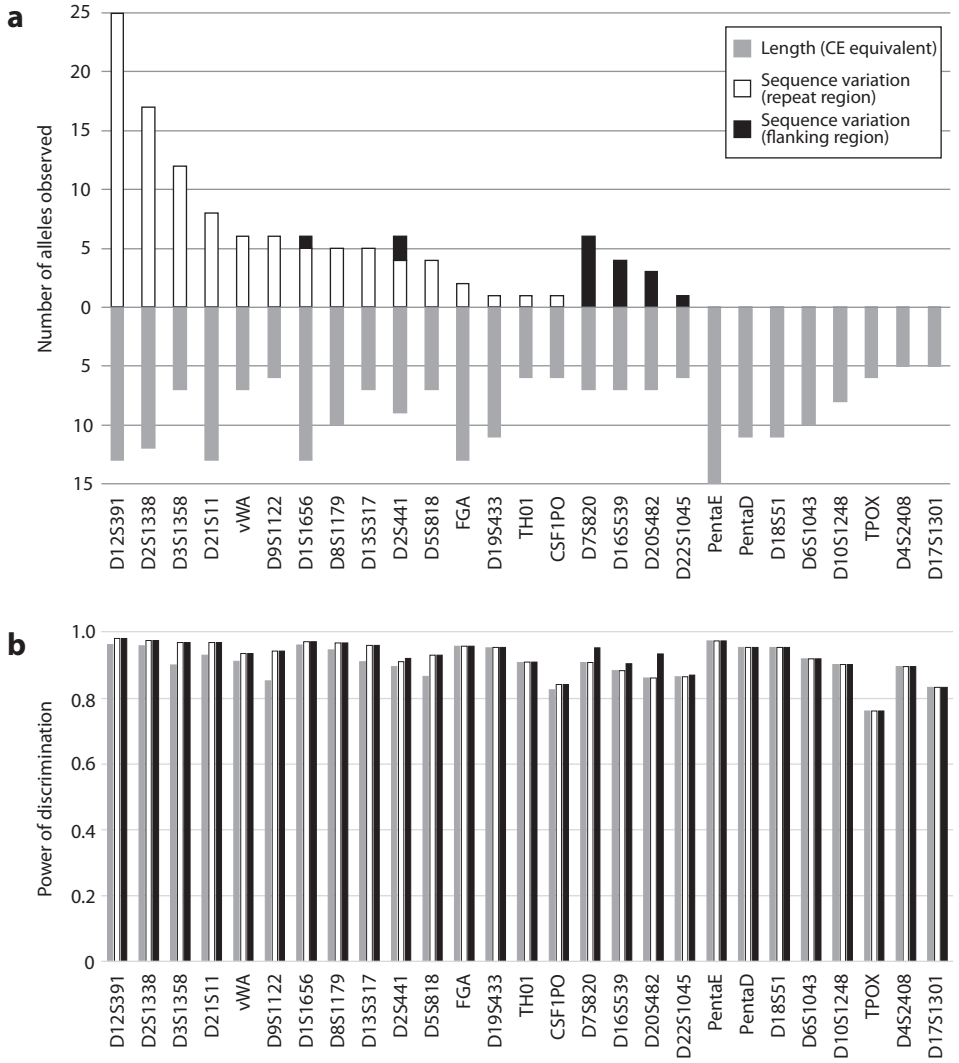

a
Number of alleles observed
25
20
15
10
5
0
5
10
15
Length (CE equivalent)
Sequence variation (repeat region)
Sequence variation (flanking region)
D12S391
D2S1338
D3S1358
D21S11
vWA
D9S1122
D1S1656
D8S1179
D13S317
D2S441
D5S818
FGA
D19S433
TH01
CSF1PO
D7S820
D16S539
D20S482
D22S1045
PentaE
PentaD
D18S51
D6S1043
D10S1248
TPOX
D4S2408
D17S1301
b
Power of discrimination
1.0
0.8
0.6
0.4
0.2
0
D12S391
D2S1338
D3S1358
D21S11
vWA
D9S1122
D1S1656
D8S1179
D13S317
D2S441
D5S818
FGA
D19S433
TH01
CSF1PO
D7S820
D16S539
D20S482
D22S1045
PentaE
PentaD
D18S51
D6S1043
D10S1248
TPOX
D4S2408
D17S1301

Figure 1.

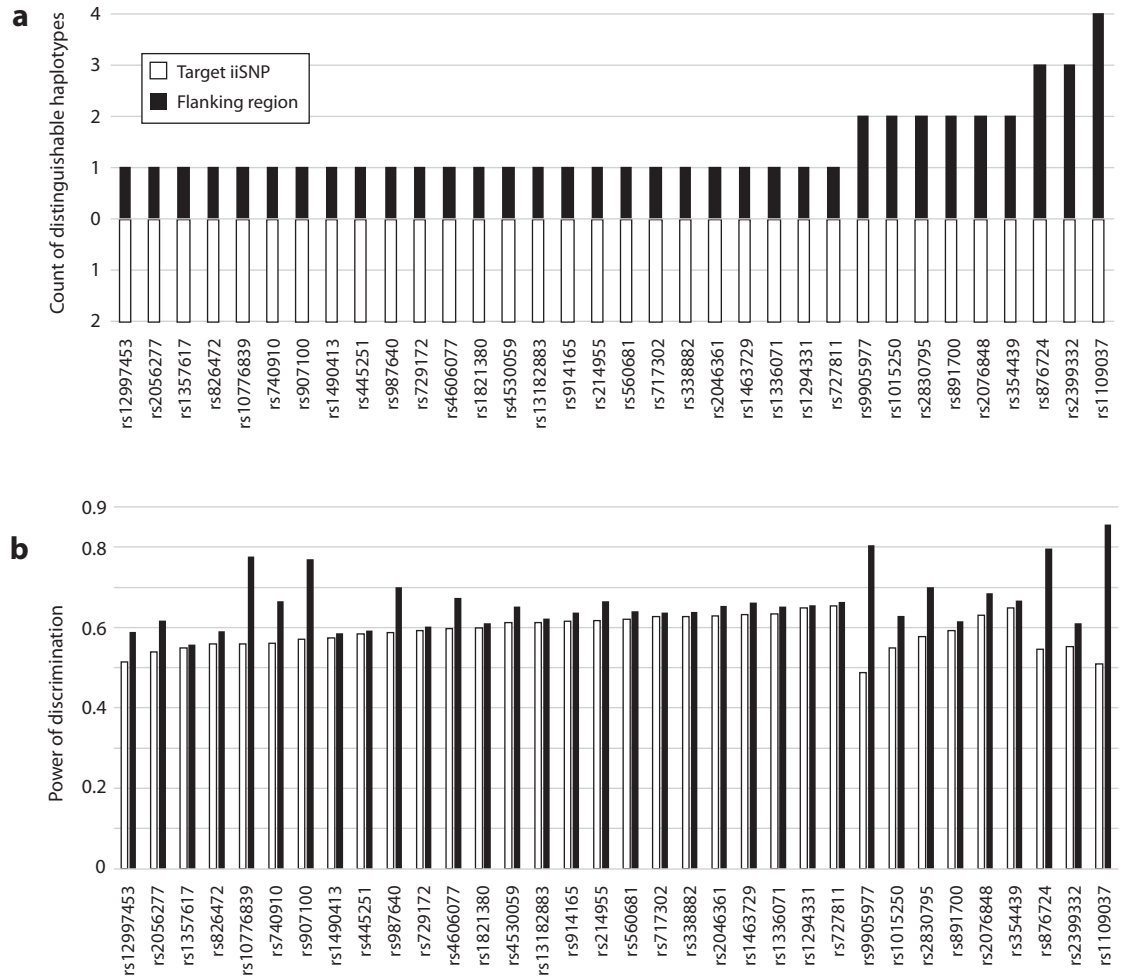

a
Count of distinguishable haplotypes
4
3
2
1
0
1
2
Target iiSNP
Flanking region
rs12997453
rs2056277
rs1357617
rs826472
rs10776839
rs740910
rs907100
rs1490413
rs445251
rs987640
rs729172
rs4606077
rs1821380
rs4530059
rs13182883
rs914165
rs214955
rs560681
rs717302
rs338882
rs2046361
rs1463729
rs1336071
rs1294331
rs727811
rs9905977
rs1015250
rs2830795
rs891700
rs2076848
rs354439
rs876724
rs2399332
rs1109037
b
Power of discrimination
0.9
0.8
0.6
0.4
0.2
0
rs12997453
rs2056277
rs1357617
rs826472
rs10776839
rs740910
rs907100
rs1490413
rs445251
rs987640
rs729172
rs4606077
rs1821380
rs4530059
rs13182883
rs914165
rs214955
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rs1463729
rs1336071
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rs354439
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rs2399332
rs1109037

Figure 2.

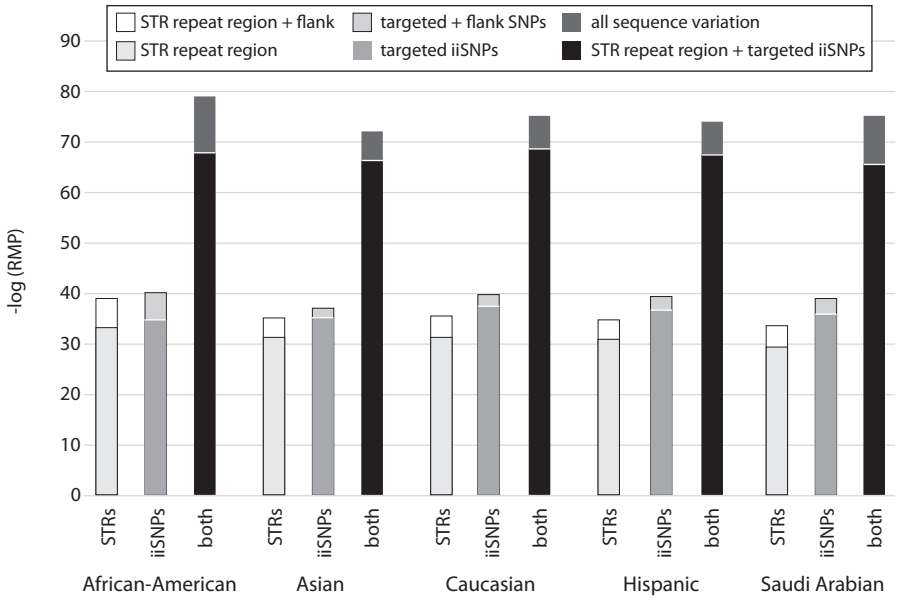

STR repeat region + flank
STR repeat region
targeted + flank SNPs
targeted iiSNPs
all sequence variation
STR repeat region + targeted iiSNPs
-log (RMP)
90
80
70
60
50
40
30
20
10
0
STRs
iiSNPs
both
African-American
Asian
Caucasian
Hispanic
Saudi Arabian

Figure 3.

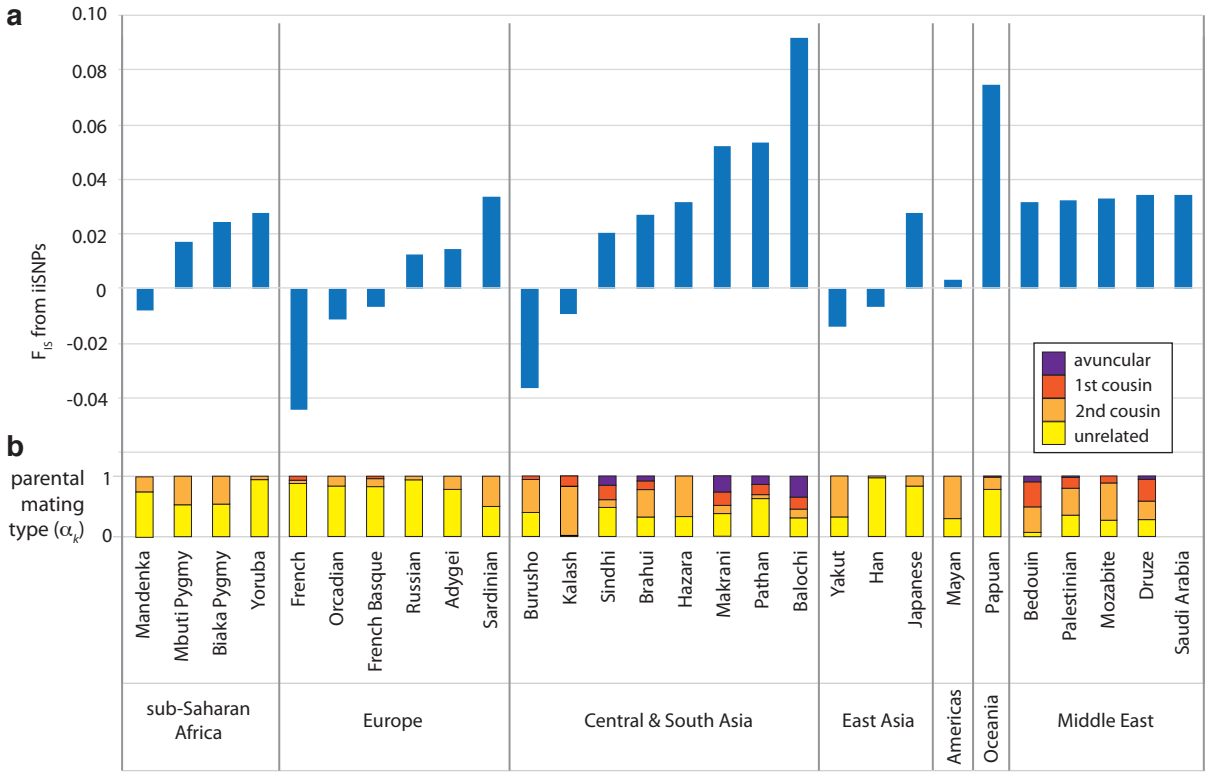

a
0.10
0.08
0.06
0.04
0.02
0
-0.02
-0.04
F_IS from iiSNPs
b
parental mating type (α_k)
1
0
avuncular
1st cousin
2nd cousin
unrelated
Mandenka
Mbuti Pygmy
Biaka Pygmy
Yoruba
French
Orcadian
French Basque
Russian
Adygei
Sardinian
Burusho
Kalash
Sindhi
Brahui
Hazara
Makrani
Pathan
Balochi
Yakut
Han
Japanese
Mayan
Papuan
Bedouin
Palestinian
Mozabite
Druze
Saudi Arabia
sub-Saharan Africa
Europe
Central & South Asia
East Asia
Americas
Oceania
Middle East

Figure 4.

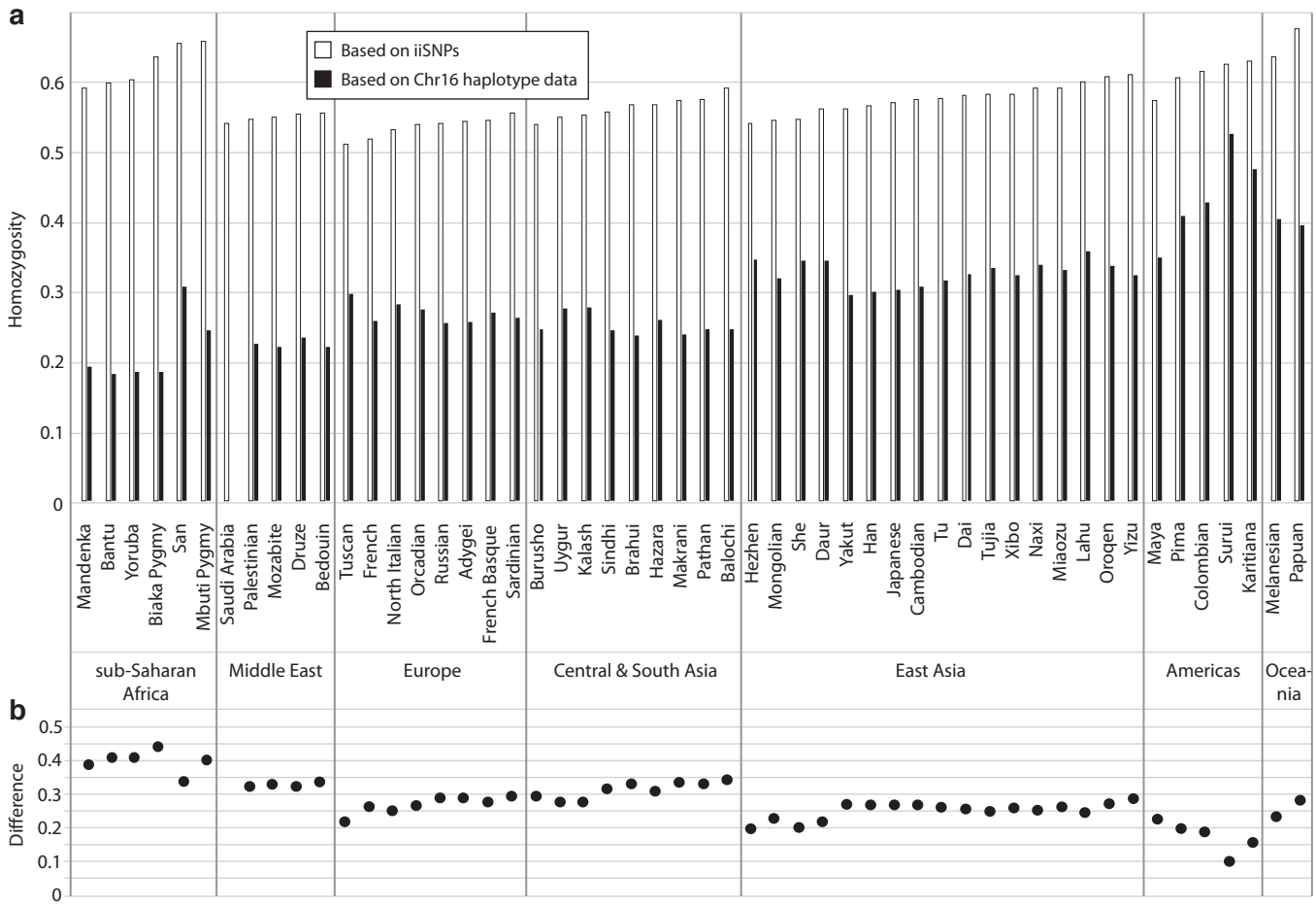


Figure S1: Observed homozygosity in HGDP populations based on iiSNPs, compared with a genomic estimate.

(a) Observed homozygosity based on 91 iiSNPs, including the value for the Saudi Arabian sample studied here (white bars), and also (for the HGDP samples only) homozygosity based on chromosome 16 haplotypes (black bars) estimated from genome-wide SNP chip data and taken from Li et al. (2008). Here, we follow Li et al. (2008) by combining the North and South Bantu samples into a single Bantu classification.

(b) The differences between iiSNP- and chromosome 16-based values, highlighting the underestimation of true homozygosity by iiSNPs in the African populations.

Figure S1.

Table S1a: Autosomal STR variants: allele length, repeat and flanking sequences with frequencies

Locus	Allele	Seq	Flank	allele/C	Seq/Cour	Flank/Co	totalGen	allele/F	Seq/Freq	Flank/Fr	Novel	Nomenclature
CSF1PO	9	AGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	2	2	2	178	0.011	0.011	0.011		CSF1PO [CE 9]-GRCh38-Chr5-150076318-150076389 (ATCT)9
CSF1PO	10	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	56	56	56	178	0.315	0.315	0.315		CSF1PO [CE 10]-GRCh38-Chr5-150076318-150076389 (ATCT)10
CSF1PO	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	47	47	47	178	0.264	0.264	0.264		CSF1PO [CE 11]-GRCh38-Chr5-150076318-150076389 (ATCT)11
CSF1PO	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	67	63	63	178	0.376	0.354	0.354		CSF1PO [CE 12]-GRCh38-Chr5-150076318-150076389 (ATCT)12
CSF1PO	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTAGATAGGAAG	67	4	4	178		0.022	0.022	Novel	CSF1PO [CE 12]-GRCh38-Chr5-150076318-150076389 ATCT ACCT (ATCT)10
CSF1PO	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	5	5	5	178	0.028	0.028	0.028		CSF1PO [CE 13]-GRCh38-Chr5-150076318-150076389 (ATCT)13
CSF1PO	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AAGATAGATAGATTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAG	1	1	1	178	0.006	0.006	0.006		CSF1PO [CE 14]-GRCh38-Chr5-150076318-150076389 (ATCT)14
D10S1248	9	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATACAACCAGAGTT	2	2	2	178	0.011	0.011	0.011	Novel	D10S1248 [CE 9]-GRCh38-Chr10 129294226-129294318 (GGAA)9
D10S1248	11	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATACAACCAGAGTT	1	1	1	178	0.006	0.006	0.006		D10S1248 [CE 11]-GRCh38-Chr10 129294226-129294318 (GGAA)11
D10S1248	12	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATACAACCAGAGTT	6	6	6	178	0.034	0.034	0.034		D10S1248 [CE 12]-GRCh38-Chr10 129294226-129294318 (GGAA)12
D10S1248	13	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATACAACCAGA	28	28	28	178	0.157	0.157	0.157		D10S1248 [CE 13]-GRCh38-Chr10 129294226-129294318 (GGAA)13
D10S1248	14	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATACAAC	62	62	62	178	0.348	0.348	0.348		D10S1248 [CE 14]-GRCh38-Chr10 129294226-129294318 (GGAA)14
D10S1248	15	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGACAATA	46	46	46	178	0.258	0.258	0.258		D10S1248 [CE 15]-GRCh38-Chr10 129294226-129294318 (GGAA)15
D10S1248	16	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGAAGAC.	27	27	27	178	0.152	0.152	0.152		D10S1248 [CE 16]-GRCh38-Chr10 129294226-129294318 (GGAA)16
D10S1248	17	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	TTGAACAAATGAGTGAGTGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAATGA.	6	6	6	178	0.034	0.034	0.034		D10S1248 [CE 17]-GRCh38-Chr10 129294226-129294318 (GGAA)17
D12S391	15	AGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGA	3	3	3	178	0.017	0.017	0.017		D12S391 [CE 15]-GRCh38-Chr12-12296981-12297168 (AGAT)8 (AGAC)6 AGAT
D12S391	16	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGA	2	2	2	178	0.011	0.011	0.011		D12S391 [CE 16]-GRCh38-Chr12-12296981-12297168 (AGAT)9 (AGAC)6 AGAT
D12S391	17	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGA	26	24	24	178	0.146	0.135	0.135		D12S391 [CE 17]-GRCh38-Chr12-12296981-12297168 (AGAT)10 (AGAC)6 AGAT
D12S391	17	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	26	2	2	178		0.011	0.011		D12S391 [CE 17]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)5 AGAT
D12S391	18	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGA	36	1	1	178	0.202	0.006	0.006		D12S391 [CE 18]-GRCh38-Chr12-12296981-12297168 (AGAT)10 (AGAC)7 AGAT
D12S391	18	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	36	32	32	178		0.180	0.180		D12S391 [CE 18]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)6 AGAT
D12S391	18	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	36	3	3	178		0.017	0.017		D12S391 [CE 18]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)5 AGAT
D12S391	18.3	AGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGAC.	2	2	2	178	0.011	0.011	0.011		D12S391 [CE 18.3]-GRCh38-Chr12-12296981-12297168 AGAT GAT (AGAT)9 (AGAC)7 AGAT
D12S391	19	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	13	3	3	178	0.073	0.017	0.017		D12S391 [CE 19]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)7 AGAT
D12S391	19	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	13	10	10	178		0.056	0.056		D12S391 [CE 19]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)6 AGAT
D12S391	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	14	2	2	178		0.011	0.011		D12S391 [CE 20]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)8 AGAT
D12S391	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	14	2	2	178	0.079	0.011	0.011		D12S391 [CE 20]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)9
D12S391	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	14	4	4	178		0.022	0.022		D12S391 [CE 20]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)7 AGAT
D12S391	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	14	5	5	178		0.028	0.028		D12S391 [CE 20]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)6 AGAT
D12S391	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	14	1	1	178		0.006	0.006		D12S391 [CE 20]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)5 AGAT
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGA	20	3	3	178	0.112	0.017	0.017		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)11 (AGAC)10
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	2	2	178		0.011	0.011		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)8 AGAT
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	8	8	178		0.045	0.045		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)9
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	2	2	178		0.011	0.011		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)7 AGAT
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	3	3	178		0.017	0.017		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)8
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	1	1	178		0.006	0.006		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)6 AGAT
D12S391	21	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	20	1	1	178		0.006	0.006		D12S391 [CE 21]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)7
D12S391	22	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	19	3	3	178	0.107	0.017	0.017		D12S391 [CE 22]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)10
D12S391	22	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	19	4	4	178		0.022	0.022		D12S391 [CE 22]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)8 AGAT
D12S391	22	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	19	11	11	178		0.062	0.062		D12S391 [CE 22]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)9
D12S391	22	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	19	1	1	178		0.006	0.006		D12S391 [CE 22]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)7 AGAT
D12S391	23	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	26	1	1	178		0.006	0.006	Novel	D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)10 AGAT
D12S391	23	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	26	1	1	178	0.146	0.006	0.006	Novel	D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)11
D12S391	23	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	26	3	3	178		0.017	0.017		D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)13 (AGAC)10
D12S391	23	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAT	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	26	11	11	178		0.062	0.062		D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)8 AGAT
D12S391	23	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGAC	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	26	10	10	178		0.056	0.056		D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)9
D12S391	24	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	13	3	3	178	0.073	0.017	0.017		D12S391 [CE 24]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)10
D12S391	24	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	13	3	3	178		0.017	0.017		D12S391 [CE 24]-GRCh38-Chr12-12296981-12297168 (AGAT)14 (AGAC)9 AGAT
D12S391	24	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	13	4	4	178		0.022	0.022		D12S391 [CE 24]-GRCh38-Chr12-12296981-12297168 (AGAT)15 (AGAC)8 AGAT
D12S391	24	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	13	3	3	178		0.017	0.017		D12S391 [CE 24]-GRCh38-Chr12-12296981-12297168 (AGAT)15 (AGAC)9
D12S391	25	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	3	2	2	178		0.011	0.011		D12S391 [CE 25]-GRCh38-Chr12-12296981-12297168 (AGAT)16 (AGAC)8 AGAT
D12S391	25	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	3	1	1	178	0.017	0.006	0.006		D12S391 [CE 25]-GRCh38-Chr12-12296981-12297168 (AGAT)16 (AGAC)9
D12S391	26	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACAGACAGACAG.	CAGAGAGAAAGAATCAACAGGATCAATGGATGCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	1	1	1	178	0.006	0.006	0.006	Novel	D12S391 [CE 26]-GRCh38-Chr12-12296981-12297168 (AGAT)17 (AGAC)8 AGAT
D13S317	8	TATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATC	18	18	18	178	0.101	0.101	0.101		D13S317 [CE 8]-GRCh38-Chr13-82147986-82148107 (TATC)8
D13S317	9	TATCTATCTATCTATCTATCTATCTATCTATCAATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCAATCATCTATC	11	1	1	178	0.062	0.006	0.006	Novel	D13S317 [CE 9]-GRCh38-Chr13-82147986-82148107 (TATC)8 AATC
D13S317	9	TATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATC	11	10	10	178		0.056	0.056		D13S317 [CE 9]-GRCh38-Chr13-82147986-82148107 (TATC)9
D13S317	10	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATC	13	11	11	178	0.073	0.062	0.062		D13S317 [CE 10]-GRCh38-Chr13-82147986-82148107 (TATC)10
D13S317	10	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCATC	13	2	2	178		0.011	0.011		D13S317 [CE 10]-GRCh38-Chr13-82147986-82148107 (TATC)10 82148069-T
D13S317	11	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAAT	49	14	14	178	0.275	0.079	0.079		D13S317 [CE 11]-GRCh38-Chr13-82147986-82148107 (TATC)11
D13S317	11	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAAT	49	35	35	178		0.197	0.197		D13S317 [CE 11]-GRCh38-Chr13-82147986-82148107 (TATC)11 82148069-T
D13S317	12	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAAT	61	35	35	178	0.343	0.197	0.197		D13S317 [CE 12]-GRCh38-Chr13-82147986-82148107 (TATC)12
D13S317	12	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT	61	26	26	178		0.146	0.146		D13S317 [CE 12]-GRCh38-Chr13-82147986-82148107 (TATC)12 82148069-T
D13S317	13	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT	19	15	15	178	0.107	0.084	0.084		D13S317 [CE 13]-GRCh38-Chr13-82147986-82148107 (TATC)13
D13S317	13	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT	19	4	4	178		0.022	0.022		D13S317 [CE 13]-GRCh38-Chr13-82147986-82148107 (TATC)13 82148069-T
D13S317	14	TATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCAATCAATCATCTATCTATCTTTCTGTCTGTC	TCTGACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT	7	7	7	178	0.039	0.039	0.039		D13S317 [CE 14]-GRCh38-Chr13-82147986-82148107 (TATC)14
D16S539	8	GATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGACAAAACAGA	3	2	2	178	0.017	0.017	0.011		D16S539 [CE 8]-GRCh38-Chr16-86352664-86352781 (GATA)8
D16S539	8	GATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGAGAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGACAAAACAGA	3	3	1	178			0.006	Novel	D16S539 [CE 8]-GRCh38-Chr16-86352664-86352781 (GATA)8 86352692-G (rs563997442)
D16S539	9	GATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGACAAAA	22	22	8	178	0.124	0.124	0.045		D16S539 [CE 9]-GRCh38-Chr16-86352664-86352781 (GATA)9
D16S539	9	GATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGACAAAC	22	22	14	178			0.079		D16S539 [CE 9]-GRCh38-Chr16-86352664-86352781 (GATA)9 86352761-C
D16S539	10	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGAC.	20	20	9	178	0.112	0.112	0.051		D16S539 [CE 10]-GRCh38-Chr16-86352664-86352781 (GATA)10
D16S539	10	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAAAGAC.	20	20	11	178			0.062		D16S539 [CE 10]-GRCh38-Chr16-86352664-86352781 (GATA)10 86352761-C
D16S539	11	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAA.	79	79	76	178	0.444	0.444	0.427		D16S539 [CE 11]-GRCh38-Chr16-86352664-86352781 (GATA)11
D16S539	11	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATCATTGAA.	79	79	3	178			0.017		D16S539 [CE 11]-GRCh38-Chr16-86352664-86352781 (GATA)11 86352761-C
D16S539	12	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATCAT	39	39	39	178	0.219	0.219	0.219		D16S539 [CE 12]-GRCh38-Chr16-86352664-86352781 (GATA)12
D16S539	13	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	11	11	11	178	0.062	0.062	0.062		D16S539 [CE 13]-GRCh38-Chr16-86352664-86352781 (GATA)13
D16S539	14	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	TCCTCTTCCCTAGATCAATACAGACAGACAGACAGGTGGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATA	4	4	4	178	0.022	0.022	0.022		D16S539 [CE 14]-GRCh38-Chr16-86352664-86352781 (GATA)14
D17S1301	10	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATATGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATCCATCATAGGAATTTT	8	8	8	178	0.045	0.045	0.045		D17S1301 [CE 10]-GRCh38-Chr17-74684846-74684918 (AGAT)10
D17S1301	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATATGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATCCATCATAGGAATTTT	52	52	52	178	0.292	0.292	0.292		D17S1301 [CE 11]-GRCh38-Chr17-74684846-74684918 (AGAT)11
D17S1301	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATATGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATCCATCATAGGAATTTT	84	84	84	178	0.472	0.472	0.472		D17S1301 [CE 12]-GRCh38-Chr17-74684846-74684918 (AGAT)12
D17S1301	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATATGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATCCATCATAGGAATTTT	30	30	30	178	0.169	0.169	0.169		D17S1301 [CE 13]-GRCh38-Chr17-74684846-74684918 (AGAT)13
D17S1301	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATATGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATCCATCATAGGAATTTT	4	4	4	178	0.022	0.022	0.022		D17S1301 [CE 14]-GRCh38-Chr17-74684846-74684918 (AGAT)14
D18S51	10	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAAAGAAAAGAAATAGTAGCAAC	1	1	1	178	0.006	0.006	0.006		D18S51 [CE 10]-GRCh38-Chr18-63281662-63281796 (AGAA)10
D18S51	11	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAAAGAAAAGAAATAGTAG	3	3	3	178	0.017	0.017	0.017		D18S51 [CE 11]-GRCh38-Chr18-63281662-63281796 (AGAA)11
D18S51	12	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAAAGAAAAGAAATA	27	27	27	178	0.152	0.152	0.152		D18S51 [CE 12]-GRCh38-Chr18-63281662-63281796 (AGAA)12
D18S51	13	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAAAGAAAAGA.	43	43	43	178	0.242	0.242	0.242		D18S51 [CE 13]-GRCh38-Chr18-63281662-63281796 (AGAA)13
D18S51	14	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAAAGAA.	21	21	21	178	0.118	0.118	0.118		D18S51 [CE 14]-GRCh38-Chr18-63281662-63281796 (AGAA)14
D18S51	15	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAGAAAA.	30	30	30	178	0.169	0.169	0.169		D18S51 [CE 15]-GRCh38-Chr18-63281662-63281796 (AGAA)15
D18S51	16	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAAAGAG.	15	15	15	178	0.084	0.084	0.084		D18S51 [CE 16]-GRCh38-Chr18-63281662-63281796 (AGAA)16
D18S51	17	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAAAGAA.	21	21	21	178	0.118	0.118	0.118		D18S51 [CE 17]-GRCh38-Chr18-63281662-63281796 (AGAA)17
D18S51	18	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAGGAA.	11	11	11	178	0.062	0.062	0.062		D18S51 [CE 18]-GRCh38-Chr18-63281662-63281796 (AGAA)18
D18S51	19	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGA	4	4	4	178	0.022	0.022	0.022		D18S51 [CE 19]-GRCh38-Chr18-63281662-63281796 (AGAA)19
D18S51	20	AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGAGAGAG	GTCTCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAAAGA	2	2	2	178	0.011	0.011	0.011		D18S51 [CE 20]-GRCh38-Chr18-63281662-63281796 (AGAA)20
D19S433	12	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG.	18	18	18	178	0.101	0.101	0.101		D19S433 [CE 12]-GRCh38-Chr19-29926205-29926352 (CCTT)10 CCTA CCTT CTTT CCTT
D19S433	13	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG.	29	28	28	178		0.157	0.157		D19S433 [CE 13]-GRCh38-Chr19-29926205-29926352 (CCTT)11 CCTA CCTT CTTT CCTT
D19S433	13	AAGGAAAGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGAAGGAAGGAAGGAAGGAAGGAAGG.	29	1	1	178	0.163	0.006	0.006		D19S433 [CE 13]-GRCh38-Chr19-29926205-29926352 (CCTT)13 CTTT CCTT
D19S433	13.2	AAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAA	2	2	2	178	0.011	0.011	0.011		D19S433 [CE 13.2]-GRCh38-Chr19-29926205-29926352 (CCTT)12 CCTA CCT TTT CCTT
D19S433	14	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG.	50	50	50	178	0.281	0.281	0.281		D19S433 [CE 14]-GRCh38-Chr19-29926205-29926352 (CCTT)12 CCTA CCTT CTTT CCTT
D19S433	14.2	AAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAA	10	10	10	178	0.056	0.056	0.056		D19S433 [CE 14.2]-GRCh38-Chr19-29926205-29926352 (CCTT)13 CCTA CCT TTT CCTT
D19S433	15	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG.	24	24	24	178	0.135	0.135	0.135		D19S433 [CE 15]-GRCh38-Chr19-29926205-29926352 (CCTT)13 CCTA CCTT CTTT CCTT
D19S433	15.2	AAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAA	10	10	10	178	0.056	0.056	0.056		D19S433 [CE 15.2]-GRCh38-Chr19-29926205-29926352 (CCTT)14 CCTA CCT TTT CCTT
D19S433	16	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG.	17	17	17	178	0.096	0.096	0.096		D19S433 [CE 16]-GRCh38-Chr19-29926205-29926352 (CCTT)14 CCTA CCTT CTTT CCTT

Locus	Allele	Seq	Flank	allele/C	Seq/Coun	Flank/Co	totalGen	allele/F	Seq/Freq	Flank/Fr	Novel	Nomenclature
D19S433	16.2	AAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAA	12	12	12	178	0.067	0.067	0.067		D19S433 [CE 16.2]-GRCh38-Chr19-29926205-29926352 (CCTT)15 CCTA CCT TTT CCTT
D19S433	17	AAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAGAAGGTAGGAAGGAAGGAAGGAAGGAAGG	4	4	4	178	0.022	0.022	0.022		D19S433 [CE 17]-GRCh38-Chr19-29926205-29926352 (CCTT)15 CCTA CCTT CTTT CCTT
D19S433	17.2	AAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAGAGAGGAAGAAAGAG	AGCTATAATTGTACCACTGCACTCCAGCCTGGGCAACAGAATAAGATTCTGTTGAAGGAAAAGGTAGGAAGGAAGGAAGGAAGGAAGGAA	2	2	2	178	0.011	0.011	0.011		D19S433 [CE 17.2]-GRCh38-Chr19-29926205-29926352 (CCTT)16 CCTA CCT TTT CCTT
D1S1656	11	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTGTTTAATTGTATGTATATATATTTGGTTCCCTAGTGA	15	15	15	178	0.084	0.084	0.084		D1S1656 [CE 11]-GRCh38-Chr1-230769555-230769682 (TCTA)11
D1S1656	12	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTGTTTAATTGTATGTATATATATTTGGTTCCCTA	28	14	14	178	0.157	0.079	0.079		D1S1656 [CE 12]-GRCh38-Chr1-230769555-230769682 (TCTA)12
D1S1656	12	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATATATATTTGGTTCCCTA	28	14	14	178		0.079	0.079		D1S1656 [CE 12]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)11
D1S1656	13	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTGTTTAATTGTATGTATATATATTTGGTTC	19	12	12	178	0.107	0.067	0.067		D1S1656 [CE 13]-GRCh38-Chr1-230769555-230769682 (TCTA)13
D1S1656	13	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATATATATTTGGTTC	19	7	7	178		0.039	0.039		D1S1656 [CE 13]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)12
D1S1656	14	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTGTTTAATTGTATGTATATATATTTG	18	2	2	178	0.101	0.011	0.011		D1S1656 [CE 14]-GRCh38-Chr1-230769555-230769682 (TCTA)14
D1S1656	14	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATATATATTTG	18	16	16	178		0.090	0.090		D1S1656 [CE 14]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)13
D1S1656	15	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATATA	35	35	35	178	0.197	0.197	0.197		D1S1656 [CE 15]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)14
D1S1656	15.3	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATAT	7	7	7	178	0.039	0.039	0.039		D1S1656 [CE 15.3]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)10 TCA (TCTA)4
D1S1656	16	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTGTGTGTGTTTAATTGTATGTATA	35	1	1	178		0.006	0.006		D1S1656 [CE 16]-GRCh38-Chr1-230769555-230769682 (TCTA)16
D1S1656	16	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGTATA	35	32	32	178		0.180	0.180		D1S1656 [CE 16]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)15
D1S1656	16	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAAGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAAGTGTGTGTGTGTTTAATTGTATGTATA	35	2	2	178	0.197	0.011	0.011		D1S1656 [CE 16]-GRCh38-Chr1-230769555-230769682 CTTA (TCTA)15
D1S1656	16.3	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATGT	6	6	6	178	0.034	0.034	0.034		D1S1656 [CE 16.3]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)11 TCA (TCTA)4
D1S1656	17	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATG	6	6	5	178	0.034	0.034	0.028		D1S1656 [CE 17]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)16
D1S1656	17	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGTATG	6	6	1	178			0.006	Novel	D1S1656 [CE 17]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)16 230769682-G (rs NA)
D1S1656	17.3	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTGT	4	4	4	178	0.022	0.022	0.022		D1S1656 [CE 17.3]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)12 TCA (TCTA)4
D1S1656	18	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAATTG	1	1	1	178	0.006	0.006	0.006		D1S1656 [CE 18]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)17
D1S1656	18.3	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTAA	3	3	3	178	0.017	0.017	0.017		D1S1656 [CE 18.3]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)13 TCA (TCTA)4
D1S1656	19	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTG	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTGTGTGTGTGTTTA	1	1	1	178	0.006	0.006	0.006		D1S1656 [CE 19]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)18
D20S482	9	AGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGGAATTGATT	5	5	5	178	0.028	0.028	0.028		D20S482 [CE 9]-GRCh38-Chr20-4525674-4525771 (AGAT)9
D20S482	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGGAATTGATT	1	1	1	178	0.006	0.006	0.006		D20S482 [CE 11]-GRCh38-Chr20-4525674-4525771 (AGAT)11
D20S482	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGGAATTGATT	6	6	6	178	0.034	0.034	0.034		D20S482 [CE 12]-GRCh38-Chr20-4525674-4525771 (AGAT)12
D20S482	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGGAATT	42	42	22	178	0.236	0.236	0.124		D20S482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13
D20S482	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACTGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGGAATT	42	42	20	178			0.112		D20S482 [CE 13]-GRCh38-Chr20-4525674-4525771 (AGAT)13 4525680-T
D20S482	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGG	82	82	64	178	0.461	0.461	0.360		D20S482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14
D20S482	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACTGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTATAGG	82	82	18	178			0.101		D20S482 [CE 14]-GRCh38-Chr20-4525674-4525771 (AGAT)14 4525680-T
D20S482	15	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTA	32	32	28	178	0.180	0.180	0.157		D20S482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15
D20S482	15	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACTGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTTATTA	32	32	4	178			0.022		D20S482 [CE 15]-GRCh38-Chr20-4525674-4525771 (AGAT)15 4525680-T
D20S482	16	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	AGACACCGAACCAATAAGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGATTT	10	10	10	178	0.056	0.056	0.056		D20S482 [CE 16]-GRCh38-Chr20-4525674-4525771 (AGAT)16
D21S11	27	TCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	4	3	3	178		0.017	0.017		D21S11 [CE 27]-GRCh38-Chr21-19181939-19182111 (TCTA)4 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)9
D21S11	27	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	4	1	1	178	0.022	0.006	0.006		D21S11 [CE 27]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)9
D21S11	28	TCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	21	21	21	178	0.118	0.118	0.118		D21S11 [CE 28]-GRCh38-Chr21-19181939-19182111 (TCTA)4 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)10
D21S11	29	TCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	54	40	40	178		0.225	0.225		D21S11 [CE 29]-GRCh38-Chr21-19181939-19182111 (TCTA)4 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	29	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	54	2	2	178		0.011	0.011		D21S11 [CE 29]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)10
D21S11	29	TCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	54	12	12	178	0.303	0.067	0.067		D21S11 [CE 29]-GRCh38-Chr21-19181939-19182111 (TCTA)6 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)10
D21S11	30	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	45	9	9	178		0.051	0.051		D21S11 [CE 30]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	30	TCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	45	21	21	178	0.253	0.118	0.118		D21S11 [CE 30]-GRCh38-Chr21-19181939-19182111 (TCTA)6 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	30	TCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	45	15	15	178		0.084	0.084		D21S11 [CE 30]-GRCh38-Chr21-19181939-19182111 (TCTA)6 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	30.2	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	3	3	3	178	0.017	0.017	0.017		D21S11 [CE 30.2]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)10 TA TCTA
D21S11	31	TCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATC	7	4	4	178		0.022	0.022		D21S11 [CE 31]-GRCh38-Chr21-19181939-19182111 (TCTA)4 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)13
D21S11	31	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	7	1	1	178		0.006	0.006		D21S11 [CE 31]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)12
D21S11	31	TCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	7	1	1	178	0.039	0.006	0.006		D21S11 [CE 31]-GRCh38-Chr21-19181939-19182111 (TCTA)6 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)12
D21S11	31	TCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTA	7	1	1	178		0.006	0.006		D21S11 [CE 31]-GRCh38-Chr21-19181939-19182111 (TCTA)6 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	31.2	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	18	18	18	178	0.101	0.101	0.101		D21S11 [CE 31.2]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11 TA TCTA
D21S11	32	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	1	1	1	178	0.006	0.006	0.006		D21S11 [CE 32]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)13
D21S11	32.2	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	14	14	14	178	0.079	0.079	0.079		D21S11 [CE 32.2]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)12 TA TCTA
D21S11	33.2	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	8	8	8	178	0.045	0.045	0.045		D21S11 [CE 33.2]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)13 TA TCTA
D21S11	34.2	TCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCATCTATCTATCCATATCTATCT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTA	1	1	1	178	0.006	0.006	0.006		D21S11 [CE 34.2]-GRCh38-Chr21-19181939-19182111 (TCTA)5 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)14 TA TCTA
D21S11	35	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTATCAT	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTGTCTG	1	1	1	178	0.006	0.006	0.006		D21S11 [CE 35]-GRCh38-Chr21-19181939-19182111 (TCTA)11 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D21S11	36	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATATCTATCTATCTA	AAATATGTGAGTCAATTCCCCAAGTGAATTGCCTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTGTCTG	1	1	1	178	0.006	0.006	0.006	Novel	D21S11 [CE 36]-GRCh38-Chr21-19181939-19182111 (TCTA)11 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11
D22S1045	11	ATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	28	28	28	178	0.157	0.157	0.157		D22S1045 [CE 11]-GRCh38-Chr22-37140181-37140357 (ATT)8 ACT (ATT)2
D22S1045	12	ATTATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	3	3	3	178	0.017	0.017	0.017		D22S1045 [CE 12]-GRCh38-Chr22-37140181-37140357 (ATT)9 ACT (ATT)2
D22S1045	14	ATTATTATTATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	11	11	11	178	0.062	0.062	0.062		D22S1045 [CE 14]-GRCh38-Chr22-37140181-37140357 (ATT)11 ACT (ATT)2
D22S1045	15	ATTATTATTATTATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	77	77	76	178			0.427		D22S1045 [CE 15]-GRCh38-Chr22-37140181-37140357 (ATT)12 ACT (ATT)2
D22S1045	15	ATTATTATTATTATTATTATTATTATTATTATTATTACTATTATT	CATTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	77	77	1	178	0.433	0.433	0.006	Novel	D22S1045 [CE 15]-GRCh38-Chr22-37140181-37140357 (ATT)12 ACT (ATT)2 37140182-A (rs554502154)
D22S1045	16	ATTATTATTATTATTATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	50	50	50	178	0.281	0.281	0.281		D22S1045 [CE 16]-GRCh38-Chr22-37140181-37140357 (ATT)13 ACT (ATT)2
D22S1045	17	ATTATTATTATTATTATTATTATTATTATTATTATTATTATTACTATTATT	CGTTGGAATTCCCCAAACTGGCCAGTTCCTCTCCACCCTATAGACCCTGTCCTAGCCTTCTTATAGCTGCTATGGGGGCTAGATTTCCC	9	9	9	178	0.051	0.051	0.051		D22S1045 [CE 17]-GRCh38-Chr22-37140181-37140357 (ATT)14 ACT (ATT)2
D2S1338	15	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	1	1	1	178	0.006	0.006	0.006	Novel	D2S1338 [CE 15]-GRCh38-Chr2-218014856-218014964 (GGAA)9 (GGCA)6
D2S1338	16	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	10	10	10	178	0.056	0.056	0.056		D2S1338 [CE 16]-GRCh38-Chr2-218014856-218014964 (GGAA)10 (GGCA)6
D2S1338	17	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	48	46	46	178	0.270	0.258	0.258		D2S1338 [CE 17]-GRCh38-Chr2-218014856-218014964 (GGAA)11 (GGCA)6
D2S1338	17	TGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	48	2	2	178		0.011	0.011		D2S1338 [CE 17]-GRCh38-Chr2-218014856-218014964 (GGAA)13 (GGCA)4
D2S1338	18	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	19	7	7	178	0.107	0.039	0.039		D2S1338 [CE 18]-GRCh38-Chr2-218014856-218014964 (GGAA)11 (GGCA)7
D2S1338	18	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	19	11	11	178		0.062	0.062		D2S1338 [CE 18]-GRCh38-Chr2-218014856-218014964 (GGAA)12 (GGCA)6
D2S1338	18	TGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCTC	19	1	1	178		0.006	0.006		D2S1338 [CE 18]-GRCh38-Chr2-218014856-218014964 (GGAA)13 (GGCA)5
D2S1338	19	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	22	13	13	178	0.124	0.073	0.073		D2S1338 [CE 19]-GRCh38-Chr2-218014856-218014964 (GGAA)12 (GGCA)7
D2S1338	19	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	22	6	6	178		0.034	0.034		D2S1338 [CE 19]-GRCh38-Chr2-218014856-218014964 (GGAA)12 (GGCA)7
D2S1338	19	TGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	22	1	1	178		0.006	0.006		D2S1338 [CE 19]-GRCh38-Chr2-218014856-218014964 (GGAA)14 (GGCA)5
D2S1338	19	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	22	2	2	178		0.011	0.011		D2S1338 [CE 19]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)10 (GGCA)6
D2S1338	20	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	33	4	4	178	0.185	0.022	0.022		D2S1338 [CE 20]-GRCh38-Chr2-218014856-218014964 (GGAA)12 (GGCA)8
D2S1338	20	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	33	3	3	178		0.017	0.017		D2S1338 [CE 20]-GRCh38-Chr2-218014856-218014964 (GGAA)14 (GGCA)6
D2S1338	20	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCC	33	18	18	178		0.101	0.101		D2S1338 [CE 20]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)10 (GGCA)7
D2S1338	20	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCC	33	8	8	178		0.045	0.045		D2S1338 [CE 20]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)10 (GGCA)7
D2S1338	21	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	11	2	2	178	0.062	0.011	0.011		D2S1338 [CE 21]-GRCh38-Chr2-218014856-218014964 (GGAA)13 (GGCA)8
D2S1338	21	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	11	7	7	178		0.039	0.039		D2S1338 [CE 21]-GRCh38-Chr2-218014856-218014964 (GGAA)14 (GGCA)7
D2S1338	21	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	11	1	1	178		0.006	0.006		D2S1338 [CE 21]-GRCh38-Chr2-218014856-218014964 (GGAA)15 (GGCA)6
D2S1338	21	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCC	11	1	1	178		0.006	0.006		D2S1338 [CE 21]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)11 (GGCA)7
D2S1338	22	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	7	1	1	178		0.006	0.006		D2S1338 [CE 22]-GRCh38-Chr2-218014856-218014964 (GGAA)15 (GGCA)7
D2S1338	22	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	7	3	3	178	0.039	0.017	0.017		D2S1338 [CE 22]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)12 (GGCA)7
D2S1338	22	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	7	3	3	178		0.017	0.017		D2S1338 [CE 22]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)13 (GGCA)6
D2S1338	23	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTTCC	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	9	9	9	178	0.051	0.051	0.051		D2S1338 [CE 23]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)13 (GGCA)7
D2S1338	24	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	9	1	1	178	0.051	0.006	0.006		D2S1338 [CE 24]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)13 (GGCA)8
D2S1338	24	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	9	7	7	178		0.039	0.039		D2S1338 [CE 24]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)14 (GGCA)7
D2S1338	24	TGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTTCCTT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	9	1	1	178		0.006	0.006		D2S1338 [CE 24]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)15 (GGCA)6
D2S1338	25	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	8	3	3	178	0.045	0.017	0.017		D2S1338 [CE 25]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)14 (GGCA)8
D2S1338	25	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGTCCTT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	8	5	5	178		0.028	0.028		D2S1338 [CE 25]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)15 (GGCA)7
D2S1338	26	TGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCGT	AAATGGCTTGGCCTTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCC	1	1	1	178	0.006	0.006	0.006		D2S1338 [CE 26]-GRCh38-Chr2-218014856-218014964 (GGAA)2 GGAC (GGAA)15 (GGCA)8
D2S441	9	TCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCACAGCCACTTA	1	1	1	178	0.006	0.006	0.006	Novel	D2S441 [CE 9]-GRCh38-Chr2-68011918-68012017 (TCTA)9
D2S441	10	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCACAGCCACT	26	19	18	178			0.101		D2S441 [CE 10]-GRCh38-Chr2-68011918-68012017 (TCTA)10
D2S441	10	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGAAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCACAGCCACT	26	19	1	178	0.146	0.107	0.006		D2S441 [CE 10]-GRCh38-Chr2-68011918-68012017 (TCTA)10 68011922-A
D2S441	10	TCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTATATCATAACACCACAGCCACT	26	7	7	178		0.039	0.039		D2S441 [CE 10]-GRCh38-Chr2-68011918-68012017 (TCTA)8 TCTG TCTA
D2S441	11	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCACAGC	61	60	55	178			0.309		D2S441 [CE 11]-GRCh38-Chr2-68011918-68012017 (TCTA)11
D2S441	11	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGAAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCACAGC	61	60	5	178	0.343	0.337	0.028		D2S441 [CE 11]-GRCh38-Chr2-68011918-68012017 (TCTA)11 68011922-A
D2S441	11	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTGTCTATATCATAACACCACAGC	61	1	1	178		0.006	0.006		D2S441 [CE 11]-GRCh38-Chr2-68011918-68012017 (TCTA)9 TCTG TCTA
D2S441	11.3	TCTATCTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATATCATAACACCAC	8	8	8	178	0.045	0.045	0.045		D2S441 [CE 11.3]-GRCh38-Chr2-68011918-68012017 (TCTA)4 TC A (TCTA)7
D2S441	12	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACACCA	19	18	18	178	0.107	0.101	0.101		D2S441 [CE 12]-GRCh38-Chr2-68011918-68012017 (TCTA)12
D2S441	12	TCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTATATCATAACACCA	19	1	1	178		0.006	0.006		D2S441 [CE 12]-GRCh38-Chr2-68011918-68012017 (TCTA)9 TTTA (TCTA)2
D2S441	12.3	TCTATCTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATCTATATCATAACA	1	1	1	178	0.006	0.006	0.006		D2S441 [CE 12.3]-GRCh38-Chr2-68011918-68012017 (TCTA)4 TC A (TCTA)8
D2S441	13	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTATATCATAAC	3	1	1	178		0.006	0.006		D2S441 [CE 13]-GRCh38-Chr2-68011918-68012017 (TCTA)10 TTTA (TCTA)2
D2S441	13	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCATAAC	3	2	2	178	0.017	0.011	0.011		D2S441 [CE 13]-GRCh38-Chr2-68011918-68012017 (TCTA)13
D2S441	14	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTATATCA	51	51	51	178	0.287	0.287	0.287		D2S441 [CE 14]-GRCh38-Chr2-68011918-68012017 (TCTA)11 TTTA (TCTA)2

Locus	Allele	Seq	Flank	allele/C	Seq/Coun	Flank/Co	totalGen	allele/F	Seq/Freq	Flank/Fr	Novel	Nomenclature
D2S441	15	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTA	CCAGGAACTGTGGCTCATCTATGAAAACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTTATCTATCTAT	8	8	8	178	0.045	0.045	0.045		D2S441 [CE 15]-GRCh38-Chr2-68011918-68012017 (TCTA)12 TTTA (TCTA)2
D3S1358	13	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	3	2	2	178	0.017	0.011	0.011		D3S1358 [CE 13]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)10
D3S1358	13	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATC	3	1	1	178		0.006	0.006	Novel	D3S1358 [CE 13]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)9
D3S1358	14	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	12	11	11	178		0.062	0.062		D3S1358 [CE 14]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)11
D3S1358	14	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATC	12	1	1	178	0.067	0.006	0.006		D3S1358 [CE 14]-GRCh38-Chr3-45540691-45540820 TCTA TCTG (TCTA)12
D3S1358	15	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	44	31	31	178	0.247	0.174	0.174		D3S1358 [CE 15]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)12
D3S1358	15	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATC	44	13	13	178		0.073	0.073		D3S1358 [CE 15]-GRCh38-Chr3-45540691-45540820 TCTA TCTG (TCTA)13
D3S1358	16	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	53	33	33	178		0.185	0.185		D3S1358 [CE 16]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)13
D3S1358	16	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATC	53	12	12	178		0.067	0.067		D3S1358 [CE 16]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)12
D3S1358	16	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATC	53	8	8	178	0.298	0.045	0.045		D3S1358 [CE 16]-GRCh38-Chr3-45540691-45540820 TCTA TCTG (TCTA)14
D3S1358	17	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	47	24	24	178		0.135	0.135		D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)14
D3S1358	17	TCTATCTGTCTGTCTCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTCTCTATCTATCTATCTATCTATCTATC	47	2	2	178		0.011	0.011	Novel	D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)13
D3S1358	17	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATC	47	19	19	178		0.107	0.107		D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)13
D3S1358	17	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATC	47	2	2	178	0.264	0.011	0.011		D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA TCTG (TCTA)15
D3S1358	18	TCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATC	17	2	2	178	0.096	0.011	0.011		D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 (TCTA)15
D3S1358	18	TCTATCTGTCTGTCTCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTCTCTATCTATCTATCTATCTATCTATC	17	1	1	178		0.006	0.006	Novel	D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)14
D3S1358	18	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATC	17	13	13	178		0.073	0.073		D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)14
D3S1358	18	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATC	17	1	1	178		0.006	0.006	Novel	D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)13
D3S1358	19	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATC	2	1	1	178	0.011	0.006	0.006		D3S1358 [CE 19]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)15
D3S1358	19	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TTTGGGGGCATCTCTTATACTCATGAAATCAACAGAGGCTTGCATGTATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATC	2	1	1	178		0.006	0.006	Novel	D3S1358 [CE 19]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)14
D4S2408	8	ATCTATCTATCTATCTATCTATCTATCTATCT	CTATGCATCTATCTATCTATCTATCTATCTATCTATCTAATGGTTA	68	68	68	178	0.382	0.382	0.382		D4S2408 [CE 8]-GRCh38-Chr4-31302792-31302841 (ATCT)8
D4S2408	9	ATCTATCTATCTATCTATCTATCTATCTATCTATCT	CTATGCATCTATCTATCTATCTATCTATCTATCTATCTATCTAATGGTTA	27	27	27	178	0.152	0.152	0.152		D4S2408 [CE 9]-GRCh38-Chr4-31302792-31302841 (ATCT)9
D4S2408	10	ATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT	CTATGCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAATGGTTA	32	32	32	178	0.180	0.180	0.180		D4S2408 [CE 10]-GRCh38-Chr4-31302792-31302841 (ATCT)10
D4S2408	11	ATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT	CTATGCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAATGGTTA	35	35	35	178	0.197	0.197	0.197		D4S2408 [CE 11]-GRCh38-Chr4-31302792-31302841 (ATCT)11
D4S2408	12	ATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT	CTATGCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAATGGTTA	16	16	16	178	0.090	0.090	0.090		D4S2408 [CE 12]-GRCh38-Chr4-31302792-31302841 (ATCT)12
D5S818	8	AGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	2	2	2	178	0.011	0.011	0.011		D5S818 [CE 8]-GRCh38-Chr5-123775543-123775606 (ATCT)8 123775552-A
D5S818	9	AGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	11	11	11	178	0.062	0.062	0.062		D5S818 [CE 9]-GRCh38-Chr5-123775543-123775606 (ATCT)9 123775552-A
D5S818	10	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGAG	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGGTATAAATA	18	15	15	178	0.101	0.084	0.084		D5S818 [CE 10]-GRCh38-Chr5-123775543-123775606 (ATCT)10
D5S818	10	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	18	3	3	178		0.017	0.017		D5S818 [CE 10]-GRCh38-Chr5-123775543-123775606 (ATCT)10 123775552-A
D5S818	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAG	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGGTATAAATA	52	44	44	178	0.292	0.247	0.247		D5S818 [CE 11]-GRCh38-Chr5-123775543-123775606 (ATCT)11
D5S818	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	52	8	8	178		0.045	0.045		D5S818 [CE 11]-GRCh38-Chr5-123775543-123775606 (ATCT)11 123775552-A
D5S818	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAG	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGGTATAAATA	72	53	53	178	0.404	0.298	0.298		D5S818 [CE 12]-GRCh38-Chr5-123775543-123775606 (ATCT)12
D5S818	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	72	19	19	178		0.107	0.107		D5S818 [CE 12]-GRCh38-Chr5-123775543-123775606 (ATCT)12 123775552-A
D5S818	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAG	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGGTATAAATA	21	19	19	178	0.118	0.107	0.107		D5S818 [CE 13]-GRCh38-Chr5-123775543-123775606 (ATCT)13
D5S818	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATGTATAAATA	21	2	2	178		0.011	0.011		D5S818 [CE 13]-GRCh38-Chr5-123775543-123775606 (ATCT)13 123775552-A
D5S818	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAG	ATTTTGAAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGGTATAAATA	2	2	2	178	0.011	0.011	0.011		D5S818 [CE 14]-GRCh38-Chr5-123775543-123775606 (ATCT)14
D6S1043	10	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGATTTATTATGGGAAGTGGCTCATACAA	6	6	6	178	0.034	0.034	0.034		D6S1043 [CE 10]-GRCh38-Chr6-91740160-91740292 (ATCT)10
D6S1043	11	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGATTTATTATGGGAAGTGGCTCAT	57	57	57	178	0.320	0.320	0.320		D6S1043 [CE 11]-GRCh38-Chr6-91740160-91740292 (ATCT)11
D6S1043	12	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGATTTATTATGGGAAGTGGC	53	53	53	178	0.298	0.298	0.298		D6S1043 [CE 12]-GRCh38-Chr6-91740160-91740292 (ATCT)12
D6S1043	13	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGATTTATTATGGGAAG	13	13	13	178	0.073	0.073	0.073		D6S1043 [CE 13]-GRCh38-Chr6-91740160-91740292 (ATCT)13
D6S1043	14	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGATTTATTATGG	5	5	5	178	0.028	0.028	0.028		D6S1043 [CE 14]-GRCh38-Chr6-91740160-91740292 (ATCT)14
D6S1043	17	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAGATAG	2	2	2	178	0.011	0.011	0.011		D6S1043 [CE 17]-GRCh38-Chr6-91740160-91740292 (ATCT)5 ATGT (ATCT)11
D6S1043	18	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAG	19	19	19	178	0.107	0.107	0.107		D6S1043 [CE 18]-GRCh38-Chr6-91740160-91740292 (ATCT)5 ATGT (ATCT)12
D6S1043	19	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAG	15	15	15	178	0.084	0.084	0.084		D6S1043 [CE 19]-GRCh38-Chr6-91740160-91740292 (ATCT)5 ATGT (ATCT)13
D6S1043	20	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATAGAT	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAG	7	7	7	178	0.039	0.039	0.039		D6S1043 [CE 20]-GRCh38-Chr6-91740160-91740292 (ATCT)5 ATGT (ATCT)14
D6S1043	25	AGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAGATACATAGATAGATAGATAGATAG	GATCAATAGATTGATAGATCAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATACATAGATAGATAGATAG	1	1	1	178	0.006	0.006	0.006	Novel	D6S1043 [CE 25]-GRCh38-Chr6-91740160-91740292 (ATCT)6 ATGT (ATCT)4 ATGT (ATCT)13
D7S820	7	GATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACTAAATA	4	4	4	178	0.022	0.022	0.022		D7S820 [CE 7]-GRCh38-Chr7-84160191-84160297 (TATC)7 84160204-A
D7S820	8	GATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACTAAATA	40	40	24	178	0.225	0.225	0.135		D7S820 [CE 8]-GRCh38-Chr7-84160191-84160297 (TATC)8 84160204-A
D7S820	8	GATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAATGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACTAAATA	40	40	16	178			0.090		D7S820 [CE 8]-GRCh38-Chr7-84160191-84160297 (TATC)8 84160204-A; 84160286-A
D7S820	9	GATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACTAAAT	19	19	17	178	0.107	0.107	0.096		D7S820 [CE 9]-GRCh38-Chr7-84160191-84160297 (TATC)9 84160204-A
D7S820	9	GATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAATGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACTAAAT	19	19	2	178			0.011		D7S820 [CE 9]-GRCh38-Chr7-84160191-84160297 (TATC)9 84160204-A; 84160286-A
D7S820	10	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTAATCTCACT	55	55	11	178	0.309	0.309	0.062		D7S820 [CE 10]-GRCh38-Chr7-84160191-84160297 (TATC)10
D7S820	10	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCTCACT	55	55	44	178			0.247		D7S820 [CE 10]-GRCh38-Chr7-84160191-84160297 (TATC)10 84160204-A
D7S820	11	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTAATCT	32	32	4	178	0.180	0.180	0.022		D7S820 [CE 11]-GRCh38-Chr7-84160191-84160297 (TATC)11
D7S820	11	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTTATCT	32	32	28	178			0.157		D7S820 [CE 11]-GRCh38-Chr7-84160191-84160297 (TATC)11 84160204-A
D7S820	12	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTA	24	24	6	178	0.135	0.135	0.034		D7S820 [CE 12]-GRCh38-Chr7-84160191-84160297 (TATC)12
D7S820	12	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTTTTTT	24	24	18	178			0.101		D7S820 [CE 12]-GRCh38-Chr7-84160191-84160297 (TATC)12 84160204-A
D7S820	13	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTT	4	4	3	178	0.022	0.022	0.017		D7S820 [CE 13]-GRCh38-Chr7-84160191-84160297 (TATC)13
D7S820	13	GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTT	ATAGTTTAGAACGAACTAACGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGATTGATAGTTTTT	4	4	1	178			0.006		D7S820 [CE 13]-GRCh38-Chr7-84160191-84160297 (TATC)13 84160204-A
D8S1179	9	TCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	2	2	2	180	0.011	0.011	0.011		D8S1179 [CE 9]-GRCh38-Chr8-124894867-124894921 (TCTA)9
D8S1179	10	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	13	13	13	180	0.072	0.072	0.072		D8S1179 [CE 10]-GRCh38-Chr8-124894867-124894921 (TCTA)10
D8S1179	11	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	22	22	22	180	0.122	0.122	0.122		D8S1179 [CE 11]-GRCh38-Chr8-124894867-124894921 (TCTA)11
D8S1179	12	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	28	28	28	180	0.156	0.156	0.156		D8S1179 [CE 12]-GRCh38-Chr8-124894867-124894921 (TCTA)12
D8S1179	13	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	37	11	11	180	0.206	0.061	0.061		D8S1179 [CE 13]-GRCh38-Chr8-124894867-124894921 (TCTA)13
D8S1179	13	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	37	5	5	180		0.028	0.028		D8S1179 [CE 13]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)10
D8S1179	13	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	37	21	21	180		0.117	0.117		D8S1179 [CE 13]-GRCh38-Chr8-124894867-124894921 TCTA TCTG (TCTA)11
D8S1179	14	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	27	5	5	180	0.150	0.028	0.028		D8S1179 [CE 14]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)11
D8S1179	14	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	27	22	22	180		0.122	0.122		D8S1179 [CE 14]-GRCh38-Chr8-124894867-124894921 TCTA TCTG (TCTA)12
D8S1179	15	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	41	31	31	180	0.228	0.172	0.172		D8S1179 [CE 15]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)12
D8S1179	15	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	41	9	9	180		0.050	0.050		D8S1179 [CE 15]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)12
D8S1179	15	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	41	1	1	180		0.006	0.006		D8S1179 [CE 15]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)12
D8S1179	16	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	8	8	8	180	0.044	0.044	0.044		D8S1179 [CE 16]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)13
D8S1179	17	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	TCTATCTATCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTCCC	1	1	1	180	0.006	0.006	0.006		D8S1179 [CE 17]-GRCh38-Chr8-124894867-124894921 (TCTA)2 TCTG (TCTA)14
D8S1179	17.1	TCTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTTA	TCTATCTATCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTTATTCCC	1	1	1	180	0.006	0.006	0.006	Novel	D8S1179 [CE 17.1]-GRCh38-Chr8-124894867-124894921 (TCTA)2 (TCTG)2 (TCTA)12 TCTTA
D9S1122	10	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	5	4	4	178	0.028	0.022	0.022		D9S1122 [CE 10]-GRCh38-Chr9-77073809-77073880 (TAGA)10
D9S1122	10	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	5	1	1	178		0.006	0.006		D9S1122 [CE 10]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)8
D9S1122	11	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	44	38	38	178	0.247	0.213	0.213		D9S1122 [CE 11]-GRCh38-Chr9-77073809-77073880 (TAGA)11
D9S1122	11	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	44	6	6	178		0.034	0.034		D9S1122 [CE 11]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)9
D9S1122	12	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	74	42	42	178	0.416	0.236	0.236		D9S1122 [CE 12]-GRCh38-Chr9-77073809-77073880 (TAGA)12
D9S1122	12	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	74	32	32	178		0.180	0.180		D9S1122 [CE 12]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)10
D9S1122	13	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	49	21	21	178	0.275	0.118	0.118		D9S1122 [CE 13]-GRCh38-Chr9-77073809-77073880 (TAGA)13
D9S1122	13	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	49	27	27	178		0.152	0.152		D9S1122 [CE 13]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)11
D9S1122	13	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGACAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGACAGATAGATAGATATTAAT	49	1	1	178		0.006	0.006	Novel	D9S1122 [CE 13]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)8 CAGA (TAGA)2
D9S1122	14	TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	5	1	1	178	0.028	0.006	0.006		D9S1122 [CE 14]-GRCh38-Chr9-77073809-77073880 (TAGA)14
D9S1122	14	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	5	4	4	178		0.022	0.022		D9S1122 [CE 14]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)12
D9S1122	15	TAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	AGATAACTGTAGATAGGTAGATCGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATTAAT	1	1	1	178	0.006	0.006	0.006		D9S1122 [CE 15]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)13
FGA	16.1	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTTCTTTCTTTCTTTCTCCTTCCTTCCTTTCTTCC	1	1	1	178	0.006	0.006	0.006	Novel	FGA [CE 16.1]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)3 A (AAAG)5 AGAA AAAA (GAAA)3 154587760-A
FGA	18	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCCT	1	1	1	178	0.006	0.006	0.006		FGA [CE 18]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)10 AGAA AAAA (GAAA)3
FGA	19	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCT	10	10	10	178	0.056	0.056	0.056		FGA [CE 19]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)11 AGAA AAAA (GAAA)3
FGA	20	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCT	23	23	23	178	0.129	0.129	0.129		FGA [CE 20]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)12 AGAA AAAA (GAAA)3
FGA	21	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	23	23	23	178	0.129	0.129	0.129		FGA [CE 21]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)13 AGAA AAAA (GAAA)3
FGA	22	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	33	33	33	178	0.185	0.185	0.185		FGA [CE 22]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)14 AGAA AAAA (GAAA)3
FGA	23	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTTCC	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	26	26	26	178	0.146	0.146	0.146		FGA [CE 23]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)15 AGAA AAAA (GAAA)3
FGA	24	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTTCCTT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	31	31	31	178	0.174	0.174	0.174		FGA [CE 24]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)16 AGAA AAAA (GAAA)3
FGA	25	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCCTT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	20	20	20	178	0.112	0.112	0.112		FGA [CE 25]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)17 AGAA AAAA (GAAA)3
FGA	26	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	5	2	2	178		0.011	0.011		FGA [CE 26]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)18 AGAA AAAA (GAAA)3
FGA	26	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCTTCTTTCTTTCTTTCTTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCTTC	5	2	2	178	0.028	0.011	0.011		FGA [CE 26]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)5 AAGG (AAAG)12 AGAA AAAA (GAAA)3
FGA	26	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTGTTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	5	1	1	178		0.006	0.006		FGA [CE 26]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG AAAG AAAC (AAAG)16 AGAA AAAA (GAAA)3
FGA	27	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	3	3	3	178	0.017	0.017	0.017		FGA [CE 27]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)19 AGAA AAAA (GAAA)3
FGA	29	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCTTCTTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	1	1	1	178	0.006	0.006	0.006		FGA [CE 29]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)5 AAGG (AAAG)15 AGAA AAAA (GAAA)3
FGA	30	TTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCTTCTTTCT	GCATATTTACAAGCTAGTTTCTTTCTTTCTTTTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	1	1	1	178	0.006	0.006	0.006		FGA [CE 30]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)5 AAGG (AAAG)16 AGAA AAAA (GAAA)3
PentaD	2.2	GAAAAGAAAAGAAAAGA	AGTAGGATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCA	5	5	5	178	0.028	0.028	0.028		PentaD [CE 2.2]-GRCh38-Chr21-43636100-43636278 (AAAGA)5 43636192-43636204 DEL
PentaD	7	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	1	1	1	178	0.006	0.006	0.006		PentaD [CE 7]-GRCh38-Chr21-43636100-43636278 (AAAGA)7

Locus	Allele	Seq	Flank	allele/C	Seq/Coun	Flank/Co	totalGen	allele/F	Seq/Freq	Flank/Fr	Novel	Nomenclature
PentaD	8	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	8	8	8	178	0.045	0.045	0.045		PentaD [CE 8]-GRCh38-Chr21-43636100-43636278 (AAAGA)8
PentaD	9	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	42	42	42	178	0.236	0.236	0.236		PentaD [CE 9]-GRCh38-Chr21-43636100-43636278 (AAAGA)9
PentaD	10	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	30	30	30	178	0.169	0.169	0.169		PentaD [CE 10]-GRCh38-Chr21-43636100-43636278 (AAAGA)10
PentaD	11	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	26	26	26	178	0.146	0.146	0.146		PentaD [CE 11]-GRCh38-Chr21-43636100-43636278 (AAAGA)11
PentaD	12	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	20	20	20	178	0.112	0.112	0.112		PentaD [CE 12]-GRCh38-Chr21-43636100-43636278 (AAAGA)12
PentaD	13	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	26	26	26	178	0.146	0.146	0.146		PentaD [CE 13]-GRCh38-Chr21-43636100-43636278 (AAAGA)13
PentaD	14	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	14	14	14	178	0.079	0.079	0.079		PentaD [CE 14]-GRCh38-Chr21-43636100-43636278 (AAAGA)14
PentaD	15	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	5	5	5	178	0.028	0.028	0.028		PentaD [CE 15]-GRCh38-Chr21-43636100-43636278 (AAAGA)15
PentaD	16	AAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	GATCACTTGAGCCTGGAAGGTCGAAGCTGAAGTGAGCCATGATCACACCACTACACTCCAGCCTAGGTGACAGAGCAAGACACCATCTCA	1	1	1	178	0.006	0.006	0.006		PentaD [CE 16]-GRCh38-Chr21-43636100-43636278 (AAAGA)16
PentaE	5	AAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	13	13	13	174	0.075	0.075	0.075		PentaE [CE 5]-GRCh38-Chr15-96830996-96831114 (TCTTT)5
PentaE	7	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	8	8	8	174	0.046	0.046	0.046		PentaE [CE 7]-GRCh38-Chr15-96830996-96831114 (TCTTT)7
PentaE	8	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	10	10	10	174	0.057	0.057	0.057		PentaE [CE 8]-GRCh38-Chr15-96830996-96831114 (TCTTT)8
PentaE	9	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	2	2	2	174	0.011	0.011	0.011		PentaE [CE 9]-GRCh38-Chr15-96830996-96831114 (TCTTT)9
PentaE	10	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	16	16	16	174	0.092	0.092	0.092		PentaE [CE 10]-GRCh38-Chr15-96830996-96831114 (TCTTT)10
PentaE	11	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	26	26	26	174	0.149	0.149	0.149		PentaE [CE 11]-GRCh38-Chr15-96830996-96831114 (TCTTT)11
PentaE	12	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	26	26	26	174	0.149	0.149	0.149		PentaE [CE 12]-GRCh38-Chr15-96830996-96831114 (TCTTT)12
PentaE	13	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	15	15	15	174	0.086	0.086	0.086		PentaE [CE 13]-GRCh38-Chr15-96830996-96831114 (TCTTT)13
PentaE	14	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTTTTCT	6	6	6	174	0.034	0.034	0.034		PentaE [CE 14]-GRCh38-Chr15-96830996-96831114 (TCTTT)14
PentaE	15	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAGGAGTT	15	15	15	174	0.086	0.086	0.086		PentaE [CE 15]-GRCh38-Chr15-96830996-96831114 (TCTTT)15
PentaE	16	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTGTAAG	19	19	19	174	0.109	0.109	0.109		PentaE [CE 16]-GRCh38-Chr15-96830996-96831114 (TCTTT)16
PentaE	16.4	AAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTG	2	2	2	174	0.011	0.011	0.011	Novel	PentaE [CE 16.4]-GRCh38-Chr15-96830996-96831114 (TCTTT)16 TCTT
PentaE	17	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATT	9	9	9	174	0.052	0.052	0.052		PentaE [CE 17]-GRCh38-Chr15-96830996-96831114 (TCTTT)17
PentaE	18	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	5	5	5	174	0.029	0.029	0.029		PentaE [CE 18]-GRCh38-Chr15-96830996-96831114 (TCTTT)18
PentaE	19	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG	AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGA	2	2	2	174	0.011	0.011	0.011		PentaE [CE 19]-GRCh38-Chr15-96830996-96831114 (TCTTT)19
TH01	6	AATGAATGAATGAATAAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATAAATGAATGAGGGAAATAAGG	48	1	1	178	0.270	0.006	0.006	Novel	TH01 [CE 6]-GRCh38-Chr11-2171056-2171127 (AATG)3 AATA (AATG)2
TH01	6	AATGAATGAATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGAGGGAAATAAGG	48	47	47	178		0.264	0.264		TH01 [CE 6]-GRCh38-Chr11-2171056-2171127 (AATG)6
TH01	7	AATGAATGAATGAATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGAATGAGGGAAATAAGG	25	25	25	178	0.140	0.140	0.140		TH01 [CE 7]-GRCh38-Chr11-2171056-2171127 (AATG)7
TH01	8	AATGAATGAATGAATGAATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGAATGAATGAGGGAAATAAGG	24	24	24	178	0.135	0.135	0.135		TH01 [CE 8]-GRCh38-Chr11-2171056-2171127 (AATG)8
TH01	9	AATGAATGAATGAATGAATGAATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAGGGAAATAAGG	60	60	60	178	0.337	0.337	0.337		TH01 [CE 9]-GRCh38-Chr11-2171056-2171127 (AATG)9
TH01	9.3	AATGAATGAATGAATGAATGAATGATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGATGAATGAATGAATGAGGGAAATAAGG	20	20	20	178	0.112	0.112	0.112		TH01 [CE 9.3]-GRCh38-Chr11-2171056-2171127 (AATG)6 ATG (AATG)3
TH01	10	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATG	TGCAGGTCACAGGGAACACAGACTCCATGGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAGGGAAATAAGG	1	1	1	178	0.006	0.006	0.006		TH01 [CE 10]-GRCh38-Chr11-2171056-2171127 (AATG)10
TPOX	7	AATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGTTTGG	1	1	1	178	0.006	0.006	0.006		TPOX [CE 7]-GRCh38-Chr2-1489651-1489689 (AATG)7
TPOX	8	AATGAATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGAATGTTTGG	105	105	105	178	0.590	0.590	0.590		TPOX [CE 8]-GRCh38-Chr2-1489651-1489689 (AATG)8
TPOX	9	AATGAATGAATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGAATGAATGTTTGG	25	25	25	178	0.140	0.140	0.140		TPOX [CE 9]-GRCh38-Chr2-1489651-1489689 (AATG)9
TPOX	10	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATGTTTGG	20	20	20	178	0.112	0.112	0.112		TPOX [CE 10]-GRCh38-Chr2-1489651-1489689 (AATG)10
TPOX	11	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGTTTGG	24	24	24	178	0.135	0.135	0.135		TPOX [CE 11]-GRCh38-Chr2-1489651-1489689 (AATG)11
TPOX	12	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATG	AATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGTTTGG	3	3	3	178	0.017	0.017	0.017		TPOX [CE 12]-GRCh38-Chr2-1489651-1489689 (AATG)12
vWA	14	TCTATCTGTCTATCTGTCTGTCTGTCTGTCTATCTATCTATCCATCTATCTATCTATCCATCCA	ATTGATCTATCTGTCTATCTGTCTGTCTGTCTGTCTATCTATCTATCCATCTATCTATCTATCCATCCATCCATCCATCCTATGTATT	6	5	5	178	0.034	0.028	0.028		vWA [CE 14]-GRCh38-Chr12-5983950-5984049 (TAGA)3 TGGA (TAGA)3 (CAGA)4 TAGA CAGA TAGA 5983970-G
vWA	14	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCTATGTATT	6	1	1	178		0.006	0.006		vWA [CE 14]-GRCh38-Chr12-5983950-5984049 (TAGA)9 (CAGA)4 TAGA 5983962-A; 5983974-A
vWA	15	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCATCCTATGTA	23	17	17	178		0.096	0.096		vWA [CE 15]-GRCh38-Chr12-5983950-5984049 (TAGA)10 (CAGA)4 TAGA
vWA	15	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCATCCTATGTA	23	6	6	178	0.129	0.034	0.034		vWA [CE 15]-GRCh38-Chr12-5983950-5984049 (TAGA)11 (CAGA)3 TAGA
vWA	16	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCATCCTA	56	49	49	178		0.275	0.275		vWA [CE 16]-GRCh38-Chr12-5983950-5984049 (TAGA)11 (CAGA)4 TAGA
vWA	16	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCATCCTA	56	7	7	178	0.315	0.039	0.039		vWA [CE 16]-GRCh38-Chr12-5983950-5984049 (TAGA)12 (CAGA)3 TAGA
vWA	17	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCAT	47	44	44	178		0.247	0.247		vWA [CE 17]-GRCh38-Chr12-5983950-5984049 (TAGA)12 (CAGA)4 TAGA
vWA	17	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCATCCAT	47	3	3	178	0.264	0.017	0.017		vWA [CE 17]-GRCh38-Chr12-5983950-5984049 (TAGA)13 (CAGA)3 TAGA
vWA	18	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTATCCAT	30	30	30	178	0.169	0.169	0.169		vWA [CE 18]-GRCh38-Chr12-5983950-5984049 (TAGA)13 (CAGA)4 TAGA
vWA	19	TCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTAT	12	1	1	178		0.006	0.006		vWA [CE 19]-GRCh38-Chr12-5983950-5984049 (TAGA)12 (CAGA)6 TAGA
vWA	19	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTAT	12	10	10	178		0.056	0.056		vWA [CE 19]-GRCh38-Chr12-5983950-5984049 (TAGA)14 (CAGA)4 TAGA
vWA	19	TCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTAT	12	1	1	178	0.067	0.006	0.006		vWA [CE 19]-GRCh38-Chr12-5983950-5984049 (TAGA)15 (CAGA)3 TAGA
vWA	20	TCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCATCTA	ATTGATCTATCTGTCTGTCTGTCTGTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCCAT	4	4	4	178	0.022	0.022	0.022		vWA [CE 20]-GRCh38-Chr12-5983950-5984049 (TAGA)15 (CAGA)4 TAGA

Allele:	CE length equivalent
Seq:	Repeat region sequence
Flank:	Full sequence including flanking region from Flanking Region Report

Table S1b: Autosomal STR variants absent from STRait Razor database: Nomenclature, allele length, repeat and flanking sequences with previous observations.

Locus	Allele	Flank	Nomenclature	Type	Obs	HGDP occurrence	GenBank
CSF1PO	12	AAGATAGATAGATTAGATAGATAGA	CSF1PO [CE 12]-GRCh38-Chr5-150076318-150076389 ATCT ACCT (ATCT)10	RS	3	MEA	Missing
D10S1248	9	TTGAACAAATGAGTGAGTGGAAGGA	D10S1248 [CE 9]-GRCh38-Chr10 129294226-129294318 (GGAA)9	RL	2	MEA/AFR	MH167056.1
D12S391	23	CAGAGAGAAAGAATCAACAGGATCA	D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)11	RS	1	EUR/OCE/SAS	MH167177.1
D12S391	23	CAGAGAGAAAGAATCAACAGGATCA	D12S391 [CE 23]-GRCh38-Chr12-12296981-12297168 (AGAT)12 (AGAC)10 AGAT	RS	1	EUR	Missing
D12S391	26	CAGAGAGAAAGAATCAACAGGATCA	D12S391 [CE 26]-GRCh38-Chr12-12296981-12297168 (AGAT)17 (AGAC)8 AGAT	RS	1	EAS	Missing
D13S317	9	TCTGACCCATCTAACGCCTATCTGT	D13S317 [CE 9]-GRCh38-Chr13-82147986-82148107 (TATC)8 AATC	RS	1	Missing	MH167205.1
D16S539	8	TCCTCTTCCCTAGATCAATACAGAC	D16S539 [CE 8]-GRCh38-Chr16-86352664-86352781 (GATA)8 86352692-G (rs563997442)	FS	1	No-Flank	MK570018.1
D1S1656	17	TAGATAGATAGATAGATAGATAGAT	D1S1656 [CE 17]-GRCh38-Chr1-230769555-230769682 CCTA (TCTA)16 230769682-G (rs NA)	FS	1	n/a	Missing
D21S11	36	AAATATGTGAGTCAATTCCCCAAGT	D21S11 [CE 36]-GRCh38-Chr21-19181939-19182111 (TCTA)11 (TCTG)6 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCA TA (TCTA)11	RS	1	Missing	Missing
D22S1045	15	CATTGGAATTCCCCAAACTGGCCAG	D22S1045 [CE 15]-GRCh38-Chr22-37140181-37140357 (ATT)12 ACT (ATT)2 37140182-A (rs554502154)	FS	1	n/a	Missing
D2S1338	15	AAATGGCTTGGCCTTGCCTGCCTGC	D2S1338 [CE 15]-GRCh38-Chr2-218014856-218014964 (GGAA)9 (GGCA)6	RS	1	EUR	Missing
D2S441	9	CCAGGAACTGTGGCTCATCTATGAA	D2S441 [CE 9]-GRCh38-Chr2-68011918-68012017 (TCTA)9	RL	1	MEA/EUR/AFR/EAS	MH167314.1
D3S1358	13	TTTGGGGGCATCTCTTATACTCATG	D3S1358 [CE 13]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)3 (TCTA)9	RS	1	Missing	Missing
D3S1358	17	TTTGGGGGCATCTCTTATACTCATG	D3S1358 [CE 17]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)13	RS	2	MEA/SAS	MK990348.1
D3S1358	18	TTTGGGGGCATCTCTTATACTCATG	D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)2 TCTC (TCTA)14	RS	1	Missing	MK990350.1
D3S1358	18	TTTGGGGGCATCTCTTATACTCATG	D3S1358 [CE 18]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)13	RS	1	MEA/SAS	MH166987.1
D3S1358	19	TTTGGGGGCATCTCTTATACTCATG	D3S1358 [CE 19]-GRCh38-Chr3-45540691-45540820 TCTA (TCTG)4 (TCTA)14	RS	1	MEA	Missing
D6S1043	25	GATCAATAGATTGATAGATCAGATA	D6S1043 [CE 25]-GRCh38-Chr6-91740160-91740292 (ATCT)6 ATGT (ATCT)4 ATGT (ATCT)13	RS/RL	1	Missing	MH166958.1
D8S1179	17.1	TCTATCTATCTGTCTGTCTATCTAT	D8S1179 [CE 17.1]-GRCh38-Chr8-124894867-124894921 (TCTA)2 (TCTG)2 (TCTA)12 TCTTA	RS	1	Missing	Missing
D9S1122	13	AGATAACTGTAGATAGGTAGATCGA	D9S1122 [CE 13]-GRCh38-Chr9-77073809-77073880 TAGA TCGA (TAGA)8 CAGA (TAGA)2	RS	1	Missing	Missing
FGA	16.1	GCATATTTACAAGCTAGTTTCTTTC	FGA [CE 16.1]-GRCh38-Chr4-154587713-154587823 (GGAA)2 GGAG (AAAG)3 A (AAAG)5 AGAA AAAA (GAAA)3 154587760-A	RS	1	Missing	Missing
PentaE	16.4	AAGAAAAGAAAAGAAAAGAAAAGAA	PentaE [CE 16.4]-GRCh38-Chr15-96830996-96831114 (TCTTT)16 TCTT	RS	2	MEA/SAS	Missing
TH01	6	TGCAGGTCACAGGGAACACAGACTC	TH01 [CE 6]-GRCh38-Chr11-2171056-2171127 (AATG)3 AATA (AATG)2	RS	1	Missing	Missing

Allele: CE length equivalent; Flank: Full sequence including flanking region from Flanking Region Report; AFR: AFRICAN; EAS: EAST ASIAN; EUR: EUROPEAN; MEA: MIDDLE EAST; OCE: OCEANIAN; SAS: SOUTH ASIAN; n/a: not available (as flanking SNP data not in Phillips et al. 2018); RL: Repeat Length; RS: Repeat Sequence; FS: Flank Sequence.

Table S2a: iiSNP Flanking Region Report with novel SNP variants.

Locus	Seq	Target bases	Detected bases	iiSNP & Variant Reference SNP	iiSNP & Variant GRCh37 Position	frequency	No. polymorphic sites
rs1005533	GCAAAAAGCAAGAGCCGTGGAATTAAGTCGCCGCTGTTCAGGGGAGGCATAAGGAGCTGGAGGACTGGGTGGGCTCGGCAGCTTCCCTGGTCTTGCCCCTGCACTCCTCACCCAGC	A	A	rs1005533	39487110	0.51	1
rs1005533	GCAAAAAGCAAGAGCCGTGGAATTGAGTCGCCGCTGTTCAGGGGAGGCATAAGGAGCTGGAGGACTGGGTGGGCTCGGCAGCTTCCCTGGTCTTGCCCCTGCACTCCTCACCCAGC	G	G	rs1005533	39487110	0.49	1
rs10092491	AAACTGAAGCTTTCCTTATAGAGATTTATCCTAGTTAGTTTGCGGGGATACTGGTTGGGCCGAAA	C	CG	rs10092491_rs757115963	28411072_28411106	0.70	1
rs10092491	AAACTGAAGTTTTCCTTATAGAGATTTATCCTAGTTAGTTTGCGGGGATACTGGTTGGGCCGAAA	T	TG	rs10092491_rs757115963	28411072_28411106	0.30	1
rs1015250	AAAGGTTACTAAGTGATGGAGTTAGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCAGTGATTTTTTCA	C	ATCGC	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	0.06	3
rs1015250	AAAGGTTACTAAGTGATGGAGTTAGGAAAAGAACCCAGGTGTTTTATTGCTGTCCCAGTGATTTTTTCA	G	ATGGC	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	0.72	3
rs1015250	AAAGGTTACTAAGTGATGGAGTTGGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCACTGATTTTTTCA	C	GTCCC	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	0.01	3
rs1015250	AAAGGTTACTAAGTGATGGAGTTGGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCAGTGATTTTTTCA	C	GTCGC	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	0.22	3
rs1024116	CATACACTTAATAAAGTATGCCTTTGTATTTACTTTTGCTCACTTCCCA	A	AG	rs1024116_rs545003555	75432386_75432370	0.50	1
rs1024116	CATGCACTTAATAAAGTATGCCTTTGTATTTACTTTTGCTCACTTCCCA	G	GG	rs1024116_rs545003555	75432386_75432370	0.50	1
rs1028528	CTTACTCGACATCACTGTGTGCAGATCCGCGGAGGT	A	A	rs1028528	48362290	0.66	1
rs1028528	CTTACTCGACATCGCTGTGTGCAGATCCGCGGAGGT	G	G	rs1028528	48362290	0.34	1
rs1031825	GTCCTTAACCTATTAAATTTTAATGAGTATTTTATTTATCTAACCCCGAGCATACTTGAAAGCAGTGATTATATCT	A	AC	rs1031825_NA	4447483_4447484	0.31	1
rs1031825	GTCCTTAACCTATTAAATTTTAATGAGTATTTTATTTATCTAACCCCGAGCATACTTGAAAGCAGTGATTATATCT	C	CC	rs1031825_NA	4447483_4447484	0.69	1
rs10488710	TTTACTGTATTAGGAGTTCCCACTTGTTCTTTTTCTGCAAATGTGGCACTCGGTTTTATTTTTA	C	C	rs10488710	115207176	0.54	1
rs10488710	TTTACTGTATTAGGAGTTCCCACTTGTTCTTTTTCTGCAAATGTGGCAGTCGGTTTTATTTTTA	G	G	rs10488710	115207176	0.46	1
rs10495407	TCTGCTTCTGGAGATCTCCACTTCCTCTTGGTTGCATTGGATTCTCATTGAAATCCTATTCCATTC	A	AT	rs10495407_rs187062753	238439308_238439314	0.36	1
rs10495407	TCTGCTTCTGGAGATCTCCACTTCCTCTTGGTTGCATTGGATTCTCATTGAAAGTCCTATTCCATTC	G	GT	rs10495407_rs187062753	238439308_238439314	0.64	1
rs1058083	TTTGCTCAGAGTATCCAGAGTTAGCCACTAGG	A	A	rs1058083	100038233	0.33	1
rs1058083	TTTGCTCAGAGTATCCGGAGTTAGCCACTAGG	G	G	rs1058083	100038233	0.67	1
rs10773760	TGTTAGCCGTCGGGACCAGCTTCTGTCTGGAAGTTCGTCAAATTGCAGTTAAGTCC	A	AA	rs185405753_rs10773760	130761684_130761696	0.54	1
rs10773760	TGTTAGCCGTCGGGACCAGCTTCTGTCTGGAAGTTCGTCAAATTGCAGTTAGGTCC	G	AG	rs185405753_rs10773760	130761684_130761696	0.46	1
rs10776839	CAGCTGAGGAGCCCAAGGTTGCCGTCAGATCAGAGCCCCAGTTGCCCGGTCTGCCGCAGCTCT	G	AG	rs7037930_rs10776839	137417305_137417308	0.19	2
rs10776839	CAGCTGAGGAGCCCGAGGTTGCCGTCAGATCAGAGCCCCAGTTGCCCGGTCTGCCGCAGCTCT	G	GG	rs7037930_rs10776839	137417305_137417308	0.30	2
rs10776839	CAGCTGAGGAGCCCGAGTTTGCCGTCAGATCAGAGCCCCAGTTGCCCGGTCTGCCGCAGCTCT	T	GT	rs7037930_rs10776839	137417305_137417308	0.51	2
rs1109037	CCAGTTTCTCCAGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG	A	CATCGGGA	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.19	4
rs1109037	CCAGTTTCTCCAGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG	A	CATCGGGG	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.20	4
rs1109037	CCAGTTTCTCCGGAGCGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG	G	CGCCGGGG	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.01	4
rs1109037	CCAGTTTCTCCGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAAG	G	CGTCGGGA	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.13	4
rs1109037	CCAGTTTCTCCGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG	G	CGTCGGGG	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.47	4
rs1109037	CCAGTTTCTCTGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG	G	TGTCGGGA	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	0.01	4
rs1294331	AGTATAGCTATGGATTTTTATTGAATTTTTG	A	GAC	NA_rs1294331	233448415_233448413	0.01	2
rs1294331	AGTATAGTTATGGATTTTTATTGAATTTTTG	A	GAT	NA_rs1294331	233448415_233448413	0.47	2
rs1294331	AGTGTAGTTATGGATTTTTATTGAATTTTTG	G	GGT	NA_rs1294331	233448415_233448413	0.52	2
rs12997453	TTTTATGCTTTAAAGATACAGGTTATCTGTATTACATTGAGTTTTTACCTACCTT	A	CA	rs72883670_rs12997453	182413238_182413259	0.17	2
rs12997453	TTTTATGCTTTAAAGATACAGGTTATCTGTATTACATTGGGTTTTTACCTACCTT	G	CG	rs72883670_rs12997453	182413238_182413259	0.75	2
rs12997453	TTTTATGCTTTAAAGATATAGGTTATCTGTATTACATTGAGTTTTTACCTACCTT	A	TA	rs72883670_rs12997453	182413238_182413259	0.08	2
rs13182883	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTACAGTGAGCATTCAAATCCTCAAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAAA	A	AA	rs13182883	136633338	0.01	2
rs13182883	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTGCAGTGAGCATTCAAATCCTCAAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAAA	A	GA	rs13182883	136633338	0.35	2
rs13182883	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTGCAGTGAGCATTCAAATCCTCGAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAAG	G	GG	rs13182883	136633338	0.65	2
rs13218440	CCTCTGAGCAGCCTCCTGGAATACTCAGCTGGGATGGGTTGGGGCTGCTTGAGGTACAGCTCCCACTGCCTCTGAGTGGCCCTCCATGAAAATGCCTCATGTCTCTGTGTCCCTAAACTGTAAA	A	AGT	rs13218440_NA_rs1011515	12059954_12060015_12060047	0.41	1
rs13218440	CCTCTGGGCAGCCTCCTGGAATACTCAGCTGGGATGGGTTGGGGCTGCTTGAGGTACAGCTCCCACTGCCTCTGAGTGGCCCTCCATGAAAATGCCTCATGTCTCTGTGTCCCTAAACTGTAAG	G	GGT	rs13218440_NA_rs1011515	12059954_12060015_12060047	0.59	1
rs1335873	AGGGTGCAGGTATGTATTGTTGGCCGTGGAATACTGAGTACATAGCTAGGTACCTGGTACGGGA	A	AG	rs1335873_NA	20901724_20901693	0.44	1
rs1335873	AGGGTGCAGGTATGTATTGTTGGCCGTGGTATACTGAGTACATAGCTAGGTACCTGGTACGGGA	T	TG	rs1335873_NA	20901724_20901693	0.56	1
rs1336071	AAAAAGCATCAGATTAAAACAAAGATAAGAAAAATTAGAATTTCAGATGGACAAAACAG	A	AT	rs1336071_rs73756355	94537255_94537233	0.58	2
rs1336071	AAAAAGCATCAGGTTAAAACAAAGATAAGAAAAATAGAATTTCAGATGGACAAAACAG	G	GA	rs1336071_rs73756355	94537255_94537233	0.01	2
rs1336071	AAAAAGCATCAGGTTAAAACAAAGATAAGAAAAATTAGAATTTCAGATGGACAAAACAG	G	GT	rs1336071_rs73756355	94537255_94537233	0.40	2
rs1355366	TTCAGAGCCACTGGAGGCCTCGAGGATGAGGACTTGCCAAAGCCAGTTGTGGCCTAAGCACATGTGCCAGCTGGAT	A	AC	rs1355366_rs573442621	190806108_190806084	0.60	1
rs1355366	TTCAGAGCCACTGGAGGCCTCGAGGATGGGGACTTGCCAAAGCCAGTTGTGGCCTAAGCACATGTGCCAGCTGGAT	G	GC	rs1355366_rs573442621	190806108_190806084	0.40	1
rs1357617	ATTTGGGGAGCTTGGTCATGTTTCTTATCAGCTATCCCTATTCTAATCTCTAATTGGGCTTTTCAATTC	A	AC	rs1357617_rs145504328	961782_961743	0.74	2
rs1357617	ATTTGGGGAGCTTGGTCATGTTTCTTATCAGCTATCCCTATTCTAATTTCTAATTGGGCTTTTCAATTC	A	AT	rs1357617_rs145504328	961782_961743	0.01	2
rs1357617	ATTTGGGGTGCTTGGTCATGTTTCTTATCAGCTATCCCTATTCTAATCTCTAATTGGGCTTTTCAATTC	T	TC	rs1357617_rs145504328	961782_961743	0.26	2
rs1360288	GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGACACTGGCTGCATCCCCTCAACAGATGCCCC	C	GCGC	rs116412791_rs1360288_NA_NA	128968017_128968063_128968068_128968092	0.66	1
rs1360288	GGGGAGAGGCTCCCTGCAGCCTCTGGGGAGTAGAGGAGACCTGGGAAGATACTGGCTGCATCCCCTCAACAGATGCCCC	T	GTGC	rs116412791_rs1360288_NA_NA	128968017_128968063_128968068_128968092	0.34	1
rs1382387	GAAGGAGAAACACCTGAACTTTCAAGTCCCTGCAGTGGGCAGATGC	G	GC	rs1382387_rs551898660	80106361_80106359	0.25	1
rs1382387	GAAGGAGAAACACCTGAACTTTCAATTCCCTGCAGTGGGCAGATGC	T	TC	rs1382387_rs551898660	80106361_80106359	0.75	1
rs1413212	GGTGGAGCATGGGACATTTCA	A	A	rs1413212	242806797	0.29	1
rs1413212	GGTGGAGCATGGGGCATTTCA	G	G	rs1413212	242806797	0.71	1
rs1454361	GGGAGGAGGGAAATACACCCTGAGCTGCATGTTGTTTCTAAATGGATACTGAAAAGTGTCTTACTGATGATGGAC	A	A	rs1454361	25850832	0.53	1
rs1454361	GGGAGGAGGGAAATACACCCTGAGCTGCTTGTTGTTTCTAAATGGATACTGAAAAGTGTCTTACTGATGATGGAC	T	T	rs1454361	25850832	0.47	1
rs1463729	CTTTGGCAGCATACACTCATAGCCACATGCAGCCATTCCCACCCAAAAGCACGCACAT	A	AAAC	rs553955089_rs1463729_NA_rs114709250	126881464_126881448_126881440_126881423	0.02	2
rs1463729	CTTTGGCAGCATACACTCATAGCCACATGCAGCCATTCCCACCCAAAAGCATGCACAT	A	AAAT	rs553955089_rs1463729_NA_rs114709250	126881464_126881448_126881440_126881423	0.47	2
rs1463729	CTTTGGCAGCATACACTCATAGCCACGTGCAGCCATTCCCACCCAAAAGCATGCACAT	G	AGAT	rs553955089_rs1463729_NA_rs114709250	126881464_126881448_126881440_126881423	0.52	2
rs1490413	TCAGAACTGCCTGGTGTGGACTGGGCTGATGTGGGTTCTTTGCAAAACTGGCTGG	A	AA	rs113167966_rs1490413	4367298_4367323	0.36	2
rs1490413	TCAGAACTGCCTGGTGTGGACTGGGCTGATGTGGGTTCTTTGCAGAACTGGCTGG	G	AG	rs113167966_rs1490413	4367298_4367323	0.63	2
rs1490413	TCAGAACTGCCTGGTGTGGGCTGGGCTGATGTGGGTTCTTTGCAAAACTGGCTGG	A	GA	rs113167966_rs1490413	4367298_4367323	0.01	2
rs1493232	TTTTGGGTGCTAGGCCACAAAATAAACA	A	A	rs1493232	1127986	0.71	1
rs1493232	TTTTGGGTGCTAGGCCCCAAAATAAACA	C	C	rs1493232	1127986	0.29	1
rs1498553	ACTTCAGATGTTCAAAGCCAGACGAGAATAAAAGGATGGCTATGAGATCTATGGAAGTGCTGAG	C	C	rs1498553	5709028	0.42	1
rs1498553	ACTTCAGATGTTCAAAGCCAGATGAGAATAAAAGGATGGCTATGAGATCTATGGAAGTGCTGAG	T	T	rs1498553	5709028	0.58	1
rs1523537	TCTTAATACATTCATTTCTGCATGGGTGGGGTTTCAGTCTGCAACAAGATCTTGTAGGGACGCTATCGCT	C	GAC	rs538906241_rs77195753_rs1523537	51296121_51296123_51296162	0.46	1
rs1523537	TCTTAATACATTCATTTCTGCATGGGTGGGGTTTCAGTCTGCAACAAGATCTTGTAGGGATGCTATCGCT	T	GAT	rs538906241_rs77195753_rs1523537	51296121_51296123_51296162	0.54	1
rs1528460	CTTAACATATTTAAGACTGAAAAATGTTACAGTAAAAGTTTTGTTTAATCCTGCATTTGCCAAAC	C	CA	rs1528460_rs764217792	55210705_55210710	0.37	1
rs1528460	CTTAACATATTTAAGATTGAAAAATGTTACAGTAAAAGTTTTGTTTAATCCTGCATTTGCCAAAC	T	TA	rs1528460_rs764217792	55210705_55210710	0.63	1
rs159606	GTTTCTCATCCTGTTATTATTTGTTTACATCTGTCTCCTATATTTTATTCTCTC	A	A	rs159606	17374898	0.33	1
rs159606	GTTTCTCATCCTGTTATTATTTGTTTACGTCTGTCTCCTATATTTTATTCTCTC	G	G	rs159606	17374898	0.67	1
rs1821380	ATGGAGCCACTGAACTGCAGTGCAAAAATGCAGTAAGGCATACAGATAGAAGAAGGAGAATGTCAGGAAAAGACAG	C	CT	rs1821380_rs76591310	39313402_39313380	0.35	2
rs1821380	ATGGAGCCACTGAACTGCAGTGCAAAAATGCAGTAAGGGATACAGATAGAAGAAGGAGAACGTCAGGAAAAGACAG	G	GC	rs1821380_rs76591310	39313402_39313380	0.01	2
rs1821380	ATGGAGCCACTGAACTGCAGTGCAAAAATGCAGTAAGGGATACAGATAGAAGAAGGAGAATGTCAGGAAAAGACAG	G	GT	rs1821380_rs76591310	39313402_39313380	0.64	2
rs1886510	GGGTAAATTTTAGTAATTCTTAAAAGAATAAGCAATATTCGCAAGTGTTGTTGTGAAAATCCAGGCGTCA	C	C	rs1886510	22374700	0.64	1

Locus	Seq	Target bases	Detected bases	iiSNP & Variant Reference SNP	iiSNP & Variant GRCh37 Position	frequency	No. polymorphic sites
rs1886510	GGGTAAATTTTAGTAATTCTTAAAAGAATAAGCAATATTTGCAAGTGTTGTTGTGAAAATCCAGGCGTCA	T	T	rs1886510	22374700	0.36	1
rs1979255	GATCAGCAAGAGTTCCAACGTTCCATGCCCTGACCAACACAAGCTA	C	C	rs1979255	190318080	0.70	1
rs1979255	GATGAGCAAGAGTTCCAACGTTCCATGCCCTGACCAACACAAGCTA	G	G	rs1979255	190318080	0.30	1
rs2040411	AAGTGCATATTTCATGA	A	A	rs2040411	47836412	0.57	1
rs2040411	AAGTGCGTATTTCATGA	G	G	rs2040411	47836412	0.43	1
rs2046361	TGAAAGATCATTTTCAAAATTAAAATTAATAGAAGGTGAAGTGTCAACAATGACCAAAAATAGACAAATC	A	AA	rs116699455_rs2046361	10969083_10969059	0.02	2
rs2046361	TGAACGATCATTTTCAAAATTAAAATTAATAGAAGGTGAAGTGTCAACAATGACCAAAAATAGACAAATC	A	CA	rs116699455_rs2046361	10969083_10969059	0.62	2
rs2046361	TGAACGATCATTTTCAAAATTAAAATTATTAGAAGGTGAAGTGTCAACAATGACCAAAAATAGACAAATC	T	CT	rs116699455_rs2046361	10969083_10969059	0.35	2
rs2056277	AAGCATGTGTCAACCGCCAAACTGGGTGTTAGGGAGACAGGCATGAATGAGACGGGGA	C	CACG	rs149318691_NA_rs2056277_rs539552840	139399078_139399106_139399116_139399117	0.70	2
rs2056277	AAGCATGTGTCAACCGCCAAACTGGGTGTTAGGGAGACAGGCATGAATGAGATGGGA	T	CATG	rs149318691_NA_rs2056277_rs539552840	139399078_139399106_139399116_139399117	0.24	2
rs2056277	AAGCATGTGTCAACTGCCAAACTGGGTGTTAGGGAGACAGGCATGAATGAGACGGGGA	C	TACG	rs149318691_NA_rs2056277_rs539552840	139399078_139399106_139399116_139399117	0.06	2
rs2076848	GAAATTATTGATAATACACAGGTATCCTGGCCTCACCACCAGAAATCAGGGCAATGATGGACCTGAAGCGGTCCCAGG	A	ACA	rs2076848_NA_rs7947725	134667546_134667538_134667524	0.01	2
rs2076848	GAAATTATTGATAATACACAGGTATCCTGGCCTCACCACCAGAAATCAGGGCATGATGGACCTGAAGCGGTCCCAGG	A	ACG	rs2076848_NA_rs7947725	134667546_134667538_134667524	0.40	2
rs2076848	GAAATTATTGATAATACACAGGTATCCTGGCCTCACCACCAGAAATCAGGGCTTGATGGACCTGAAGCGGTCCCAGG	T	TCA	rs2076848_NA_rs7947725	134667546_134667538_134667524	0.03	2
rs2076848	GAAATTATTGATAATACACAGGTATCCTGGCCTCACCACCAGAAATCAGGGCTTGATGGACCTGAAGCGGTCCCGGG	T	TCG	rs2076848_NA_rs7947725	134667546_134667538_134667524	0.56	2
rs2107612	ACTAATTATGTGTTTTTTCTAAATCATATTGTCTACTTTTCTCCAAAACA	A	A	rs2107612	888320	0.62	1
rs2107612	ACTAATTATGTGTTTTTTCTAAATCATATTGTCTGCTTTTCTCCAAAACA	G	G	rs2107612	888320	0.38	1
rs2111980	CCTTCAAGCTCCAGCCTGGTGCCTCCGCTCCGTGACTCACTGGCAAAGATCT	A	AG	rs2111980_rs79578959	106328254_106328228	0.64	1
rs2111980	CCTTCGAGCTCCAGCCTGGTGCCTCCGCTCCGTGACTCACTGGCAAAGATCT	G	GG	rs2111980_rs79578959	106328254_106328228	0.36	1
rs214955	CCTGCCATTAAATTTTTGCATCACCTTTTCAGTCTTTGTTTGCAAGCATCAAAGGGCTGCCAGAATAAAGAA	A	AA	rs214955_rs117020413	152697706_152697675	0.03	2
rs214955	CCTGCCATTAAATTTTTGCATCACCTTTTCAGTCTTTGTTTGCAAGCATCCAAGGGCTGCCAGAATAAAGAA	A	AC	rs214955_rs117020413	152697706_152697675	0.57	2
rs214955	CCTGCCATTAAATTTTTGCGTCACCTTTTCAGTCTTTGTTTGCAAGCATCCAAGGGCTGCCAGAATAAAGAA	G	GC	rs214955_rs117020413	152697706_152697675	0.39	2
rs221956	TTCCCTCCAGCTCTCCTCTCCCCTTTCTGAGCCCTCAGCAAACTGACTTTAG	C	CA	rs221956_rs182328575	43606997_43607005	0.67	1
rs221956	TTCCCTCCAGCTCTCCTCTCCCCTTTCTGAGCCCTCAGCAAATTGACTTTAG	T	TA	rs221956_rs182328575	43606997_43607005	0.33	1
rs2269355	TCCCGAGTTCTCTCCACAGTCCC	C	C	rs2269355	6945914	0.56	1
rs2269355	TCCCGAGTTCTCTGCACAGTCCC	G	G	rs2269355	6945914	0.44	1
rs2342747	GGAGGAAGAAAACAGAGAGTCTTGACCGTAGAGGGGACAACAAAGAATGAGCTT	A	ACA	rs2342747_NA_rs140745596	5868700_5868708_5868716	0.23	1
rs2342747	GGAGGAAGAAAACAGAGAGTCTTGACCGTGGAGGGGACAACAAAGAATGAGCTT	G	GCA	rs2342747_NA_rs140745596	5868700_5868708_5868716	0.77	1
rs2399332	ATTAAAAAATCAGCAAAATACATGAACAGATACTTCTCAAAAGAAGCCAACAAACTTGAAAAAATGTTCAACGTCACTAATCATGAGAGAAATGTAAATCAAAACCCAAT	A	ACA	rs2399332_rs2399333_rs2399334	110301126_110301062_110301025	0.01	3
rs2399332	ATTAAAAAATCAGCAAAATACATGAACAGATACTTCTCAAAAGAAGCCAACAAACTTGAAAAAATGTTCAACGTCACTAATCATGAGAGAAATGTAAATCAAAACCCAGT	A	ACG	rs2399332_rs2399333_rs2399334	110301126_110301062_110301025	0.34	3
rs2399332	ATTAAAACATCAGCAAAATACATGAACAGATACTTCTCAAAAGAAGCCAACAAACTTGAAAAAATGTTCAAAGTCACTAATCATGAGAGAAATGTAAATCAAAACCCAAT	C	CAA	rs2399332_rs2399333_rs2399334	110301126_110301062_110301025	0.63	3
rs2399332	ATTAAAACATCAGCAAAATACATGAACAGATACTTCTCAAAAGAAGCCAACAAACTTGAAAAAATGTTCAACGTCACTAATCATGAGAGAAATGTAAATCAAAACCCAAT	C	CCA	rs2399332_rs2399333_rs2399334	110301126_110301062_110301025	0.01	3
rs2399332	ATTAAAACATCAGCAAAATACATGAACAGATACTTCTCAAAAGAAGCCAACAAACTTGAAAAAATGTTCAACGTCACTAATCATGAGAGAAATGTAAATCAAAACCCAGT	C	CCG	rs2399332_rs2399333_rs2399334	110301126_110301062_110301025	0.01	3
rs251934	GAGGCTTTTAAGTAGACGGGACAGCCAGATATCTACTACTTCATCTGCCCCAGAC	C	C	rs251934	174778678	0.40	1
rs251934	GAGGCTTTTAAGTAGATGGGACAGCCAGATATCTACTACTTCATCTGCCCCAGAC	T	T	rs251934	174778678	0.60	1
rs279844	AAGGATAACAGATTAAGTTCAGTGTCAATTTTGACCAGATATTAAAACTCACAACTCTCTAAACTTCCTTGATATTAACTACTGAACTAATTAATATCCCAGTAGCTTCTGGAGTTT	A	ACAT	rs279844_rs61621790_NA_rs279845	46329655_46329665_46329709_46329723	0.69	2
rs279844	AAGGATAACAGATTAAGTTCAGTGTCAATTTTGACCAGATATTAAATCTCACAACTCTCTAAACTTCCTTGATATTAACTACTGAACTAATTAATATCCCAGTAGCTTCTGGAGATT	T	TCAA	rs279844_rs61621790_NA_rs279845	46329655_46329665_46329709_46329723	0.31	2
rs2830795	ACTGGGTTCACCTCTATAGACATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTAT	A	CAA	rs12626695_rs79319609_rs2830795	28608125_28608161_28608163	0.08	2
rs2830795	ACTGGGTTCACCTCTATAGACATAGGACACACCATTTTATTGTCTAAAGGGCAAAGAAGTCCTATTAT	G	CAG	rs12626695_rs79319609_rs2830795	28608125_28608161_28608163	0.02	2
rs2830795	ACTGGGTTCACTTCTATAGACATAGGACACACCATTTTATTGTCTAAAGAGCAAAGAAGTCCTATTAT	A	TAA	rs12626695_rs79319609_rs2830795	28608125_28608161_28608163	0.66	2
rs2830795	ACTGGGTTCACTTCTATAGACATAGGACACACCATTTTATTGTCTAAAGGGCAAAGAAGTCCTATTAT	G	TAG	rs12626695_rs79319609_rs2830795	28608125_28608161_28608163	0.25	2
rs2831700	ATTTGGCTAAACTATTGCCGGAGATAAGTTAGAA	A	TA	NA_rs2831700	29679677_29679687	0.41	1
rs2831700	ATTTGGCTAAACTATTGCCGGAGATGAGTTAGAA	G	TG	NA_rs2831700	29679677_29679687	0.59	1
rs321198	ATACAATTCTCAAATGAAATAACTAAATAAGGAAGCTGTGTTCCTTTCTCCTACACACAGGCTTCAGGTTACCTGTTTTCCTTTTGTGATTCCACTTCCGTGTGAAGCAAGCAGT	C	TCT	rs147098090_rs321198_rs186446125	137029829_137029838_137029840	0.59	1
rs321198	ATACAATTCTCAAATGAAATAACTAAATAAGGAAGCTGTGTTCCTTTCTCCTACACACAGGCTTCAGGTTACCTGTTTTCCTTTTGTGATTCCACTTCTGTGTGAAGCAAGCAGT	T	TTT	rs147098090_rs321198_rs186446125	137029829_137029838_137029840	0.41	1
rs338882	GCCTGTGCACACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGCGCCACG	C	CCGCC	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	0.49	2
rs338882	GCCTGTGCATACACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGCGCCACG	T	TCGCC	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	0.50	2
rs338882	GCCTGTGCATACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGTGCCACG	T	TCGTC	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	0.01	2
rs354439	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATATCATTCACGGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA	A	CAGAGC	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	0.01	3
rs354439	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATATCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA	A	CAGATC	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	0.55	3
rs354439	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATATCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA	A	CAGCTC	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	0.01	3
rs354439	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTTTTAAGCACAATATTCTGAATATCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA	T	CTGATC	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	0.44	3
rs3780962	CTGTCCTCACGGGTGAAAGCTGATATCTTGACCTTGTTCATC	C	CC	rs3780962_NA	17193346_17193344	0.56	1
rs3780962	CTGTCCTTACGGGTGAAAGCTGATATCTTGACCTTGTTCATC	T	TC	rs3780962_NA	17193346_17193344	0.44	1
rs430046	AAGGTCATACAATGAATGGTGTGATGTAAAAGCTTGGGAGGTGATTTTTGAGGGTAGGTGCTGGGTTT	T	ATTG	rs409820_rs430044_rs430046_NA	78017034_78017045_78017051_78017056	0.49	3
rs430046	AAGGTCATACAATGAATGGTGTGATGTAAACGCTTGGGAGGCGATTTCTGAGGGTAGGTGCTGGGTTT	C	CCG	rs409820_rs430044_rs430046_NA	78017034_78017045_78017051_78017056	0.51	3
rs4364205	TTCCAGTCCTAGATATCCACCCATGAGAAATATATCCACAAAAAGATTGAGCAA	G	AG	NA_rs4364205	32417643_32417644	0.58	1
rs4364205	TTCCAGTCCTAGATATCCACCCATGAGAAATATATCCACAAAAATATTGAGCAA	T	AT	NA_rs4364205	32417643_32417644	0.42	1
rs445251	CATGTGCATTGGAGTTTTGATCACCAACCACTTGCAGTTTTTACATTAATTTGAATTGTAGGCCAGGT	C	CTCA	rs117702247_rs535095356_rs445251_rs369438	15124957_15124953_15124933_15124893	0.31	3
rs445251	CATGTGCATTGGAGTTTTGATCACGAACCACTTGCAGTTTTTACATTAATTTGAATTGTAGGCCGGGT	G	CTGG	rs117702247_rs535095356_rs445251_rs369438	15124957_15124953_15124933_15124893	0.69	3
rs445251	TATGTGCATTGGAGTTTTGATCACCAACCACTTGCAGTTTTTACATTAATTTGAATTGTAGGCCAGGT	C	TTCA	rs117702247_rs535095356_rs445251_rs369438	15124957_15124953_15124933_15124893	0.01	3
rs4530059	CAGAGCTCCAGAAGCAACTCCAGCACACAGAGAGGCGCTGATGTGCCTGTCAGGTGCTGCTACTGAGGAAGCCGTTGCTGGTCTCCGGAAGCTCTTGTATCCCCAGGAGTGCCGTCTGCCTGCA	A	ACTGC	rs4530059_NA_rs535737392_NA_rs4450333	104769149_104769158_104769168_104769194_104769223	0.02	2
rs4530059	CAGAGCTCCAGAAGCAACTCCAGCACACAGAGAGGCGCTGATGTGCCTGTCAGGTGCTGCTACTGAGGAAGCCGTTGCTGGTCTCCGGAAGCTCTTGTATCCTCAGGAGTGCCGTCTGCCTGA	A	ACTGT	rs4530059_NA_rs535737392_NA_rs4450333	104769149_104769158_104769168_104769194_104769223	0.39	2
rs4530059	CAGAGCTCCAGAAGCAACTCCAGCACACGGAGAGGCGCTGATGTGCCTGTCAGGTGCTGCTACTGAGGAAGCCGTTGCTGGTCTCCGGAAGCTCTTGTATCCCCAGGAGTGCCGTCTGCCTGG	G	GCTGC	rs4530059_NA_rs535737392_NA_rs4450333	104769149_104769158_104769168_104769194_104769223	0.58	2
rs4606077	TGGGATCTGACTCCCCACAGCCCACCCAAAGCCAGGGAACTCCTCACTGCCCTTCGGGCTTCAGCACAGGGCTGTCTCCCACGCCGGCAGGGCCTGTGCTTTCACTGG	C	TCCA	NA_rs4606077_rs58774517_rs1869434	144656732_144656754_144656764_144656765	0.65	3
rs4606077	TGGGATCTGACTCCCCACAGCCTACCCAAAGCCGGGGAACTCCTCACTGCCCTTCGGGCTTCAGCACAGGGCTGTCTCCCACGCCGGCAGGGCCTGTGCTTTCACTGG	T	TTCG	NA_rs4606077_rs58774517_rs1869434	144656732_144656754_144656764_144656765	0.28	3
rs4606077	TGGGATCTGACTCCCCACAGCCTACCCAAAGCTGGGGAACTCCTCACTGCCCTTCGGGCTTCAGCACAGGGCTGTCTCCCACGCCGGCAGGGCCTGTGCTTTCACTGG	T	TTTG	NA_rs4606077_rs58774517_rs1869434	144656732_144656754_144656764_144656765	0.07	3
rs560681	TCCATCTCTATTTACTCAGGTCACAGGACCTTGGGGCCTCCAAGAGTT	A	ACA	rs560681_rs186550433_rs60615385	160786670_160786675_160786688	0.58	2
rs560681	TCCATCTCTATTTACTCAGGTCACAGGGCCTTGGGGCCTCCAAGAGTT	A	ACG	rs560681_rs186550433_rs60615385	160786670_160786675_160786688	0.01	2
rs560681	TCCATCTCTGTTTACTCAGGTCACAGGACCTTGGGGCCTCCAAGAGTT	G	GCA	rs560681_rs186550433_rs60615385	160786670_160786675_160786688	0.41	2
rs576261	GTCACCAACCCTGGCCTCACAACTCTCTC	A	A	rs576261	39559807	0.66	1
rs576261	GTCACCACCCCTGGCCTCACAACTCTCTC	C	C	rs576261	39559807	0.34	1
rs6444724	TTGGAATGGGAGGAAAGGGAAAGGACTAAATTGTTGAACACTGGTTACCGTGCTAGGTATTTACAAACTTG	C	C	rs6444724	193207380	0.38	1
rs6444724	TTGGAATGGGAGGAAAGGGAAAGGACTAAATTGTTGAACACTGGTTACTGTGCTAGGTATTTACAAACTTG	T	T	rs6444724	193207380	0.62	1
rs6811238	CACTGAGAGGAGAAGACTGTGTGTTTTAAAGCCAGGTTTGTTTAAAGGTTATGATAGTATTAA	G	GG	NA_rs6811238	169663590_169663615	0.44	1
rs6811238	CACTGAGAGGAGAAGACTGTGTGTTTTAAAGCCAGGTTTGTTTAAAGTGTTATGATAGTATTAA	T	GT	NA_rs6811238	169663590_169663615	0.56	1
rs6955448	TAAGTTGGAATAGGTGATGCAAAGCCCTGCCGTTACTACTATTGTTGAAAAGTTCATGGGAGAAAGTTGTAAA	T	AGAT	rs6950322_rs140855431_rs143117431_rs6955448	4310317_4310327_4310349_4310365	0.34	2
rs6955448	TAAGTTGGGATAGGTGATGCAAAGCCCTGCCGTTACTACTATTGTTGAAAAGTTCACGGGAGAAAGTTGTAAA	C	GGAC	rs6950322_rs140855431_rs143117431_rs6955448	4310317_4310327_4310349_4310365	0.66	2
rs7041158	TCAATTTCCTCTCCAACCCAAGACACTTCTCACTGGAAAACTCTCACAATCACATTTATAACAAAGGAGAGG	C	CA	rs7041158_rs117776421	27985938_27985976	0.62	1
rs7041158	TCAATTTCCTTTCCAACCCAAGACACTTCTCACTGGAAAACTCTCACAATCACATTTATAACAAAGGAGAGG	T	TA	rs7041158_rs117776421	27985938_27985976	0.38	1
rs717302	AATAAGCTTTAGAAAGGCATATCATATTAACTGTGTGGTGAACGTCTGTCATTAGGTTTAGCTC	G	AG	rs149072431_rs717302	2879382_2879395	0.01	2
rs717302	AATAAGCTTTAGAAAGGCATATCGTATTAACTGTGTAGTGAACGTCTGTCATTAGGTTTAGCTC	A	GA	rs149072431_rs717302	2879382_2879395	0.57	2

Locus	Seq	Target bases	Detected bases	iiSNP & Variant Reference SNP	iiSNP & Variant GRCh37 Position	frequency	No. polymorphic sites
rs717302	AATAAGCTTTAGAAAGGCATATCGTATTAACTGTGTGGTGAACGTCTGTCATTAGGTTTAGCTC	G	GG	rs149072431_rs717302	2879382_2879395	0.43	2
rs722098	GAAATATCCTTGATAAGGATTTAAATTTTGGATGTGCTGAATATTTCTT	A	A	rs722098	16685598	0.73	1
rs722098	GAAATATCCTTGGTAAGGATTTAAATTTTGGATGTGCTGAATATTTCTT	G	G	rs722098	16685598	0.27	1
rs722290	GTGTTTCAGATTTCAGATTTTGAAATATTTGCATATACATACTCAGATGTCTTGGG	C	TC	NA_rs722290	53216765_53216723	0.63	1
rs722290	GTGTTTCAGATTTCAGATTTTGAAATATTTGCATATACATACTGAGATGTCTTGGG	G	TG	NA_rs722290	53216765_53216723	0.37	1
rs727811	CAACGACTTAAAATCATCTGCATCTCCCAGCAATCTCATGATTTCATTCACTTTATATTTTTGCT	A	AA	rs727811_rs1390470	165045334_165045290	0.47	2
rs727811	CAACGACTTACAATCATCTGCATCTCCCAGCAATCTCATGATTTCATTCACTTTATATTTTTGCT	C	CA	rs727811_rs1390470	165045334_165045290	0.53	2
rs727811	CAACGACTTACAATCATCTGCATCTCCCAGCAATCTCATGATTTCATTCACTTTGTATTTTTGCT	C	CG	rs727811_rs1390470	165045334_165045290	0.01	2
rs729172	AGCCTCATTAATATGACCAAGGCTCCTCTGCAGACAGAATGTATGTAACCG	A	CA	rs729172	5606197	0.32	2
rs729172	AGCCTCATTAATATGACCAAGGCTCCTCTGCAGACCGAATGTATGTAACCG	C	CC	rs729172	5606197	0.67	2
rs729172	AGCTTCATTAATATGACCAAGGCTCCTCTGCAGACCGAATGTATGTAACCG	C	TC	rs729172	5606197	0.01	2
rs733164	CCAGGCTCAGCTTTCAGCCCCAGGTCCCACCAACAGGCCATCCCACTTGGAAAATTTGCCTGACATTCCTGAGCCGGGCC	A	A	rs733164	27816784	0.38	1
rs733164	CCAGGCTCAGCTTTCAGCCCCAGGTCCCACCAACAGGCCATCCCACTTGGAAAGTTTGCCTGACATTCCTGAGCCGGGCC	G	G	rs733164	27816784	0.62	1
rs735155	GACGCCGGCTCCAGAAGGGACCTAACCTGGAGAAAACCGGAGAGCTGGCGCTGAAGGGTCGGGAGAGGCCTGCTGGGCCGCGCTGGAGAGGGAGACCTGCTGACTTCCCGTTGAATTCGGTGTA	A	GAAT	rs79799511_rs735155_rs373487413_rs79059653374199_3374178_3374156_3374154	0.62	1
rs735155	GACGCCGGCTCCAGAAGGGACCTAACCTGGAGAAAACCGGAGAGCTGGCGCTGAAGGGTCGGGAGAGGCCTGCTGGGCCGCGCTGGAGAGGGAGACCTGCTGGCTTCCCGTTGAATTCGGTGTG	G	GGAT	rs79799511_rs735155_rs373487413_rs79059653374199_3374178_3374156_3374154	0.38	1
rs737681	CCGCGGGAGCTCTGCACAAGCCGCAGGGTCACATGTGAGGCCATCTCCACCCTTCATCCCTGGGCCCAGGTGCAGTCTCTC	C	CCGCG	NA_rs535138178_rs553538445_rs737681_NA	155990763_155990783_155990787_155990813_155990824	0.54	1
rs737681	CCGCGGGAGCTCTGCACAAGCCGCAGGGTCACATGTGAGGCCATCTCCACCTTCATCCCTGGGCCCAGGTGCAGTCTCTC	T	CCGTG	NA_rs535138178_rs553538445_rs737681_NA	155990763_155990783_155990787_155990813_155990824	0.46	1
rs740598	TCAAATAGCAATGGCTCGTCTATGGTTAGTCTCAAGCCACATTCTCAGAACTGCTCAAACCCTGGCCCTGC	A	GAC	rs151017734_rs740598_rs189367495	118506883_118506899_118506910	0.51	1
rs740598	TCAAATAGCAATGGCTCGTCTATGGTTAGTCTCGCAGCCACATTCTCAGAACTGCTCAAACCCTGGCCCTGC	G	GGC	rs151017734_rs740598_rs189367495	118506883_118506899_118506910	0.49	1
rs740910	AAGTATAACAGTTTGCTAAGTAAGGTGAGTGGTATAATCATATAATTGTAAAAAGCAAAACAAA	A	AA	rs60810599_rs740910	5706584_5706623	0.69	2
rs740910	AAGTATAACAGTTTGCTAAGTAAGGTGAGTGGTATAATCATATGTTTGTAAAAAGCAAAACAAA	G	AG	rs60810599_rs740910	5706584_5706623	0.23	2
rs740910	AAGTGTAACAGTTTGCTAAGTAAGGTGAGTGGTATAATCATATATTGTAAAAAGCAAAACAAA	A	GA	rs60810599_rs740910	5706584_5706623	0.08	2
rs763869	TGTTTATATTATTTCTAACTCAACTGCATTACATT	C	C	rs763869	1375610	0.42	1
rs763869	TGTTTATATTATTTCTAACTCAATTGCATTACATT	T	T	rs763869	1375610	0.58	1
rs8037429	GAGTTACGTAG	C	C	rs8037429	53616909	0.56	1
rs8037429	GAGTTATGTAG	T	T	rs8037429	53616909	0.44	1
rs8078417	GGGGACGCCTGGCGCTGCGAGGGAGGCCCCGAGCCTCGTGCCCCCGTGAAGCTTCAGCTCCCCTCCCCGGCTGTCCTTGAGGCTCTTCTCACACTCAGATGC	C	GGCCGGC	rs78650971_NA_rs182919351_rs567092265_rs138638046187180461878_80461880_80461904_80461905_80461913_804619350.60	1
rs8078417	GGGGACGCCTGGCGCTGCGAGGGAGGCCCCGAGCCTCGTGCCCCCGTGAAGCTTCAGCTCCCCTCCCTGGCTGTCCTTGAGGCTCTTCTCACACTCAGATGC	T	GGCCGGT	rs78650971_NA_rs182919351_rs567092265_rs138638046187180461878_80461880_80461904_80461905_80461913_804619350.40	1
rs826472	TAGCATTTTTATGCATCAATAAGATGTTAATTATGATCAGATATTTTACAATGATGCTGAATTTTGTCTCTGTTATATTAGCCACCTATCTCTCACCAGGAT	C	CC	rs138540224_rs826472	2406617_2406631	0.02	2
rs826472	TAGCATTTTTATGCATCAATAAGATGTTAATTATGATCAGATATTTTACAATGATGCTGAATTTTGTCTCTGTTATATTAGTCACCTATCTCTCACCAGGAT	C	TC	rs138540224_rs826472	2406617_2406631	0.68	2
rs826472	TAGCATTTTTATGCATCAATAAGATGTTAATTATGATCAGATATTTTACAATGATGCTGAATTTTGTCTCTGTTATATTAGTCACCTATCTCTCATCAGGAT	T	TT	rs138540224_rs826472	2406617_2406631	0.30	2
rs873196	TGCCCCTTGTAATGTGAACATGCCTGATTGACTCCAACTCCTGCCAGCCTTGGCATGCTCATTTGTGAACC	C	C	rs873196	98845531	0.29	1
rs873196	TGCCCTTTGTAATGTGAACATGCCTGATTGACTCCAACTCCTGCCAGCCTTGGCATGCTCATTTGTGAACC	T	T	rs873196	98845531	0.71	1
rs876724	AGTACATTTTTTCTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTAGATA	C	CCGT	rs876724_rs77642176_rs114448669_rs300773	114974_114982_115033_115035	0.01	4
rs876724	AGTACATTTTTTGTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTACATA	C	CGCT	rs876724_rs77642176_rs114448669_rs300773	114974_114982_115033_115035	0.02	4
rs876724	AGTACATTTTTTGTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTAGACA	C	CGGC	rs876724_rs77642176_rs114448669_rs300773	114974_114982_115033_115035	0.22	4
rs876724	AGTACATTTTTTGTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTAGATA	C	CGGT	rs876724_rs77642176_rs114448669_rs300773	114974_114982_115033_115035	0.51	4
rs876724	AGTATATTTTTTGTCACACTCTGCTAACTGCCTGCTCATAGATATTCAAATTTAGTAGATGTAGATA	T	TGGT	rs876724_rs77642176_rs114448669_rs300773	114974_114982_115033_115035	0.24	4
rs891700	GTGTTAACAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTGCTTGCATAGTTCTAAGG	G	AG	rs12047255_rs891700	239881878_239881926	0.01	3
rs891700	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTACTTGCATAGTTCTAAGG	A	GA	rs12047255_rs891700	239881878_239881926	0.42	3
rs891700	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTGCTTGCATAGTTCTAAGG	G	GG	rs12047255_rs891700	239881878_239881926	0.57	3
rs891700	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTACTTGCATAGTTCTAAGG	A	GTA	rs12047255_rs891700	239881878_239881926	0.01	3
rs901398	GTGCAAACTAGCTGAATATCAGCCCCGTTGATAGCTAACATTAGT	C	C	rs901398	11096221	0.29	1
rs901398	GTGCAAACTAGCTGAATATCAGCCCTGTTGATAGCTAACATTAGT	T	T	rs901398	11096221	0.71	1
rs907100	TGATGCCCTGGCATCAAAGAAGGCTCCAACTGAGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	C	CA	rs907100_rs11689319	239563579_239563597	0.20	2
rs907100	TGATGCCCTGGCATCAAAGAAGGCTCCAACTGGGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	C	CG	rs907100_rs11689319	239563579_239563597	0.24	2
rs907100	TGATGCCCTGGCATGAAAGAAGGCTCCAACTGGGCTTCTTTTCTGTGTTTTCCAAGGCTTGGAAAG	G	GG	rs907100_rs11689319	239563579_239563597	0.56	2
rs914165	CAAGCAGCAGAGCCTGGATGCTGATGGGCACCAAAGAGGGCAACACCCTCAGGCAGCTCTGCTGAGCCCGCCCCCCACCCAGTGCAAAACAGGTGACTGGTCTGCACTC	A	AC	rs914165_rs755095	42415929_42415976	0.45	2
rs914165	CAAGCAGCAGAGCCTGGATGCTGATGGGCACCAAAGAGGGCAACACCCTCAGGCAGCTCTGCTGAGCCCGCCCCCCACCCAGTGCAAAAGAGGTGACTGGTCTGCACTC	A	AG	rs914165_rs755095	42415929_42415976	0.01	2
rs914165	CAAGCAGCAGAGCCTGGATGCTGATGGGCACCAAAGAGGGCGACACCCTCAGGCAGCTCTGCTGAGCCCGCCCCCCACCCAGTGCAAAACAGGTGACTGGTCTGCACTC	G	GC	rs914165_rs755095	42415929_42415976	0.54	2
rs917118	CCATGAAGATGGAGTCAACATTTTACAAGACGGCTCGTTGACCTCAGTCATCTCTTACCACTTGTGCTC	C	CG	rs917118_NA	4457003_4457008	0.72	1
rs917118	CCATGAAGATGGAGTCAACATTTTACAAGATGCTCGTTGACCTCAGTCATCTCTTACCACTTGTGCTC	T	TG	rs917118_NA	4457003_4457008	0.28	1
rs938283	CATACATTGAAGTCCTAACCCCTAGTACGTTAGATGTGACCGCATTTGGAGAT	C	C	rs938283	77468498	0.21	1
rs938283	CATACATTGAAGTCCTAACCCCTAGTACGTTAGATGTGACCGTATTTGGAGAT	T	T	rs938283	77468498	0.79	1
rs964681	GACACGGGCATTTGGGGCCACAGTGCTCAGACAGCAACCTCTGGTTCTTACCAATCC	C	C	rs964681	132698419	0.34	1
rs964681	GACATGGGCATTTGGGGCCACAGTGCTCAGACAGCAACCTCTGGTTCTTACCAATCC	T	T	rs964681	132698419	0.66	1
rs987640	ACAGGTACATTCACTTAACAGGCTCTCTTTCCACCCATGTAGAAATACAAAAATAAGACTTAATACAGACGATGG	A	AA	rs17793354_rs987640	33559474_33559508	0.42	2
rs987640	ACAGGTACATTCACTTAACAGGCTCTCTTTCCACCCTTGTAGAAATACAAAAATAAGACTTAATACAGACGATGG	T	AT	rs17793354_rs987640	33559474_33559508	0.52	2
rs987640	ACCGGTACATTCACTTAACAGGCTCTCTTTCCACCCATGTAGAAATACAAAAATAAGACTTAATACAGACGATGG	A	CA	rs17793354_rs987640	33559474_33559508	0.06	2
rs9905977	TGGTGTCCAAGGAGGGCTGGGTGACTCGTGGCTCAGTCAGGATCAAGATTCCTTTCGTCTTTCCCCTCTGCCCTCCCTGGCTTGTCAGCTTTGTCCCTCAGGCTTGGCCCCTCGTGGCC	A	AGC	rs9905977_rs28582109_rs73298992	2919393_2919430_2919461	0.26	3
rs9905977	TGGTGTCCAAGGAGGGCTGGGTGACTCGTGGCTCAGTCAGCGTCAAGATTCCTTTCGTCTTTCCCCTCTGCCCTCCCTAGCTTGTCAGCTTTGTCCCTCAGGCTTGGCCCCTCGTGGCC	G	GAC	rs9905977_rs28582109_rs73298992	2919393_2919430_2919461	0.01	3
rs9905977	TGGTGTCCAAGGAGGGCTGGGTGACTCGTGGCTCAGTCAGCGTCAAGATTCCTTTCGTCTTTCCCCTCTGCCCTCCCTGGCTTGTCAGCTTTGTCCCTCAGGCTTGGCCCCTCGTGGCC	G	GGC	rs9905977_rs28582109_rs73298992	2919393_2919430_2919461	0.43	3
rs9905977	TGGTGTCCAAGGAGGGCTGGGTGACTCGTGGCTCAGTCAGCGTCAAGATTCCTTTCGTCTTTCCCCTCTGCCCTCCCTGGCTTGTCAGCTTTGTCCCTCAGGCTTGGCCTCTCGTGGCC	G	GGT	rs9905977_rs28582109_rs73298992	2919393_2919430_2919461	0.30	3
rs993934	TTACGAACTAAGCTAATATACTCTGGAGACTGTTATCACAATACTTTGCTCTATTGCCTTACAAAGCAAA	C	CA	rs993934_NA	124109213_124109179	0.44	1
rs993934	TTATGAACTAAGCTAATATACTCTGGAGACTGTTATCACAATACTTTGCTCTATTGCCTTACAAAGCAAA	T	TA	rs993934_NA	124109213_124109179	0.56	1
rs9951171	GGGAGAAAAAGTCCTCGTTGTTCCTCTGGGATGCAACATGAGAGAGCAGCACACTGAGGCTTTATGGATTGCCCTG	A	AA	rs145524126_rs9951171	9749820_9749879	0.42	1
rs9951171	GGGAGAAAAAGTCCTCGTTGTTCCTCTGGGATGCAACATGAGAGAGCAGCACACTGAGGCTTTATGGGTTGCCCTG	G	AG	rs145524126_rs9951171	9749820_9749879	0.58	1

Extract from the Flanking Region Report using the Verogen colour scheme whereby information pertaining to the target SNP is shown in black (with the base highlighted in bold in the sequence string) and certain known flanking SNP details are shown in blue (with the base highlighted in bold in the sequence string)

Polymorphisms detected in this study which were not highlighted and therefore could go unnoticed are now highlighted in red (see Table S2b for additional detail).

Pale yellow highlighting shows sequences distinguished only by these potentially overlooked variant positions

Green highlighting indicates three amplicons which show variation at more than one SNP but which are perfectly linked to yeild just two microhaplotypes in this population

Salmon highlighting indicates four amplicons where recombination or recurrent mutation must be invoked due to the presence of all four combinations of alleles at two biallelic SNPs

Table S2b: iiSNP variants (not highlighted in Flanking Region Report): Flanking sequences with previous observations.

locus	iSNP & Variant Reference SNP	iSNP & Variant GRCh37 Position	Detected bases	Format of UAS Flanking Region Report with new SNPs highlighted in red and bold font (NB these variants are in plain text in the original report)	UAS reported strand	Unreported SNP	GRCh37 Variant (Ref>Alt)	GRCh37 Position
rs1015250	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	ATCC	AAAGGTTACTAAGTGATGGAGTTAGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCAGTGATTTTTCA	plus			
rs1015250	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	ATGC	AAAGGTTACTAAGTGATGGAGTTAGGAAAAGAACCCAGGTGTTTTATTGCTGTCCCAGTGATTTTTCA				
rs1015250	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	GTCC	AAAGGTTACTAAGTGATGGAGTTGGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCACTGATTTTTCA		rs130727885	G>C	1823783
rs1015250	rs6475200_NA_rs1015250_rs145984676	1823749_1823767_1823774_1823792	GTCC	AAAGGTTACTAAGTGATGGAGTTGGGAAAAGAACCCAGGTGTTTTATTCCTGTCCCAGTGATTTTTCA				
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	ACGGGA	CCAGTTTCTCCAGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG	plus			
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	ACGGGG	CCAGTTTCTCCAGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG				
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	GCGGGG	CCAGTTTCTCCGGAGCGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG		NA	T>C	10085726
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	GCGGGG	CCAGTTTCTCCGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGGGG				
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	GCGGGA	CCAGTTTCTCCGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG				
rs1109037	rs1109037_rs183533496_NA_NA_NA_rs1109038	10085722_10085753_10085760_10085768_10085785_10085786	GCGGGA	CCAGTTTCTCTGGAGTGGAAAGACTTTCATCTCGCACTGGCACGACCTTGAGACCCCGGGTTCTGATGAACTGGGAGG		rs99975532(	C>T	10085721
rs1294331	NA_rs1294331	233448415_233448413	GA	AGTATAGCTATGGATTTTTATTGAATTTTTG	minus	rs92280418	A>G	2.33E+08
rs1294331	NA_rs1294331	233448415_233448413	GA	AGTATAGTTATGGATTTTTATTGAATTTTTG				
rs1294331	NA_rs1294331	233448415_233448413	GG	AGTGTAGTTATGGATTTTTATTGAATTTTTG				
rs13182883	rs13182883	136633338	A	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTACAGTGAGCATTCAAATCCTCAAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAGACA	plus	NA	G>A	1.37E+08
rs13182883	rs13182883	136633338	A	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTGCAGTGAGCATTCAAATCCTCAAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAGACA				
rs13182883	rs13182883	136633338	G	TGAGGGGAGGGGTCCCTTCTGGCCTAGTAGAGGGCCTGGCCTGCAGTGAGCATTCAAATCCTCGAGGAACAGGGTGGGGAGGTGGGACAAAGGCAGGAAGAAAGTAACGGAGAGCCTGGGGAGACA				
rs338882	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	CCGC	GCCTGTGCACACACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGCGCCACG	minus			
rs338882	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	TCGC	GCCTGTGCATACACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGCGCCACG				
rs338882	rs338882_rs746755126_NA_NA	178690725_178690719_178690640_178690620	TCGC	GCCTGTGCATACACACGTTTGGGACAAGGGCTGGATTCTTCGGCTGGGATGTCTCTCAGAGCTCTTGACTTGGTCCCTTTGGCTGGGGCTTGCCGTGAGGTGTGGGCTGTGCCACG		rs527589535	G>A	1.79E+08
rs354439	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	CAGAC	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATATCATTCACGGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA	minus	NA	A>C	1.07E+08
rs354439	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	CAGAC	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATATCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA				
rs354439	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	CAGCC	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTATTAAGCACAATATTCTGAATCTCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA				
rs354439	NA_rs354439_rs564750466_rs144284297_NA	106938442_106938411_106938406_106938390_106938362	CTGAC	TGTTCTGGTGGCTTCTCTTTCCCTTATGTATCTCTCTCATGTATCACATTCCTTTTAAGCACAATATTCTGAATATCATTCACTGTTTTCTATCGCAACCTGCAATTTGAGAGTTAAGAA				
rs729172	rs729172	5606197	A	AGCCTCATTAATATGACCAAGGCTCCTCTGCAGACAGAATGTATGTAACCG	minus			
rs729172	rs729172	5606197	C	AGCCTCATTAATATGACCAAGGCTCCTCTGCAGACCGAATGTATGTAACCG				
rs729172	rs729172	5606197	C	AGCTTCATTAATATGACCAAGGCTCCTCTGCAGACCGAATGTATGTAACCG		rs556717755	G>A	2.33E+08
rs891700	rs12047255_rs891700	239881878_239881926	AG	GTGTTAACAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTGCTTGCATAGTTCTAAGG	plus			
rs891700	rs12047255_rs891700	239881878_239881926	GG	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTGCTTGCATAGTTCTAAGG				
rs891700	rs12047255_rs891700	239881878_239881926	GA	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTGAAGCCTACTTGCATAGTTCTAAGG				
rs891700	rs12047255_rs891700	239881878_239881926	GA	GTGTTAGCAGTAAAACATTTTCATCAAATTTCCATTCTTTTTTTTTTTGAAGCCTACTTGCATAGTTCTAAGG		rs54356353(	T insertio	2.4E+08
UAS Flanking Region Report								Additional data on novel SNPs

Extract from the Flanking Region Report using the Verogen colour scheme whereby information pertaining to the target SNP is shown in black (with the base highlighted in bold in the sequence string) and certain known flanking SNP details are shown in blue (with the base highlighted in bold in the sequence string)

Polymorphisms detected in this study which were not highlighted and therefore could go unnoticed are now highlighted in red and bold with additional data pertaining to these shown to the right.

Pale yellow highlighting shows sequences distinguished only by these potentially overlooked variant positions

Table S3: STR forensic statistics (allele length, repeat region sequence & flanking region).

Allele length

locus	N	Nall	GD	PIC	PM	PD	Hobs	PE	TPI
TPOX	178	6	0.6046	0.5641	0.2382	0.7618	0.4944	0.1826	0.9889
D9S1122	178	6	0.6926	0.6311	0.1468	0.8532	0.6404	0.3423	1.3906
D17S1301	178	5	0.6648	0.6038	0.1668	0.8332	0.6517	0.3575	1.4355
D20S482	178	7	0.6986	0.6506	0.1380	0.8620	0.6966	0.4231	1.6481
D16S539	178	7	0.7266	0.6870	0.1148	0.8852	0.7079	0.4405	1.7115
D3S1358	178	7	0.7708	0.7285	0.0983	0.9017	0.7079	0.4405	1.7115
D4S2408	178	5	0.7562	0.7149	0.1034	0.8966	0.7191	0.4584	1.7800
D5S818	178	7	0.7269	0.6804	0.1327	0.8673	0.7191	0.4584	1.7800
D22S1045	178	6	0.7065	0.6560	0.1345	0.8655	0.7303	0.4767	1.8542
D10S1248	178	8	0.7660	0.7253	0.0968	0.9032	0.7303	0.4767	1.8542
CSF1PO	178	6	0.6926	0.6265	0.1741	0.8259	0.7416	0.4955	1.9348
TH01	178	6	0.7674	0.7261	0.0910	0.9090	0.7416	0.4955	1.9348
vWA	178	7	0.7844	0.7474	0.0867	0.9133	0.7528	0.5146	2.0227
D13S317	178	7	0.7788	0.7434	0.0877	0.9123	0.7753	0.5540	2.2250
D6S1043	178	10	0.7858	0.7521	0.0792	0.9208	0.7753	0.5540	2.2250
D8S1179	178	10	0.8421	0.8167	0.0519	0.9481	0.7753	0.5540	2.2250
D19S433	178	11	0.8502	0.8290	0.0463	0.9537	0.7753	0.5540	2.2250
D2S1338	178	12	0.8553	0.8351	0.0400	0.9600	0.7753	0.5540	2.2250
PentaE	174	15	0.9092	0.8962	0.0252	0.9748	0.7816	0.5654	2.2895
D2S441	178	9	0.7677	0.7285	0.1031	0.8969	0.7865	0.5743	2.3421
D1S1656	178	13	0.8694	0.8501	0.0375	0.9625	0.7865	0.5743	2.3421
D21S11	178	13	0.8138	0.7858	0.0686	0.9314	0.7978	0.5949	2.4722
D7S820	178	7	0.7956	0.7607	0.0900	0.9100	0.8090	0.6158	2.6176
D18S51	178	11	0.8553	0.8334	0.0443	0.9557	0.8090	0.6158	2.6176
FGA	178	13	0.8685	0.8483	0.0408	0.9592	0.8202	0.6371	2.7812
D12S391	178	13	0.8796	0.8620	0.0357	0.9643	0.8427	0.6805	3.1786
PentaD	178	11	0.8556	0.8335	0.0453	0.9547	0.8539	0.7026	3.4231

Repeat region sequence

locus	Nall	GD	PIC	PM	PD	Hobs	PE	TPI
TPOX	6	0.6046	0.5641	0.2382	0.7618	0.4944	0.1826	0.9889
D9S1122	12	0.8319	0.8043	0.0554	0.9446	0.7978	0.5949	2.4722
D17S1301	5	0.6648	0.6038	0.1668	0.8332	0.6517	0.3575	1.4355
D20S482	7	0.6986	0.6506	0.1380	0.8620	0.6966	0.4231	1.6481
D16S539	7	0.7266	0.6870	0.1148	0.8852	0.7079	0.4405	1.7115
D3S1358	19	0.8890	0.8732	0.0302	0.9698	0.8539	0.7026	3.4231
D4S2408	5	0.7562	0.7149	0.1034	0.8966	0.7191	0.4584	1.7800
D5S818	11	0.8184	0.7911	0.0688	0.9312	0.8202	0.6371	2.7812
D22S1045	6	0.7065	0.6560	0.1345	0.8655	0.7303	0.4767	1.8542
D10S1248	8	0.7660	0.7253	0.0968	0.9032	0.7303	0.4767	1.8542
CSF1PO	7	0.7086	0.6477	0.1569	0.8431	0.7528	0.5146	2.0227
TH01	7	0.7704	0.7300	0.0893	0.9107	0.7416	0.4955	1.9348
vWA	13	0.8227	0.7954	0.0638	0.9362	0.7978	0.5949	2.4722
D13S317	12	0.8735	0.8551	0.0383	0.9617	0.8539	0.7026	3.4231
D6S1043	10	0.7858	0.7521	0.0792	0.9208	0.7753	0.5540	2.2250
D8S1179	15	0.8932	0.8778	0.0312	0.9688	0.8427	0.6805	3.1786
D19S433	12	0.8520	0.8312	0.0453	0.9547	0.7753	0.5540	2.2250
D2S1338	29	0.9023	0.8913	0.0234	0.9766	0.8427	0.6805	3.1786
PentaE	15	0.9092	0.8962	0.0252	0.9748	0.7816	0.5654	2.2895
D2S441	13	0.7812	0.7469	0.0882	0.9118	0.7865	0.5743	2.3421
D1S1656	18	0.8954	0.8812	0.0276	0.9724	0.8202	0.6371	2.7812
D21S11	21	0.8926	0.8781	0.0302	0.9698	0.8876	0.7702	4.4500
D7S820	7	0.7956	0.7607	0.0900	0.9100	0.8090	0.6158	2.6176
D18S51	11	0.8553	0.8334	0.0443	0.9557	0.8090	0.6158	2.6176
FGA	15	0.8690	0.8489	0.0408	0.9592	0.8202	0.6371	2.7812
D12S391	38	0.9323	0.9232	0.0173	0.9827	0.8539	0.7026	3.4231
PentaD	11	0.8556	0.8335	0.0453	0.9547	0.8539	0.7026	3.4231

Flanking sequence

locus	Nall	GD	PIC	PM	PD	Hobs	PE	TPI
TPOX	6	0.6046	0.5641	0.2382	0.7618	0.4944	0.1826	0.9889
D9S1122	12	0.8319	0.8043	0.0554	0.9446	0.7978	0.5949	2.4722
D17S1301	5	0.6648	0.6038	0.1668	0.8332	0.6517	0.3575	1.4355
D20S482	10	0.8068	0.7810	0.0648	0.9352	0.7528	0.5146	2.0227
D16S539	11	0.7546	0.7236	0.0946	0.9054	0.7303	0.4767	1.8542
D3S1358	19	0.8890	0.8732	0.0302	0.9698	0.8539	0.7026	3.4231
D4S2408	5	0.7562	0.7149	0.1034	0.8966	0.7191	0.4584	1.7800
D5S818	11	0.8184	0.7911	0.0688	0.9312	0.8202	0.6371	2.7812
D22S1045	7	0.7114	0.6618	0.1294	0.8706	0.7303	0.4767	1.8542
D10S1248	8	0.7660	0.7253	0.0968	0.9032	0.7303	0.4767	1.8542
CSF1PO	7	0.7086	0.6477	0.1569	0.8431	0.7528	0.5146	2.0227
TH01	7	0.7704	0.7300	0.0893	0.9107	0.7416	0.4955	1.9348
vWA	13	0.8227	0.7954	0.0638	0.9362	0.7978	0.5949	2.4722
D13S317	12	0.8735	0.8551	0.0383	0.9617	0.8539	0.7026	3.4231
D6S1043	10	0.7858	0.7521	0.0792	0.9208	0.7753	0.5540	2.2250
D8S1179	15	0.8932	0.8778	0.0312	0.9688	0.8427	0.6805	3.1786
D19S433	12	0.8520	0.8312	0.0453	0.9547	0.7753	0.5540	2.2250
D2S1338	29	0.9023	0.8913	0.0234	0.9766	0.8427	0.6805	3.1786
PentaE	15	0.9092	0.8962	0.0252	0.9748	0.7816	0.5654	2.2895
D2S441	15	0.7998	0.7695	0.0779	0.9221	0.7978	0.5949	2.4722
D1S1656	19	0.8958	0.8816	0.0276	0.9724	0.8202	0.6371	2.7812
D21S11	21	0.8926	0.8781	0.0302	0.9698	0.8876	0.7702	4.4500
D7S820	13	0.8670	0.8481	0.0463	0.9537	0.8764	0.7475	4.0455
D18S51	11	0.8553	0.8334	0.0443	0.9557	0.8090	0.6158	2.6176
FGA	15	0.8690	0.8489	0.0408	0.9592	0.8202	0.6371	2.7812
D12S391	38	0.9323	0.9232	0.0173	0.9827	0.8539	0.7026	3.4231
PentaD	11	0.8556	0.8335	0.0453	0.9547	0.8539	0.7026	3.4231

N: Number of alleles sampled, Nall: Number of different alleles observed, GD: Genetic Diversity or expected Heterozygosity, PIC: Polymorphism Information Content, PM: Random Match Probability, PD: Power of Discrimination, Hobs: observed heterozygosity, PE: Power of Exclusion, TPI: Typical Paternity Index. All calculated using STRAF (http://cmpg.unibe.ch/shiny/STRAF/)

Table S4: iiSNP forensic statistics (target SNP only & whole amplicon).

Targeted iiSNPs

locus	N	Nall	GD	PIC	PM	PD	Hobs	PE	TPI
rs1005533	178	2	0.5028	0.3750	0.3839	0.6161	0.5169	0.2027	1.0349
rs10092491	178	2	0.4206	0.3307	0.4172	0.5828	0.3708	0.0971	0.7946
rs1015250	178	2	0.3908	0.3131	0.4501	0.5499	0.3933	0.1099	0.8241
rs1024116	178	2	0.5028	0.3750	0.3577	0.6423	0.4607	0.1553	0.9271
rs1028528	178	2	0.4531	0.3490	0.3882	0.6118	0.3933	0.1099	0.8241
rs1031825	172	2	0.4333	0.3380	0.4135	0.5865	0.4186	0.1256	0.8600
rs10488710	178	2	0.4997	0.3734	0.4001	0.5999	0.5393	0.2243	1.0854
rs10495407	178	2	0.4631	0.3545	0.3804	0.6196	0.4045	0.1167	0.8396
rs1058083	178	2	0.4457	0.3450	0.4238	0.5762	0.4831	0.1732	0.9674
rs10773760	178	2	0.4988	0.3730	0.3943	0.6057	0.5281	0.2133	1.0595
rs10776839	178	2	0.4988	0.3730	0.4405	0.5595	0.5955	0.2855	1.2361
rs1109037	178	2	0.4866	0.3668	0.4910	0.5090	0.6404	0.3423	1.3906
rs1294331	178	2	0.5018	0.3745	0.3508	0.6492	0.4382	0.1389	0.8900
rs12997453	178	2	0.3504	0.2877	0.4859	0.5141	0.3596	0.0911	0.7807
rs13182883	178	2	0.4565	0.3509	0.3869	0.6131	0.4045	0.1167	0.8396
rs13218440	178	2	0.4866	0.3668	0.3832	0.6168	0.4831	0.1732	0.9674
rs1335873	178	2	0.4951	0.3712	0.3612	0.6388	0.4494	0.1470	0.9082
rs1336071	178	2	0.4866	0.3668	0.3660	0.6340	0.4382	0.1389	0.8900
rs1355366	178	2	0.4845	0.3657	0.3647	0.6353	0.4270	0.1312	0.8725
rs1357617	178	2	0.3855	0.3098	0.4501	0.5499	0.3371	0.0800	0.7542
rs1360288	178	2	0.4531	0.3490	0.3993	0.6007	0.4382	0.1389	0.8900
rs1382387	178	2	0.3743	0.3029	0.4617	0.5383	0.3146	0.0697	0.7295
rs1413212	178	2	0.4112	0.3253	0.4488	0.5512	0.4607	0.1553	0.9271
rs1454361	178	2	0.5005	0.3739	0.3521	0.6479	0.4382	0.1389	0.8900
rs1463729	178	2	0.5018	0.3745	0.3680	0.6320	0.4831	0.1732	0.9674
rs1490413	178	2	0.4663	0.3562	0.4266	0.5734	0.5281	0.2133	1.0595
rs1493232	178	2	0.4112	0.3253	0.4258	0.5742	0.3034	0.0649	0.7177
rs1498553	178	2	0.4904	0.3687	0.3700	0.6300	0.4607	0.1553	0.9271
rs1523537	178	2	0.4988	0.3730	0.4589	0.5411	0.6180	0.3130	1.3088
rs1528460	178	2	0.4692	0.3577	0.3869	0.6131	0.4494	0.1470	0.9082
rs159606	178	2	0.4418	0.3428	0.4016	0.5984	0.4045	0.1167	0.8396
rs1821380	178	2	0.4599	0.3528	0.4003	0.5997	0.4607	0.1553	0.9271
rs1886510	178	2	0.4631	0.3545	0.3859	0.6141	0.4270	0.1312	0.8725
rs1979255	178	2	0.4251	0.3333	0.4309	0.5691	0.4494	0.1470	0.9082
rs2040411	178	2	0.4921	0.3696	0.3572	0.6428	0.4270	0.1312	0.8725
rs2046361	178	2	0.4663	0.3562	0.3718	0.6282	0.3708	0.0971	0.7946
rs2056277	178	2	0.3908	0.3131	0.4612	0.5388	0.4382	0.1389	0.8900
rs2076848	178	2	0.4904	0.3687	0.3700	0.6300	0.4607	0.1553	0.9271
rs2107612	178	2	0.4748	0.3607	0.4001	0.5999	0.4944	0.1826	0.9889
rs2111980	178	2	0.4631	0.3545	0.4016	0.5984	0.4719	0.1641	0.9468
rs214955	178	2	0.4866	0.3668	0.3832	0.6168	0.4831	0.1732	0.9674
rs221956	178	2	0.4418	0.3428	0.4071	0.5929	0.4270	0.1312	0.8725
rs2269355	178	2	0.4965	0.3718	0.3561	0.6439	0.4382	0.1389	0.8900
rs2342747	178	2	0.3566	0.2917	0.4829	0.5171	0.2809	0.0560	0.6953
rs2399332	178	2	0.4599	0.3528	0.4468	0.5532	0.5506	0.2357	1.1125
rs251934	178	2	0.4845	0.3657	0.4021	0.5979	0.5169	0.2027	1.0349
rs279844	178	2	0.4337	0.3383	0.4223	0.5777	0.4494	0.1470	0.9082
rs2830795	178	2	0.4378	0.3406	0.4223	0.5777	0.4607	0.1553	0.9271
rs2831700	178	2	0.4845	0.3657	0.3804	0.6196	0.4719	0.1641	0.9468
rs321198	178	2	0.4866	0.3668	0.3660	0.6340	0.4382	0.1389	0.8900
rs338882	178	2	0.5028	0.3750	0.3723	0.6277	0.4944	0.1826	0.9889
rs354439	178	2	0.4977	0.3724	0.3516	0.6484	0.4270	0.1312	0.8725
rs3780962	178	2	0.4951	0.3712	0.3915	0.6085	0.5169	0.2027	1.0349
rs430046	178	2	0.5028	0.3750	0.3410	0.6590	0.4045	0.1167	0.8396
rs4364205	178	2	0.4885	0.3678	0.3763	0.6237	0.4719	0.1641	0.9468
rs445251	178	2	0.4294	0.3359	0.4165	0.5835	0.4157	0.1238	0.8558
rs4530059	178	2	0.4823	0.3646	0.3875	0.6125	0.4831	0.1732	0.9674
rs4606077	178	2	0.4378	0.3406	0.4034	0.5966	0.3933	0.1099	0.8241
rs560681	178	2	0.4904	0.3687	0.3794	0.6206	0.4831	0.1732	0.9674
rs576261	178	2	0.4531	0.3490	0.4071	0.5929	0.4607	0.1553	0.9271
rs6444724	178	2	0.4748	0.3607	0.4001	0.5999	0.4944	0.1826	0.9889
rs6811238	178	2	0.4965	0.3718	0.3733	0.6267	0.4831	0.1732	0.9674
rs6955448	178	2	0.4494	0.3470	0.4152	0.5848	0.4719	0.1641	0.9468
rs7041158	178	2	0.4721	0.3593	0.3660	0.6340	0.3708	0.0971	0.7946
rs717302	178	2	0.4921	0.3696	0.3728	0.6272	0.4719	0.1641	0.9468
rs722098	178	2	0.3961	0.3163	0.4395	0.5605	0.3371	0.0800	0.7542
rs722290	178	2	0.4692	0.3577	0.3869	0.6131	0.4494	0.1470	0.9082
rs727811	178	2	0.5005	0.3739	0.3458	0.6542	0.4157	0.1238	0.8558
rs729172	178	2	0.4418	0.3428	0.4071	0.5929	0.4270	0.1312	0.8725
rs733164	178	2	0.4721	0.3593	0.3976	0.6024	0.4831	0.1732	0.9674
rs735155	178	2	0.4721	0.3593	0.4084	0.5916	0.5056	0.1925	1.0114
rs737681	178	2	0.4997	0.3734	0.3652	0.6348	0.4719	0.1641	0.9468
rs740598	178	2	0.5028	0.3750	0.3723	0.6277	0.4944	0.1826	0.9889
rs740910	178	2	0.4251	0.3333	0.4395	0.5605	0.4719	0.1641	0.9468
rs763869	178	2	0.4904	0.3687	0.4319	0.5681	0.5730	0.2598	1.1711
rs8037429	178	2	0.4951	0.3712	0.4046	0.5954	0.5393	0.2243	1.0854
rs8078417	178	2	0.4823	0.3646	0.3703	0.6297	0.4382	0.1389	0.8900
rs826472	178	2	0.4337	0.3383	0.4410	0.5590	0.4944	0.1826	0.9889
rs873196	178	2	0.4159	0.3281	0.4208	0.5792	0.3596	0.0911	0.7807
rs876724	178	2	0.4378	0.3406	0.4549	0.5451	0.5281	0.2133	1.0595
rs891700	178	2	0.4921	0.3696	0.4077	0.5923	0.5393	0.2243	1.0854
rs901398	178	2	0.4159	0.3281	0.4273	0.5727	0.4045	0.1167	0.8396
rs907100	178	2	0.4774	0.3621	0.4294	0.5706	0.5506	0.2357	1.1125
rs914165	178	2	0.4965	0.3718	0.3842	0.6158	0.5056	0.1925	1.0114
rs917118	178	2	0.4063	0.3224	0.4496	0.5504	0.4494	0.1470	0.9082
rs938283	178	2	0.3312	0.2751	0.5061	0.4939	0.3708	0.0971	0.7946
rs964681	178	2	0.4531	0.3490	0.4071	0.5929	0.4607	0.1553	0.9271
rs987640	178	2	0.5012	0.3742	0.4132	0.5868	0.5618	0.2475	1.1410
rs9905977	178	2	0.4866	0.3668	0.5124	0.4876	0.6629	0.3733	1.4833
rs993934	178	2	0.4951	0.3712	0.3698	0.6302	0.4719	0.1641	0.9468
rs9951171	178	2	0.4904	0.3687	0.3622	0.6378	0.4382	0.1389	0.8900

Targeted and Flanking SNPs

locus	Nall	GD	PIC	PM	PD	Hobs	PE	TPI
rs1005533	2	0.5028	0.3750	0.3839	0.6161	0.5169	0.2027	1.0349
rs10092491	2	0.4206	0.3307	0.4172	0.5828	0.3708	0.0971	0.7946
rs1015250	4	0.4416	0.3859	0.3715	0.6285	0.3933	0.1099	0.8241
rs1024116	2	0.5028	0.3750	0.3577	0.6423	0.4607	0.1553	0.9271
rs1028528	2	0.4531	0.3490	0.3882	0.6118	0.3933	0.1099	0.8241
rs1031825	2	0.4333	0.3380	0.4135	0.5865	0.4186	0.1256	0.8600
rs10488710	2	0.4997	0.3734	0.4001	0.5999	0.5393	0.2243	1.0854
rs10495407	2	0.4631	0.3545	0.3804	0.6196	0.4045	0.1167	0.8396
rs1058083	2	0.4457	0.3450	0.4238	0.5762	0.4831	0.1732	0.9674
rs10773760	2	0.4988	0.3730	0.3943	0.6057	0.5281	0.2133	1.0595
rs10776839	3	0.6157	0.5398	0.2238	0.7762	0.5955	0.2855	1.2361
rs1109037	6	0.6931	0.6430	0.1433	0.8567	0.6404	0.3423	1.3906
rs1294331	3	0.5123	0.3906	0.3453	0.6547	0.4382	0.1389	0.8900
rs12997453	3	0.4075	0.3640	0.4109	0.5891	0.3596	0.0911	0.7807
rs13182883	3	0.4638	0.3599	0.3781	0.6219	0.4045	0.1167	0.8396
rs13218440	2	0.4866	0.3668	0.3832	0.6168	0.4831	0.1732	0.9674
rs1335873	2	0.4951	0.3712	0.3612	0.6388	0.4494	0.1470	0.9082
rs1336071	3	0.4977	0.3831	0.3471	0.6529	0.4382	0.1389	0.8900
rs1355366	2	0.4845	0.3657	0.3647	0.6353	0.4270	0.1312	0.8725
rs1357617	3	0.3883	0.3158	0.4427	0.5573	0.3371	0.0800	0.7542
rs1360288	2	0.4531	0.3490	0.3993	0.6007	0.4382	0.1389	0.8900
rs1382387	2	0.3743	0.3029	0.4617	0.5383	0.3146	0.0697	0.7295
rs1413212	2	0.4112	0.3253	0.4488	0.5512	0.4607	0.1553	0.9271
rs1454361	2	0.5005	0.3739	0.3521	0.6479	0.4382	0.1389	0.8900
rs1463729	3	0.5181	0.3987	0.3372	0.6628	0.4831	0.1732	0.9674
rs1490413	3	0.4703	0.3634	0.4150	0.5850	0.5281	0.2133	1.0595
rs1493232	2	0.4112	0.3253	0.4258	0.5742	0.3034	0.0649	0.7177
rs1498553	2	0.4904	0.3687	0.3700	0.6300	0.4607	0.1553	0.9271
rs1523537	2	0.4988	0.3730	0.4589	0.5411	0.6180	0.3130	1.3088
rs1528460	2	0.4692	0.3577	0.3869	0.6131	0.4494	0.1470	0.9082
rs159606	2	0.4418	0.3428	0.4016	0.5984	0.4045	0.1167	0.8396
rs1821380	3	0.4671	0.3617	0.3902	0.6098	0.4607	0.1553	0.9271
rs1886510	2	0.4631	0.3545	0.3859	0.6141	0.4270	0.1312	0.8725
rs1979255	2	0.4251	0.3333	0.4309	0.5691	0.4494	0.1470	0.9082
rs2040411	2	0.4921	0.3696	0.3572	0.6428	0.4270	0.1312	0.8725
rs2046361	3	0.4881	0.3874	0.3463	0.6537	0.3708	0.0971	0.7946
rs2056277	3	0.4479	0.3843	0.3832	0.6168	0.4382	0.1389	0.8900
rs2076848	4	0.5229	0.4159	0.3142	0.6858	0.4607	0.1553	0.9271
rs2107612	2	0.4748	0.3607	0.4001	0.5999	0.4944	0.1826	0.9889
rs2111980	2	0.4631	0.3545	0.4016	0.5984	0.4719	0.1641	0.9468
rs214955	3	0.5188	0.4132	0.3354	0.6646	0.4831	0.1732	0.9674
rs221956	2	0.4418	0.3428	0.4071	0.5929	0.4270	0.1312	0.8725
rs2269355	2	0.4965	0.3718	0.3561	0.6439	0.4382	0.1389	0.8900
rs2342747	2	0.3566	0.2917	0.4829	0.5171	0.2809	0.0560	0.6953
rs2399332	5	0.4858	0.3912	0.3887	0.6113	0.5506	0.2357	1.1125
rs251934	2	0.4845	0.3657	0.4021	0.5979	0.5169	0.2027	1.0349
rs279844	2	0.4337	0.3383	0.4223	0.5777	0.4494	0.1470	0.9082
rs2830795	4	0.5032	0.4412	0.2998	0.7002	0.4607	0.1553	0.9271
rs2831700	2	0.4845	0.3657	0.3804	0.6196	0.4719	0.1641	0.9468
rs321198	2	0.4866	0.3668	0.3660	0.6340	0.4382	0.1389	0.8900
rs338882	3	0.5084	0.3833	0.3614	0.6386	0.4944	0.1826	0.9889
rs354439	4	0.5076	0.3883	0.3332	0.6668	0.4270	0.1312	0.8725
rs3780962	2	0.4951	0.3712	0.3915	0.6085	0.5169	0.2027	1.0349
rs430046	2	0.5028	0.3750	0.3410	0.6590	0.4045	0.1167	0.8396
rs4364205	2	0.4885	0.3678	0.3763	0.6237	0.4719	0.1641	0.9468
rs445251	3	0.4372	0.3450	0.4074	0.5926	0.4157	0.1238	0.8558
rs4530059	3	0.5063	0.3974	0.3473	0.6527	0.4831	0.1732	0.9674
rs4606077	3	0.4970	0.4245	0.3266	0.6734	0.3933	0.1099	0.8241
rs560681	3	0.4997	0.3841	0.3587	0.6413	0.4831	0.1732	0.9674
rs576261	2	0.4531	0.3490	0.4071	0.5929	0.4607	0.1553	0.9271
rs6444724	2	0.4748	0.3607	0.4001	0.5999	0.4944	0.1826	0.9889
rs6811238	2	0.4965	0.3718	0.3733	0.6267	0.4831	0.1732	0.9674
rs6955448	2	0.4494	0.3470	0.4152	0.5848	0.4719	0.1641	0.9468
rs7041158	2	0.4721	0.3593	0.3660	0.6340	0.3708	0.0971	0.7946
rs717302	3	0.4985	0.3783	0.3625	0.6375	0.4719	0.1641	0.9468
rs722098	2	0.3961	0.3163	0.4395	0.5605	0.3371	0.0800	0.7542
rs722290	2	0.4692	0.3577	0.3869	0.6131	0.4494	0.1470	0.9082
rs727811	3	0.5065	0.3824	0.3367	0.6633	0.4157	0.1238	0.8558
rs729172	3	0.4454	0.3497	0.3978	0.6022	0.4270	0.1312	0.8725
rs733164	2	0.4721	0.3593	0.3976	0.6024	0.4831	0.1732	0.9674
rs735155	2	0.4721	0.3593	0.4084	0.5916	0.5056	0.1925	1.0114
rs737681	2	0.4997	0.3734	0.3652	0.6348	0.4719	0.1641	0.9468
rs740598	2	0.5028	0.3750	0.3723	0.6277	0.4944	0.1826	0.9889
rs740910	3	0.4727	0.4128	0.3342	0.6658	0.4719	0.1641	0.9468
rs763869	2	0.4904	0.3687	0.4319	0.5681	0.5730	0.2598	1.1711
rs8037429	2	0.4951	0.3712	0.4046	0.5954	0.5393	0.2243	1.0854
rs8078417	2	0.4823	0.3646	0.3703	0.6297	0.4382	0.1389	0.8900
rs826472	3	0.4481	0.3602	0.4094	0.5906	0.4944	0.1826	0.9889
rs873196	2	0.4159	0.3281	0.4208	0.5792	0.3596	0.0911	0.7807
rs876724	5	0.6330	0.5664	0.2044	0.7956	0.5281	0.2133	1.0595
rs891700	4	0.5016	0.3852	0.3842	0.6158	0.5393	0.2243	1.0854
rs901398	2	0.4159	0.3281	0.4273	0.5727	0.4045	0.1167	0.8396
rs907100	3	0.5947	0.5252	0.2294	0.7706	0.5506	0.2357	1.1125
rs914165	3	0.5088	0.3888	0.3625	0.6375	0.5056	0.1925	1.0114
rs917118	2	0.4063	0.3224	0.4496	0.5504	0.4494	0.1470	0.9082
rs938283	2	0.3312	0.2751	0.5061	0.4939	0.3708	0.0971	0.7946
rs964681	2	0.4531	0.3490	0.4071	0.5929	0.4607	0.1553	0.9271
rs987640	3	0.5546	0.4533	0.3003	0.6997	0.5618	0.2475	1.1410
rs9905977	4	0.6577	0.5823	0.1958	0.8042	0.6629	0.3733	1.4833
rs993934	2	0.4951	0.3712	0.3698	0.6302	0.4719	0.1641	0.9468
rs9951171	2	0.4904	0.3687	0.3622	0.6378	0.4382	0.1389	0.8900

N: Number of alleles sampled, Nall: Number of different alleles observed, GD: Genetic Diversity or expected Heterozygosity, PIC: Polymorphism Information Content, PM: Random Match Probability, PD:Power of Discrimination, Hobs: observed heterozygosity, PE: Power of Exclusion, TPI: Typical Paternity Index. All calculated using STRAF (http://cmpg.unibe.ch/shiny/STRAF/)

Table S5: Deviation from expected heterozygosity under Hardy Weinberg equilibrium at each of the autosomal STR loci.

Allele repeat length

Locus	n	Obs. Het.	Exp. Het.	P-value	s.d.	Obs.-Exp.
CSF1PO	89	0.7416	0.6926	0.6930	0.0005	0.0490
D10S1248	89	0.7303	0.7660	0.1771	0.0003	-0.0357
D12S391	89	0.8427	0.8796	0.5453	0.0004	-0.0369
D13S317	89	0.7753	0.7788	0.8523	0.0004	-0.0036
D16S539	89	0.7079	0.7266	0.6363	0.0004	-0.0187
D17S1301	89	0.6517	0.6648	0.7951	0.0004	-0.0131
D18S51	89	0.8090	0.8553	0.5284	0.0004	-0.0463
D19S433	89	0.7753	0.8502	0.3043	0.0004	-0.0749
D1S1656	89	0.7865	0.8694	0.2991	0.0004	-0.0829
D20S482	89	0.6966	0.6986	0.9019	0.0003	-0.0020
D21S11	89	0.7978	0.8138	0.1240	0.0002	-0.0161
D22S1045	89	0.7303	0.7065	0.8808	0.0003	0.0238
D2S1338	89	0.7753	0.8553	0.6928	0.0003	-0.0801
D2S441	89	0.7865	0.7677	0.2196	0.0004	0.0189
D3S1358	89	0.7079	0.7708	0.1985	0.0004	-0.0629
D4S2408	89	0.7191	0.7562	0.2979	0.0005	-0.0371
D5S818	89	0.7191	0.7269	0.6178	0.0004	-0.0078
D6S1043	89	0.7753	0.7858	0.8351	0.0004	-0.0105
D7S820	89	0.8090	0.7956	0.1191	0.0003	0.0134
D8S1179	89	0.7753	0.8421	0.4247	0.0005	-0.0669
D9S1122	89	0.6405	0.6926	0.7315	0.0005	-0.0521
FGA	89	0.8202	0.8685	0.3625	0.0004	-0.0483
PentaD	89	0.8539	0.8556	0.5661	0.0004	-0.0017
PentaE	87	0.7816	0.9092	0.0891	0.0002	-0.1276
TH01	89	0.7416	0.7674	0.9739	0.0001	-0.0258
TPOX	89	0.4944	0.6046	0.0000	0.0000	-0.1102
vWA	89	0.7528	0.7844	0.3448	0.0004	-0.0316

Repeat region sequence variation

Locus	n	Obs. Het.	Exp. Het.	P-value	s.d.	Obs.-Exp.
CSF1PO	89	0.7528	0.7086	0.6331	0.0004	0.0443
D10S1248	89	0.7303	0.7660	0.1750	0.0004	-0.0357
D12S391	89	0.8539	0.9323	0.1584	0.0001	-0.0784
D13S317	89	0.8539	0.8736	0.5957	0.0003	-0.0196
D16S539	89	0.7079	0.7266	0.6489	0.0005	-0.0187
D17S1301	89	0.6517	0.6648	0.7935	0.0004	-0.0131
D18S51	89	0.8090	0.8553	0.5301	0.0005	-0.0463
D19S433	89	0.7753	0.8520	0.3043	0.0004	-0.0767
D1S1656	89	0.8202	0.8955	0.3410	0.0003	-0.0752
D20S482	89	0.6966	0.6986	0.9014	0.0003	-0.0020
D21S11	89	0.8876	0.8926	0.4373	0.0003	-0.0050
D22S1045	89	0.7303	0.7065	0.8820	0.0003	0.0238
D2S1338	89	0.8427	0.9023	0.4320	0.0002	-0.0596
D2S441	89	0.7865	0.7812	0.3738	0.0004	0.0053
D3S1358	89	0.8539	0.8890	0.6302	0.0003	-0.0350
D4S2408	89	0.7191	0.7562	0.3038	0.0004	-0.0371
D5S818	89	0.8202	0.8185	0.6368	0.0004	0.0018
D6S1043	89	0.7753	0.7858	0.8379	0.0004	-0.0105
D7S820	89	0.8090	0.7956	0.1175	0.0003	0.0134
D8S1179	89	0.8427	0.8932	0.3324	0.0003	-0.0505
D9S1122	89	0.7978	0.8319	0.7697	0.0003	-0.0342
FGA	89	0.8202	0.8690	0.2694	0.0002	-0.0488
PentaD	89	0.8539	0.8556	0.5791	0.0004	-0.0017
PentaE	87	0.7816	0.9092	0.0878	0.0003	-0.1276
TH01	89	0.7416	0.7704	0.9483	0.0002	-0.0288
TPOX	89	0.4944	0.6046	0.0000	0.0000	-0.1102
vWA	89	0.7978	0.8227	0.3361	0.0003	-0.0250

All sequence variation (repeat region and flanking)

Locus	n	Obs. Het.	Exp. Het.	P-value	s.d.	Obs.-Exp.
CSF1PO	89	0.7528	0.7086	0.6370	0.0005	0.0443
D10S1248	89	0.7303	0.7660	0.1816	0.0003	-0.0357
D12S391	89	0.8539	0.9323	0.1828	0.0002	-0.0784
D13S317	89	0.8539	0.8736	0.5994	0.0004	-0.0196
D16S539	89	0.7303	0.7546	0.4970	0.0004	-0.0243
D17S1301	89	0.6517	0.6648	0.7928	0.0004	-0.0131
D18S51	89	0.8090	0.8553	0.5310	0.0004	-0.0463
D19S433	89	0.7753	0.8520	0.3123	0.0004	-0.0767
D1S1656	89	0.8202	0.8958	0.3102	0.0002	-0.0756
D20S482	89	0.7528	0.8068	0.5958	0.0004	-0.0540
D21S11	89	0.8876	0.8926	0.4997	0.0002	-0.0050
D22S1045	89	0.7303	0.7114	0.8752	0.0003	0.0190
D2S1338	89	0.8427	0.9023	0.4778	0.0002	-0.0596
D2S441	89	0.7978	0.7998	0.3034	0.0003	-0.0020
D3S1358	89	0.8539	0.8890	0.6257	0.0003	-0.0350
D4S2408	89	0.7191	0.7562	0.2974	0.0004	-0.0371
D5S818	89	0.8202	0.8185	0.6288	0.0003	0.0018
D6S1043	89	0.7753	0.7858	0.8332	0.0004	-0.0105
D7S820	89	0.8764	0.8670	0.3712	0.0004	0.0094
D8S1179	89	0.8427	0.8932	0.3353	0.0004	-0.0505
D9S1122	89	0.7978	0.8319	0.7682	0.0004	-0.0342
FGA	89	0.8202	0.8690	0.2807	0.0004	-0.0488
PentaD	89	0.8539	0.8556	0.5831	0.0003	-0.0017
PentaE	87	0.7816	0.9092	0.1043	0.0002	-0.1276
TH01	89	0.7416	0.7704	0.9472	0.0002	-0.0288
TPOX	89	0.4944	0.6046	0.0000	0.0000	-0.1102
vWA	89	0.7978	0.8227	0.3103	0.0003	-0.0250

n: number of samples; Obs.Het.: observed heterozygosity; Exp.Het.: expected heterozygosity; s.d.: standard deviation

Table S6: Deviation from expected heterozygosity under Hardy Weinberg equilibrium at each of the autosomal iiSNP loci.

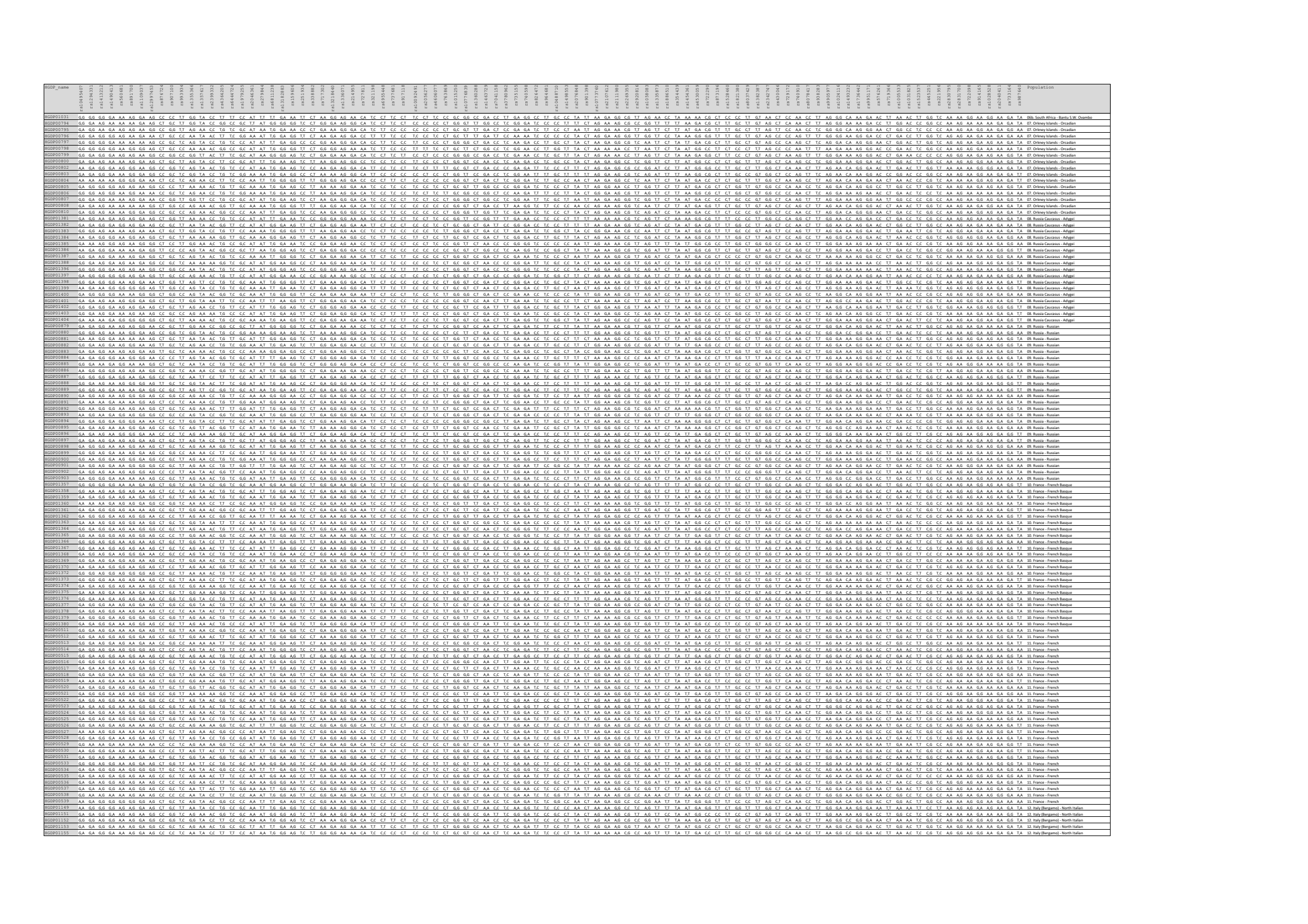
Locus	n	Obs.Het.	Exp.Het.	P-value	s.d.	Obs.-Exp.
rs1005533	89	0.5169	0.5028	0.8342	0.0004	0.014
rs10092491	89	0.3708	0.4206	0.3112	0.0005	-0.050
rs1015250	89	0.3933	0.4416	0.2865	0.0005	-0.048
rs1024116	89	0.4607	0.5028	0.5250	0.0005	-0.042
rs1028528	89	0.3933	0.4531	0.2420	0.0004	-0.060
rs1031825	86	0.4186	0.4333	0.8045	0.0004	-0.015
rs10488710	89	0.5393	0.4997	0.5235	0.0005	0.040
rs10495407	89	0.4045	0.4632	0.2525	0.0004	-0.059
rs1058083	89	0.4832	0.4457	0.4789	0.0005	0.037
rs10773760	89	0.5281	0.4988	0.6692	0.0005	0.029
rs10776839	89	0.5955	0.6157	0.0991	0.0003	-0.020
rs1109037	89	0.6405	0.6931	0.3464	0.0005	-0.053
rs1294331	89	0.4382	0.5124	0.0041	0.0001	-0.074
rs12997453	89	0.3596	0.4075	0.1511	0.0004	-0.048
rs13182883	89	0.4045	0.4639	0.1519	0.0004	-0.059
rs13218440	89	0.4832	0.4866	1.0000	0.0000	-0.003
rs1335873	89	0.4494	0.4951	0.3965	0.0005	-0.046
rs1336071	89	0.4382	0.4977	0.4307	0.0005	-0.059
rs1355366	89	0.4270	0.4845	0.2787	0.0005	-0.058
rs1357617	89	0.3371	0.3883	0.4515	0.0005	-0.051
rs1360288	89	0.4382	0.4531	0.8161	0.0004	-0.015
rs1382387	89	0.3146	0.3743	0.1564	0.0004	-0.060
rs1413212	89	0.4607	0.4112	0.3064	0.0005	0.050
rs1454361	89	0.4382	0.5005	0.2904	0.0004	-0.062
rs1463729	89	0.4832	0.5181	0.6435	0.0005	-0.035
rs1490413	89	0.5281	0.4703	0.4624	0.0005	0.058
rs1493232	89	0.3034	0.4112	0.0191	0.0001	-0.108
rs1498553	89	0.4607	0.4904	0.6641	0.0005	-0.030
rs1523537	89	0.6180	0.4988	0.0330	0.0002	0.119
rs1528460	89	0.4494	0.4692	0.8204	0.0004	-0.020
rs159606	89	0.4045	0.4418	0.4710	0.0005	-0.037
rs1821380	89	0.4607	0.4672	0.5149	0.0005	-0.006
rs1886510	89	0.4270	0.4632	0.4935	0.0005	-0.036
rs1979255	89	0.4494	0.4251	0.6247	0.0005	0.024
rs2040411	89	0.4270	0.4921	0.2754	0.0004	-0.065
rs2046361	89	0.3708	0.4881	0.0039	0.0001	-0.117
rs2056277	89	0.4382	0.4479	0.1443	0.0004	-0.010
rs2076848	89	0.4607	0.5229	0.4323	0.0004	-0.062
rs2107612	89	0.4944	0.4748	0.8228	0.0004	0.020
rs2111980	89	0.4719	0.4632	1.0000	0.0000	0.009
rs214955	89	0.4832	0.5188	0.1258	0.0003	-0.036
rs221956	89	0.4270	0.4418	0.8102	0.0004	-0.015
rs2269355	89	0.4382	0.4965	0.2912	0.0005	-0.058
rs2342747	89	0.2809	0.3566	0.0683	0.0003	-0.076
rs2399332	89	0.5506	0.4858	0.4584	0.0005	0.065
rs251934	89	0.5169	0.4845	0.6592	0.0004	0.032
rs279844	89	0.4494	0.4337	0.8087	0.0004	0.016

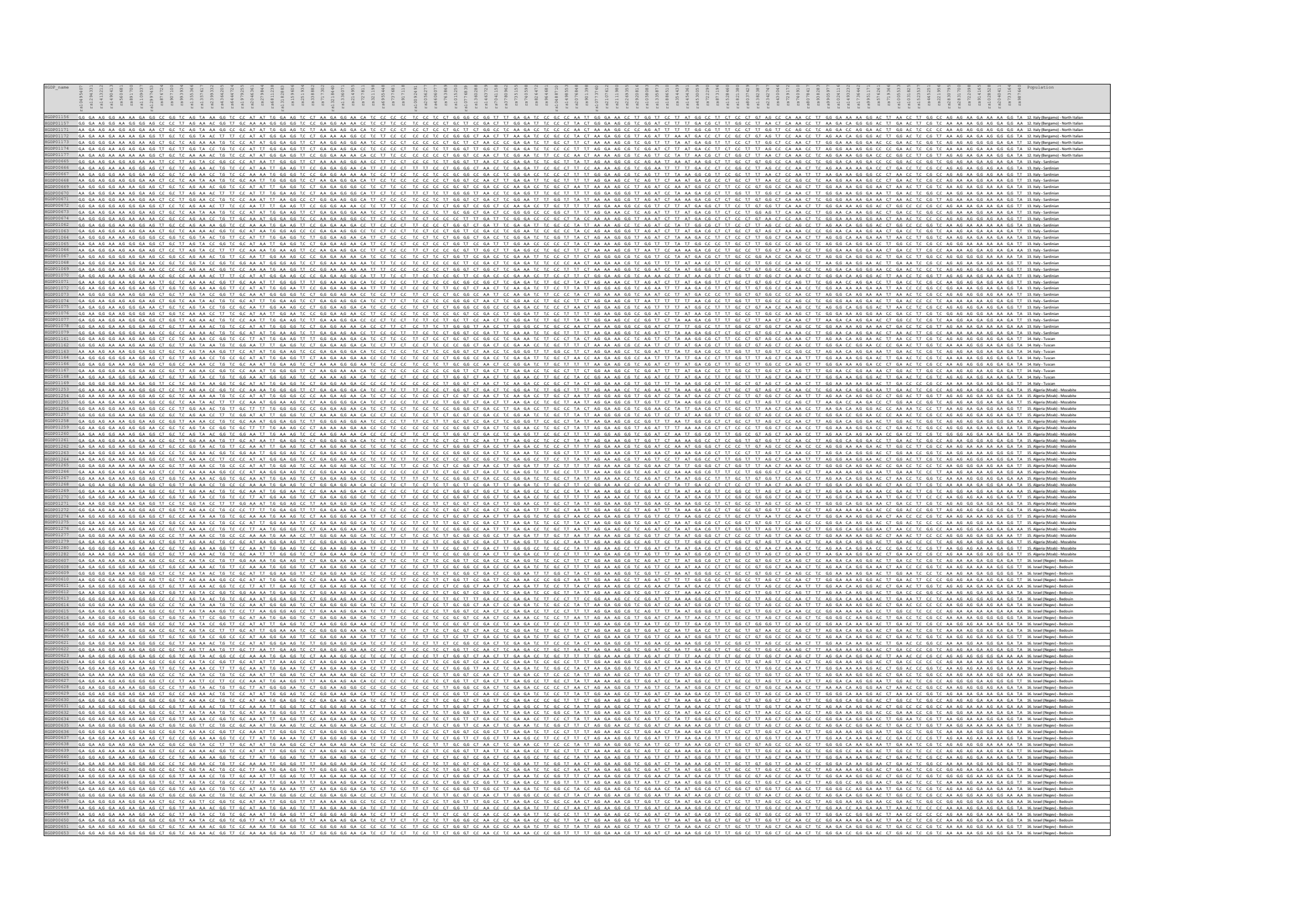
Locus	n	Obs.Het.	Exp.Het.	P-value	s.d.	Obs.-Exp.
rs2830795	89	0.4607	0.5032	0.5043	0.0005	-0.043
rs2831700	89	0.4719	0.4845	0.8283	0.0004	-0.013
rs321198	89	0.4382	0.4866	0.3848	0.0005	-0.048
rs338882	89	0.4944	0.5084	0.8324	0.0004	-0.014
rs354439	89	0.4270	0.5077	0.1528	0.0003	-0.081
rs3780962	89	0.5169	0.4951	0.8290	0.0004	0.022
rs430046	89	0.4045	0.5028	0.0886	0.0003	-0.098
rs4364205	89	0.4719	0.4885	0.8276	0.0004	-0.017
rs445251	89	0.4157	0.4372	0.3424	0.0005	-0.021
rs4530059	89	0.4832	0.5063	0.4195	0.0005	-0.023
rs4606077	89	0.3933	0.4970	0.0547	0.0002	-0.104
rs560681	89	0.4832	0.4997	0.6380	0.0005	-0.017
rs576261	89	0.4607	0.4531	1.0000	0.0000	0.008
rs6444724	89	0.4944	0.4748	0.8223	0.0004	0.020
rs6811238	89	0.4832	0.4965	0.8320	0.0004	-0.013
rs6955448	89	0.4719	0.4494	0.8130	0.0004	0.022
rs7041158	89	0.3708	0.4721	0.0682	0.0003	-0.101
rs717302	89	0.4719	0.4985	0.5074	0.0005	-0.027
rs722098	89	0.3371	0.3961	0.1804	0.0004	-0.059
rs722290	89	0.4494	0.4692	0.8206	0.0004	-0.020
rs727811	89	0.4157	0.5065	0.0931	0.0003	-0.091
rs729172	89	0.4270	0.4454	0.8678	0.0003	-0.018
rs733164	89	0.4832	0.4721	1.0000	0.0000	0.011
rs735155	89	0.5056	0.4721	0.6508	0.0005	0.034
rs737681	89	0.4719	0.4997	0.6708	0.0005	-0.028
rs740598	89	0.4944	0.5028	1.0000	0.0000	-0.008
rs740910	89	0.4719	0.4727	0.0845	0.0003	-0.001
rs763869	89	0.5730	0.4904	0.1293	0.0003	0.083
rs8037429	89	0.5393	0.4951	0.5167	0.0005	0.044
rs8078417	89	0.4382	0.4823	0.5062	0.0005	-0.044
rs826472	89	0.4944	0.4481	0.5818	0.0005	0.046
rs873196	89	0.3596	0.4159	0.2081	0.0004	-0.056
rs876724	89	0.5281	0.6330	0.0289	0.0002	-0.105
rs891700	89	0.5393	0.5016	0.8360	0.0004	0.038
rs901398	89	0.4045	0.4159	0.8013	0.0004	-0.011
rs907100	89	0.5506	0.5947	0.7155	0.0005	-0.044
rs914165	89	0.5056	0.5088	0.4172	0.0005	-0.003
rs917118	89	0.4494	0.4063	0.4317	0.0005	0.043
rs938283	89	0.3708	0.3312	0.3427	0.0005	0.040
rs964681	89	0.4607	0.4531	1.0000	0.0000	0.008
rs987640	89	0.5618	0.5546	0.3155	0.0005	0.007
rs9905977	89	0.6629	0.6577	0.9304	0.0003	0.005
rs993934	89	0.4719	0.4951	0.6725	0.0005	-0.023
rs9951171	89	0.4382	0.4904	0.3844	0.0005	-0.052

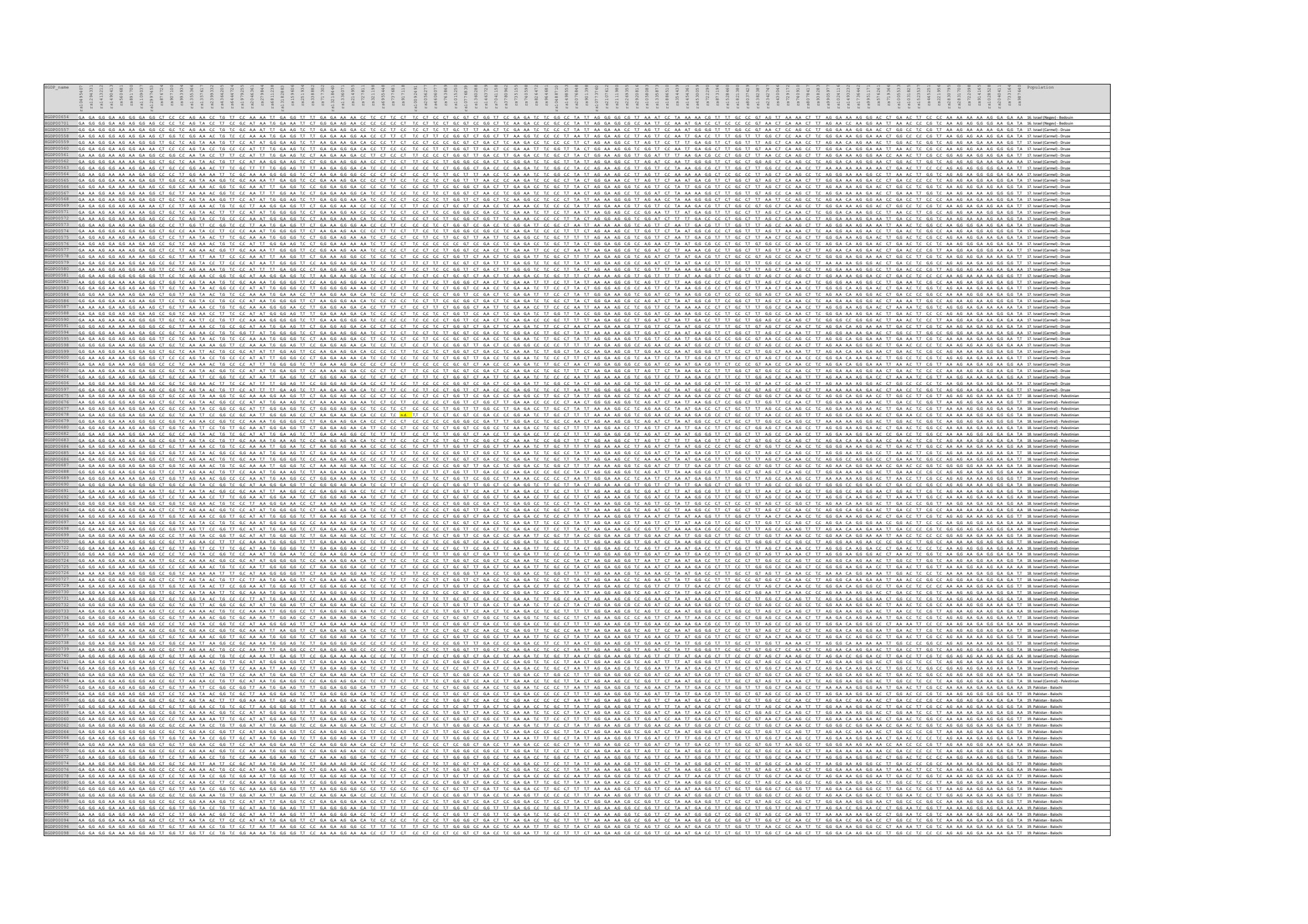
n: number of samples; Obs.Het.: observed heterozygosity; Exp.Het.: expected heterozygosity; s.d.: standard deviation

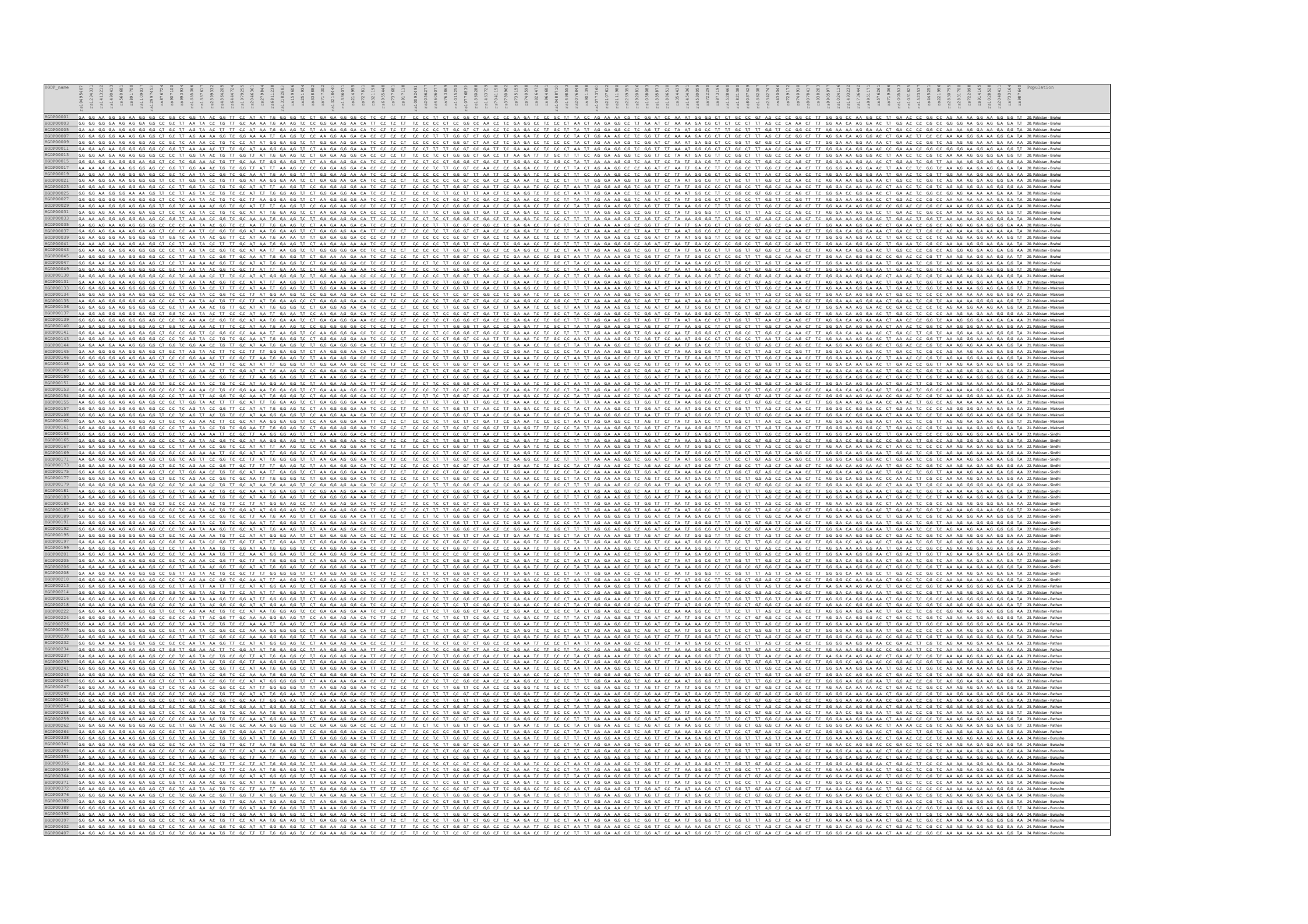
Table S7: HGDP iiSNP genotypes

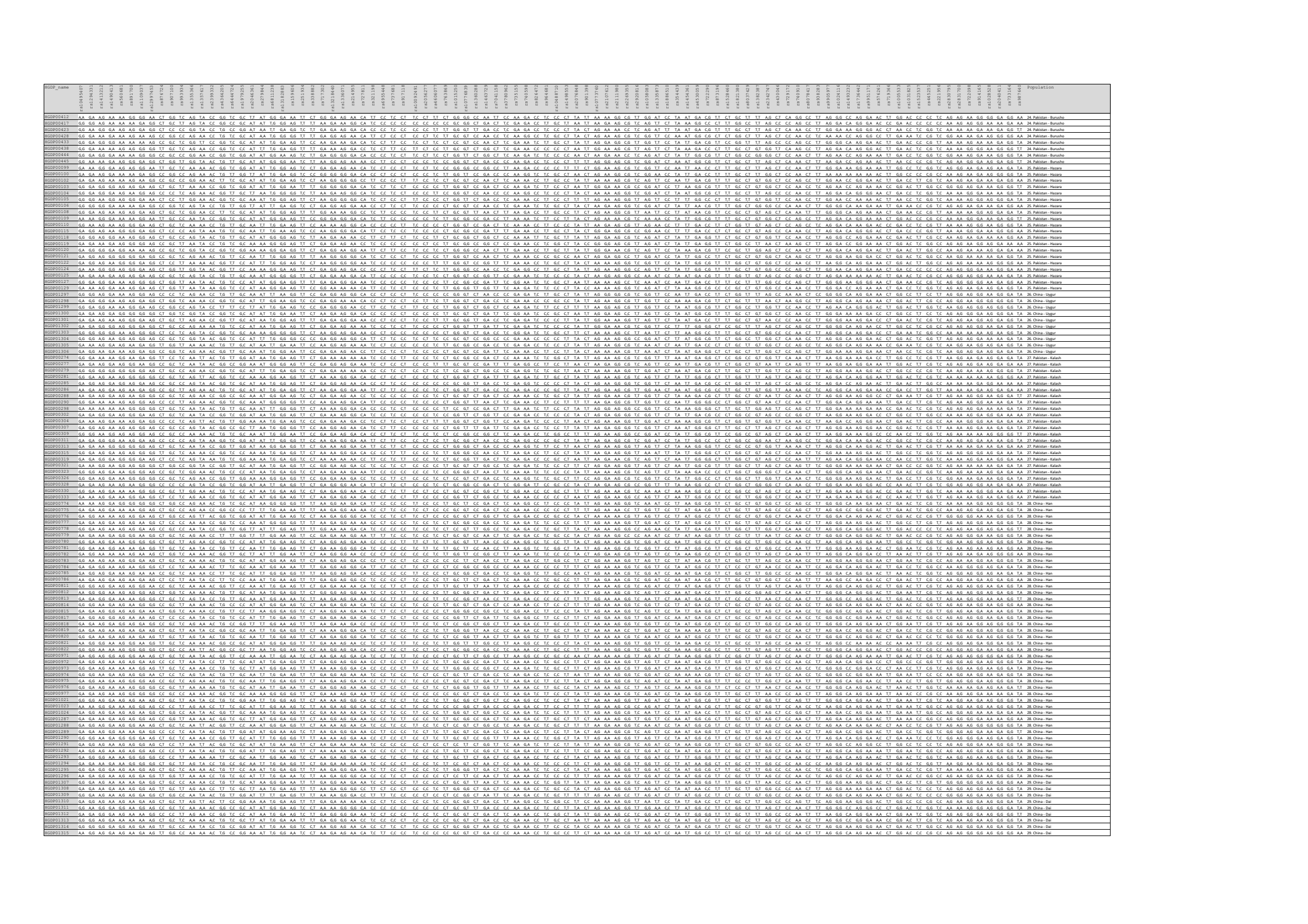
HGDP_name	rs… (SNP genotypes)	Population
HGDP01405	[illegible]	01. Kenya - Bantu N.E.
HGDP01406	[illegible]	01. Kenya - Bantu N.E.
HGDP01408	[illegible]	01. Kenya - Bantu N.E.
HGDP01411	[illegible]	01. Kenya - Bantu N.E.
HGDP01412	[illegible]	01. Kenya - Bantu N.E.
HGDP01414	[illegible]	01. Kenya - Bantu N.E.
HGDP01415	[illegible]	01. Kenya - Bantu N.E.
HGDP01416	[illegible]	01. Kenya - Bantu N.E.
HGDP01417	[illegible]	01. Kenya - Bantu N.E.
HGDP01418	[illegible]	01. Kenya - Bantu N.E.
HGDP01419	[illegible]	01. Kenya - Bantu N.E.
HGDP01413	[illegible]	01. Kenya - Bantu N.E.
HGDP00904	[illegible]	02. Senegal - Mandenka
HGDP00905	[illegible]	02. Senegal - Mandenka
HGDP00906	[illegible]	02. Senegal - Mandenka
HGDP00907	[illegible]	02. Senegal - Mandenka
HGDP00908	[illegible]	02. Senegal - Mandenka
HGDP00909	[illegible]	02. Senegal - Mandenka
HGDP00910	[illegible]	02. Senegal - Mandenka
HGDP00911	[illegible]	02. Senegal - Mandenka
HGDP00912	[illegible]	02. Senegal - Mandenka
HGDP00913	[illegible]	02. Senegal - Mandenka
HGDP00914	[illegible]	02. Senegal - Mandenka
HGDP00915	[illegible]	02. Senegal - Mandenka
HGDP00916	[illegible]	02. Senegal - Mandenka
HGDP00917	[illegible]	02. Senegal - Mandenka
HGDP00918	[illegible]	02. Senegal - Mandenka
HGDP00919	[illegible]	02. Senegal - Mandenka
HGDP01199	[illegible]	02. Senegal - Mandenka
HGDP01200	[illegible]	02. Senegal - Mandenka
HGDP01201	[illegible]	02. Senegal - Mandenka
HGDP01202	[illegible]	02. Senegal - Mandenka
HGDP01283	[illegible]	02. Senegal - Mandenka
HGDP01284	[illegible]	02. Senegal - Mandenka
HGDP01285	[illegible]	02. Senegal - Mandenka
HGDP01286	[illegible]	02. Senegal - Mandenka
HGDP00920	[illegible]	03. Nigeria - Yoruba
HGDP00924	[illegible]	03. Nigeria - Yoruba
HGDP00925	[illegible]	03. Nigeria - Yoruba
HGDP00926	[illegible]	03. Nigeria - Yoruba
HGDP00927	[illegible]	03. Nigeria - Yoruba
HGDP00928	[illegible]	03. Nigeria - Yoruba
HGDP00929	[illegible]	03. Nigeria - Yoruba
HGDP00930	[illegible]	03. Nigeria - Yoruba
HGDP00931	[illegible]	03. Nigeria - Yoruba
HGDP00932	[illegible]	03. Nigeria - Yoruba
HGDP00933	[illegible]	03. Nigeria - Yoruba
HGDP00934	[illegible]	03. Nigeria - Yoruba
HGDP00935	[illegible]	03. Nigeria - Yoruba
HGDP00936	[illegible]	03. Nigeria - Yoruba
HGDP00937	[illegible]	03. Nigeria - Yoruba
HGDP00938	[illegible]	03. Nigeria - Yoruba
HGDP00939	[illegible]	03. Nigeria - Yoruba
HGDP00940	[illegible]	03. Nigeria - Yoruba
HGDP00941	[illegible]	03. Nigeria - Yoruba
HGDP00942	[illegible]	03. Nigeria - Yoruba
HGDP00943	[illegible]	03. Nigeria - Yoruba
HGDP00944	[illegible]	03. Nigeria - Yoruba
HGDP00987	[illegible]	04. Namibia - San
HGDP00991	[illegible]	04. Namibia - San
HGDP00992	[illegible]	04. Namibia - San
HGDP01029	[illegible]	04. Namibia - San
HGDP01032	[illegible]	04. Namibia - San
HGDP01036	[illegible]	04. Namibia - San
HGDP00449	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00450	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00456	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00462	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00463	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00467	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
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HGDP00471	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00474	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00476	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00478	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00982	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00983	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00984	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP01081	[illegible]	05. Democratic Republic of Congo - Mbuti Pygmies
HGDP00461	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00464	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00465	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00466	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00469	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00470	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00473	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00475	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00452	[illegible]	06. Central African Republic - Biaka Pygmies
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HGDP00457	[illegible]	06. Central African Republic - Biaka Pygmies
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HGDP00460	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00472	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00479	[illegible]	06. Central African Republic - Biaka Pygmies
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HGDP00985	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00986	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP01086	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP01087	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP01090	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP01092	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP01094	[illegible]	06. Central African Republic - Biaka Pygmies
HGDP00993	[illegible]	06b. South Africa - Bantu S.E. Pedi
HGDP00994	[illegible]	06b. South Africa - Bantu S.E. S.Sotho
HGDP01030	[illegible]	06b. South Africa - Bantu S.E. Tswana
HGDP01034	[illegible]	06b. South Africa - Bantu S.E. Tswana
HGDP01033	[illegible]	06b. South Africa - Bantu S.E. Zulu
HGDP01028	[illegible]	06b. South Africa - Bantu S.W. Herero
HGDP01035	[illegible]	06b. South Africa - Bantu S.W. Herero

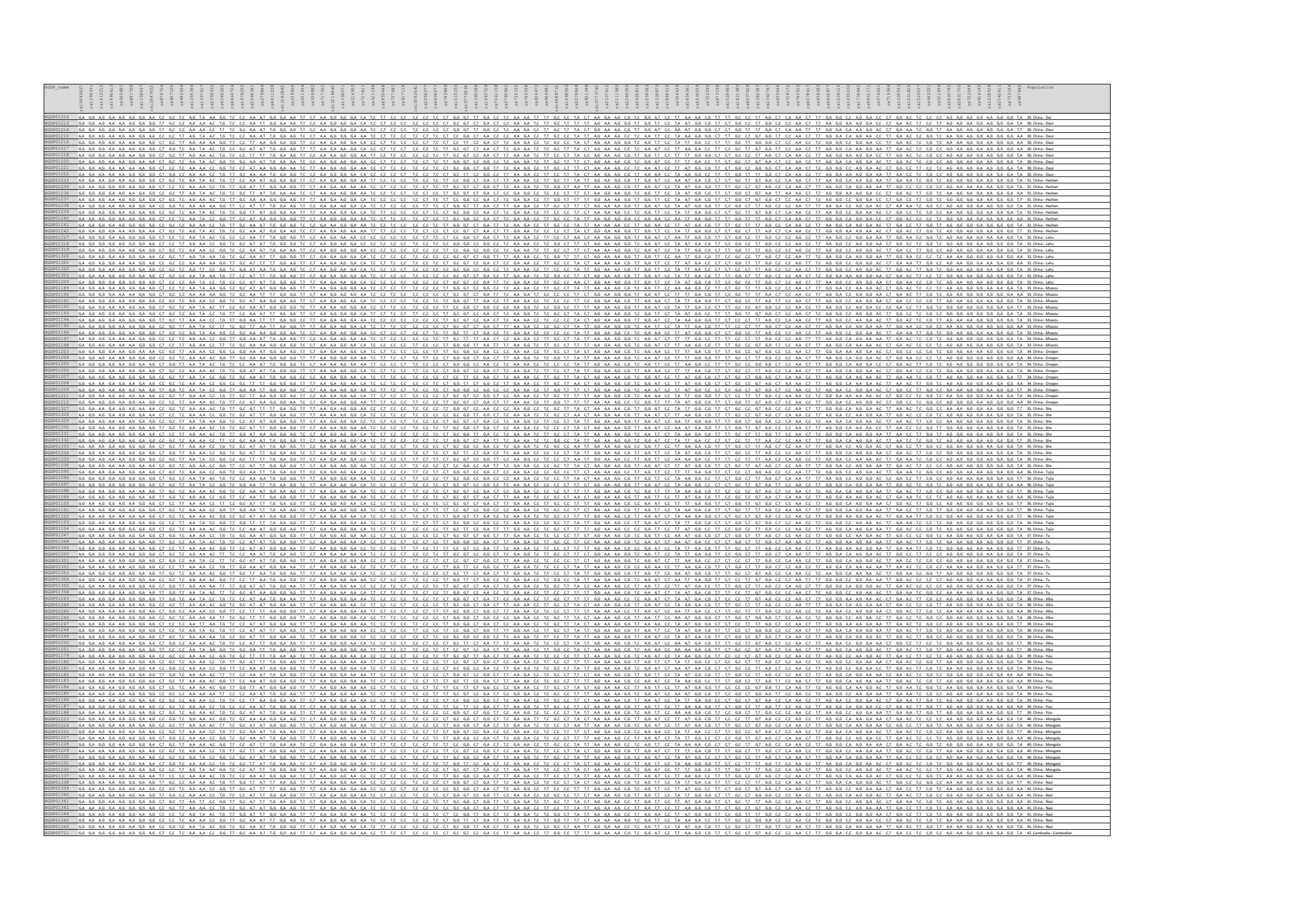


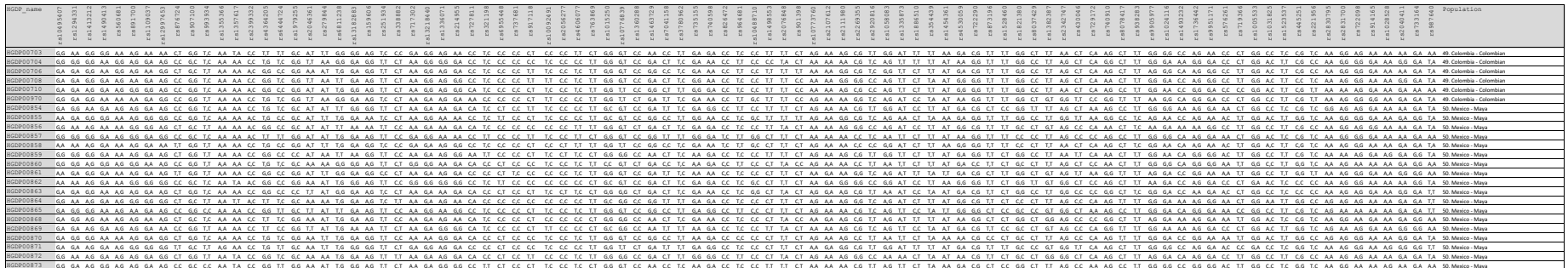












n.d.: no data