Appendix A

Parameters and commands for Chapter 2 simulations

***cosi* parameters:**

#random_seed 1001

in bp.

length 1000000

per bp per generation

mutation_rate 1.9e-8

recomb_file ../cosi_files/rec_r1

population info

pop_define 1 european

pop_define 4 asian

pop_define 5 african

#european

pop_size 1 7700

sample_size 1 10

#asian

pop_size 4 7700

sample_size 4 1540

#african

pop_size 5 24000

sample_size 5 4800

pop_event split "asian and european split" 1 4 0

pop_event bottleneck "OoA bottleneck" 1 1499 .085

pop_event split "out of Africa" 5 1 1500

pop_event change_size "african pop size" 5 15000 12500

***mpop* commands:**

mpop commands for Asian population (selection coefficient 0.007)

./mpop -i mpop_input_r1_Asian -o mpop_out_r1_Asian_1 -N 1540 -S -m 0.09 -r 0.46 -s 0.01 -h 0.5 -g 1;

./mpop -i mpop_out_r1_Asian_1 -o mpop_out_r1_Asian_2 -N 145 -g 1;

./mpop -i mpop_out_r1_Asian_2 -o mpop_out_r1_Asian_3 -N 1540 -g 318;

./mpop -i mpop_out_r1_Asian_3 -o mpop_out_r1_Asian_4 -N 20000 -g 80;

./mpop -i mpop_out_r1_Asian_4 -o mpop_out_r1_Asian -N 50 -g 0;

mpop commands for African population (neutral)

./mpop -i mpop_input_r1_African -o mpop_out_r1_African_1 -N 4800 -m 0.09 -r 0.46 -g 360;

./mpop -i mpop_out_r1_African_1 -o mpop_out_r1_African_2 -N 20000 -g 40;

./mpop -i mpop_out_r1_African_2 -o mpop_out_r1_African -N 50 -g 0;

Appendix B

Chapter 2 targeted resequencing of two regions: PCR primers and protocols

PCR enrichments*:

Primer Name	Primer sequences	PCR product coordinates F=start, R=end	PCR product size (bp)
Region1_1F	TCTATCTCCTCCCTTACCCTTTG	chr4:158702285	
Region1_1R	GATTCTTTCAGTGTTGATCTGGG	chr4:158708600	6316
Region1_2F	TAATGCACCTTTGTTCTTGGTCT	chr4:158708036	
Region1_2R	CTTGTAGTCCCATCATCTCCTTG	chr4:158715605	7570
Region1_3F	ACCTCTCCCTACTCCCAGAGTC	chr4:158715109	
Region1_3R	ATCTGCCATGAATACAGAAAGGA	chr4:158722818	7710
Region1_4F	CTCCATGACTTTAGAGGCTACGA	chr4:158722140	
Region1_4R	GAAGTAGGGTTGGAGAGGGTCTA	chr4:158730090	7951
Region1_5F	TCCTCCTATCTTGTCTCTTGCTG	chr4:158729433	
Region1_5R	GAGAAAGAAATTGTGTTGCATCC	chr4:158735391	5959
Region1_6F	AGCCAGCCACACTTACTATGAAC	chr4:158734888	
Region1_6R	GCAACTTCCCTCTAATATGCCTT	chr4:158741661	6774
Region1_7F	AAATGGACTGTGCTTTCAAAGAG	chr4:158740885	
Region1_7R	GTATTTGTCCTTCTGTGCCTGAC	chr4:158747831	6947
Region1_8F	AAACGATTGACAGAGTGAAGAGC	chr4:158747100	
Region1_8R	CCAGTCAGAAATATTGCAAGTCC	chr4:158753068	5969
Region1_9F	CTGGAATTTCTTATCCTCGTCCT	chr4:158752465	
Region1_9R	AGGTCTCGGATTACAGACATGAA	chr4:158758682	6218
Region1_10F	GCAAGCTTCTCAATGGAGTTAAA	chr4:158757964	
Region1_10R	TTGGGTGGAGAAGAAGTAATGAA	chr4:158767669	9705

Region1_11F	AAGACCTGGAATCAGTAGAAGGG	chr4:158762445	
Region1_11R	GGAGATTTACCAAGGCTTCACTT	chr4:158772142	9697
Region1_12F	CTCACTATGGATATTGACGAGGC	chr4:158770930	
Region1_12R	CCTTAATTTCGTTCTCCTGCTTT	chr4:158778727	7798
Region1_13F	GGGCTCCTCACTTACCCAGTAG	chr4:158777605	
Region1_13R	TGCTTCCGAAATTATTGTTCTGT	chr4:158785309	7704
Region1_14F	ACAGCTGCCATTCAATAAATGTT	chr4:158783817	
Region1_14R	TGCCAGGTAACCTAGATGAGGTA	chr4:158791494	7678
Region1_15F	TGACTGACCATTATTGACCATGA	chr4:158790760	
Region1_15R	TAGCTATGATTGATTGGGTGCTT	chr4:158797058	6299
Region1_16F	TTGAACAGACGAATGAATGATTG	chr4:158796560	
Region1_16R	TTTATGCTAATTGGCTCTGGGTA	chr4:158802768	6209
Region1_17F	TCTTTATCTTGCCAGTTGAGCAT	chr4:158802175	
Region1_17R	TATTTGTGTTCCCTTTCCTGCTA	chr4:158808423	6249
Region1_18F	GTGAGAATTCATCTCAAAGCCAC	chr4:158807818	
Region1_18R	GGAAGCTATTTACAGTTTGCCCT	chr4:158815385	7568
Region1_19F	CAGTAAGCCCAAATGTTAAGGTG	chr4:158814909	
Region1_19R	ACCTGACTTTATTTCCCTCTTCG	chr4:158822313	7405
Region1_20F	GGATGCTGATCAATACCTGATGT	chr4:158821535	
Region1_20R	CTACTTACGGCAACTCACAGCTT	chr4:158829166	7632
Region1_21F	AGGAATGCTCAGTTCTTGTTCTG	chr4:158827934	
Region1_21R	TTATTTCTGAGGGCTCTGTTCTG	chr4:158836728	8794
Region1_22F	CATGGAAACTGAATAACCTGCTC	chr4:158834952	
Region1_22R	ACAAGGATTCTCATTTGAGTGGA	chr4:158840977	6026
Region1_23F	GGAAGTTGAAAGATGAATAGAACAAA	chr4:158840377	
Region1_23R	ACGGTCAATATTCTCTCCTCACA	chr4:158847471	7095
Region1_24F	ATCATGAGCCAAGTAAGCACAAT	chr4:158846985	
Region1_24R	GGCACCTATGTGAAATCTGACTC	chr4:158853923	6939
Region1_25F	ATGCCTTGCTTTCATAACTCTTG	chr4:158853372	

Region1_25R	CGGAAAGTCTAATTTGAACAACG	chr4:158860928	7557
Region1_26F	TCAAACTGAGTCTCTGGGAATGT	chr4:158859085	
Region1_26R	TGGCTGGTAACTCATTAGGTCAT	chr4:158868003	8918
Region1_27F	CACACAATTTATCCAACATCCCT	chr4:158866183	
Region1_27R	TTACATTGATTGGATGCAGTGAG	chr4:158874110	7928
Region1_28F	CTGAGGAATACTGCCGTATCAAG	chr4:158872529	
Region1_28R	ACCAATCCCAGTCCTTTATGAAT	chr4:158881348	8819
Region1_29F	GCAAAGCTAATTCGATACACCTG	chr4:158880521	
Region1_29R	TCAAGATCAAATGCAGTCAGAGA	chr4:158887599	7079
Region1_30F	CAAAGGTAATTGTGAGGTGAAGG	chr4:158886844	
Region1_30R	TTGGGAGTTGAAGCTGGTATAAA	chr4:158894432	7589
Region1_31F	TTCCTCTCTGTAAATGTGGCAAT	chr4:158893844	
Region1_31R	AGTTTGAACAAAGCAGCAGGTAG	chr4:158901107	7264
Region1_32F	GCTTGTCTATGCTTCACGAAGTT	chr4:158900212	
Region1_32R	TTCTATCGCAATACTCCCTTTCA	chr4:158907520	7308
Region1_33F	CACCAGGCTACAGTTTCTTCATC	chr4:158906161	
Region1_33R	CATTGCTCCACATTCTCATTACA	chr4:158913779	7619
Region1_34F	CTGAAGTGTGTAGAATGGTGCTG	chr4:158913234	
Region1_34R	TTGAATCCACAAGGTGAAGCTAT	chr4:158920243	7010
Region1_35F	AAGGATCATTTCTCTGCCCTAAC	chr4:158919497	
Region1_35R	TTATTAGTGGTGCTTTCAGGGAA	chr4:158927302	7806
Region1_36F	CAGTGGGTACTCTATGTTGAGGC	chr4:158926740	
Region1_36R	CCTCTTCATGGTACAGATTCCTG	chr4:158934735	7996
Region1_37F	AGGTCCAACTATAGGAGGAGTGG	chr4:158934050	
Region1_37R	AATCACAAGTCAAGGGAGATTCA	chr4:158940035	5986
Region1_38F	TGAGCAGTGTGAGAGTGGACTAA	chr4:158939317	
Region1_38R	GTGGGATGGACACATATTCTGTT	chr4:158945415	6099
Region1_39F	AGAGCTCCCTTCTCTCTGACATT	chr4:158944781	
Region1_39R	TTCTGTGAGATTCCAACCCTTTA	chr4:158951872	7092

Region1_40F	TGAGAATTTAGGTGAGGCTGTGT	chr4:158951262	
Region1_40R	TCTTTCCTTCTCTCAGCCCTACT	chr4:158958029	6768
Region1_41F	TTTGACAGAAGGGAAGTAAACCA	chr4:158956621	
Region1_41R	GAGCTTGTCTTCATGCTCTGAAT	chr4:158966261	9640
Region1_42F	AGAAGGAACTCTCCAGCTGATCT	chr4:158964566	
Region1_42R	TTTGGCATAAACCACTCCTCTAA	chr4:158972100	7535
Region1_43F	GCCCATCCATGTATGTTCTGTAT	chr4:158971591	
Region1_43R	CACCCTGAAAGCATTCTTAATTG	chr4:158979627	8037
Region1_44F	CATCCACCAAGGTTATAGCTCAG	chr4:158979058	
Region1_44R	ATGGAGAAGAATGGACAAACTCA	chr4:158986215	7158
Region1_45F	CATAGTGCTTCAAGATGTCCTCC	chr4:158985263	
Region1_45R	TAAAGACAGCCTACAGAATGGGA	chr4:158994297	9034
Region1_46F	CCCACTGTTCACCTTACAGACTC	chr4:158992842	
Region1_46R	TGCCAAGATAATTGTTAGAGGGA	chr4:158999198	6356
Region1_47F	GGACAATGACACTATGCTTCACA	chr4:158998528	
Region1_47R	ACATCCTCCTAGCACTAACTCCC	chr4:159006314	7786
Region1_48F	AAATCCAACATTAGAGCGACAAA	chr4:159004387	
Region1_48R	ATGCGACAGAAAGAGAATCAGAG	chr4:159010873	6487
Region1_49F	CACTTGCTCATGAACTAAAGCCT	chr4:159010262	
Region1_49R	GATCCTCAAATGGTGAGTCTGTC	chr4:159016211	5950

*PCR protocol: Xue et al. [183]

In total, 49 pairs of PCR primers were designed for chr4:158Mb, 42 for chr10:22Mb and 4 pairs for the Y chromosome to amplify 5-11 kb PCR products with overlap of >500 bp, using a Perl script (http://droog.gs.washington.edu/PCR-Overlap.html). Two previous pairs for *CASP12* [105] were also used. The three base pairs at the 3' end of all primers were

confirmed not to overlap with any SNP in dbSNP127 (http://www.ncbi.nlm.nih.gov/projects/SNP/). The primer sequences and PCR conditions are listed in above table. Forty-four out of 49 fragments from chr4:158Mb, 37 out of 42 from chr10:22Mb and all from the Y chromosome and *CASP12* were successfully amplified in initial tests. These fragments were subsequently amplified in 28 CHB and 2 YRI samples from the HapMap collection. Three CHB provided poor quality data for chr4:158Mb, and four for chr10:22Mb, and were excluded from all subsequent analyses. Amplification was tested by agarose gel electrophoresis followed by ethidium bromide staining, and approximate quantification was performed from the band intensity. Thirty nine out of 49 (~80%) long PCR primer pairs worked well for 22 or more samples for chr4:158Mb, and 32/42 (~75%) for 20 or more samples for chr10:22Mb. The PCR products from each individual sample were pooled, approximately equalizing the molar yield for the Illumina sequencing paired end library construction.

Appendix C

Parameters and commands for Chapter 3 simulations

***cosi* parameters:**

#random_seed 1001 # Specifies a particular random number seed

in bp.

length 300000

per bp per generation

mutation_rate 1.0e-8

recomb_file rec_file

population info

pop_define 1 european

pop_define 4 asian

pop_define 5 african

#european

pop_size 1 100000

sample_size 1 120

#asian

pop_size 4 100000

sample_size 4 120

#african

pop_size 5 100000

sample_size 5 120

pop_event migration_rate "afr->eur migration" 5 1 0 0.000032

pop_event migration_rate "eur->afr migration" 1 5 0 0.000032

pop_event migration_rate "afr->as migration" 5 4 0 0.000008

pop_event migration_rate "as->afr migration" 4 5 0 0.000008

#pop_event admix "african american admix" 3 1 5. .2

#pop_event split "african to aa" 5 3 7.0

pop_event change_size "agriculture - african" 5 200 24000

pop_event change_size "agriculture - european" 1 350 7700

pop_event change_size "agriculture - asian" 4 400 7700

pop_event bottleneck "african bottleneck" 5 1997 .008

pop_event bottleneck "asian bottleneck" 4 1998 .067

pop_event bottleneck "european bottleneck" 1 1999 .02

pop_event sweep "European selection" 1 0 0.01 0.5 0.9

pop_event split "asian and european split" 1 4 2000

pop_event migration_rate "afr->eur migration" 5 1 1996 0

pop_event migration_rate "eur->afr migration" 1 5 1995 0

pop_event migration_rate "afr->as migration" 5 4 1994 0

pop_event migration_rate "as->afr migration" 4 5 1993 0

pop_event bottleneck "OoA bottleneck" 1 3499 .085

pop_event split "out of Africa" 5 1 3500

pop_event change_size "african pop size" 5 17000 12500

***mpop* commands:**

Neutral:

CHBJPT:

./mpop -i ms_out_Eurasian -o mpop_tmp1 -N 3080 -m 0.015 -r rec -g 19;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 290 -g 1;

./mpop -i mpop_tmp2 -o mpop_tmp3-N 3080 -g 300;

./mpop -i mpop_tmp3 -o mpop_tmp4 -N 40000 -g 80;

./mpop -i mpop_tmp4 -o mpop_out -N 120 -g 0;

CEU:

./mpop -i ms_out_Eurasian -o mpop_tmp1 -N 3080 -m 0.015 -r rec -g 5;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 287 -g 1;

./mpop -i mpop_tmp2 -o mpop_tmp3-N 3080 -g 324;

./mpop -i mpop_tmp3 -o mpop_tmp4 -N 40000 -g 70;

./mpop -i mpop_tmp4 -o mpop_out -N 120 -g 0;

YRI:

./mpop -i ms_out_African -o mpop_tmp1 -N 9600 -m 0.015 -r rec -g 360;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 40000 -g 40;

./mpop -i mpop_tmp2 -o mpop_out -N 120 -g 0;

Selection coefficient = 0.01, age of sweep = 2000 generations:

CHBJPT:

./mpop -i ms_out_Eurasian -o mpop_tmp1 -N 3080 -m 0.015 -r rec -S -s 0.05 -h 0.5 -g 19;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 290 -g 1;

./mpop -i mpop_tmp2 -o mpop_tmp3-N 3080 -g 300;

./mpop -i mpop_tmp3 -o mpop_tmp4 -N 40000 -g 80;

./mpop -i mpop_tmp4 -o mpop_out -N 120 -g 0;

CEU:

./mpop -i ms_out_Eurasian -o mpop_tmp1 -N 3080 -m 0.015 -r rec -S -s 0.05 -h 0.5 -g 5;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 287 -g 1;

./mpop -i mpop_tmp2 -o mpop_tmp3-N 3080 -g 324;

./mpop -i mpop_tmp3 -o mpop_tmp4 -N 40000 -g 70;

./mpop -i mpop_tmp4 -o mpop_out -N 120 -g 0;

YRI:

./mpop -i ms_out_African -o mpop_tmp1 -N 9600 -m 0.015 -r rec -S -s 0.05 -h 0.5 -g 360;

./mpop -i mpop_tmp1 -o mpop_tmp2 -N 40000 -g 40;

./mpop -i mpop_tmp2 -o mpop_out -N 120 -g 0;

Appendix D

Candidate regions and genes in each population

Coordinates are in NCBI36.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
CEU							
1	797099	906801	847099	856801	2.29E-08	ENSG00000187634	*SAMD11*
1	10068896	10178302	10118896	10128302	1.96E-08	ENSG00000130939	*UBE4B*
1	13821389	13931321	13871389	13881321	5.17E-09	ENSG00000116731	*PRDM2*
1	27831079	27940924	27881079	27890924	5.47E-09	ENSG00000126709	*IFI6*
1	35355105	35464358	35405105	35414358	1.36E-08	ENSG00000116560	*SFPQ*
1	53228676	53338605	53278676	53288605	2.00E-09	ENSG00000116171	*SCP2*
1	53788087	53897937	53838087	53847937	6.93E-09	ENSG00000174332	*GLIS1*
1	66419956	66529521	66469956	66479521	1.20E-08	ENSG00000184588	*PDE4B*
1	76884112	76994105	76934112	76944105	6.54E-09	n.a.	n.a.
1	86596670	86706639	86646670	86656639	3.51E-09	ENSG00000122417	*ODF2L*
1	86596670	86706639	86646670	86656639	3.51E-09	ENSG00000137975	*CLCA2*
1	101748396	101970549	101798396	101808232	2.33E-09	n.a.	n.a.
1	102471628	102611505	102541801	102551773	4.81E-09	n.a.	n.a.
1	103207706	103327893	103268059	103277893	3.59E-09	ENSG00000060718	*COL11A1*
1	104387351	104573771	104459973	104468954	9.67E-10	n.a.	n.a.
1	105857859	105967516	105907859	105917516	4.12E-10	n.a.	n.a.
1	106474162	106584135	106524162	106534135	1.36E-08	n.a.	n.a.
1	117217385	117327315	117267385	117277315	4.30E-09	ENSG00000134247	*PTGFRN*
1	118134064	118264087	118184064	118193499	9.06E-09	ENSG00000196505	*GDAP2*
1	151028501	151159115	151099455	151109115	1.31E-10	ENSG00000163206	*SMCP*
1	154773501	154893188	154834024	154843188	4.42E-09	ENSG00000183856	*IQGAP3*
1	161195217	161304900	161245217	161254900	1.98E-10	n.a.	n.a.
1	162325660	162434777	162375660	162384777	5.87E-09	n.a.	n.a.
1	163721017	163830863	163771017	163780863	3.10E-09	ENSG00000162763	*LRRC52*
1	166615355	166725170	166665355	166675170	2.09E-08	n.a.	n.a.
1	181833404	181942458	181883404	181892458	1.87E-08	ENSG00000143344	*RGL1*
1	181833404	181942458	181883404	181892458	1.87E-08	ENSG00000173627	*APOBEC4*
1	183788556	183908552	183848976	183858552	2.17E-10	n.a.	n.a.
1	187028219	187158523	187088277	187097830	5.68E-09	n.a.	n.a.
1	187987903	188148535	188037903	188047844	2.52E-08	n.a.	n.a.
1	190884961	191004182	190945032	190954182	1.77E-08	ENSG00000127074	*RGS13*
1	206899055	207008768	206949055	206958768	2.54E-09	n.a.	n.a.
1	212081680	212191240	212131680	212141240	3.35E-08	n.a.	n.a.
1	212827867	212937843	212877867	212887843	1.42E-08	ENSG00000117724	*CENPF*

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
1	219734611	219854641	219784611	219794242	5.86E-09	n.a.	n.a.
1	232425142	232534909	232475142	232484909	4.62E-09	ENSG00000183780	*SLC35F3*
1	234895573	235004711	234945573	234954711	1.53E-08	ENSG00000077522	*ACTN2*
1	236273131	236403322	236323131	236333113	2.28E-10	n.a.	n.a.
2	6148356	6268236	6198356	6207722	1.10E-09	n.a.	n.a.
2	7533894	7643810	7583894	7593810	1.23E-08	n.a.	n.a.
2	21596445	21841341	21646445	21655066	5.01E-12	n.a.	n.a.
2	24385849	24504568	24435849	24445846	2.03E-10	ENSG00000198399	*ITSN2*
2	39917077	40027005	39967077	39977005	3.09E-08	n.a.	n.a.
2	69025791	69134554	69075791	69084554	2.67E-10	ENSG00000169605	*GKN1*
2	69025791	69134554	69075791	69084554	2.67E-10	ENSG00000169604	*ANTXR1*
2	83128877	83238859	83178877	83188859	2.47E-08	n.a.	n.a.
2	107231463	107340791	107281463	107290791	8.59E-10	n.a.	n.a.
2	121376537	121486418	121426537	121436418	8.08E-09	ENSG00000074047	*GLI2*
2	150814344	150924100	150864344	150874100	2.50E-08	n.a.	n.a.
2	167686338	167796283	167736338	167746283	2.62E-08	ENSG00000163092	*XIRP2*
2	182245152	182439132	182295152	182305057	2.13E-11	ENSG00000162992	*NEUROD1*
2	195721849	195831681	195771849	195781681	1.86E-08	n.a.	n.a.
2	224178700	224288695	224228700	224238695	3.11E-11	n.a.	n.a.
2	237029301	237139132	237079301	237089132	2.46E-08	ENSG00000132321	*IQCA1*
3	355682	773168	426407	436102	7.65E-11	ENSG00000134121	*CHL1*
3	3835933	3945844	3885933	3895844	8.43E-09	ENSG00000144455	*SUMF1*
3	4050353	4170446	4110452	4120446	3.55E-09	n.a.	n.a.
3	7018406	7128393	7068406	7078393	3.53E-08	ENSG00000196277	*GRM7*
3	7296272	7406271	7346272	7356271	5.74E-09	n.a.	n.a.
3	8482559	8592440	8532559	8542440	3.17E-08	ENSG00000071282	*LMCD1*
3	11925199	12035027	11975199	11985027	4.46E-09	ENSG00000157152	*SYN2*
3	14825904	14935524	14875904	14885524	6.04E-09	ENSG00000154783	*FGD5*
3	15972893	16082532	16022893	16032532	4.36E-09	n.a.	n.a.
3	29593202	29773402	29643202	29652970	7.48E-09	ENSG00000144642	*RBMS3*
3	40617631	40894999	40667631	40677443	2.99E-09	n.a.	n.a.
3	41645755	41755115	41695755	41705115	3.59E-08	ENSG00000168038	*ULK4*
3	58659078	58768392	58709078	58718392	1.16E-08	ENSG00000163689	*C3orf67*
3	59781034	59890749	59831034	59840749	7.59E-09	ENSG00000189283	*FHIT*
3	66556933	66665955	66606933	66615955	7.96E-09	ENSG00000144749	*LRIG1*
3	89800572	89910474	89850572	89860474	3.23E-08	n.a.	n.a.
3	97896644	98017341	97957359	97967341	8.19E-09	ENSG00000080224	*EPHA6*
3	99217131	99327009	99267131	99277009	2.23E-08	ENSG00000196578	*OR5AC2*
3	104252756	104362666	104302756	104312666	2.53E-08	n.a.	n.a.
3	107434455	107544376	107484455	107494376	1.75E-09	n.a.	n.a.
3	111775748	111882789	111825748	111832789	2.83E-08	n.a.	n.a.
3	112565463	112675318	112615463	112625318	3.98E-08	n.a.	n.a.
3	113254707	113364412	113304707	113314412	2.29E-08	ENSG00000114529	*C3orf52*
3	124864552	124973930	124914552	124923930	2.86E-08	ENSG00000065534	*MYLK*
3	136816358	136926078	136866358	136876078	3.16E-08	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
3	144995803	145115822	145055942	145065822	6.06E-10	ENSG00000181804	*SLC9A9*
3	147407375	147517084	147457375	147467084	2.45E-08	ENSG00000114698	*PLSCR4*
3	157455823	157565750	157505823	157515750	2.91E-08	ENSG00000169282	*KCNAB1*
3	174493364	174603316	174543364	174553316	1.25E-08	n.a.	n.a.
3	175277765	175387764	175327765	175337764	2.31E-08	ENSG00000169760	*NLGN1*
3	177707190	177816865	177757190	177766865	2.94E-09	n.a.	n.a.
3	178886726	178996686	178936726	178946686	1.96E-09	n.a.	n.a.
3	187149342	187258965	187199342	187208965	1.40E-08	ENSG00000171656	*ETV5*
3	190059450	190189991	190109450	190119392	6.72E-09	ENSG00000145012	*LPP*
3	191940911	192050897	191990911	192000897	3.86E-08	n.a.	n.a.
3	193235593	193345464	193285593	193295464	3.08E-09	ENSG00000114279	*FGF12*
3	194163940	194364328	194304531	194314328	1.32E-09	n.a.	n.a.
3	195632688	195742208	195682688	195692208	1.82E-08	ENSG00000133657	*ATP13A3*
3	196051892	196161845	196101892	196111845	7.44E-09	n.a.	n.a.
4	3505256	3615203	3555256	3565203	1.45E-08	ENSG00000216560	n.a.
4	4938663	5048572	4988663	4998572	1.42E-08	n.a.	n.a.
4	5261778	5505182	5352718	5362388	1.65E-09	ENSG00000152953	*STK32B*
4	14278140	14387761	14328140	14337761	3.16E-09	n.a.	n.a.
4	15278537	15388271	15328537	15338271	3.03E-08	ENSG00000109743	*BST1*
4	24338604	24448532	24388604	24398532	7.18E-09	ENSG00000109610	*SOD3*
4	32806311	32936928	32877427	32886928	4.69E-10	n.a.	n.a.
4	33216406	33326273	33266406	33276273	8.53E-09	n.a.	n.a.
4	34349592	34479595	34409609	34419485	2.04E-09	n.a.	n.a.
4	38403778	38513647	38453778	38463647	2.70E-08	ENSG00000174123	*TLR10*
4	42316679	42426548	42366679	42376548	1.65E-09	ENSG00000124406	*ATP8A1*
4	43008451	43128526	43058451	43068071	2.04E-09	n.a.	n.a.
4	55697521	55891731	55757643	55766818	9.58E-11	n.a.	n.a.
4	57067392	57176318	57117392	57126318	2.37E-08	ENSG00000196503	*ARL9*
4	60560440	60670150	60610440	60620150	1.95E-09	n.a.	n.a.
4	64226667	64336107	64276667	64286107	4.77E-09	n.a.	n.a.
4	64772668	64882457	64822668	64832457	3.29E-08	ENSG00000205678	n.a.
4	67269221	67378380	67319221	67328380	3.71E-09	n.a.	n.a.
4	71736097	71845931	71786097	71795931	1.40E-08	ENSG00000132467	*UTP3*
4	71736097	71845931	71786097	71795931	1.40E-08	ENSG00000018189	*RUFY3*
4	74361956	74512708	74411956	74421185	5.95E-09	n.a.	n.a.
4	75543994	75653814	75593994	75603814	3.95E-08	n.a.	n.a.
4	75931273	76041154	75981273	75991154	1.31E-08	ENSG00000174808	*BTC*
4	79977676	80087610	80027676	80037610	2.69E-09	ENSG00000138756	*BMP2K*
4	79977676	80087610	80027676	80037610	2.69E-09	ENSG00000163291	*PAQR3*
4	84281633	84391554	84331633	84341554	1.42E-08	n.a.	n.a.
4	85482704	85591519	85532704	85541519	8.85E-09	n.a.	n.a.
4	89092930	89202832	89142930	89152832	3.97E-08	ENSG00000118762	*PKD2*
4	93758997	93868355	93808997	93818355	9.60E-09	ENSG00000152208	*GRID2*
4	94797451	94907355	94847451	94857355	5.56E-09	n.a.	n.a.
4	96065573	96175204	96115573	96125204	1.92E-08	ENSG00000138696	*BMPR1B*

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4	96856764	96966688	96906764	96916688	3.90E-09	n.a.	n.a.
4	134308254	134437993	134368280	134377531	1.21E-09	ENSG00000138650	*PCDH10*
4	148389178	148499112	148439178	148449112	2.21E-08	n.a.	n.a.
4	156963127	157082944	157013127	157022938	2.51E-09	ENSG00000023843	*ACCN5*
4	163364280	163474168	163414280	163424168	2.18E-08	n.a.	n.a.
4	163663033	163772877	163713033	163722877	8.85E-09	n.a.	n.a.
4	165662952	165772885	165712952	165722885	1.12E-08	n.a.	n.a.
4	167365959	167485922	167415959	167425306	8.65E-10	n.a.	n.a.
4	168404471	168514387	168454471	168464387	2.77E-08	n.a.	n.a.
4	171478904	171745218	171528904	171538771	3.81E-09	n.a.	n.a.
4	172691703	172811785	172741703	172751630	2.54E-08	n.a.	n.a.
4	176393686	176746676	176443686	176453372	2.98E-09	n.a.	n.a.
4	178045518	178155489	178095518	178105489	5.98E-10	n.a.	n.a.
4	179180564	179290500	179230564	179240500	1.21E-08	n.a.	n.a.
4	180031210	180141029	180081210	180091029	8.48E-09	n.a.	n.a.
4	180379745	180530927	180439785	180449666	1.18E-09	n.a.	n.a.
4	182020705	182140717	182081056	182090717	2.01E-08	n.a.	n.a.
4	186586040	186695933	186636040	186645933	5.95E-09	ENSG00000168491	*CCDC110*
4	186586040	186695933	186636040	186645933	5.95E-09	ENSG00000154553	*PDLIM3*
5	888770	998682	938770	948682	3.66E-08	ENSG00000188818	*ZDHHC11*
5	4195348	4326216	4266360	4276216	1.21E-10	n.a.	n.a.
5	5251501	5361050	5301501	5311050	3.20E-08	ENSG00000145536	*ADAMTS16*
5	6149837	6259708	6199837	6209708	3.74E-08	n.a.	n.a.
5	11405272	11513912	11455272	11463912	3.55E-08	ENSG00000169862	*CTNND2*
5	11754601	11916207	11856492	11866207	3.11E-11	n.a.	n.a.
5	13602516	13712488	13652516	13662488	3.90E-08	n.a.	n.a.
5	15068086	15177819	15118086	15127819	2.60E-08	n.a.	n.a.
5	16291882	16411560	16341882	16351531	3.96E-09	n.a.	n.a.
5	18046735	18156677	18096735	18106677	2.35E-10	n.a.	n.a.
5	20108845	20217295	20158845	20167295	1.74E-08	n.a.	n.a.
5	23609527	23719495	23659527	23669495	1.16E-08	n.a.	n.a.
5	26369074	26478948	26419074	26428948	2.04E-09	n.a.	n.a.
5	29692634	29802426	29742634	29752426	5.32E-09	n.a.	n.a.
5	30484474	30594443	30534474	30544443	1.32E-08	n.a.	n.a.
5	31453154	31562933	31503154	31512933	2.65E-08	ENSG00000113360	*RNASEN*
5	31453154	31562933	31503154	31512933	2.65E-08	ENSG00000082213	*C5orf22*
5	33000096	33109984	33050096	33059984	2.14E-08	n.a.	n.a.
5	34402524	34512413	34452524	34462413	4.78E-10	n.a.	n.a.
5	38021327	38131205	38071327	38081205	3.11E-08	n.a.	n.a.
5	53958992	54068710	54008992	54018710	2.74E-08	n.a.	n.a.
5	54902588	55012059	54952588	54962059	3.19E-08	ENSG00000177058	*SLC38A9*
5	55766947	55875700	55816947	55825700	5.86E-09	n.a.	n.a.
5	67955416	68072958	68005416	68015396	2.63E-10	n.a.	n.a.
5	75151384	75261335	75201384	75211335	2.75E-08	n.a.	n.a.
5	97070120	97220944	97162942	97170944	1.06E-08	n.a.	n.a.

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5	99506633	99616542	99556633	99566542	3.89E-08	n.a.	n.a.
5	100710045	100840352	100780449	100790352	1.98E-10	n.a.	n.a.
5	100927427	101047459	100977427	100987371	3.92E-10	n.a.	n.a.
5	102002354	102112090	102052354	102062090	2.39E-09	n.a.	n.a.
5	109214330	109324059	109264330	109274059	9.91E-10	ENSG00000112893	*MAN2A1*
5	111946180	112055873	111996180	112005873	6.96E-09	n.a.	n.a.
5	115908166	116017795	115958166	115967795	2.92E-08	ENSG00000092421	*SEMA6A*
5	116405732	116515721	116455732	116465721	3.02E-08	n.a.	n.a.
5	117899353	118009270	117949353	117959270	2.00E-08	n.a.	n.a.
5	121071350	121234503	121121350	121131298	4.34E-11	n.a.	n.a.
5	126209968	126462023	126259968	126266104	7.17E-10	ENSG00000173926	*Mar-03*
5	144884095	144992878	144934095	144942878	2.16E-09	n.a.	n.a.
5	147361224	147471200	147411224	147421200	3.71E-09	ENSG00000133710	*SPINK5*
5	147566850	147676554	147616850	147626554	1.41E-08	ENSG00000178172	*SPINK6*
5	159112961	159232971	159173066	159182971	5.64E-10	n.a.	n.a.
5	168674391	168784360	168724391	168734360	2.04E-09	n.a.	n.a.
5	175034965	175144944	175084965	175094944	1.95E-08	ENSG00000113749	*HRH2*
6	2031068	2140862	2081068	2090862	1.17E-09	ENSG00000112699	*GMDS*
6	3808344	3917849	3858344	3867849	2.50E-08	n.a.	n.a.
6	10675596	10785508	10725596	10735508	1.72E-08	ENSG00000111846	*GCNT2*
6	29470141	29580071	29520141	29530071	6.31E-09	ENSG00000112462	*OR12D3*
6	30022655	30132654	30072655	30082654	3.94E-08	ENSG00000204623	*C6orf12*
6	30022655	30132654	30072655	30082654	3.94E-08	ENSG00000204622	*HLA-J*
6	30755426	30865118	30805426	30815118	1.83E-08	ENSG00000196230	*TUBBP2*
6	30755426	30865118	30805426	30815118	1.83E-08	ENSG00000137312	*FLOT1*
6	34095971	34205789	34145971	34155789	5.31E-09	ENSG00000124493	*GRM4*
6	40298670	40418882	40348670	40358454	1.21E-09	n.a.	n.a.
6	40493514	40603300	40543514	40553300	1.27E-08	ENSG00000156564	*LRFN2*
6	43507550	43617547	43557550	43567547	1.37E-08	ENSG00000171462	*DLK2*
6	51550467	51670722	51600467	51610364	1.41E-09	ENSG00000170927	*PKHD1*
6	56563975	56673746	56613975	56623746	2.87E-08	ENSG00000151914	*DST*
6	57648043	57757862	57698043	57707862	1.82E-08	n.a.	n.a.
6	58818960	58928887	58868960	58878887	1.20E-08	n.a.	n.a.
6	71801383	71911333	71851383	71861333	2.61E-09	n.a.	n.a.
6	72283845	72393767	72333845	72343767	5.93E-09	n.a.	n.a.
6	73805330	73966332	73865381	73875098	2.63E-10	ENSG00000185760	*KCNQ5*
6	75527921	75637322	75577921	75587322	7.22E-09	n.a.	n.a.
6	78105977	78215941	78155977	78165941	2.97E-08	n.a.	n.a.
6	85292936	85401929	85342936	85351929	1.33E-08	n.a.	n.a.
6	95457138	95567100	95507138	95517100	3.18E-08	n.a.	n.a.
6	97524281	97634118	97574281	97584118	1.29E-08	ENSG00000186231	*KLHL32*
6	102420908	102530890	102470908	102480890	2.63E-08	ENSG00000164418	*GRIK2*
6	103306890	103427375	103367406	103377375	7.08E-11	n.a.	n.a.
6	121576846	121697335	121637341	121647335	1.25E-08	ENSG00000146350	*C6orf170*
6	124072425	124234953	124175144	124184953	8.87E-09	ENSG00000188580	*NKAIN2*

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6	125760855	126018604	125810855	125820802	6.44E-09	n.a.	n.a.
6	128435397	128544982	128485397	128494982	5.86E-09	ENSG00000152894	*PTPRK*
6	131672420	131782151	131722420	131732151	4.60E-09	n.a.	n.a.
6	132479486	132589184	132529486	132539184	1.24E-08	n.a.	n.a.
6	137332672	137442017	137382672	137392017	1.63E-09	ENSG00000016402	*IL20RA*
6	145265416	145375412	145315416	145325412	3.22E-09	n.a.	n.a.
6	150643133	150762907	150703492	150712907	5.46E-09	ENSG00000009765	*IYD*
7	1211748	1321585	1261748	1271585	1.07E-08	ENSG00000164853	*UNCX*
7	3349469	3459397	3399469	3409397	1.32E-08	ENSG00000146555	*SDK1*
7	3688578	3797977	3738578	3747977	1.34E-08	n.a.	n.a.
7	10067005	10176870	10117005	10126870	3.94E-09	n.a.	n.a.
7	18395394	18504697	18445394	18454697	4.17E-09	ENSG00000048052	*HDAC9*
7	19093001	19202990	19143001	19152990	3.81E-08	ENSG00000146618	*FERD3L*
7	19437502	19557610	19497666	19507610	3.73E-09	n.a.	n.a.
7	27995905	28105595	28045905	28055595	1.19E-09	ENSG00000153814	*JAZF1*
7	30172426	30292686	30222426	30232347	2.03E-08	n.a.	n.a.
7	30797248	30906903	30847248	30856903	1.66E-08	ENSG00000106121	*C7orf67*
7	32286745	32396675	32336745	32346675	3.58E-08	ENSG00000154678	*PDE1C*
7	38567244	38675831	38617244	38625831	2.64E-08	ENSG00000078053	*AMPH*
7	38887364	38997130	38937364	38947130	1.47E-08	ENSG00000006715	*VPS41*
7	42336317	42446204	42386317	42396204	1.06E-08	n.a.	n.a.
7	46043377	46153174	46093377	46103174	9.18E-09	n.a.	n.a.
7	48479572	48589536	48529572	48539536	1.22E-08	ENSG00000179869	*ABCA13*
7	78616613	78726128	78666613	78676128	4.04E-09	ENSG00000187391	*MAGI2*
7	79049197	79158088	79099197	79108088	5.45E-10	n.a.	n.a.
7	80886668	80996120	80936668	80946120	1.63E-09	n.a.	n.a.
7	86760734	86870643	86810734	86820643	1.21E-08	ENSG00000182165	*TP53TG1*
7	86760734	86870643	86810734	86820643	1.21E-08	ENSG00000005471	*ABCB4*
7	93306422	93416374	93356422	93366374	1.33E-08	ENSG00000105825	*TFPI2*
7	96169763	96279575	96219763	96229575	2.24E-08	ENSG00000127922	*SHFM1*
7	107961491	108071157	108011491	108021157	3.42E-08	ENSG00000128590	*DNAJB9*
7	109257448	109367225	109307448	109317225	1.86E-09	n.a.	n.a.
7	112927739	113037473	112977739	112987473	8.09E-09	n.a.	n.a.
7	120256851	120397509	120306851	120315576	4.15E-09	ENSG00000106025	*TSPAN12*
7	134888399	134998230	134938399	134948230	1.49E-08	ENSG00000155561	*NUP205*
7	135322320	135432160	135372320	135382160	2.74E-09	n.a.	n.a.
7	136841043	137051779	136992020	137001779	8.31E-09	ENSG00000157680	*DGKI*
7	139165373	139275331	139215373	139225331	4.21E-09	ENSG00000059377	*TBXAS1*
7	145185621	145295288	145235621	145245288	3.29E-09	n.a.	n.a.
7	145531771	145683118	145623501	145633118	3.63E-09	ENSG00000174469	*CNTNAP2*
7	145978272	146088244	146028272	146038244	1.51E-08	n.a.	n.a.
7	152157001	152378499	152207001	152216725	5.74E-09	ENSG00000133627	*ACTR3B*
7	155550844	155660839	155600844	155610839	8.66E-09	n.a.	n.a.
8	208415	318356	258415	268356	3.69E-08	ENSG00000182366	*FAM87A*
8	1705411	1815223	1755411	1765223	2.23E-08	ENSG00000104728	*ARHGEF10*

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8	2012608	2122585	2062608	2072585	2.86E-09	ENSG00000036448	*MYOM2*
8	2805335	2914910	2855335	2864910	2.20E-08	ENSG00000183117	*CSMD1*
8	5089077	5199074	5139077	5149074	2.12E-09	n.a.	n.a.
8	9715838	9824929	9765838	9774929	1.48E-08	n.a.	n.a.
8	15971622	16465601	16021622	16031379	3.61E-09	ENSG00000038945	*MSR1*
8	16558329	16668184	16608329	16618184	3.95E-08	n.a.	n.a.
8	17745658	17855653	17795658	17805653	1.08E-08	ENSG00000104760	*FGL1*
8	18537864	18657976	18587864	18597648	4.24E-09	ENSG00000156011	*PSD3*
8	19774737	19882676	19824737	19832676	2.68E-08	ENSG00000175445	*LPL*
8	21035976	21145846	21085976	21095846	4.78E-09	n.a.	n.a.
8	23872153	24053220	23993884	24003220	1.19E-09	n.a.	n.a.
8	30040446	30254387	30195378	30204387	7.39E-09	ENSG00000104671	*DCTN6*
8	34429457	34538406	34479457	34488406	6.82E-09	n.a.	n.a.
8	35652255	35869146	35723988	35733305	8.39E-10	ENSG00000156687	*UNC5D*
8	39384731	39515235	39455323	39465235	1.43E-09	ENSG00000197475	n.a.
8	43282130	43401494	43332130	43342076	1.55E-09	ENSG00000188877	*POTEA*
8	51648670	51758579	51698670	51708579	2.51E-09	ENSG00000147481	*SNTG1*
8	53198222	53308206	53248222	53258206	3.95E-08	ENSG00000147488	*ST18*
8	56092434	56202352	56142434	56152352	2.19E-08	ENSG00000206579	*XKR4*
8	58405055	58514501	58455055	58464501	1.15E-08	n.a.	n.a.
8	75090808	75200595	75140808	75150595	1.98E-09	ENSG00000154589	*LY96*
8	82752068	82861800	82802068	82811800	1.98E-08	ENSG00000164695	*CHMP4C*
8	90213031	90322251	90263031	90272251	6.97E-10	n.a.	n.a.
8	101654683	101764371	101704683	101714371	1.33E-08	ENSG00000174226	*SNX31*
8	102425851	102535707	102475851	102485707	2.71E-09	n.a.	n.a.
8	102665235	102774334	102715235	102724334	7.18E-09	ENSG00000083307	*GRHL2*
8	108836877	108946357	108886877	108896357	3.38E-08	n.a.	n.a.
8	123762254	123871894	123812254	123821894	1.41E-08	ENSG00000178764	*ZHX2*
8	124847797	124957595	124897797	124907595	4.01E-09	ENSG00000176853	*FAM91A1*
8	125030117	125139840	125080117	125089840	1.20E-08	ENSG00000214814	*FER1L6*
8	125030117	125139840	125080117	125089840	1.20E-08	ENSG00000181171	*C8orf54*
9	828249	937949	878249	887949	2.84E-08	ENSG00000137090	*DMRT1*
9	9068470	9178227	9118470	9128227	8.33E-10	ENSG00000212829	*RPS26P3*
9	12422510	12532330	12472510	12482330	2.69E-08	n.a.	n.a.
9	15034374	15144031	15084374	15094031	3.09E-08	n.a.	n.a.
9	16060688	16170630	16110688	16120630	3.10E-08	n.a.	n.a.
9	16493888	16654533	16596474	16604533	6.02E-10	ENSG00000173068	*BNC2*
9	16834638	16944635	16884638	16894635	2.22E-09	n.a.	n.a.
9	23423526	23533213	23473526	23483213	1.16E-09	n.a.	n.a.
9	25141263	25251193	25191263	25201193	1.85E-09	n.a.	n.a.
9	26520067	26629986	26570067	26579986	8.75E-09	n.a.	n.a.
9	29746957	29856465	29796957	29806465	8.91E-09	n.a.	n.a.
9	33156428	33264833	33206428	33214833	1.40E-08	ENSG00000122711	*SPINK4*
9	75515677	75625498	75565677	75575498	2.15E-08	n.a.	n.a.
9	78889455	78999267	78939455	78949267	2.49E-08	ENSG00000197969	*VPS13A*

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9	86242046	86351675	86292046	86301675	9.67E-10	n.a.	n.a.
9	92846673	92956032	92896673	92906032	1.73E-08	n.a.	n.a.
9	101043505	101152971	101093505	101102971	2.79E-08	n.a.	n.a.
9	106948244	107058151	106998244	107008151	3.24E-08	ENSG00000070214	*SLC44A1*
9	114690945	114810936	114740945	114750746	2.42E-09	ENSG00000119457	*SLC46A2*
9	124528802	124638591	124578802	124588591	2.33E-08	ENSG00000148215	*OR5C1*
9	125932298	126041700	125982298	125991700	6.06E-09	n.a.	n.a.
10	457451	567339	507451	517339	2.24E-08	ENSG00000151240	*DIP2C*
10	2964799	3074760	3014799	3024760	8.02E-09	n.a.	n.a.
10	9500977	9610968	9550977	9560968	4.16E-10	n.a.	n.a.
10	10338229	10448024	10388229	10398024	3.87E-09	n.a.	n.a.
10	28448769	28558609	28498769	28508609	2.56E-08	ENSG00000150054	*MPP7*
10	52636659	52746506	52686659	52696506	1.91E-08	ENSG00000185532	*PRKG1*
10	55947070	56056778	55997070	56006778	2.35E-08	ENSG00000150275	*PCDH15*
10	57976303	58086266	58026303	58036266	1.81E-09	n.a.	n.a.
10	58447738	58556956	58497738	58506956	1.41E-08	n.a.	n.a.
10	59350285	59460215	59400285	59410215	3.51E-08	n.a.	n.a.
10	67839770	67960010	67900085	67910010	8.10E-10	ENSG00000183230	*CTNNA3*
10	68095045	68205021	68145045	68155021	2.66E-08	n.a.	n.a.
10	72364993	72474888	72414993	72424888	5.61E-09	n.a.	n.a.
10	77030367	77139863	77080367	77089863	3.91E-08	ENSG00000148655	*C10orf11*
10	80845369	80955098	80895369	80905098	2.08E-08	ENSG00000165424	*ZCCHC24*
10	91042186	91152142	91092186	91102142	1.73E-08	ENSG00000107798	*LIPA*
10	91042186	91152142	91092186	91102142	1.73E-08	ENSG00000119917	*IFIT3*
10	107959593	108069331	108009593	108019331	3.67E-09	n.a.	n.a.
10	118102470	118212240	118152470	118162240	3.25E-08	ENSG00000203837	*PNLIPRP3*
10	119927194	120036247	119977194	119986247	4.24E-09	ENSG00000165669	*C10orf84*
10	121821212	121940070	121881671	121890070	1.49E-08	n.a.	n.a.
10	122491162	122601064	122541162	122551064	2.24E-08	ENSG00000120008	*BRWD2*
10	122845219	122965152	122905267	122915152	2.88E-10	n.a.	n.a.
10	129358894	129478427	129418898	129428427	5.64E-09	ENSG00000186766	*FOXI2*
10	130720206	130830092	130770206	130780092	2.66E-09	n.a.	n.a.
10	132063026	132193172	132113026	132122982	1.98E-09	n.a.	n.a.
11	19599663	19709441	19649663	19659441	1.44E-08	ENSG00000166833	*NAV2*
11	20333900	20443811	20383900	20393811	1.32E-08	ENSG00000185238	*PRMT3*
11	21498292	21608073	21548292	21558073	1.71E-08	ENSG00000165973	*NELL1*
11	38081876	38397628	38131876	38141394	7.65E-11	n.a.	n.a.
11	42656749	42766347	42706749	42716347	2.98E-08	n.a.	n.a.
11	43967603	44077272	44017603	44027272	1.46E-08	ENSG00000205126	*ACCSL*
11	58330409	58440287	58380409	58390287	2.16E-10	ENSG00000156689	*GLYATL2*
11	59269972	59379867	59319972	59329867	3.84E-08	ENSG00000166900	*STX3*
11	59269972	59379867	59319972	59329867	3.84E-08	ENSG00000166902	*MRPL16*
11	60117880	60237203	60167880	60177422	4.66E-09	ENSG00000181995	*C11orf64*
11	62313644	62423505	62363644	62373505	3.53E-08	ENSG00000133316	*WDR74*
11	79189185	79298636	79239185	79248636	1.36E-08	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
11	87039769	87149407	87089769	87099407	2.92E-08	n.a.	n.a.
11	94189954	94340418	94281500	94290418	8.28E-10	ENSG00000166025	*AMOTL1*
11	94189954	94340418	94281500	94290418	8.28E-10	ENSG00000150316	*CWC15*
11	98546472	98656077	98596472	98606077	3.93E-08	n.a.	n.a.
11	104211100	104320241	104261100	104270241	5.27E-09	ENSG00000204403	*CASP12*
11	108856049	108965664	108906049	108915664	1.72E-08	n.a.	n.a.
11	115314545	115424243	115364545	115374243	2.90E-09	n.a.	n.a.
11	117032884	117142563	117082884	117092563	8.07E-10	ENSG00000177103	*DSCAML1*
11	133741819	133851594	133791819	133801594	7.41E-09	ENSG00000149328	*GLB1L2*
11	133741819	133851594	133791819	133801594	7.41E-09	ENSG00000109956	*B3GAT1*
12	8514544	8749273	8689395	8699273	1.00E-08	ENSG00000197614	*MFAP5*
12	10216569	10357713	10297834	10307713	7.14E-09	ENSG00000139112	*GABARAPL1*
12	10940252	11050194	10990252	11000194	1.98E-10	ENSG00000212127	*TAS2R14*
12	15367046	15551364	15491436	15501364	7.99E-09	ENSG00000151490	*PTPRO*
12	15642821	15752509	15692821	15702509	1.65E-08	ENSG00000151491	*EPS8*
12	27468053	27578003	27518053	27528003	2.82E-08	ENSG00000165935	*C12orf70*
12	27829119	27938883	27879119	27888883	9.22E-09	ENSG00000087448	*KLHDC5*
12	37373017	37482558	37423017	37432558	3.81E-08	ENSG00000139117	*CPNE8*
12	39042747	39152452	39092747	39102452	8.62E-09	ENSG00000188906	*LRRK2*
12	42947052	43056574	42997052	43006574	5.99E-09	ENSG00000139173	*TMEM117*
12	43903077	44012159	43953077	43962159	1.31E-08	ENSG00000177119	*ANO6*
12	47976799	48086591	48026799	48036591	1.28E-08	ENSG00000178401	*DNAJC22*
12	51471942	51591311	51532039	51541311	1.19E-10	ENSG00000170423	*KRT78*
12	53447620	53557566	53497620	53507566	9.93E-09	ENSG00000172551	*MUCL1*
12	53672209	53782077	53722209	53732077	1.00E-08	ENSG00000123307	*NEUROD4*
12	57487096	57596550	57537096	57546550	5.07E-09	ENSG00000139263	*LRIG3*
12	82082786	82192689	82132786	82142689	1.25E-08	n.a.	n.a.
12	90069420	90188955	90119420	90129118	3.52E-09	ENSG00000011465	*DCN*
12	92512995	92622599	92562995	92572599	1.65E-08	ENSG00000220515	n.a.
12	104744718	104854597	104794718	104804597	3.23E-08	n.a.	n.a.
12	111651772	111761376	111701772	111711376	5.77E-09	ENSG00000089169	*RPH3A*
12	124796117	124905655	124846117	124855655	9.75E-09	n.a.	n.a.
12	125697760	125807745	125747760	125757745	1.76E-09	ENSG00000189238	n.a.
12	127336467	127446321	127386467	127396321	6.75E-09	n.a.	n.a.
12	129970602	130080381	130020602	130030381	6.14E-10	ENSG00000111452	*GPR133*
13	18826967	18936302	18876967	18886302	1.23E-08	ENSG00000132958	*TPTE2*
13	21811159	21920958	21861159	21870958	6.31E-09	n.a.	n.a.
13	33045825	33155700	33095825	33105700	9.43E-09	n.a.	n.a.
13	37735362	37897881	37817996	37825888	5.96E-09	ENSG00000120686	*UFM1*
13	38709451	38819343	38759451	38769343	1.47E-08	ENSG00000183722	*LHFP*
13	41080309	41190243	41130309	41140243	1.32E-08	ENSG00000102763	*KIAA0564*
13	59019597	59129025	59069597	59079025	4.14E-10	n.a.	n.a.
13	67205241	67315076	67255241	67265076	1.65E-09	n.a.	n.a.
13	69250850	69381120	69310997	69320981	6.02E-10	ENSG00000150361	*KLHL1*
13	69935300	70045211	69985300	69995211	2.64E-08	n.a.	n.a.

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13	78100336	78210043	78150336	78160043	1.43E-08	ENSG00000152193	*RNF219*
13	88515298	88696158	88575469	88585278	1.82E-09	n.a.	n.a.
13	90985406	91095220	91035406	91045220	1.96E-08	ENSG00000179399	*GPC5*
13	92591140	92700988	92641140	92650988	3.90E-08	ENSG00000183098	*GPC6*
13	102790532	102900338	102840532	102850338	3.11E-08	n.a.	n.a.
13	103029936	103264439	103204988	103214439	7.73E-10	n.a.	n.a.
13	104117902	104227897	104167902	104177897	1.65E-08	n.a.	n.a.
13	107473958	107583809	107523958	107533809	8.43E-09	n.a.	n.a.
14	33332299	33475474	33415622	33425474	3.46E-09	ENSG00000129521	*EGLN3*
14	39502985	39633018	39563054	39573038	9.36E-10	n.a.	n.a.
14	44235814	44503667	44285814	44295703	1.64E-08	n.a.	n.a.
14	51451495	51561385	51501495	51511385	1.73E-08	ENSG00000186469	*GNG2*
14	56863240	56973172	56913240	56923172	3.43E-08	ENSG00000139977	*NAT12*
14	66785355	66895034	66835355	66845034	3.86E-08	ENSG00000072415	*MPP5*
14	78298536	78408276	78348536	78358276	3.02E-08	ENSG00000021645	*NRXN3*
14	79894340	80004336	79944340	79954336	1.58E-08	n.a.	n.a.
14	80497989	80607253	80547989	80557253	1.85E-08	ENSG00000165409	*TSHR*
14	83493714	83603697	83543714	83553697	4.67E-09	n.a.	n.a.
14	89445739	89565316	89495739	89505678	1.48E-09	ENSG00000140025	*C14orf143*
14	92505675	92615092	92555675	92565092	3.81E-09	ENSG00000100605	*ITPK1*
14	97037280	97146999	97087280	97096999	1.67E-10	n.a.	n.a.
14	102737704	102847561	102787704	102797561	1.14E-08	n.a.	n.a.
14	105544863	105652736	105594863	105602736	1.37E-08	n.a.	n.a.
14	105896339	106004171	105946339	105954171	2.05E-08	ENSG00000214398	n.a.
15	24522549	24632371	24572549	24582371	9.68E-09	ENSG00000166206	*GABRB3*
15	25983676	26093570	26033676	26043570	1.32E-09	ENSG00000104044	*OCA2*
15	31915235	32024854	31965235	31974854	9.65E-09	ENSG00000198838	*RYR3*
15	34045559	34155535	34095559	34105535	4.91E-10	n.a.	n.a.
15	42143313	42263882	42193313	42203285	1.17E-08	ENSG00000171877	*FRMD5*
15	46107395	46216678	46157395	46166678	5.27E-09	ENSG00000188467	*SLC24A5*
15	50280355	50389827	50330355	50339827	1.60E-08	ENSG00000128833	*MYO5C*
15	58233152	58342375	58283152	58292375	2.46E-08	n.a.	n.a.
15	66850000	66959768	66900000	66909768	6.04E-09	ENSG00000140350	*ANP32A*
15	91574654	91684241	91624654	91634241	1.92E-09	n.a.	n.a.
15	98331160	98451106	98381160	98390857	8.01E-09	ENSG00000140470	*ADAMTS17*
16	6192831	6302510	6242831	6252510	3.99E-08	n.a.	n.a.
16	7465646	7575546	7515646	7525546	1.13E-08	ENSG00000078328	n.a.
16	8237634	8357193	8297823	8307193	4.72E-09	n.a.	n.a.
16	8431090	8695537	8635588	8645537	2.59E-09	ENSG00000067365	*C16orf68*
16	46456451	46587768	46527985	46537768	1.67E-08	n.a.	n.a.
16	50453993	50563859	50503993	50513859	2.11E-08	n.a.	n.a.
16	52889717	52999318	52939717	52949318	2.56E-08	n.a.	n.a.
16	56644417	56753769	56694417	56703769	1.66E-08	ENSG00000070761	*C16orf80*
16	76961320	77071263	77011320	77021263	3.50E-09	ENSG00000186153	*WWOX*
16	81740232	81860227	81790232	81800178	5.64E-10	ENSG00000140945	*CDH13*

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16	83598485	83708477	83648485	83658477	2.73E-08	ENSG00000153786	*ZDHHC7*
17	21088013	21198002	21138013	21148002	1.31E-08	ENSG00000034152	*MAP2K3*
17	37028879	37138251	37078879	37088251	2.57E-09	ENSG00000173812	*EIF1*
17	51318754	51428539	51368754	51378539	7.16E-10	n.a.	n.a.
17	56142640	56252518	56192640	56202518	6.68E-09	ENSG00000141376	*BCAS3*
17	60365115	60474458	60415115	60424458	5.28E-09	ENSG00000120063	*GNA13*
17	60778059	60907702	60848310	60857702	1.98E-10	n.a.	n.a.
17	63844587	63954520	63894587	63904520	9.55E-09	ENSG00000141337	*ARSG*
17	72195918	72325982	72266413	72275982	8.53E-09	ENSG00000182534	*MXRA7*
18	28618964	28791790	28732104	28741790	2.52E-10	ENSG00000166960	*C18orf34*
18	36029899	36139593	36079899	36089593	1.01E-08	n.a.	n.a.
18	53189468	53299216	53239468	53249216	3.43E-08	ENSG00000119547	*ONECUT2*
18	59529215	59639135	59579215	59589135	1.01E-08	ENSG00000166396	*SERPINB7*
18	64138301	64248289	64188301	64198289	1.25E-08	n.a.	n.a.
18	64754914	64958486	64804914	64814826	5.60E-10	ENSG00000150636	*CCDC102B*
18	65711578	65821486	65761578	65771486	1.81E-09	ENSG00000150637	*CD226*
18	68603842	68713818	68653842	68663818	3.16E-08	ENSG00000166342	*NETO1*
18	71520972	71640987	71581089	71590987	4.17E-09	n.a.	n.a.
19	11669484	11778917	11719484	11728917	2.16E-08	ENSG00000197933	*ZNF823*
19	11898124	12007462	11948124	11957462	3.98E-08	ENSG00000197054	*ZNF763*
19	33747932	33869312	33797932	33807586	1.88E-09	n.a.	n.a.
19	36767849	36884574	36827973	36834574	1.42E-09	n.a.	n.a.
19	39135597	39255304	39185597	39195195	1.92E-08	ENSG00000186008	n.a.
19	41007576	41117442	41057576	41067442	8.14E-10	ENSG00000167595	*C19orf55*
19	45223926	45374319	45314937	45324319	4.80E-09	ENSG00000197782	*ZNF780A*
19	48579080	48688321	48629080	48638321	1.21E-09	ENSG00000131126	*TEX101*
19	48579080	48688321	48629080	48638321	1.21E-09	ENSG00000124466	*LYPD3*
19	51237331	51347303	51287331	51297303	1.49E-08	ENSG00000204866	*IGFL2*
19	52471796	52580956	52521796	52530956	1.97E-08	ENSG00000197405	*C5AR1*
19	52471796	52580956	52521796	52530956	1.97E-08	ENSG00000134830	*GPR77*
19	56427836	56536923	56477836	56486923	3.91E-08	n.a.	n.a.
19	57575452	57716035	57636087	57646041	8.83E-10	ENSG00000167555	*ZNF534*
19	59434571	59544505	59484571	59494505	9.68E-09	ENSG00000204577	*LILRA6*
19	59736464	59846379	59786464	59796379	4.88E-09	ENSG00000187095	*LILRA2*
20	951502	1061318	1001502	1011318	1.04E-08	ENSG00000125818	*PSMF1*
20	6241475	6351403	6291475	6301403	5.52E-09	n.a.	n.a.
20	19170791	19280743	19220791	19230743	1.89E-08	ENSG00000185052	*SLC24A3*
20	20622014	20731953	20672014	20681953	3.55E-08	ENSG00000188559	*C20orf74*
20	24173207	24293349	24223207	24233177	4.23E-10	n.a.	n.a.
20	41716665	41826636	41766665	41776636	2.99E-08	ENSG00000101057	*MYBL2*
20	43279190	43399244	43329190	43338818	1.23E-08	ENSG00000124107	*SLPI*
20	44708708	44818465	44758708	44768465	3.91E-09	ENSG00000172315	*TP53RK*
20	44708708	44818465	44758708	44768465	3.91E-09	ENSG00000197496	*SLC2A10*
20	49288547	49398425	49338547	49348425	2.89E-08	n.a.	n.a.
20	52190430	52422425	52362487	52372425	1.90E-08	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
20	57837075	57947032	57887075	57897032	2.15E-08	ENSG00000196074	*SYCP2*
20	58623432	58743393	58683447	58693393	1.24E-09	n.a.	n.a.
21	21295000	21404989	21345000	21354989	6.10E-10	ENSG00000154654	*NCAM2*
21	22932648	23042420	22982648	22992420	1.98E-09	n.a.	n.a.
21	27938947	28048735	27988947	27998735	1.36E-09	n.a.	n.a.
21	29727785	29837153	29777785	29787153	1.23E-09	ENSG00000171189	*GRIK1*
21	30380160	30489836	30430160	30439836	3.09E-10	ENSG00000156282	*CLDN17*
21	35817141	35926909	35867141	35876909	2.92E-09	n.a.	n.a.
21	37893505	38003502	37943505	37953502	2.25E-09	ENSG00000157542	*KCNJ6*
22	24480901	24590850	24530901	24540850	9.59E-09	ENSG00000133454	*MYO18B*
22	32730938	32840882	32780938	32790882	2.61E-08	n.a.	n.a.
CHB+JPT							
1	37025194	37133411	37075194	37083411	1.44E-10	ENSG00000163873	*GRIK3*
1	63942953	64052760	63992953	64002760	8.65E-09	ENSG00000185483	*ROR1*
1	64184683	64293968	64234683	64243968	3.12E-09	n.a.	n.a.
1	75416996	75526492	75466996	75476492	1.35E-09	ENSG00000137968	*SLC44A5*
1	103469185	103578851	103519185	103528851	8.47E-09	n.a.	n.a.
1	109758910	109868628	109808910	109818628	3.05E-10	ENSG00000143028	*SYPL2*
1	179416676	179526507	179466676	179476507	2.53E-10	ENSG00000179452	n.a.
1	181805606	181915529	181855606	181865529	3.83E-08	ENSG00000162704	*ARPC5*
1	181805606	181915529	181855606	181865529	3.83E-08	ENSG00000143344	*RGL1*
1	194034592	194144585	194084592	194094585	6.22E-09	n.a.	n.a.
1	206138351	206248286	206188351	206198286	2.39E-10	ENSG00000174059	*CD34*
1	245170726	245280081	245220726	245230081	7.94E-09	ENSG00000197472	*ZNF695*
2	4161943	4271354	4211943	4221354	9.47E-09	n.a.	n.a.
2	7544018	7653585	7594018	7603585	6.78E-09	n.a.	n.a.
2	15042617	15152501	15092617	15102501	3.62E-09	n.a.	n.a.
2	24383855	24503789	24433855	24443679	1.57E-09	ENSG00000198399	*ITSN2*
2	37629764	37739660	37679764	37689660	9.21E-09	ENSG00000163171	*CDC42EP3*
2	81642954	81752433	81692954	81702433	9.19E-09	n.a.	n.a.
2	86420650	86530548	86470650	86480548	2.24E-08	ENSG00000115548	*JMJD1A*
2	107132184	107252362	107182184	107191113	7.87E-10	n.a.	n.a.
2	151224799	151334526	151274799	151284526	4.69E-09	n.a.	n.a.
2	177424441	177533521	177474441	177483521	4.74E-09	n.a.	n.a.
2	188528149	188638106	188578149	188588106	1.73E-08	n.a.	n.a.
2	194687010	194817154	194737010	194746818	4.07E-11	n.a.	n.a.
2	202052305	202162058	202102305	202112058	3.38E-08	ENSG00000155754	*ALS2CR11*
2	215921581	216031383	215971581	215981383	1.74E-08	ENSG00000115414	*FN1*
2	223625575	223755822	223695838	223705822	4.62E-10	n.a.	n.a.
3	17757230	17867059	17807230	17817059	2.06E-08	ENSG00000131374	*TBC1D5*
3	18971639	19080822	19021639	19030822	5.05E-09	n.a.	n.a.
3	97781565	97890978	97831565	97840978	1.94E-08	n.a.	n.a.
3	99331808	99441778	99381808	99391778	1.07E-08	ENSG00000198068	*OR5H15*
3	109057897	109167716	109107897	109117716	2.94E-09	n.a.	n.a.
3	110294094	110403858	110344094	110353858	3.76E-08	ENSG00000114487	*MORC1*

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
3	136796133	136906087	136846133	136856087	1.69E-08	n.a.	n.a.
3	146472561	146582522	146522561	146532522	2.04E-10	n.a.	n.a.
3	155702265	155812163	155752265	155762163	5.66E-09	n.a.	n.a.
3	160810006	160919764	160860006	160869764	5.02E-09	ENSG00000151967	*SCHIP1*
3	164187145	164297136	164237145	164247136	8.85E-09	n.a.	n.a.
4	6288142	6408528	6338142	6348095	1.32E-09	ENSG00000109501	*WFS1*
4	17250145	17360122	17300145	17310122	4.34E-09	ENSG00000047662	*FAM184B*
4	19648308	19758257	19698308	19708257	1.02E-08	n.a.	n.a.
4	32612876	32722011	32662876	32672011	2.20E-08	n.a.	n.a.
4	41648592	41835140	41719050	41728350	5.46E-10	ENSG00000014824	*SLC30A9*
4	70013085	70122666	70063085	70072666	8.97E-09	ENSG00000213759	*UGT2B11*
4	86616416	86725866	86666416	86675866	8.25E-09	ENSG00000138639	*ARHGAP24*
4	135610281	135720147	135660281	135670147	3.01E-10	n.a.	n.a.
4	159516223	159637555	159577788	159587555	1.27E-10	n.a.	n.a.
4	167024921	167134656	167074921	167084656	9.55E-09	ENSG00000038295	*TLL1*
4	170916232	171026110	170966232	170976110	3.74E-08	n.a.	n.a.
4	176524029	176633194	176574029	176583194	1.15E-08	n.a.	n.a.
4	178028544	178158603	178078544	178088424	1.57E-09	n.a.	n.a.
4	178841769	178951541	178891769	178901541	2.14E-08	n.a.	n.a.
5	8941824	9051609	8991824	9001609	1.67E-08	n.a.	n.a.
5	97214622	97324613	97264622	97274613	7.33E-09	n.a.	n.a.
5	117563179	117693097	117623357	117632864	4.50E-09	n.a.	n.a.
5	124457396	124567289	124507396	124517289	1.22E-08	n.a.	n.a.
5	127902655	128012328	127952655	127962328	2.80E-08	n.a.	n.a.
5	137003365	137113016	137053365	137063016	8.45E-09	ENSG00000146021	*KLHL3*
5	141304610	141413293	141354610	141363293	2.17E-09	ENSG00000113552	*GNPDA1*
6	25155429	25265396	25205429	25215396	1.27E-08	ENSG00000168405	*CMAH*
6	63776582	63886531	63826582	63836531	1.15E-08	n.a.	n.a.
6	67166270	67276239	67216270	67226239	4.07E-11	n.a.	n.a.
6	112815920	112925256	112865920	112875256	3.33E-08	n.a.	n.a.
6	129338050	129447104	129388050	129397104	2.23E-08	ENSG00000196569	*LAMA2*
7	3992147	4101869	4042147	4051869	1.63E-09	ENSG00000146555	*SDK1*
7	19431848	19541741	19481848	19491741	2.70E-08	n.a.	n.a.
7	49162814	49271468	49212814	49221468	1.34E-08	n.a.	n.a.
7	54604266	54714221	54654266	54664221	7.81E-09	ENSG00000170419	*VSTM2A*
7	101468685	101578345	101518685	101528345	2.17E-08	ENSG00000160967	*CUX1*
7	110928160	111037066	110978160	110987066	3.93E-11	ENSG00000184903	*IMMP2L*
7	119178681	119288390	119228681	119238390	3.92E-08	n.a.	n.a.
7	131201425	131311164	131251425	131261164	3.69E-10	n.a.	n.a.
7	155367424	155477353	155417424	155427353	1.63E-08	ENSG00000204876	n.a.
8	10846529	10956442	10896529	10906442	3.98E-08	ENSG00000171044	*XKR6*
8	11780143	11890010	11830143	11840010	2.21E-10	ENSG00000205882	*DEFB134*
8	50218674	50338697	50278737	50288697	1.07E-08	n.a.	n.a.
8	56934254	57044165	56984254	56994165	2.47E-08	ENSG00000147507	*LYN*
8	120373469	120483155	120423469	120433155	2.05E-09	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
8	120935575	121045403	120985575	120995403	7.94E-09	ENSG00000155792	*DEPDC6*
9	10600129	10709873	10650129	10659873	1.97E-09	n.a.	n.a.
9	11045707	11165140	11095707	11105500	2.33E-12	n.a.	n.a.
9	16551692	16660889	16601692	16610889	1.24E-08	ENSG00000173068	*BNC2*
9	75961384	76071044	76011384	76021044	5.75E-09	n.a.	n.a.
9	123769116	123878892	123819116	123828892	2.53E-09	ENSG00000175764	*TTLL11*
9	131607709	131717544	131657709	131667544	1.48E-08	ENSG00000136878	*USP20*
10	3902232	4012090	3952232	3962090	1.11E-11	n.a.	n.a.
10	55577106	55687093	55627106	55637093	1.69E-09	ENSG00000150275	*PCDH15*
10	55782701	55892539	55832701	55842539	7.64E-09	n.a.	n.a.
10	59322139	59575727	59402926	59412905	6.56E-11	n.a.	n.a.
10	82071433	82253516	82121433	82129901	1.34E-09	ENSG00000133665	*DYDC2*
10	87117583	87226925	87167583	87176925	1.84E-08	n.a.	n.a.
10	127061186	127170208	127111186	127120208	3.95E-08	n.a.	n.a.
11	4718977	4828330	4768977	4778330	1.32E-08	ENSG00000167346	*MMP26*
11	23620797	23730561	23670797	23680561	5.83E-09	n.a.	n.a.
11	25087541	25208180	25137541	25146942	7.38E-09	n.a.	n.a.
11	25971643	26090783	26021643	26031382	5.98E-10	n.a.	n.a.
11	37908714	38018331	37958714	37968331	8.80E-09	n.a.	n.a.
11	39263416	39372951	39313416	39322951	3.73E-09	n.a.	n.a.
11	39692796	39802176	39742796	39752176	7.02E-09	n.a.	n.a.
11	87138674	87248425	87188674	87198425	1.43E-08	n.a.	n.a.
11	96698477	96807835	96748477	96757835	5.68E-09	n.a.	n.a.
11	97528280	97638256	97578280	97588256	7.40E-09	n.a.	n.a.
12	32672358	32782327	32722358	32732327	2.36E-08	ENSG00000087470	*DNM1L*
12	53231280	53340940	53281280	53290940	5.61E-10	ENSG00000135447	*PPP1R1A*
12	53231280	53340940	53281280	53290940	5.61E-10	ENSG00000135413	*LACRT*
12	84618003	84727973	84668003	84677973	5.94E-11	ENSG00000198774	*RASSF9*
12	97169923	97278998	97219923	97228998	1.40E-08	n.a.	n.a.
12	129969331	130079205	130019331	130029205	3.46E-08	ENSG00000111452	*GPR133*
13	45225436	45333565	45275436	45283565	7.00E-09	ENSG00000215475	*SIAH3*
13	60298813	60408388	60348813	60358388	3.47E-08	n.a.	n.a.
13	104456061	104566048	104506061	104516048	3.36E-09	n.a.	n.a.
13	105018750	105128603	105068750	105078603	7.58E-09	n.a.	n.a.
15	40336454	40446426	40386454	40396426	2.39E-09	ENSG00000214013	*GANC*
15	61892963	62002122	61942963	61952122	2.60E-08	ENSG00000103657	*HERC1*
15	61892963	62002122	61942963	61952122	2.60E-08	ENSG00000035664	*DAPK2*
15	86513328	86623194	86563328	86573194	1.31E-09	ENSG00000140538	*NTRK3*
15	98336682	98446142	98386682	98396142	8.46E-09	ENSG00000140470	*ADAMTS17*
16	5482839	5592836	5532839	5542836	1.45E-08	n.a.	n.a.
16	79629749	79739291	79679749	79689291	1.22E-08	ENSG00000140905	*GCSH*
16	81746275	81854494	81796275	81804494	6.43E-11	ENSG00000140945	*CDH13*
17	8891763	9001519	8941763	8951519	1.57E-09	ENSG00000065320	*NTN1*
17	36944831	37054809	36994831	37004809	3.60E-08	ENSG00000186847	*KRT14*
17	53182090	53291839	53232090	53241839	6.13E-10	ENSG00000181610	*MRPS23*

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
17	56131340	56240825	56181340	56190825	9.07E-11	ENSG00000141376	*BCAS3*
17	65545487	65655093	65595487	65605093	1.40E-09	ENSG00000153822	*KCNJ16*
18	11005451	11115425	11055451	11065425	9.09E-10	n.a.	n.a.
18	53823966	53933503	53873966	53883503	5.42E-10	ENSG00000049759	*NEDD4L*
18	59506677	59616415	59556677	59566415	4.61E-09	ENSG00000166396	*SERPINB7*
18	61582394	61702170	61632394	61642103	7.88E-09	ENSG00000081138	*CDH7*
18	63684655	63794519	63734655	63744519	8.11E-09	n.a.	n.a.
18	70573244	70683006	70623244	70633006	2.16E-08	ENSG00000215421	*ZNF407*
19	6087442	6197373	6137442	6147373	1.45E-09	ENSG00000130377	*ACSBG2*
19	36749293	36858184	36799293	36808184	3.01E-08	n.a.	n.a.
20	11938626	12048402	11988626	11998402	4.46E-09	n.a.	n.a.
20	22404140	22513528	22454140	22463528	2.92E-08	ENSG00000125798	*FOXA2*
20	31120574	31230422	31170574	31180422	9.59E-09	ENSG00000186191	*C20orf186*
21	20989362	21099246	21039362	21049246	3.26E-09	n.a.	n.a.
21	21707908	21816420	21757908	21766420	5.02E-09	ENSG00000154654	*NCAM2*
YRI							
1	4870735	4980651	4920735	4930651	8.07E-09	n.a.	n.a.
1	13823309	13933241	13873309	13883241	4.48E-10	ENSG00000116731	*PRDM2*
1	20413206	20522555	20463206	20472555	1.10E-08	ENSG00000158816	*VWA5B1*
1	36934932	37097131	37037187	37047131	1.91E-09	ENSG00000163873	*GRIK3*
1	42809335	42918788	42859335	42868788	2.70E-08	ENSG00000186409	n.a.
1	59811568	59921231	59861568	59871231	6.47E-09	ENSG00000172456	*FGGY*
1	73159742	73269292	73209742	73219292	8.16E-09	n.a.	n.a.
1	79829438	79949721	79889943	79899721	3.87E-09	n.a.	n.a.
1	86419276	86528838	86469276	86478838	3.96E-08	n.a.	n.a.
1	99855589	100046207	99966739	99976721	8.25E-11	ENSG00000156869	*FRRS1*
1	106377980	106487733	106427980	106437733	4.08E-10	n.a.	n.a.
1	155242061	155351428	155292061	155301428	3.18E-09	ENSG00000132694	*ARHGEF11*
1	173448741	173558687	173498741	173508687	1.74E-11	ENSG00000116147	*TNR*
1	184419087	184529045	184469087	184479045	1.94E-09	ENSG00000143341	*HMCN1*
1	191738540	191848404	191788540	191798404	2.65E-08	n.a.	n.a.
1	213667620	213777582	213717620	213727582	3.91E-08	n.a.	n.a.
1	221394736	221504627	221444736	221454627	1.05E-08	ENSG00000143502	*SUSD4*
1	246384277	246494129	246434277	246444129	2.86E-09	ENSG00000177233	*OR2M3*
2	24382278	24502243	24432278	24441844	1.94E-11	ENSG00000198399	*ITSN2*
2	54476778	54586707	54526778	54536707	2.70E-08	ENSG00000115306	*SPTBN1*
2	84191980	84311960	84241980	84251876	3.48E-09	n.a.	n.a.
2	114848255	114958065	114898255	114908065	7.01E-09	ENSG00000175497	*DPP10*
2	132735607	132855558	132785607	132795561	2.37E-09	n.a.	n.a.
2	141894443	142004338	141944443	141954338	7.28E-09	ENSG00000168702	*LRP1B*
2	182246665	182369058	182296665	182306170	1.81E-10	ENSG00000162992	*NEUROD1*
2	205719400	205828370	205769400	205778370	1.14E-09	ENSG00000116117	*PARD3B*
3	536594	646563	586594	596563	4.57E-09	n.a.	n.a.
3	2373053	2482381	2423053	2432381	2.66E-08	ENSG00000144619	*CNTN4*
3	5320406	5430190	5370406	5380190	2.13E-08	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
3	23081221	23202040	23142243	23152040	1.08E-09	n.a.	n.a.
3	36364625	36494650	36414625	36424144	8.25E-11	ENSG00000144681	*STAC*
3	41349401	41459183	41399401	41409183	2.20E-09	ENSG00000168038	*ULK4*
3	43693436	43801778	43743436	43751778	2.54E-08	ENSG00000011198	*ABHD5*
3	64426658	64536323	64476658	64486323	1.77E-09	ENSG00000163638	*ADAMTS9*
3	75304187	75414076	75354187	75364076	8.48E-09	n.a.	n.a.
3	78245678	78355243	78295678	78305243	7.75E-09	n.a.	n.a.
3	79104378	79213990	79154378	79163990	2.04E-09	ENSG00000169855	*ROBO1*
3	95290048	95399666	95340048	95349666	7.15E-09	ENSG00000178694	*NSUN3*
3	95751850	95861845	95801850	95811845	1.67E-08	n.a.	n.a.
3	99247597	99357585	99297597	99307585	8.66E-09	ENSG00000196578	*OR5AC2*
3	104242065	104352042	104292065	104302042	1.93E-10	n.a.	n.a.
3	105261477	105371078	105311477	105321078	2.11E-08	ENSG00000214405	n.a.
3	108157665	108267642	108207665	108217642	2.86E-10	n.a.	n.a.
3	141867812	141977715	141917812	141927715	1.92E-08	ENSG00000155890	*TRIM42*
3	146485421	146594742	146535421	146544742	1.81E-10	n.a.	n.a.
3	149306627	149416518	149356627	149366518	2.48E-08	n.a.	n.a.
3	167698224	167807954	167748224	167757954	2.84E-08	n.a.	n.a.
3	179975850	180085645	180025850	180035645	4.38E-09	ENSG00000197584	*KCNMB2*
3	184434340	184544050	184484340	184494050	1.91E-10	ENSG00000053524	*MCF2L2*
3	189887078	189996944	189937078	189946944	2.79E-08	ENSG00000145012	*LPP*
3	190943750	191053505	190993750	191003505	1.54E-08	ENSG00000073282	*TP63*
3	193191467	193301396	193241467	193251396	1.40E-08	n.a.	n.a.
3	197331035	197441026	197381035	197391026	1.81E-08	ENSG00000163958	*ZDHHC19*
4	983248	1093172	1033248	1043172	1.97E-08	ENSG00000178222	*RNF212*
4	3500900	3621054	3550900	3560375	1.03E-08	ENSG00000163956	*LRPAP1*
4	8971648	9081406	9021648	9031406	2.09E-08	ENSG00000186146	*DEFB131*
4	11616229	11726216	11666229	11676216	3.61E-08	n.a.	n.a.
4	14278121	14387775	14328121	14337775	1.98E-08	n.a.	n.a.
4	17782634	17912613	17832634	17842088	8.48E-09	n.a.	n.a.
4	21263121	21372734	21313121	21322734	3.79E-08	ENSG00000185774	*KCNIP4*
4	35748496	35858336	35798496	35808336	2.26E-10	ENSG00000047365	*ARAP2*
4	42709663	42819646	42759663	42769646	3.38E-09	ENSG00000215203	*GRXCR1*
4	43806692	43916412	43856692	43866412	4.00E-09	ENSG00000183783	*KCTD8*
4	55388408	55497816	55438408	55447816	3.62E-09	n.a.	n.a.
4	57065485	57175425	57115485	57125425	3.65E-08	ENSG00000196503	*ARL9*
4	58080145	58190090	58130145	58140090	1.06E-09	n.a.	n.a.
4	63343946	63453869	63393946	63403869	1.29E-08	n.a.	n.a.
4	64015330	64125212	64065330	64075212	8.39E-09	n.a.	n.a.
4	88950767	89060764	89000767	89010764	1.54E-08	ENSG00000152595	*MEPE*
4	88950767	89060764	89000767	89010764	1.54E-08	ENSG00000183199	*HSP90AB3P*
4	93811847	93921502	93861847	93871502	1.91E-09	ENSG00000152208	*GRID2*
4	97557869	97790761	97730837	97740761	5.04E-09	n.a.	n.a.
4	100210496	100330411	100270745	100280411	3.38E-11	ENSG00000198099	*ADH4*
4	108083711	108193607	108133711	108143607	1.36E-08	ENSG00000155011	*DKK2*

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
4	119894987	120075813	119944987	119954789	4.92E-11	ENSG00000150961	*SEC24D*
4	131910075	132020008	131960075	131970008	5.68E-09	n.a.	n.a.
4	138091938	138201765	138141938	138151765	1.84E-08	n.a.	n.a.
4	143671542	143781515	143721542	143731515	2.12E-09	n.a.	n.a.
4	148291906	148475054	148415209	148425054	4.79E-11	n.a.	n.a.
4	153392228	153502206	153442228	153452206	2.83E-10	ENSG00000109670	*FBXW7*
4	157265631	157375276	157315631	157325276	1.37E-09	n.a.	n.a.
4	159758019	159867896	159808019	159817896	7.97E-09	ENSG00000205208	*C4orf46*
4	159758019	159867896	159808019	159817896	7.97E-09	ENSG00000171503	*ETFDH*
4	162172027	162281987	162222027	162231987	2.79E-08	n.a.	n.a.
4	163615182	163725014	163665182	163675014	4.34E-09	n.a.	n.a.
4	176361854	176471559	176411854	176421559	3.73E-08	n.a.	n.a.
4	176790390	176900273	176840390	176850273	3.38E-11	ENSG00000150625	*GPM6A*
4	184204236	184313605	184254236	184263605	7.42E-09	ENSG00000151718	*WWC2*
4	189969174	190079118	190019174	190029118	3.34E-09	n.a.	n.a.
4	190658887	190819031	190739050	190749027	1.14E-09	n.a.	n.a.
5	4255299	4365223	4305299	4315223	1.33E-09	n.a.	n.a.
5	18324455	18434442	18374455	18384442	2.15E-08	n.a.	n.a.
5	21505816	21655905	21565840	21575831	9.29E-09	ENSG00000198014	n.a.
5	23155746	23265626	23205746	23215626	2.28E-09	n.a.	n.a.
5	65647250	65780812	65720959	65730812	2.16E-09	ENSG00000205619	n.a.
5	71514708	71624621	71564708	71574621	2.00E-08	ENSG00000113048	*MRPS27*
5	83807680	83917381	83857680	83867381	1.52E-08	n.a.	n.a.
5	94619514	94729254	94669514	94679254	2.25E-08	ENSG00000175471	*MCTP1*
5	103953314	104062812	104003314	104012812	2.55E-09	n.a.	n.a.
5	104967588	105076529	105017588	105026529	1.95E-08	n.a.	n.a.
5	117597895	117707254	117647895	117657254	1.27E-09	n.a.	n.a.
5	117763488	118019158	117959270	117969158	1.14E-08	n.a.	n.a.
5	128649555	128759390	128699555	128709390	5.72E-09	n.a.	n.a.
5	141305842	141415580	141355842	141365580	1.95E-08	ENSG00000113552	*GNPDA1*
5	151213949	151323931	151263949	151273931	5.66E-10	ENSG00000145888	*GLRA1*
5	152869545	152989663	152919545	152929422	5.98E-10	ENSG00000155511	*GRIA1*
5	160127170	160257093	160187277	160197053	1.61E-10	ENSG00000118322	*ATP10B*
5	163518471	163628135	163568471	163578135	1.41E-08	n.a.	n.a.
5	166345073	166454989	166395073	166404989	5.64E-11	n.a.	n.a.
5	174377023	174486770	174427023	174436770	3.47E-08	n.a.	n.a.
6	29434364	29554196	29484364	29494303	2.02E-09	ENSG00000112462	*OR12D3*
6	30433695	30543670	30483695	30493670	9.33E-09	n.a.	n.a.
6	30844975	30954911	30894975	30904911	3.09E-08	ENSG00000214894	n.a.
6	31345585	31455426	31395585	31405426	3.38E-09	ENSG00000204525	*HLA-C*
6	32669640	32859076	32719640	32729569	2.71E-10	ENSG00000179344	*HLA-DQB1*
6	38950190	39060170	39000190	39010170	2.67E-09	ENSG00000124721	*DNAH8*
6	48315912	48580494	48520533	48530494	1.55E-08	n.a.	n.a.
6	57420721	57767987	57698266	57707862	7.48E-09	n.a.	n.a.
6	63776582	63886526	63826582	63836526	2.72E-09	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
6	64056119	64166056	64106119	64116056	1.25E-09	ENSG00000146166	*LGSN*
6	66513711	66623618	66563711	66573618	4.55E-09	n.a.	n.a.
6	75710972	75832458	75772925	75782458	2.11E-08	n.a.	n.a.
6	75932671	76042343	75982671	75992343	3.55E-08	ENSG00000111799	*COL12A1*
6	75932671	76042343	75982671	75992343	3.55E-08	ENSG00000112695	*COX7A2*
6	77147061	77257059	77197061	77207059	3.09E-08	n.a.	n.a.
6	82353052	82462699	82403052	82412699	2.95E-08	n.a.	n.a.
6	85803437	85913316	85853437	85863316	3.48E-08	n.a.	n.a.
6	95133876	95243862	95183876	95193862	3.61E-08	n.a.	n.a.
6	109231959	109371825	109281959	109291853	2.40E-09	ENSG00000118690	*ARMC2*
6	120421792	120531600	120471792	120481600	1.08E-08	n.a.	n.a.
6	122083715	122193546	122133715	122143546	2.94E-08	n.a.	n.a.
6	124400554	124510298	124450554	124460298	2.84E-08	ENSG00000188580	*NKAIN2*
6	140346414	140456180	140396414	140406180	1.23E-08	n.a.	n.a.
6	151154546	151263329	151204546	151213329	1.77E-08	ENSG00000120278	*PLEKHG1*
6	154853049	154962780	154903049	154912780	7.90E-09	ENSG00000153721	*CNKSR3*
6	157990558	158100241	158040558	158050241	6.16E-09	ENSG00000175048	*ZDHHC14*
6	158409833	158519226	158459833	158469226	2.23E-08	ENSG00000122335	*SERAC1*
6	160592439	160702211	160642439	160652211	2.49E-08	ENSG00000112499	*SLC22A2*
6	168799357	168909344	168849357	168859344	2.95E-09	ENSG00000112562	*SMOC2*
6	169488931	169598810	169538931	169548810	2.33E-08	n.a.	n.a.
6	170511524	170621330	170561524	170571330	1.99E-08	ENSG00000112584	*FAM120B*
7	3735339	3845287	3785339	3795287	1.74E-09	ENSG00000146555	*SDK1*
7	4163560	4273457	4213560	4223457	2.02E-08	n.a.	n.a.
7	17913563	18106534	17963563	17973313	2.51E-09	ENSG00000071189	*SNX13*
7	18439265	18549221	18489265	18499221	1.05E-09	ENSG00000048052	*HDAC9*
7	19430315	19540260	19480315	19490260	1.05E-08	n.a.	n.a.
7	29893633	30003330	29943633	29953330	1.58E-08	ENSG00000136193	*SCRN1*
7	35376998	35497388	35426998	35436796	1.10E-09	n.a.	n.a.
7	41972250	42081762	42022250	42031762	1.51E-08	ENSG00000106571	*GLI3*
7	42335633	42445581	42385633	42395581	8.62E-10	n.a.	n.a.
7	53396948	53506758	53446948	53456758	5.19E-09	n.a.	n.a.
7	54410200	54529392	54470275	54479392	8.08E-10	n.a.	n.a.
7	55320648	55430641	55370648	55380641	1.45E-11	ENSG00000132434	*LANCL2*
7	64855038	64964875	64905038	64914875	2.04E-08	ENSG00000169921	n.a.
7	91012764	91121597	91062764	91071597	2.57E-09	n.a.	n.a.
7	92435168	92545093	92485168	92495093	1.31E-09	n.a.	n.a.
7	118474018	118614637	118554731	118564637	5.68E-09	n.a.	n.a.
7	125428929	125538905	125478929	125488905	2.87E-09	n.a.	n.a.
7	133069253	133229109	133170018	133179109	2.45E-10	ENSG00000131558	*EXOC4*
7	134848292	134967619	134908327	134917619	5.37E-09	ENSG00000155561	*NUP205*
7	139169143	139278799	139219143	139228799	4.18E-10	ENSG00000059377	*TBXAS1*
7	140963597	141073140	141013597	141023140	6.74E-11	ENSG00000127359	*KIAA1147*
7	146943839	147053376	146993839	147003376	7.56E-10	ENSG00000174469	*CNTNAP2*
7	158732284	158852296	158792304	158802296	1.68E-09	n.a.	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
8	1702312	1812271	1752312	1762271	1.62E-08	ENSG00000104728	*ARHGEF10*
8	3654876	3764742	3704876	3714742	5.43E-10	n.a.	n.a.
8	3906844	4016736	3956844	3966736	2.18E-09	n.a.	n.a.
8	4594679	4704634	4644679	4654634	9.24E-09	n.a.	n.a.
8	5710355	5820327	5760355	5770327	1.14E-08	n.a.	n.a.
8	23016243	23126155	23066243	23076155	1.10E-09	ENSG00000173530	*TNFRSF10D*
8	32897840	33007836	32947840	32957836	3.44E-08	n.a.	n.a.
8	79200198	79310061	79250198	79260061	1.11E-08	n.a.	n.a.
8	82332049	82441679	82382049	82391679	1.90E-08	ENSG00000164687	*FABP5L2*
8	85398122	85518354	85458531	85468354	9.92E-10	n.a.	n.a.
8	92489226	92598877	92539226	92548877	1.76E-08	n.a.	n.a.
8	120051706	120161675	120101706	120111675	2.73E-08	ENSG00000184374	*COLEC10*
8	127158213	127268063	127208213	127218063	2.24E-08	n.a.	n.a.
8	130241742	130351579	130291742	130301579	4.31E-09	n.a.	n.a.
8	130816197	130926195	130866197	130876195	1.04E-08	ENSG00000147697	*GSDMC*
8	132362634	132472596	132412634	132422596	1.63E-08	n.a.	n.a.
8	134440359	134550339	134490359	134500339	1.67E-09	ENSG00000008513	*ST3GAL1*
8	135926238	136036101	135976238	135986101	1.93E-08	n.a.	n.a.
8	137092623	137212194	137142623	137152586	6.95E-10	n.a.	n.a.
8	138496674	138606420	138546674	138556420	3.61E-08	n.a.	n.a.
9	9680605	9790514	9730605	9740514	7.64E-09	n.a.	n.a.
9	10388782	10498677	10438782	10448677	1.67E-09	n.a.	n.a.
9	12037077	12147065	12087077	12097065	2.49E-08	n.a.	n.a.
9	12652157	12762146	12702157	12712146	1.88E-08	ENSG00000107165	*TYRP1*
9	15955008	16064891	16005008	16014891	2.29E-08	ENSG00000164989	*C9orf93*
9	24653105	24763039	24703105	24713039	2.10E-09	n.a.	n.a.
9	31644278	31754115	31694278	31704115	2.44E-08	n.a.	n.a.
9	44684944	44794637	44734944	44744637	2.62E-08	n.a.	n.a.
9	91690411	91800172	91740411	91750172	3.98E-08	n.a.	n.a.
9	100412521	100522373	100462521	100472373	4.75E-09	ENSG00000136928	*GABBR2*
9	107308722	107417306	107358722	107367306	3.38E-09	ENSG00000106701	*FSD1L*
9	107308722	107417306	107358722	107367306	3.38E-09	ENSG00000106692	*FKTN*
9	138250273	138356368	138300273	138306368	7.29E-09	ENSG00000165661	*QSOX2*
9	138822720	138930998	138872720	138880998	1.76E-08	ENSG00000177943	*MAMDC4*
9	138822720	138930998	138872720	138880998	1.76E-08	ENSG00000107223	*EDF1*
10	25169318	25279195	25219318	25229195	8.03E-09	ENSG00000099256	*PRTFDC1*
10	47057619	47167276	47107619	47117276	5.69E-09	ENSG00000198250	*ANTXRL*
10	55093068	55202990	55143068	55152990	4.29E-10	n.a.	n.a.
10	57604041	57723632	57664215	57673632	4.23E-09	n.a.	n.a.
10	58913807	59023667	58963807	58973667	3.30E-08	n.a.	n.a.
10	68147491	68256569	68197491	68206569	3.31E-08	ENSG00000183230	*CTNNA3*
10	92049635	92159497	92099635	92109497	1.31E-08	n.a.	n.a.
10	107134271	107244178	107184271	107194178	2.75E-08	n.a.	n.a.
10	109003054	109112833	109053054	109062833	1.19E-08	n.a.	n.a.
10	118507959	118617886	118557959	118567886	2.26E-08	ENSG00000188316	*C10orf134*

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10	134207902	134412074	134278316	134287774	3.45E-10	ENSG00000068383	*INPP5A*
11	5007434	5117204	5057434	5067204	1.41E-08	ENSG00000176787	*OR52E2*
11	6015825	6125787	6065825	6075787	4.43E-10	n.a.	n.a.
11	6753243	6873391	6813393	6823391	1.79E-08	n.a.	n.a.
11	34336403	34446297	34386403	34396297	1.06E-08	ENSG00000121691	*CAT*
11	48255938	48387052	48305938	48315892	3.94E-09	ENSG00000176547	*OR4C3*
11	55119145	55229067	55169145	55179067	3.75E-08	ENSG00000181927	*OR4P4*
11	55119145	55229067	55169145	55179067	3.75E-08	ENSG00000174982	*OR4S2*
11	58322153	58432053	58372153	58382053	8.66E-09	ENSG00000156689	*GLYATL2*
11	71924296	72034209	71974296	71984209	2.46E-10	ENSG00000186642	*PDE2A*
11	93804371	93913922	93854371	93863922	3.48E-08	ENSG00000020922	*MRE11A*
11	93804371	93913922	93854371	93863922	3.48E-08	ENSG00000168876	*ANKRD49*
11	97528804	97638753	97578804	97588753	1.40E-08	n.a.	n.a.
11	98832809	98942728	98882809	98892728	1.77E-08	n.a.	n.a.
11	126138569	126248207	126188569	126198207	6.92E-09	n.a.	n.a.
12	2190860	2300493	2240860	2250493	8.07E-09	ENSG00000151067	*CACNA1C*
12	10945041	11167569	10995041	11004915	1.82E-08	ENSG00000212127	*TAS2R14*
12	17722238	17832178	17772238	17782178	9.18E-09	n.a.	n.a.
12	41400616	41510579	41450616	41460579	1.10E-09	n.a.	n.a.
12	43420652	43530560	43470652	43480560	1.45E-09	ENSG00000184613	*NELL2*
12	57301424	57411025	57351424	57361025	3.59E-09	n.a.	n.a.
12	72491600	72611625	72541600	72551447	1.14E-09	n.a.	n.a.
12	86107277	86217091	86157277	86167091	7.17E-10	n.a.	n.a.
12	113947438	114057220	113997438	114007220	1.48E-08	n.a.	n.a.
12	124356881	124466320	124406881	124416320	3.05E-08	ENSG00000139364	*TMEM132B*
12	125356974	125466886	125406974	125416886	6.52E-09	n.a.	n.a.
13	18795614	18905535	18845614	18855535	9.58E-09	n.a.	n.a.
13	25176123	25285418	25226123	25235418	1.74E-08	ENSG00000132932	*ATP8A2*
13	28986360	29096326	29036360	29046326	2.39E-08	ENSG00000139514	*SLC7A1*
13	42430804	42540355	42480804	42490355	3.69E-10	ENSG00000133106	*EPSTI1*
13	45940089	46050084	45990089	46000084	2.24E-09	ENSG00000136141	*LRCH1*
13	51855900	51965708	51905900	51915708	1.22E-08	ENSG00000136100	*VPS36*
13	62485115	62595091	62535115	62545091	8.65E-09	n.a.	n.a.
13	67284250	67393806	67334250	67343806	7.20E-09	n.a.	n.a.
13	100825274	100945266	100885429	100895266	5.51E-09	ENSG00000198542	*ITGBL1*
14	21811403	21921291	21861403	21871291	5.73E-09	n.a.	n.a.
14	22482624	22592369	22532624	22542369	3.14E-08	ENSG00000100802	*C14orf93*
14	37655799	37765761	37705799	37715761	3.52E-08	ENSG00000139874	*SSTR1*
14	54006122	54115972	54056122	54065972	1.38E-08	ENSG00000100532	*CGRRF1*
14	68858623	68978676	68918680	68928676	2.00E-10	ENSG00000100632	*ERH*
14	69034751	69144401	69084751	69094401	8.14E-10	ENSG00000175985	n.a.
14	72302462	72412083	72352462	72362083	7.67E-09	ENSG00000205683	*DPF3*
14	76462869	76572825	76512869	76522825	1.92E-08	ENSG00000119669	*C14orf4*
14	87461459	87571399	87511459	87521399	8.04E-10	ENSG00000054983	*GALC*
14	105942432	106052419	105992432	106002419	2.73E-08	ENSG00000187156	n.a.

Chr	Region start	Region end	Peak start	Peak end	Peak p value	Gene EnsemblID	Gene name
15	21711179	21821057	21761179	21771057	1.83E-08	n.a.	n.a.
15	25872564	25982406	25922564	25932406	2.22E-09	ENSG00000104044	*OCA2*
15	57479321	57589164	57529321	57539164	2.77E-08	ENSG00000157470	*FAM81A*
15	83658565	83768373	83708565	83718373	9.70E-09	ENSG00000170776	*AKAP13*
15	93371423	93481402	93421423	93431402	4.12E-09	n.a.	n.a.
15	93607440	93716802	93657440	93666802	4.09E-09	n.a.	n.a.
15	95867099	95976469	95917099	95926469	3.00E-09	n.a.	n.a.
16	7005291	7115269	7055291	7065269	1.73E-08	n.a.	n.a.
16	8082635	8192555	8132635	8142555	2.50E-08	n.a.	n.a.
16	8576022	8706045	8646123	8656045	7.08E-11	ENSG00000067365	*C16orf68*
16	9090535	9200491	9140535	9150491	7.41E-09	ENSG00000182831	*C16orf72*
16	10229060	10337712	10279060	10287712	2.45E-08	n.a.	n.a.
16	22817413	22988761	22877911	22887894	1.78E-12	ENSG00000122254	*HS3ST2*
16	46790944	46900813	46840944	46850813	1.12E-09	ENSG00000102910	*LONP2*
16	59901557	60011534	59951557	59961534	2.33E-08	n.a.	n.a.
16	74887489	74997217	74937489	74947217	1.87E-08	ENSG00000152910	*CNTNAP4*
16	75724465	75834452	75774465	75784452	2.50E-09	ENSG00000103111	*MON1B*
16	80663239	80773163	80713239	80723163	6.43E-09	ENSG00000135698	*MPHOSPH6*
17	21091602	21213130	21141602	21151092	1.24E-08	ENSG00000034152	*MAP2K3*
17	23649233	23768988	23709249	23718988	1.96E-08	ENSG00000160629	*TMEM199*
17	23649233	23768988	23709249	23718988	1.96E-08	ENSG00000109072	*VTN*
17	48778049	48887499	48828049	48837499	5.42E-09	n.a.	n.a.
18	11654262	11764260	11704262	11714260	1.88E-09	ENSG00000141404	*GNAL*
18	48518185	48628069	48568185	48578069	1.41E-08	ENSG00000187323	*DCC*
18	49678230	49788193	49728230	49738193	6.28E-09	n.a.	n.a.
18	71336451	71446441	71386451	71396441	3.88E-09	n.a.	n.a.
18	74017896	74127878	74067896	74077878	3.10E-08	n.a.	n.a.
19	1518037	1627456	1568037	1577456	7.77E-09	ENSG00000181588	*MEX3D*
19	21556254	21676350	21606254	21615861	8.48E-09	ENSG00000213976	n.a.
19	33428608	33548642	33488767	33498642	9.10E-09	n.a.	n.a.
19	33814772	33924767	33864772	33874767	3.29E-09	ENSG00000205243	n.a.
19	34459241	34569238	34509241	34519238	1.11E-08	n.a.	n.a.
19	36871058	36981031	36921058	36931031	1.66E-08	n.a.	n.a.
19	43457904	43567429	43507904	43517429	5.59E-10	ENSG00000099337	*KCNK6*
19	52474978	52583615	52524978	52533615	4.57E-09	ENSG00000134830	*GPR77*
19	56816295	56926116	56866295	56876116	1.42E-08	n.a.	n.a.
20	18733277	18839699	18783277	18789699	4.15E-09	ENSG00000149443	*C20orf78*
20	24163282	24293922	24233949	24243922	9.10E-12	n.a.	n.a.
20	51860627	51970421	51910627	51920421	7.26E-09	n.a.	n.a.
20	58592629	58702351	58642629	58652351	2.22E-10	n.a.	n.a.
21	21293678	21403136	21343678	21353136	2.53E-08	ENSG00000154654	*NCAM2*
21	27493692	27603684	27543692	27553684	2.83E-08	n.a.	n.a.
21	29759048	29878999	29819050	29828999	6.23E-09	ENSG00000171189	*GRIK1*
21	35819529	35929507	35869529	35879507	4.01E-09	n.a.	n.a.

Appendix E

The table below lists regions in Akey's review that overlap with our candidate regions, and the number of previous genome-wide scans that identified the region as positively selected. Coordinates are in NCBI36.

Chr	Start	End	No. of scans
1	35091347	36450032	7
1	52834684	53397600	5
1	63896341	64300000	4
1	73110567	73763239	2
1	75412213	75792745	4
1	102950280	103520567	5
1	186911638	187544804	2
1	187734833	188413044	2
1	212836722	213574853	2
1	245200000	245400000	2
2	5937460	6624193	2
2	21520822	21691853	2
2	39873524	40313548	2
2	69000000	69100000	2
2	83200000	83491853	3
2	84300000	85001443	7
2	86420824	86700685	3
2	107252946	107707862	4
2	121388162	121500000	2
2	167488441	167829843	3
2	177021882	178332739	8
2	194388441	194872739	4
2	195445042	197337972	5
2	215700000	216047276	4
2	237100000	237806446	4
3	17174903	17918047	7
3	43171008	43826735	3
3	59659140	59859140	2
3	66549620	66649620	2
3	108648481	109250364	5
3	110200000	110400000	3
3	124800000	124908517	3
3	144980752	145392790	4
3	189890333	190421069	3
3	195600000	195700000	2

Chr	Start	End	No. of scans
4	1000000	1100000	2
4	3500000	3600000	2
4	14117624	14591044	5
4	32715092	33416543	6
4	33453829	34600000	4
4	41100000	42012240	9
4	60433581	60833044	2
4	71712335	71739976	2
4	85052048	85711845	2
4	93711845	93911845	2
4	96559478	96900000	2
4	99861845	100861845	4
4	135100000	135637586	3
4	147933837	148461845	4
4	159500000	160383102	5
4	165478100	165764287	2
4	170733084	171062639	4
4	171504228	172245075	4
4	172390869	173690711	2
4	176402530	177137450	5
4	177900000	178108882	2
5	11428374	11964581	3
5	21591332	22138852	4
5	54919872	55028135	2
5	75118302	75321300	2
5	100585818	101100000	3
5	109051683	109351683	2
5	116900000	118039500	6
5	124199397	124569221	3
5	141324037	141367520	2
6	48261123	48400000	2
6	56600000	56700000	2
6	67209702	67610632	2
6	95545225	95800000	3
6	102261123	102461123	2
6	125797887	126100000	4
6	129300000	129400000	2
6	132524241	132708765	2
6	144769146	145480251	2
6	158164208	158660281	4
7	3616258	3831778	2
7	19000000	19100000	2
7	28092602	28200000	2
7	30117938	30486920	3
7	100190728	102393972	4

Chr	Start	End	No. of scans
7	118426018	118562339	2
7	119136728	119800000	3
7	135077048	135518370	3
7	136703651	137238735	3
7	145499216	145879474	4
8	9245944	9900000	3
8	10630705	11614773	7
8	16087027	16507429	3
8	20836402	21282410	3
8	34000000	35059528	3
8	35611003	36378014	3
8	50212593	50500000	3
8	50580000	52150000	8
8	56962654	57180754	2
8	82065718	82400000	4
9	12500000	12800000	3
9	15900000	16100000	3
9	24300000	24679974	3
9	25922398	27000000	3
10	2950000	3100000	3
10	55489628	55857080	6
10	58559648	59725403	6
10	92000000	92100000	2
10	107024983	107512933	4
10	118125403	118276595	4
11	23600000	23730424	2
11	24900000	25092267	2
11	37368196	38750000	7
11	39594336	40051695	3
11	48292267	48392267	2
12	10900000	11100000	2
12	42500000	43185479	6
12	48000000	48300000	2
12	84396635	85067701	2
13	18774831	19612163	6
13	21669520	22133385	2
13	33055423	33455792	2
13	37603687	38490126	5
13	51800000	51909915	2
13	62067478	62850000	4
13	67150000	67350000	2
13	102845482	103213227	2
13	103955437	104200000	2
13	104398149	104598149	2
13	104950261	105324693	2

Chr	Start	End	No. of scans
14	44280000	44770503	6
14	56700000	57000000	3
14	66779712	66900000	2
14	87235602	87763024	2
14	89492048	89579438	2
14	105800000	105900000	2
15	25800000	26378746	6
15	42200000	42300000	2
15	45937993	46804624	6
15	49844415	50441408	3
15	61145232	62319917	9
15	86550993	87140285	3
16	22840948	23040948	2
16	45959870	47212009	5
16	76927006	77155299	4
17	55211782	56901284	6
17	60400000	60500000	2
18	28600000	29361325	7
18	61600000	61700000	2
18	64675139	64941495	3
18	65689235	66040000	5
19	11875627	12000000	2
19	43400000	43600000	2
19	45194869	45300000	2
20	19831968	20720000	3
20	31200000	31300000	2
20	57849002	58049002	2
21	29719326	30020705	2

Appendix F

This table shows genes within each enriched functional cluster in the CEU and YRI populations. Genes are shown in Ensembl ID.

Functional cluster	No. of genes	Bonferroni p-value	Genes
CEU			
Cell adhesion	27	0.001	ENSG00000138650, ENSG00000164853, ENSG00000183230, ENSG00000140945, ENSG00000138696, ENSG00000152894, ENSG00000169760, ENSG00000156282, ENSG00000174469, ENSG00000177103, ENSG00000165973, ENSG00000118762, ENSG00000169862, ENSG00000077522, ENSG00000169604, ENSG00000060718, ENSG00000112699, ENSG00000134121, ENSG00000021645, ENSG00000146555, ENSG00000151914, ENSG00000170927, ENSG00000150275, ENSG00000154654, ENSG00000137975, ENSG00000150637, ENSG00000145012.
Signal	74	0.002	ENSG00000138650, ENSG00000152208, ENSG00000144749, ENSG00000104974, ENSG00000183117, ENSG00000162763, ENSG00000138696, ENSG00000152894, ENSG00000174808, ENSG00000174469, ENSG00000156687, ENSG00000109743, ENSG00000126709, ENSG00000016402, ENSG00000154589, ENSG00000124159, ENSG00000204866, ENSG00000149328, ENSG00000169604, ENSG00000102763, ENSG00000092421, ENSG00000169605, ENSG00000134121, ENSG00000188467, ENSG00000021645, ENSG00000214510, ENSG00000203837, ENSG00000105825, ENSG00000151490, ENSG00000166342, ENSG00000131126, ENSG00000164418, ENSG00000150275, ENSG00000124493, ENSG00000179399, ENSG00000172551, ENSG00000137975, ENSG00000165409, ENSG00000166206, ENSG00000111452, ENSG00000011465, ENSG00000150637, ENSG00000133710, ENSG00000140945, ENSG00000169760, ENSG00000175445, ENSG00000156564, ENSG00000107798, ENSG00000177103, ENSG00000145536, ENSG00000165973, ENSG00000144455, ENSG00000171189, ENSG00000109610, ENSG00000060718, ENSG00000142549, ENSG00000196277, ENSG00000183722, ENSG00000183098, ENSG00000122711, ENSG00000146555, ENSG00000170927, ENSG00000134247, ENSG00000197614, ENSG00000104760, ENSG00000141337, ENSG00000187095, ENSG00000154654, ENSG00000080224, ENSG00000174123, ENSG00000124107, ENSG00000140470, ENSG00000009765, ENSG00000139263.
Ig-like C2-type 3 domain	12	0.001	ENSG00000154654, ENSG00000134121, ENSG00000144749, ENSG00000104974, ENSG00000146555, ENSG00000065534, ENSG00000036448, ENSG00000177103, ENSG00000134247, ENSG00000139263, ENSG00000142549, ENSG00000187095

Functional cluster	No. of genes	Bonferroni p-value	Genes
YRI			
N-linked glycosylation site	60	0.0007	ENSG00000152208, ENSG00000139364, ENSG00000163638, ENSG00000174469, ENSG00000112562, ENSG00000163956, ENSG00000112499, ENSG00000143341, ENSG00000204525, ENSG00000112462, ENSG00000109072, ENSG00000187323, ENSG00000155011, ENSG00000150625, ENSG00000165661, ENSG00000152910, ENSG00000169855, ENSG00000173530, ENSG00000151067, ENSG00000158816, ENSG00000155511, ENSG00000179344, ENSG00000152595, ENSG00000107165, ENSG00000145888, ENSG00000008513, ENSG00000116147, ENSG00000099337, ENSG00000099338, ENSG00000106692, ENSG00000122254, ENSG00000168702, ENSG00000198542, ENSG00000177233, ENSG00000171189, ENSG00000143502, ENSG00000197584, ENSG00000184374, ENSG00000139514, ENSG00000156869, ENSG00000175497, ENSG00000184613, ENSG00000144619, ENSG00000134830, ENSG00000146555, ENSG00000212127, ENSG00000176787, ENSG00000139874, ENSG00000196578, ENSG00000054983, ENSG00000166363, ENSG00000154654, ENSG00000177943, ENSG00000174982, ENSG00000136928, ENSG00000176555, ENSG00000163873, ENSG00000197865, ENSG00000176547, ENSG00000104044.
RhoGEF domain	6	0.01	ENSG00000170776, ENSG00000104728, ENSG00000198399, ENSG00000120278, ENSG00000132694, ENSG00000053524.
glutamate receptor activity	5	0.04	ENSG00000152208, ENSG00000155511, ENSG00000171189, ENSG00000136928, ENSG00000163873.

Appendix G

Command lines for GENETREE

Generate tree structure:
./seq2tr seq2tr_input seq2tr_output;

Estimate the best theta:
./genetree seq2tr_output seed_theta 100000 6666 -f surf_output -g seed_theta/10 seed_theta*10 500 -m mg_3pop -y 100 -2 -x 1000 > estimate_theta_out;

Estimate TMRCA:
./genetree seq2tr_output estimated_theta 10000000 6666 -m mg_3pop -y 100 -x 1000 > estimate_TMRCA_output;

Appendix H

Phylogenetic networks of two regions with recent TMRCAs. A: chr1:28,465,001-28,480,000; TMRCA 1.992 N_e generations. B: chr1:28,920,001-28,940,000; TMRCA 1.962 N_e generations.