Supplemental Discussion

The following comparison of enrichment methods for targeted sequencing was added at the request of the reviewers to address concerns that the reader be able to compare the performance of the microdroplet PCR enrichment process to other already established methods. We wish to note that each of the published technical studies has selected different targets (with different GC contents and homologs in the genome), have sequenced the captured DNA to different levels of coverage, and have performed different analyses to measure performance. Furthermore, the definition of "target", "background" and "fraction of reads mapping on target" are used in different contexts in the various technical studies describing enrichment methods. Thus, we recognize that there are limitations to being able to fairly compare performance measures of targeting efficiencies between the different technologies.

A. Comparison of enrichment methods for targeted sequencing

Here we clearly define "target", "background" and "fraction of reads mapping on target" used for the microdroplet PCR enrichment method as well as for a recently published hybridization method and a recent publication on molecular inversion probes. In addition to defining these terms for all three technologies we provide published performance measures (Supplemental Table 8).

Microdroplet PCR

For the scale-up phase after trimming primer sequences from the amplicons there is a total of 1.35 Mb of targeted bases. The fraction of the 10,603,854 total reads generated that map to the targeted bases is 65.1%. The fraction of targeted bases that are covered by at least 1 base is 99.8%, and the fraction that passes our threshold for calling variants (covered by 5 or more reads and a consensus score for 50 or greater) is 94.5%. The average coverage was 185 and variant concordance based on comparison with 2226 HapMap genotypes was 98.8%. The uniformity of coverage: 96.6% of bases within 25-fold

Hybridization-based methods

We use the data from Gnirke et al.[1] for the basis of comparing the Solution Hybridization enrichment method. The study used 22,000 bait sequences of 170 bases in length for a total of 3.74 Mb of targeted bases. The authors report that 321 Mb of the total sequence (851 Mb) and of uniquely mapping sequence (492 Mb) map directly on the bait itself. Due to the fact that Gnirke et al. uses all sequence reads while we use filtered sequence reads for performance measures, direct comparisons is difficult and may result in an underrepresentation for solution

hybridization performance. Therefore to perform this comparison we acquired the hybridization sequence raw data (851 Mb)[2] and mapped back to HG18 using the same analysis methods we used to assess micro-droplet PCR performance. We obtained similar mapping efficiency for the unfiltered reads (523 Mb uniquely mapping to HG18 and 331 Mb uniquely mapping on target) as described in Gnirke et al. with the slight variation due to differing mapping strategies. We filtered the reads assuming the GERALD filter flag is still properly represented in the archive obtaining 524 Mb. Of the filtered reads 439 Mb mapped uniquely to HG18 of which 278 Mb fell on the baited region. Thus, 53.1% (278/524) of the filtered reads mapped on to the baited regions. For all other coverage statistics we used values given in the original paper. The fraction of targeted bases that are covered by at least 1 read is 88.0%, and the fraction that passes the threshold for calling variants (best-to-next-best ratio of 10^5 or greater) is 64% of the exonic sequence in the GA-I run and 89% in the GA-II run. The average coverage was 86x and variant concordance based on 7712 HapMap genotypes was 99.6% for the GA-I run, concordance was not reported for the GA-II run. The uniformity of coverage: 80% of bases within 25-fold.

Molecular Inversion probes

We use the data from Turner et al.[3] for the basis of comparing the Molecular Inversion Probe (MIP) enrichment method. Our comparisons are based on the sequence data generated using the End Sequencing approach (13,000 MIPs), which had greater targeting efficiency than the Shotgun approach (55,000 MIPs). The study used 13,000 MIPs ranging in length from 100-191 bp, which total ~1.7 Mb. However, only 1.4 Mb were considered the targeted bases because 0.3 Mb were not accessible by end sequencing. The MIPs method showed high specificity with 90% of reads mapping on target. However, the study generated 76 bp reads with the first 20 bp of each read corresponding to the MIP primer, thus 56 of the bases are informative. 90*(56/76) = 66.3% = the proportion of reads mapping to targeted bases. The fraction of targeted bases that are covered by at least 1 read is 98.0%, and the fraction that passes the threshold for calling variants (covered by 8 or more reads) is 75%. In Turner et al. there is no direct mention of average sequence depth per sample. We calculate an estimated average coverage of ~224X coverage per sample by multiplying the average number of reads mapping on target (8.4 million reads x 90% mapping on target) by the ratio of the read that was on target (56 bases of 76 bp read) divided by the total sequence captured (1.4 Mb). The variant concordance based on 9489 HapMap genotypes was 99.7%. The uniformity of coverage: 58% of bases with 10-fold and 88% of bases within 100-fold.

B. Reduction in DNA requirements for microdroplet PCR

In the RDT 1000: Merge step described above we started with 4.5 ug of genomic DNA in 20 ul of buffer and divided it evenly into 1.5 million droplets of 14 pl. Each microdroplet thus contains ~3 pg of genomic DNA, corresponding roughly to 1 haploid genome equivalent. Hence, if the amount of starting genomic DNA were to be halved, the number of productive microdroplets would also be halved. However, in some cases, researchers have a need to be able to work with less starting DNA and therefore we have examined the effects of whole genome amplification on data quality and are developing the ability to perform microdroplet PCR with multiple primer pairs in each droplet.

Whole-genome amplification

The effects of whole-genome amplification ("WGA") on data quality were examined. Two WGA kits were used for this experiment: Rapisome pWGA Kit (Biohelix, H0300S) which utilizes a primase and helicase for WGA; and REPLI-g Mini kit (Qiagen, 150023) which utilizes random hexamers and phi29 for WGA. 100 ng of input DNA (Coriell HapMap sample NA18858) was amplified according to the manufacturers' instructions for both kits. Quality of WGA template was assessed by agarose gel electrophoresis, followed by WGA template purification using QIAmp Mini DNA Kit (Qiagen) according to manufacturer's instructions. Purified WGA DNA samples were then sheared to 2 to 4 kb by nebulization (Invitrogen) using an air pump at 10 psi. Following nebulization, a small aliquot of the sheared samples was assessed by agarose gel electrophoresis to determine correct sizing of the sheared DNA fragments. Sheared WGA samples were then precipitated by isopropyl alcohol precipitation, and the air-dried DNA pellets were resusupended by vigorous pipetting in 1 mM Tris-HCl pH 8.0. Samples were resuspended in 12 µL and DNA concentrations were determined by picogreen fluorescence using 1 µL of the DNA sample.

The purified, sheared WGA DNA templates (4 ug) were amplified using the same 3976 primer pair library and sequence enrichment protocol as used in the scale-up phase alongside unamplified genomic DNA from HapMap sample NA18858. The SNP calls made from the sequencing data were compared with the data in the HapMap database and the two WGA samples had similar call rates (97%) and the same concordance rate (98.7%) as the unamplified genomic sample. These data demonstrate that equivalently accurate SNP calling can be performed using the microdroplet PCR sequence enrichment procedure whether the DNA is unamplified or whole genome amplified.

Expanded content microdroplet PCR

Another possibility exists to increase the number of active PCR droplets without increasing the starting amount of template DNA. If one starts with 1/4 of a haploid genome per droplet and includes 4 sets of primer pairs in each of the primer droplets, essentially all of the droplets will generate a single PCR product and 2.0 million active reactions can be achieved from 1.5 ug of input DNA. To demonstrate this, we prepared 21 uL of template buffer solution with 375 ng of template DNA and a 384-member library where each library droplet contains 4 sets of primer pairs; 96 different types of droplets. Gel electrophoresis curves indicate that the yield is consistent with what is expected if all droplets are producing a single amplification product.

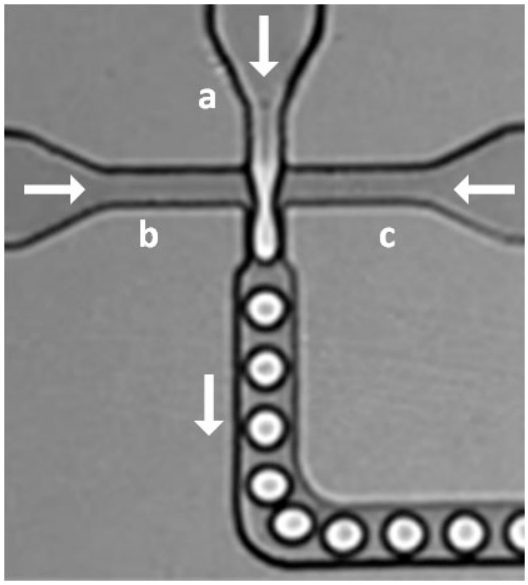
Additionally, we generated a 1536 primer pair droplet library such that each of 384 different types of droplets contained four primer pairs. The procedure for generating the library was identical to the procedure used for the library generation described above except that four primer pairs instead of one were mixed in the solutions used to generate the library droplets. The 1536 primer pair library was merged with Coriell sample NA18858 using the sequence enrichment procedure under the same conditions as described in the corresponding section above. The sample was sequenced on an Illumina GAII instrument and the sequencing data was used to make SNP calls. The SNP calls were compared to those in the HapMap database. The concordant rate for the droplets containing 4 sets of primers was similar (98.8%) as for the individually encapsulated primers (98.7%). This data demonstrates that using up to 4 primer pairs in the droplet library does not affect the performance of primer droplet libraries while allowing a significant decrease in required template. When the expanded content format is scaled to 5 to 10 primer pairs in each droplet we anticipate that the current libraries with 4000 types of primer droplets will be sufficient to capture 20,000 to 40,000 amplicons representing 1/10th to 1/5th of the exome.

References

1. Gnirke, A. et al. Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. *Nat Biotechnol* **27**, 182-189 (2009).
2. http://www.broadinstitute.org/annotation/hybrid_selection/hybrid_selection.html.
3. Turner, E.H., Lee, C., Ng, S.B., Nickerson, D.A. & Shendure, J. Massively parallel exon capture and library-free resequencing across 16 genomes. *Nat Methods*, 1-2 (2009).

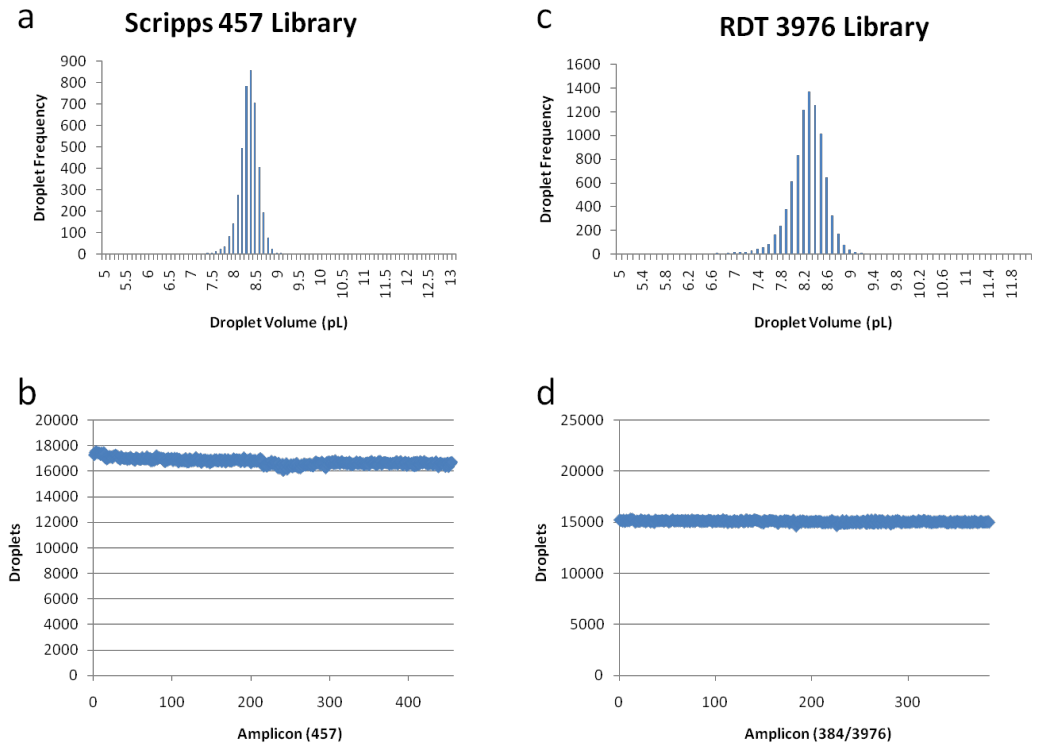
Supplemental Figure 1.

Microfluidic nozzle for generation of primer pair droplets. An aqueous solution of the forward and reverse primers for a single amplicon is infused through channel (a) into the nozzle where opposing streams of a fluorocarbon oil (b) and (c) focus the flow through the orifice to generate uniform primer droplets.



Supplemental Figure 2.

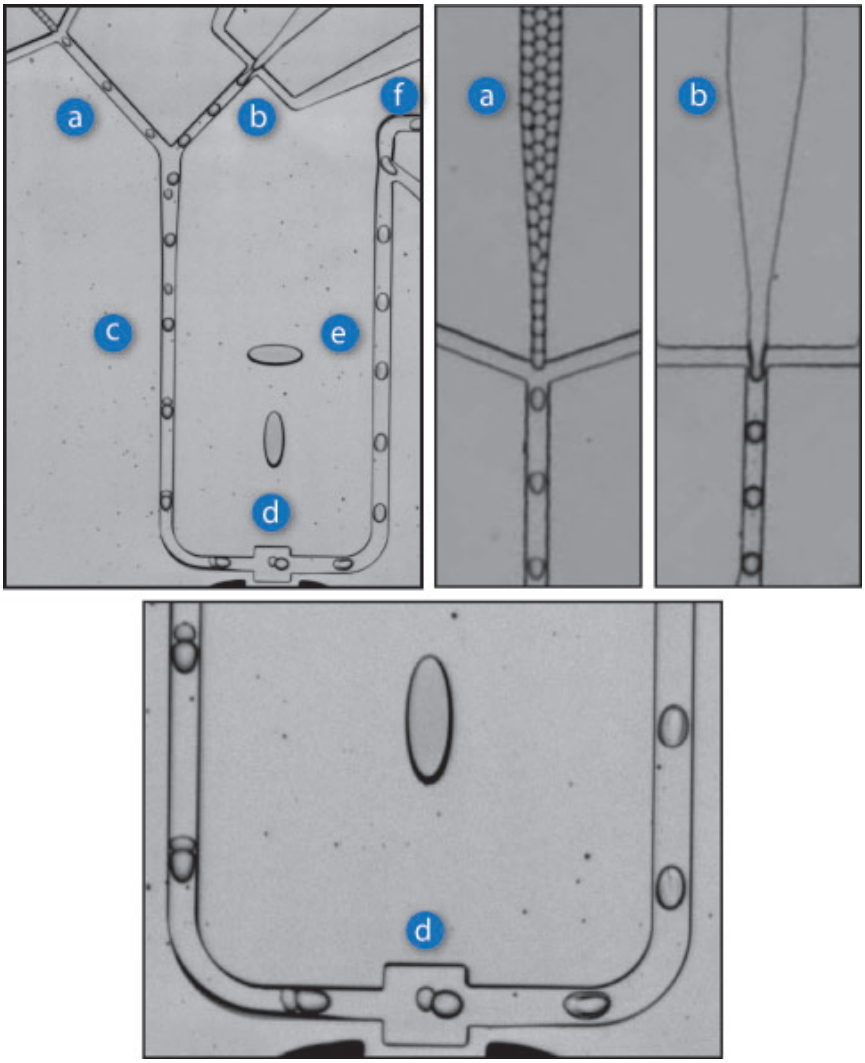
Primer Library Quality Control for the validation phase 457 amplicon and the scale-up phase 3976 amplicon libraries. Primer libraries are tested for primer pair droplet size and uniformity as well as library element representation within the primer library. (**a**) droplet size and uniformity data for the validation phase 457 amplicon library: Avg. droplet volume = 8.3 pL, CV = 3.4%. (**b**) library element representation data within the validation phase 457 amplicon library: Min = 16069; Max = 17574; Avg. = 16773; Std. Dev. = 239.523; CV = 8.9% (**c**) droplet size and uniformity data for the scale-up phase 3976 amplicon library: Avg. droplet volume = 8.2 pL, CV = 4.4%. (**d**) library element representation data within the scale-up phase 3976 amplicon library: Min = 14653; Max = 15323 Avg. = 15084; Std. Dev. = 93.84; CV = 3.6%.



Supplemental Figure 3

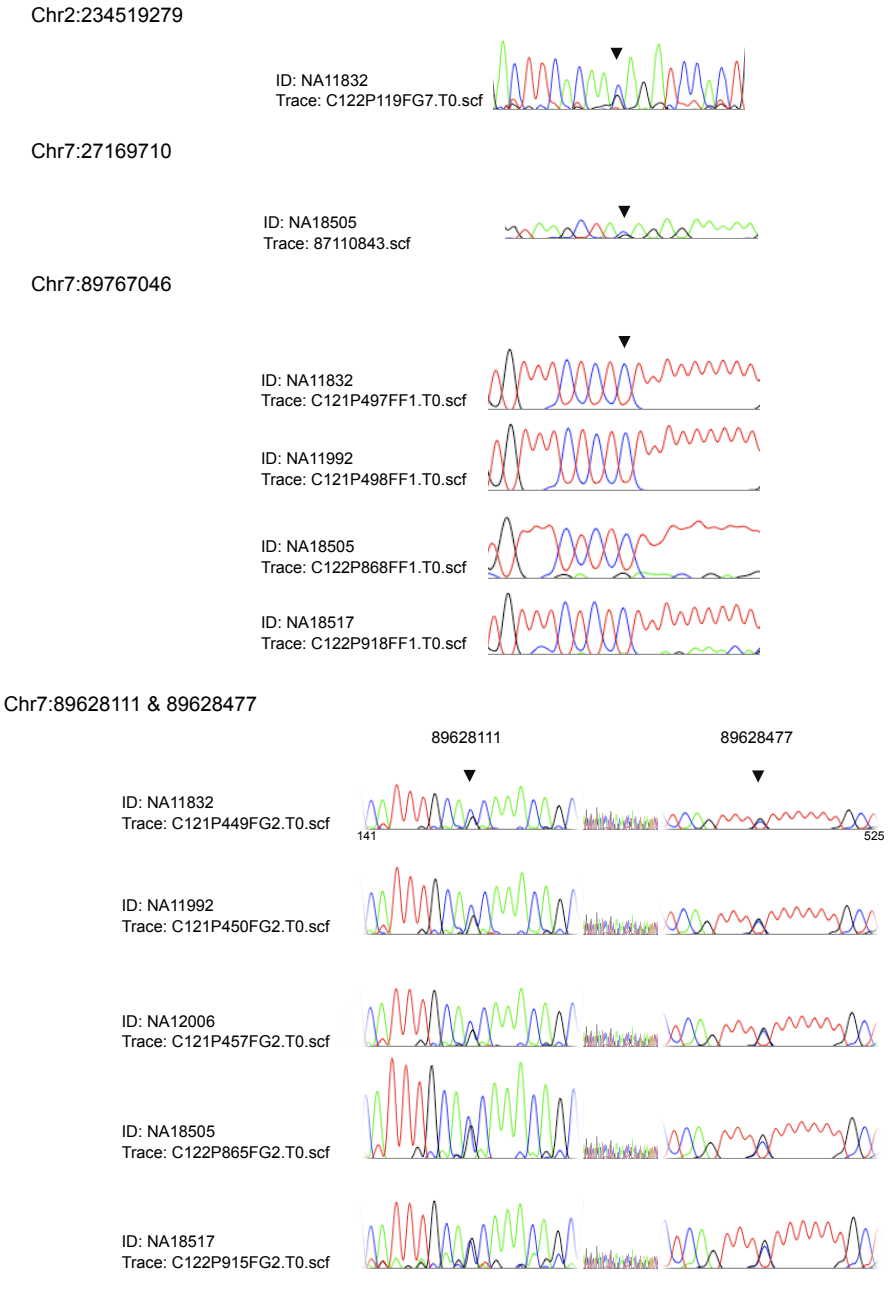
Processing droplets in a microfluidic chip. The optical image shows all key microfluidic elements for processing droplets. These include: (**a**) Spacing of the Library droplets with carrier-oil. (**b**) Generation of Template droplets of uniform size. (**c**) One-to-one pairing of Template and Library droplets. Pairing is achieved by actively matching the rate of library droplet introduction to the rate of template droplet generation and by using the property that small droplets move faster than large droplets and will catch-up to the preceding large droplet. (**d**) Merging of Template and Library droplets by field-induced coalescence to make individual PCR droplets. (**e**) PCR droplets are transported to a collect line. (**f**) PCR droplets are collected off chip into a standard 0.2 ml PCR tube. Enlarged regions of the image show: (**a**) library droplets before they are spaced, (**b**) template droplets being generated and (**d**) the region where droplets merge in an electric field.

The PCR droplet generation can be viewed in the attached movie (Supplemental Movie 1).



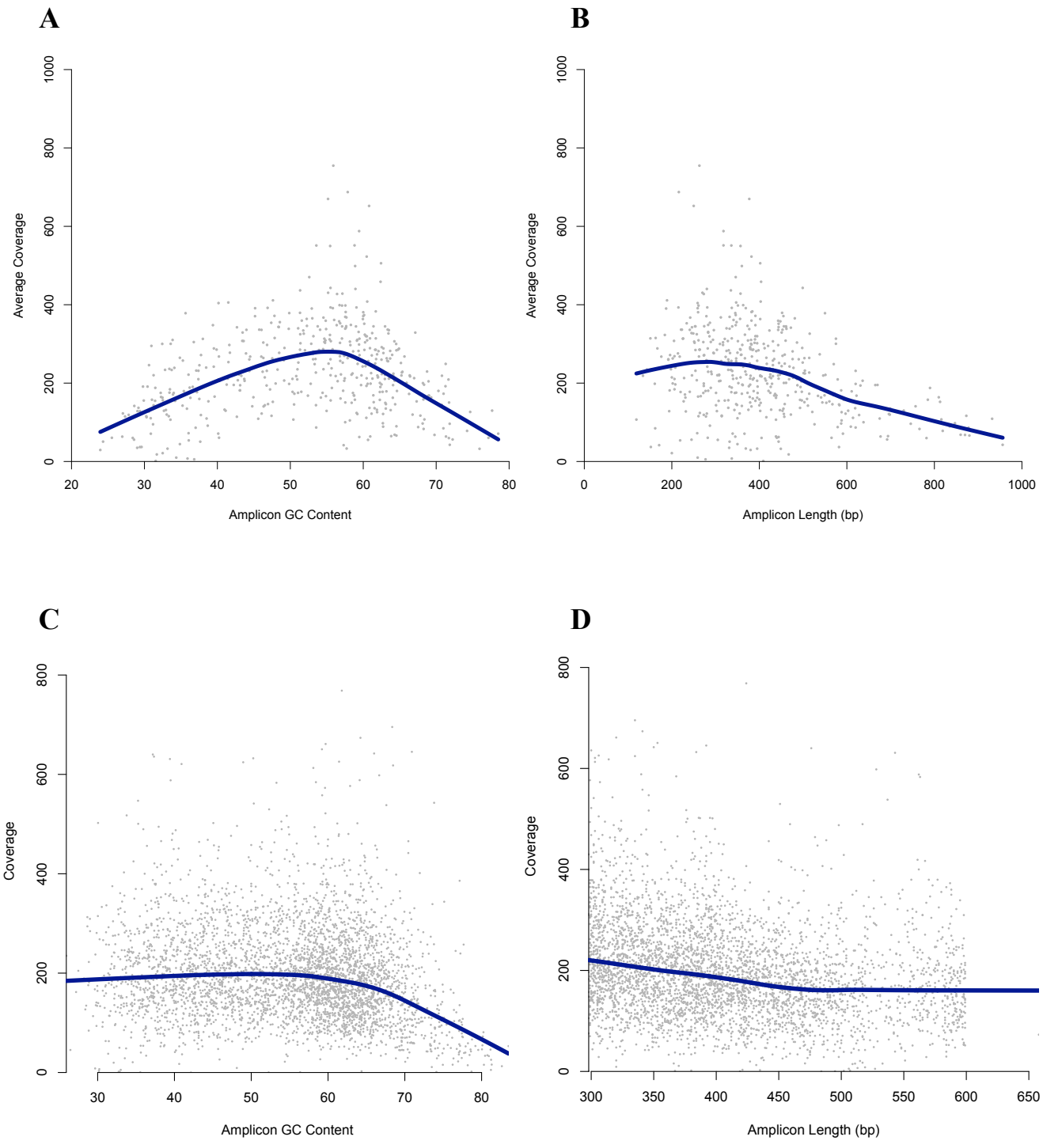
Supplemental Figure 4

HapMap Sequence traces for discordant alleles in the ENCODE regions.



Supplemental Figure 5

Effect of GC% and amplicon length on average sequence coverage. Average sequence coverage of the primer trimmed amplicons for the 456 amplicons in the validation phase (A,B) and 3976 amplicons in the scale-up phase (C,D) plotted against the full amplicons GC% (A,C) and length (B,D).



Supplemental Table 1. Summary of targeted genes in Validation Phase. In total, 435 exons from 47 genes were targeted. The 435 exons were split into 457 amplicons, each under 1 kb in total length (Supplemental Methods).

Chr.	Gene	No. Exon	No. Amplicon	Median Size (bp)	Size Range (bp)	Category
Chr2	HJURP	9	11	358	135-814	ENCODE
Chr2	UGT1A10	5	6	444	362-604	ENCODE
Chr7	C7orf63	22	22	344.5	193-583	ENCODE
Chr7	CLDN12	1	2	627.5	623-632	ENCODE
Chr7	EVX1	3	3	767	589-783	ENCODE
Chr7	GTPBP10	8	8	335	153-479	ENCODE
Chr7	HOXA1	2	3	584	580-589	ENCODE
Chr7	HOXA2	2	3	621	583-697	ENCODE
Chr7	HOXA3	2	3	700	699-861	ENCODE
Chr7	HOXA4	2	3	621	522-747	ENCODE
Chr7	HOXA5	2	2	658	621-695	ENCODE
Chr7	HOXA6	2	2	576	554-598	ENCODE
Chr7	HOXA7	2	2	527.5	445-610	ENCODE
Chr7	HOXA9	2	2	690.5	500-881	ENCODE
Chr7	HOXA10	3	4	575.5	375-693	ENCODE
Chr7	HOXA11	2	3	434	360-588	ENCODE
Chr7	HOXA13	2	3	566	499-957	ENCODE
Chr7	STEAP1	4	4	450	246-879	ENCODE
Chr7	STEAP2	6	6	528	220-676	ENCODE
Chr9	C9orf106	1	2	510.5	445-576	ENCODE
Chr9	CRAT	14	14	349	152-444	ENCODE
Chr9	NUP188	44	44	336	177-516	ENCODE
Chr9	DOLPP1	8	8	317	235-461	ENCODE
Chr9	FAM73B	15	15	380	242-539	ENCODE
Chr9	IER5L	1	3	731	515-820	ENCODE
Chr9	PHYHD1	11	11	284	120-391	ENCODE
Chr9	PPP2R4	11	11	338	188-588	ENCODE
Chr9	SH3GLB2	11	11	383	209-592	ENCODE
Chr11	APOA1	3	4	488.5	221-568	Haemostatis/Thrombosis
Chr16	CETP	16	16	362.5	162-457	Haemostatis/Thrombosis
Chr5	F2R	2	3	874	401-933	Haemostatis/Thrombosis
Chr17	GP1BA	1	4	711.5	576-791	Haemostatis/Thrombosis
Chr1	LRP8	19	19	396	164-678	Haemostatis/Thrombosis
Chr20	PLTP	15	15	297	216-418	Haemostatis/Thrombosis
Chr2	PROC	8	8	393	163-848	Haemostatis/Thrombosis
Chr20	PROCR	4	4	402.5	347-561	Haemostatis/Thrombosis
Chr20	THBD	1	3	836	817-871	Haemostatis/Thrombosis
Chr9	UGCG	9	9	392	308-473	Haemostatis/Thrombosis
Chr8	TRPA1	27	27	329	197-504	TRP Channels
Chr4	TRPC3	11	12	451	330-666	TRP Channels
Chr11	TRPM5	24	24	400	262-542	TRP Channels
Chr2	TRPM8	24	24	347	209-671	TRP Channels & ENCODE
Chr17	TRPV1	15	15	439	281-639	TRP Channels
Chr17	TRPV2	14	14	400	172-612	TRP Channels
Chr17	TRPV3	17	17	349	144-515	TRP Channels
Chr12	TRPV4	15	15	396	193-620	TRP Channels
Chr12	PAH	13	13	330	168-462	Phenylketonuria
Total	47	435	457	434	120-957	

Supplemental Table 2. Primer Design Strategy for Validation Phase. The primer sets were designed using five stages. The parameters used in the first stage were the most stringent and were loosened in the following stages to allow for primer design of all 457 amplicons (Supplemental Methods).

Stage		Masking		Padding	Primer3 Parameter*	Number of Primer Sets	
		Repeat	SNP	Sequence (bp)	Tm (°C)	Designed	Failed
1	5'-primer	+	+	200	59.5-60.5	424	33
	3'-primer	+	+				
2	5'-primer	+	+	200	59.5-60.5	10	23
	3'-primer	-	+				
3	5'-primer	-	+	200	59.5-60.5	17	6
	3'-primer	+	+				
4	5'-primer	+	+	300	57.5-62.5	5	1
	3'-primer	-	+				
5	5'-primer	-	+	300	57.5-62.5	1	0
	3'-primer	+	+				
					Total	457	

*Primer length was kept constant at 18-27 bp.

Supplemental Table 3. List of 457 primer pairs for validation phase.

Gene	Exon No.	Forward (F)-primer	Reverse (R)-Primer	F-Tm	R-Tm	Length (bp)	GC (%)
APOA1	1	CTCTATTCTCCCAAAAGAAAGAAGC	CAGGAGATGAGCAAGGATCTG	60.2	60	568	64.4
APOA1	1	CCGTTCTCCTTGAGAGCCT	TGAGAGTGTACTGGAAATGCTAGG	59.5	59.8	547	64.2
APOA1	2	ATCAGATATTAGGTGAGGACTCGG	TAACCTAGGGAGCCAACCATC	59.9	60.3	430	60.5
APOA1	3	GATGGTTGGCTCCCTAGGTTA	TCTGGGTACCTGAGGTCTTCTC	60.3	59.7	221	62.4
C9orf106	1	CAGTGTGAATTGGGAGTAAGAGTTC	GTCACAGAGCAGAGGATTCAGAT	60.4	59.9	445	60.2
C9orf106	1	CTTCCTCTGGGAAGTCCTCTCT	AGTGCCTCCTATAGGTCAGTATGTG	60.4	60	576	59.5
CETP	1	TTGAATGTCTGGCTCTGAACTCTA	TCCTCTCTCTGGGCTAGTGTG	60.4	59.6	425	61.9
CETP	2	GAGCTCTCTGTGTCCCCTAGAAT	GTAGGGAAGGTGTCAGGCTCT	60.3	59.8	457	61.5
CETP	3	TAGACAAAATTGGAGGCTCACTC	CATACTCAGCTGTGTGTTGATCTG	59.8	59.9	378	55
CETP	4	ATTCAGAACGTGTCTGTGGTCTT	GAGTCCAGCTCCCACTTCC	60.1	59.8	264	55.7
CETP	5	ATACCATCTGATAGCGGAGGC	GTTATTGTTGTTTCCAGCCTTTG	60.5	59.9	333	57.4
CETP	6	GGGATGGTGCCACAGTTAAT	ACATGGAGAAGGTGGGAGTG	59.7	60	370	55.9
CETP	7	CACTCCCACCTTCTCCATGT	TTGCCAAAGTATGCTCATAACTAATC	60	60	352	55.7
CETP	8	AGACAGACTTGGGAAAAGAGAGAAT	ACTCTTGGCTGCCATAAGGTT	60.2	60.1	383	57.4
CETP	9	GGGTACAGCTCTTTCCTCAGTTT	CTATTGCTCCAGCTTAGTTCTTTTG	60.2	60	444	58.3
CETP	10	AGTTTTCTTCTGAGGAGTGGACTTT	GGATTGGGGTACGTGAGATAAA	60.2	60.1	162	52.5
CETP	11	CCAGCTTTGTCCTTCCCAT	TTACTTGCATGATGTGATTTTGATT	60.1	59.8	426	57
CETP	12	CTCACAGCAAATTTGGTTTCTCT	TCTATCTAGGCAGGGTCTTATCTCC	59.8	60.5	255	54.1
CETP	13	CAGAATAGCAAATCTCAAGGGAATA	CCCCAGTCTATCCAAGACTACCTA	60	59.9	224	46
CETP	14	AGGAAAGACCACTCAGGAAGG	GCTAAGTATCAATGACTGGGAAGAG	59.7	59.7	364	56.6
CETP	15	TAAATCAAAGTGAAACGCATGTTTA	CTCTGTCTGTCTCCCCAACAG	60	59.9	321	57
CETP	16	CTGTTGGGGAGACAGACAGAG	CAGCTCTTGGATACAGCACTTTAAT	59.9	60.2	361	59
CLDN12	1	CTTTGCATTGACATTTCATCATTAG	GATGGATGTTATAAAAGATGACCCA	59.9	60.3	623	52.5
CLDN12	1	TGTACGACACTACTTGGTACTCATCA	GGTCAAAAACAAAGGAAAATGTATG	60	60	632	46.7
CRAT	1	AAGGAAGAGGGAACCAAGGA	AAGGTAGGGGAGCTGAGAGC	60	60	348	63.9
CRAT	2	CATCAAACTACCAGTGGGTTCTC	AATACTCTGGTCTTGTGGTTTTGAG	59.9	60	326	63.8
CRAT	3	ACACTAAGGGACAAGTGAGTAGGC	AAGAGAAGGGACAGTGCTTCAG	60.1	60.1	152	60.5
CRAT	4	GCTCAATTATTGTGTTGACTGAG	CACCATTTTGGAAAAGACTTCC	60.1	59.9	404	60.6
CRAT	5	TAGATCCTGGTGGGAAATGG	GCAGAACCTCAGCATGTAAGTG	59.7	59.9	403	62.3
CRAT	6	GAAGAGCAGGTGAGGAGCAG	GTGGTTTTCAGAACAAACTCACAC	60.3	60	405	62.5
CRAT	7	TAGGCGAGAGATGTGACTGTACTC	TAATAAGTCATCATAGCCCCTTGAG	60	59.9	252	57.9
CRAT	8	TCCTGTTCAGGTGTGTGTGAG	GTACAAATGGGTCAGAAGAGCC	59.8	60	334	62.6
CRAT	9	TAACCTGTCTCTTCTCATTCCTTTG	ACTCAGCTCCCTCCTCTTACCT	60.2	59.9	339	56.9
CRAT	10	CTTGGATCACCCTTCTGGG	TAGCAGGTCCCTGTCTACCCT	60.4	60.1	444	65.3
CRAT	11	CAGAGGTGGCTGTGGTAATTAAG	CGCAGCTTCTAATCTCTAATCAATC	60.1	59.9	154	51.3
CRAT	12	CTTGTGGGGCAGAAAGATAAAC	TTACTTTGAGAATCTCCATAGCCAG	60	60.2	348	63.8
CRAT	13	AGTGGGCACTGGAGAACTGT	AATGAACAGGATGTTCTGCTACCT	59.8	60.4	358	61.5
CRAT	14	TTTAATCCCGCTTCTGACCTT	GGCTGTAACTCAGCGACCTT	60.1	59.5	350	70.6
DOLPP1	1	TACCTATATTGGCCTCCGATTG	TTCACTATTTGACAGTTCCCACC	60.2	60.3	315	67.6
DOLPP1	2	TGCTAAGTAGTAGACAGCATCACGTA	CAACAGGTGAGTAACCTAGAACCAG	59.6	60.5	461	59
DOLPP1	3	CTGGTTCTAGGTTACTCACCTGTTG	GAATAGACGGAGAAGAACCACATAA	60.5	59.9	383	60.6
DOLPP1	4	GGTCAACTGGCTGATCAAAAA	TAGCAGTGAGTCCCTAGCAGAAC	60.1	60.1	319	58.9
DOLPP1	5	GTTCTGCTAGGGACTCACTGCTA	GTCCTTTTAAAACTAGAGGTCTGGG	60.1	60	413	61
DOLPP1	6	GGCTCTCACATACTTCGCTTCT	TGGGGTCAAGACTCCTAGGTC	60	60.5	255	63.1
DOLPP1	7	GTGACATAGCTGGGTCTCTCAGT	TGCTGTCCCCTGAACTCAC	59.8	59.8	275	59.6
DOLPP1	8	CATTTGCCTACTTAGTTGGGACTAC	TCTGTAGAGGTCTCTGCTTCGTC	59.5	60.2	235	57
EVX1	1	CTTCACAAGGTGACCCTAGCTC	CAGATAGCAGAGAGAGTTGCTCAG	60.3	60	767	68.3
EVX1	2	AGAAACAGTTACTGAGGTGGCTG	TATTTAACCAGGAAAGGGACAGAG	59.9	59.9	589	61.8
EVX1	3	AGACTACTGGCCTCTGAGCATC	CACTTCCTAGGCTTTCCAATTCT	60	60.1	783	71.6
F2R	1	CGCTTGGACCCTGATCTTAC	CCACCTAAACGTGACTGGAAA	59.7	60	401	68.3
F2R	2	ATTTGTGCATTATCTGCTCTTTACC	ATAGACACATAACAGACCGTGGAA	59.9	59.8	933	45.6
F2R	2	TTCGTCACTGCAGCATTTTACT	TATGCAAGTCGTACATCTGTTGTTT	59.9	60	874	47.4
FAM73B	1	ACGTTCTCTTATCTGACTTGGTCAT	TATAGTCTCAGGCTAAAGAACAGGC	59.6	59.5	454	57.3
FAM73B	2	GCTGCCTCTCAGTCTCTCATCT	ACATCACCCTCCAGTACAGTGAC	60.3	60.3	539	62
FAM73B	3	CCTCTGTTCCCCTGACTTAGAA	CTACCAGTCTATAAGCTTGCTGAGG	59.7	60	338	61.8
FAM73B	4	CTTCACTCTTTCTTCTTGCACTGAT	TAGACACTGTCCCTTGTTCAGAAAT	60.5	60.4	313	57.8
FAM73B	5	ATTTCTGAACAAGGGACAGTGTCTA	TCCTGTGCTGCCAACTTTATC	60.4	60.3	385	60
FAM73B	6	TTTTGGAGTTTATGTGCTTAGCTG	AACTTCTCCCTCACCTCCATCC	59.9	59.5	318	60.1
FAM73B	7	TTTCTCTCACTGCTCTTCCCA	CAAATTCTCCCATCAGAGGAAA	60.1	60.4	242	62.4
FAM73B	8	GCCAGTGTTCCCTCTGACAT	ACTCACTCAGGCTAAGTCCTCG	60.1	60.1	380	65
FAM73B	9	TTGTGTGACGCCGTCTGT	GCCACATAAGAGGCCAGGTA	59.9	60.1	263	65.4
FAM73B	10	CATGGCTGTGTGGCATGTA	CAGAGTCTACAGAACGGAGTAGGAG	60.1	60	392	60.5
FAM73B	11	TGCTGAGTAGGAGACACTTCTCTG	GGGACTATGAGCAGTGATGGA	60.2	60.1	380	62.4
FAM73B	12	AGTCTCCCCATCTGGAAAGTG	GAGCAAGTGTGGGTCTGAGAG	60.5	60	250	63.2
FAM73B	13	GGAGGAAGCAGCAGAGCTTA	AGAGGAAGTGGGTCTACACGAG	59.9	59.8	396	64.1
FAM73B	14	ATCTAGCAGGAAAGTACATGAGCTG	GGTCAGGAAAGAACGAGAACTG	60.3	60.3	275	57.5
FAM73B	15	ACATGGGTCCAGAGGAAGC	CACCACAGCTGTCAGATACCA	60.1	59.8	437	66.1
C7orf63	1	CACTGTAGGACAGGAAGATCCC	AAAGCACAGACACCTGCTCATA	60	59.9	193	62.7
C7orf63	2	TTCTCCCCTTACTATCGTAGTGTCA	TGTTACCTTTCAGGGAAATAGTTTG	60.4	59.8	262	33.2
C7orf63	3	AAAGCACAAAAGAACTAAAATAGGTGA	TTACAACAGCAATGGAAAACTAACA	60	60	195	29.2
C7orf63	4	CACATTTGGCAAAATAGTTGGA	CAAGTGATGAACTGAAGTTTTCTGA	59.9	59.8	356	27.2
C7orf63	5	TAGTTAATAATTGTCAATCCCCAGG	GGAGAAGGAGTCCTCTTAGTGAAAC	59.6	60.2	330	32.7
C7orf63	6	ACATGATCCAGTTTGAATCTCTGA	TGCAAATCAAAAACTGAAAAATACA	60	59.9	417	30.2
C7orf63	7	AAAAGTTTTTCTTGCTGTTGCTTAAT	CATTGAGGTGAGTACAGATTCCAC	60.1	59.9	421	30.9
C7orf63	8	AAATCAACTTGTTGAGAAACTTTGG	ATGTTAGTTATGTCACTGGCTGTCA	60	60	411	32.4
C7orf63	9	CTCACTCCTAAAACCATCACATTG	CACACTGGTGACCATCAAGATATTA	59.9	60.2	379	32.5
C7orf63	10	TGAATTCAAATGAATGACAGTAGGA	GATTTTGACTTTTAACTGTGAGGGA	59.9	59.9	279	27.2
C7orf63	11	TTTGATACTGTTTGCCACCTTTAAT	TTATTGATTTTCCTGCCTTGATTAC	60.2	59.8	274	27.7
C7orf63	12	TTGCCTTAAAGTATTTTTGGCTATG	TGAGCATTCAGTTGAAATATGAAGA	59.9	60.1	337	37.1
C7orf63	13	CATTTGAGTAAAATTCCAAAACACA	GTTGAAGAAATAAATGCTTAAAGGG	59.4	58.8	583	29.5
C7orf63	14	GATTAGCCTAGGCAACATAATGAGA	TATAGTGTTAGGTGACTGGGAGACC	60	59.8	351	31.1
C7orf63	15	AACAATGTTGCTGTATTTCTCTGGT	GGCTATACCATCTAGCCTAAGTGTG	60.3	59.6	417	34.8
C7orf63	16	GAAAATGCTTTGATAAAGATAAAGCTG	TGTTTAAGACCGTACCTTTGAACAT	60.1	60.2	302	32.5
C7orf63	17	AGGAGATTTTCCTGACTCTGAGTTT	AAAACTTTAGACAAAGGGGTGAAAG	60.2	60.3	432	30.6
C7orf63	18	TCTTAGAATCACTTGCTCTGCTAAAG	ATGAAATCTTATCCCATGAAAAACA	59.8	60	332	28.9
C7orf63	19	TCCCAGGAAGTAATTTAGGAAAAGT	CATCCCCTTAAACACTTATCATTTCT	59.8	60	527	31.1
C7orf63	20	TTTTTAAAAGGCAGAGAGATACTTGAG	AATAGTGCTGGTATTGTACGGAAAG	59.9	59.9	338	36.1
C7orf63	21	GCAGATTTCAGCGCTATCTAATAAA	GGGTAAAATTCAATGGTTTTCAGTA	60.3	59.6	333	30.6
C7orf63	22	TCTTGTTGAAAATTGTGTAAATGGA	TTCTGATATTACATGTTGATGTTTTCC	59.8	59.6	410	31.5
GP1BA	1	AGTAGTTTTAAGTTCTGCAGGCAAG	CCTTTGGTATTGTATACAGCGAGTT	59.6	59.9	786	58.8
GP1BA	1	AACTCCAAGAGCTCTACCTGAAAG	AAGCAGTGGACCATGAGTAGAATAG	59.6	60.1	576	52.8
GP1BA	1	CAGTGTGACAATTCAGACAAGTTTC	AAGAGACCCAAGACATAGAAGCC	60.1	60.1	791	55.8
GP1BA	1	AAAACCCGTATCACTCTTAGAATCC	TACAGAAAAAGGAACTAAGACCCCT	60.1	60	637	57.3
GTPBP10	1	AGAAGGTTTCCTGGCCTGTT	AGAAGTCTATGGGAAAACCAAGC	60.1	60	185	55.1
GTPBP10	2	GTGGAGGTGAGCTAAGAAAATGTTA	GCTTTTGCTTGGTTATAAATACAGG	60.1	59.5	479	34.2
GTPBP10	3	CCAGCATGAATTATCTTTACCTTTT	CAGTTAAGGATACCCTCCGAGTTA	60.1	59.9	361	28.8
GTPBP10	4	CCTTAATTTATTGCTGTGTTTCCTTT	AATATCCAAGTACGTACCAAAACCA	60.2	60	153	30.1
GTPBP10	5	GTAATTGAACTTGCGGTTTTCATAC	TAGTAAACAATGTCACTTCCATCCC	60.2	60.5	322	30.1
GTPBP10	6	TCTTCGTATGTTAAAGGCTGTCTCT	TCAAAGCTTTAAAGGTGGAGTATGT	59.9	59.6	232	32.3
GTPBP10	7	TCATTTTCTGAAATTCTTCCTTTTG	TTCAAACTTGACTTTTAAGAGCAGAA	60	60	396	33.1
GTPBP10	8	AGCTTTGTTTGTGCTCTTTCTTTTA	AAGGATTTCCTTGTTTTTAAGCATT	60	59.8	348	33.3
HJURP	1	GGGAAGATAAATAACACTCCGAAAT	GGTTGCCATTATATTTTTGTTGTTT	60	59.5	290	31.7
HJURP	2	ACAGGGACACATTCTTGATAGAGAC	ATTCATCTTCATCACTTCCAAAGAC	59.9	59.9	814	47.5
HJURP	2	CAATACATAAAGGCACTGTCATCTG	GCATTAAGAGATTGCAAGAACGTAT	60	60.1	811	45
HJURP	2	TATATGTTGCACTGGAGTCGAAGTA	ACTCCTACACATTTGTGGTGTTTTT	60.1	60.1	758	44.7
HJURP	3	TCTTAATCTTCCAGTGAAATCCAAG	TTAGTAGGACATATTTTCTTCCCACTG	60	60.2	426	50.9
HJURP	4	TGTCAGCATGTGAATAAAACAATTT	AGATTTGTACATTAATGAGCTTGCC	59.8	59.9	345	33.9
HJURP	5	CCATTCATTACTAAAGGCAGCAC	CTTCCTGAAAATCCTGATTGAGAT	60	60	135	43.7
HJURP	6	CAGAAGGAATCAACAGGGTACTTTA	GTGTTAACAGAAGGATTGCAGTTTT	59.9	60	358	46.6
HJURP	7	GGTTATTTGGCAATAAAATTTGACA	CCTGAAACTTTACAAAGAGGAACAA	60.3	60.1	255	37.6
HJURP	8	AACTACTCCATTCACACTCTTCACC	CCAGACTAACGGCCTCTCAC	60	59.9	222	63.1
HJURP	9	CTGCCTCCTTTTTCCCCTCTC	GGAGTCTCCTATTTGAGTTTGTGG	60.3	60.4	380	68.4
HOXA1	1	CCCAGATAGGATTAGAAAGGAAGAA	GATCTTTTCTTTACCTGAGTGTTGC	60.3	59.7	584	53.6

HOXA1	2	TAAAATCCTTGAAAACACACCAATC	CTACTCCCACTCAAGTTGTGGTC	60.5	60.1	580	50.9
HOXA1	2	CATATGAGTGGTGAATGTATTGAGG	ACATTCATATCATTTTTCTTCTCCG	59.7	59.8	589	58.2
HOXA10	1	AGCAAACACAAAGAAACAAAAAGTC	CTGTGACTTGGGACATCTCTCTTAT	60.1	60.1	571	53.2
HOXA10	2	TAGTTTTCTGATCCTTCTCCTCCTT	CCATAGACCTGTGGCTAGACG	60.1	59.8	693	72.2
HOXA10	2	GAGACTTTGGGGCATTTGTC	ATTGCTAATCGTATTCAGCATGTTT	59.5	60.3	580	67.6
HOXA10	3	AAGGAGCTAAAATCCTCAACTTTTC	CTAAGAGCAGCACGGTACATTATTT	59.7	60.1	375	54.7
HOXA11	1	TATTATCTCATGTGTATGAAGCCCC	TTCTCCTCAGCTATGGGCTCT	60.4	60.5	360	50.8
HOXA11	2	TAGATTTCCAACTCCCCTTTCATA	CGAAGTGACCTTCAGAGAGTACG	60.2	60.5	588	68
HOXA11	2	TGCTATAGAAATTGGACGAGACTG	AGAATCATGTTAAGCTCGGCTACT	59.8	59.9	434	59.2
HOXA13	1	AGCATTATTATCATTATCTGGGCAA	AGAACTAACTACCTTCCCCACTGAC	60.1	60.3	499	49.1
HOXA13	2	AAGCTAGCCGAGGTCTCCAC	AGGGGGCAACTTCTCGGT	60.9	62	957	71.8
HOXA13	2	GTAGTAGCCGCTGCCGAA	ACTGGGGTCTTCTCCATGC	60.1	60.1	566	77.2
HOXA2	1	CAGAAAATCCTCAACACTTAAAGGA	CTTGAGGACTCCGAGAAAGTAGAG	60	60.1	621	46.9
HOXA2	1	AAATGTTTCAGATTTTTCTCATTGC	CATTTTGTTGCAGTTGATCTTTTC	59.9	60	583	50.4
HOXA2	2	ATCTCTCCCTCTCCTCCTTCTCT	TCAATAGTTTAATAGTAGCGGCGGTC	60.3	60.1	697	59.1
HOXA3	1	CGTCACATAAACTATAAAAACGCCT	TGGCTATCTGAACTCTATGCATTC	59.9	59.8	700	63.1
HOXA3	1	CTTCCCTGTATGTGTGGGGT	TAGTTCCTACTTCTCTCTGGGACCT	59.7	60.2	699	66.8
HOXA3	2	AGACTATGAAAACCTTTTTGGTGG	GCTATTGAGAGTAAGATGGATTTGC	59.8	59.7	861	64.2
HOXA4	1	TTTTGGTGTCTATTATGGTCCAGAT	CATTTTCTTTGCCGTTTTATGTATC	60	60.1	621	53.5
HOXA4	2	GTACAAAAGGGTTCTCATGTTGG	GACACCGCCTACCCCTATG	59.8	60.3	522	74.7
HOXA4	2	ATCTTCTTCATCCAGGGGTACA	GAGGAGTGGGCACTTGACAG	59.8	60.9	747	71.8
HOXA5	1	AGCAGATCTACTTATACAGGCGCTA	GGTCCAAATCGTATTGTTTTCTTT	60	59.7	621	49.8
HOXA5	2	AGAAATGAGACCAAGAGAGACTGG	ACAAATCAAGCACACATATCAAAAA	60.3	59.8	695	63.7
HOXA6	1	GAAATAAATGCACAGACGCTTG	CATCTCGCTTGGTATGAAATAATCT	59.8	59.9	598	61.2
HOXA6	2	TCCACTGTCTTGGGATATGTCTTA	AGAAACAAACCAGTTCGATGACTAC	59.9	60	554	58.3
HOXA7	1	TTTCCCATTTTTGTAAGTAAAACCA	TACTTGTCTGTCCTTGTGTTCATGT	60	60	445	59.3
HOXA7	2	CTCCAATTAAAACCAGAAAGGCT	TATCACTCTACCTCGTAAAACCGAC	60	60	610	62.8
HOXA9	1	GACGGACAGTTCTTTCTTTTTCTC	AAGTTTTACTGCGTGCAATTTTAAG	59.8	60.1	500	51.2
HOXA9	2	TCTTCACTGCTCTCCAGACTTG	CGGCAACTTATTAGGTGACTGTACT	59.8	60	881	64.5
IER5L	1	TTGCCGAGTCTTTGTCTGG	CCGTGCTGGACCTAGACACT	60	60.3	515	70.9
IER5L	1	GTCGTCTTCCTCCTCCTCCT	AGCACCAGCACCTAGCGTA	59.8	59.6	731	77.7
IER5L	1	CAGAGGCTCCAAGGGCTG	AGAGCTCCTATTGGCTCTTCTCAT	62.1	61.2	820	74.3
LRP8	1	TGTTTGCAGTTCATCATAACTTTGT	TGGATCTAATGATGAATTCTTTGGT	60	60.1	258	42.6
LRP8	2	TCTGTGACTAACCCATTTTTCTTCT	GTCACTGTTATACAGCACAGTCAGG	59.6	60.2	403	56.1
LRP8	3	AAGGAAGGAAAGAAGGAAAGAAAA	GAGCAAAGGGTAGTAAAAGTGGAGT	60.1	60.4	463	49.7
LRP8	4	CTAAGCAGGGTCTCTCTTTTCTCTT	GACACACAGTGATAGAGCATCATTC	60.1	60.1	164	48.2
LRP8	5	ATGCAGTAACCTCCTCAAAGATATG	CAAAATTATCTGTCCAAGTGACCTC	59.9	60.3	396	53
LRP8	6	ATGAGCATTCAAGGAAGGTAAAAA	AAAAGTATAGGGCAAGCTTTTTGAG	60.3	60.5	435	53.3
LRP8	7	CCAACAAGAGGGATTGTTGTTATTA	GATTTCAGGGAAGTTCTTGTGACTA	60.5	60.1	383	51.7
LRP8	8	GACTCATCCTATTTGAACAAGCATT	TGCCAGTGACTTTGTTTCCTAAT	59.9	60	357	52.4
LRP8	9	ATCAGGACAAGGCACTAGAATAGG	ACAACTAGTCAATGGGTTATTGAGC	60	59.9	264	51.1
LRP8	10	TTGGGGATTAACAAGACTTTCTTC	TCCACGTTCCTCTAAAAATCTATTG	59.9	59.9	498	55.4
LRP8	11	GTAAAGTCCCAGAAGTTCCATATCC	CTGCAACCTGTAAAGTAGGAATTGT	60.5	60	482	53.1
LRP8	12	TAATTGTCTCTTGGCTGAATTCTTT	ACCTCAAGATTGGCTTTGAATG	59.7	60.5	454	54
LRP8	13	CACTCACACTTAAAATAGCCCTTGT	TGCTTCTGCTCTAGGTCCTACC	60	60	352	57.7
LRP8	14	TATCCTTTCCTCTCCACCACC	CTAAGCTATGCATGGACGTCTG	60.3	59.9	283	62.5
LRP8	15	AAGAAAGTCCAGAAACAGGTCAGTA	ATGAAGAAGCTTGTCTCTCCTGTC	59.8	60.4	449	56.6
LRP8	16	CCCCACCGTTCCTTTTCT	ATAATCGCCCCCTTTCCTC	59.9	60.2	284	65.5
LRP8	17	AAATTCAGGAATAGCCGCTTC	GTCACCGAACCTGCTTGAA	59.7	59.8	450	75.8
LRP8	18	TTACAAATCCAGTTCTGGTGCTACT	ACCACACTGACTCTGATCCTCTC	60.4	59.8	358	57
LRP8	19	GTATTCAGGTAAGGCAATGAAAGG	GTCACCTAGCATGTCCGTGTT	60.2	60.1	678	71.4
NUP188	1	GCAGCCTTCCTCACAGTTACA	GGACCGTTTGGACGTAACC	60.4	60.2	380	71.8
NUP188	2	TTTGCTTTTAGAGAGCAGACAAAAT	GTAACAAAAGCTACACAAAGAACCC	60	59.6	206	43.2
NUP188	3	GAGAATCACTTGAACCTGGGAG	ACCCTACAATATCATCAAAGCACAT	60.1	60	312	61.1
NUP188	4	CTGAAGGGCAGAAAATAGTCTGTAG	CTATGATATGCAGTGAATGGATCAG	59.9	59.9	382	33.8
NUP188	5	ATCTTTAAATTCTCTGCATCCTGTG	GAAAAGGATAAAGGCAGAAGAAAG	60	60.1	196	42.9
NUP188	6	TCTTGAAGGATGAAGTGAAGGTATC	TCTTCATAAAGACCTCCATGCTTAC	60	60	261	39.5
NUP188	7	ATTCAGTATGTTTGCATTTCTGTGA	CCTTCTCCAATTTATCAACACAGTC	60	60.3	397	29.7
NUP188	8	AAGAACCTGTATTCTTCGTTGTGTC	TACAGGAGAGCACAGTAACCACATA	60	60.1	336	33.6
NUP188	9	TCATGTTATTTCTCTCCCATTTTGT	AGTGAAAAGTACACCTACCCCCTAC	60.1	60.1	351	41.6
NUP188	10	CTCTAGTGAGTTTCAGAACGGGATA	ACACTGAAAATTTTATGCAGCAGTT	60.2	60.4	260	40.4
NUP188	11	GGAAGAGTAATTGTAATTGAGGGGT	CAACATGATCCCATTATCCACA	60	60.4	487	46.4
NUP188	12	TAATATTTGTGGTTCCTGCTTTCTC	ATAATATCAGATCCAATGGGGGTAT	59.9	59.9	371	42.9
NUP188	13	ATAGACTGGTTCAGCTAGGGAAAAT	TGAAGATTAAATGAGAAAATGCACA	59.9	60	228	38.6
NUP188	14	TCCTTTTTCAGTGGAAATATGAAAG	TTTAGAATTGAGGTGCTATCTTTGG	59.9	60	441	40.1
NUP188	15	AAGAAGTTTGAGAGTCTGGTTGAAA	TAAAAGGGGGATCTCTTTATCTCAC	59.9	60.2	247	42.5
NUP188	16	TGTGAGTTTGTGTATCTCTGTGTGTT	TTCTATTTTCTAAATCCTCCAAGCA	60.1	59.7	331	41.4
NUP188	17	GAGACTGTTCAGTGATCTTAAAGGG	TATAAAAACAGGAAAACCCTCACAG	59.7	59.8	349	48.7
NUP188	18	GTGAGGGAACCAGTTGTATTATTTG	ACCTGAGAAGGAAAGGAAGAGTTA	60.1	60.2	242	44.2
NUP188	19	ATACCTGAAGATATGTGGGCATTTA	GGCTAGATCTGAGACATATGTGGTT	60	59.9	190	47.4
NUP188	20	GAAACCTTGAAATTTCCCTATCATT	ACAAGACTGGACCTTTTCTTTTTCT	60	60.1	219	44.7
NUP188	21	TTCCTTTGGACCTATCTATGGTTTT	CCTTATCTCAAGAAAGGGAAAGAAA	60.4	60.4	302	46.4
NUP188	22	ATCATTCCTCTGTCTTTTCTGGAG	TCTGTCCACAGTGAGAAATGATAAA	60.1	60	274	47.8
NUP188	23	TCCAGTGTCCAGTAGGTTAGGTTAG	CTATACAGCAGCCACTAGGGTATGT	60	60	392	47.7
NUP188	24	GAGTTGATTACTCCTCCTCTCTCCT	ATTTATGAGCAAAAATGACTGGAAG	59.8	59.9	364	45.6
NUP188	25	ATATCTAAACTGTTTCCTGTGCTGC	CCTCATATAAACAGTGTGTGTGCAT	60.1	60.2	177	45.8
NUP188	26	ATTACTGTCTTTCCTGTGAATTTGC	AGAAGGGACAGGTAAGAGTTCAGTT	60	60.1	516	51.7
NUP188	27	GAACTGTTTCTGAACCTGGAAGTTA	GACTAAGCACTCTTATTCCCAGTGA	60.1	60.2	453	51.4
NUP188	28	GACTGTGAGAGGGAAAAAGTTATGA	CTGAGAAAGACGTTTCTAGTGAAGG	60.1	60	260	45.4
NUP188	29	GTGCTAACTTGTTCTGCAAGTGTT	ACCTTCAGTTAAAATCTCAAGAGGG	59.9	60.4	215	44.2
NUP188	30	TATTCCCATCTGCTTTCAAAATCTA	TGCTAAGGTACCAAAGTGAAAACTC	60.3	60.1	291	46
NUP188	31	TTTTACCAATGACTAATTGCCTAGC	GAAATGTAAAATCTCCCAGACACAC	59.9	60.2	207	43.5
NUP188	32	CTTTCCACTGACTTCTGACTGGT	ACCCTCCTATCTGCTATGTCACTC	59.8	60	271	55.4
NUP188	33	TTTTAGTAGAGACAGGGTTTCACCA	GAAACTCAAAAGTCCCAGAAGAAAT	60.4	60.4	403	55.6
NUP188	34	AAGGAAACCTTGGTGTACAGTGA	GCACTTCTCTCCTGCAGTACAAT	60	60	444	54.7
NUP188	35	TGTTACTCAAGCTCACTTAGCAATG	GAGGGAAAGACAGGAAATGAGAT	60	60	477	58.5
NUP188	36	ATCTCATTTCCTGTCTTTCCCTC	GATTCCTCACCATCAGTGTATTAGG	60	60.1	253	54.5
NUP188	37	GCCTTAGTTGCTGTACTACAAGGAG	CAGTGAGCCAGCAGAGTACTTAGA	59.9	60.3	390	56.9
NUP188	38	TGGTTGTACCACTAAGCCATTTC	TTGACTATGGAAGGAAACATTTAGC	60.3	59.9	459	55.1
NUP188	39	GGGTGTTACATGGAGGGCTAT	CCATTTTTGTTCTAAGGAGAGTCAA	60.1	60	258	51.6
NUP188	40	GCATTACTTACAGGTAAGCGTCCTA	AGTCAAAGGTGGGAGTGGTAAA	60.1	59.9	500	55.6
NUP188	41	AGTATGGCCTTCTCAAGATCCTC	GACAGTGTCTGACAGAACCAACTTA	60.1	59.8	358	55.3
NUP188	42	ACTGATTAAATTTGCTTAGTGCAGG	AGATGAGCAGGTAGAAGCAGTTTT	60.1	60	336	51.2
NUP188	43	AAAGTAAGTGCTCTTTCTGGGATTT	CCCTCCGTATCCCTATCCAT	60.1	60	274	56.2
NUP188	44	TCTGAGTTGGTACGGATGGATAG	TCCATTGTATAGGCCCTAGCAG	60.4	60.5	414	61.1
PAH	1	AAATAGTTGGATCTCCATCAACAGA	AGGACACTTGAAGAGTTTTTGCTTA	60.2	59.9	168	39.3
PAH	2	TTCTGACCTTTTTGTCAAGTTCTTC	AAAAGAAGTAAAATGCCACTGAGAA	60.2	59.7	380	41.3
PAH	3	GAGAACATGGGAGAGAAACTGTCTA	AGGTTTTAGATGAGCTATGAAGGGT	60.2	59.9	462	48.5
PAH	4	CCATTTCTATCTGTAAAACCCACAG	GAGTGTGCTCTCAGATTGACTTTC	60.2	59.6	318	41.8
PAH	5	GAGTAGGAAAGTTTCAAAGACCTGAG	CAAGTACTAGGTTGGTTCTGTGGTT	60.2	59.9	203	47.8
PAH	6	AACTCATTTGAGAAATTCAGGTCAC	CCTTCCTTTTCTTCTTTTTACCTTG	59.9	60	330	44.2
PAH	7	TATCTACTTGGATGGAGCAAATCTC	GAGTTTTCTTTCTTCTTTTCATCCC	60	60	341	50.1
PAH	8	CTTTCATACTTGCCTCCACATACTT	TCAAGATGTGGAATTTTTCTCTTTC	60	60	459	47.1
PAH	9	ATCATGTGTTATTAAAGGGAGGGTT	AAAAATCAGGTGTCTCTTTTCTCCT	60.2	60.1	288	47.2
PAH	10	AGTGAACAAGTACATTGCTCCAAGT	ATAGTAATTTGGGGGTTATCTGGAA	60.5	60.2	326	50.9
PAH	11	AGACAGTGTGGAGTTACTTATGTTGC	ACAACTTTTGCAAATTTAAGGACTTT	60.1	59.9	392	39.3
PAH	12	AGTTTGCTACGACATTATCCAAGAC	AATTGCCCTGGACTTACTTATTTTC	60	60.1	338	35.8
PAH	13	TTCTTACTGAGCTTATGAAACCAGG	ACACCCTTTGTAACTCTCTTCTCCT	60.2	60.1	290	54.5
PHYHD1	1	CCAGGCTCCTAAACTTTCTCCT	AGGGCTATGTGTGAAGAAGTCAG	60.2	59.8	278	64.7
PHYHD1	2	ATTTGCAGACTGGGGAAGC	CTCAAAAGCCACATCCCATC	60.2	60.5	243	54.3
PHYHD1	3	ACTTGAAGTTCTGGCTCACTGTC	ACAAAGAACAGATAAAGGCAGAGAA	60	59.9	391	55.2
PHYHD1	4	CAGTTCTCTGCCTTTATCTGTTCTT	CCGATCTTCTTTCCTGTACCC	59.5	59.9	120	50.8
PHYHD1	5	CAGAAGGGTTAATGCCTACAAAGTA	AGATGTACATGCTCTGCACCAC	60	60.2	319	59.6
PHYHD1	6	GGCATATGGTAGGTGCTCAGTAG	CCTTCTGAAGATCTGAGAACCATT	60.1	60.1	254	53.9
PHYHD1	7	GAGGAATAGGTAATGAGGCCAAG	CTTAAACTCCTCCTTTCTCAAGGTC	60.3	60.2	287	60.6
PHYHD1	8	GACCTTGAGAAAGGAGGAGTTTAAG	CTTTCTGTGACTTCACTGCCC	60.2	59.9	284	59.5
PHYHD1	9	AGGAACATGCATCTCAATAGCTTAG	CTTTAGGTGTACAGTTGGGGAAAG	60.2	60.3	462	58.9

PHYHD1	10	CTCAAGGTTGTTTCTCCTCTATCC	CAGAGAGGTGAAGATCTTAGGGAA	59.7	60.2	261	60.2
PHYHD1	11	CAAGAGCATCACACACTCCTTC	GATCAACTAAGTTCCAGGTGCTTTA	59.9	60.1	337	53.7
PLTP	1	GAATTAAATTGGGTACAGCTTCAAA	TAACTGAATGAATAAATGAGGCTCC	59.8	59.9	309	55.7
PLTP	2	AGTCTAAGATTAAAATGGGAGGGG	GTGTGAGGATGGAGGAAGAAAG	60.1	60.1	274	60.9
PLTP	3	CTTTCTTCCTCCATCCTCACAC	AATCTATTCCAACCATTCTGCACT	60.1	60.3	284	58.5
PLTP	4	CGCAGGTGAGCAGTTATATGAG	AGGATACCTGGAAAGTTGTAGCAC	59.9	60	281	59.1
PLTP	5	CTCTCAGTGGCTTACAGGTATCACT	TGACCTTCTGGGTCAGTAACATC	60.2	60.4	216	59.3
PLTP	6	AGGATGTTACTGACCCAGAAGGT	AAGGCTAGATGCAGATGTGAGAG	60.3	60.1	418	59.1
PLTP	7	GACAGGAACAGCCATGACAA	GTATGTGGCCTTCTCTGAGTTCTT	59.7	60.2	385	61.8
PLTP	8	GAATCAGGAGTGAGGGAGTGAG	CCTTTTAAGAGATGTGCTTGTGAAT	60.3	60.1	403	60
PLTP	9	AAAATCTTGCAACTTAGCAGAGAAA	TTAATGAGCACCTAACTACACACCA	60	60	346	49.7
PLTP	10	CTGCACACCCAGACTCACC	CACAGGAAGGTGTATGATTTTCTCT	60.3	59.9	251	61
PLTP	11	AGAGTCAGGGCCTTCTCAAAG	ATTTCCCTAGTCACTGATTTCTCCT	60	59.9	217	57.6
PLTP	12	CAGATGAGCTGTGGGGCT	AACCTTATTAAGAGGTATGGTGATGC	59.9	60.1	297	57.2
PLTP	13	TCCTGACCCACTCTCCACTC	ACTTTGAGCCACCCAAGTCTAA	60.2	60.2	342	55.8
PLTP	14	CCATCCGGTTTCTTAAGTCTTG	TAAGTAAGGGTTTCTCTGCTGCTT	60	60	274	60.6
PLTP	15	GTTGTAGTAGAAGTGGCCTTCTTTG	TTTAAGCGGCTCAGATAACTCC	59.8	59.9	348	63.5
PPP2R4	1	ACTTTAACTCTCGGTTTTCGGTTAT	CTAAGGCCATTCAACTCAGTCC	59.9	60.1	340	66.2
PPP2R4	2	TGTGTTGTAGGGGAGGATTCTATT	TAAAGCATCTCTGAGTACTGCCTCT	60.1	60.1	338	46.7
PPP2R4	3	GTCAGGGTCAGGAGAAGTAGAAAG	GACTCTGGAGCTATTTTTGGAAAG	59.8	59.8	262	57.3
PPP2R4	4	ATATTCAGAACAGTGGGGAAGAAA	ATATGCCTAGAAGCGCTATACAATG	60.2	60.1	381	55.6
PPP2R4	5	CACCACTTTGTGTCTCTTGTGTTAC	AGTGAAGCTAGATAAGTACAGAGCCC	60	59.9	188	53.2
PPP2R4	6	ACTAAAACAATCCCAGTCCTTTACC	TTGCTTTTACTTGGAGGTTAATTTG	60.1	60	361	50.4
PPP2R4	7	TTTTTACTTTTTGCTACCTTCCCTT	ACAGTAAACAGCCTCCCTCAATAG	60	60.1	337	56.7
PPP2R4	8	TTACTTATTGCTCCTTCAAGGTGAG	TGGCTCTTCTGATCCACTGTAA	60.2	59.9	333	57.4
PPP2R4	9	AGAACCTGTCTCTTCAGCTTGTG	GGTTCCACATCTTTTGCTTTGT	60.1	60.4	227	56.8
PPP2R4	10	GTCTTTGGATAGAAGGAGTGAGGA	AGTAAACAGCCTCTCATCAAACG	60.1	59.8	368	63.3
PPP2R4	11	ACCTCTGACTCCGATTCTACTTCTT	CCTGGCCTACACTAAACATTTTAAC	60.2	59.4	588	43
PROC	1	GCTATGTCTCTAGCGAACAAGGA	TACCTGGGACTTGTCAGTTGATT	60.1	59.9	400	62
PROC	2	CTAGAATTAGAATGAGTCTTGAGGGG	AGCTTCTTCCTGAATTCTGTTTCTT	60	60.3	505	58.6
PROC	3	CTGTTTGTCTGGAAGCCCTC	GGGGATCTAGAACGCACTCA	59.8	60.2	163	71.2
PROC	4	AGTGCGTTCTAGATCCCCG	CTAGGCAGTAATGCGTGCAG	60.2	59.7	386	71.5
PROC	5	GAGGGGGAGAGGTGGATG	CCTCCCTAGAAACCCTCCTG	60.4	60.1	339	71.4
PROC	6	TGGAGTGGTCTAAGTATCATTGGTT	GTTTCTGCACCCTGAGCATAG	60.2	59.9	368	60.1
PROC	7	ACACTGTAAAATGGGCAAAAATAGA	AAAATACTGGGTGTACATGGGTG	60.2	59.9	466	58.6
PROC	8	ATAGGGTTCCACGGCATAGAC	CTTGTTACATGTCCCTTTAATGTCC	60.2	60.1	848	62.6
PROCR	1	GTCCTCACTTCTCTTTTCCCTAGAC	AATGTACTAACTCACCTTGGCTTTG	60.2	60	347	56.5
PROCR	2	GCACATTATAGTTTATGAAGGGTCG	GGACAACTGCCTCTCTCCAG	60.2	60	561	67.4
PROCR	3	ACTCTTGCCTTCTCATGTTCTTTT	CTTCAGGTCCATCCATTTGTCT	59.8	60.4	448	58.3
PROCR	4	GCAGCTTCAGTCAGTTGGTAAAC	GAGCTGTCACTCCAAACCTTCT	60.3	59.9	357	54.6
SH3GLB2	1	CTGTGTCACCAACAAACAAGTTAAG	ATATCCAGCTCTGAGGAAAGGAT	60	59.6	383	59.5
SH3GLB2	2	GAGCTGGATATGCCCTCTTTAAC	CTGCTAAGATGTATCCCTCCTCTC	60.5	59.8	406	66.5
SH3GLB2	3	CCACTCCACCCTCATACACAT	GAGGTTAGAAGTCAGCCTCTGG	59.7	59.5	304	61.8
SH3GLB2	4	TGCTGAGGGTTAGGTTTAGTGAG	AGGTAGGCTCCAGGAGAAGACT	59.8	59.9	209	62.2
SH3GLB2	5	GAGAAAACATTTCCCCACAGAG	GCATGTTAGAGGGACTGGGA	60	60.1	396	64.4
SH3GLB2	6	TCTAGCTCCTGTGCAGTCAGAG	GTTTGTGTTGTGTTTGTATCCCC	60	60.4	292	62.3
SH3GLB2	7	GGAGAGAGGTCATGCCAAATAC	GTGCTGGGGCTACAAAACTC	60	59.7	379	61.7
SH3GLB2	8	TGGAAGAGAGCCTGTACTCAAAG	CCTCTCCTGTAGATCAGAGTAGCC	60.1	59.9	282	55.3
SH3GLB2	9	CAAAACTGGTTAAGAGAAGATTCCA	GTATAGTGCTGGGTCAATCACAAC	60	59.8	484	50.4
SH3GLB2	10	CCATTTTCTTTTAACTGTCCCTCTT	AGTATCACACTCAGGGCTGGTT	60.3	60.1	452	60.4
SH3GLB2	11	AGCAGGGTAACCCAACCAG	CTCTAGCTCCGCCCCACT	60	60.5	592	78.4
STEAP1	1	TTTTTATTTTTACAGGTGGCTGAAG	TATCAGCAGACTAGGGTGAAAAATC	60	60	246	28.5
STEAP1	2	CTAAAGACAAAAGTCTTTCAGTGCC	CTCAATATAAAACCGACTGACAACC	59.9	60.2	879	37.1
STEAP1	3	GACCTGTTATCAGGGCTTCATAGTA	GAAAACAACAGGAGAGCACATTATT	59.9	60	432	35.4
STEAP1	4	TATTGAACCAATCTTCACCAATTTT	TTTTGCTTTGAATAAAATCTGCAA	60	60.1	468	31.6
STEAP2	1	CTAGGATATTCTTGGTGATCTTGGA	TTGGAAAGTGTCAGAGTTTGGTATT	59.9	60.3	629	37.8
STEAP2	2	TGGTAATGCTGAGTCTTTTTGTTTT	GCAGTATACCAAAATCAAATTTCCA	60.4	60.4	676	38.5
STEAP2	3	AGCAGTATCATCCAGTAACAGGTTC	TTCACTTATTTAACCAGAGCAATCC	60	59.9	505	37
STEAP2	4	TCAGTAGAGGACAAAGGTTAACTTGA	ATTTAACAAGTTTCAACCCACGATA	59.8	60.1	551	35.6
STEAP2	5	TCAGTAGAGGACAAAGGTTAACTTGA	CTTCTTCCAGAAATTGGCTCTTT	59.8	60.2	382	33.8
STEAP2	6	TTATTGAATTTCCATCATGCATTC	TCAATAGGAAGACAAATTCCAGTTC	60.1	59.9	220	35.9
THBD	1	CAGTTAGCCATGGAATAGAAGAAAA	GAGTGCCACTGCTACCCTAACTA	60	59.9	836	64.6
THBD	1	AACCGTCGTCCAGGATGTAG	TTCCTCTGCGAGTTCCACTT	60	60	817	68.3
THBD	1	GCACATTAGCTGTAAGCCGAG	CACTTATAAACTCGAGCCCTGG	60.1	60.1	871	69.8
TRPA1	1	TTCTGCTTCTTCCTCACTCTTTTTA	GGTTAAAACCTATGCCTTCCTACAT	60.1	60	384	40.1
TRPA1	2	AATAGTGGCAAATATGTTGTTGGTT	TGCTTAAGAAAAAGTTCCTGAATTG	60	60.2	346	26.9
TRPA1	3	GGTTAACACAATGAATGAATGTCAA	ATTTTGCTGTATTAATGATTGCCTC	60	59.8	273	36.3
TRPA1	4	AAATGCCCATTTTTGACTTGTAATA	TGGACCATTCAACTGTAGTGATTTA	60	59.8	203	38.9
TRPA1	5	TTTCAAATGATCAACAAACAGAAAA	TTCATTGTAGAAACTTTGCATTTCA	59.9	60.1	278	36.7
TRPA1	6	TAATTCACAGCGACAAAATCAACTA	TGTTTTCTTTTTCAAAATAACTGGC	60.1	59.9	315	30.2
TRPA1	7	TTGAAACAACTGGAAAAGGAATAAG	TAACCATCCATAGATGCTAGGTCTC	59.9	59.9	344	32.8
TRPA1	8	TTCTGCATATGAAAATATGTGCAAC	TTTTCTGTTTAACTCAAAGTGGACAG	60.3	60.1	283	25.4
TRPA1	9	TCCTGATATGTCAGATTTATTATGGG	TTTACCAACAAGGTTTCTGAAAGAG	59.5	60.1	367	30.8
TRPA1	10	TTTGAAGGCTTTGTAATAGATCCAA	ACCAAACACAGTTATAAAACCAGACA	60.3	60.1	233	30.5
TRPA1	11	TGTATCAAAACATTTTAGAACCCAAC	TTTGTTCAAATCACTTAATTTTCAGC	59.6	60	406	28.3
TRPA1	12	ATTAAAATATTCGGGGAAAACTGAG	TTCCTAATATGTAGTGTACTGCCCC	60	59.7	304	28.9
TRPA1	13	CAACAACATATGTCAAGCATAAACC	TGTTGTACAGAACAGAAGGATGAAG	59.7	59.7	207	33.8
TRPA1	14	ACTAAATGACAGTGGACAGGAAGAC	TGTCTTTTAAGCAGTTAAGCAGTGA	60	59.7	280	45
TRPA1	15	ATAGAGCAAGGAAGGTAAAAGGTGT	CAATAATGCTTTTTGTTGTCATCAG	60	60	329	43.5
TRPA1	16	AAAAGATAGCCTGAAAATGGCTAAT	TCCAAAAGCAAAGATAAGAAATCAC	59.9	60	358	38.5
TRPA1	17	ATTCAGAAGCCTCGTATCACTTATG	AATACATATTGACCCTTGTTGGAAA	60.1	59.9	427	37.5
TRPA1	18	AGTTAATGGCAATCCACAGATATACA	ATACAGACACACACACACAGAGA	60.1	59.7	330	29.1
TRPA1	19	AATGTTCATCCAACCAAATTGAG	CTAAGCTCTTTGTTGAATGGTTTGT	60.1	60.1	197	37.6
TRPA1	20	TCCAAGTATGTCAATCATCATTTTG	TGAAAATGCTACCCTAATCAGAATC	60.1	59.9	381	23.9
TRPA1	21	TTCACTCATGAAGATGAAAAATCTG	ATTTTATGAACCTGGGAAGAAAAAG	59.7	60.1	288	38.5
TRPA1	22	TGAAACTTGGGATATTCTCTTGTTC	TAAACACAAGCTTTTATGTGTCTCG	59.9	59.8	439	33.5
TRPA1	23	TCAAATTAATAGCATCCACCAAAAT	TTTTTCATTTTGTCTTTTCTTCCAG	60	60	201	32.3
TRPA1	24	CATGAAAAGATAAAGAAAGCAGACAG	CATGATTATTTCATCTAATGGGGAA	59.9	60.3	351	35
TRPA1	25	GTAATAATTGCATTTTGTTTGCCAT	ATATTCCCACTAGGTTCCCATTAAA	60.3	60.2	488	43.2
TRPA1	26	TAATTGAATGGGATGAATGATTTCT	CATAAGTTTTGCATATGCTTGTTTG	59.9	60	260	34.2
TRPA1	27	GGACAAACAAGCAAACAAAATAGAT	AACTCCTTCCAGAAGTTCTCCAG	59.8	60.3	494	63.3
TRPC3	1	CACTGTAATGTCAAAGCAGACAAAT	TTCATTTCTAAATCCAAAGAGCAAC	59.7	60	401	31.4
TRPC3	2	TTAGAGGCATCCAAACTATAACCTG	GGTGGATTATGCAGTAAGTCTCAGT	59.9	60	393	33.3
TRPC3	3	TGTTGAATCATTTTCTTTGTTCTGA	GACTCCAGAAATGTTATCAAGGAGA	60	60	330	32.4
TRPC3	4	GACTCAGTGACTTCTTGAAACATCA	GAGGCATATGAAAAAGAATGAGTATCT	59.8	59.5	594	31.1
TRPC3	5	CACCTAGAAGACAGCAGAATGTGTA	TCTTGGAGTATATTATGGTGGCATT	59.9	60	512	35.4
TRPC3	6	AGAAATTTTTCCTTTGCTTCCTCTA	TGGTTTAAGATGAAAATAGTCCCTG	60.1	59.8	510	37.5
TRPC3	7	AAATGTGGTTCCAATACCTTTCC	AGTGACCATACAGTCAGTCAGTCAA	60.3	60.1	444	45.9
TRPC3	8	ATGTAGTGTTAAGGGACACCTTTTG	CAAACTTTTCCTCTTTGGTTTGTTA	59.8	60	439	36.2
TRPC3	9	TCTTGAATCAATTAACATTCAGGGT	AATGGAGGGAAAGCTAAGAAGAATA	60.1	60	458	42.6
TRPC3	10	TTTCCTAGGATTATGGCATAGTTTG	TTCTAATTCACCCAAATACTTTCCA	59.8	60.1	340	40
TRPC3	11	TGAGAGGGAGAAAGAAAACATTAGA	GCTGCTCAAGAAGGAGAACCT	59.8	60.1	666	59.6
TRPC3	11	ACCACTTCGTATTTCTGGCAGT	TTTATCGTTGCTACTGATTAGGTCC	60.1	59.9	552	62.9
TRPM5	1	GTTCCTTTGGGTGAGGGTCT	CTTTCCTAGTCCCAGGAGTGC	60.3	60.3	462	66
TRPM5	2	AAGGCAGAGCACACAGCAC	TCTCAGAGGGAGGAGTCACAG	60.2	59.6	284	66.9
TRPM5	3	CTGCCTCATCTCTGTGAGTGAC	CATGAGGGAGGAAGGGAAA	60.1	60	311	64.6
TRPM5	4	CAGCTCAGATCCTCTGTCACTG	CATGCTCTAGTAATGCTGGCTG	60.2	60.1	262	60.7
TRPM5	5	AGGTCTCTCCAGACCTGCCT	GAAGACCCAAGGAGAGTGGAC	60.4	60.1	446	65
TRPM5	6	CAGGCTATGCCACCTTCTATCT	TCTGGTTCTGGTTTGCTGTG	59.8	59.9	502	61.2
TRPM5	7	GACCTCTCTGGAGAGCCTCAT	GATCCATATCTTTGCCATACACAA	60	60.1	432	64.4
TRPM5	8	GCTCAGAAAGAAGAGGAAGAAGAA	ATCAGCCTCCCATCCTCC	59.8	60	297	63.6
TRPM5	9	ACCTGAGTGGCTTCATCTGG	ATAGATGGAACCCTGATCCTTACA	60.3	60.1	295	59
TRPM5	10	ATGCTGTTCTTGTTTTACAGTTGG	CTCACCACTGCGAACTTCTCT	59.6	59.7	404	62.9
TRPM5	11	AGAGAAGTTCGCAGTGGTGAG	CTGGTGGTAGCCTGACTCTGTAG	59.7	60.4	369	68.6
TRPM5	12	CTACAGAGTCAGGCTACCACCAG	GCAAAGGTGCAGAGTTGGA	60.4	60	265	64.9
TRPM5	13	GAAGTCAACTCAAGCTGGGC	GACAGAGCCGGAGAAGGAC	60	59.9	422	70.4
TRPM5	14	GAGCCGTCTGTCCTCTCCTA	ACGAGATGGCCACCTACTTCT	59.6	60.1	377	71.4

TRPM5	15	ACATCTCTTTGAGGATTTTGCAG	GAGGCTTCTACCAGGACGG	59.8	59.8	381	70.6
TRPM5	16	GCTCTTCTGGTTCAGGTCCCA	CTGTCTCTCGCTCACTCTCTTGT	60.4	60.4	542	69.4
TRPM5	17	ATGATGGGGAGGTGGGTAG	GCTTTCTCCTGCGGTTTGTA	59.6	60.4	348	62.9
TRPM5	18	ATAAAACTTGCCAAATACAGACAGC	AGGGAGCAGAGAGACCCAG	60	59.5	461	64
TRPM5	19	ATTGCAGGAACTCTCCCAGA	CCTGCATCCAGATGTCGTC	59.8	60.2	331	64.4
TRPM5	20	AGATCCTCTGAGACGGGGA	GTAATAAGCAGCCTGTGTCACG	59.7	59.8	396	63.1
TRPM5	21	AGACAGCTCCTCCTCCCAG	TCCTTTTGTCTGAAGGGTGG	59.5	60.1	535	68.8
TRPM5	22	CCGTTCCCTATGCGGTACT	CCAGGTAACTGGCTGCTGAT	60	60.3	440	69.1
TRPM5	23	CCTGGAGAGTCAGGGGGT	CTCCCAGTGCCCAGTGTC	60	60.3	497	69
TRPM5	24	CTCTGGAACTCTGCCTGTCTG	CCTGGCTGGAGAGAAGGTC	60.2	59.9	462	65.4
TRPM8	1	GTCTTGGAGGGTAAAGAGGAATTAG	CACTGAGCATTAAGTAGTGAAAGGAA	59.9	60.2	445	48.5
TRPM8	2	TGTGTTATTCAATGTTCTCTCTCCA	AGTAACAACTATAAGCTCCTTGCCA	60	59.8	273	36.6
TRPM8	3	AAGACTTGAAGGTATCCTTTGTGTG	TTCCTGTTGAGCATAGCCTAATAAC	60	60.1	452	43.4
TRPM8	4	GAACACAGGCCTATCCTGATACTT	TTTGAGGATATGGCTTTCAATAAGA	59.9	60.3	374	54.5
TRPM8	5	TGACCATTTACTCTTCCTATTTGTTG	AACTCTTTCCCAGCAGTTAATTAGG	59.8	60.4	399	51.9
TRPM8	6	TCTCAAAGACAAGTTTCCCTGTACT	GTTCTTTGGCAATAAAAATACCTGA	59.8	59.8	339	44.2
TRPM8	7	CAACTTTTCACAGAGGTAGGTGAGT	CCAAATCTTCTTGACTGAGGAATAA	60.1	60	322	38.2
TRPM8	8	AGGTCTCTGATCTGTCTGACTCTGT	TATCACACTTGGTGAGTCACGTATC	60	60.3	424	51.7
TRPM8	9	GTTGGCTGACACTTTGTTCTTTAAT	AGAAATGTAAGTCATGAAAAGCCAC	60	60	209	38.8
TRPM8	10	GAATGACAGTTTGAGTGTCTGAATG	AGATTTGGTATTGAAGACCTTGTTG	60.1	59.8	362	47
TRPM8	11	AGGTTTGAACTGTAATCCTCTGTTG	GCAGAGACTCACCCTATAGACAGAC	60	59.9	671	42.2
TRPM8	12	GAGATGAAAATCCCATCACTGTACT	ATATTTGGTGTAAATCTGATGTGGG	59.8	60.2	280	49.3
TRPM8	13	GGCAGTAGAATCACTTGAACCC	ATTCTTGGAAAATTCCATATGTGC	60	60.4	498	51.6
TRPM8	14	GCATTTTCTATGCCTTTTGTAAGAA	AAACCACTCCTTCTATGGCTTTTAT	60	59.8	416	49.3
TRPM8	15	CTTAGAATCCAGGCAACTGGTATAA	AATGTAAACATCATAAGTTCCAGGC	59.9	59.7	387	40.1
TRPM8	16	TCCTGGCTATGGGTCTGTATTTA	GACTAGCACCCAAAGAGAACATTTA	59.9	60.1	459	51.6
TRPM8	17	TGGCATATGAAAGAATAAACAAACA	TCCACTTTTGTAGTCAAAACACAGA	59.8	60.1	282	39.4
TRPM8	18	TTTGGAATGTTTTGTCAATATCTCA	GAAATACATCAAAGAAAGCGAATGT	59.8	59.9	333	37.5
TRPM8	19	AATTAGTCAGTGAACTCTGGGTGAC	AAGAGGTTTTGAGGAGTGAGTTTTT	60	60.1	473	57.5
TRPM8	20	CTATGACTTGTTTGGACAAAGTGC	CAGTGAACATGTGACTGAACACATA	60.1	60	347	52.7
TRPM8	21	GAGTTATTTTGGCTCGTGTATCACT	TCTCTAGAGTAATTCATTGGTTGGC	60	60	515	46.4
TRPM8	22	AAGCCATTACTATTCCATCACTCTG	CCTACGTTCTATGGGCTTATGTCTA	59.9	60	348	41.4
TRPM8	23	AATAGCCCTCTCTCAATCTGTTTTT	CCCTGCTCTTAGACAGTGAATTAAG	60	59.9	231	33.8
TRPM8	24	AAATATCACATGCCACTCTCATTCT	CTTAAAAGATGCAAATCTTCAGAGC	60.3	59.9	305	31.1
TRPV1	1	ACAGCTTGTCCAGCACAGATT	CAAGAAGTGAATGTTTGTTTTGTTG	59.9	60	378	54.8
TRPV1	2	ATGAGTGAGGTGCTCAAGTCAG	GTGTCCAAAAATCAAGTCCTCTCT	59.5	60	448	63.6
TRPV1	3	AGATGAGATCTAAGATGGTCCCC	CCCTTGTATACAGTGTACCCCC	59.8	59.5	504	61.3
TRPV1	4	CTTTCTGCTCCCTCCTCAAAT	GGGATGCTTTAAAAATAACTTGTCA	59.8	59.8	639	57.6
TRPV1	5	TTAAAGCATTTTATATAACACGTGGC	CTGAGAACCAGCAAAGCAAAC	59.8	60	386	56.7
TRPV1	6	ATTGCTTGATTCTTGGAAAATAGG	CAACCCTAGCTCCTATTGCG	59.9	59.9	435	58.6
TRPV1	7	GACTGGGAATGAGTCAAAGTGTC	TTTTTAACCATCTCTACTGACTGGG	60	59.9	296	48.6
TRPV1	8	TTTTGTTTTGGTGATAATGGAAACT	TAACACACTGTCTTTGTGTGTCCTT	60	60	281	45.9
TRPV1	9	ATACGAGGTTCTCCACGTTCTC	GCTCAGACCTCCCATCTCAC	59.6	59.8	457	62.1
TRPV1	10	ATAATCACGTATGGTTGCTATGCTT	CTGGTTGTTGAGGTACTGTCTGAG	60.2	60.3	445	63.4
TRPV1	11	TTTCTCAGACTTATTCTAACAGCCCT	GATTCTACTTCGGTAGGGAGACAG	60.2	59.7	615	60.3
TRPV1	12	TTAGCAAAAGCCAAAAAGATCAG	CACTTTCTGCCCAGTTCCTC	59.9	59.8	306	60.5
TRPV1	13	AGTAAGGATCCCAGAGAAGCAAG	TATGATCGCAGGAGTATCTTTGAA	60.3	60.1	439	60.8
TRPV1	14	TGTCTCAGGGTCTGAAAGACATAA	TATATCATTTTTCCCCTTTTTGGTT	60.2	60.2	370	57.6
TRPV1	15	CTTTGTGACATTTAGCCCAGAAG	AGTCCTTACTTTGGGAGTCAACC	60.2	59.9	457	62.8
TRPV2	1	GAAGACAGGACCCTTGACATCT	GAAGCCTCTGGAAAGAGCAAT	59.6	60	470	60
TRPV2	2	GTGTGTACAGGACTCCCTGAAAG	ACTATCAGCTCACAGGATGCCTA	60.1	60.3	284	57.4
TRPV2	3	TGTGTAGCATCTCTTTTAATCCTCC	GCCTGGACAAAAGACAAACTG	60	59.8	586	54.1
TRPV2	4	GTAAAGAAGCCTGACCTGTTTCA	CAGAAATTTTGGGATGAGACCTAC	59.8	60.2	478	59.2
TRPV2	5	GCGTGTGTGTGTTTAAGAGTTTAGA	TTGGATGGGACTAGAGTATGGATT	59.8	60.1	545	57.6
TRPV2	6	CAAGCCCCTTAGTCACACTGTAG	GCACTATTACTGCCCCATCTTC	60.2	60	425	55.8
TRPV2	7	CCTAGGTCTCATCTGAGTGTGTCTT	AATTCTAGGTTTGCTTCTTGGTAGG	60.2	60.4	172	57.6
TRPV2	8	CCAAGCTATCTCAGCTATCAGAAGT	AGAGACAGTTGAGAGAAGGAGGAGT	59.6	60.5	267	55.1
TRPV2	9	GTCAGGACCTTGGTCAGCATA	TACTTAAGCTTCCATCCAGCAAG	60.1	59.9	397	58.7
TRPV2	10	ATATGTATGTGTGCGTATGTGCAG	GTGTACAGGGTGGACAAGGAA	59.9	59.9	247	59.5
TRPV2	11	GATCTACTTAGTCTTCCTTTTCGGC	CTGACAAGGTAGAGCTGCCC	60.2	60	612	63.2
TRPV2	12	GCGTTATACTGTGAAGTGCTGC	GAGATCCAGACCCCTGACCT	60	60.5	403	62
TRPV2	13	AGAGAAAAAGCCTGTCCTCCTC	GTTTTAAGGAGGCAATCCCTCTA	60.4	60	388	60.3
TRPV2	14	CTACAGTGCTTGCCATCTGTTTAC	ATATATTTGCCACCAGAATTCACTG	60.2	60.5	226	54.9
TRPV3	1	CACTCAGACAAATTGACAACTGC	AGAGGGAAACTCCATCTCAAAAA	59.8	60.5	383	46.5
TRPV3	2	ATGTCACCTCACAGCGACAG	AGGCACTGGTGAAATAGTAAGAATG	59.9	60	144	47.9
TRPV3	3	GTAGCTGTGGTTATGGTTAGCAAGT	TTGAATTCTGTAGATTAGCCAAACC	60	59.9	374	52.4
TRPV3	4	CTAGGCTAAGGCCTCCTCAAA	GCTTGTAGAGTAATTACCAGGCAGA	60	60.2	491	55.6
TRPV3	5	TATAAAGGTAATGCTTGGAAAATGC	CTTGCACCTTACACTTGAATTATGTT	59.8	59.9	259	35.9
TRPV3	6	GGTCTTGACACTTAAAGCCTGG	TCTACAGGCTGAATTCTATGGTAGC	60.2	60.2	515	53.6
TRPV3	7	AGTAGGATATTTGTTCAAGAGGCG	GTGCACTGTTTCTTTCCTTCCT	60	59.8	199	54.3
TRPV3	8	GAGAGGGATGGAGGCTGTC	TATACTGACCACCCCTCTTCTTTC	59.7	59.9	201	62.2
TRPV3	9	TGAAGACATATTCAGTTCCCTGG	ATGGTGACTGGTGGCATTCTA	60.4	60.4	349	57.3
TRPV3	10	ACAGAGTGGGGTATGCAGATG	ATTCCACAGATAAAGACGGGG	60	60.2	477	61.6
TRPV3	11	CTGAGGCTGTGGTTTGTGAAT	CATCCTGCTGAGATAGGATATGG	60.2	60	487	63
TRPV3	12	CTTCCTTCCTCCTTCCCTCTT	AAGGAAGCAAAGAACAAAGCTG	60.2	60.1	428	67.1
TRPV3	13	AGAGACTCCTGTCTGCACAGC	GTAAGGTCTGGGAGTGGAGATG	59.8	60	347	59.9
TRPV3	14	CTGCCAGGCTCAGACACTC	GTGTTGAGTTGGAAACATTTTCTG	59.7	59.9	207	57
TRPV3	15	AATTCAATACTCCACTCCTTCCC	AAAACTTTAAAACCCTCTCTGTTCC	59.7	59.5	309	56.3
TRPV3	16	ACCCAGGGCAAGTCACTG	GACACAGGCAGACAGGCTC	59.7	59.5	246	61
TRPV3	17	AGAGTCTCAGGTCTCCCCAAG	CAGCTTCTCTGTCCTTGAAGAAG	59.9	59.8	394	61.9
TRPV4	1	ACTAGAAATGAGTGGGCAGAGAAG	CCTCCCTCTGATGTGCTCTC	60.3	59.9	229	63.3
TRPV4	2	ATTCACAAGCAGCAGAGGAAG	GCATGGAGAGCGTCTCTGA	59.6	60.2	324	58.3
TRPV4	3	GAAATTGCAATGGGTAGACGA	TGTCTAGTGGGGAGTAGGAGTCTAA	60	59.7	359	64.1
TRPV4	4	AGAAGACACTGCTTGCTCAGAGT	TCAGTGAGTGCCACCCCTA	59.9	60.3	456	59.9
TRPV4	5	CCCCTATACATCATGGCTACTGTT	TGAGAAACCATGTGTCTCCTCTT	60.5	60.2	193	53.4
TRPV4	6	AGGAGACACATGGTTTCTCACTTT	TGCTAATCCACTTTGTTTCTTTTCT	60.4	59.7	504	57.7
TRPV4	7	TAGCAATCAGAATTTTTCTTGAACC	GGAAAGAGTCCTTTGTCTTTTCTCT	60	59.8	396	51.3
TRPV4	8	GAGAAGAGAAAAAGAGGGAGAGAAA	AAGACTCAGGAGGAAGAGAGTGAA	60	60.1	314	60.8
TRPV4	9	TTCACTCTCTTCCTCCTGAGTCTT	AATAGGGTGGAAAGGTACATTGAG	60.1	59.7	550	61.3
TRPV4	10	GACACTGTTCTGGGCACTTAGTT	GCAAGAATTAAACAAGATGAGGAAA	59.7	60	494	60.9
TRPV4	11	AGAGGGGTACGAGTAGGTGGA	AGAGAAACGTGCAGTTCATATCC	60	59.7	495	62.2
TRPV4	12	CAACCAGTATCATGCTATCTCCC	GAATATCCAAGGACCTATTTGCTG	59.9	60.2	376	62
TRPV4	13	CAGATCAAAAGTCTCAGGAGTCAG	GTCATCTTGTGTGTCTCTCTTGCTA	59.6	60	265	59.2
TRPV4	14	AAGAAAGAAGCTGAGGGGAAAG	TAGTTTTTACATCTGCCCCAACTAC	60.4	59.9	419	60.9
TRPV4	15	ATAGATAGAGGGGTGGATGATGAAT	CTGTCATTACAACGGTGGCTT	60.3	60	620	61.5
UGCG	1	CCTTTCCTCTCCCCACCTT	CTGACGATCAGCTTTCTCCAC	60.4	60	353	68.3
UGCG	2	TGGTTCTACTTCCCTTCATGTTTAG	TCAACCTATTTCTGTTCTGTGATGA	59.9	60	473	33
UGCG	3	TTATCATAAGTGTTTGCATCCATTG	AACACCTCTCAGTACTCCAACAAAC	60.1	60	392	31.4
UGCG	4	TACAGTTTTCCTTTTGAGAATGGAC	AGCATAACTGGACATATTACCATGAA	59.9	60.1	445	24.3
UGCG	5	CCCTTTTGAAATTTTGTATTCTCCT	ATACCTAATTCCAGCTCCCATAGTC	60.1	60.1	388	35.6
UGCG	6	GAACACCATGCTTTTAACATGAAAT	AGGTTGAACAAAAAGAATAAACCAAC	60.5	60.1	309	36.2
UGCG	7	TTGCCTGGTCTTTATAATGATTACTG	TCTGCAACTAAACAAAAATCTTCAAC	59.8	60.1	308	34.1
UGCG	8	GAATGGTCTTTCTATCACAGGGTAA	TAAGTTTTGCATCAACATTCCACTA	59.8	60	469	37.5
UGCG	9	GGCAGTTAAATTACATAAGGAAGCA	AAGTGCCATGCAAAAATAAATTAAA	59.9	60.1	454	32.8
UGT1A10	1	CTGTACTTCTTCCGCCTACTGTATC	ACAATTAAGCCACAGGTATCAAAAG	59.8	59.9	541	47.3
UGT1A10	1	AGGAGTTTGTTTAATGACCGAAAAT	TAAACTGGAAAGAAATTTGAAATGC	60.5	59.9	604	41.1
UGT1A10	2	GAAGGAAGTAAAGGAGAGGAAAATG	AACCTTTGGATTAATAGTTGGGAAG	60	60	456	36
UGT1A10	3	CTGTTAAAGACTGTTCCTTCAGAGG	CAGAAGAAAATGTGGGTTGAGATAC	59.9	60.3	362	41.4
UGT1A10	4	CATGTGAGTAACACTGAGTCTTTGG	ATTTGAAACAACGCTATTAAATGCT	60.1	59.5	428	41.1
UGT1A10	5	AAAGAGAGGATTGTTCATACCACAG	CACTGATTCTGTTTTCAAGTTTGG	59.9	60.1	432	50.7

Supplemental Table 4. Coverage statistics per sample for validation phase.
Precentage of all bases that had a sequence depth of 1/5 the mean coverage or greater, less then 5 times the mean, and fell between 1/5 and 5 times the mean.

			Proportion of Mapped Bases		
Sample	PCR Method	Mean Coverage	>1/5 Mean	<5x Mean	> 1/5 & <5x
NA11832	Traditional	294	93.5%	100%	93.5%
NA11832	Microdroplet	274	89.93%	99.91%	89.83%
NA11992	Traditional	235	92.78%	99.96%	92.73%
NA11992	Microdroplet	188	89.95%	99.98%	89.93%
NA12006	Traditional	247	93.46%	100%	93.46%
NA12006	Microdroplet	186	90.08%	99.98%	90.06%
NA18505	Traditional	242	91.16%	99.97%	91.13%
NA18505	Microdroplet	193	90.03%	99.96%	89.99%
NA18517[a]	Traditional	165	91.06%	99.91%	90.97%
NA18517[a]	Microdroplet	82	89.14%	99.98%	89.11%
NA18489	Traditional	271	94.88%	99.98%	94.86%
NA18489	Microdroplet	342	91.77%	99.9%	91.67%

a - NA18517 had fewer reads than the other 5 samples for both traditional and microdroplet PCR. This

Supplemental Table 5. Discordant variants between sequence data and HapMap genotypes in validation phase.

					HapMap Alleles		Sequencing Alleles						
Method	Sample	Chr	Position	Reference Allele	A	B	A	B	Variant Quality	Neighbor Quality	Base Frequency[a]	Amplicon	Amplicon[d]
Microdroplet	NA11832	2	234519279	G	G	G	**C**	**G**	213	62	46.31	TRPM8_6_1	
Traditional	NA11832	2	234519279	G	G	G	**C**	**G**	209	62	52.12	TRPM8_6_1	
Microdroplet	NA18505	7	27169710[c]	C	**C**	**G**	C	C	49	40	65.91	HOXA9_1_1	
Microdroplet	NA11832	7	89628111	C	G	G	**C**	**C**	209	62	90.43	STEAP1_2_1	
Traditional	NA11832	7	89628111	C	G	G	**C**	**C**	255	62	80.33	STEAP1_2_1	
Microdroplet	NA11992	7	89628111	C	G	G	**C**	**C**	165	62	80.34	STEAP1_2_1	
Traditional	NA11992	7	89628111	C	G	G	**C**	**C**	255	62	84	STEAP1_2_1	
Microdroplet	NA12006	7	89628111	C	G	G	**C**	**C**	255	62	90.79	STEAP1_2_1	
Traditional	NA12006	7	89628111	C	G	G	**C**	**C**	255	62	86.08	STEAP1_2_1	
Microdroplet	NA11832	7	89628477	C	G	G	**C**	**C**	255	62	100	STEAP1_2_1	
Traditional	NA11832	7	89628477	C	G	G	**C**	**C**	255	62	94.37	STEAP1_2_1	
Microdroplet	NA11992	7	89628477	C	G	G	**C**	**C**	255	62	100	STEAP1_2_1	
Traditional	NA11992	7	89628477	C	G	G	**C**	**C**	255	62	98.19	STEAP1_2_1	
Microdroplet	NA12006	7	89628477	C	G	G	**C**	**C**	255	62	99.21	STEAP1_2_1	
Traditional	NA12006	7	89628477	C	G	G	**C**	**C**	255	62	97.08	STEAP1_2_1	
Microdroplet	NA18505	7	89628477	C	G	G	**C**	**C**	199	62	100	STEAP1_2_1	
Traditional	NA18505	7	89628477	C	G	G	**C**	**C**	255	62	97.25	STEAP1_2_1	
Microdroplet	NA18517	7	89628477	C	G	G	**C**	**C**	202	62	100	STEAP1_2_1	
Traditional	NA18517	7	89628477	C	G	G	**C**	**C**	255	62	96	STEAP1_2_1	
Microdroplet	NA11832	7	89767046	C	C	T	**C**	**C**	255	62	93.57	FLJ21062_17_1	
Traditional	NA11832	7	89767046	C	C	T	**C**	**C**	255	62	89.93	FLJ21062_17_1	
Microdroplet	NA11992	7	89767046	C	C	T	**C**	**C**	140	62	88.52	FLJ21062_17_1	
Traditional	NA11992	7	89767046	C	C	T	**C**	**C**	127	62	92.73	FLJ21062_17_1	
Microdroplet	NA18505	7	89767046	C	C	T	**C**	**C**	54	56	81.48	FLJ21062_17_1	
Traditional	NA18505	7	89767046	C	C	T	**C**	**C**	84	62	94.12	FLJ21062_17_1	
Microdroplet	NA18517	7	89767046	C	C	T	**C**	**C**	86	62	96.43	FLJ21062_17_1	
Traditional	NA18517	7	89767046	C	C	T	**C**	**C**	96	62	85.07	FLJ21062_17_1	
Microdroplet	NA11832	8	73104764	G	G	T	T	T	177	62	18.71	TRPA1_4_1	
Traditional	NA11832	8	73104764	G	G	T	T	T	112	62	9.52	TRPA1_4_1	
Microdroplet	NA12006	8	73104764	G	G	T	T	T	132	62	14.43	TRPA1_4_1	
Traditional	NA12006	8	73104764	G	G	T	T	T	102	62	8.16	TRPA1_4_1	
Traditional	NA18517	8	73134059[c]	T	G	T	T	T	65	22	79.22	TRPA1_20_1	
Microdroplet	NA18505	9	130979840	G	A	A	G	G	205	62	98.59	IER5L_1_2	IER5L_1_3
Traditional	NA18505	9	130979840	G	A	A	G	G	57	50	100	IER5L_1_2	IER5L_1_3
Microdroplet	NA18517	11	2396484	G	G	G	A	G	167	62	41.82	TRPM5_20_1	
Traditional	NA18517	11	2396484	G	G	G	A	G	165	62	52.5	TRPM5_20_1	
Microdroplet	NA11832	12	101764760	C	C	C	A	C	187	62	50.28	PAH_5_1	
Traditional	NA11832	12	101764760	C	C	C	A	C	138	62	52.45	PAH_5_1	
Microdroplet	NA11992	12	101764760	C	C	C	A	C	143	62	50.4	PAH_5_1	
Traditional	NA11992	12	101764760	C	C	C	A	C	121	62	49.15	PAH_5_1	
Microdroplet	NA18505	12	101764760	C	C	C	A	C	176	62	53.28	PAH_5_1	
Traditional	NA18505	12	101764760	C	C	C	A	C	149	62	44.35	PAH_5_1	
Microdroplet	NA18489	16	55562390	G	A	G	G	G	255	62	98.27	CETP_6_1	
Traditional	NA18489	16	55562390	G	A	G	G	G	255	62	97.88	CETP_6_1	

a - Frequency of reads mapped that contains the reference allele. **b** - class 1: homozygote reference by PCR, homozygote alternate in HapMap, class 2: heterozygote by PCR, homozygote reference in HapMap, class3: homozygote reference by PCR, heterzygote in HapMap. **c** - For variants at both 27169710 and 73134059 the PCR method not shown produced a no call at the position. **d** - Variants amplified by two PCR primer pairs

Supplemental Table 6. False positives in validation phase.

						HapMap Alleles		Sequencing Alleles	
Chr	Position	Position	Method	Sample	Reference Allele	A	B	A	B
2	234210504	234210504	Microdroplet	NA18517	T	T	T	C	T
2	234210504		Traditional	NA18517	T	T	T	C	T
2	234341152	234341152	Microdroplet	NA18505	T	T	T	C	T
2	234341152		Traditional	NA18505	T	T	T	C	T
2	234345991	234345991	Traditional	NA11992	T	T	T	C	T
2	234414008	234414008	Microdroplet	NA18517	G	G	G	A	G
2	234414008		Traditional	NA18517	G	G	G	A	G
2	234427637	234427637	Microdroplet	NA18505	C	C	C	C	T
2	234427637		Traditional	NA18505	C	C	C	C	T
2	234427663	234427663	Microdroplet	NA11832	C	C	C	G	G
2	234427663		Microdroplet	NA11992	C	C	C	C	G
2	234427663		Microdroplet	NA12006	C	C	C	C	G
2	234427663		Traditional	NA11832	C	C	C	G	G
2	234427663		Traditional	NA11992	C	C	C	C	G
2	234427663		Traditional	NA12006	C	C	C	C	G
2	234427685	234427685	Microdroplet	NA11832	C	C	C	C	G
2	234427685		Traditional	NA11832	C	C	C	C	G
2	234511046	234511046	Traditional	NA11832	C	C	C	A	C
2	234537961	234537961	Microdroplet	NA11992	G	G	G	A	G
2	234537961		Microdroplet	NA12006	G	G	G	A	G
2	234537961		Microdroplet	NA18517	G	G	G	A	G
2	234537961		Traditional	NA11992	G	G	G	A	G
2	234537961		Traditional	NA18517	G	G	G	A	G
2	234542947	234542947	Traditional	NA12006	A	A	A	A	G
2	234542947		Traditional	NA18505	A	A	A	A	G
2	234542947		Traditional	NA18517	A	A	A	A	G
7	27101313	27101313	Microdroplet	NA18505	A	A	A	T	T
7	27101313		Traditional	NA18505	A	A	A	T	T
7	27101883	27101883	Traditional	NA18517	C	C	C	C	G
7	27106771	27106771	Microdroplet	NA18517	C	C	C	A	C
7	27113998	27113998	Microdroplet	NA12006	C	C	C	A	C
7	27114800	27114800	Microdroplet	NA12006	G	G	G	C	G
7	27114800		Traditional	NA12006	G	G	G	C	G
7	27136142	27136142	Microdroplet	NA11832	T	T	T	C	C
7	27136142		Microdroplet	NA11992	T	T	T	C	C
7	27136142		Microdroplet	NA12006	T	T	T	C	C
7	27136142		Microdroplet	NA18505	T	T	T	C	C
7	27136142		Microdroplet	NA18517	T	T	T	C	C
7	27136142		Traditional	NA11832	T	T	T	C	C
7	27136142		Traditional	NA11992	T	T	T	C	C
7	27136142		Traditional	NA12006	T	T	T	C	C
7	27136142		Traditional	NA18505	T	T	T	C	C
7	27136142		Traditional	NA18517	T	T	T	C	C
7	27136459	27136459	Microdroplet	NA11832	A	A	A	G	G
7	27136459		Microdroplet	NA11992	A	A	A	G	G
7	27136459		Microdroplet	NA12006	A	A	A	G	G
7	27136459		Microdroplet	NA18505	A	A	A	G	G
7	27136459		Microdroplet	NA18517	A	A	A	G	G
7	27136459		Traditional	NA11832	A	A	A	G	G
7	27136459		Traditional	NA11992	A	A	A	G	G
7	27136459		Traditional	NA12006	A	A	A	G	G
7	27136459		Traditional	NA18505	A	A	A	G	G
7	27136459		Traditional	NA18517	A	A	A	G	G
7	27136670	27136670	Microdroplet	NA11832	T	T	T	G	G
7	27136670		Microdroplet	NA11992	T	T	T	G	G
7	27136670		Microdroplet	NA12006	T	T	T	G	G
7	27136670		Microdroplet	NA18505	T	T	T	G	G
7	27136670		Microdroplet	NA18517	T	T	T	G	G
7	27136670		Traditional	NA11832	T	T	T	G	G
7	27136670		Traditional	NA11992	T	T	T	G	G
7	27136670		Traditional	NA12006	T	T	T	G	G
7	27136670		Traditional	NA18505	T	T	T	G	G
7	27136670		Traditional	NA18517	T	T	T	G	G
7	27149158	27149158	Microdroplet	NA18505	G	G	G	A	G
7	27149158		Microdroplet	NA18517	G	G	G	A	G
7	27149158		Traditional	NA18505	G	G	G	A	G
7	27149158		Traditional	NA18517	G	G	G	A	G
7	27152045	27152045	Microdroplet	NA18505	G	G	G	A	G
7	27152045		Microdroplet	NA18517	G	G	G	A	G
7	27152045		Traditional	NA18505	G	G	G	A	G
7	27152045		Traditional	NA18517	G	G	G	A	G
7	27162519	27162519	Microdroplet	NA12006	G	G	G	A	G
7	27162519		Traditional	NA12006	G	G	G	A	G
7	27171257	27171257	Microdroplet	NA11992	C	C	C	A	C
7	27171257		Microdroplet	NA12006	C	C	C	A	C
7	27171257		Traditional	NA11992	C	C	C	A	C
7	27171257		Traditional	NA12006	C	C	C	A	C
7	27171684	27171684	Traditional	NA18517	C	C	C	C	G
7	27205216	27205216	Microdroplet	NA11832	C	C	C	G	G
7	27205216		Microdroplet	NA11992	C	C	C	G	G
7	27205216		Microdroplet	NA12006	C	C	C	G	G
7	27205216		Microdroplet	NA18505	C	C	C	G	G
7	27205216		Microdroplet	NA18517	C	C	C	G	G
7	27205216		Traditional	NA11832	C	C	C	G	G
7	27205216		Traditional	NA11992	C	C	C	G	G
7	27205216		Traditional	NA12006	C	C	C	G	G
7	27205216		Traditional	NA18505	C	C	C	G	G
7	27205216		Traditional	NA18517	C	C	C	G	G
7	27205718	27205718	Microdroplet	NA18517	C	C	C	T	T
7	27205718		Traditional	NA18517	C	C	C	C	T
7	27205726	27205726	Traditional	NA18517	G	G	G	G	T

7	27206075	27206075	Microdroplet	NA18517	C	C	C	C	T
7	27206075		Traditional	NA18517	C	C	C	C	T
7	27249029	27249029	Traditional	NA11992	G	G	G	A	G
7	27249654	27249654	Microdroplet	NA11992	C	C	C	C	T
7	27249654		Traditional	NA11992	C	C	C	C	T
7	27252215	27252215	Microdroplet	NA18505	A	A	A	A	C
7	27252215		Traditional	NA18505	A	A	A	A	C
7	89631723	89631723	Traditional	NA11832	G	G	G	G	T
7	89699558	89699558	Traditional	NA11992	G	G	G	G	T
7	89729133	89729133	Microdroplet	NA12006	C	C	C	A	C
7	89744582	89744582	Microdroplet	NA18505	C	C	C	A	C
7	89753393	89753393	Microdroplet	NA11992	C	C	C	A	C
7	89753393		Traditional	NA18517	C	C	C	A	C
7	89774976	89774976	Microdroplet	NA18505	G	G	G	A	G
7	89839432	89839432	Microdroplet	NA12006	G	G	G	C	G
7	89839432		Traditional	NA12006	G	G	G	C	G
7	89852431	89852431	Microdroplet	NA18517	C	C	C	A	C
9	130738637	130738637	Microdroplet	NA18505	G	G	G	A	G
9	130738637		Traditional	NA18505	G	G	G	A	G
9	130749838	130749838	Microdroplet	NA18505	G	G	G	A	G
9	130749838		Traditional	NA18505	G	G	G	A	G
9	130749946	130749946	Microdroplet	NA18505	A	A	A	A	G
9	130749946		Traditional	NA18505	A	A	A	A	G
9	130749988	130749988	Microdroplet	NA18517	G	G	G	A	G
9	130749988		Traditional	NA18517	G	G	G	A	G
9	130782645	130782645	Microdroplet	NA18517	T	T	T	C	T
9	130782645		Traditional	NA18517	T	T	T	C	T
9	130788934	130788934	Microdroplet	NA18517	T	T	T	C	T
9	130788934		Traditional	NA18517	T	T	T	C	T
9	130800813	130800813	Microdroplet	NA11992	A	A	A	A	T
9	130800813		Traditional	NA11992	A	A	A	A	T
9	130803835	130803835	Microdroplet	NA18517	A	A	A	A	C
9	130803835		Traditional	NA18517	A	A	A	A	C
9	130808083	130808083	Microdroplet	NA18517	G	G	G	A	G
9	130808083		Traditional	NA18517	G	G	G	A	G
9	130811326	130811326	Microdroplet	NA11832	C	C	C	C	T
9	130811326		Microdroplet	NA11992	C	C	C	T	T
9	130811326		Microdroplet	NA12006	C	C	C	T	T
9	130811326		Traditional	NA11832	C	C	C	C	T
9	130811326		Traditional	NA11992	C	C	C	T	T
9	130811326		Traditional	NA12006	C	C	C	T	T
9	130830351	130830351	Microdroplet	NA18517	G	G	G	C	G
9	130830352	130830352	Microdroplet	NA11832	C	C	C	C	T
9	130830352		Microdroplet	NA11992	C	C	C	T	T
9	130830352		Microdroplet	NA12006	C	C	C	T	T
9	130830352		Microdroplet	NA18517	C	C	C	C	T
9	130830352		Traditional	NA11992	C	C	C	T	T
9	130830454	130830454	Microdroplet	NA11832	T	T	T	G	G
9	130830454		Microdroplet	NA11992	T	T	T	G	G
9	130830454		Microdroplet	NA12006	T	T	T	G	G
9	130830454		Microdroplet	NA18505	T	T	T	G	G
9	130830454		Microdroplet	NA18517	T	T	T	G	G
9	130830454		Traditional	NA11992	T	T	T	G	G
9	130851869	130851869	Microdroplet	NA18517	C	C	C	C	T
9	130851869		Traditional	NA18517	C	C	C	C	T
9	130887224	130887224	Microdroplet	NA18517	G	G	G	A	G
9	130887224		Traditional	NA18517	G	G	G	A	G
9	130888884	130888884	Microdroplet	NA18517	C	C	C	C	T
9	130888884		Traditional	NA18517	C	C	C	C	T
9	130897438	130897438	Microdroplet	NA11832	G	G	G	A	G
9	130897438		Traditional	NA11832	G	G	G	A	G
9	130900088	130900088	Microdroplet	NA18505	C	C	C	C	T
9	130900088		Traditional	NA18505	C	C	C	C	T
9	130902602	130902602	Microdroplet	NA11832	G	G	G	A	A
9	130902602		Microdroplet	NA11992	G	G	G	A	A
9	130902602		Microdroplet	NA12006	G	G	G	A	A
9	130902602		Microdroplet	NA18505	G	G	G	A	G
9	130902602		Traditional	NA11832	G	G	G	A	A
9	130902602		Traditional	NA11992	G	G	G	A	A
9	130902602		Traditional	NA12006	G	G	G	A	A
9	130902602		Traditional	NA18505	G	G	G	A	G
9	130902815	130902815	Microdroplet	NA18505	C	C	C	C	T
9	130902815		Traditional	NA18505	C	C	C	C	T
9	130922582	130922582	Microdroplet	NA11832	T	T	T	C	C
9	130922582		Microdroplet	NA11992	T	T	T	C	C
9	130922582		Microdroplet	NA12006	T	T	T	C	C
9	130922582		Microdroplet	NA18505	T	T	T	C	C
9	130922582		Microdroplet	NA18517	T	T	T	C	C
9	130922582		Traditional	NA11832	T	T	T	C	C
9	130922582		Traditional	NA11992	T	T	T	C	C
9	130922582		Traditional	NA12006	T	T	T	C	C
9	130922582		Traditional	NA18505	T	T	T	C	C
9	130922582		Traditional	NA18517	T	T	T	C	C
9	130925100	130925100	Traditional	NA18517	G	G	G	A	G
9	130938701	130938701	Microdroplet	NA18505	A	A	A	G	G
9	130938701		Microdroplet	NA18517	A	A	A	G	G
9	130938701		Traditional	NA18505	A	A	A	G	G
9	130938701		Traditional	NA18517	A	A	A	G	G
9	130939667	130939667	Microdroplet	NA11832	T	T	T	C	C
9	130939667		Microdroplet	NA11992	T	T	T	C	C
9	130939667		Microdroplet	NA12006	T	T	T	C	C
9	130939667		Traditional	NA11832	T	T	T	C	C
9	130939667		Traditional	NA11992	T	T	T	C	C
9	130939667		Traditional	NA12006	T	T	T	C	C

a - Frequency of reads mapped which the reference allele **b** - Variant calls between traditional and microdroplet PCR differed. For a

Supplemental Table 7. Scale up phase discordant variants between sequence data and HapMap genotypes.

			HapMap Alleles		Sequencing Alleles				Illumina GAII					Roche 454			
					GA II		454										
Chr	Position	Reference Allele	A	B	A	B	A	B	Variant Quality	Neighbor Quality	Base Frequency[a]	Base Called[b]	Base Discrepent	Variant Probability[a]	Base Frequency	Base Called[b]	Base Discrepent
1	35431339	G	C	C	G	G	G	G	255	62	99.05	yes	yes	-	100	yes	yes
1	159911794	G	G	G	G	G	C	G	255	62	98.76	yes	no	2.04E-27	68.57	yes	yes
1	226499840	A	A	G	A	A	A	A	230	62	99.1	yes	yes	-	100	yes	yes
1	226510920	T	G	G	T	T	T	T	253	62	100	yes	yes	-	100	yes	yes
3	12398113	G	G	G	C	G	C	G	165	62	48.1	yes	yes	6.61E-23	47.3	yes	yes
3	37510988	C	G	G	C	G	C	G	189	62	52.05	yes	yes	2.86E-10	43.37	yes	yes
3	136127326	G	T	T	T	T	G	T	255	62	0	yes	no	3.04E-09	33.33	yes	yes
3	185781762	G	A	G	A	G	A	A	53	62	22.94	yes	no	1.03E-14	17.14	yes	yes
5	176828423	G	G	G	A	G	A	G	165	62	57.14	yes	yes	3.36E-31	47.86	yes	yes
6	30967283	C	C	G	C	C	C	C	255	62	98.69	yes	yes	-	100	yes	yes
6	33051323	C	C	T	C	C	C	C	241	62	100	yes	yes	-	100	yes	yes
6	44326098	A	A	G	A	A	A	G	63	62	72	yes	yes	1.73E-08	34.62	yes	no
6	109091842	T	C	T	T	T	C	T	255	62	100	yes	yes	3.63E-25	72.19	yes	no
6	160401527	T	C	C	C	T	C	T	182	62	52.52	yes	yes	8.73E-19	60.94	yes	yes
7	5993514	G	G	G	A	G	A	G	62	62	57.36	yes	yes	8.45E-09	75	yes	yes
7	100248593	A	A	A	A	G	-	-	171	62	50.85	yes	yes	1.41E-05	52.38	no	-
7	150795122	A	G	G	A	A	A	A	255	62	100	yes	yes	-	100	yes	yes
9	133054166	T	C	C	C	C	C	T	255	62	0	yes	no	1.07E-32	28	yes	yes
10	76458866	C	C	T	-	-	C	C	1	62	81.93	no	-	3.27E-01	94.12	yes	yes
11	85369990	A	C	C	A	C	A	C	255	62	48.13	yes	yes	2.20E-27	39.34	yes	yes
11	116582149	C	C	C	C	C	C	T	255	62	99.3	yes	no	1.92E-06	63.16	yes	yes
11	116582159	G	A	A	G	G	-	-	255	62	97.76	yes	yes	2.47E-04	63.16	no	-
11	116582219	A	C	C	A	A	A	C	255	62	100	yes	yes	1.84E-09	61.54	yes	yes
12	4253419	T	C	C	C	C	C	T	255	62	1.09	yes	no	1.01E-06	25	yes	yes
15	82279640	A	G	G	G	G	A	G	255	62	0.46	yes	no	8.30E-08	45.1	yes	yes
17	21142143	T	T	T	C	T	C	T	162	62	60.34	yes	yes	4.15E-18	47.37	yes	yes
17	21142312	T	T	T	C	T	C	T	175	62	44.96	yes	yes	1.53E-20	55	yes	yes
17	21144883	G	G	G	G	G	C	G	97	62	83.97	yes	no	7.49E-13	77.06	yes	yes
17	21157990	A	A	A	A	G	A	G	120	62	68.25	yes	yes	7.88E-25	42.68	yes	yes
17	21158106	G	G	G	A	G	A	G	192	62	51.59	yes	yes	2.17E-65	42.42	yes	yes
18	7024464	T	A	T	A	A	A	A	255	62	0.67	yes	yes	6.99E-12	0	yes	yes
19	5953701	C	C	C	C	T	C	T	168	62	45.28	yes	yes	5.61E-09	30	yes	yes
19	50563876	C	T	T	C	T	T	T	159	62	61.73	yes	yes	6.72E-69	0.96	yes	no
20	35448117	G	G	G	A	G	A	G	181	62	53.96	yes	yes	6.04E-16	46.94	yes	yes
20	35464469	C	T	T	C	T	C	T	176	62	45.86	yes	yes	6.52E-11	51.16	yes	yes
X	107863596	G	C	G	C	G	G	G	175	62	54.29	yes	no	5.31E-11	80.56	yes	yes

a - Frequency of reads mapped which the reference allele. b - Filter criteria for variant calling explained are explained in the supplemental methods

Supplemental Table 8. Comparison of enrichment methods for targeted sequencing. Please see Supplemental Discussion starting on page 9 for supporting text.

Method		Targeted Bases	Fraction of Reads On Target		Coverage of targeted bases		Concordance	Uniformity of coverage
			All Reads	Uniquely Mapping	≥ 1 read	Passed for Variant Detection		
Microdrolet PCR		1.35 Mb	64.2%	79.2%	99.8%	94.5%	98.8%	96.6% within 1/5 the mean (25-fold)
MIP[1]	Shotgun	6.5 Mb	58.4%	99.0%	85.0%	58.8%	99.7 / 96.4[2]	N/A
	End Sequence	1.4 Mb[3]	66.3%[4]	73.1%	98.0%	75.0%	99.7%	58% within tenfold, 88% within 100-fold
Solution Hybridization[5]		3.7 Mb	*53.1%*[6]	65.2%	88.0%	64.0% / 89%[7,8]	99.6% / NA[8]	80% within 1/5 the mean (25-fold)

1 - MIP = Molecular inversion probe. Turner et al. N. Meth 2009. 2 - Concordance reported seperately for homozygotes (99.7%) and heterozygotes (96.4%). 3 - 1.4 Mb represents a proportion of 1.7 Mb of the exonic sequence that could be aquired by 76 bp end sequenceing 4 - Calculated by multiplying the proportion of the 76 base reads that did not consist of primer sequence (56/76 * 90.0). 5 - Gnirke et al. N. Biotech 2009 6 - Gnirke et al. mapped 37.7% of all reads. For a fairer assesment we report mapping of filtered reads using methods discribed in the supplemental discussion. 7 - Gnirke et al. only reported the call rate for exonic sequence (2.5 Mb) and not the entire bait. 8 - The concordance for the GA-II run was not reported, because of this exclusion we have provided call rates for the GA-I (first value) and GA-II runs (second value).