Supplementary Information

Using population admixture to help complete maps of the human genome

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Supplementary Note

CARe and ICDB dataset analysis.

For the analysis of the SNPs mismapped in the Affymetrix 6.0 array, we selected all samples from the union of the ARIC, CARDIA, JHS, and MESA datasets combined[1]. To infer local ancestry across the genome, we used a simple Hidden Markov Model similar to the one used in ANCESTRYMAP[2] selecting 4,323 ancestry-informative SNPs which form a subset of the Affymetrix 6.0 SNP panel[3]. After estimating African ancestry for each sample, we selected ~7,800 samples that had at least 20% West African ancestry. Average West African ancestry for the selected group was 79.5%±11.0%.

For the analysis of SNPs mismapped in the Illumina HumanHap550 array, we downloaded all genotype data from 2,161 African Americans for the Hap550v1 and Hap550v3 arrays available from the Illumina iControlDB online database. To infer local ancestry across the genome, we used the 4,174 SNPs shared with the admixture map designed for the Illumina 610 array[3]. After removing outliers and samples with less than 20% West African ancestry, we selected a group of ~1,800 samples with 80.9%±8.6% average West African ancestry.

To assign rsIDs to the 906,703 SNPs in the Affymetrix 6.0 array and the 566,714 SNPs in the HumanHap550 array, we used annotations provided by Affymetrix (http://www.affymetrix.com/support/technical/byproduct.affx?product=genomewidesnp_6) and Illumina and we converted names for SNPs that have been merged in dbSNP (ftp://ftp.ncbi.nih.gov/snp/database/organism_data/human_9606/RsMergeArch.bcp.gz). We noticed that several SNP mapping annotations from dbSNP relative to hg19 were incorrect, so we used mapping annotations from HapMap available through the UCSC table browser, which we found to be more reliable.

In the Affymetrix 6.0 array there were overall 577 SNPs with no HapMap annotations. Of these, 50 belong to the Human T cell Receptor Beta Variable locus at 7q34 and 23 to the 17q23.3 locus which have been modified between reference genomes hg18 and hg19 leaving these SNPs unmapped in hg19. For the remaining SNPs, using dbSNP 131 annotations, 427 have unique mappings, 42 have dual placement in the X-transposed region, a segmental duplication from Xq21.3 to Yp11.2[4], 33 have multiple autosomal placements, one has no autosomal placement in hg19 (rs6656783), and one has been retracted (rs41400850).

In the HumanHap550 array there were 689 SNPs with no HapMap annotations. Of these, 39 belong to the Human T cell Receptor Beta Variable locus at 7q34 and 16 to the 17q23.3 locus. For the remaining SNPs, using dbSNP 131 annotations, 588 have unique mappings, 37 have multiple autosomal placements, and 9 have no autosomal placements in hg19.

While performing the test for the initial set of 4,323 ancestry-informative SNPs in the Affymetrix 6.0 array, we realized that SNP rs4293623, the most centromeric SNP on acrocentric chromosome 21 in the African American admixture map[3], is actually a chromosome 13 SNP. We therefore excluded this SNP from computation of local ancestry and repeated the analysis. Notably, SNP rs1877468 is an ancestry-informative marker in the *HYDIN* locus and was confirmed to be a 16q22.2 SNP rather than a 1q21.1 SNP. SNP rs9964056 has been incorrectly mapped in dbSNP 131 to 13q14.2 in hg19 while it is correctly mapped to 18p11.21 in HapMap. These findings should raise awareness of the importance of correcting mismapping issues before using ancestry-informative admixture maps.

We recorded all SNPs whose adjusted genotype did not correlate with local ancestry at the locus where they are annotated but correlated at a genome-wide significant level ($p<5\times10^{-8}$) at a different locus, and all SNPs whose best mapping matched the best mapping of a nearby SNP already recorded.

We noticed that SNP rs159093 maps to 20q13.2 in the Affymetrix 6.0 array (minor allele frequency 0.27) and to 17q12 in the HumanHap550 array (minor allele frequency 0.14), most likely because the two arrays, due to design differences, are genotyping different SNPs. With the exception of SNPs from the *HYDIN* locus, we report all SNPs with HapMap annotations or unique dbSNP 131 mapping which were incompatible with our placements, 63 for the Affymetrix 6.0 array and 7 for HumanHap550 array (**Supplementary Table 3**). The substantially larger number of mismapped SNPs discovered in the Affymetrix 6.0 array relative to the HumanHap550 array is both a consequence of the lower number of SNPs in the latter array and the smaller size of the ICDB cohort compared to the cohort from CARe. Approximately a third of these SNPs failed Hardy-Weinberg equilibrium test, but they were still informative enough to be reliably mapped.

Among the 114 SNPs in the Affymetrix 6.0 array and 14 SNPs in the HumanHap550 array mapped within the *HYDIN* segmental duplication, only 7 SNPs could not be mapped. For these SNPs we analyzed patterns of local LD, which allowed us to place them with confidence in the correct region. We concluded that 58 out of 114 SNPs from the Affymetrix 6.0 array and 8 out of 14 SNPs in the HumanHap550 were SNPs from the 1q21.1 paralog (**Supplementary Tables 4 and 5**), which essentially means that SNPs assayed in this locus were equally likely to be ascertained from either paralog.

Theoretical derivations for correlation between SNP genotype and local ancestry.

With the possible exclusion of the short arms of the acrocentric chromosomes, most of the missing euchromatic parts of the genome are at a short genetic distance (say less than 5cM) from locations in the genome assayed by the Affymetrix 6.0 array or any other array with comparable marker density. By simulating African American chromosomes as a mix of 20% European and 80% West African chromosomes admixing for 6 generations, we estimated the Pearson correlation coefficient between local ancestry at 5cM distance as $r^2>90\%$ (**Supplementary Fig. 1**). Therefore, if we had perfect local ancestry estimation at two different loci, it would be straightforward to test if they are closely linked, that is, at a distance less than 5cM from each other, with fewer than 60 samples.

For a bi-allelic SNP, given x the frequency of an allele in the ancestral European population, y the frequency of the same allele in the ancestral West African population, and m the amount of European ancestry, the correlation between the genotype for the locus and the number of European chromosomes at the locus is given by:

$$r^2(x,y,m)=\frac{m(1-m)(x-y)^2}{(y-my+mx)(1-y+my-m)}.$$

Theorem. With the constraints that $0\leq x,y,m\leq 1$, it follows that

$$4\mathrm{m}(1-m)(x-y)^2\leq r^2(x,y,m)\leq|x-y|.$$

Proof. First notice that

$$(y-my+mx)(1-y+my-mx)=\ldots$$
$$\ldots=(1/2-1/2+y-my+mx)(1/2+1/2-y+my-mx)=\ldots$$
$$\ldots=1/4-[y-1/2+m(x-y)]^2\leq 1/4,$$

from which the first inequality follows. For the second inequality, it is enough to show that

$$1/4-[y-1/2+m(x-y)]^2\geq\ldots$$

$$\ldots \geq 1/4-(1/2-m|x-y|)^2=\ldots$$
$$\ldots = m|x-y|-m^2(x-y)^2=\ldots$$
$$\ldots = m|x-y|(1-m|x-y|).$$

and therefore it follows that

$$r^2(x,y,m)\leq \frac{m(1-m)(x-y)^2}{m|x-y|(1-m|x-y|)}=\frac{(1-m)|x-y|}{1-m|x-y|}\leq |x-y|.$$

Notice that $r^2(x,y,m)$ is not a symmetric function in x and y. For example, for SNPs rare in one population and monomorphic for the common allele in the other, we get

$$r^2(x,0,m)=\frac{(1-m)x}{1-mx}\approx(1-m)x \text{ for } x\ll 1,$$

$$r^2(0,x,m)=\frac{mx}{1-x+mx}\approx mx \text{ for } x\ll 1.$$

Therefore when $m<1/2$ and $x\ll 1$, $r^2(x,0,m)$ is greater than $r^2(0,x,m)$, by approximately a factor of (1-m)/m, which for African Americans corresponds to a factor of 4. This is also an upper bound.

Theorem. With the constraints $0\leq x,y\leq 1$ and $0<m<1/2$, it follows that, when $x\neq y$,

$$\frac{r^2(x,y,m)}{r^2(y,x,m)}<\frac{1-m}{m}.$$

Proof. By using the previous formula for $r^2(x,y,m)$, the statement becomes

$$\frac{(x-mx+my)(1-x+mx-my)}{(y-my+mx)(1-y+my-mx)}<\frac{1-m}{m}.$$

As each term is positive, this is equivalent to

$$m(x-mx+my)(1-x+mx-my)<(1-m)(y-my+mx)(1-y+my-mx),$$

and with a few algebraic steps this is the same as

$$(2\mathrm{m}-1)\left[(1-m)m(x-y)^2+y(1-y)\right]<0,$$

which is true by the hypothesis $0<m<1/2$.

In general, genotypes for SNPs with larger allele frequency differentiation between Europeans and West Africans tend to have larger correlation with local ancestry state, though for a given allele frequency difference, the genotype for a SNP which is more polymorphic in Europeans will have better correlation since $m<1/2$ (**Supplementary Fig. 2**). Notice that this measure is similar, up to the factor m(1-m), to the Shannon Information Content used to generate admixture maps[5,6].

List of loci with cryptic segmental duplications

2p22.2 locus. We identified three SNPs assigned in the chr2:37,958,019-38,003,219 region at 2p22.2, where a large increase in heterozygosity was observed (**Supplementary Fig. 12**), mapping to the pericentromeric region of chromosome 22. The region does not contain known segmental duplications in hg19, although SCAF_1103279187616 aligns to it with ~4% sequence divergence. Analysis of 1000 Genomes Project data shows increased read depth and realigning the reads to the hg19 region and the HuRef unlocalized scaffold also shows that the latter is highly polymorphic (**Supplementary Fig. 7**). This is an interesting example of a common CNV of sequence missing from the reference genome.

2p11.1 locus. We identified two SNPs assigned in the chr2:91,737,476-91,880,745 region at 2p11.1, where an increase in heterozygosity was observed (**Supplementary Fig. 13**), mapping to the pericentromeric region of chromosome 1. We identified BAC clones RP11-247L13/AC144898.3, RP11-400J9/AC010098.8, and RP11-1210E1/AC145614.3, as carrying the alternate allele for SNP rs11240831. The region contains a copy of gene *OTOP1*, belonging to a gene family for which the reference genome has 5 or more fewer copies than the median present in the human genome (Supplementary Table S6 of [7]).

2q21.2 locus. We identified three SNPs assigned in the chr2:133,005,020-133,120,083 region at 2q21.2, where a large increase in heterozygosity was observed (**Supplementary Fig. 14**), mapping to the pericentromeric region of chromosome 20, confirmed by FISH analysis (**Fig. 4**). The hg19 reference contains a segmental duplication of part of this region at 19q13.31, also confirmed by FISH. We identified BAC clone RP11-462H3/AC018688.9 as carrying the alternate allele for SNP rs2677646. This region resides in the vestigial centromere on chromosome 2[8] and harbors of a segmental duplication that took place when the region was still functioning as a centromere.

3p26.3 locus. We identified one SNP localized in the chr3:612,223-663,367 region at 3p26.3, where a large increase in heterozygosity was observed (**Supplementary Fig. 15**), mapping to the pericentromeric region of chromosome 22, confirmed by FISH analysis (**Fig. 4**). The hg19 reference contains two segmental duplications of this region at 21p11.2 and in contig GL000217, while FISH predicts the other two copies to be present in the pericentromeric regions of chromosome 14 and 22, possibly indicating the presence of more than three copies.

***ZNF717* locus.** We identified one SNP assigned in the chr3:75,761,051-75,871,577 region at 3p12.3 (**Supplementary Fig. 16**), mapping to the pericentromeric region of chromosome 21. We identified BAC clone RP4-813B7/AL137861.5 as carrying the alternate allele for SNP rs6656783. The region contains gene *ZNF717*, belonging to a gene family with one of the most variable copy number and for which the reference genome has 5 or more fewer copies than the median present in the human genome (Fig. 2A and Supplementary Table S6 of [7]).

***ZNF595* locus.** We identified one SNP assigned in the chr4:25,709-68,702 region at 4p16.3 (**Supplementary Fig. 17**), mapping to the pericentromeric region of chromosome 22. We identified BAC clone RP11-85C8/AC237676.1 as carrying the alternate allele for SNP rs2859203. The region contains gene *ZNF595*, belonging to a gene family for which the reference genome has 5 or more fewer copies than the median present in the human genome and that has continued to expand in the primate lineage (Supplementary Table S6 and S11 of [7]).

4p16.3 locus. We identified one SNP assigned in the chr4:3,536,207-3,636,136 region at 4p16.3, where a large increase in heterozygosity was observed (**Supplementary Fig. 18**), mapping to the pericentromeric region of chromosome 9, confirmed by FISH analysis (**Fig. 4**). HuRef contig SCAF_1103279188214, assembled as part of chromosome 9, aligns to this region and is likely to be the missing paralog which, after being duplicated in the pericentromeric region of chromosome 9, gave rise to further segmental duplications annotated and present in hg19.

4q35.2 locus. We identified one SNP assigned in the chr4:190,470,115-190,684,480 region at 4q35.2, where a large increase in heterozygosity was observed[9] (**Supplementary Fig. 19**), mapping to the pericentromeric region of chromosome 21. According to FISH analysis of clone RP11-119M6/AC146634.1 there are three additional copies in the pericentromeric regions or short arms of acrocentric chromosomes 13, 14, and 21[10]. The copy on chromosome 14 is known to be highly polymorphic (Supplementary Fig. S24a of [7]). Analysis of 1000 Genomes Project data shows increased read depth and copy number variability (**Supplementary Fig. 8**), and we speculate this to be due to a common deletion polymorphism on chromosome 14, although it was not possible to identify with certainty which of the missing copies are variable, as we had no reference sequence for them. Given our localization of unmapped contig GL000193 to chromosome 21, as clone bP-21201H5/CR382285.2 at 21p11.2 and RP11-499D3/AL360154.30 from GL000193 each contain ~35kbp of homologous sequence with ~0.27% divergence, it is possible the overlap represents the same human sequence on chromosome 21. BAC clones RP11-570J4/AC124864.3 (aligned to 190,630,692-190,684,480) and RP11-312L16/AC116622.6 (aligned to 190,579,576-190,684,480), erroneously mapped to chromosome 4, are likely to partially represent two of these three cryptic paralogs.

5p14.3 locus. We identified two HapMap SNPs (rs1901495 and rs10520871) assigned in the chr5:21,506,326-21,573,437 region at 5p14.3 (**Supplementary Fig. 20**) in LD with HapMap SNPs at 6p11.2 (rs3805798, rs2472932, rs9404721, rs1841579, and rs1517230). This suggest the presence of a cryptic segmental duplication between the two regions only partially annotated in the reference that we could confirm by FISH analysis (**Fig. 4**). We could identify sequence from this missing paralog in clone CH17-92N24/FP325329.6, which overlaps clone 55C20/AL021368.1 next to the gap at 6p11.2.

***DUSP22* locus.** We identified one SNP assigned in the chr6:256,518-382,461 region at 6p25.3 (**Supplementary Fig. 21**) mapping to 16p11.2. FISH analysis had confirmed the presence of this second copy[11]. Analysis of 1000 Genomes Project data shows increased read depth and copy number variability (**Supplementary Fig. 9**). The region contains gene *DUSP22*, one of the 23 genes duplicated specifically in the human lineage and diploid in great apes (Fig. 2B of [7]) and known to be present in a second copy at 16p11.2[11,12], although this copy is missing from hg19.

***PRIM2* locus.** We identified three SNPs assigned in the chr6:57,369,236-57,608,453 region at 6p11.2, where a large increase in heterozygosity was observed[9] (**Supplementary Fig. 22**), mapping to the pericentromeric regions of chromosome 3. We identified BAC clone RP1-216J23/AL354926.17 as carrying the alternate allele for SNP rs185540 and we determined that the same sequence for this clone is located in SCAF_1103279180085 which contains a partial copy of the *PRIM2* gene. Previous FISH assays showed the presence of two copies on chromosome 6[13] but failed to uncover the third copy on chromosome 3 that was instead detected by FISH analysis of clones RP3-401D24/AL137184.15 and RP11-91K21[10]. Our FISH analysis confirmed the presence of all three copies (**Fig. 3b**).

We noticed that the two clones RP3-422B11/AL121975.10 and RP1-71H19/AL121958.6 over the *PRIM2* gene belong to two of these distinct paralogs. They overlap over a ~30kbp segment with ~2% sequence divergence but they have been incorrectly joined together in the reference genome . This also explains the presence of rs4535533, one of the PSVs over the duplicated region, which is a nonsense mutation present in the reference genome acting as a stop-codon in the 11th exon of the *PRIM2* gene (**Supplementary Table 10**) and apparently disrupting the only full copy of the evolutionary conserved *PRIM2* gene. Once the misassembly is taken into account, this nonsense mutation is actually present in the partial copy on chromosome 6. By analyzing read depths of sample HG00155/GBR, which has an extra copy of the partial *PRIM2* duplication on chromosome 6 (**Supplementary Fig. 5**), we confirmed this hypothesis, as sample HG00155/GBR was found to have a copy number of 2 over the sequence from clone RP3-422B11/AL121975.10 and a copy number of 3 over the sequence from clone RP1-71H19/AL121958.6 (**Supplementary Fig. 6**). It has been speculated that the correct location of the *PRIM2* partial copy contained in chr6:57,314,070-58,087,659 is actually at 6q11.1[14] and this is further suggested by the missed joining of clone RP11-452D24/AL356672.9 at 6p11.1 and clone RP1-173A13/AL035688.8 at 6q11.1, containing ~10kb of homologous sequence with ~0.17% divergence, well within the range of human haplotypic variation.

The original copy of the *PRIM2* gene at 6p11.2 is actually contained in HuRef contig SCAF_1103279188350, mapped to chromosome 6, and Huref scaffold SCAF_1103279188406 mapped to chromosome 5. This is likely an artifact of misassembly due to a recent ~65kbp segmental duplication between 5p14.3 and 6p11.2 and should not be interpreted as an extra copy on chromosome 5[15]. The partial copy of *PRIM2* that we speculate being at 6q11.1 is fully contained in HuRef contig SCAF_1103279188263.

***HYDIN* locus.** We identified 58 out of 114 SNPs from the Affymetrix 6.0 array and 8 out of 14 SNPs from the Illumina HumanHap550 array originally assigned to the chr16:70,845,287-71,202,573 region at 16q22.2 (**Supplementary Fig. 23**) but actually mapping to 1q21.1 (**Supplementary Tables 4 and 5**). The corresponding missing paralog is entirely contained in the GL000192 unplaced contig, included in hg19. The exact location of this unplaced contig is within the gap next to clone RP11-47D6/AL359176.20 at 1q21.1, added to hg19 and absent from hg18. The rationale for this observation is that this clone and clone RP11-499D3/AL360154.30 from GL000192 contain each ~85kbp of homologous sequence with ~0.15% divergence, well within the range of human haplotypic variation, and should have been joined together. The region contains the gene *HYDIN*, one of the 23 genes duplicated specifically in the human lineage and diploid in great apes (Fig. 2B of [7]). Rare CNVs of the copy at 1q21.1 have been observed in samples NA19190/YRI and NA19201/YRI from the 1000 Genomes Project (Supplementary Fig. S39 of [7]).

17p11.2 locus. We identified 3 HuRef unlocalized scaffolds, SCAF_1103279180438, SCAF_1103279188241, and SCAF_1103279187931, aligning to the 17p11.2 region, with corresponding increase in read depth in data from the 1000 Genomes Project (**Supplementary Fig. 10**). Scaffold SCAF_1103279180438 contains gene *KCNJ17* and scaffold SCAF_1103279187931 contains gene *KCNJ18*, both known to play important biological roles[16,17]. The absence of these segmental duplications from the reference genome has resulted in the identification of many of the PSVs among the three copies as SNPs (**Supplementary Fig. 24**).

Additional loci. Scaffold SCAF_1103279182504 contains the gene *UGT2B17* and HuRef scaffold SCAF_1103279180463 contains the gene *TRY6*, both genes known to be polymorphic and stratified among populations[7,18]. We could confirm that the *TRY6* copy, missing from hg19 but present in hg18, maps to the Human T cell Receptor Beta Variable locus at 7q34. Furthermore, HuRef scaffolds SCAF_1103279179890 contains the gene *RAB7B* and we verified that this scaffold is located at 1q32.1[19,20]. Scaffold SCAF_1103279180486 contains a paralog of gene *MUC3* and we could verify that this scaffold is located at 7q22.1[21]. Among the HuRef scaffolds mapping to the pericentromeric region of chromosome 1, SCAF_1103279187792 contains a paralog of the gene *FAM27C* and, interestingly, we could not find any region across the genome with low sequence divergence from sequence in this scaffold, indicating that this copy of the gene must have resulted from duplication early in primate evolution.

Supplementary Tables

Supplementary Table 1. SNPs genotyped with Sequenom from unlocalized scaffolds.

SCAF: genomic scaffold; BP: coordinate within scaffold; LENGTH: full length of the scaffold; REF, ALT: reference and alternate alleles observed; AF: alternate allele frequency observed in JHS samples; CEU, YRI: alternate allele frequency observed in CEU and YRI samples; R2: Pearson correlation coefficient r² between genotype and local ancestry, as estimated from CEU and YRI frequencies; HWE: p-value from Hardy-Weinberg equilibrium test; P: p-value for correlation of genotypes with local ancestry at the best representative SNP; CHR, ID, BP', BAND: chromosome, hg19 coordinates, and localization of the SNP for which the local ancestry best represents the location of the SNP in the unlocalized scaffold.

SCAF	BP	LENGTH	REF	ALT	AF	CEU	YRI	R2	HWE	P	ID	CHR	BP'	BAND
GL000191	27,316	106,433	T	C	0.91	0.55	1	0.4	1	2.4E-028	rs3211051	chr1	24,160,991	1p36.11
GL000192	101,317	547,496	A	C	0.15	0.68	0	0.63	0.0002753	7.7E-069	rs1932366	chr1	146,268,901	1q21.1
GL000192	105,841	547,496	A	G	NaN	0.67	0	0.62	1	NA	NA	NA	NA	NA
GL000192	108,915	547,496	G	A	NaN	0.62	0	0.57	1	NA	NA	NA	NA	NA
GL000192	123,920	547,496	A	T	0.15	0.64	0	0.59	0.000272	1.2E-065	rs4950584	chr1	146,245,271	1q21.1
GL000193	2,822	189,789	C	T	NaN	0.24	0	0.2	1	NA	NA	NA	NA	NA
GL000193	25,476	189,789	G	T	0	0.32	0	0.27	1	0.0000016	rs2260895	chr21	13,564,335	21q11.2
GL000193	26,272	189,789	C	G	NaN	0.31	0.02	0.19	1	NA	NA	NA	NA	NA
GL000193	30,855	189,789	C	T	0.09	0.33	0.02	0.2	0.09004	5.4E-016	rs2334600	chr21	13,938,843	21q11.2
GL000193	114,174	189,789	T	C	0	0.41	0.04	0.22	1	0.000063	rs6062363	chr20	62,382,907	20q13.33
GL000193	151,546	189,789	T	C	NaN	0.77	1	0.19	1	NA	NA	NA	NA	NA
GL000194	72,564	191,469	G	A	0.09	0.3	0.02	0.18	0.04333	NA	NA	NA	NA	NA
GL000194	81,542	191,469	T	C	NaN	0.31	0.02	0.19	1	NA	NA	NA	NA	NA
GL000195	4,865	182,896	G	T	0.11	0.34	0.01	0.25	0.1464	NA	NA	NA	NA	NA
GL000195	21,980	182,896	T	A	0.01	0.34	0.02	0.21	1	0.000022	rs2019048	chr7	46,652,626	7p12.3
GL000195	22,624	182,896	G	A	0	0.33	0.02	0.2	1	NA	NA	NA	NA	NA
GL000195	80,280	182,896	G	A	0.5	0.27	0	0.23	3.346E-071	NA	NA	NA	NA	NA
GL000195	142,420	182,896	C	G	0.02	0.27	0	0.23	1	0.00019	rs1148825	chr1	178,040,788	1q25.2
GL000199	2,656	169,874	C	T	0.15	0.49	0.08	0.2	0.5038	1.9E-019	rs35882728	chr9	44,804,684	9p11.2
GL000204	61,571	81,310	A	G	0.68	0.08	0.79	0.35	0.4152	8.6E-043	rs4889908	chr17	75,272,116	17q25.3
GL000204	61,666	81,310	C	T	0.69	0.08	0.8	0.37	0.4065	2E-035	rs4889908	chr17	75,272,116	17q25.3
GL000204	75,440	81,310	G	T	0.19	0.69	0.08	0.37	0.43	2.3E-019	rs7215564	chr17	76,351,882	17q25.3
GL000204	79,997	81,310	C	T	0.18	0.6	0.05	0.36	0.4196	7.6E-022	rs7215564	chr17	76,351,882	17q25.3
GL000204	80,788	81,310	G	A	NaN	0.63	0.07	0.34	1	NA	NA	NA	NA	NA
GL000205	142,251	174,588	C	A	0.05	0.8	1	0.17	1	NA	NA	NA	NA	NA
GL000205	154,786	174,588	T	G	0.78	0.39	0.88	0.23	0.02749	0.000038	rs10849105	chr12	4,589,936	12p13.32

GL000205	158,044	174,588	C	T	NaN	0.8	1	0.17	1	NA	NA	NA	NA	NA
GL000208	70,457	92,689	C	T	0	0.3	0.01	0.21	1	NA	NA	NA	NA	NA
GL000212	9,128	186,858	G	A	0.24	0.65	0.04	0.44	0.1124	1.3E-033	rs2775533	chr13	18,064,576	13q11
GL000212	27,092	186,858	A	C	0.01	0.54	0.01	0.44	1	0.000000028	rs2775533	chr13	18,064,576	13q11
GL000212	36,207	186,858	G	A	0.05	0.73	0.06	0.46	1	1.8E-013	rs9509040	chr13	19,584,272	13q12.11
GL000212	80,151	186,858	A	G	NaN	0.95	0.2	0.4	1	NA	NA	NA	NA	NA
GL000214	66,287	137,718	G	C	0.92	0.93	0.42	0.17	0.3759	NA	NA	NA	NA	NA
GL000214	75,893	137,718	G	T	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
GL000214	85,170	137,718	A	C	0.99	0.93	0.39	0.19	1	NA	NA	NA	NA	NA
GL000214	94,868	137,718	G	A	0.07	0.2	0	0.17	0.3789	0.0000066	rs2822991	chr21	15,275,402	21q11.2
GL000214	116,077	137,718	T	C	0.71	0.88	0.38	0.16	8.486E-010	NA	NA	NA	NA	NA
GL000216	63,796	172,294	C	A	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
GL000218	156,904	161,147	A	G	0.6	0.56	0.94	0.2	2.127E-023	NA	NA	NA	NA	NA
GL000219	66,846	179,198	C	T	0.85	0.24	0.01	0.16	1	NA	NA	NA	NA	NA
GL000219	157,526	179,198	C	G	0.06	0.22	0.01	0.14	0.07501	NA	NA	NA	NA	NA
GL000219	167,734	179,198	A	G	0.45	0	0.54	0.19	9.266E-015	0.0000043	rs10787464	chr10	114,542,952	10q25.2
GL000219	178,845	179,198	C	A	0	0.2	0	0.17	1	NA	NA	NA	NA	NA
GL000220	7,291	161,802	A	G	NaN	0.23	0	0.19	1	NA	NA	NA	NA	NA
GL000220	58,883	161,802	T	C	0	0.28	0.01	0.19	1	0.000028	rs1788849	chr18	55,669,956	18q21.32
GL000220	61,838	161,802	T	A	0.01	0.28	0.01	0.19	1	0.00000029	rs1448356	chr11	130,841,892	11q25
GL000220	65,261	161,802	T	A	NaN	0.24	0	0.2	1	NA	NA	NA	NA	NA
GL000220	70,395	161,802	T	G	NaN	0.28	0.01	0.19	1	NA	NA	NA	NA	NA
GL000220	77,225	161,802	A	T	NaN	0.21	0	0.18	1	NA	NA	NA	NA	NA
GL000221	2,470	155,397	G	A	NaN	0.33	0	0.28	1	NA	NA	NA	NA	NA
GL000222	19,610	186,861	T	C	0.13	0.38	0.01	0.28	0.1274	1.1E-021	rs17013856	chr3	76,262,091	3p12.3
GL000224	57,717	179,693	A	G	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
GL000224	101,290	179,693	T	A	0.02	0.26	0	0.22	1	0.0000053	rs8138488	chr22	14,870,204	22q11.1
GL000224	154,610	179,693	G	A	0	0.27	0.01	0.19	1	NA	NA	NA	NA	NA
GL000224	157,091	179,693	C	A	0.05	0.23	0.01	0.15	0.0001314	NA	NA	NA	NA	NA
GL000230	4,861	43,691	C	T	NaN	0.32	0	0.27	1	NA	NA	NA	NA	NA
GL000230	5,653	43,691	G	C	NaN	0.32	0.01	0.23	1	NA	NA	NA	NA	NA
GL000230	7,699	43,691	G	T	NaN	0.29	0.01	0.2	1	NA	NA	NA	NA	NA
GL000230	14,024	43,691	C	G	0.1	0.33	0.01	0.24	0.3312	3.5E-019	rs1878705	chr14	19,975,355	14q11.2
GL000230	15,352	43,691	T	G	0.49	0.3	0.01	0.21	2.254E-047	NA	NA	NA	NA	NA
GL000230	19,697	43,691	A	T	0.02	0.31	0	0.26	1	0.000052	rs11156677	chr14	20,337,669	14q11.2
GL000233	24,395	45,941	T	G	0.33	0.25	0	0.21	1	0.000015	rs1565078	chr2	187,642,721	2q32.1
GL000234	22,268	40,531	C	T	NaN	0.21	0	0.18	1	NA	NA	NA	NA	NA
GL000235	5,365	34,474	G	C	NaN	0.26	0	0.22	1	NA	NA	NA	NA	NA

GL000235	5,525	34,474	C	G	NaN	0.33	0.03	0.18	1	NA	NA	NA	NA	NA
GL000235	6,064	34,474	G	A	NaN	0.27	0	0.23	1	NA	NA	NA	NA	NA
GL000235	7,959	34,474	C	A	0.11	0.32	0	0.27	0.03388	2.1E-021	rs1878705	chr14	19,975,355	14q11.2
GL000235	20,608	34,474	G	A	NaN	0.25	0.01	0.17	1	NA	NA	NA	NA	NA
GL000235	24,671	34,474	T	A	0	0.27	0	0.23	1	NA	NA	NA	NA	NA
GL000237	944	45,867	T	A	NaN	0.6	0.94	0.17	1	NA	NA	NA	NA	NA
GL000240	32,364	41,933	G	T	NaN	0.26	0.01	0.18	1	NA	NA	NA	NA	NA
GL000248	10,594	39,786	A	C	NaN	0.78	0.24	0.21	1	NA	NA	NA	NA	NA
GL000248	10,636	39,786	T	G	0.38	0.76	0.26	0.17	1.845E-033	1.6E-009	rs16991084	chr22	31,443,375	22q12.3
SCAF_1103279188373	774	1,612,812	A	G	0.69	0.14	0.8	0.31	0.4888	8.7E-013	rs5939329	chrX	2,728,135	Xp22.33
SCAF_1103279188373	2,014	1,612,812	A	C	0.73	0.35	0.84	0.2	0.7708	1.5E-013	rs2010818	chrX	3,508,557	Xp22.33
SCAF_1103279188373	762,163	1,612,812	T	C	0.46	0.07	0.57	0.16	0.7257	0.00015	rs17090623	chrX	2,717,734	Xp22.33
SCAF_1103279188373	1,384,762	1,612,812	A	G	0.17	0.38	0.04	0.19	4.385E-008	NA	NA	NA	NA	NA
SCAF_1103279188373	1,455,486	1,612,812	G	A	0.07	0.47	0	0.42	0.000005047	NA	NA	NA	NA	NA
SCAF_1103279188110	72,042	716,511	C	A	NaN	0.44	0.02	0.3	1	NA	NA	NA	NA	NA
SCAF_1103279188110	79,305	716,511	C	T	0.5	0.3	0	0.26	1	NA	NA	NA	NA	NA
SCAF_1103279188110	89,436	716,511	C	T	NaN	0.37	0.01	0.28	1	NA	NA	NA	NA	NA
SCAF_1103279188110	324,884	716,511	A	G	0	0.35	0	0.3	1	NA	NA	NA	NA	NA
SCAF_1103279188197	70,458	688,672	G	T	0.09	0.41	0.03	0.24	0.1484	0.0000001	rs6060089	chr20	29,628,788	20q11.21
SCAF_1103279188197	81,348	688,672	C	G	NaN	0.68	0.19	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279188197	92,818	688,672	C	T	0.38	0.58	0.12	0.2	2.808E-049	2.8E-009	rs6057602	chr20	30,645,469	20q11.21
SCAF_1103279188197	557,118	688,672	C	T	0.1	0.34	0.02	0.21	1	0.000000015	rs750144	chr20	29,642,688	20q11.21
SCAF_1103279188197	581,035	688,672	C	T	0.2	0.49	0.09	0.18	1	9.4E-014	rs11699392	chr20	25,135,575	20p11.21
SCAF_1103279188252	326,398	392,061	T	C	0.01	0.48	0.09	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279187452	134,707	363,655	T	A	0.84	0.37	0.89	0.26	0.0002646	1.3E-017	rs6060341	chr20	33,327,047	20q11.22
SCAF_1103279187452	197,024	363,655	G	T	0	0.52	0.07	0.24	1	NA	NA	NA	NA	NA
SCAF_1103279187452	205,259	363,655	A	G	0.1	0.31	0	0.26	0.5382	7.1E-018	rs6119410	chr20	31,906,268	20q11.22
SCAF_1103279187452	223,425	363,655	C	T	0.02	0.58	0.07	0.29	1	0.000077	rs6060316	chr20	33,279,435	20q11.22
SCAF_1103279180085	60,734	305,597	A	G	0.2	0.61	0.07	0.32	0.4766	3.6E-009	rs7429932	chr3	90,366,641	3p11.1
SCAF_1103279180085	294,790	305,597	G	A	0	0.47	0.08	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279187930	31,787	280,839	G	A	0.1	0.4	0	0.35	1.413E-010	1.7E-013	rs6587170	chr17	21,437,192	17p11.2
SCAF_1103279187930	241,525	280,839	A	G	0.95	0.72	0.99	0.19	4.768E-017	0.000001	rs2729352	chr17	28,037,201	17q11.2
SCAF_1103279188164	22,291	275,343	G	A	0.77	0.28	0.8	0.2	0.0004463	0.0000079	rs3135338	chr6	32,509,195	6p21.32
SCAF_1103279188164	26,392	275,343	G	A	0.73	0.46	0.9	0.2	2.409E-029	0.000096	rs3135338	chr6	32,509,195	6p21.32
SCAF_1103279188164	139,443	275,343	A	T	0.14	0.26	0.81	0.23	1.208E-018	NA	NA	NA	NA	NA
SCAF_1103279188164	156,167	275,343	A	G	0.03	0.31	0.01	0.22	1	0.00000021	rs3117324	chr6	33,432,505	6p21.32
SCAF_1103279188164	168,609	275,343	C	A	0.09	0.38	0	0.33	7.104E-009	2.1E-014	rs9268856	chr6	32,537,697	6p21.32
SCAF_1103279188164	168,626	275,343	T	C	0.14	0.27	0	0.23	2.728E-021	0.00000073	rs9268856	chr6	32,537,697	6p21.32

SCAF_1103279181781	57,886	263,990	A	T	NaN	0.74	1	0.22	1	NA	NA	NA	NA	NA
SCAF_1103279181781	68,126	263,990	C	T	0.5	0.32	0	0.27	1.589E-086	NA	NA	NA	NA	NA
SCAF_1103279181781	237,445	263,990	T	C	0.08	0.23	0	0.19	1	7.4E-021	rs4889736	chr17	21,944,094	17p11.2
SCAF_1103279181222	934	261,077	C	T	0	0.33	0.03	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279181222	9,135	261,077	T	C	NaN	0.61	0.99	0.29	1	NA	NA	NA	NA	NA
SCAF_1103279181222	12,417	261,077	C	T	0.08	0.24	0	0.2	0.4199	NA	NA	NA	NA	NA
SCAF_1103279181222	42,383	261,077	C	T	0	0.29	0.01	0.2	1	0.000034	rs17007543	chr4	85,000,448	4q21.23
SCAF_1103279187792	46,115	251,763	A	T	0.9	0.55	0.97	0.28	1	2E-012	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279187792	47,682	251,763	A	G	NaN	0.59	0.98	0.28	1	NA	NA	NA	NA	NA
SCAF_1103279187792	132,443	251,763	G	T	0.87	0.59	0.97	0.24	0.000000082	3.6E-009	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279187792	133,164	251,763	G	A	0.93	0.57	0.99	0.33	0.6643	4.5E-013	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279187792	227,994	251,763	G	C	0.9	0.61	0.98	0.26	1	1.9E-014	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279188241	181,972	245,808	T	C	0.9	0.34	0.97	0.48	0.00005635	2.4E-019	rs7406339	chr17	21,926,683	17p11.2
SCAF_1103279188241	220,331	245,808	C	A	0.51	0.62	0.01	0.52	5.312E-032	NA	NA	NA	NA	NA
SCAF_1103279188241	226,453	245,808	G	C	0.09	0.7	0	0.65	4.052E-009	1.1E-018	rs1824900	chr17	22,496,341	17q11.1
SCAF_1103279188305	21,267	238,759	A	T	0.13	0.49	0.08	0.2	0.004214	3.9E-013	rs6606438	chr9	44,806,024	9p11.2
SCAF_1103279188305	21,909	238,759	A	C	0.22	0.45	0.07	0.19	2.022E-014	4.1E-012	rs7848562	chr9	44,840,522	9p11.2
SCAF_1103279188305	47,504	238,759	C	T	NaN	0.39	0.05	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279179615	197,014	225,507	G	A	0.33	0.72	1	0.24	1	0.000064	rs13004371	chr2	61,693,429	2p15
SCAF_1103279179615	203,707	225,507	C	T	0.62	0.11	0.72	0.25	0.7109	5.4E-024	rs6115515	chr20	26,020,582	20p11.1
SCAF_1103279179615	210,373	225,507	T	C	0.59	0.01	0.68	0.29	0.0002009	8E-032	rs6115515	chr20	26,020,582	20p11.1
SCAF_1103279179615	219,425	225,507	T	C	NaN	0.17	0.81	0.3	1	NA	NA	NA	NA	NA
SCAF_1103279179615	219,605	225,507	C	T	NaN	0.28	0	0.24	1	NA	NA	NA	NA	NA
SCAF_1103279188307	46,575	215,476	T	G	0.11	0.36	0.01	0.27	0.00009958	2.1E-026	rs833942	chr1	144,192,023	1q21.1
SCAF_1103279188307	166,097	215,476	T	C	0.12	0.34	0.03	0.18	0.0002879	1.4E-021	rs833942	chr1	144,192,023	1q21.1
SCAF_1103279188266	66,064	210,595	G	T	0.06	0.31	0	0.26	0.3243	NA	NA	NA	NA	NA
SCAF_1103279188266	67,416	210,595	G	A	0.1	0.33	0	0.28	0.1268	NA	NA	NA	NA	NA
SCAF_1103279188266	105,915	210,595	A	G	0.91	0.64	1	0.31	0.327	NA	NA	NA	NA	NA
SCAF_1103279188266	140,457	210,595	C	T	0.02	0.36	0.01	0.27	1	0.000028	rs278546	chr8	94,290,220	8q22.1
SCAF_1103279188266	141,028	210,595	G	C	0.09	0.36	0.01	0.27	0.03726	0.00018	rs2866792	chr4	106,708,112	4q24
SCAF_1103279188429	160,508	182,978	C	G	0.02	0.22	0	0.18	1	0.0000002	rs1258540	chr7	62,746,705	7q11.21
SCAF_1103279187926	74,230	176,562	T	A	0.01	0.51	0.04	0.3	1	0.00000023	rs17359629	chr1	145,059,743	1q21.1
SCAF_1103279187926	75,590	176,562	C	T	NaN	0.27	0.01	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279187926	78,243	176,562	T	C	NaN	0.29	0.02	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279187926	97,497	176,562	G	A	0.51	0.34	0.01	0.25	6.837E-060	0.00018	rs12036859	chr1	153,126,564	1q21.3
SCAF_1103279187926	136,168	176,562	A	T	NaN	0.25	0.01	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279180438	132,606	169,268	C	T	0.16	0.52	0.09	0.2	1	1.7E-026	rs747959	chr17	23,026,451	17q11.1
SCAF_1103279180438	152,054	169,268	A	G	0.93	0.68	1	0.27	0.000000001	1.1E-012	rs7406339	chr17	21,926,683	17p11.2

SCAF_1103279180438	153,938	169,268	C	G	0.22	0.47	0.05	0.24	1.25E-014	9E-023	rs9891469	chr17	23,032,179	17q11.1
SCAF_1103279180438	155,176	169,268	C	A	0.17	0.54	0.08	0.24	0.8452	2.7E-027	rs747959	chr17	23,026,451	17q11.1
SCAF_1103279187484	27,293	156,877	C	T	0	0.27	0.01	0.19	1	0.000035	rs3859935	chrX	67,047,373	Xq12
SCAF_1103279187475	123,734	140,524	A	G	0.87	0.61	0.96	0.2	0.000001725	2.7E-013	rs7179358	chr15	18,451,755	15q11.2
SCAF_1103279180259	12,833	118,878	C	T	NaN	0.27	0.02	0.15	1	NA	NA	NA	NA	NA
SCAF_1103279180259	16,978	118,878	G	A	NaN	0.36	0.03	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279180259	82,791	118,878	C	A	NaN	0.34	0.03	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279180259	90,065	118,878	A	T	0	0.21	0	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279187477	72,717	116,983	C	T	0.13	0.43	0.06	0.19	0.0006164	1E-014	rs7179358	chr15	18,451,755	15q11.2
SCAF_1103279187375	1,286	92,983	G	A	NaN	0.26	0.01	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279184675	45,022	88,285	T	G	0.71	0.24	0.76	0.19	1.615E-026	6.5E-014	rs6120328	chr20	31,663,533	20q11.22
SCAF_1103279184675	45,566	88,285	A	T	0.78	0.22	0.77	0.22	3.547E-017	1.1E-017	rs845784	chr20	26,140,655	20p11.1
SCAF_1103279187460	43,714	87,440	C	A	0.21	0.62	0.12	0.23	0.2223	0.000000011	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187460	80,674	87,440	C	A	0.17	0.47	0.04	0.27	0.001023	0.000000001	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187460	81,471	87,440	G	A	0.12	0.36	0	0.31	1	6E-024	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187460	82,865	87,440	T	A	0.83	0.35	0.83	0.19	0.001172	0.0000089	rs6490178	chr12	117,370,705	12q24.23
SCAF_1103279184115	5,672	85,204	G	A	0.12	0.4	0.05	0.19	0.0121	NA	NA	NA	NA	NA
SCAF_1103279184115	79,913	85,204	A	T	0	0.22	0	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279188124	10,878	83,573	A	T	0.18	0.54	0.06	0.28	0.05893	3E-013	rs7179358	chr15	18,451,755	15q11.2
SCAF_1103279188124	41,740	83,573	G	A	0.02	0.44	0.05	0.22	1	0.00000012	rs7179358	chr15	18,451,755	15q11.2
SCAF_1103279188124	43,835	83,573	T	C	NaN	0.25	0.01	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279184412	19,430	82,586	A	G	0.84	0.31	1	0.64	0.1483	1.1E-051	rs1151446	chr13	110,926,861	13q34
SCAF_1103279184412	39,752	82,586	G	A	0.25	0.69	0.11	0.31	0.03672	9E-022	rs4773388	chr13	110,993,251	13q34
SCAF_1103279184412	46,435	82,586	T	C	0.57	0.03	0.73	0.32	0.3475	5.4E-022	rs9555829	chr13	111,136,682	13q34
SCAF_1103279184412	71,648	82,586	C	T	0.76	0.28	0.92	0.4	0.1577	2.3E-029	rs1111850	chr13	111,085,977	13q34
SCAF_1103279184412	72,536	82,586	G	C	0.76	0.3	0.93	0.4	0.03891	6.7E-031	rs9522315	chr13	111,070,181	13q34
SCAF_1103279184412	74,517	82,586	A	T	0.81	0.26	0.99	0.65	0.4658	4.3E-043	rs9515471	chr13	111,118,097	13q34
SCAF_1103279181012	35,678	79,524	C	T	0.02	0.29	0.01	0.2	1	0.00002	rs17277515	chr14	20,178,749	14q11.2
SCAF_1103279181012	74,625	79,524	G	T	0.05	0.22	0	0.18	0.00663	0.000000065	rs6517933	chr21	13,984,840	21q11.2
SCAF_1103279181399	1,942	76,390	T	C	NaN	0.19	0	0.16	1	NA	NA	NA	NA	NA
SCAF_1103279181399	69,978	76,390	G	A	0.06	0.32	0.01	0.23	1	NA	NA	NA	NA	NA
SCAF_1103279184990	73,384	73,893	A	C	0.07	0.35	0.03	0.19	0.3939	1E-011	rs11850906	chr14	19,496,544	14q11.2
SCAF_1103279187626	46,163	69,204	A	C	0	0.7	0.09	0.36	1	NA	NA	NA	NA	NA
SCAF_1103279187626	47,976	69,204	C	G	0.16	0.64	0.07	0.35	0.6556	2.7E-018	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187626	51,038	69,204	T	C	0.07	0.61	0.09	0.28	0.6093	0.000000086	rs8138488	chr22	14,870,204	22q11.1
SCAF_1103279187626	54,749	69,204	C	T	0.11	0.64	0.04	0.43	0.0001058	0.000000042	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187626	59,504	69,204	C	T	NaN	0.32	0.93	0.38	1	NA	NA	NA	NA	NA
SCAF_1103279187720	45,300	59,016	T	C	0.12	0.5	0	0.44	0.4377	4.5E-028	rs7324712	chr13	112,080,916	13q34

SCAF_1103279187720	56,014	59,016	C	T	0.38	0.88	0.23	0.29	1	2.1E-022	rs1163858	chr13	110,957,160	13q34
SCAF_1103279187720	57,041	59,016	T	C	0.11	0.46	0.02	0.32	0.002709	8.5E-031	rs9577637	chr13	111,876,415	13q34
SCAF_1103279187720	58,477	59,016	T	C	0.62	0.1	0.8	0.35	0.9032	3E-024	rs1163858	chr13	110,957,160	13q34
SCAF_1103279187778	14,311	55,715	C	A	NaN	0.23	0	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279188326	23,015	55,597	C	T	0.25	0.48	0	0.42	1	NA	NA	NA	NA	NA
SCAF_1103279188326	45,606	55,597	T	C	0.12	0.48	0	0.42	2.117E-009	8.8E-023	rs445659	chr9	40,085,483	9p13.1
SCAF_1103279182087	2,870	53,383	T	A	0.06	0.33	0	0.28	0.3357	1.4E-015	rs10908850	chr9	65,336,138	9q12
SCAF_1103279182087	43,005	53,383	C	T	0.06	0.35	0.01	0.26	0.3295	1.4E-017	rs7041252	chr9	67,788,172	9q12
SCAF_1103279181352	34,142	43,897	C	A	0.15	0.37	0.04	0.18	0.002066	0.0000038	rs5993792	chr22	15,509,738	22q11.1
SCAF_1103279179919	417	42,263	G	C	0.19	0.31	0.01	0.22	1	0.00014	rs7714420	chr5	74,376,083	5q13.3
SCAF_1103279187736	36,315	42,066	T	C	0.76	0.43	0.89	0.21	0.001209	3.1E-009	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187736	37,900	42,066	A	G	0.76	0.39	0.91	0.28	0.0000172	6.4E-009	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187736	39,138	42,066	G	A	0.13	0.58	0.09	0.25	0.002335	5.2E-013	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279182252	41,642	41,864	G	A	0.09	0.25	0	0.21	0.00007273	2.5E-011	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279181033	734	41,438	G	A	0	0.26	0	0.22	1	NA	NA	NA	NA	NA
SCAF_1103279181033	38,383	41,438	G	C	NaN	0.34	0.02	0.21	1	NA	NA	NA	NA	NA
SCAF_1103279182133	1,991	41,222	C	T	0.1	0.47	0.05	0.24	0.3746	0.00000019	rs2027649	chr22	14,880,040	22q11.1
SCAF_1103279182133	2,225	41,222	C	A	NaN	0.46	0	0.41	1	NA	NA	NA	NA	NA
SCAF_1103279185831	4,435	41,060	G	A	NaN	0.21	0	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279185831	39,359	41,060	G	A	NaN	0.22	0.01	0.14	1	NA	NA	NA	NA	NA
SCAF_1103279180032	10,218	39,368	G	A	NaN	0.23	0	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279185329	1,465	39,011	G	T	0.85	0.23	0	0.19	0.02621	NA	NA	NA	NA	NA
SCAF_1103279180967	1,970	39,004	G	C	NaN	0.52	0.98	0.34	1	NA	NA	NA	NA	NA
SCAF_1103279180967	36,678	39,004	T	C	0.88	0.39	0.99	0.51	6.792E-013	4.3E-018	rs1953991	chr14	19,590,944	14q11.2
SCAF_1103279180967	36,932	39,004	A	G	NaN	0.4	0.88	0.22	1	NA	NA	NA	NA	NA
SCAF_1103279187122	3,932	38,711	A	T	0.93	0.7	0.99	0.21	0.000003297	4.8E-010	rs4124921	chr1	143,584,684	1q21.1
SCAF_1103279187122	36,213	38,711	G	A	0.06	0.19	0	0.16	1.189E-010	4.9E-012	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279187122	38,109	38,711	G	T	0.01	0.27	0.01	0.19	1	0.000079	rs11846846	chr14	20,361,138	14q11.2
SCAF_1103279187122	38,468	38,711	G	A	NaN	0.39	0	0.34	1	NA	NA	NA	NA	NA
SCAF_1103279185794	34,463	38,069	T	C	0.55	0.41	0.97	0.41	0.1385	NA	NA	NA	NA	NA
SCAF_1103279188052	7,044	36,577	C	T	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279188017	20,258	34,319	A	G	0.88	0.35	0.96	0.44	7.56E-013	1.3E-016	rs1953991	chr14	19,590,944	14q11.2
SCAF_1103279188017	31,805	34,319	A	G	0.8	0.35	0.97	0.47	0.001081	4.8E-012	rs11158599	chr14	19,608,234	14q11.2
SCAF_1103279179733	6,639	31,033	G	C	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279187369	6,972	28,964	C	T	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279179890	5,000	27,533	A	G	0.7	0.29	0.77	0.17	0.4217	6.2E-024	rs11584983	chr1	204,835,670	1q32.1
SCAF_1103279179890	13,607	27,533	G	T	0.73	0.29	0.86	0.27	0.8874	1E-029	rs11584983	chr1	204,835,670	1q32.1
SCAF_1103279179890	13,701	27,533	C	T	0.72	0.33	0.88	0.27	0.8883	1.2E-027	rs11584983	chr1	204,835,670	1q32.1

SCAF_1103279179890	13,784	27,533	G	A	0.75	0.39	0.02	0.26	1	6.4E-009	rs10784709	chr12	67,084,267	12q15
SCAF_1103279187934	9,494	26,514	T	C	NaN	0	0.63	0.25	1	NA	NA	NA	NA	NA
SCAF_1103279187526	12,615	25,584	G	A	0.03	0.19	0	0.16	0.2045	1.4E-009	rs17277515	chr14	20,178,749	14q11.2
SCAF_1103279187526	20,185	25,584	G	A	0.09	0.24	0	0.2	0.1443	1.1E-017	rs17111750	chr14	19,980,248	14q11.2
SCAF_1103279182830	1,870	22,526	T	C	0.77	0.54	0.93	0.19	0.003497	3.3E-010	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279182830	2,753	22,526	T	C	0.83	0.53	0.96	0.27	0.003759	6E-014	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279183386	13,224	21,096	C	G	0.51	0.03	0.57	0.19	0.02003	6.9E-019	rs10438921	chr18	17,049,476	18q11.1
SCAF_1103279183386	13,323	21,096	G	T	NaN	0.03	0.65	0.25	1	NA	NA	NA	NA	NA
SCAF_1103279180463	18,061	21,025	C	T	0.46	0.02	0.62	0.23	2.89E-008	3.1E-012	rs2855981	chr7	142,176,424	7q34
SCAF_1103279187972	13,065	20,990	C	A	0.55	0.12	0.69	0.21	0.000003202	2E-020	rs845796	chr20	26,173,145	20p11.1
SCAF_1103279187072	433	17,538	G	T	0.16	0.52	0.05	0.29	1.641E-007	1.3E-016	rs12146056	chr1	120,991,757	1p11.2
SCAF_1103279186364	9,142	17,346	T	C	NaN	0.32	0.01	0.23	1	NA	NA	NA	NA	NA
SCAF_1103279186364	9,686	17,346	T	A	0	0.57	0.12	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279186364	11,853	17,346	C	A	NaN	0.44	0.06	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279186364	14,696	17,346	T	A	NaN	0.25	0	0.21	1	NA	NA	NA	NA	NA
SCAF_1103279182869	12,885	16,214	C	T	0.03	0.19	0	0.16	1	0.000048	rs1406987	chrX	50,400,324	Xp11.22
SCAF_1103279182884	15,315	15,900	A	C	0.83	0.48	0.89	0.17	0.02909	0.00014	rs6047484	chr20	21,489,737	20p11.22
SCAF_1103279180486	11,648	15,015	G	T	0.11	0.29	0.02	0.17	0.007188	0.0000019	rs2740566	chr7	99,253,341	7q22.1
SCAF_1103279185707	1,128	14,392	C	G	NaN	0.54	0.97	0.29	1	NA	NA	NA	NA	NA
SCAF_1103279185707	1,897	14,392	A	G	NaN	0.55	0.08	0.25	1	NA	NA	NA	NA	NA
SCAF_1103279185707	2,065	14,392	T	C	NaN	0.53	0.1	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279182409	11,698	14,313	A	G	0.78	0.38	0.83	0.17	0.2395	0.000000018	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279182011	10,656	14,258	G	C	NaN	0.24	0	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279180476	3,836	14,211	A	G	0.48	0	0.61	0.24	0.3561	3.4E-019	rs4307023	chr4	1,510,197	4p16.3
SCAF_1103279180476	3,852	14,211	C	G	0.48	0	0.67	0.29	0.2486	4.4E-019	rs4307023	chr4	1,510,197	4p16.3
SCAF_1103279180476	3,926	14,211	A	G	0.48	0.01	0.67	0.28	0.5611	2.7E-019	rs10050053	chr4	1,533,980	4p16.3
SCAF_1103279180476	4,694	14,211	C	T	0.48	0	0.68	0.3	0.3561	7.2E-019	rs4307023	chr4	1,510,197	4p16.3
SCAF_1103279180476	6,103	14,211	C	T	0.48	0	0.63	0.25	0.3561	1.2E-018	rs10050053	chr4	1,533,980	4p16.3
SCAF_1103279183743	10,873	13,950	C	T	0.96	0.29	0.94	0.44	1	0.000000011	rs4539525	chr14	19,551,185	14q11.2
SCAF_1103279186290	1,523	13,155	G	C	0.46	0.55	0.96	0.25	3.774E-035	1.8E-025	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279180693	1,884	12,732	G	A	NaN	0.27	0.01	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279180693	1,970	12,732	G	A	NaN	0.22	0.01	0.14	1	NA	NA	NA	NA	NA
SCAF_1103279181016	9,958	12,716	T	C	0.47	0	0.5	0.17	1.61E-035	0.00000074	rs11180159	chr12	73,365,636	12q21.1
SCAF_1103279183150	9,341	12,207	T	G	0.8	0.39	0.87	0.21	0.1101	1.4E-016	rs4911368	chr20	31,885,403	20q11.22
SCAF_1103279183297	9,965	12,068	G	T	0.73	0.27	0.93	0.43	7.048E-048	1.7E-021	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279188035	3,214	11,897	G	A	0.02	0.3	0.01	0.21	1	NA	NA	NA	NA	NA
SCAF_1103279186405	960	11,846	A	G	0.13	0.46	0	0.41	1.195E-009	4.5E-026	rs445659	chr9	40,085,483	9p13.1
SCAF_1103279186312	10,066	11,331	C	A	0	0.43	0.05	0.21	1	NA	NA	NA	NA	NA

SCAF_1103279180654	7,266	11,273	G	T	0	0.3	0	0.26	1	NA	NA	NA	NA	NA
SCAF_1103279184048	10,064	11,060	A	G	NaN	0.27	0.01	0.19	1	NA	NA	NA	NA	NA
SCAF_1103279180200	335	10,712	T	C	0.88	0.55	0.99	0.35	0.06153	2.7E-015	rs17111750	chr14	19,980,248	14q11.2
SCAF_1103279180200	8,812	10,712	A	G	0.46	0.05	0.57	0.17	3.643E-009	0.0000011	rs10484226	chr14	19,580,947	14q11.2
SCAF_1103279180743	6,691	9,219	T	A	0.01	0.41	0.06	0.17	1	0.000012	rs11633626	chr15	93,072,382	15q26.2
SCAF_1103279180743	6,693	9,219	G	A	0.24	0.45	0.05	0.23	1.118E-008	5.1E-009	rs4239845	chr22	15,332,978	22q11.1
SCAF_1103279184705	580	8,311	G	C	0.1	0.39	0	0.34	1.487E-009	3.3E-017	rs41347645	chr3	164,714,286	3q26.1
SCAF_1103279184705	2,064	8,311	G	C	0.1	0.31	0	0.26	0.000000004	6.6E-020	rs41347645	chr3	164,714,286	3q26.1
SCAF_1103279184705	3,272	8,311	A	T	0.1	0.38	0	0.33	0.000000008	2E-019	rs41347645	chr3	164,714,286	3q26.1
SCAF_1103279184705	5,183	8,311	G	A	0.12	0.29	0.02	0.17	1.782E-015	0.0000019	rs16853454	chr3	170,504,122	3q26.2
SCAF_1103279188008	3,224	8,133	A	G	0.17	0.84	0.13	0.41	0.00004331	1.4E-015	rs12577327	chr11	24,355,673	11p14.3
SCAF_1103279180372	952	6,413	T	C	0.66	0.22	0.94	0.51	2.121E-021	1E-042	rs12047343	chr1	30,696,373	1p35.2
SCAF_1103279180372	1,175	6,413	A	G	0.83	0.2	0.95	0.56	0.0001373	4.3E-043	rs12047343	chr1	30,696,373	1p35.2
SCAF_1103279180372	1,593	6,413	T	C	0.65	0.16	0.97	0.68	3.652E-018	1.3E-038	rs419355	chr1	30,762,790	1p35.2
SCAF_1103279180372	2,885	6,413	T	A	0.65	0.2	0.87	0.37	4.379E-023	1.4E-034	rs419355	chr1	30,762,790	1p35.2
SCAF_1103279180372	5,715	6,413	A	G	0.62	0.16	0.94	0.57	9.023E-024	3.4E-029	rs419355	chr1	30,762,790	1p35.2
SCAF_1103279187968	4,075	6,193	C	A	0.41	0.35	0.04	0.17	2.442E-015	NA	NA	NA	NA	NA
SCAF_1103279182969	334	5,851	G	A	0.23	0.46	0.06	0.21	5.263E-009	4.7E-042	rs2821796	chr21	13,571,669	21q11.2
SCAF_1103279182969	3,537	5,851	T	A	NaN	0.31	0.01	0.22	1	NA	NA	NA	NA	NA
SCAF_1103279183789	2,662	5,748	G	A	0.12	0.51	0.1	0.18	0.002478	3.6E-019	rs12146056	chr1	120,991,757	1p11.2
SCAF_1103279187432	3,872	5,567	T	G	NaN	0.23	0.01	0.15	1	NA	NA	NA	NA	NA
SCAF_1103279180389	4,741	5,542	T	A	0	0.08	0.61	0.18	1	NA	NA	NA	NA	NA
SCAF_1103279187875	3,772	5,520	T	C	0.15	0.48	0.08	0.19	0.4247	0.000017	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279181625	4,835	5,487	C	T	NaN	0.33	0	0.28	1	NA	NA	NA	NA	NA
SCAF_1103279187902	3,165	5,451	C	A	NaN	0.76	0.99	0.16	1	NA	NA	NA	NA	NA
SCAF_1103279180133	4,138	5,409	T	G	0.06	0.23	0	0.19	0.1335	5E-014	rs35882728	chr9	44,804,684	9p11.2
SCAF_1103279188031	1,130	5,318	T	C	NaN	0.8	1	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279183543	2,037	5,204	A	C	0.34	0	0.51	0.17	1.816E-029	0.000036	rs2477849	chr6	67,365,655	6q12
SCAF_1103279186877	1,243	4,819	T	C	0.78	0.31	0.87	0.27	0.001173	1.2E-009	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279186877	1,490	4,819	G	C	NaN	0.36	0.89	0.27	1	NA	NA	NA	NA	NA
SCAF_1103279186877	4,004	4,819	T	C	0.79	0.42	0.92	0.27	0.0008758	1.3E-012	rs2027649	chr22	14,880,040	22q11.1
SCAF_1103279186877	4,081	4,819	T	C	0.77	0.42	0.86	0.18	0.002392	0.000000002	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279186877	4,182	4,819	T	C	0.76	0.39	0.86	0.2	0.00007126	0.00000024	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279183691	2,483	4,672	G	T	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279184070	3,007	4,648	T	G	0.91	0.34	0.83	0.2	0.1492	1.7E-011	rs2319971	chr1	120,928,505	1p11.2
SCAF_1103279187659	972	4,505	C	T	0.03	0.32	0.01	0.23	1	1.6E-010	rs9618954	chr22	15,850,779	22q11.1
SCAF_1103279187659	1,103	4,505	A	G	0.18	0.34	0.03	0.18	0.5718	3.8E-011	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187753	1,272	4,339	A	G	0.53	0.52	0.09	0.2	5.966E-045	NA	NA	NA	NA	NA

SCAF_1103279187753	3,721	4,339	C	T	0.38	0.48	0.06	0.23	1	0.00000006	rs6986204	chr8	77,407,886	8q21.11
SCAF_1103279180853	2,469	4,329	C	A	0.01	0.38	0	0.33	1	0.000006	rs2027649	chr22	14,880,040	22q11.1
SCAF_1103279180853	3,459	4,329	G	C	0.18	0.55	0.06	0.29	0.5678	2.1E-013	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279187631	2,414	4,290	G	A	0.03	0.38	0.02	0.25	1	0.000000056	rs2027649	chr22	14,880,040	22q11.1
SCAF_1103279187631	3,052	4,290	G	A	NaN	0.19	0	0.16	1	NA	NA	NA	NA	NA
SCAF_1103279187631	3,608	4,290	C	G	NaN	0.68	0.98	0.2	1	NA	NA	NA	NA	NA
SCAF_1103279187631	4,116	4,290	G	A	0.02	0.32	0.02	0.2	0.1351	0.000079	rs17277515	chr14	20,178,749	14q11.2
SCAF_1103279182164	1,738	4,274	A	G	NaN	0.33	0.01	0.24	1	NA	NA	NA	NA	NA
SCAF_1103279186561	1,628	4,103	T	A	0.83	0.32	1	0.63	5.129E-011	9.9E-020	rs10484226	chr14	19,580,947	14q11.2
SCAF_1103279187445	1,597	3,987	C	T	NaN	0.41	0.92	0.28	1	NA	NA	NA	NA	NA
SCAF_1103279180207	2,996	3,965	G	C	0.11	0.25	0	0.21	0.03405	1.4E-019	rs1953991	chr14	19,590,944	14q11.2
SCAF_1103279187012	3,010	3,910	G	A	0.19	0.46	0.07	0.19	6.867E-007	4.8E-009	rs5748662	chr22	15,272,858	22q11.1
SCAF_1103279188030	1,493	3,859	T	C	NaN	0.37	0.88	0.24	1	NA	NA	NA	NA	NA
SCAF_1103279187639	2,645	3,766	G	A	NaN	0.2	0	0.17	1	NA	NA	NA	NA	NA
SCAF_1103279181079	3,077	3,640	G	A	0.5	0.55	0.04	0.34	1.577E-089	NA	NA	NA	NA	NA
SCAF_1103279181192	1,163	3,483	A	G	0.5	0.51	1	0.43	1.277E-074	0.00011	rs7921170	chr10	70,802,255	10q21.3
SCAF_1103279187162	1,215	3,448	C	G	0.66	0.32	0.78	0.16	0.2476	0.000000001	rs12709102	chr16	87,239,820	16q24.3
SCAF_1103279187162	3,333	3,448	G	T	0.66	0.34	0.81	0.17	0.4392	1.1E-010	rs3751679	chr16	87,182,252	16q24.2
SCAF_1103279187285	421	3,421	G	A	NaN	0	0.67	0.29	1	NA	NA	NA	NA	NA
SCAF_1103279184284	676	3,190	G	T	NaN	0.33	0	0.28	1	NA	NA	NA	NA	NA
SCAF_1103279187453	2,266	3,012	G	C	0.23	0.29	0	0.25	0.04807	NA	NA	NA	NA	NA
SCAF_1103279187453	2,271	3,012	T	C	0.75	0.56	0.98	0.3	2.067E-007	NA	NA	NA	NA	NA

Supplementary Table 2. Unlocalized scaffolds analyzed in this study.

SCAF: genomic scaffold; SNPS: number of SNPs from the scaffold successfully mapped; MAPTO: identified localization; LENGTH: full length of the scaffold; SATELLITE: amount of satellite sequence; NOSEQ: amount of missing sequence; CHR, FROM, TO, BAND: best alignments to hg19 from the UCSC segmental duplication track for hg19 unplaced contigs and computed in this study for HuRef unplaced scaffolds; PRIMARY / SECONDARY: chromosomal assignments and FISH assignments for hg19 unplaced contigs and primary and secondary FISH assignments for HuRef unplaced scaffolds. Unplaced scaffolds SCAF_1103279188373, SCAF_1103279182504, SCAF_1103279187554, and SCAF_1103279188164 are almost certainly alternative haplotypes of sequence already present in hg19 rather than novel sequence missing from the human reference genome. Due to lack of SNPs assayed in the short arms of acrocentric chromosomes, scaffolds mapped to regions 13q11, 14q11.2, 15q11.2, 21q11.2, and 22q11.1 should be interpreted as mapped to any locus in the corresponding pericentromeric region or short arm.

SCAF	SNPS	MAPTO	LENGTH	SATELLITE	NOSEQ	CHR	FROM	TO	BAND	PRIMARY / SECONDARY
GL000191	1	1p36.11	106,433	0	0	chr1	24,256,638	24,363,222	1p36.11	chr1
GL000192	2	1q21.1	547,496	0	0	chr16	70,845,287	71,202,573	16q22.2	chr1
GL000193	2	21q11.2	189,789	27,021	0	chr21	10,365,977	10,400,000	21p11.2	chr4 / 13p11.1-13p11.2 21q11.1-21q11.2 4q28 9q12 14p11.1-14p11.2 4q35 9p12
GL000194	0	NA	191,469	13,222	0	NA	NA	NA	NA	chr4
GL000195	0	NA	182,896	10,867	0	NA	NA	NA	NA	chr7 / 15p13 14p13 13p13 22p13 21p13
GL000196	0	NA	38,914	0	0	chr8	48,180,605	48,216,171	8q11.21	chr8
GL000197	0	NA	37,175	0	0	chr8	21,624,542	21,662,068	8p21.3	chr8
GL000198	0	NA	90,085	56,883	0	NA	NA	NA	NA	chr9
GL000199	1	9p11.2	169,874	166,937	0	NA	NA	NA	NA	chr9
GL000200	0	NA	187,035	0	0	chr9	44,451,829	44,639,037	9p11.2	chr9
GL000201	0	NA	36,148	0	0	chr9	136,416,914	136,453,838	9q34.2	chr9
GL000202	0	NA	40,103	0	0	chr11	69,717,484	69,788,767	11q13.3	chr11
GL000203	0	NA	37,498	0	0	chr17	21,670,281	21,700,252	17p11.2	chr17
GL000204	4	17q25.3	81,310	0	0	chr17	77,462,381	77,494,566	17q25.3	chr17
GL000205	0	NA	174,588	50,795	0	NA	NA	NA	NA	chr17 / 15p13 14p13 13p13 22p13 21p13
GL000206	0	NA	41,001	0	0	chr17	81,110,123	81,150,656	17q25.3	chr17
GL000207	0	NA	4,262	0	0	NA	NA	NA	NA	chr18
GL000208	0	NA	92,689	71,831	0	NA	NA	NA	NA	chr19 / 9q32-9q34.11
GL000209	0	NA	159,169	0	0	NA	NA	NA	NA	chr19
GL000210	0	NA	27,682	0	0	chr21	44,682,665	44,710,462	21q22.3	chr21
GL000211	0	NA	166,566	8,434	0	NA	NA	NA	NA	
GL000212	3	13q11	186,858	1,793	0	NA	NA	NA	NA	13cen 22cen 2p11.2-2p12
GL000213	0	NA	164,239	0	0	chr21	14,957,544	15,121,905	21q11.2	
GL000214	0	NA	137,718	7,069	0	NA	NA	NA	NA	
GL000215	0	NA	172,545	0	0	chr21	15,028,102	15,200,573	21q11.2	

GL000216	0	NA	172,294	112,373	0	NA	NA	NA	NA	
GL000217	0	22q11.1	172,149	45	0	chr21	9,421,761	9,593,540	21p11.2	
GL000218	0	NA	161,147	7,862	0	NA	NA	NA	NA	
GL000219	0	NA	179,198	23,907	0	NA	NA	NA	NA	
GL000220	1	11q25	161,802	0	0	NA	NA	NA	NA	
GL000221	0	NA	155,397	2,196	0	chr1	142,811,462	142,966,511	1q21.1	
GL000222	1	3p12.3	186,861	16,939	0	chr3	75,615,943	75,802,717	3p12.3	
GL000223	0	NA	180,455	0	0	chr12	133,502,306	133,682,662	12q24.33	
GL000224	0	NA	179,693	69,138	0	NA	NA	NA	NA	
GL000225	0	NA	211,173	127,131	0	NA	NA	NA	NA	
GL000226	0	NA	15,008	15,003	0	NA	NA	NA	NA	
GL000227	0	NA	128,374	0	0	chr6	74,669	202,273	6p25.3	
GL000228	0	NA	129,120	13,589	0	chr4	190,915,843	191,014,418	4q35.2	
GL000229	0	NA	19,913	0	0	NA	NA	NA	NA	
GL000230	2	14q11.2	43,691	14,367	0	NA	NA	NA	NA	
GL000231	0	NA	27,386	784	0	NA	NA	NA	NA	
GL000232	0	NA	40,652	439	0	NA	NA	NA	NA	
GL000233	0	NA	45,941	14,463	0	NA	NA	NA	NA	
GL000234	0	NA	40,531	646	0	NA	NA	NA	NA	
GL000235	1	14q11.2	34,474	1,484	0	NA	NA	NA	NA	
GL000236	0	NA	41,934	0	0	chr22	16,961,913	17,003,620	22q11.1	
GL000237	0	NA	45,867	0	0	NA	NA	NA	NA	
GL000238	0	NA	39,939	0	0	chr22	17,156,570	17,196,365	22q11.1	
GL000239	0	NA	33,824	0	0	NA	NA	NA	NA	
GL000240	0	NA	41,933	3,610	0	NA	NA	NA	NA	
GL000241	0	NA	42,152	0	0	NA	NA	NA	NA	
GL000242	0	NA	43,523	0	0	chr22	25,411,158	25,454,636	22q11.23	
GL000243	0	NA	43,341	7,992	0	chr21	9,678,584	9,721,852	21p11.2	
GL000244	0	NA	39,929	2,779	0	chr22	16,073,977	16,113,899	22q11.1	
GL000245	0	NA	36,651	0	0	chr1	142,918,834	142,955,514	1q21.1	
GL000246	0	NA	38,154	0	0	chr22	17,240,160	17,278,332	22q11.1	
GL000247	0	NA	36,422	5,059	0	chr1	143,425,582	143,462,000	1q21.1	
GL000248	1	22q12.3	39,786	0	0	chr22	33,050,701	33,090,472	22q12.3	
GL000249	0	NA	38,502	0	0	chr22	28,217,109	28,255,612	22q12.1	
SCAF_1103279188373	2	Xp22.33	1,612,812	142	112,063	chrX	284,308	2,068,238	Xp22.33	
SCAF_1103279188110	0	NA	716,511	508,890	23,941	chr18	15,165,346	15,187,027	18p11.21	
SCAF_1103279188197	4	20p11.21	688,672	169,187	4,015	chr7	57,721,772	57,750,628	7p11.2	15p13 20cen 22cen 14cen / 2q13
SCAF_1103279188252	0	NA	392,061	199,366	21,032	chrUn_gl000234	0	37,526	NA	

SCAF_1103279187452	3	20q11.22	363,655	174,743	45,424	chr9_gl000198_random	55,900	90,085	NA	20q11 / 9qh 13cen 14cen 15cen 21cen 22cen
SCAF_1103279187554	0	4p16.1	356,219	11,754	5,290	chr4	8,818,203	9,158,154	4p16.1	4p16 8p22 / 3q21 3p12 11p15 11q13 7q22
SCAF_1103279180085	1	3p11.1	305,597	53,956	21,262	chr6	57,369,236	57,608,453	6p11.2	6p12.1 3p14
SCAF_1103279186763	0	NA	299,293	88,411	664	chrUn_gl000224	41,064	179,656	NA	
SCAF_1103279187930	2	17p11.2	280,839	193,529	11,357	chr7	61,747,443	61,803,068	7q11.21	7cen 22cen 16cen / 1cen 2cen 17cen
SCAF_1103279188164	5	6p21.32	275,343	0	30,524	chr6_mann_hap4	3,945,017	4,121,517	6p21.32	
SCAF_1103279188189	0	NA	274,328	15,004	3,717	chrUn_gl000211	41,610	166,160	NA	13cen 22cen 9q13 / 14cen 15cen 21cen 1q12 4p12
SCAF_1103279181781	1	17p11.2	263,990	174,138	3,780	chr2	91,639,392	91,669,482	2p11.1	
SCAF_1103279181222	0	NA	261,077	16,481	24,687	chr2	92,150,858	92,205,985	2p11.1	2cen 14cen 22cen 16cen / 9q21 9cen 15cen 13cen 10cen 1q11
SCAF_1103279187792	4	1p11.2	251,763	161,398	4,490	NA	NA	NA	NA	1q11 16q21 / 2p12 7q12
SCAF_1103279188241	2	17p11.2	245,808	129,699	21,351	chr17	21,207,781	21,245,119	17p11.2	17cen / 17p
SCAF_1103279188290	0	NA	239,334	97,673	111,702	chrUn_gl000216	19,591	81,397	NA	
SCAF_1103279188305	2	9p11.2	238,759	130,831	28,111	chr16	46,447,878	46,469,228	16q11.2	9p11
SCAF_1103279179615	2	20p11.1	225,507	81,686	2,450	chrUn_gl000232	6,701	40,652	NA	
SCAF_1103279188307	2	1q21.1	215,476	56,688	46,598	NA	NA	NA	NA	1q11 16q11.2 7cen / 2p11.2 3p21.3 17p11
SCAF_1103279188266	0	NA	210,595	97,218	60,385	chr10	135,461,048	135,474,303	10q26.3	
SCAF_1103279181001	0	NA	196,548	75,195	90,307	chrUn_gl000225	0	47,891	NA	
SCAF_1103279188429	1	7q11.21	182,978	58,865	10,465	NA	NA	NA	NA	1q12 7cen 16q11 / 2cen 9cen 13cen 14cen 15cen 22cen
SCAF_1103279187926	1	1q21.1	176,562	62,905	92,471	NA	NA	NA	NA	
SCAF_1103279180438	4	17q11.1	169,268	9,516	6,136	chr17	21,193,718	21,353,727	17p11.2	17p11
SCAF_1103279187484	0	NA	156,877	15,369	88	chrUn_gl000224	58,402	110,666	NA	1q12 16p13 15q11 / 14cen 13cen
SCAF_1103279187475	1	15q11.2	140,524	0	85	chrUn_gl000220	93,145	101,616	NA	20cen / 15cen 13cen 22cen
SCAF_1103279187442	0	NA	138,126	120,288	458	chr21	10,740,238	10,753,197	21p11.2	
SCAF_1103279184113	0	NA	128,177	74,286	46,491	NA	NA	NA	NA	
SCAF_1103279182504	0	4q13.2	119,939	0	11,286	chr4	69,372,276	69,488,104	4q13.2	
SCAF_1103279180259	0	NA	118,878	37,920	63,617	NA	NA	NA	NA	
SCAF_1103279187477	1	15q11.2	116,983	42,556	16,278	NA	NA	NA	NA	
SCAF_1103279187589	0	NA	112,505	71,533	28,494	NA	NA	NA	NA	
SCAF_1103279187167	0	NA	89,142	2,559	0	NA	NA	NA	NA	9cen 13cen 15cen 20cen 21cen 22cen / 9q2 14cen 4q3
SCAF_1103279181475	0	NA	88,633	63,846	22,688	NA	NA	NA	NA	
SCAF_1103279184675	2	20p11.1	88,285	32,597	53,012	NA	NA	NA	NA	
SCAF_1103279187460	3	22q11.1	87,440	21,156	61,297	NA	NA	NA	NA	
SCAF_1103279188124	2	15q11.2	83,573	68,769	219	chr16	33,969,092	33,990,762	16p11.2	
SCAF_1103279184412	6	13q34	82,586	0	1,297	NA	NA	NA	NA	13q34
SCAF_1103279181012	1	21q11.2	79,524	19,750	50,213	NA	NA	NA	NA	
SCAF_1103279184990	1	14q11.2	73,893	33,687	3,736	chrUn_gl000231	12,658	25,586	NA	13cen 14cen 15cen 20cen 21cen 22cen
SCAF_1103279187931	0	17p11.1	72,524	10,516	1,043	chr17	21,303,089	21,353,727	17p11.2	
SCAF_1103279187626	3	22q11.1	69,204	26,166	13,923	NA	NA	NA	NA	22p11.2 / 20cen 9p13 14cen 15cen

SCAF_1103279187720	4	13q34	59,016	0	443	NA	NA	NA	NA	13q33
SCAF_1103279181301	0	NA	58,705	15,505	4,982	chr2	91,635,751	91,657,138	2p11.1	7p11 / 2cen 1qh 16qh
SCAF_1103279188326	1	9p13.1	55,597	35,769	17,300	NA	NA	NA	NA	
SCAF_1103279182997	0	NA	55,026	0	13,476	chr7	65,255,106	65,286,510	7q11.21	7q11
SCAF_1103279182087	2	9q12	53,383	19,547	31,867	NA	NA	NA	NA	
SCAF_1103279185025	0	NA	52,016	13,997	36,717	NA	NA	NA	NA	9q12
SCAF_1103279183688	0	NA	50,612	561	0	chrUn_gl000232	0	14,986	NA	1q42
SCAF_1103279187616	0	22q11.1	48,268	912	0	chr2	37,958,019	38,003,219	2p22.2	
SCAF_1103279187736	3	22q11.1	42,066	8,727	31,235	NA	NA	NA	NA	
SCAF_1103279182252	1	22q11.1	41,864	7,147	32,600	NA	NA	NA	NA	
SCAF_1103279182133	1	22q11.1	41,222	4,324	33,170	NA	NA	NA	NA	
SCAF_1103279180967	1	14q11.2	39,004	5,546	30,466	NA	NA	NA	NA	
SCAF_1103279187122	2	1p11.2	38,711	3,357	31,341	NA	NA	NA	NA	
SCAF_1103279188017	2	14q11.2	34,319	18,527	13,907	NA	NA	NA	NA	
SCAF_1103279179890	4	1q32.1	27,533	0	1,578	NA	NA	NA	NA	
SCAF_1103279187526	2	14q11.2	25,584	0	0	chrUn_gl000224	96,542	110,555	NA	
SCAF_1103279182830	2	22q11.1	22,526	2,992	14,982	NA	NA	NA	NA	
SCAF_1103279183386	1	18q11.1	21,096	12,699	6,752	NA	NA	NA	NA	
SCAF_1103279180463	1	7q34	21,025	0	532	chr7	142,466,550	142,486,382	7q34	
SCAF_1103279187972	1	20p11.1	20,990	15,498	5,488	NA	NA	NA	NA	
SCAF_1103279187072	1	1p11.2	17,538	10,461	6,236	NA	NA	NA	NA	
SCAF_1103279180486	1	7q22.1	15,015	0	7,893	chr7	100,546,668	100,611,888	7q22.1	
SCAF_1103279182409	1	22q11.1	14,313	2,830	9,783	NA	NA	NA	NA	
SCAF_1103279180476	5	4p16.3	14,211	0	875	NA	NA	NA	NA	
SCAF_1103279183743	1	14q11.2	13,950	6,159	7,095	NA	NA	NA	NA	
SCAF_1103279186290	1	22q11.1	13,155	4,677	7,860	NA	NA	NA	NA	
SCAF_1103279181016	1	12q21.1	12,716	8,919	3,139	NA	NA	NA	NA	
SCAF_1103279183150	1	20q11.22	12,207	6,666	4,969	NA	NA	NA	NA	
SCAF_1103279183297	1	22q11.1	12,068	7,117	3,308	NA	NA	NA	NA	
SCAF_1103279186405	1	9p13.1	11,846	4,661	6,844	NA	NA	NA	NA	
SCAF_1103279180200	2	14q11.2	10,712	2,912	7,169	NA	NA	NA	NA	
SCAF_1103279180743	1	22q11.1	9,219	7,221	0	NA	NA	NA	NA	
SCAF_1103279184705	4	3q26.1	8,311	0	0	chr3	163,104,167	163,104,610	3q26.1	
SCAF_1103279188008	1	11p14.3	8,133	0	0	chr11	24,392,500	24,394,019	11p14.3	
SCAF_1103279180372	5	1p35.2	6,413	0	0	chr1	30,878,560	30,879,782	1p35.2	
SCAF_1103279182969	1	21q11.2	5,851	5,850	0	NA	NA	NA	NA	
SCAF_1103279183789	1	1p11.2	5,748	5,568	0	NA	NA	NA	NA	
SCAF_1103279180133	1	9p11.2	5,409	5,407	0	chr9	66,860,506	66,863,343	9q13	

SCAF_1103279186877	4	22q11.1	4,819	2,807	378	NA	NA	NA	NA	
SCAF_1103279184070	1	1p11.2	4,648	4,647	0	NA	NA	NA	NA	
SCAF_1103279187659	2	22q11.1	4,505	4,447	0	NA	NA	NA	NA	
SCAF_1103279187753	1	8q21.11	4,339	4,338	0	NA	NA	NA	NA	
SCAF_1103279180853	2	22q11.1	4,329	3,944	0	NA	NA	NA	NA	
SCAF_1103279187631	1	22q11.1	4,290	2,160	0	NA	NA	NA	NA	
SCAF_1103279186561	1	14q11.2	4,103	1,994	317	NA	NA	NA	NA	
SCAF_1103279180207	1	14q11.2	3,965	0	0	NA	NA	NA	NA	
SCAF_1103279187012	1	22q11.1	3,910	2,469	369	NA	NA	NA	NA	
SCAF_1103279187162	2	16q24.2	3,448	0	0	NA	NA	NA	NA	

Supplementary Table 3. Re-mapped SNPs in the CARe and ICDB dataset outside of the *HYDIN* locus.

CHR, ID, BP, BAND: assigned chromosome, SNP rsID, hg19 coordinate, and localization; MAF: minor allele frequency; HWE: p-value from Hardy-Weinberg equilibrium test; P: p-value for association from a one-tailed Pearson correlation test of the adjusted genotypes for the mismapped SNP with the local ancestry inferred at the ancestry-informative SNP; CHR', ID', BP', BAND': chromosome, SNP rsID, hg19 coordinate, and localization of the ancestry-informative SNP for which the local ancestry best represents the location of the mismapped SNP; SEGDUP, RMSK, DGVSV, MULT, SUNS: whether the SNP falls within a known segmental duplication, a repetitive element, a structural variation from the database of Genomic Variants, if it has multiple locations according to dbSNP, if it localizes over a single unique nucleotide.

CHR	ID	BP	BAND	MAF	HWE	P	CHR'	ID'	BP'	BAND'	SEGDUP	RMSK	DGVSV	MULT	SUNS
chr1	rs2533899	83,609,311	1p31.1	0.11	0.000058	9.7E-054	chr7	rs3898649	75,546,892	7q11.23	yes	yes	yes	yes	yes
chr1	rs17841791	83,788,830	1p31.1	0.02	0.29	6.6E-110	chr7	rs1167796	75,173,180	7q11.23	yes	no	yes	no	no
chr1	rs4241009	142,569,068	1q12	0.2	0.00000097	1.9E-100	chr4	rs6554227	52,984,391	4q12	yes	yes	yes	yes	yes
chr1	rs6668639	143,373,529	1q21.1	0.08	2E-042	4.5E-012	chr22	rs5748662	16,892,858	22q11.1	yes	no	yes	yes	no
chr1	rs4058419	143,982,530	1q21.1	0.17	0.36	4.1E-273	chr1	rs291090	207,114,037	1q32.1	yes	no	yes	yes	no
chr1	rs6700467	144,048,591	1q21.1	0.08	0.0074	7.6E-027	chr1	rs1041311	205,456,028	1q32.1	yes	no	yes	no	no
chr1	rs477524	144,052,046	1q21.1	0.05	0.059	1.5E-014	chr1	rs10900456	205,145,005	1q32.1	yes	yes	yes	no	yes
chr1	rs41450550	188,446,241	1q31.1	0.06	0.92	9.6E-241	chr6	rs1495543	65,485,019	6q12	no	yes	no	no	no
chr2	rs41509444	37,960,683	2p22.2	0.31	0.00000048	5.9E-061	chr22	rs8139954	17,238,335	22q11.1	no	no	yes	no	no
chr2	rs41421545	37,960,995	2p22.2	0.34	0.00006	6.2E-063	chr22	rs5992665	17,810,483	22q11.1	no	no	yes	no	no
chr2	rs2373298	37,987,192	2p22.2	0.34	0.092	1.5E-058	chr22	rs5992665	17,810,483	22q11.1	no	no	yes	no	no
chr2	rs11240831	91,773,332	2p11.1	0.12	2.2E-029	2.8E-047	chr1	rs4246521	145,625,979	1q21.1	yes	yes	yes	no	no
chr2	rs232162	91,814,117	2p11.1	0.09	4.3E-020	6E-019	chr1	rs11803553	118,522,545	1p12	yes	yes	yes	no	no
chr2	rs7340336	133,114,536	2q21.2	0.12	0.21	1.6E-039	chr20	rs11906851	30,154,237	20q11.21	yes	no	yes	no	no
chr2	rs7425124	180,221,453	2q31.2	0.14	0.031	3.3E-044	chr4	rs7682828	186,012,464	4q35.1	no	yes	no	no	no
chr3	rs6765000	619,034	3p26.3	0.08	0.00000012	3.3E-018	chr22	rs928832	17,524,190	22q11.1	yes	no	yes	no	no
chr3	rs7632506	5,785,451	3p26.1	0.18	1.8E-025	1.7E-034	chr4	rs7682828	186,012,464	4q35.1	no	yes	no	no	no
chr3	rs6656783	75,796,979	3p12.3	0.16	3.8E-013	1.3E-047	chr21	rs2822081	15,153,248	21q11.2	yes	yes	yes	yes	no
chr3	rs2313099	197,856,433	3q29	0.23	0.57	5.5E-012	chr16	rs6600162	1,753,332	16p13.3	yes	no	yes	no	no
chr4	rs2859203	45,410	4p16.3	0.13	2.3E-018	0.000000028	chr22	rs5748662	16,892,858	22q11.1	no	no	yes	no	no
chr4	rs6817919	3,582,651	4p16.3	0.21	0.42	1.4E-223	chr9	rs6606438	44,866,028	9p11.2	no	yes	yes	no	no
chr4	rs1163095	49,579,167	4p11	0.09	0.14	8.8E-023	chr22	rs5748662	16,892,858	22q11.1	yes	yes	yes	no	no
chr4	rs1848259	49,584,109	4p11	0.24	5E-011	1.2E-111	chr22	rs8139954	17,238,335	22q11.1	yes	yes	yes	no	no
chr4	rs1344424	190,557,109	4q35.2	0.08	1	9.5E-133	chr21	rs2155965	15,424,368	21q11.2	no	no	yes	no	no
chr4	rs2025529	190,637,996	4q35.2	0.15	0.00013	0.0000097	chr21	rs2821796	14,649,798	21q11.2	no	no	yes	no	no
chr6	rs1855410	57,419,605	6p11.2	0.06	0.35	2.3E-097	chr3	rs11128080	90,056,453	3p11.1	no	no	yes	no	no
chr6	rs9885765	57,462,600	6p11.2	0.02	0.022	0.0000024	chr3	rs11128080	90,056,453	3p11.1	no	yes	yes	no	no

chr6	rs3857620	57,496,076	6p11.2	0.19	0.72	4E-114	chr3	rs11128080	90,056,453	3p11.1	no	no	yes	no	no
chr6	rs2134484	66,024,729	6q12	0.08	0.25	1.1E-227	chr1	rs1415282	219,842,900	1q41	yes	yes	yes	yes	no
chr7	rs4454721	65,309,327	7q11.21	0.36	0.42	1.2E-051	chr11	rs10896596	57,020,516	11q12.1	no	yes	yes	no	no
chr7	rs4078393	65,309,486	7q11.21	0.25	0.59	6E-135	chr11	rs10896596	57,020,516	11q12.1	no	no	yes	yes	no
chr7	rs1856151	76,450,465	7q11.23	0.16	0.0043	2E-106	chr1	rs10782812	84,025,511	1p31.1	yes	no	yes	no	yes
chr7	rs2868260	76,475,878	7q11.23	0.22	0.19	3.7E-012	chr1	rs11161436	85,206,477	1p22.3	yes	no	yes	yes	yes
chr7	rs2536396	76,481,072	7q11.23	0.42	0.98	0.00016	chr1	rs6428492	89,467,787	1p22.2	yes	yes	yes	no	yes
chr7	rs2538225	76,509,506	7q11.23	0.43	0.9	8.9E-009	chr1	rs1609519	97,781,039	1p21.3	yes	no	yes	yes	yes
chr9	rs368353	38,876,225	9p13.1	0.25	1	1E-061	chr9	rs2297231	71,606,315	9q21.11	yes	no	yes	yes	no
chr9	rs11791792	72,822,973	9q21.12	0.04	0.33	7.6E-016	chr9	rs4879686	33,343,397	9p13.3	no	yes	no	no	no
chr10	rs1923940	88,778,049	10q23.2	0.09	0.000000021	1.1E-013	chr19	rs4801281	56,331,249	19q13.43	yes	no	yes	no	no
chr12	rs1500095	161,382	12p13.33	0.21	0.0058	2E-061	chr20	rs186332	62,159,468	20q13.33	yes	no	yes	no	no
chr12	rs7299571	166,333	12p13.33	0.18	0.054	<2.2e-308	chr6	rs2788237	744,998	6p25.3	no	yes	yes	no	no
chr12	rs4079417	180,472	12p13.33	0.03	0.82	0.000000058	chr6	rs10793858	1,016,984	6p25.3	yes	no	yes	no	no
chr12	rs16930856	3,955,141	12p13.32	0.03	1	1.3E-085	chr4	rs336406	143,072,608	4q31.21	yes	no	no	no	no
chr12	rs10506218	43,152,484	12q12	0.08	0.94	8.4E-015	chr1	rs1563468	2,833,743	1p36.32	no	no	yes	no	no
chr12	rs587756	123,188,731	12q24.31	0.17	0.54	7.7E-038	chr13	rs9578595	23,996,255	13q12.12	yes	yes	yes	no	no
chr13	rs3874211	19,045,720	13q11	0.01	0.0063	4.9E-012	chr21	rs2823676	17,611,773	21q21.1	yes	yes	yes	no	no
chr15	rs7179169	94,887,534	15q26.2	0.1	0.012	3.1E-029	chr12	rs305396	73,022,080	12q21.1	no	no	yes	no	no
chr21	rs240446	10,979,098	21p11.1	0.05	6.9E-009	0.00000036	chr13	rs2105076	20,905,957	13q12.11	yes	yes	yes	no	no
chr21	rs3915345	11,039,570	21p11.1	0.09	0.036	2.9E-232	chr14	rs1713411	20,822,495	14q11.2	yes	no	yes	no	no
chr21	rs4111253	11,083,847	21p11.1	0.05	0.21	1.6E-018	chr13	rs472708	19,166,576	13q11	yes	no	yes	no	no
chr21	rs209047	11,156,072	21p11.1	0.03	0.000035	9.2E-013	chr13	rs472708	19,166,576	13q11	yes	no	yes	no	no
chr21	rs4293623	14,369,207	21q11.2	0.14	0.08	1.8E-042	chr13	rs472708	19,166,576	13q11	no	yes	yes	no	no
chr21	rs11088650	14,386,013	21q11.2	0.14	0.37	2E-012	chr13	rs1345067	21,570,310	13q12.11	yes	no	yes	no	no
chr21	rs3875341	14,540,019	21q11.2	0.09	0.9	3.4E-028	chr13	rs472708	19,166,576	13q11	yes	no	yes	yes	no
chr22	rs10154759	16,061,342	22q11.1	0.05	0.3	0.000000074	chr14	rs1713411	20,822,495	14q11.2	yes	no	yes	no	no
chr22	rs2844871	16,079,243	22q11.1	0.04	0.36	7.9E-009	chr14	rs1713411	20,822,495	14q11.2	yes	yes	yes	yes	yes
chr22	rs7354790	16,081,115	22q11.1	0.15	1.3E-017	6.7E-158	chr14	rs1713411	20,822,495	14q11.2	yes	no	yes	yes	no
chr22	rs2212062	16,108,388	22q11.1	0.03	1	0.00013	chr14	rs7153404	20,550,111	14q11.2	yes	no	yes	yes	no
chr22	rs1041770	16,223,201	22q11.1	0.04	0.36	3.7E-085	chr14	rs1713411	20,822,495	14q11.2	yes	no	yes	yes	no
chr22	rs9712893	16,347,194	22q11.1	0.01	0.18	1.5E-011	chr14	rs1957333	21,227,592	14q11.2	yes	no	yes	no	no
chr22	rs8138488	16,490,204	22q11.1	0.39	0.22	0.0000012	chr14	rs1957333	21,227,592	14q11.2	yes	no	yes	yes	yes
chr22	rs2027649	16,500,040	22q11.1	0.23	0.42	0.0000014	chr14	rs1713411	20,822,495	14q11.2	yes	yes	yes	yes	no
chrX	rs5918679	66,162,538	Xq12	0.13	0.085	1.3E-028	chr5	rs2241583	132,561,277	5q31.1	no	yes	yes	no	no
chrX	rs5929223	111,768,483	Xq23	0.14	0.19	1.3E-046	chr2	rs4073566	119,161,638	2q14.2	no	yes	no	no	no
chr1	rs3929252	83,895,896	1p31.1	0.16	2E-021	0.0001	chr7	rs7794510	75,240,915	7q11.23	yes	no	yes	no	no
chr1	rs2050890	238,641,278	1q43	0.48	0.9	1.5E-028	chr16	rs2292326	84,028,123	16q23.3	no	no	yes	no	no

chr2	rs2677646	133,055,128	2q21.2	0.08	0.00001	1.8E-014	chr20	rs6120890	30,207,659	20q11.21	no	no	yes	no	no
chr6	rs7762811	344,878	6p25.3	0.16	1.5E-022	7E-014	chr16	rs7500616	31,947,241	16p11.2	no	no	yes	no	no
chr11	rs5016282	88,741,660	11q14.3	0.36	0.88	4.9E-022	chr11	rs6485802	48,051,442	11p11.2	yes	no	yes	no	no
chr20	rs159093	53,635,581	20q13.2	0.14	0.37	1E-034	chr17	rs11080292	32,998,577	17q12	no	yes	no	no	no
chr21	rs10439884	10,971,951	21p11.1	0.01	1	0.0000079	chr13	rs1335870	20,905,776	13q12.11	yes	no	yes	no	yes

Supplementary Table 4. SNPs mapped to the 16q22.2 *HYDIN* locus.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; MAF: minor allele frequency; HWE: p-value from Hardy-Weinberg equilibrium test; P: best p-value from association through admixture mapping.

CHR	ID	BP	BAND	MAF	HWE	P
chr16	rs6416701	70,850,893	16q22.2	0.47	0.9636	3.4E-279
chr16	rs13339158	70,858,121	16q22.2	0.13	0.3385	2.2E-052
chr16	rs9927184	70,874,792	16q22.2	0.15	0.5139	2.2E-045
chr16	rs13331105	70,883,845	16q22.2	0.09	0.3902	3.9E-037
chr16	rs7200463	70,884,562	16q22.2	0.13	0.5481	1.4E-060
chr16	rs9930231	70,886,409	16q22.2	0.06	0.3052	8.4E-030
chr16	rs1774414	70,891,236	16q22.2	0.11	0.7756	5E-088
chr16	rs1532832	70,894,889	16q22.2	0.47	0.4654	1.3e-308
chr16	rs13338730	70,899,939	16q22.2	0.12	0.0009412	1.5E-048
chr16	rs13338821	70,900,111	16q22.2	0.12	0.633	1.7E-049
chr16	rs1774509	70,901,176	16q22.2	0.25	0.9031	5.4E-126
chr16	rs9935910	70,902,206	16q22.2	0.1	0.9499	2.6E-045
chr16	rs7188340	70,904,026	16q22.2	0.06	0.9237	9.8E-031
chr16	rs2456147	70,905,640	16q22.2	0.08	0.7091	2E-038
chr16	rs4985432	70,913,651	16q22.2	0.06	7.446E-008	5E-019
chr16	rs9922872	70,918,800	16q22.2	0.08	0.2066	4.4E-020
chr16	rs10445012	70,924,781	16q22.2	0.06	0.008523	2E-018
chr16	rs8056750	70,927,078	16q22.2	0.08	0.8723	5.3e-312
chr16	rs8063609	70,928,414	16q22.2	0.1	0.008877	4.7E-023
chr16	rs1798459	70,930,637	16q22.2	0.02	0.38	5E-059
chr16	rs11860140	70,944,218	16q22.2	0.15	0.7145	1E-070
chr16	rs2502714	70,960,990	16q22.2	0.3	0.6838	7.9E-171
chr16	rs1774364	70,970,795	16q22.2	0.02	1	4.8E-108
chr16	rs8062472	70,971,743	16q22.2	0.13	0.05592	2.7E-060
chr16	rs2456141	70,978,362	16q22.2	0.17	0.09798	<2.2e-308
chr16	rs1877468	70,985,899	16q22.2	0.18	0.05183	<2.2e-308
chr16	rs8056914	70,990,192	16q22.2	0.08	0.6094	1.7E-039
chr16	rs8061245	70,990,985	16q22.2	0.1	0.007023	1.1E-015
chr16	rs1847594	70,993,264	16q22.2	0.45	0.8544	1.8E-019
chr16	rs6499365	70,994,202	16q22.2	0.24	0.7296	<2.2e-308
chr16	rs1774273	70,997,913	16q22.2	0.22	0.9732	2.9E-272
chr16	rs1774275	70,999,657	16q22.2	0.38	0.4551	1.2E-052
chr16	rs1798357	71,000,598	16q22.2	0.02	0.2904	9.9E-158
chr16	rs4985443	71,018,471	16q22.2	0.1	0.1326	0.0000041
chr16	rs2795675	71,022,529	16q22.2	0.22	0.8937	4.5E-253
chr16	rs1512635	71,028,623	16q22.2	0.17	0.00001312	9.7E-074
chr16	rs2458375	71,031,777	16q22.2	0.33	0.5545	3.8e-312
chr16	rs6416707	71,048,781	16q22.2	0.09	0.1112	<2.2e-308
chr16	rs6499386	71,049,391	16q22.2	0.12	0.379	<2.2e-308
chr16	rs4788728	71,066,078	16q22.2	0.22	0.4726	6E-049
chr16	rs8046772	71,068,143	16q22.2	0.09	0.1833	7.2E-031

chr16	rs9935325	71,093,625	16q22.2	0.31	0.2894	2.1E-033
chr16	rs2356033	71,097,724	16q22.2	0.3	0.7655	5.6E-043
chr16	rs6416719	71,103,114	16q22.2	0.26	0.2881	1.2E-271
chr16	rs4327057	71,107,315	16q22.2	0.01	1	8.8E-015
chr16	rs4606725	71,107,568	16q22.2	0.12	0.004089	1.8E-037
chr16	rs6499437	71,110,354	16q22.2	0.26	0.2101	6.2E-282
chr16	rs7189917	71,135,472	16q22.2	0.06	0.06662	4.1E-235
chr16	rs4502222	71,157,423	16q22.2	0	1	NA
chr16	rs16964541	71,166,556	16q22.2	0.29	0.2379	1.5E-133
chr16	rs13331166	71,184,898	16q22.2	0.1	0.5394	2.5E-039
chr16	rs8045566	71,188,799	16q22.2	0.09	0.0568	<2.2e-308
chr16	rs8058211	71,191,405	16q22.2	0.29	0.2855	2.4E-134
chr16	rs7187738	71,196,153	16q22.2	0.3	0.2293	3.1E-133
chr16	rs2017666	71,200,049	16q22.2	0.09	0.006295	<2.2e-308
chr16	rs9933375	71,202,489	16q22.2	0.16	0.1282	4.3E-066
chr16	rs4985430	70,871,031	16q22.2	0.05	0.0086	0.00000081
chr16	rs7192013	70,901,188	16q22.2	0.12	4.4E-013	0.000000051
chr16	rs4985432	70,913,651	16q22.2	0.05	0.78	NA
chr16	rs2456141	70,978,362	16q22.2	0.18	0.87	1.1E-146
chr16	rs10852481	71,070,698	16q22.2	0.16	2.3E-009	NA
chr16	rs7499876	71,070,878	16q22.2	0.36	0.76	1.2E-014

Supplementary Table 5. SNPs mapped to the 1q21.1 *HYDIN* locus.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; MAF: minor allele frequency; HWE: p-value from Hardy-Weinberg equilibrium test; P: best p-value from association through admixture mapping.

CHR	ID	BP	BAND	MAF	HWE	P
chr1_gl000192_random	rs1770421	49,508	1q21.1	0.04	0.011	0.0002
chr1_gl000192_random	rs7204551	57,972	1q21.1	0.19	0.3	6.1E-033
chr1_gl000192_random	rs1798473	59,070	1q21.1	0.41	0.56	0.00000025
chr1_gl000192_random	rs12447241	59,224	1q21.1	0.13	0.26	4.4E-043
chr1_gl000192_random	rs11075785	64,954	1q21.1	0.24	0.19	NA
chr1_gl000192_random	rs2791867	74,611	1q21.1	0.04	0.03	4.4E-018
chr1_gl000192_random	rs12103046	78,956	1q21.1	0.04	1	4.4E-018
chr1_gl000192_random	rs1891343	88,869	1q21.1	0.07	0.047	2.6E-009
chr1_gl000192_random	rs1394575	99,633	1q21.1	0.3	0.87	2.8E-020
chr1_gl000192_random	rs1539301	99,799	1q21.1	0.07	0.4	6.8E-024
chr1_gl000192_random	rs1626593	101,228	1q21.1	0.25	1	5.6E-009
chr1_gl000192_random	rs12102532	101,821	1q21.1	0.22	0.84	1.7E-040
chr1_gl000192_random	rs7201503	104,084	1q21.1	0.31	1.3E-029	3.7E-097
chr1_gl000192_random	rs4788625	104,364	1q21.1	0.17	0.17	1.2E-023
chr1_gl000192_random	rs1342172	106,301	1q21.1	0.26	0.55	6E-012
chr1_gl000192_random	rs8052250	110,325	1q21.1	0.4	0.00069	3.4E-141
chr1_gl000192_random	rs10852475	116,511	1q21.1	0.13	0.16	9.4E-043
chr1_gl000192_random	rs1974350	122,167	1q21.1	0.34	0.12	6.2E-202
chr1_gl000192_random	rs7197263	123,158	1q21.1	0.08	1	2.2E-025
chr1_gl000192_random	rs11075806	124,695	1q21.1	0.34	0.58	3.6E-088
chr1_gl000192_random	rs7192929	131,599	1q21.1	0.45	0.96	5.6E-111
chr1_gl000192_random	rs12102545	132,321	1q21.1	0.07	0.0016	6.3E-027
chr1_gl000192_random	rs1774433	133,444	1q21.1	0.28	1.1E-010	1.7E-009
chr1_gl000192_random	rs8047724	148,588	1q21.1	0.07	0.73	3.5E-024
chr1_gl000192_random	rs1774388	163,864	1q21.1	0.06	0.38	1.1E-015
chr1_gl000192_random	rs1798405	169,064	1q21.1	0.27	0.26	0.000000014
chr1_gl000192_random	rs7193277	170,629	1q21.1	0.15	0.6	1.8E-055
chr1_gl000192_random	rs12051071	176,451	1q21.1	0.04	0.19	NA
chr1_gl000192_random	rs1620815	177,480	1q21.1	0.29	0.55	0.00028
chr1_gl000192_random	rs12102764	181,710	1q21.1	0.17	0.75	4.5E-056
chr1_gl000192_random	rs1798348	197,459	1q21.1	0.42	0.61	1.1E-097
chr1_gl000192_random	rs12149261	201,824	1q21.1	0.24	0.8	<2.2e-308
chr1_gl000192_random	rs783724	204,814	1q21.1	0.1	0.18	3.1E-040
chr1_gl000192_random	rs783719	206,365	1q21.1	0.11	0.72	6.4E-038
chr1_gl000192_random	rs783718	206,465	1q21.1	0.2	0.89	1.4E-009
chr1_gl000192_random	rs2174409	214,090	1q21.1	0.08	0.24	1.9E-030
chr1_gl000192_random	rs12103040	215,123	1q21.1	0.1	0.3	2.3E-038
chr1_gl000192_random	rs1774524	222,551	1q21.1	0.49	0.55	1E-148
chr1_gl000192_random	rs2795674	225,964	1q21.1	0.19	0.56	2E-065
chr1_gl000192_random	rs1974348	238,974	1q21.1	0.15	0.37	NA
chr1_gl000192_random	rs1543087	240,824	1q21.1	0.11	0.61	6.2E-041

chr1_gl000192_random	rs6499381	256,372	1q21.1	0.03	1.2E-009	1.3E-014
chr1_gl000192_random	rs195655	256,732	1q21.1	0.07	0.037	3E-119
chr1_gl000192_random	rs8054021	258,139	1q21.1	0.36	0.62	2.1E-098
chr1_gl000192_random	rs2356024	259,746	1q21.1	0.5	0.0097	1.4E-201
chr1_gl000192_random	rs6499388	260,395	1q21.1	0.33	0.54	2.6E-083
chr1_gl000192_random	rs7191383	275,493	1q21.1	0.41	0.45	1E-067
chr1_gl000192_random	rs7203379	277,026	1q21.1	0.21	0.21	0.00031
chr1_gl000192_random	rs7204163	277,322	1q21.1	0.44	0.52	6.6E-088
chr1_gl000192_random	rs11075838	277,984	1q21.1	0.09	0.052	1.6E-030
chr1_gl000192_random	rs11075850	305,473	1q21.1	0.2	0.78	1.6E-051
chr1_gl000192_random	rs7200126	313,538	1q21.1	0.01	1	3.7E-039
chr1_gl000192_random	rs7184770	323,633	1q21.1	0.08	0.55	1.8E-026
chr1_gl000192_random	rs12597227	331,588	1q21.1	0.08	0.82	4E-023
chr1_gl000192_random	rs10735140	352,535	1q21.1	0.09	0.89	5E-017
chr1_gl000192_random	rs195672	353,625	1q21.1	0.4	0.72	7.2E-025
chr1_gl000192_random	rs11075865	359,899	1q21.1	0.04	0.45	1E-010
chr1_gl000192_random	rs8060499	378,662	1q21.1	0.14	0.7	2.3E-079
chr1_gl000192_random	rs12102979	101,548	1q21.1	0.11	1.2E-010	0.00000059
chr1_gl000192_random	rs12149070	119,141	1q21.1	0.15	9.3E-012	0.000027
chr1_gl000192_random	rs783756	208,871	1q21.1	0.17	2.6E-026	0.0013
chr1_gl000192_random	rs12103040	215,123	1q21.1	0.09	0.000082	0.00000051
chr1_gl000192_random	rs195656	257,321	1q21.1	0.15	0.0000034	NA
chr1_gl000192_random	rs7206076	278,861	1q21.1	0.46	0.037	1.6E-022
chr1_gl000192_random	rs7205580	335,063	1q21.1	0.09	0.0000095	0.00000021
chr1_gl000192_random	rs11075875	376,097	1q21.1	0.21	0.28	0.00011

Supplementary Table 6. Regions with increased heterozygosity.

List of regions >40kbp with increased density of SNPs failing Hardy-Weinberg equilibrium test (p<10-6) for CEU and YRI samples from the 1000 Genomes Project pilot. CHR, FROM, TO, BAND: chromosome, hg19 coordinates, and localization of the region of increased observed heterozygosity; GENE: protein coding gene(s) overlapping the region; SIZE: estimated size of the cryptic segmental duplication; SNPS: indicates if mismapped SNPs from the CARe or ICDB datasets were identified for the region.

CHR	FROM	TO	BAND	GENE	SIZE	SNPS
chr1	16,902,113	16,978,230	1p36.13	*NBPF1*	76,117	no
chr1	120,555,746	120,596,847	1p12	*NOTCH2*	41,101	no
chr1	142,569,420	142,675,590	1q12	NA	106,170	no
chr1	143,138,772	143,192,121	1q21.1	NA	53,349	no
chr1	143,984,142	144,028,315	1q21.1	*SRGAP2P2*	44,173	yes
chr1	144,835,832	144,950,925	1q21.1	*PDE4DIP*	115,093	no
chr1	144,986,081	145,128,744	1q21.1	*PDE4DIP*	142,663	no
chr1	145,184,519	145,253,351	1q21.1	*NOTCH2NL*	68,832	no
chr1	149,250,978	149,368,223	1q21.2	NA	117,245	no
chr1	149,680,310	149,752,366	1q21.2	NA	72,056	no
chr2	37,958,755	38,002,829	2p22.2	NA	44,074	yes
chr2	91,757,505	91,872,635	2p11.2	*OTOP1*	115,130	yes
chr2	92,028,614	92,108,796	2p11.1	NA	80,182	no
chr2	97,809,814	97,857,733	2q11.2	NA	47,919	no
chr2	132,768,246	132,813,362	2q21.2	NA	45,116	no
chr2	133,008,065	133,120,630	2q21.2	NA	112,565	yes
chr3	615,289	663,155	3p26.3	NA	47,866	yes
chr3	75,824,118	75,875,184	3p12.3	*ZNF717*	51,066	yes
chr4	27,712	68,443	4p16.3	*ZNF595*	40,731	yes
chr4	3,536,889	3,636,047	4p16.3	*FLJ35424*	99,158	yes
chr4	4,185,518	4,239,516	4p16.3	*OTOP1*	53,998	no
chr4	190,539,915	190,684,209	4q35.2	NA	144,294	yes
chr4	190,796,314	190,915,597	4q35.2	*FRG1*	119,283	no
chr5	21,510,015	21,573,393	5p14.3	NA	63,378	yes
chr6	256,765	380,843	6p25.3	*DUSP22*	124,078	yes
chr6	57,205,693	57,608,310	6p11.2	*PRIM2*	402,617	yes
chr7	57,605,689	57,666,779	7p11.2	NA	61,090	no
chr7	57,692,731	57,775,133	7p11.2	NA	82,402	no
chr7	61,737,146	61,793,587	7q11.21	NA	56,441	no
chr7	65,249,248	65,303,925	7q11.21	NA	54,677	no
chr7	100,546,719	100,619,245	7q22.1	*MUC3*	72,526	no
chr7	142,099,601	142,180,704	7q34	*TRBV*	81,103	no
chr7	151,928,341	151,989,542	7q36.1	*MLL3*	61,201	no
chr7	152,073,527	152,113,724	7q36.1	*MLL3*	40,197	no
chr8	12,397,894	12,454,130	8p23.1	NA	56,236	no
chr9	66,454,796	66,545,565	9q13	NA	90,769	no
chr9	68,378,693	68,506,434	9q13	NA	127,741	no
chr9	69,799,583	69,846,339	9q21.11	NA	46,756	no
chr10	42,604,351	42,682,615	10q11.21	NA	78,264	no

chr10	46,948,842	47,151,288	10q11.22	*GPRIN2*	202,446	no
chr11	48,340,191	48,388,899	11p11.2	*OR4C45*	48,708	no
chr13	63,602,751	63,649,007	13q21.31	NA	46,256	no
chr14	19,079,063	19,120,560	14q11	NA	41,497	no
chr15	20,029,776	20,088,237	15q11.1	NA	58,461	no
chr15	20,417,406	20,466,064	15q11.1	NA	48,658	no
chr15	20,557,396	20,625,590	15q11.1	NA	68,194	no
chr16	32,372,363	32,492,671	16p11.2	NA	120,308	no
chr16	32,605,080	32,657,164	16p11.2	NA	52,084	no
chr16	33,360,162	33,641,499	16p11.2	NA	281,337	no
chr16	33,922,089	33,981,135	16p11.2	NA	59,046	no
chr16	46,437,498	46,478,563	16q11.2	NA	41,065	no
chr17	21,193,755	21,254,703	17p11.2	*MAP2K3*	60,948	no
chr17	21,303,128	21,353,258	17p11.2	*KCNJ12*	50,130	no
chr17	21,506,608	21,566,448	17p11.2	NA	59,840	no
chr17	25,263,483	25,337,342	17q11.1	NA	73,859	no
chr19	44,857,649	44,905,909	19q13.31	*ZNF285*	48,260	no
chr20	25,859,611	25,945,375	20p11.1	NA	85,764	no
chr20	26,054,859	26,149,544	20p11.1	*FAM182A*	94,685	no
chr20	29,420,001	29,494,077	20q11.21	NA	74,076	no
chr20	29,527,718	29,653,843	20q11.21	*FRG1B*	126,125	no
chr21	10,858,755	10,950,631	21p11	*TPTE*	91,876	yes
chr21	11,021,723	11,186,824	21p11.1	*BAGE*	165,101	yes
chr22	16,865,913	16,907,698	22q11.1	NA	41,785	no

Supplementary Table 7. SNP pairs in linkage disequilibrium.

Significant pairwise linkage disequilibrium among SNPs genotyped with Sequenom from unlocalized scaffolds. SCAF: genomic scaffold of first SNP in the pair; BP: coordinate within scaffold of first SNP in the pair; MAPTO: identified localization for scaffold of first SNP in the pair; R2: observed Pearson correlation coefficient r² between SNPs genotypes after correcting genotype for global ancestry; P: p-value for correlation of SNP pairs genotypes; SCAF’: genomic scaffold of second SNP in the pair; BP’: coordinate within scaffold of second SNP in the pair; MAPTO’: identified localization for scaffold of second SNP in the pair.

SCAF	BP	MAPTO	R2	P	SCAF'	BP'	MAPTO'
SCAF_1103279180372	952	1p35.2	0.85	2.1E-118	SCAF_1103279180372	1,175	1p35.2
SCAF_1103279187659	1,103	22q11.1	0.45	1.4E-045	SCAF_1103279186877	1,243	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.54	1.8E-028	SCAF_1103279186290	1,523	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.21	3.9E-010	SCAF_1103279186290	1,523	22q11.1
SCAF_1103279180372	952	1p35.2	1	0	SCAF_1103279180372	1,593	1p35.2
SCAF_1103279180372	1,175	1p35.2	0.73	1.4E-087	SCAF_1103279180372	1,593	1p35.2
SCAF_1103279180200	335	14q11.2	0.67	9.1E-084	SCAF_1103279186561	1,628	14q11.2
SCAF_1103279187659	1,103	22q11.1	0.49	3.4E-053	SCAF_1103279182830	1,870	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.93	2.5E-203	SCAF_1103279182830	1,870	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.25	1.1E-012	SCAF_1103279182830	1,870	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.34	3.8E-018	SCAF_1103279182133	1,991	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.59	4.3E-037	SCAF_1103279182133	1,991	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.33	0.000000012	SCAF_1103279182133	1,991	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.56	3E-035	SCAF_1103279182133	1,991	22q11.1
SCAF_1103279188373	774	Xp22.33	0.43	1.9E-042	SCAF_1103279188373	2,014	Xp22.33
SCAF_1103279184705	580	3q26.1	1	0	SCAF_1103279184705	2,064	3q26.1
SCAF_1103279186877	1,243	22q11.1	0.21	2.8E-010	SCAF_1103279187453	2,271	NA
SCAF_1103279182830	1,870	22q11.1	0.22	7E-011	SCAF_1103279187453	2,271	NA
SCAF_1103279186405	960	9p13.1	0.45	7.6E-050	GL000199	2,656	9p11.2
SCAF_1103279187072	433	1p11.2	0.69	9.2E-095	SCAF_1103279183789	2,662	1p11.2
SCAF_1103279187659	1,103	22q11.1	0.37	1E-035	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.78	4.1E-114	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.32	1.1E-014	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.82	1.8E-132	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.67	2.1E-045	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279187453	2,271	NA	0.29	9.4E-014	SCAF_1103279182830	2,753	22q11.1
SCAF_1103279186405	960	9p13.1	0.19	8.1E-019	SCAF_1103279182087	2,870	9q12
GL000199	2,656	9p11.2	0.08	0.000000025	SCAF_1103279182087	2,870	9q12
SCAF_1103279180372	952	1p35.2	0.92	3E-163	SCAF_1103279180372	2,885	1p35.2
SCAF_1103279180372	1,175	1p35.2	0.71	3.6E-083	SCAF_1103279180372	2,885	1p35.2
SCAF_1103279180372	1,593	1p35.2	0.91	2.6E-158	SCAF_1103279180372	2,885	1p35.2
SCAF_1103279180200	335	14q11.2	0.87	3.2E-164	SCAF_1103279180207	2,996	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.76	3.5E-108	SCAF_1103279180207	2,996	14q11.2
SCAF_1103279187659	1,103	22q11.1	0.46	3E-049	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.81	7E-130	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.19	0.000000001	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.76	4.6E-117	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.49	5.6E-030	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279187453	2,271	NA	0.18	2.3E-009	SCAF_1103279187012	3,010	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.62	2.1E-076	SCAF_1103279187012	3,010	22q11.1

SCAF_1103279184705	580	3q26.1	1	0	SCAF_1103279184705	3,272	3q26.1
SCAF_1103279184705	2,064	3q26.1	1	0	SCAF_1103279184705	3,272	3q26.1
SCAF_1103279187162	1,215	16q24.2	0.83	1.7E-139	SCAF_1103279187162	3,333	16q24.2
SCAF_1103279187659	1,103	22q11.1	0.38	1.6E-037	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.69	1.2E-089	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.27	1.9E-013	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.73	4.1E-105	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.6	2.5E-039	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279187453	2,271	NA	0.23	2.4E-011	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.9	3.3E-173	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.6	1.5E-075	SCAF_1103279180853	3,459	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.13	1.4E-009	SCAF_1103279187875	3,772	NA
SCAF_1103279186290	1,523	22q11.1	0.3	6.6E-012	SCAF_1103279187875	3,772	NA
SCAF_1103279182830	1,870	22q11.1	0.14	9.9E-011	SCAF_1103279187875	3,772	NA
SCAF_1103279182830	2,753	22q11.1	0.24	6.5E-018	SCAF_1103279187875	3,772	NA
SCAF_1103279187012	3,010	22q11.1	0.11	3.1E-009	SCAF_1103279187875	3,772	NA
SCAF_1103279180853	3,459	22q11.1	0.26	2.7E-020	SCAF_1103279187875	3,772	NA
SCAF_1103279180476	3,836	4p16.3	0.99	0	SCAF_1103279180476	3,852	4p16.3
SCAF_1103279180476	3,836	4p16.3	0.98	0	SCAF_1103279180476	3,926	4p16.3
SCAF_1103279180476	3,852	4p16.3	0.98	1.4E-307	SCAF_1103279180476	3,926	4p16.3
SCAF_1103279184070	3,007	1p11.2	0.13	8.8E-013	SCAF_1103279187122	3,932	1p11.2
SCAF_1103279187659	1,103	22q11.1	0.33	4E-032	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.83	2.7E-134	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.25	2.6E-012	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.8	3.6E-131	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.68	3.5E-048	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279187453	2,271	NA	0.27	1.3E-013	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.95	1.1E-228	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.67	1.4E-089	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.83	5.6E-140	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279187875	3,772	NA	0.19	8.5E-015	SCAF_1103279186877	4,004	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.46	6.5E-048	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.98	3.6E-285	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.21	3.4E-010	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.96	2.7E-254	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.59	4E-038	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279187453	2,271	NA	0.23	2.3E-011	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.79	2.5E-118	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.82	1.7E-135	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.72	1.8E-099	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279187875	3,772	NA	0.13	7.7E-010	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.85	1.2E-151	SCAF_1103279186877	4,081	22q11.1
SCAF_1103279186405	960	9p13.1	0.2	1.8E-019	SCAF_1103279180133	4,138	9p11.2
GL000199	2,656	9p11.2	0.28	2.7E-028	SCAF_1103279180133	4,138	9p11.2
SCAF_1103279187659	1,103	22q11.1	0.39	5E-039	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.83	1.2E-132	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.2	1.3E-009	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.91	1.3E-188	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.54	2.4E-033	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279187453	2,271	NA	0.24	1.1E-011	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.68	9E-087	SCAF_1103279186877	4,182	22q11.1

SCAF_1103279187012	3,010	22q11.1	0.69	1.4E-094	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.66	1.5E-084	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279187875	3,772	NA	0.09	0.00000025	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.85	2.3E-148	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279186877	4,081	22q11.1	1	0	SCAF_1103279186877	4,182	22q11.1
SCAF_1103279180476	3,836	4p16.3	0.99	0	SCAF_1103279180476	4,694	4p16.3
SCAF_1103279180476	3,852	4p16.3	0.99	0	SCAF_1103279180476	4,694	4p16.3
SCAF_1103279180476	3,926	4p16.3	0.98	4.3E-307	SCAF_1103279180476	4,694	4p16.3
SCAF_1103279180372	952	1p35.2	0.98	1.4E-251	SCAF_1103279180372	5,715	1p35.2
SCAF_1103279180372	1,175	1p35.2	0.52	6.6E-052	SCAF_1103279180372	5,715	1p35.2
SCAF_1103279180372	1,593	1p35.2	0.96	9.9E-217	SCAF_1103279180372	5,715	1p35.2
SCAF_1103279180372	2,885	1p35.2	0.88	1.4E-137	SCAF_1103279180372	5,715	1p35.2
SCAF_1103279180476	3,836	4p16.3	0.98	4.3e-311	SCAF_1103279180476	6,103	4p16.3
SCAF_1103279180476	3,852	4p16.3	0.97	1.2E-291	SCAF_1103279180476	6,103	4p16.3
SCAF_1103279180476	3,926	4p16.3	0.96	9.3E-263	SCAF_1103279180476	6,103	4p16.3
SCAF_1103279180476	4,694	4p16.3	0.98	0	SCAF_1103279180476	6,103	4p16.3
SCAF_1103279184115	5,672	NA	0.24	2.4E-019	SCAF_1103279180743	6,693	22q11.1
SCAF_1103279180200	335	14q11.2	0.78	1.1E-119	GL000235	7,959	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.83	2.5E-136	GL000235	7,959	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.9	9.3E-185	GL000235	7,959	14q11.2
SCAF_1103279180200	335	14q11.2	0.13	2.7E-011	SCAF_1103279180200	8,812	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.16	4.7E-014	SCAF_1103279180200	8,812	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.14	5.3E-012	SCAF_1103279180200	8,812	14q11.2
GL000235	7,959	14q11.2	0.15	6.6E-013	SCAF_1103279180200	8,812	14q11.2
SCAF_1103279187659	1,103	22q11.1	0.4	4.2E-039	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.31	7.7E-029	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.86	1.2E-075	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.33	2.9E-032	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.33	2.3E-017	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.43	8.8E-043	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.32	1.6E-031	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.43	3.1E-043	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279187875	3,772	NA	0.13	7.6E-010	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.37	4.8E-036	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.31	3.4E-029	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.27	2.2E-024	SCAF_1103279183297	9,965	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.28	6.8E-025	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.52	3.4E-054	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.54	2.7E-059	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.48	1.7E-026	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279187453	2,271	NA	0.23	2.8E-011	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.64	1.7E-074	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.49	1.2E-052	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.74	1.1E-099	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279187875	3,772	NA	0.12	8.8E-009	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.66	1.7E-081	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.56	5.4E-061	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.49	5.2E-051	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.33	4.3E-030	SCAF_1103279182409	11,698	22q11.1
SCAF_1103279180200	335	14q11.2	0.12	2.7E-011	SCAF_1103279181222	12,417	NA
SCAF_1103279186561	1,628	14q11.2	0.09	0.000000021	SCAF_1103279181222	12,417	NA

SCAF_1103279180207	2,996	14q11.2	0.13	4.4E-012	SCAF_1103279181222	12,417	NA
GL000235	7,959	14q11.2	0.13	1.7E-012	SCAF_1103279181222	12,417	NA
SCAF_1103279179890	5,000	1q32.1	0.69	7.5E-098	SCAF_1103279179890	13,607	1q32.1
SCAF_1103279179890	5,000	1q32.1	0.67	1.9E-093	SCAF_1103279179890	13,701	1q32.1
SCAF_1103279179890	13,607	1q32.1	0.95	1.8E-250	SCAF_1103279179890	13,701	1q32.1
SCAF_1103279180200	335	14q11.2	0.84	5.5E-142	GL000230	14,024	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.77	6.8E-109	GL000230	14,024	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.96	1.3E-253	GL000230	14,024	14q11.2
GL000235	7,959	14q11.2	0.84	9.8E-145	GL000230	14,024	14q11.2
SCAF_1103279180200	8,812	14q11.2	0.14	1.5E-011	GL000230	14,024	14q11.2
SCAF_1103279181222	12,417	NA	0.1	2.6E-009	GL000230	14,024	14q11.2
SCAF_1103279180200	335	14q11.2	0.83	2.9E-134	SCAF_1103279187526	20,185	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.79	9.4E-113	SCAF_1103279187526	20,185	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.98	3.7E-292	SCAF_1103279187526	20,185	14q11.2
GL000235	7,959	14q11.2	0.9	1.5E-180	SCAF_1103279187526	20,185	14q11.2
SCAF_1103279180200	8,812	14q11.2	0.16	4.4E-013	SCAF_1103279187526	20,185	14q11.2
SCAF_1103279181222	12,417	NA	0.12	1.2E-010	SCAF_1103279187526	20,185	14q11.2
GL000230	14,024	14q11.2	0.98	7.8E-299	SCAF_1103279187526	20,185	14q11.2
SCAF_1103279180200	335	14q11.2	0.56	4E-066	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.71	4.4E-094	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.65	1.1E-082	SCAF_1103279188017	20,258	14q11.2
GL000235	7,959	14q11.2	0.6	1.1E-073	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279180200	8,812	14q11.2	0.15	6.5E-013	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279181222	12,417	NA	0.1	2.1E-009	SCAF_1103279188017	20,258	14q11.2
GL000230	14,024	14q11.2	0.7	5.5E-093	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279187526	20,185	14q11.2	0.75	2.7E-105	SCAF_1103279188017	20,258	14q11.2
SCAF_1103279186405	960	9p13.1	0.4	1.1E-042	SCAF_1103279188305	21,267	9p11.2
GL000199	2,656	9p11.2	0.84	4E-150	SCAF_1103279188305	21,267	9p11.2
SCAF_1103279182087	2,870	9q12	0.08	0.000000046	SCAF_1103279188305	21,267	9p11.2
SCAF_1103279180133	4,138	9p11.2	0.25	2.9E-025	SCAF_1103279188305	21,267	9p11.2
SCAF_1103279186405	960	9p13.1	0.34	4.9E-032	SCAF_1103279188305	21,909	9p11.2
GL000199	2,656	9p11.2	0.81	1.1E-124	SCAF_1103279188305	21,909	9p11.2
SCAF_1103279182087	2,870	9q12	0.07	0.00000088	SCAF_1103279188305	21,909	9p11.2
SCAF_1103279180133	4,138	9p11.2	0.25	1.1E-022	SCAF_1103279188305	21,909	9p11.2
SCAF_1103279188305	21,267	9p11.2	0.83	9.1E-133	SCAF_1103279188305	21,909	9p11.2
SCAF_1103279188164	22,291	6p21.32	0.84	1.4E-125	SCAF_1103279188164	26,392	6p21.32
SCAF_1103279180372	1,175	1p35.2	0.08	0.000000029	GL000191	27,316	1p36.11
SCAF_1103279182969	334	21q11.2	0.09	2.5E-009	GL000193	30,855	21q11.2
SCAF_1103279180200	335	14q11.2	0.74	1.5E-047	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.65	5.5E-037	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.79	5.1E-054	SCAF_1103279188017	31,805	14q11.2
GL000235	7,959	14q11.2	0.72	3.2E-045	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279180200	8,812	14q11.2	0.23	1.3E-009	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279181222	12,417	NA	0.18	0.000000035	SCAF_1103279188017	31,805	14q11.2
GL000230	14,024	14q11.2	0.77	1.2E-050	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279187526	20,185	14q11.2	0.74	6.8E-045	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279188017	20,258	14q11.2	0.67	1.3E-039	SCAF_1103279188017	31,805	14q11.2
SCAF_1103279184115	5,672	NA	0.24	7.4E-016	SCAF_1103279181352	34,142	NA
SCAF_1103279180743	6,693	22q11.1	0.58	1.8E-056	SCAF_1103279181352	34,142	NA
GL000212	9,128	13q11	0.54	2.2E-053	GL000212	36,207	13q11
SCAF_1103279187072	433	1p11.2	0.18	5E-017	SCAF_1103279187122	36,213	1p11.2

SCAF_1103279183789	2,662	1p11.2	0.15	7.4E-014	SCAF_1103279187122	36,213	1p11.2
SCAF_1103279187659	1,103	22q11.1	0.47	3.8E-049	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.96	3.6E-244	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.19	1.1E-009	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.93	3E-208	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.59	1.3E-038	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279187453	2,271	NA	0.2	4.2E-010	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.76	2.6E-108	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.82	2.8E-138	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.68	4.2E-091	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279187875	3,772	NA	0.11	9.5E-009	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.83	7.8E-141	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.99	0	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.99	0	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.3	8.4E-029	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.55	5.2E-061	SCAF_1103279187736	36,315	22q11.1
SCAF_1103279180200	335	14q11.2	0.62	8.3E-077	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279186561	1,628	14q11.2	0.78	1.7E-113	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.72	6.2E-102	SCAF_1103279180967	36,678	14q11.2
GL000235	7,959	14q11.2	0.66	4.1E-088	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279180200	8,812	14q11.2	0.14	1.3E-012	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279181222	12,417	NA	0.13	9E-012	SCAF_1103279180967	36,678	14q11.2
GL000230	14,024	14q11.2	0.75	1.1E-109	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279187526	20,185	14q11.2	0.78	8.5E-117	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279188017	20,258	14q11.2	0.94	2.6E-221	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279188017	31,805	14q11.2	0.65	1.7E-037	SCAF_1103279180967	36,678	14q11.2
SCAF_1103279187659	1,103	22q11.1	0.47	4.6E-049	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.94	5.4E-220	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.2	6.9E-010	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.92	3.5E-198	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.61	5.6E-040	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279187453	2,271	NA	0.18	6.4E-009	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.74	8.8E-105	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.81	3.9E-136	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.68	8E-090	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279187875	3,772	NA	0.12	3.5E-009	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.8	1E-128	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.97	1.6E-286	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.88	7E-166	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.3	3.3E-028	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.51	4E-054	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.96	8E-262	SCAF_1103279187736	37,900	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.34	2.7E-031	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.7	3.2E-087	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.29	2.8E-012	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.65	1E-077	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.72	4.8E-053	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279187453	2,271	NA	0.26	2.8E-012	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.79	1.1E-112	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.77	9.6E-112	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.77	8.3E-108	SCAF_1103279187736	39,138	22q11.1

SCAF_1103279187875	3,772	NA	0.23	9.1E-017	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.85	1.6E-137	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.71	1.1E-091	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.62	1.1E-071	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.4	1.6E-036	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.59	1.4E-063	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.7	3.4E-089	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.69	2.4E-088	SCAF_1103279187736	39,138	22q11.1
SCAF_1103279184412	19,430	13q34	0.37	2.5E-037	SCAF_1103279184412	39,752	13q34
SCAF_1103279187659	1,103	22q11.1	0.18	9E-017	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.24	1E-022	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.24	1.9E-011	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.28	1.1E-026	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.3	1.5E-015	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.35	2.7E-033	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.15	1.9E-014	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.27	5.6E-026	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279187875	3,772	NA	0.1	0.00000017	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.33	3.1E-032	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.28	2.8E-026	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.3	5.4E-028	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.28	4.1E-026	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.23	4.2E-020	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.26	7.9E-025	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.24	2E-022	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.24	1.4E-021	SCAF_1103279182252	41,642	22q11.1
SCAF_1103279186405	960	9p13.1	0.19	3.8E-019	SCAF_1103279182087	43,005	9q12
GL000199	2,656	9p11.2	0.09	4.3E-009	SCAF_1103279182087	43,005	9q12
SCAF_1103279182087	2,870	9q12	0.96	4.1E-259	SCAF_1103279182087	43,005	9q12
SCAF_1103279188305	21,267	9p11.2	0.08	0.000000057	SCAF_1103279182087	43,005	9q12
SCAF_1103279187659	1,103	22q11.1	0.49	1.4E-050	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.91	1.4E-184	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.19	9.9E-009	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.88	2.2E-159	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.58	8.8E-036	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187453	2,271	NA	0.17	0.000000023	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.71	1.5E-093	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.84	3.8E-142	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.65	2E-080	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187875	3,772	NA	0.11	0.000000043	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.76	1.1E-107	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.95	1.7E-229	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.84	6.4E-138	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.29	3.5E-026	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.48	9.3E-048	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.94	8.2E-216	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.94	2.5E-212	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.68	6.8E-081	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.14	3.3E-013	SCAF_1103279187460	43,714	22q11.1
SCAF_1103279183150	9,341	20q11.22	0.56	2.7E-063	SCAF_1103279184675	45,022	20p11.1
SCAF_1103279184412	19,430	13q34	0.16	1.7E-015	SCAF_1103279187720	45,300	13q34

SCAF_1103279184412	39,752	13q34	0.07	0.0000002	SCAF_1103279187720	45,300	13q34
SCAF_1103279183150	9,341	20q11.22	0.66	6.7E-086	SCAF_1103279184675	45,566	20p11.1
SCAF_1103279184675	45,022	20p11.1	0.77	6.6E-107	SCAF_1103279184675	45,566	20p11.1
SCAF_1103279186405	960	9p13.1	0.85	4E-145	SCAF_1103279188326	45,606	9p13.1
GL000199	2,656	9p11.2	0.45	1.6E-046	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279182087	2,870	9q12	0.21	4E-019	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279180133	4,138	9p11.2	0.2	1.2E-018	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279188305	21,267	9p11.2	0.45	1.4E-046	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279188305	21,909	9p11.2	0.34	2.3E-030	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279182087	43,005	9q12	0.21	1.8E-019	SCAF_1103279188326	45,606	9p13.1
SCAF_1103279184070	3,007	1p11.2	0.81	3.5E-130	SCAF_1103279187792	46,115	1p11.2
SCAF_1103279187122	3,932	1p11.2	0.2	1.5E-018	SCAF_1103279187792	46,115	1p11.2
SCAF_1103279184412	19,430	13q34	0.17	7.6E-016	SCAF_1103279184412	46,435	13q34
SCAF_1103279184412	39,752	13q34	0.26	1.4E-026	SCAF_1103279184412	46,435	13q34
SCAF_1103279187720	45,300	13q34	0.08	0.000000022	SCAF_1103279184412	46,435	13q34
SCAF_1103279187072	433	1p11.2	0.42	2.1E-045	SCAF_1103279188307	46,575	1q21.1
SCAF_1103279183789	2,662	1p11.2	0.48	2.2E-052	SCAF_1103279188307	46,575	1q21.1
SCAF_1103279187122	36,213	1p11.2	0.32	4E-032	SCAF_1103279188307	46,575	1q21.1
SCAF_1103279187659	1,103	22q11.1	0.46	3.3E-047	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.59	8.6E-069	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.47	2.2E-024	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.64	2.4E-081	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.69	4.1E-048	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187453	2,271	NA	0.29	3.3E-014	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.79	1.6E-117	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.53	1.2E-060	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.81	9.1E-127	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187875	3,772	NA	0.24	2.9E-018	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.71	2.1E-096	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.61	3.9E-072	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.55	5.5E-061	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.51	1.5E-054	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.6	1.5E-067	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.58	1.4E-068	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.57	7.5E-067	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.67	3.2E-080	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.32	1.5E-031	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.56	5.5E-064	SCAF_1103279187626	47,976	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.21	6.4E-016	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.29	3.1E-021	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.48	9.5E-017	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.35	7.8E-028	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.4	4.2E-019	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187453	2,271	NA	0.23	9.7E-009	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.43	4.1E-035	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.2	3.9E-015	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.38	3.5E-031	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187875	3,772	NA	0.15	2.8E-009	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.43	3.6E-035	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.32	1E-024	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.3	2.3E-023	SCAF_1103279187626	51,038	22q11.1

SCAF_1103279183297	9,965	22q11.1	0.31	3.2E-023	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.26	4.3E-019	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.3	3.3E-023	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.29	2E-022	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.36	1.6E-028	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.3	7.4E-023	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.21	4.6E-015	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187626	47,976	22q11.1	0.53	8E-046	SCAF_1103279187626	51,038	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.17	7.7E-016	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.28	2.7E-026	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.24	2.3E-011	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.32	7.8E-032	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.25	1.7E-013	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187453	2,271	NA	0.17	0.00000003	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.37	4.9E-037	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.23	1.4E-022	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.41	4.7E-042	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187875	3,772	NA	0.2	1.2E-015	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.36	4.7E-036	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.3	3.7E-029	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.26	7.7E-025	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.29	8E-027	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.33	7E-031	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.28	2.4E-027	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.27	5.6E-026	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.33	1.5E-031	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.25	1.1E-023	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.24	1.6E-022	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187626	47,976	22q11.1	0.5	5.2E-054	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279187626	51,038	22q11.1	0.67	2.9E-069	SCAF_1103279187626	54,749	22q11.1
SCAF_1103279184412	19,430	13q34	0.19	4.7E-018	SCAF_1103279187720	56,014	13q34
SCAF_1103279184412	39,752	13q34	0.1	2.8E-010	SCAF_1103279187720	56,014	13q34
SCAF_1103279187720	45,300	13q34	0.15	4.6E-015	SCAF_1103279187720	56,014	13q34
SCAF_1103279184412	46,435	13q34	0.11	1.1E-010	SCAF_1103279187720	56,014	13q34
SCAF_1103279184412	19,430	13q34	0.19	3.2E-018	SCAF_1103279187720	57,041	13q34
SCAF_1103279187720	45,300	13q34	0.34	9.7E-035	SCAF_1103279187720	57,041	13q34
SCAF_1103279184412	46,435	13q34	0.15	1.7E-014	SCAF_1103279187720	57,041	13q34
SCAF_1103279187720	56,014	13q34	0.17	3.6E-017	SCAF_1103279187720	57,041	13q34
SCAF_1103279184412	19,430	13q34	0.2	4.7E-019	SCAF_1103279187720	58,477	13q34
SCAF_1103279184412	39,752	13q34	0.11	9.2E-011	SCAF_1103279187720	58,477	13q34
SCAF_1103279187720	45,300	13q34	0.15	4.7E-015	SCAF_1103279187720	58,477	13q34
SCAF_1103279184412	46,435	13q34	0.11	4E-011	SCAF_1103279187720	58,477	13q34
SCAF_1103279187720	56,014	13q34	0.96	1.3E-270	SCAF_1103279187720	58,477	13q34
SCAF_1103279187720	57,041	13q34	0.18	5.1E-018	SCAF_1103279187720	58,477	13q34
GL000204	61,571	17q25.3	0.83	6E-139	GL000204	61,666	17q25.3
GL000235	7,959	14q11.2	0.07	0.00000076	SCAF_1103279188266	66,064	NA
SCAF_1103279181222	12,417	NA	0.77	7.2E-109	SCAF_1103279188266	66,064	NA
SCAF_1103279180967	36,678	14q11.2	0.08	0.00000021	SCAF_1103279188266	66,064	NA
SCAF_1103279180200	335	14q11.2	0.09	0.000000013	SCAF_1103279188266	67,416	NA
SCAF_1103279180207	2,996	14q11.2	0.1	1.8E-009	SCAF_1103279188266	67,416	NA
GL000235	7,959	14q11.2	0.1	5.5E-010	SCAF_1103279188266	67,416	NA

SCAF_1103279181222	12,417	NA	0.79	1E-117	SCAF_1103279188266	67,416	NA
GL000230	14,024	14q11.2	0.07	0.0000006	SCAF_1103279188266	67,416	NA
SCAF_1103279187526	20,185	14q11.2	0.09	0.000000033	SCAF_1103279188266	67,416	NA
SCAF_1103279188017	20,258	14q11.2	0.08	0.000000087	SCAF_1103279188266	67,416	NA
SCAF_1103279188017	31,805	14q11.2	0.19	8.2E-009	SCAF_1103279188266	67,416	NA
SCAF_1103279180967	36,678	14q11.2	0.1	5.9E-010	SCAF_1103279188266	67,416	NA
SCAF_1103279188266	66,064	NA	0.91	1.1E-174	SCAF_1103279188266	67,416	NA
SCAF_1103279183150	9,341	20q11.22	0.21	1.5E-019	SCAF_1103279188197	70,458	20p11.21
SCAF_1103279184675	45,022	20p11.1	0.18	2.4E-015	SCAF_1103279188197	70,458	20p11.21
SCAF_1103279184675	45,566	20p11.1	0.21	3.8E-019	SCAF_1103279188197	70,458	20p11.21
SCAF_1103279184412	19,430	13q34	0.34	1.3E-034	SCAF_1103279184412	71,648	13q34
SCAF_1103279184412	39,752	13q34	0.59	2.1E-075	SCAF_1103279184412	71,648	13q34
SCAF_1103279187720	45,300	13q34	0.09	6.4E-009	SCAF_1103279184412	71,648	13q34
SCAF_1103279184412	46,435	13q34	0.3	3.5E-031	SCAF_1103279184412	71,648	13q34
SCAF_1103279187720	56,014	13q34	0.13	5.6E-013	SCAF_1103279184412	71,648	13q34
SCAF_1103279187720	57,041	13q34	0.12	1.3E-011	SCAF_1103279184412	71,648	13q34
SCAF_1103279187720	58,477	13q34	0.12	2.2E-012	SCAF_1103279184412	71,648	13q34
SCAF_1103279184412	19,430	13q34	0.36	4E-036	SCAF_1103279184412	72,536	13q34
SCAF_1103279184412	39,752	13q34	0.59	5.4E-074	SCAF_1103279184412	72,536	13q34
SCAF_1103279187720	45,300	13q34	0.09	7.5E-009	SCAF_1103279184412	72,536	13q34
SCAF_1103279184412	46,435	13q34	0.32	2.8E-033	SCAF_1103279184412	72,536	13q34
SCAF_1103279187720	56,014	13q34	0.12	6.3E-012	SCAF_1103279184412	72,536	13q34
SCAF_1103279187720	57,041	13q34	0.12	2.9E-012	SCAF_1103279184412	72,536	13q34
SCAF_1103279187720	58,477	13q34	0.12	1.9E-012	SCAF_1103279184412	72,536	13q34
SCAF_1103279184412	71,648	13q34	0.95	3.6E-242	SCAF_1103279184412	72,536	13q34
GL000235	7,959	14q11.2	0.07	0.0000002	GL000194	72,564	NA
SCAF_1103279181222	12,417	NA	0.31	3.6E-029	GL000194	72,564	NA
SCAF_1103279187526	20,185	14q11.2	0.07	0.00000037	GL000194	72,564	NA
SCAF_1103279188266	66,064	NA	0.3	1.5E-027	GL000194	72,564	NA
SCAF_1103279188266	67,416	NA	0.33	5.6E-032	GL000194	72,564	NA
SCAF_1103279188124	10,878	15q11.2	0.59	9.6E-072	SCAF_1103279187477	72,717	15q11.2
SCAF_1103279180200	335	14q11.2	0.08	0.00000016	SCAF_1103279184990	73,384	14q11.2
SCAF_1103279180207	2,996	14q11.2	0.1	2.4E-009	SCAF_1103279184990	73,384	14q11.2
GL000235	7,959	14q11.2	0.07	0.00000026	SCAF_1103279184990	73,384	14q11.2
SCAF_1103279182884	15,315	NA	0.22	3.8E-011	SCAF_1103279184990	73,384	14q11.2
SCAF_1103279184412	19,430	13q34	0.46	1.3E-049	SCAF_1103279184412	74,517	13q34
SCAF_1103279184412	39,752	13q34	0.45	1.1E-050	SCAF_1103279184412	74,517	13q34
SCAF_1103279187720	45,300	13q34	0.12	2.4E-012	SCAF_1103279184412	74,517	13q34
SCAF_1103279184412	46,435	13q34	0.28	4.1E-028	SCAF_1103279184412	74,517	13q34
SCAF_1103279187720	56,014	13q34	0.16	6.7E-016	SCAF_1103279184412	74,517	13q34
SCAF_1103279187720	57,041	13q34	0.13	5.3E-013	SCAF_1103279184412	74,517	13q34
SCAF_1103279187720	58,477	13q34	0.16	4.4E-016	SCAF_1103279184412	74,517	13q34
SCAF_1103279184412	71,648	13q34	0.73	5.5E-110	SCAF_1103279184412	74,517	13q34
SCAF_1103279184412	72,536	13q34	0.73	2E-108	SCAF_1103279184412	74,517	13q34
GL000204	61,571	17q25.3	0.19	3.8E-018	GL000204	75,440	17q25.3
GL000204	61,666	17q25.3	0.14	6E-014	GL000204	75,440	17q25.3
GL000204	61,571	17q25.3	0.22	6E-022	GL000204	79,997	17q25.3
GL000204	61,666	17q25.3	0.19	3.3E-018	GL000204	79,997	17q25.3
GL000204	75,440	17q25.3	0.83	2.3E-145	GL000204	79,997	17q25.3
SCAF_1103279187659	1,103	22q11.1	0.32	2.3E-026	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.66	1.9E-072	SCAF_1103279187460	80,674	22q11.1

SCAF_1103279186290	1,523	22q11.1	0.24	2.4E-010	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.62	5.2E-066	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.7	3.6E-044	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187453	2,271	NA	0.25	4.1E-011	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.74	1.5E-088	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.74	1.3E-093	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.74	2E-091	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187875	3,772	NA	0.15	1.6E-009	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.8	4.9E-109	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.68	7.7E-077	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.62	7.6E-065	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.39	7.9E-033	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.58	3.9E-056	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.67	1E-074	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.66	2.4E-072	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.96	6.9E-206	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.18	8.9E-015	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.66	9.3E-073	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187626	47,976	22q11.1	0.64	3.3E-070	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187626	51,038	22q11.1	0.29	2E-019	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187626	54,749	22q11.1	0.25	2.8E-020	SCAF_1103279187460	80,674	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.51	3.4E-053	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.44	4.1E-044	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.68	7.9E-041	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.49	1.6E-053	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.52	1.7E-030	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187453	2,271	NA	0.17	0.000000034	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.64	1.9E-076	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187012	3,010	22q11.1	0.43	2.2E-044	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.52	1.3E-057	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187875	3,772	NA	0.13	7.5E-010	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.56	4.4E-064	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.46	4.8E-047	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.41	9E-041	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.64	1.4E-074	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.4	1.4E-037	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.45	3E-046	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.44	2E-045	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.55	2.2E-057	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.38	2E-036	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.43	6.1E-043	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187626	47,976	22q11.1	0.67	2.3E-084	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187626	51,038	22q11.1	0.43	2E-034	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187626	54,749	22q11.1	0.27	4.7E-025	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187460	80,674	22q11.1	0.5	2.7E-046	SCAF_1103279187460	81,471	22q11.1
SCAF_1103279187659	1,103	22q11.1	0.51	9.2E-053	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279186877	1,243	22q11.1	0.88	1.1E-155	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279186290	1,523	22q11.1	0.21	4.5E-009	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279182830	1,870	22q11.1	0.86	2.3E-146	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279182133	1,991	22q11.1	0.43	2.7E-023	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279182830	2,753	22q11.1	0.7	2.9E-087	SCAF_1103279187460	82,865	22q11.1

SCAF_1103279187012	3,010	22q11.1	0.97	1.1E-275	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279180853	3,459	22q11.1	0.67	6E-083	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187875	3,772	NA	0.11	0.000000012	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279186877	4,004	22q11.1	0.75	3.2E-102	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279186877	4,081	22q11.1	0.93	1.8E-192	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279186877	4,182	22q11.1	0.75	3.1E-101	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279183297	9,965	22q11.1	0.33	1.1E-029	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279182409	11,698	22q11.1	0.5	3.5E-049	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187736	36,315	22q11.1	0.91	2.6E-177	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187736	37,900	22q11.1	0.89	3.7E-164	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187736	39,138	22q11.1	0.75	6.1E-096	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279182252	41,642	22q11.1	0.16	2.5E-014	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187460	43,714	22q11.1	0.94	7.1E-198	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187626	47,976	22q11.1	0.59	1.8E-066	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187626	51,038	22q11.1	0.17	1.6E-012	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187626	54,749	22q11.1	0.24	4.6E-022	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187460	80,674	22q11.1	0.73	2.8E-083	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279187460	81,471	22q11.1	0.49	1.2E-049	SCAF_1103279187460	82,865	22q11.1
SCAF_1103279183150	9,341	20q11.22	0.38	7E-037	SCAF_1103279188197	92,818	20p11.21
SCAF_1103279184675	45,022	20p11.1	0.38	5E-035	SCAF_1103279188197	92,818	20p11.21
SCAF_1103279184675	45,566	20p11.1	0.45	3.3E-044	SCAF_1103279188197	92,818	20p11.21
SCAF_1103279188197	70,458	20p11.21	0.3	2.5E-026	SCAF_1103279188197	92,818	20p11.21
SCAF_1103279187072	433	1p11.2	0.09	7.8E-009	GL000192	101,317	1q21.1
SCAF_1103279183789	2,662	1p11.2	0.09	4.3E-009	GL000192	101,317	1q21.1
SCAF_1103279187122	3,932	1p11.2	0.09	7.6E-009	GL000192	101,317	1q21.1
SCAF_1103279188307	46,575	1q21.1	0.15	1.5E-014	GL000192	101,317	1q21.1
SCAF_1103279180200	335	14q11.2	0.13	3E-012	SCAF_1103279188266	105,915	NA
SCAF_1103279186561	1,628	14q11.2	0.09	0.000000013	SCAF_1103279188266	105,915	NA
SCAF_1103279180207	2,996	14q11.2	0.14	2.7E-013	SCAF_1103279188266	105,915	NA
GL000235	7,959	14q11.2	0.15	2.1E-014	SCAF_1103279188266	105,915	NA
SCAF_1103279181222	12,417	NA	0.81	9E-127	SCAF_1103279188266	105,915	NA
GL000230	14,024	14q11.2	0.1	8.1E-010	SCAF_1103279188266	105,915	NA
SCAF_1103279187526	20,185	14q11.2	0.12	4.2E-011	SCAF_1103279188266	105,915	NA
SCAF_1103279188017	20,258	14q11.2	0.11	1.4E-010	SCAF_1103279188266	105,915	NA
SCAF_1103279188017	31,805	14q11.2	0.2	8.2E-009	SCAF_1103279188266	105,915	NA
SCAF_1103279180967	36,678	14q11.2	0.14	1.8E-013	SCAF_1103279188266	105,915	NA
SCAF_1103279188266	66,064	NA	0.82	1.8E-125	SCAF_1103279188266	105,915	NA
SCAF_1103279188266	67,416	NA	0.8	2.3E-124	SCAF_1103279188266	105,915	NA
GL000194	72,564	NA	0.39	1.3E-038	SCAF_1103279188266	105,915	NA
GL000214	66,287	NA	0.28	1.8E-014	GL000214	116,077	NA
SCAF_1103279188124	10,878	15q11.2	0.61	1.2E-076	SCAF_1103279187475	123,734	15q11.2
SCAF_1103279187477	72,717	15q11.2	0.91	9.4E-195	SCAF_1103279187475	123,734	15q11.2
SCAF_1103279187072	433	1p11.2	0.07	0.00000026	GL000192	123,920	1q21.1
SCAF_1103279183789	2,662	1p11.2	0.08	0.000000094	GL000192	123,920	1q21.1
SCAF_1103279187122	3,932	1p11.2	0.09	2.3E-009	GL000192	123,920	1q21.1
SCAF_1103279187792	46,115	1p11.2	0.08	0.00000008	GL000192	123,920	1q21.1
SCAF_1103279188307	46,575	1q21.1	0.1	5E-010	GL000192	123,920	1q21.1
GL000192	101,317	1q21.1	0.92	2.4E-201	GL000192	123,920	1q21.1
SCAF_1103279184070	3,007	1p11.2	0.72	5.5E-104	SCAF_1103279187792	132,443	1p11.2
SCAF_1103279187122	3,932	1p11.2	0.14	8.3E-014	SCAF_1103279187792	132,443	1p11.2
SCAF_1103279187792	46,115	1p11.2	0.85	1.1E-148	SCAF_1103279187792	132,443	1p11.2

SCAF_1103279184070	3,007	1p11.2	0.46	1.3E-050	SCAF_1103279187792	133,164	1p11.2
SCAF_1103279187122	3,932	1p11.2	0.32	7.7E-032	SCAF_1103279187792	133,164	1p11.2
SCAF_1103279187792	46,115	1p11.2	0.58	1.6E-070	SCAF_1103279187792	133,164	1p11.2
SCAF_1103279187792	132,443	1p11.2	0.52	5.4E-062	SCAF_1103279187792	133,164	1p11.2
SCAF_1103279183150	9,341	20q11.22	0.73	4.8E-105	SCAF_1103279187452	134,707	20q11.22
SCAF_1103279184675	45,022	20p11.1	0.57	3.1E-062	SCAF_1103279187452	134,707	20q11.22
SCAF_1103279184675	45,566	20p11.1	0.64	3.1E-078	SCAF_1103279187452	134,707	20q11.22
SCAF_1103279188197	70,458	20p11.21	0.14	1.6E-012	SCAF_1103279187452	134,707	20q11.22
SCAF_1103279188197	92,818	20p11.21	0.38	4E-035	SCAF_1103279187452	134,707	20q11.22
SCAF_1103279188164	22,291	6p21.32	0.19	3.4E-012	SCAF_1103279188164	139,443	6p21.32
SCAF_1103279188164	26,392	6p21.32	0.24	2.6E-012	SCAF_1103279188164	139,443	6p21.32
SCAF_1103279180438	132,606	17q11.1	0.13	1.4E-012	SCAF_1103279180438	152,054	17q11.1
SCAF_1103279180438	132,606	17q11.1	0.76	2.8E-115	SCAF_1103279180438	153,938	17q11.1
SCAF_1103279180438	152,054	17q11.1	0.29	8.2E-030	SCAF_1103279180438	153,938	17q11.1
SCAF_1103279180438	132,606	17q11.1	0.92	2.2E-204	SCAF_1103279180438	155,176	17q11.1
SCAF_1103279180438	152,054	17q11.1	0.2	6.9E-020	SCAF_1103279180438	155,176	17q11.1
SCAF_1103279180438	153,938	17q11.1	0.82	3.5E-139	SCAF_1103279180438	155,176	17q11.1
SCAF_1103279187072	433	1p11.2	0.49	5.2E-056	SCAF_1103279188307	166,097	1q21.1
SCAF_1103279183789	2,662	1p11.2	0.55	1.2E-065	SCAF_1103279188307	166,097	1q21.1
SCAF_1103279187122	36,213	1p11.2	0.27	1.5E-026	SCAF_1103279188307	166,097	1q21.1
SCAF_1103279188307	46,575	1q21.1	0.92	1.1E-202	SCAF_1103279188307	166,097	1q21.1
GL000192	101,317	1q21.1	0.12	2.5E-011	SCAF_1103279188307	166,097	1q21.1
GL000192	123,920	1q21.1	0.07	0.00000014	SCAF_1103279188307	166,097	1q21.1
SCAF_1103279188164	22,291	6p21.32	0.21	4.3E-021	SCAF_1103279188164	168,609	6p21.32
SCAF_1103279188164	26,392	6p21.32	0.28	2.2E-024	SCAF_1103279188164	168,609	6p21.32
SCAF_1103279188164	26,392	6p21.32	0.3	6.4E-025	SCAF_1103279188164	168,626	6p21.32
SCAF_1103279188164	168,609	6p21.32	0.47	2.2E-050	SCAF_1103279188164	168,626	6p21.32
SCAF_1103279187930	31,787	17p11.2	0.56	6E-063	SCAF_1103279188241	181,972	17p11.2
SCAF_1103279180438	152,054	17q11.1	0.1	6.1E-010	SCAF_1103279188241	181,972	17p11.2
SCAF_1103279187972	13,065	20p11.1	0.73	5E-097	SCAF_1103279179615	203,707	20p11.1
SCAF_1103279183150	9,341	20q11.22	0.43	1.3E-046	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279184675	45,022	20p11.1	0.27	1.9E-025	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279184675	45,566	20p11.1	0.3	1.1E-029	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279188197	70,458	20p11.21	0.27	1.4E-025	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279188197	92,818	20p11.21	0.17	5.2E-015	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279187452	134,707	20q11.22	0.44	3.7E-047	SCAF_1103279187452	205,259	20q11.22
SCAF_1103279187972	13,065	20p11.1	0.61	6.1E-070	SCAF_1103279179615	210,373	20p11.1
SCAF_1103279179615	203,707	20p11.1	0.77	6.7E-117	SCAF_1103279179615	210,373	20p11.1
SCAF_1103279187930	31,787	17p11.2	0.7	2.8E-090	SCAF_1103279188241	226,453	17p11.2
SCAF_1103279180438	152,054	17q11.1	0.09	0.000000011	SCAF_1103279188241	226,453	17p11.2
SCAF_1103279188241	181,972	17p11.2	0.78	8.1E-119	SCAF_1103279188241	226,453	17p11.2
SCAF_1103279184070	3,007	1p11.2	0.8	9.6E-132	SCAF_1103279187792	227,994	1p11.2
SCAF_1103279187122	3,932	1p11.2	0.21	1.3E-020	SCAF_1103279187792	227,994	1p11.2
SCAF_1103279187792	46,115	1p11.2	0.92	1E-204	SCAF_1103279187792	227,994	1p11.2
GL000192	123,920	1q21.1	0.07	0.00000015	SCAF_1103279187792	227,994	1p11.2
SCAF_1103279187792	132,443	1p11.2	0.84	1.9E-151	SCAF_1103279187792	227,994	1p11.2
SCAF_1103279187792	133,164	1p11.2	0.64	7.6E-086	SCAF_1103279187792	227,994	1p11.2
SCAF_1103279180438	132,606	17q11.1	0.1	1.5E-010	SCAF_1103279181781	237,445	17p11.2
SCAF_1103279180438	153,938	17q11.1	0.09	6.8E-009	SCAF_1103279181781	237,445	17p11.2
SCAF_1103279180438	155,176	17q11.1	0.11	2.9E-011	SCAF_1103279181781	237,445	17p11.2
SCAF_1103279183150	9,341	20q11.22	0.32	8.7E-033	SCAF_1103279188197	557,118	20p11.21

SCAF_1103279184675	45,022	20p11.1	0.25	4.9E-023	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279184675	45,566	20p11.1	0.26	1.5E-025	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279188197	70,458	20p11.21	0.73	2E-103	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279188197	92,818	20p11.21	0.27	6.6E-025	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279187452	134,707	20q11.22	0.22	2.3E-021	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279187452	205,259	20q11.22	0.46	1.7E-051	SCAF_1103279188197	557,118	20p11.21
SCAF_1103279183150	9,341	20q11.22	0.71	1.1E-102	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279184675	45,022	20p11.1	0.58	7.2E-068	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279184675	45,566	20p11.1	0.69	9.9E-093	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279188197	70,458	20p11.21	0.29	1.1E-027	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279188197	92,818	20p11.21	0.55	2.5E-061	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279187452	134,707	20q11.22	0.67	2.5E-087	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279187452	205,259	20q11.22	0.33	4.6E-034	SCAF_1103279188197	581,035	20p11.21
SCAF_1103279188197	557,118	20p11.21	0.41	1.5E-044	SCAF_1103279188197	581,035	20p11.21

Supplementary Table 8. List of patches from GRCh37.p10.

Coordinates for the location where the patch replaces or adds sequence from the GRCh37/hg19 human reference genome are displayed. Analysis of overlaps with scaffolds mapped in this study shows that sequence from patch GL877877.1 is contained in HuRef scaffold SCAF_1103279188373, and sequence from BAC clone RP11-247L13/AC144898.3 is contained in patch JH636052.3.

SEQUENCE	ACCESSION	NAME	BAND	CHR	START	STOP
JH806574.1		REGION77	1p36.32	chr1	3,823,584	3,845,268
GL949741.1	NW_003571030.1	REGION60	1p35.2	chr1	31,872,759	32,017,063
JH636053.1	NW_003871056.1	1P11	1p12-1p11.2	chr1	120,471,050	121,346,350
JH636052.3		1Q21	1q21.1-1q21.3	chr1	143,871,003	150,440,213
GL383518.1	NW_003315905.1	REGION2	1q21.3	chr1	153,673,007	153,838,214
GL383519.1	NW_003315906.1	MTX1	1q22	chr1	155,180,173	155,275,036
GL383520.1	NW_003315907.1	REGION3	1q31.3	chr1	198,339,213	198,694,304
JH806573.1		REGION78	1q32.1	chr1	205,916,833	205,922,707
JH636054.1	NW_003871057.1	1Q32	1q32.1	chr1	206,072,708	206,940,869
JH806575.1		REGION79	1q42.3	chr1	235,167,042	235,192,211
GL383516.1	NW_003315903.1	REGION1	1q44	chr1	248,865,779	249,098,883
GL383517.1	NW_003315904.1	REGION1	1q44	chr1	248,865,779	249,098,883
GL383521.1	NW_003315908.1	REGION4	2p22.3	chr2	36,453,102	36,590,458
GL877871.1	NW_003571032.1	REGION55	2q11.1	chr2	95,326,172	95,618,108
GL582966.2	NW_003571033.2	REGION44	2q23.1	chr2	149,790,583	149,880,633
GL383522.1	NW_003315909.1	SPC25	2q24.3-2q31.1	chr2	169,686,873	169,793,704
GL877870.2	NW_003571031.1	REGION54	2q37.3	chr2	243,059,660	243,189,373
JH636055.1	NW_003871060.1	REGION73	3p25.2	chr3	11,856,742	12,027,971
JH159132.1	NW_003871059.1	SEMA3B	3p21.31	chr3	50,267,585	50,368,277
GL383523.1	NW_003315910.1	VPRBP	3p21.2	chr3	51,416,109	51,584,055
GL383524.1	NW_003315911.1	DNAH12	3p14.3	chr3	57,369,478	57,399,969
JH159131.1	NW_003871058.1	REGION64	3p14.2	chr3	60,558,332	60,952,039
GL383525.1	NW_003315912.1	SLC25A26	3p14.1	chr3	66,270,271	66,308,065
GL383526.1	NW_003315913.1	REGION5	3q25.1	chr3	151,307,154	151,477,286
GL383528.1	NW_003315915.1	REGION6	4p15.1	chr4	34,519,577	34,885,480
GL383529.1	NW_003315916.1	LPHN3	4q13.1	chr4	62,777,687	62,877,254
GL582967.1	NW_003571035.1	REGION45	4q13.3	chr4	75,382,210	75,689,879
GL383527.1	NW_003315914.1	REGION7	4q32.1	chr4	156,756,530	156,908,416
GL877872.1	NW_003571034.1	REGION56	4q35.2	chr4	190,828,226	191,044,276
GL383532.1	NW_003315920.1	REGION9	5p15.2	chr5	12,681,538	12,744,122
GL949742.1	NW_003571036.1	REGION61	5p13.3	chr5	29,036,605	29,254,576
GL339449.2	NW_003315917.2	SMA	5q13.2	chr5	68,512,646	70,910,270
GL383530.1	NW_003315918.1	MCTP1	5q15	chr5	94,505,561	94,590,195
JH159133.1	NW_003871061.1	PPIP5K2	5q21.1	chr5	102,420,838	102,687,150
GL383531.1	NW_003315919.1	REGION8	5q34	chr5	161,800,673	161,968,654
JH806576.1		REGION80	6p22.2	chr6	26,585,843	26,826,779
JH636057.1	NW_003871063.1	MHC	6p22.1-6p21.32	chr6	28,477,797	33,448,354
GL383533.1	NW_003315921.1	REGION10	6q14.1	chr6	80,059,725	80,156,628
JH636056.1	NW_003871062.1	LAMA4	6q21	chr6	112,323,682	112,586,593
GL582970.1	NW_003571039.1	REGION48	7p11.2	chr7	56,835,596	57,190,579
GL582969.1	NW_003571038.1	REGION46	7p11.2	chr7	57,342,227	57,586,048
JH159134.2	NW_003871064.1	WILLIAMS	7q11.22-7q11.23	chr7	71,935,722	75,921,852

GL582972.1	NW_003571041.1	REGION47	7q22.1	chr7	98,260,131	98,556,215
GL582968.1	NW_003571037.1	SH2B2	7q22.1	chr7	101,718,951	102,072,447
JH636058.1	NW_003871065.1	COPG2	7q32.2-7q32.3	chr7	129,984,424	130,721,755
GL383534.2	NW_003315922.2	REGION11	7q34	chr7	141,333,209	141,446,383
GL582971.1	NW_003571040.1	TRB	7q34	chr7	141,557,850	142,778,624
GL949743.1	NW_003571042.1	REGION62	8p23.3-8p23.2	chr8	1,965,390	2,498,608
JH159135.1	NW_003871066.1	JRK	8q24.3	chr8	143,711,229	143,813,536
GL383535.1	NW_003315923.1	EPPK1_SPATC1	8q24.3	chr8	144,743,526	145,146,062
GL383536.1	NW_003315924.1	SCXB	8q24.3	chr8	145,285,645	145,659,901
GL383539.1	NW_003315928.1	REGION14	9p24.1	chr9	7,428,994	7,577,169
JH636059.1	NW_003871067.1	CBWD3	9q21.11	chr9	70,835,469	71,130,847
GL383540.1	NW_003315929.1	REGION13	9q21.11	chr9	72,028,659	72,092,013
GL383541.1	NW_003315930.1	MAMDC2	9q21.12	chr9	72,639,029	72,804,234
GL383542.1	NW_003315931.1	REGION15	9q22.1	chr9	90,793,962	90,842,895
JH806579.1		REGION81	9q34.11	chr9	132,892,850	133,073,060
GL339450.1	NW_003315925.1	ABO	9q34.2	chr9	136,049,442	136,369,192
JH806577.1		REGION82	9q34.2	chr9	137,025,633	137,247,659
JH806578.1		REGION82	9q34.2	chr9	137,025,633	137,247,659
GL383537.1	NW_003315926.1	REGION12	9q34.3	chr9	139,136,890	139,252,828
GL383538.1	NW_003315927.1	REGION12	9q34.3	chr9	139,136,890	139,252,828
GL877873.1	NW_003571043.1	REGION57	10p15.3	chr10	60,001	224,405
JH636060.1	NW_003871071.1	AKR1CL1	10p15.1	chr10	5,012,527	5,450,243
GL383543.1	NW_003315932.1	FAM23A_MRC1	10p12.33	chr10	17,613,209	18,252,930
GL383545.1	NW_003315934.1	REGION16	10p12.1	chr10	27,574,584	27,706,537
GL383546.1	NW_003315935.1	REGION18	10q11.21	chr10	45,670,681	45,964,419
JH591181.2	NW_003871068.1	10Q11	10q11.22-10q11.23	chr10	46,224,334	51,664,310
JH591183.1	NW_003871070.1	ZNF518A	10q24.1	chr10	97,861,451	98,039,369
JH591182.1	NW_003871069.1	PNLIPRP2	10q25.3	chr10	118,348,517	118,544,777
GL383544.1	NW_003315933.1	REGION17	10q26.3	chr10	133,258,319	133,381,404
JH806580.1		PPP2R2D	10q26.3	chr10	133,727,528	133,781,577
JH591184.1	NW_003871075.1	SPON1	11p15.2	chr11	13,963,464	14,425,744
JH591185.1	NW_003871082.1	CALCA	11p15.2	chr11	14,873,971	15,041,407
GL383547.1	NW_003315936.1	REGION19	11p14.3	chr11	25,191,953	25,340,626
GL582973.1	NW_003571045.1	REGION49	11p11.12	chr11	49,862,648	50,121,284
JH159136.1	NW_003871073.1	OLFACTORY_REGION_1	11q12.1	chr11	55,956,728	56,641,043
JH159137.1	NW_003871074.1	OLFACTORY_REGION_1	11q12.1	chr11	55,956,728	56,641,043
GL949744.1	NW_003571046.1	REGION63	11q13.3	chr11	69,614,786	69,922,571
JH806581.1		SHANK2	11q13.3-11q13.4	chr11	70,301,893	71,088,948
JH159143.1	NW_003871081.1	B3GNT6	11q13.5	chr11	76,709,408	76,900,812
JH159141.2	NW_003871079.1	CWC15_SRSF8	11q21	chr11	94,611,846	94,852,618
JH159139.1	NW_003871077.1	MMP12	11q22.2	chr11	102,702,497	102,822,936
JH159142.2	NW_003871080.1	DIXDC1_ALG9	11q23.1	chr11	111,618,733	111,945,380
JH159140.1	NW_003871078.1	NCAM1	11q23.2	chr11	112,687,997	113,234,431
JH720443.1	NW_003871072.1	TREH	11q23.3	chr11	118,245,278	118,653,701
JH159138.1	NW_003871076.1	SLC37A4	11q23.3	chr11	118,849,111	118,957,986
GL582974.1	NW_003571048.1	REGION50	12p13.33	chr12	60,001	282,464
GL877875.1	NW_003571049.1	REGION50	12p13.33	chr12	60,001	282,464
JH720444.1	NW_003871083.1	EMG1	12p13.31	chr12	6,907,581	7,178,849
GL877876.1	NW_003571050.1	REGION58	12p13.2	chr12	10,953,894	11,330,216
GL949745.1	NW_003571047.1	REGION58	12p13.2	chr12	10,953,894	11,330,216
GL383549.1	NW_003315938.1	REGION21	12p11.22	chr12	28,148,967	28,263,711

GL383550.1	NW_003315939.1	REGION22	12q14.1	chr12	58,326,520	58,486,538
GL383552.1	NW_003315941.1	REGION23	12q14.1	chr12	59,323,046	59,454,651
GL383553.2	NW_003315942.2	REGION24	12q23.1-12q23.2	chr12	101,505,377	101,652,073
GL383551.1	NW_003315940.1	REGION20	12q24.32	chr12	126,711,744	126,890,020
GL383548.1	NW_003315937.1	GALNT9	12q24.33	chr12	132,806,993	132,967,794
GL582975.1	NW_003571051.1	REGION51	13q34	chr13	115,085,142	115,109,878
GL383554.1	NW_003315943.1	REGION25	15q13.1	chr15	28,557,187	28,842,093
GL383555.1	NW_003315944.1	MEGF11	15q22.31	chr15	66,200,521	66,577,156
JH720445.1	NW_003871084.1	SYNM	15q26.3	chr15	99,529,037	99,696,045
GL383556.1	NW_003315945.1	REGION26	16q12.2	chr16	55,822,434	56,002,460
JH720446.1	NW_003871085.1	REGION74	16q21	chr16	57,774,022	57,871,358
GL383557.1	NW_003315946.1	SNTB2	16q22.1	chr16	69,174,054	69,258,593
GL383563.1	NW_003315952.1	DOC2B_RPH3AL	17p13.3	chr17	1	252,428
JH806582.1		DOC2B_RPH3AL	17p13.3	chr17	1	252,428
GL383562.1	NW_003315951.1	FAM101B	17p13.3	chr17	252,429	296,626
GL383561.1	NW_003315950.1	REGION27	17p11.2	chr17	21,250,948	21,566,608
JH159145.1	NW_003871090.1	SLC46A1	17q11.2	chr17	26,645,159	26,840,019
GL383560.1	NW_003315949.1	MYO19	17q12	chr17	34,442,621	35,005,379
GL383559.1	NW_003315948.1	SOCS7	17q12	chr17	36,372,617	36,711,255
GL383564.1	NW_003315953.1	KRTAP_REGION_1	17q21.2	chr17	39,006,985	39,589,187
JH159146.1	NW_003871091.1	KRTAP_REGION_1	17q21.2	chr17	39,006,985	39,589,187
JH159147.1	NW_003871092.1	KRTAP_REGION_1	17q21.2	chr17	39,006,985	39,589,187
JH159148.1	NW_003871093.1	KRTAP_REGION_1	17q21.2	chr17	39,006,985	39,589,187
GL582976.1	NW_003571052.1	TTC25	17q21.2	chr17	39,869,611	40,277,911
JH720447.1	NW_003871086.1	MAPT	17q21.31-17q21.32	chr17	43,384,864	44,913,631
GL383558.1	NW_003315947.1	PECAM1	17q23.3-17q24.1	chr17	62,273,514	62,649,312
JH159144.1	NW_003871088.1	REGION65	17q24.2	chr17	65,936,106	66,324,470
GL383565.1	NW_003315954.1	REGION28	17q24.3	chr17	68,302,419	68,520,360
GL383566.1	NW_003315955.1	REGION30	17q25.2	chr17	75,216,812	75,295,408
JH591186.1	NW_003871089.1	REGION69	17q25.3	chr17	77,412,077	77,766,016
JH636061.1	NW_003871087.1	BAHCC1	17q25.3	chr17	79,319,163	79,498,447
GL383567.1	NW_003315956.1	REGION31	18q21.1	chr18	47,818,564	48,101,162
GL383570.1	NW_003315959.1	REGION32	18q21.2	chr18	49,189,306	49,348,012
GL383571.1	NW_003315960.1	REGION33	18q22.1	chr18	65,090,960	65,219,788
GL383568.1	NW_003315957.1	REGION34	18q22.3	chr18	70,600,357	70,692,016
GL383569.1	NW_003315958.1	REGION35	18q23	chr18	76,253,467	76,412,030
GL383572.1	NW_003315961.1	REGION36	18q23	chr18	76,694,886	76,848,997
JH159149.1	NW_003871094.1	REGION66	19p13.2	chr19	8,634,915	8,926,179
GL582977.1	NW_003571053.1	REGION52	19p12	chr19	20,193,557	20,845,946
GL383573.1	NW_003315962.1	ZNF66	19p12	chr19	20,845,947	21,225,187
GL383575.2	NW_003315964.2	REGION37	19p12	chr19	21,831,092	21,991,834
GL383576.1	NW_003315965.1	REGION39	19p12	chr19	22,303,652	22,483,468
GL383574.1	NW_003315963.1	REGION38	19q13.11	chr19	34,643,165	34,791,855
GL949746.1	NW_003571054.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949747.1	NW_003571055.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949748.1	NW_003571056.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949749.1	NW_003571057.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949750.1	NW_003571058.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949751.1	NW_003571059.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949752.1	NW_003571060.1	LRC	19q13.42	chr19	54,528,888	55,595,686
GL949753.1	NW_003571061.1	LRC	19q13.42	chr19	54,528,888	55,595,686

GL383577.1	NW_003315966.1	REGION40	20p12.1	chr20	17,751,747	17,874,115
JH720448.1	NW_003871095.1	DLGAP4	20q11.23	chr20	34,883,261	34,994,224
GL582979.2	NW_003571063.2	REGION53	20q13.33	chr20	61,031,539	61,267,733
GL383578.1	NW_003315967.1	REGION41	21q11.2	chr21	15,796,462	15,847,792
GL383579.1	NW_003315968.1	REGION42	21q21.1	chr21	23,474,793	23,669,288
GL383580.1	NW_003315969.1	REGION43	21q22.11	chr21	34,141,390	34,210,247
GL383581.1	NW_003315970.1	TMEM50B	21q22.11	chr21	34,777,735	34,884,866
JH806584.1		REGION83	22q11.1	chr22	16,050,001	16,087,693
JH806583.1		REGION84	22q11.1	chr22	16,656,462	16,697,850
JH806585.1		REGION85	22q11.1	chr22	16,847,851	16,884,805
JH720449.1	NW_003871096.1	CLTCL1	22q11.21	chr22	19,134,297	19,346,604
GL383583.1	NW_003315972.1	APOBEC	22q13.1	chr22	39,280,299	39,407,165
GL383582.1	NW_003315971.1	CYP2D6	22q13.2	chr22	42,477,964	42,648,568
JH806586.1		REGION86	22q13.33	chr22	51,203,354	51,244,566
GL877877.1	NW_003571064.1	REGION59	Xp22.33	chrX	803,878	1,227,822
JH720451.1	NW_003871098.1	REGION75	Xp21.1-Xp11.4	chrX	36,202,464	37,669,766
JH720452.1	NW_003871099.1	REGION75	Xp21.1-Xp11.4	chrX	36,202,464	37,669,766
JH806589.1		REGION87	Xp11.3	chrX	45,534,581	45,805,400
JH806587.1		DGKK_REGION98	Xp11.23-Xp11.22	chrX	47,619,971	54,424,077
JH806590.1		DGKK_REGION98	Xp11.23-Xp11.22	chrX	47,619,971	54,424,077
JH806591.1		REGION88	Xq11.1-Xq11.2	chrX	62,203,738	63,086,230
JH806592.1		REGION89	Xq13.1-Xq13.2	chrX	71,530,834	72,366,730
JH720453.1	NW_003871100.1	REGION76	Xq13.3-Xq21.1	chrX	75,200,416	77,452,502
JH720454.2		REGION76	Xq13.3-Xq21.1	chrX	75,200,416	77,452,502
JH806593.1		REGION90	Xq22.1	chrX	100,573,313	100,962,928
JH806594.1		REGION91	Xq22.1	chrX	101,383,115	101,773,566
JH806595.1		REGION92	Xq22.2	chrX	103,118,514	103,552,339
JH720455.1	NW_003871102.1	TEX13A	Xq22.3	chrX	104,423,968	104,489,003
JH806588.1		REGION93	Xq23	chrX	112,661,943	115,918,761
JH806601.1		REGION93	Xq23	chrX	112,661,943	115,918,761
JH806602.1		REGION93	Xq23	chrX	112,661,943	115,918,761
JH806603.1		REGION93	Xq23	chrX	112,661,943	115,918,761
JH806596.1		REGION94	Xq24	chrX	119,081,534	119,495,352
JH806597.1		REGION95	Xq26.3	chrX	134,202,887	135,196,638
JH806598.1		REGION96	Xq27.1-Xq27.2	chrX	139,986,363	140,891,303
JH806599.1		REGION97	Xq27.3-Xq28	chrX	142,299,066	150,174,083
JH806600.1		REGION97	Xq27.3-Xq28	chrX	142,299,066	150,174,083
JH159150.2		REGION67	Xq28	chrX	151,734,490	154,906,585

Supplementary Table 9. List of identified PSVs between the two *DUSP22* paralogs.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; REF, ALT: reference and alternate alleles; CLASS: functional class of the polymorphism; CHANGE: amino acid change.

CHR	ID	BP	BAND	REF	ALT	CLASS	CHANGE
chr6	rs11242812	348,906	6p25.3	G	A	cds-synon	p.P191
chr6	rs11242813	349,016	6p25.3	C	T	utr3	NA
chr6	rs6927235	349,317	6p25.3	T	C	utr3	NA
chr6	rs3778605	349,343	6p25.3	T	A	utr3	NA
chr6	rs1129085	350,829	6p25.3	G	A	cds-synon	p.P172
chr6	rs1046656	351,156	6p25.3	C	T	utr3	NA

Supplementary Table 10. List of identified PSVs between the three *PRIM2* paralogs.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; REF, 6p11.2, 6q11.1, 3p11.1: reference allele and alleles predicted at the three distinct paralogs; CLASS: functional class of the polymorphism; CHANGE: amino acid change.

CHR	ID	BP	BAND	REF	6p11.2	6q11.1	3p11.1	CLASS	CHANGE
chr6	rs5011403	57,244,780	6p11.2	G	G	A	NA	missense	p.E181K
chr6	rs6913546	57,246,884	6p11.2	A	A	G	NA	missense	p.D204G
chr6	rs927192	57,393,125	6p11.2	A	G	A	G	missense	p.S259G
chr6	rs76686926	57,393,160	6p11.2	G	G	G	A	cds-synon	p.K270
chr6	rs80081867	57,398,154	6p11.2	T	C	T	C	missense	p.L286P
chr6	rs9476080	57,398,157	6p11.2	A	G	A	G	missense	p.Y287C
chr6	rs9476081	57,398,163	6p11.2	A	G	A	G	missense	p.H289R
chr6	rs62398997	57,398,201	6p11.2	T	C	T	C	missense	p.C302R
chr6	rs71214816	57,398,207	6p11.2	G	G	G	T	nonsense	p.G304X
chr6	rs77436138	57,398,226	6p11.2	T	G	T	A	missense	p.V310D/G
chr6	rs62398998	57,398,264	6p11.2	A	G	A	G	missense	p.T323A
chr6	rs62398999	57,398,270	6p11.2	C	C	C	T	nonsense	p.Q325X
chr6	rs9885913	57,467,084	6p11.2	A	A	A	G	missense	p.D342G
chr6	rs9885916	57,467,093	6p11.2	A	A	A	G	missense	p.Y345C
chr6	rs4535533	57,467,100	6p11.2	G	C	G	C	readthrough	p.X347Y
chr6	rs9885751	57,467,107	6p11.2	C	C	C	T	missense	p.R350C
chr6	rs4406234	57,467,175	6p11.2	A	G	A	A	cds-synon	p.L372
chr6	rs4307164	57,512,476	6p11.2	G	A	G	A	missense	p.G435D
chr6	rs4294007	57,512,510	6p11.2	T	G	T	G	missense	p.H446Q
chr6	rs5001076	57,512,529	6p11.2	C	C	C	A	missense	p.R453S
chr6	rs4294008	57,512,565	6p11.2	T	C	T	C	missense	p.S465P
chr6	rs4398719	57,512,678	6p11.2	G	A	G	A	cds-synon	p.E502
chr6	rs5001484	57,512,711	6p11.2	G	A	G	C	utr3	NA
chr6	rs5001483	57,512,718	6p11.2	T	T	T	A	utr3	NA
chr6	rs7773110	57,512,775	6p11.2	T	G	T	G	utr3	NA
chr6	rs76296076	57,512,779	6p11.2	G	T	G	T	utr3	NA
chr6	rs72880943	57,512,825	6p11.2	C	T	C	T	utr3	NA
chr6	rs7752845	57,512,826	6p11.2	A	G	A	G	utr3	NA
chr6	rs78256005	57,512,841	6p11.2	A	A	A	G	utr3	NA
chr6	rs77911716	57,512,850	6p11.2	C	C	C	G	utr3	NA
chr6	rs75351177	57,512,889	6p11.2	C	C	C	T	utr3	NA
chr6	rs77348569	57,512,893	6p11.2	C	T	C	C	utr3	NA
chr6	rs77563921	57,512,902	6p11.2	G	G	G	A	utr3	NA
chr6	rs75209982	57,512,903	6p11.2	C	A	C	C	utr3	NA
chr6	rs77519815	57,512,906	6p11.2	T	A	T	A	utr3	NA
chr6	rs77947729	57,512,933	6p11.2	G	G	G	A	utr3	NA
chr6	rs75636132	57,512,969	6p11.2	G	C	G	C	utr3	NA
chr6	rs74695174	57,512,974	6p11.2	G	G	G	A	utr3	NA
chr6	rs79119670	57,512,999	6p11.2	C	G	C	G	utr3	NA
chr6	rs76730673	57,513,042	6p11.2	C	C	C	T	utr3	NA
chr6	rs74581130	57,513,047	6p11.2	C	T	C	C	utr3	NA

chr6	rs75390508	57,513,082	6p11.2	C	C	C	T	utr3	NA
chr6	rs56375552	57,513,126	6p11.2	C	G	C	C	utr3	NA
chr6	rs76503032	57,513,160	6p11.2	G	G	G	A	utr3	NA
chr6	rs1801400	57,513,182	6p11.2	A	G	A	A	utr3	NA
chr6	rs74617308	57,513,205	6p11.2	C	C	C	T	utr3	NA
chr6	rs1801352	57,513,221	6p11.2	C	T	C	T	utr3	NA
chr6	rs1801399	57,513,248	6p11.2	C	G	C	G	utr3	NA
chr6	rs79506978	57,513,292	6p11.2	C	C	C	T	utr3	NA
chr6	rs9367774	57,513,317	6p11.2	T	C	T	C	utr3	NA
chr6	rs74652947	57,513,366	6p11.2	A	A	A	G	utr3	NA

Supplementary Table 11. List of identified PSVs between the two *HYDIN* paralogs.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; REF, ALT: reference and alternate alleles; CLASS: functional class of the polymorphism; CHANGE: amino acid change.

CHR	ID	BP	BAND	REF	ALT	CLASS	CHANGE
chr16	rs77602727	70,852,297	16q22.2	C	T	missense	p.R4868Q
chr16	rs77347409	70,852,305	16q22.2	C	T	cds-synon	p.T4865
chr16	rs117615754	70,866,760	16q22.2	C	T	cds-synon	p.A4629
chr16	rs140880761	70,866,832	16q22.2	G	T	missense	p.N4605K
chr16	rs78139131	70,867,815	16q22.2	T	A	missense	p.M4551L
chr16	rs76311501	70,867,831	16q22.2	T	C	cds-synon	p.T4545
chr16	rs117585639	70,868,062	16q22.2	A	G	cds-synon	p.L4468
chr16	rs114164853	70,871,601	16q22.2	T	C	missense	p.K4411E
chr16	rs148248201	70,871,747	16q22.2	G	C	missense	p.S4362C
chr16	rs1798314	70,884,524	16q22.2	C	G	missense	p.E4159Q
chr16	rs79931006	70,884,534	16q22.2	T	A	cds-synon	p.T4155
chr16	rs2502698	70,889,147	16q22.2	A	G	cds-synon	p.I4108
chr16	rs1774416	70,891,640	16q22.2	T	C	missense	p.K4087R
chr16	rs1626593	70,896,033	16q22.2	C	T	missense	p.V3898M
chr16	rs1774421	70,896,118	16q22.2	A	G	cds-synon	p.H3869
chr16	rs1798325	70,897,039	16q22.2	C	G	missense	p.V3839L
chr16	rs77739958	70,902,559	16q22.2	C	T	missense	p.V3741I
chr16	rs1774504	70,902,568	16q22.2	C	T	missense	p.A3738T
chr16	rs2502690	70,902,683	16q22.2	G	A	cds-synon	p.H3699
chr16	rs1774311	70,908,239	16q22.2	G	A	cds-synon	p.I3638
chr16	rs1354550	70,908,736	16q22.2	A	G	cds-synon	p.N3547
chr16	rs1774331	70,917,855	16q22.2	A	G	missense	p.L3315P
chr16	rs1798440	70,917,931	16q22.2	C	G	missense	p.A3290P
chr16	rs1774423	70,926,334	16q22.2	G	C	missense	p.T3115R
chr16	rs79428476	70,934,994	16q22.2	C	T	cds-synon	p.G2986
chr16	rs1774449	70,942,688	16q22.2	A	C	missense	p.I2693S
chr16	rs78978478	70,954,513	16q22.2	T	C	missense	p.K2588R
chr16	rs74249266	70,954,571	16q22.2	C	T	missense	p.D2569N
chr16	rs74249267	70,954,572	16q22.2	T	A	cds-synon	p.L2568
chr16	rs74249268	70,954,606	16q22.2	C	T	missense	p.G2557E
chr16	rs1798528	70,954,691	16q22.2	T	C	missense	p.K2529E
chr16	rs77472425	70,954,774	16q22.2	A	G	missense	p.L2501S
chr16	rs76023477	70,954,809	16q22.2	C	A	cds-synon	p.A2489
chr16	rs1798531	70,954,915	16q22.2	G	T	missense	p.P2454Q
chr16	rs1798532	70,954,945	16q22.2	T	A	missense	p.N2444I
chr16	rs77513448	70,972,620	16q22.2	G	C	missense	p.R2297G
chr16	rs117922041	70,975,565	16q22.2	T	C	missense	p.Q2275R
chr16	rs117379722	70,975,667	16q22.2	T	C	missense	p.Q2241R
chr16	rs115852469	70,986,480	16q22.2	G	A	cds-synon	p.T2124
chr16	rs115844546	70,989,299	16q22.2	C	T	missense	p.V2098M
chr16	rs116739010	70,989,335	16q22.2	G	A	missense	p.R2086C
chr16	rs1774266	70,993,566	16q22.2	A	G	cds-synon	p.H2041

chr16	rs783762	71,007,809	16q22.2	C	T	missense	p.V1717M
chr16	rs115159786	71,008,169	16q22.2	T	C	cds-synon	p.L1647
chr16	rs1774303	71,012,855	16q22.2	T	C	missense	p.I1533V
chr16	rs1774516	71,025,245	16q22.2	C	T	cds-synon	p.T1280
chr16	rs1774513	71,026,076	16q22.2	C	G	missense	p.V1228L
chr16	rs117718337	71,054,178	16q22.2	T	C	missense	p.I1077V
chr16	rs116016318	71,061,056	16q22.2	A	G	utr3	NA
chr16	rs118185262	71,061,121	16q22.2	T	C	utr3	NA
chr16	rs76641962	71,061,292	16q22.2	T	C	utr3	NA
chr16	rs79616449	71,061,321	16q22.2	T	C	utr3	NA
chr16	rs78093086	71,061,364	16q22.2	T	C	utr3	NA
chr16	rs1022220	71,061,495	16q22.2	A	G	readthrough	p.X1018Q
chr16	rs3817211	71,098,649	16q22.2	T	C	missense	p.N724D
chr16	rs6416717	71,100,830	16q22.2	T	C	utr3	NA
chr16	rs10744982	71,101,200	16q22.2	T	C	missense	p.T690A
chr16	rs10735134	71,101,270	16q22.2	C	T	cds-synon	p.V666
chr16	rs1398391	71,103,269	16q22.2	T	C	cds-synon	p.P625
chr16	rs62040318	71,122,408	16q22.2	C	T	missense	p.G489D
chr16	rs929311	71,163,579	16q22.2	C	T	cds-synon	p.K397
chr16	rs79679861	71,163,606	16q22.2	C	T	cds-synon	p.Q388

Supplementary Table 12. List of identified PSVs between the three *MAP2K3* paralogs.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; REF, 80438, 88241: reference allele and corresponding alleles predicted in SCAF_1103279180438 and SCAF_1103279188241; CLASS: functional class of the polymorphism; CHANGE: amino acid change.

CHR	ID	BP	BAND	REF	80438	88241	CLASS	CHANGE
chr17	rs33911218	21,202,191	17p11.2	C	A	NA	missense	p.P11T
chr17	rs36047035	21,202,237	17p11.2	G	C	NA	missense	p.R26T
chr17	rs34105301	21,203,893	17p11.2	T	C	NA	missense	p.S39P
chr17	rs62057672	21,203,934	17p11.2	G	A	NA	cds-synon	p.V52
chr17	rs2305873	21,203,941	17p11.2	G	A	NA	missense	p.A55T
chr17	rs62057673	21,203,949	17p11.2	C	T	NA	cds-synon	p.S57
chr17	rs34458870	21,203,964	17p11.2	C	G	NA	cds-synon	p.A62
chr17	rs56067280	21,204,187	17p11.2	G	T	NA	missense	p.R65L
chr17	rs56216806	21,204,192	17p11.2	C	T	NA	missense	p.R67W
chr17	rs55796947	21,204,210	17p11.2	C	T	NA	nonsense	p.Q73X
chr17	rs56166328	21,204,257	17p11.2	G	A	NA	cds-synon	p.T88
chr17	rs2305872	21,204,290	17p11.2	G	C	NA	cds-synon	p.G99
chr17	rs62057721	21,205,460	17p11.2	C	T	NA	cds-synon	p.D106
chr17	rs74575904	21,207,813	17p11.2	T	T	G	missense	p.L186W
chr17	rs58609466	21,207,834	17p11.2	C	T	C	missense	p.T193M
chr17	rs76111309	21,207,835	17p11.2	G	G	A	cds-synon	p.T193
chr17	rs1657695	21,208,413	17p11.2	C	C	T	cds-synon	p.S220
chr17	rs55935757	21,215,483	17p11.2	C	NA	T	cds-synon	p.Y239
chr17	rs55736474	21,215,537	17p11.2	C	NA	A	cds-synon	p.S257
chr17	rs56369732	21,215,552	17p11.2	C	NA	T	cds-synon	p.A262
chr17	rs35206134	21,215,557	17p11.2	G	NA	A	missense	p.R264H
chr17	rs1657688	21,216,846	17p11.2	G	NA	C	cds-synon	p.L290
chr17	rs2363198	21,217,513	17p11.2	G	NA	A	missense	p.V310M
chr17	rs2363197	21,217,547	17p11.2	T	NA	C	utr3	NA
chr17	rs2363196	21,217,554	17p11.2	C	NA	T	utr3	NA
chr17	rs2363375	21,217,566	17p11.2	C	NA	T	utr3	NA
chr17	rs2363374	21,217,586	17p11.2	G	NA	T	utr3	NA
chr17	rs2363373	21,217,596	17p11.2	C	NA	G	utr3	NA
chr17	rs2363195	21,217,660	17p11.2	C	NA	T	utr3	NA
chr17	rs2363194	21,217,690	17p11.2	C	NA	T	utr3	NA
chr17	rs2363370	21,217,727	17p11.2	T	NA	C	utr3	NA
chr17	rs2363369	21,217,749	17p11.2	G	NA	C	utr3	NA
chr17	rs2363193	21,217,763	17p11.2	T	NA	C	utr3	NA
chr17	rs2363192	21,217,764	17p11.2	G	NA	A	utr3	NA
chr17	rs2363191	21,217,782	17p11.2	T	NA	A	utr3	NA
chr17	rs7502445	21,217,827	17p11.2	G	NA	A	utr3	NA
chr17	rs2363190	21,217,862	17p11.2	A	NA	G	utr3	NA
chr17	rs2363189	21,217,866	17p11.2	T	NA	C	utr3	NA
chr17	rs2363188	21,217,870	17p11.2	A	NA	C	utr3	NA
chr17	rs2363187	21,217,871	17p11.2	G	NA	A	utr3	NA
chr17	rs2363186	21,217,873	17p11.2	G	NA	A	utr3	NA

chr17	rs4021726	21,218,040	17p11.2	C	NA	T	utr3	NA
chr17	rs4021725	21,218,072	17p11.2	G	NA	A	utr3	NA
chr17	rs4021724	21,218,087	17p11.2	C	NA	T	utr3	NA
chr17	rs4021723	21,218,115	17p11.2	A	NA	G	utr3	NA
chr17	rs2363185	21,218,173	17p11.2	G	NA	T	utr3	NA
chr17	rs4416071	21,218,268	17p11.2	C	NA	T	utr3	NA
chr17	rs56254869	21,218,337	17p11.2	A	NA	T	utr3	NA
chr17	rs56125869	21,218,415	17p11.2	G	NA	C	utr3	NA
chr17	rs72838584	21,218,463	17p11.2	G	NA	A	utr3	NA
chr17	rs62055368	21,218,498	17p11.2	G	NA	T	utr3	NA

Supplementary Table 13. List of identified PSVs between *KCNJ12* and the two cryptic paralogs, *KCNJ17* and *KCNJ18*.

CHR, ID, BP, BAND: chromosome, SNP rsID, hg19 coordinate, and localization; REF, 80438, 87931: reference allele and corresponding alleles predicted in SCAF_1103279180438 and SCAF_1103279187931; CLASS: functional class of the polymorphism; CHANGE: amino acid change.

CHR	ID	BP	BAND	REF	80438	87931	CLASS	CHANGE
chr17	rs4021088	21,308,476	17p11.2	C	C	T	utr5	NA
chr17	rs4021087	21,308,521	17p11.2	C	C	T	utr5	NA
chr17	rs3866977	21,308,524	17p11.2	G	A	G	utr5	NA
chr17	rs3866978	21,308,541	17p11.2	G	C	G	utr5	NA
chr17	rs3866979	21,308,542	17p11.2	G	A	G	utr5	NA
chr17	rs4021055	21,308,623	17p11.2	T	C	C	utr5	NA
chr17	rs9889444	21,311,859	17p11.2	T	C	C	utr5	NA
chr17	rs9911150	21,311,885	17p11.2	A	T	A	utr5	NA
chr17	rs9908707	21,311,911	17p11.2	G	A	G	utr5	NA
chr17	rs1657716	21,311,916	17p11.2	C	C	T	utr5	NA
chr17	rs1714904	21,311,932	17p11.2	A	G	G	utr5	NA
chr17	rs1714903	21,311,940	17p11.2	T	T	C	utr5	NA
chr17	rs79809401	21,318,603	17p11.2	C	T	C	utr5	NA
chr17	rs58862472	21,318,629	17p11.2	C	A	T	utr5	NA
chr17	rs72846666	21,318,663	17p11.2	G	A	G	cds-synon	p.A3
chr17	rs1657738	21,318,698	17p11.2	C	C	T	missense	p.S15L
chr17	rs78117732	21,318,782	17p11.2	G	A	G	missense	p.R43H
chr17	rs1714865	21,318,821	17p11.2	A	A	C	missense	p.E56A
chr17	rs73979893	21,318,867	17p11.2	G	A	G	missense	p.M71I
chr17	rs1657739	21,318,897	17p11.2	G	G	C	cds-synon	p.R81
chr17	rs79626424	21,318,918	17p11.2	G	A	G	cds-synon	p.S88
chr17	rs112314728	21,318,948	17p11.2	C	T	C	cds-synon	p.F98
chr17	rs75757803	21,318,951	17p11.2	C	T	C	cds-synon	p.G99
chr17	rs8076599	21,318,952	17p11.2	A	G	G	missense	p.I100V
chr17	rs79666990	21,318,969	17p11.2	C	T	C	cds-synon	p.I105
chr17	rs9909970	21,318,981	17p11.2	C	T	C	cds-synon	p.H109
chr17	rs1657740	21,319,007	17p11.2	G	G	A	missense	p.R118Q
chr17	rs1657741	21,319,008	17p11.2	G	C	C	cds-synon	p.R118
chr17	rs76265595	21,319,069	17p11.2	G	A	G	missense	p.E139K
chr17	rs76518282	21,319,079	17p11.2	C	A	C	missense	p.T142N
chr17	rs75029097	21,319,087	17p11.2	G	A	G	missense	p.G145S
chr17	rs77283567	21,319,110	17p11.2	G	A	G	cds-synon	p.T152
chr17	rs1714864	21,319,121	17p11.2	C	C	T	missense	p.P156L
chr17	rs73313922	21,319,171	17p11.2	G	A	G	missense	p.D173N
chr17	rs73979896	21,319,208	17p11.2	C	T	C	missense	p.A185V
chr17	rs1657742	21,319,230	17p11.2	G	G	C	missense	p.Q192H
chr17	rs73313923	21,319,251	17p11.2	C	T	C	cds-synon	p.N199
chr17	rs73313926	21,319,272	17p11.2	C	T	C	cds-synon	p.D206
chr17	rs72846667	21,319,285	17p11.2	C	T	C	missense	p.L211F
chr17	rs1657743	21,319,302	17p11.2	T	C	C	cds-synon	p.G216

chr17	rs72846668	21,319,311	17p11.2	C	T	C	cds-synon	p.R219
chr17	rs77048459	21,319,369	17p11.2	G	A	G	missense	p.E239K
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chr17	rs16962951	21,319,407	17p11.2	C	T	C	cds-synon	p.I251
chr17	rs77270326	21,319,436	17p11.2	G	A	G	missense	p.R261H
chr17	rs76684759	21,319,439	17p11.2	T	G	T	missense	p.I262S
chr17	rs73313929	21,319,452	17p11.2	G	A	G	cds-synon	p.S266
chr17	rs1657744	21,319,473	17p11.2	G	G	A	cds-synon	p.E273
chr17	rs77176173	21,319,488	17p11.2	C	T	C	cds-synon	p.S278
chr17	rs78113532	21,319,519	17p11.2	G	C	G	missense	p.E289Q
chr17	rs77987694	21,319,523	17p11.2	C	T	C	missense	p.T290M
chr17	rs80022364	21,319,527	17p11.2	C	T	C	cds-synon	p.D291
chr17	rs80335301	21,319,543	17p11.2	G	A	G	missense	p.V297I
chr17	rs74801394	21,319,560	17p11.2	G	T	G	missense	p.M302I
chr17	rs80203231	21,319,682	17p11.2	C	T	C	missense	p.S343L
chr17	rs78135255	21,319,716	17p11.2	G	A	G	cds-synon	p.T354
chr17	rs76681424	21,319,728	17p11.2	T	C	T	cds-synon	p.S358
chr17	rs76267885	21,319,743	17p11.2	A	G	A	cds-synon	p.V363
chr17	rs1612176	21,319,767	17p11.2	C	G	T	cds-synon	p.S371
chr17	rs1657745	21,319,785	17p11.2	C	C	T	cds-synon	p.Y377
chr17	rs78547883	21,319,786	17p11.2	G	A	G	missense	p.E378K
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chr17	rs2917720	21,319,860	17p11.2	C	A	T	cds-synon	p.D402
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chr17	rs66981137	21,319,908	17p11.2	C	T	C	cds-synon	p.G418
chr17	rs5021699	21,319,943	17p11.2	A	A	G	missense	p.E430G
chr17	rs76506689	21,319,955	17p11.2	G	A	G	cds-synon	p.X434
chr17	rs5021700	21,319,989	17p11.2	C	A	T	utr3	NA
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chr17	rs78435971	21,320,008	17p11.2	C	T	C	utr3	NA
chr17	rs77515828	21,320,012	17p11.2	C	T	C	utr3	NA
chr17	rs5021702	21,320,025	17p11.2	C	C	T	utr3	NA
chr17	rs34808513	21,320,041	17p11.2	G	A	G	utr3	NA
chr17	rs5021703	21,320,102	17p11.2	C	C	A	utr3	NA
chr17	rs5021704	21,320,114	17p11.2	T	T	G	utr3	NA
chr17	rs79945769	21,320,197	17p11.2	G	C	G	utr3	NA
chr17	rs62049520	21,320,210	17p11.2	C	T	C	utr3	NA
chr17	rs5021705	21,320,212	17p11.2	A	G	G	utr3	NA
chr17	rs62049521	21,320,252	17p11.2	G	T	G	utr3	NA
chr17	rs5021706	21,320,263	17p11.2	T	T	C	utr3	NA
chr17	rs73313932	21,320,279	17p11.2	C	T	C	utr3	NA
chr17	rs73981226	21,320,350	17p11.2	G	A	G	utr3	NA
chr17	rs62049522	21,320,365	17p11.2	T	T	C	utr3	NA
chr17	rs111237557	21,320,436	17p11.2	T	C	T	utr3	NA
chr17	rs67199304	21,320,440	17p11.2	C	T	T	utr3	NA
chr17	rs74591721	21,320,451	17p11.2	A	T	A	utr3	NA
chr17	rs74336563	21,320,480	17p11.2	A	G	A	utr3	NA
chr17	rs73313941	21,320,499	17p11.2	A	G	G	utr3	NA

chr17	rs67680166	21,320,529	17p11.2	T	C	C	utr3	NA
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chr17	rs72846673	21,320,555	17p11.2	C	T	T	utr3	NA
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chr17	rs72846675	21,320,595	17p11.2	C	T	T	utr3	NA
chr17	rs72842109	21,320,596	17p11.2	A	G	G	utr3	NA
chr17	rs75211783	21,320,605	17p11.2	A	G	A	utr3	NA
chr17	rs73981232	21,320,658	17p11.2	C	C	T	utr3	NA
chr17	rs75614171	21,320,659	17p11.2	G	T	G	utr3	NA
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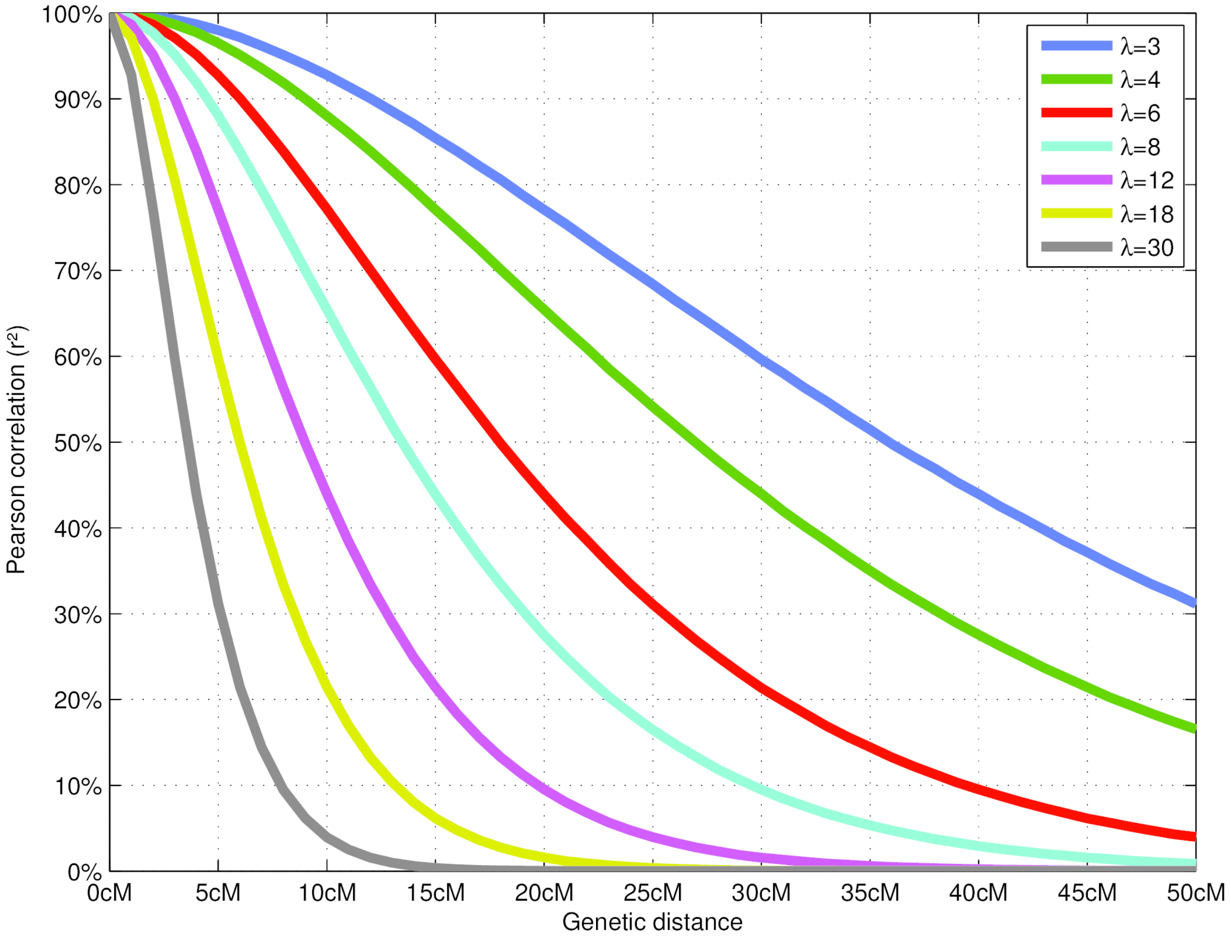
chr17	rs78556043	21,320,681	17p11.2	G	T	T	utr3	NA
chr17	rs76283231	21,320,690	17p11.2	G	C	C	utr3	NA
chr17	rs72842113	21,320,699	17p11.2	G	T	T	utr3	NA
chr17	rs74883261	21,320,711	17p11.2	C	C	G	utr3	NA
chr17	rs76105604	21,320,787	17p11.2	G	A	G	utr3	NA
chr17	rs73981233	21,320,796	17p11.2	C	T	T	utr3	NA
chr17	rs73981234	21,320,798	17p11.2	G	C	C	utr3	NA
chr17	rs76498462	21,320,826	17p11.2	C	C	T	utr3	NA
chr17	rs76059352	21,320,855	17p11.2	A	C	A	utr3	NA
chr17	rs76852423	21,320,867	17p11.2	G	A	G	utr3	NA
chr17	rs72842114	21,320,882	17p11.2	T	C	C	utr3	NA
chr17	rs35334103	21,320,884	17p11.2	T	C	T	utr3	NA
chr17	rs80028685	21,320,890	17p11.2	G	G	A	utr3	NA
chr17	rs35676232	21,320,896	17p11.2	G	G	C	utr3	NA
chr17	rs73313944	21,320,916	17p11.2	G	A	A	utr3	NA
chr17	rs73313947	21,320,980	17p11.2	C	G	G	utr3	NA
chr17	rs77190255	21,320,991	17p11.2	C	T	C	utr3	NA
chr17	rs72842115	21,320,993	17p11.2	G	T	T	utr3	NA
chr17	rs77513008	21,321,005	17p11.2	C	A	C	utr3	NA
chr17	rs72842117	21,321,016	17p11.2	T	C	C	utr3	NA
chr17	rs75958771	21,321,028	17p11.2	C	C	T	utr3	NA
chr17	rs72842119	21,321,029	17p11.2	C	G	G	utr3	NA
chr17	rs72842121	21,321,050	17p11.2	C	T	T	utr3	NA
chr17	rs72842122	21,321,052	17p11.2	T	G	G	utr3	NA
chr17	rs78581302	21,321,064	17p11.2	A	A	G	utr3	NA
chr17	rs73313949	21,321,104	17p11.2	G	T	T	utr3	NA
chr17	rs73313952	21,321,145	17p11.2	G	A	G	utr3	NA
chr17	rs73313955	21,321,173	17p11.2	A	G	A	utr3	NA
chr17	rs73313957	21,321,207	17p11.2	G	G	A	utr3	NA
chr17	rs62049523	21,321,250	17p11.2	G	A	A	utr3	NA
chr17	rs77231477	21,321,252	17p11.2	C	C	T	utr3	NA
chr17	rs77331608	21,321,278	17p11.2	T	C	C	utr3	NA
chr17	rs73313962	21,322,847	17p11.2	G	G	T	utr3	NA
chr17	rs79110818	21,322,880	17p11.2	A	C	C	utr3	NA
chr17	rs78171447	21,322,883	17p11.2	G	A	A	utr3	NA
chr17	rs73313965	21,322,933	17p11.2	C	T	T	utr3	NA

chr17	rs72842124	21,322,972	17p11.2	G	C	C	utr3	NA
chr17	rs72842125	21,322,973	17p11.2	T	C	C	utr3	NA
chr17	rs66506990	21,323,001	17p11.2	C	T	T	utr3	NA
chr17	rs76263531	21,323,015	17p11.2	C	C	T	utr3	NA
chr17	rs72842126	21,323,033	17p11.2	C	T	T	utr3	NA
chr17	rs72842128	21,323,034	17p11.2	G	A	A	utr3	NA
chr17	rs79085110	21,323,056	17p11.2	G	G	T	utr3	NA
chr17	rs73981249	21,323,074	17p11.2	T	T	C	utr3	NA
chr17	rs73981250	21,323,096	17p11.2	G	A	A	utr3	NA
chr17	rs2164678	21,323,116	17p11.2	A	A	G	utr3	NA
chr17	rs79684471	21,323,119	17p11.2	T	T	C	utr3	NA
chr17	rs78724389	21,323,136	17p11.2	G	G	A	utr3	NA
chr17	rs78952493	21,323,154	17p11.2	C	C	T	utr3	NA
chr17	rs75484234	21,323,163	17p11.2	A	A	G	utr3	NA

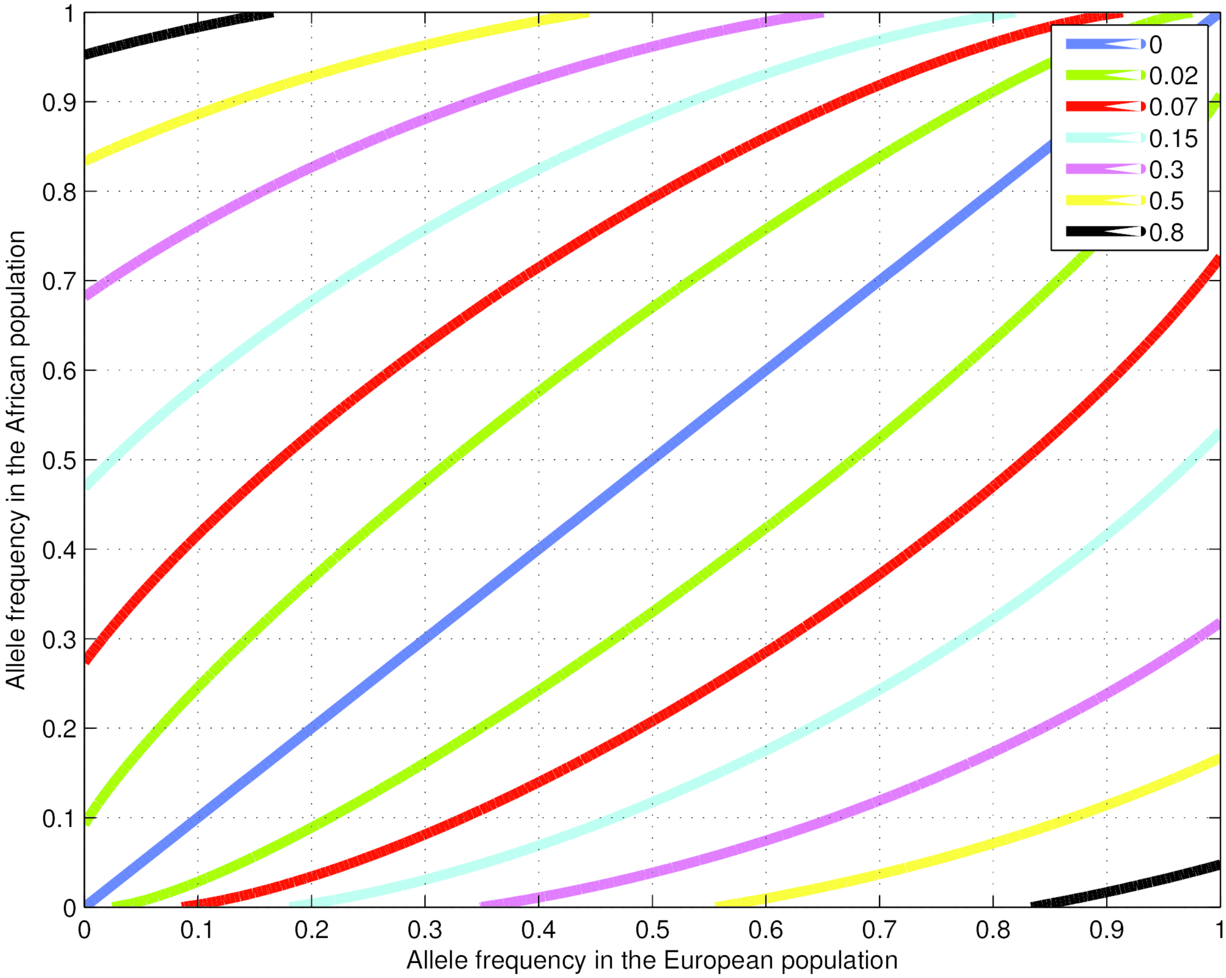
Supplementary Figures

Supplementary Figure 1. Estimates for Pearson correlation between local ancestries at physically close loci.

It is assumed that in African Americans 20% of loci descend from European chromosomes, the remaining 80% descend from West African chromosomes, and the number λ of generations since admixture is modeled increasing from 3 to 30 with 6, in red, the estimated number in African Americans.

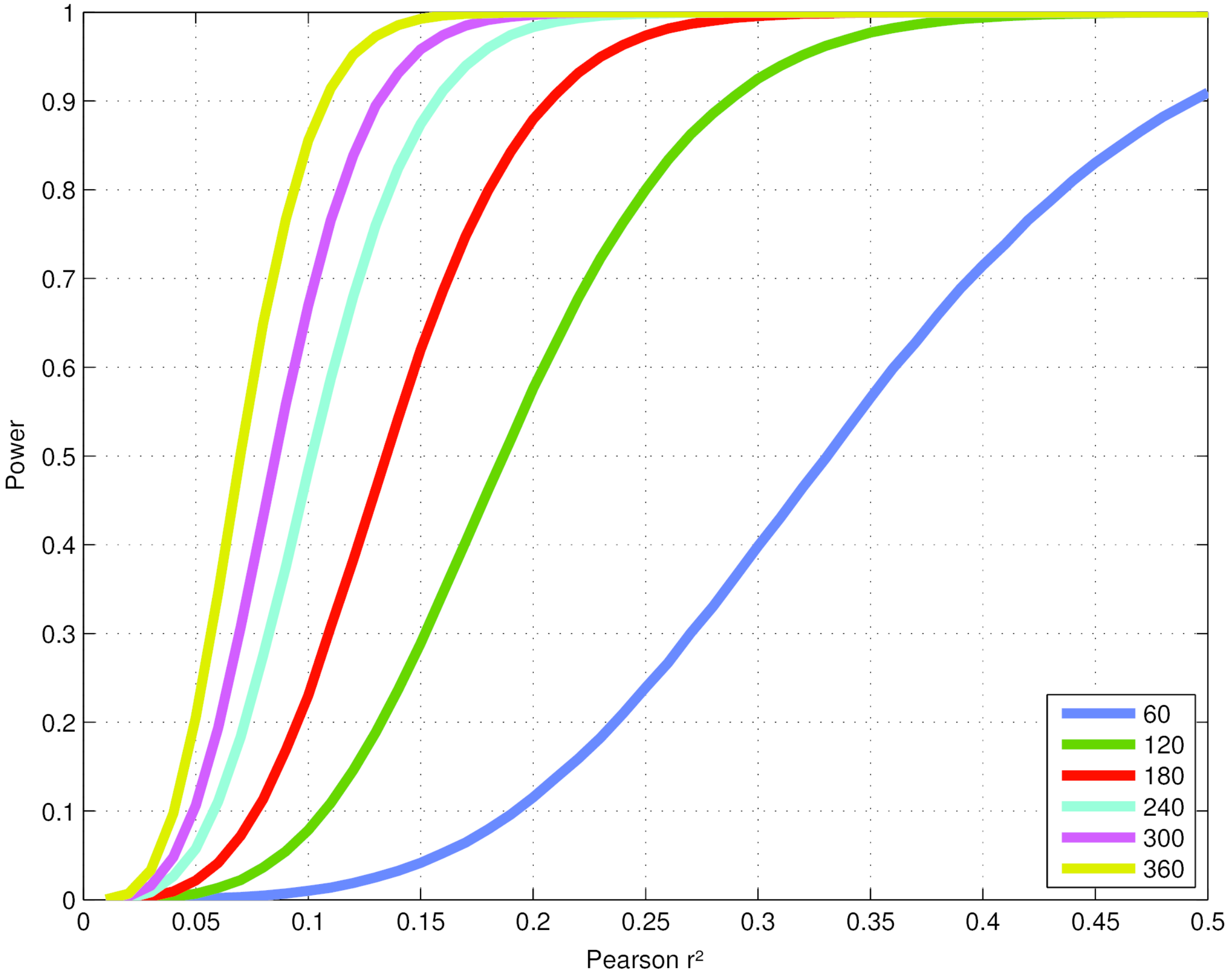


Supplementary Figure 2. Estimates for Pearson correlation between local ancestry and SNP genotype. Level curves for squared Pearson correlation (r^2) between amount of European local ancestry at the locus of a bi-allelic polymorphism and genotype at the same locus as a function of the allele frequencies of that polymorphism in the European and West African population.



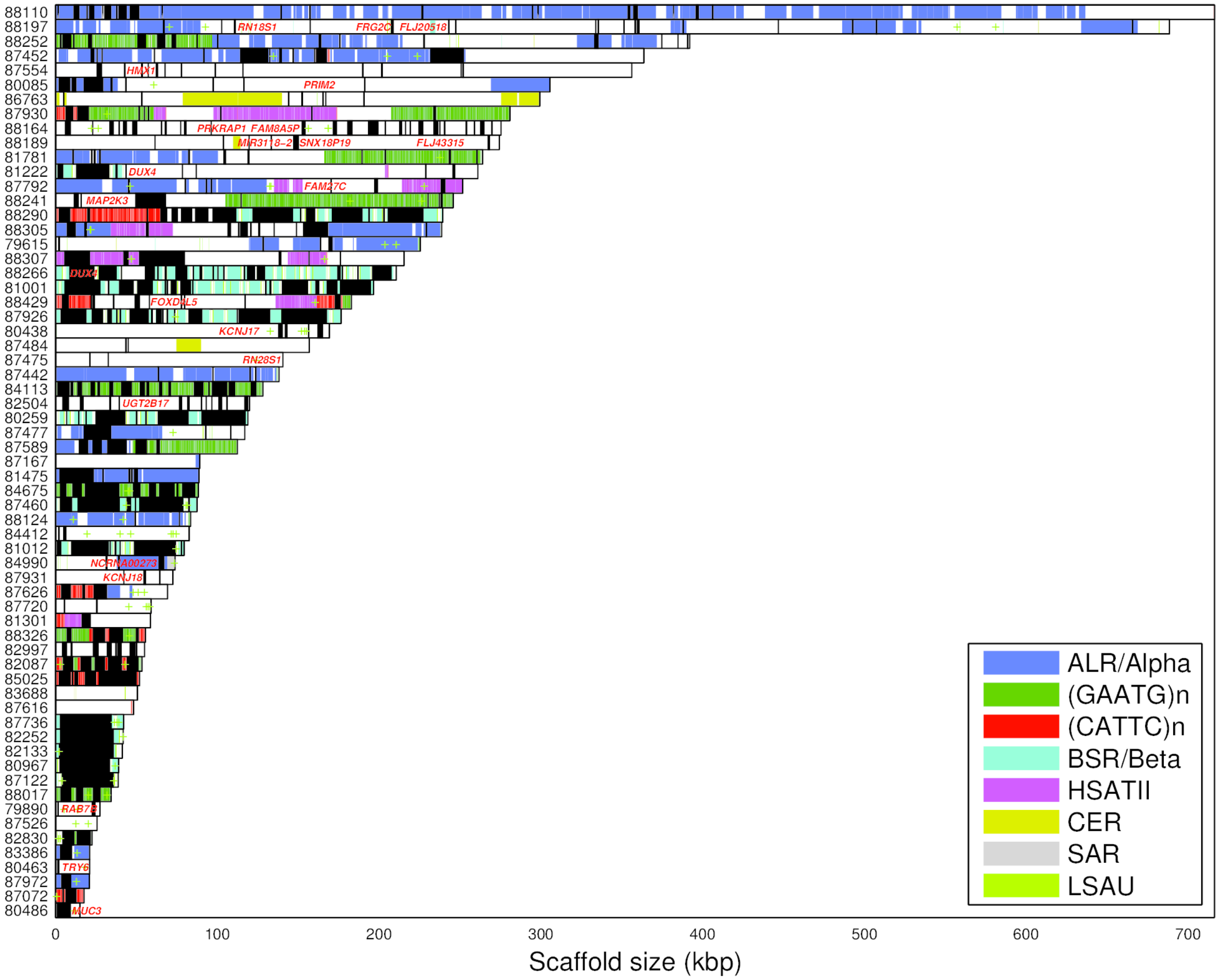
Supplementary Figure 3. Power calculations for admixture mapping.

Probability of obtaining a p-value $p<10^{-6}$ for a one-tailed Pearson correlation test between genotype and local ancestry at the same locus as a function of the correlation between genotype and local ancestry for an increasing sample size from 60 to 360. With a sample size of 360 and perfect genotype, almost all SNPs with $r^2>15\%$ are expected to be mapped.



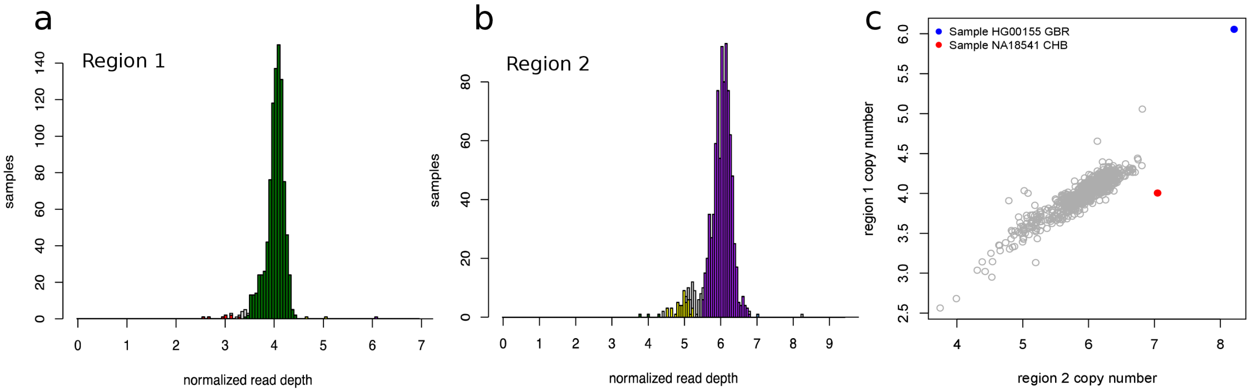
Supplementary Figure 4. Satellite repeats distribution over HuRef unplaced scaffolds.

Distribution of satellite sequences for the eight most common classes identified by RepeatMasker over HuRef unplaced scaffolds larger than 100kbp or larger than 15kbp and mapped. Black regions indicate gaps in the scaffolds. Genes identified in the scaffolds are displayed in red. Green “+” symbols indicate the location of mapped ancestry -informative SNPs. HuRef unplaced scaffolds are denoted with five digits and stand for SCAF_11032791#####.



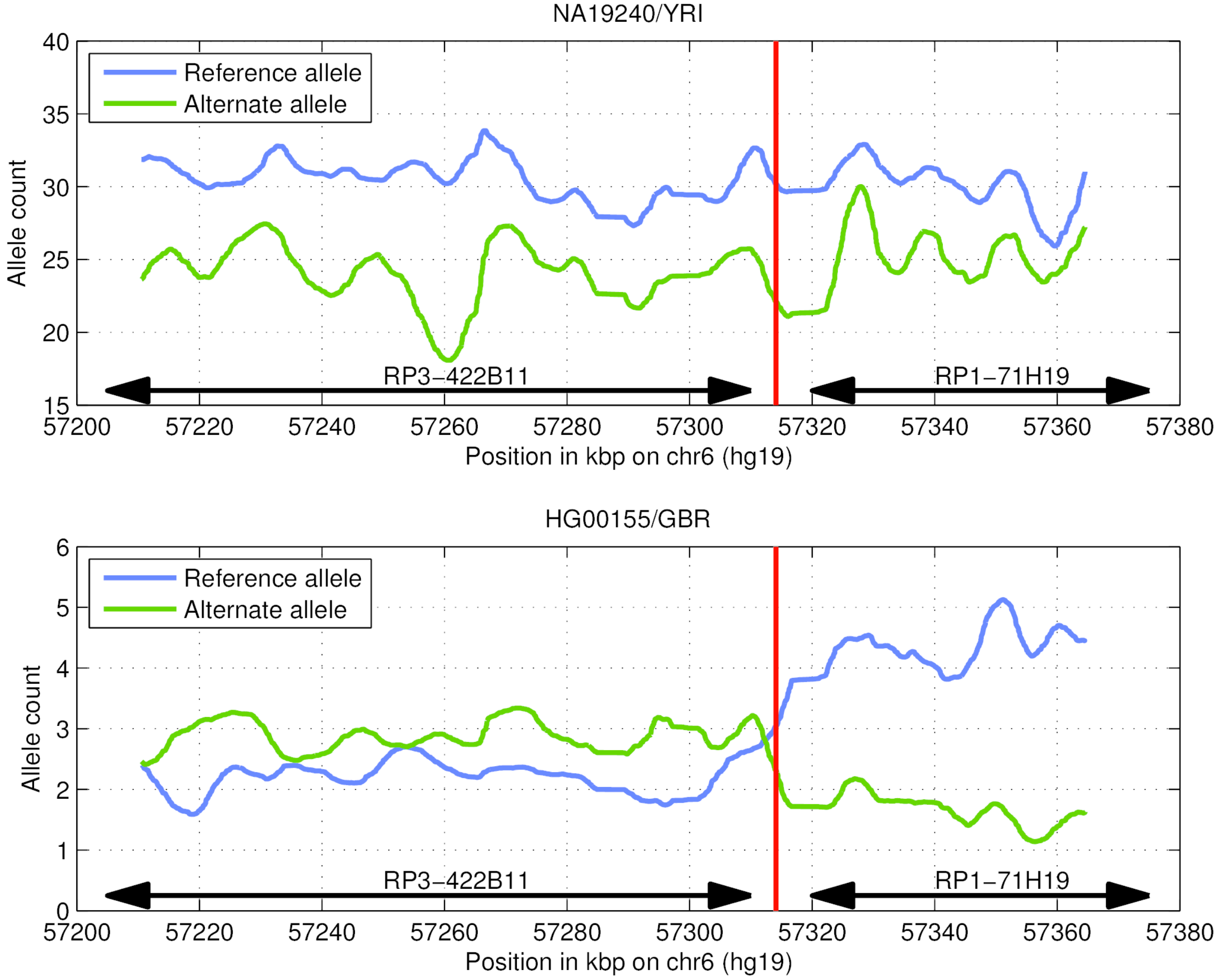
Supplementary Figure 5. Sequencing coverage depth at the *PRIM2* locus.

Genotyping region 1 (chr6:57,204,729-57,369,236) and region 2 (chr6:57,369,236-57,570,618) separately (a,b) and comparing the diploid copy number from each region (c) suggests the presence of copy number variants affecting region 2 only, corresponding to the *PRIM2* copy in 3p11.1, for sample NA18541/CHB and region 1 and region 2 together, corresponding to the *PRIM2* copy in 6q11.1, for sample HG00155/GBR. The observed smear in scatterplot (c) is possibly due to differential alignment drops from the cryptic paralogs across samples from the 1000 Genomes Project rather than a more complex CNV structure at the locus, although a few outliers point to additional structural variants at the locus.



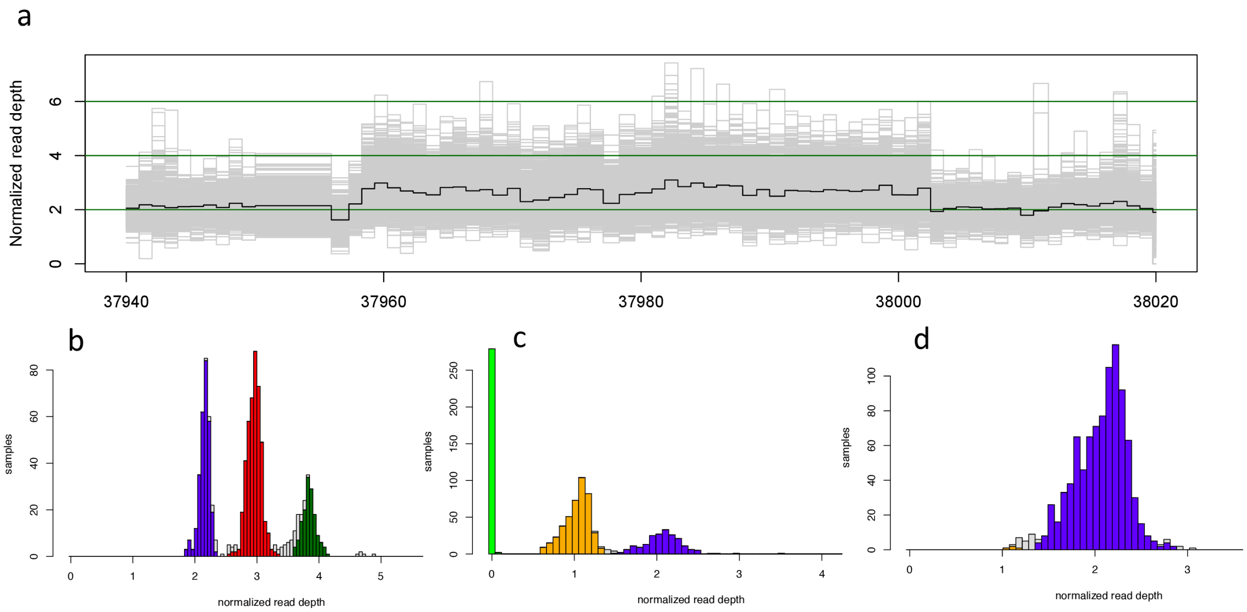
Supplementary Figure 6. Sequencing coverage depth for HG00155/GBR at the *PRIM2* locus.

All 2,671 heterozygous loci detected as heterozygous in the chr6:57,204,730-57,369,237 region in sample NA19240/YRI, sequenced at high coverage, were analyzed for number of reference alleles and alternate alleles in the aligned reads from samples NA19240/YRI and HG00155/GBR, this latter sample known to carry an extra copy of this region. As this region contains an old cryptic segmental duplication, almost all of these putative heterozygous loci are PSVs and counting reference and alternate alleles effectively gives a counting of reads from the two different paralogs. The counts are then smoothed over a window of 100 PSVs. A red line indicates the location where the two clones RP3-422B11/AL121975.10 and RP1-71H19/AL121958.6 have been joined. The increase in reference allele count on the right for HG00155/GBR confirms that this sample is copy number variant for sequence homologous to clone RP1-71H19/AL121958.6 but only paralogous to clone RP3-422B11/AL121975.10, and thus confirm that the sequences from the two clones should not have been joined together.



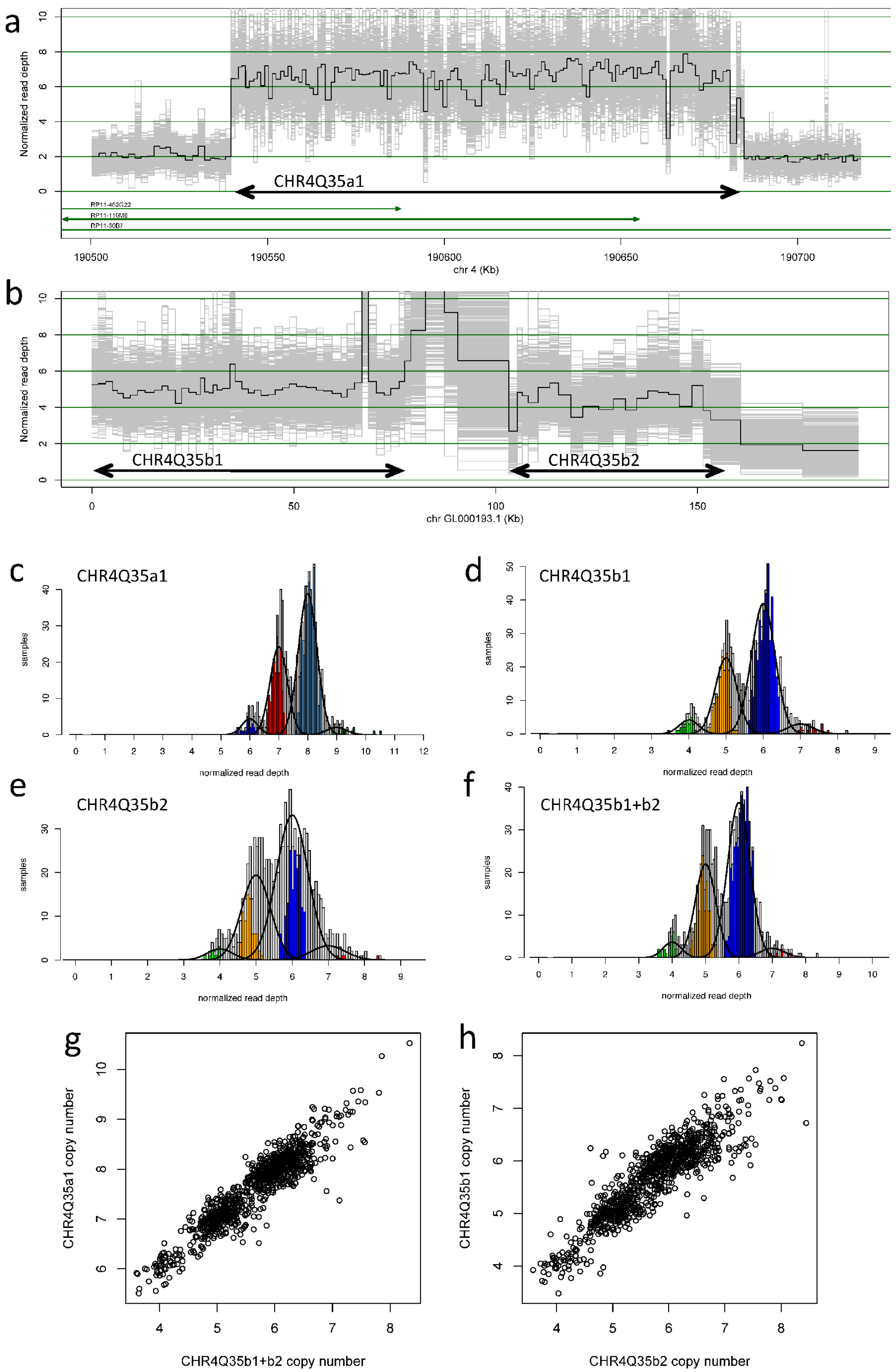
Supplementary Figure 7. Sequencing coverage depth at the 2p22.2 locus.

Analysis of sequencing read depth from the 1000 Genomes Project indicates a region with elevated copy number on chromosome 2 when reads from 946 samples (gray lines, median black line) are aligned to the hg19 reference genome (a). Genotyping this region indicates total copy number of 2 to 5 in this population (b). Realigning the 1000 Genomes Project reads to a new reference that includes extra human sequence suggests that the majority of this variation is a polymorphic copy of SCAF_1103279187616 located near the pericentromeric region of chromosome 22 (c) and not a duplication of the reference sequence from chromosome 2 (d).



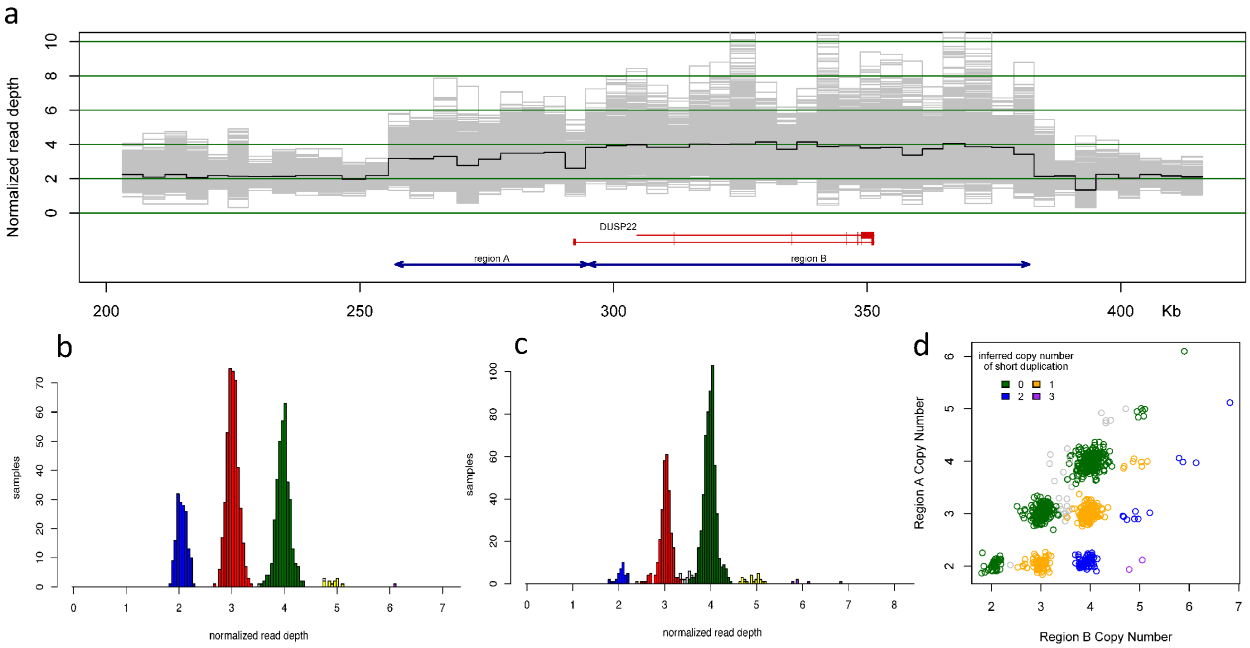
Supplementary Figure 8. Sequencing coverage depth at the 4q35.2 locus.

Sequence read depth analysis of the 1000 Genomes Project data indicates segments with elevated copy number at 4q35.2 and on unplaced contig GL000193 (a, b). Genotyping these segments in the 1000 Genomes Project samples indicates variable (c-f) but strongly correlated (g-h) copy number across all three segments. FISH data from previous studies (Supplementary Fig. S24a of [7]) suggest that there are additional copies of the 4q35.2 segment on chromosomes 13, 14 and 22, with the copy on 14 being variably present in different individuals. One parsimonious model includes copies of segments a1, b1 and b2 co-located as a polymorphic unit on chromosome 14 with additional fixed copies of this unit on chromosome 13 and chromosome 22.


a
Normalized read depth
CHR4Q35a1
RP11-462G22
RP11-119M6
RP11-30B7
190500
190550
190600
190650
190700
chr 4 (Kb)
b
Normalized read depth
CHR4Q35b1
CHR4Q35b2
0
50
100
150
chr GL000193.1 (Kb)
c
CHR4Q35a1
samples
normalized read depth
d
CHR4Q35b1
samples
normalized read depth
e
CHR4Q35b2
samples
normalized read depth
f
CHR4Q35b1+b2
samples
normalized read depth
g
CHR4Q35a1 copy number
CHR4Q35b1+b2 copy number
h
CHR4Q35b1 copy number
CHR4Q35b2 copy number

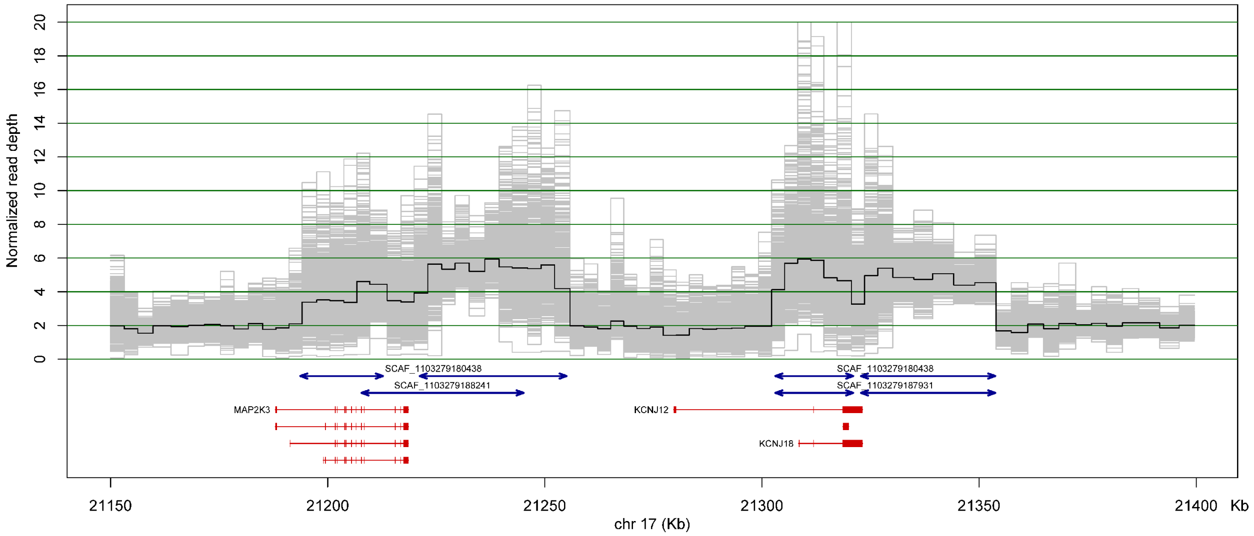
Supplementary Figure 9. Sequencing coverage depth at the *DUSP22* locus.

Analysis of sequencing read depth from the 1000 Genomes Project indicates a region with elevated copy number at 6p25.3 when reads from 946 samples (gray lines, median black line) are aligned to the hg19 reference genome (a) and indicates evidence of two distinct CNV alleles overlapping two isoforms of *DUSP22*. Genotyping region A and region B separately (b,c) and comparing the diploid copy number from each region (d) suggests two main duplication alleles, the short duplication allele containing region B only and the long allele containing regions A+B. The data also suggest the possible presence of an additional duplication allele at low frequency that is similar to the long duplication allele but more diverged from the reference genome sequence.

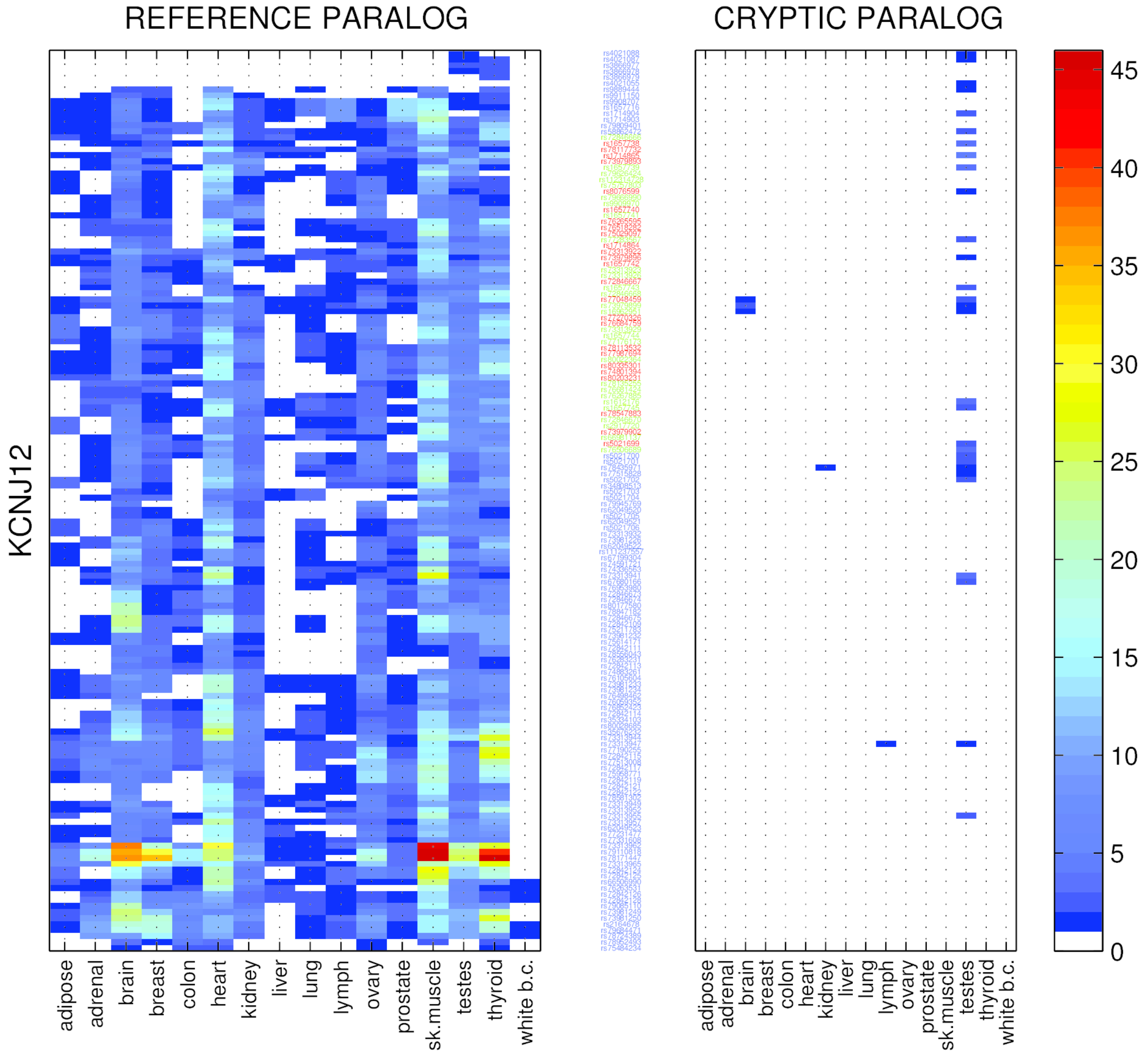


Supplementary Figure 10. Sequencing coverage depth at the 17p11.2 locus.

Analysis of sequencing read depth of the 1000 Genomes Project data shows increased read depth coincident with the location of the alignments of HuRef scaffolds SCAF_1103279180438, SCAF_1103279188241, and SCAF_1103279187931. By measuring the read depth elevation in the region, we predict no further sequence from the human genome is paralogous to this region.

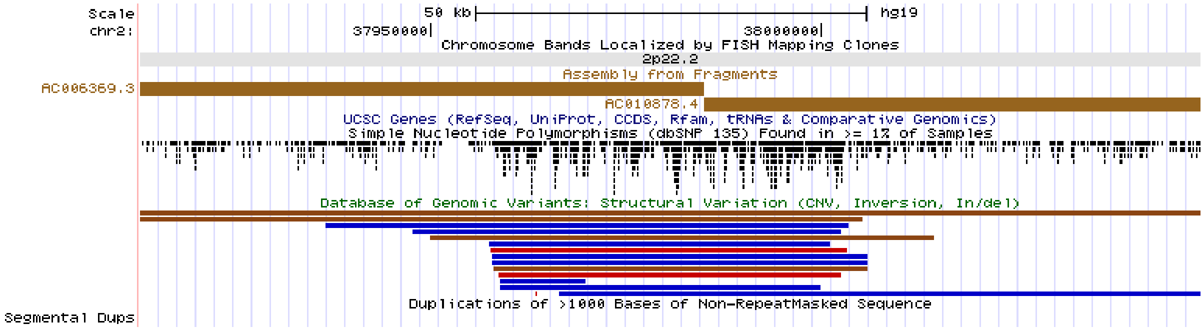


Supplementary Figure 11. Expression levels of gene *KCNJ12* and its cryptic paralogs. Paralogous sequence variants are used to distinguish expression between paralogs. Variants in the utr regions are encoded in blue and variants predicted to change the protein product of the paralog are encoded in red while synonymous variants are encoded in green.

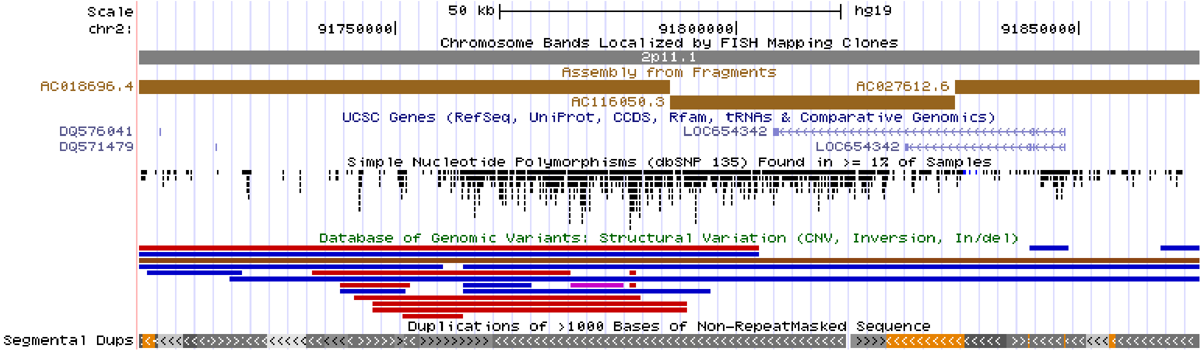


Nature Genetics: doi:10.1038/ng.2565

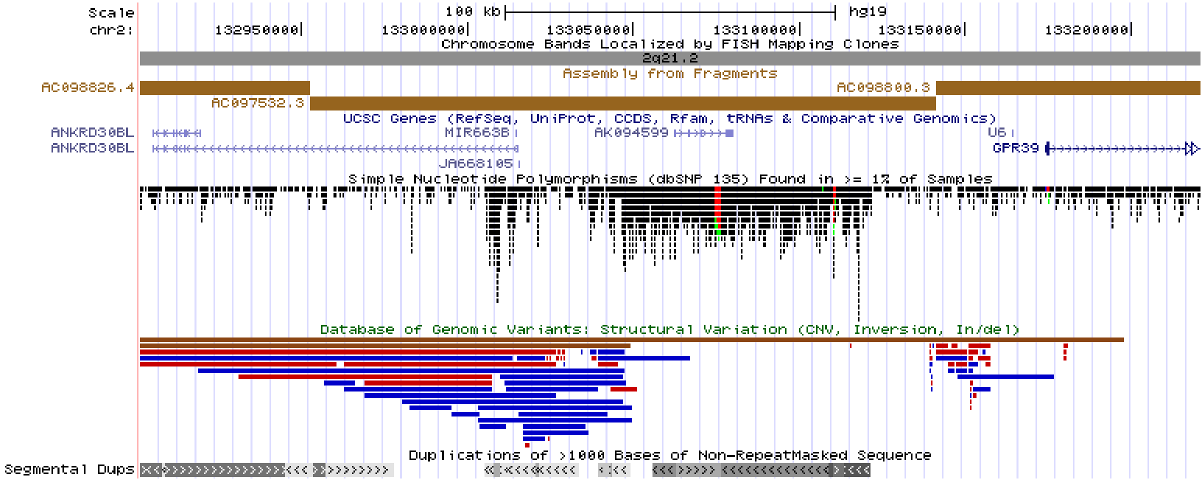
Supplementary Figure 12. Region of increased heterozygosity at 2p22.2.



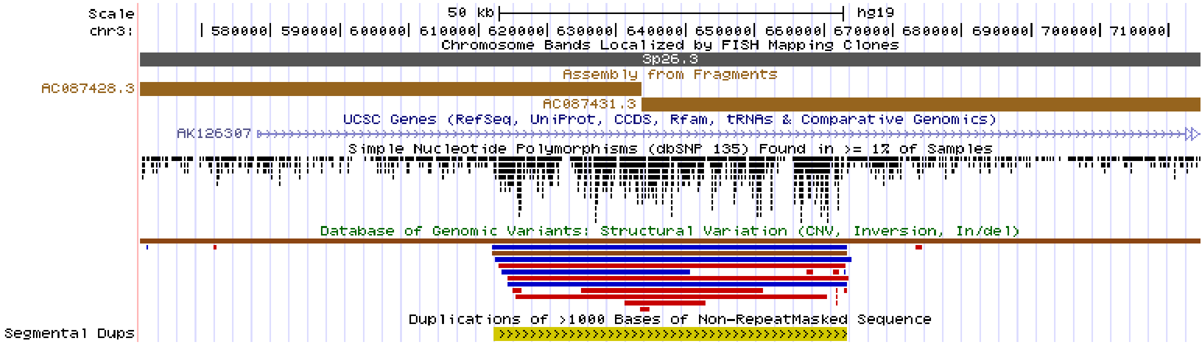
Supplementary Figure 13. Region of increased heterozygosity at 2p11.1 containing a paralog of gene *OTOP1*.



Supplementary Figure 14. Region of increased heterozygosity at 2q21.2.



Supplementary Figure 15. Region of increased heterozygosity at 3p26.3.



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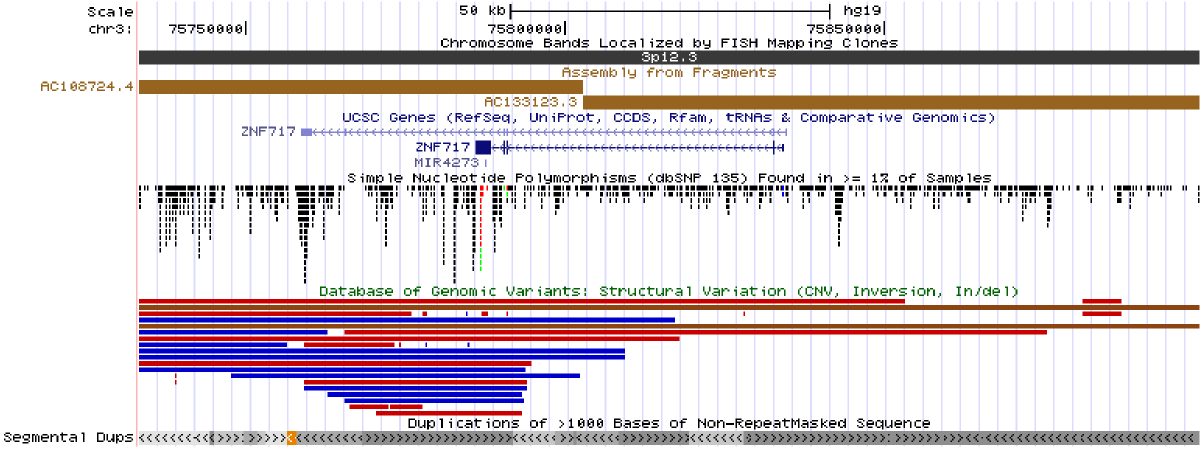
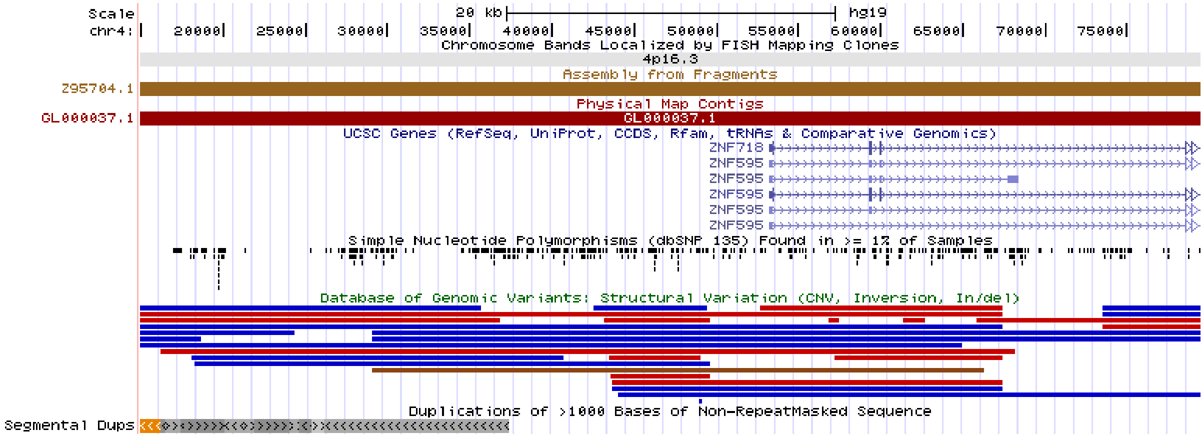
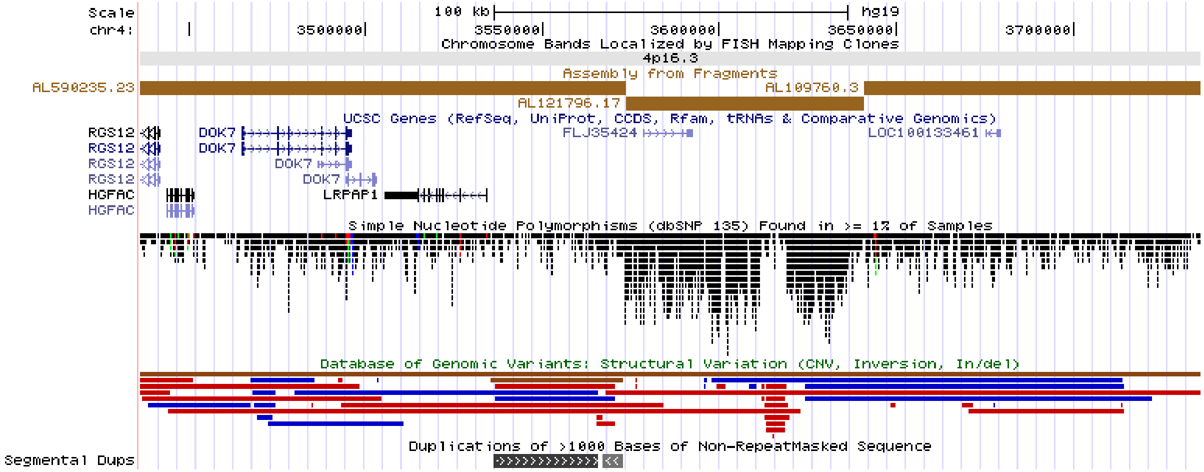
Supplementary Figure 16. Region at 3p12.3 containing gene *ZNF717*.



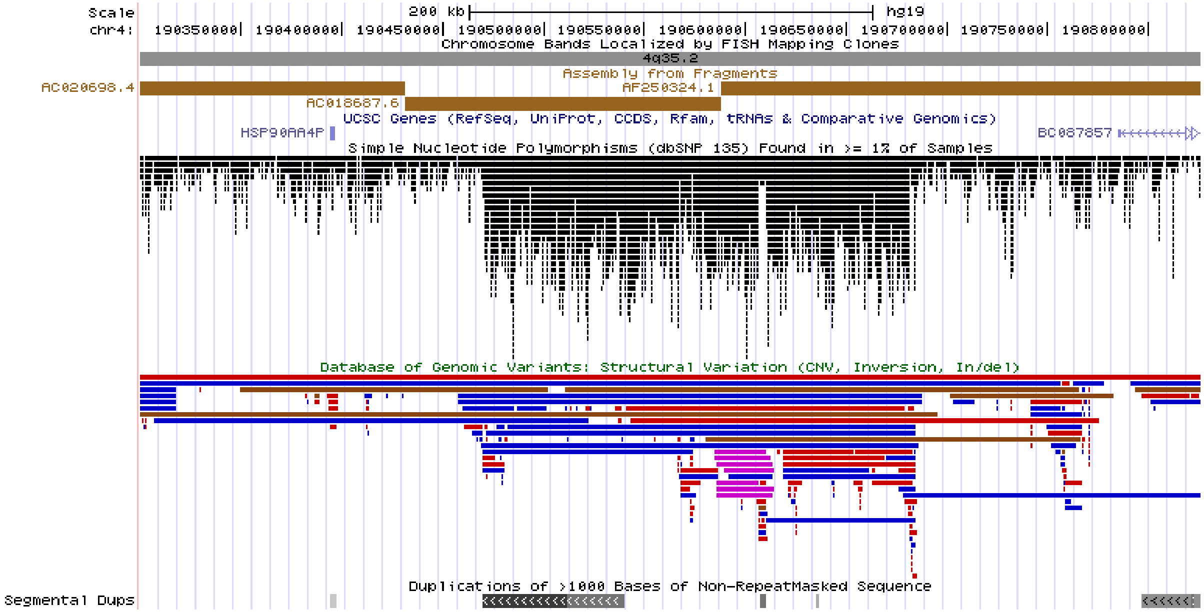
Supplementary Figure 17. Telomeric region at 4p16.3 containing gene *ZNF595*.



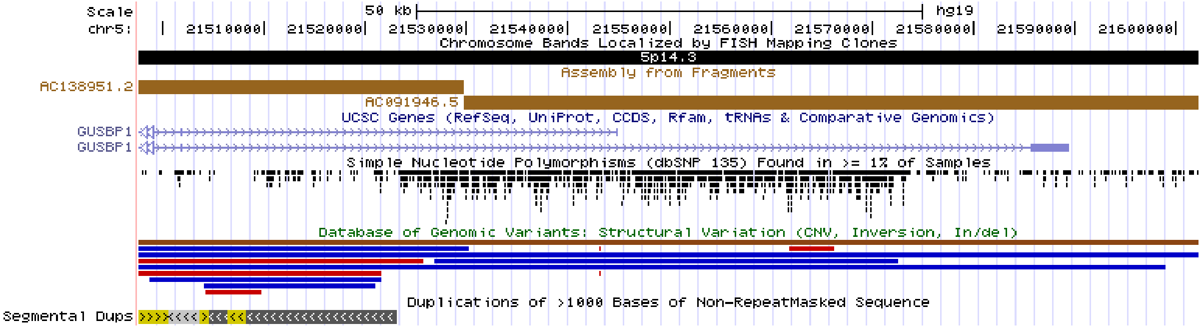
Supplementary Figure 18. Region of increased heterozygosity at 4p16.3 containing gene *FLJ35424*.



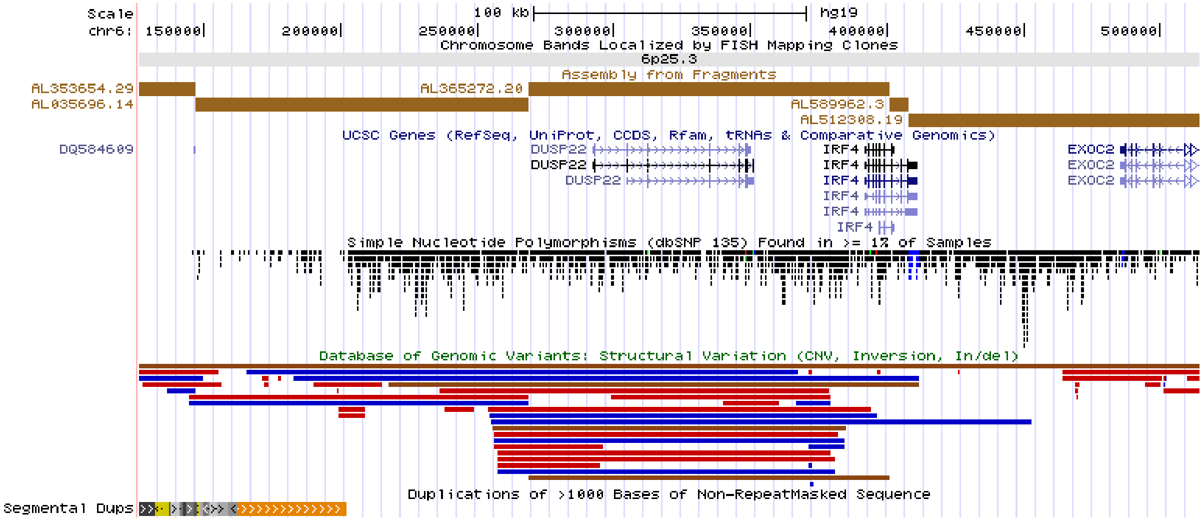
Supplementary Figure 19. Telomeric region of increased heterozygosity at 4q35.2.



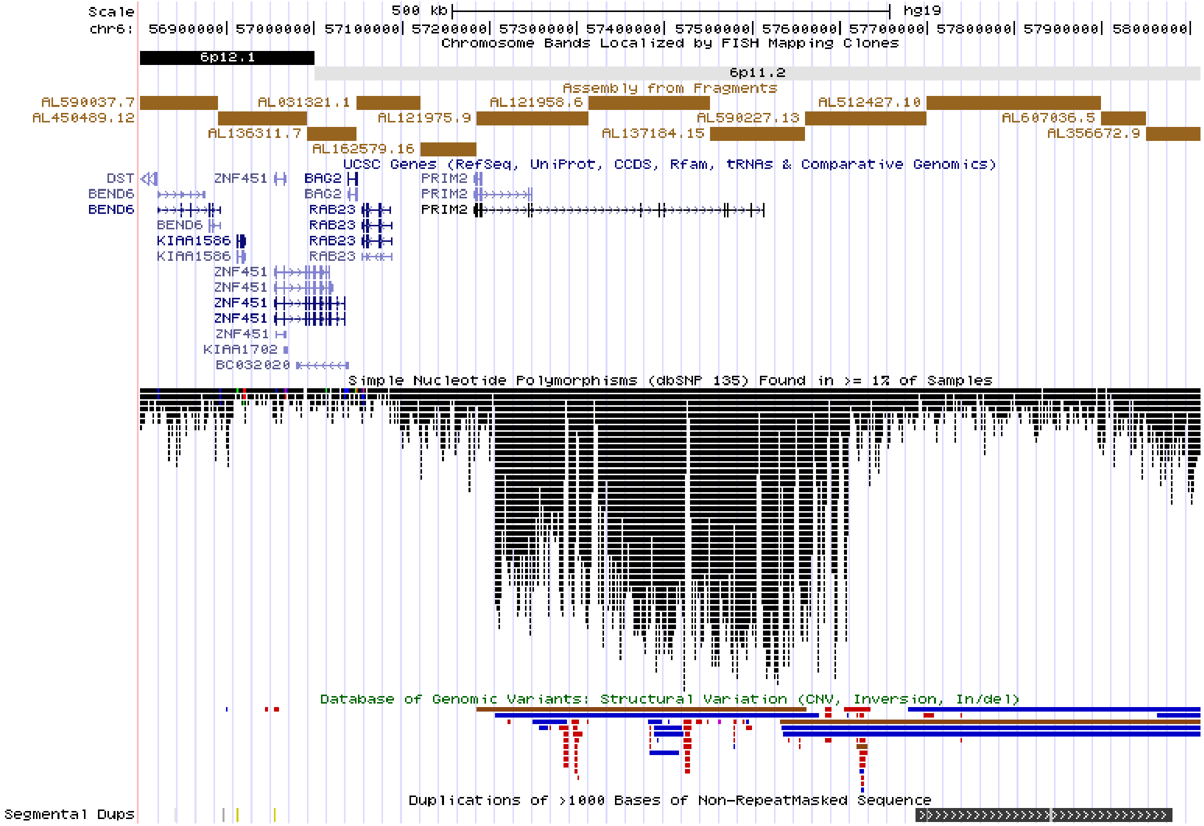
Supplementary Figure 20. Region of increased heterozygosity at 5p14.3.



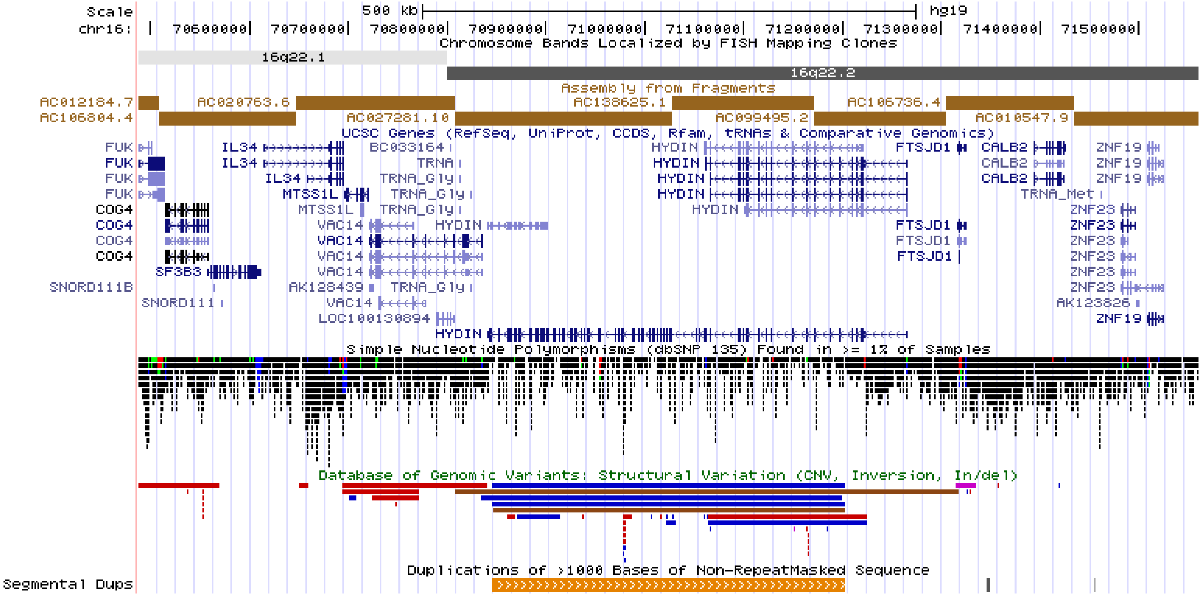
Supplementary Figure 21. Telomeric region at 6p25.3 containing gene *DUSP22*.



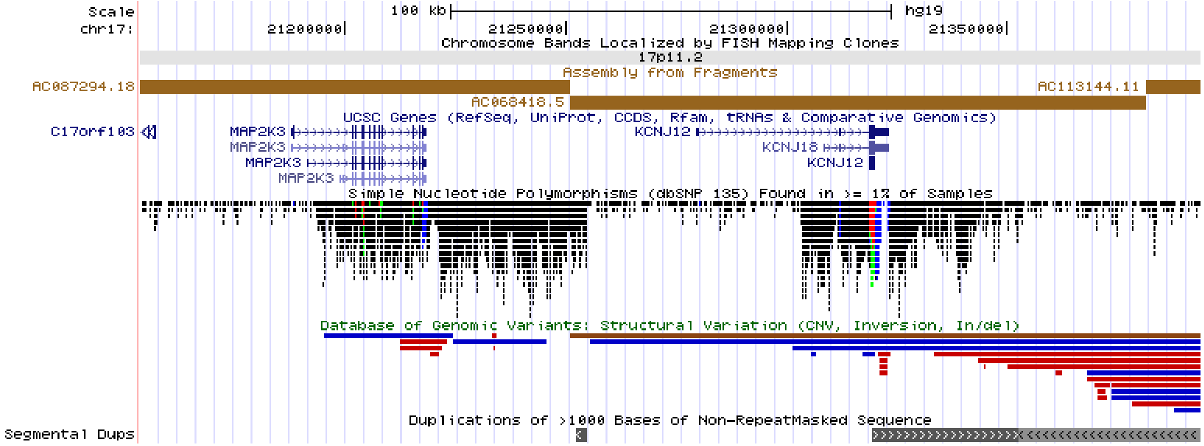
Supplementary Figure 22. Region of increased heterozygosity at 6p11.2 containing gene *PRIM2*.



Supplementary Figure 23. Region at 16q22.2 containing gene *HYDIN*.



Supplementary Figure 24. Region of increased heterozygosity at 17p11.2 containing genes *MAP2K3* and *KCNJ12*.



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