

Appendix A

A list of all sample names used in genotyping (A.1) and resequencing (A.2) is available on the accompanying CD.

Appendix B

B.1. The Illumina primers used for genotyping are on accompanying CD.

B.2. Long-Range PCR primers for *MAGEE2* and *SIGLEC12*

Primers	Primer Sequence	Product Size
Magee2_Hs_MS1_F	CAATGGCTATTCTTGTGTCTTCC	
Magee2_Hs_MS1_R	CCATCAGAGCACCTATTTTCATC	7046
Magee2_Hs_MS2_F	CCTCAATCAGAGACAACCCATAG	
Magee2_Hs_MS2_R	GTGAACACCCACATCCTTTACAT	7053
Siglec12_Hs_MS1_F	TGTGTTCAAAGTCATTGATGGAG	
Siglec12_Hs_MS1_R	CACCCTTTTAATTTTGTGCTCTG	7019
Siglec12_Hs_MS2_F	AATGCAAATCAAAGCCTTAATGA	
Siglec12_Hs_MS2_R	CAGAACAAGGATTGTACCCTGAG	7059

B.3. Nested PCR primers for *MAGEE2* and *SIGLEC12*

STS_name	forward_primer	reverse_primer	STS_size
Siglec12_1	TTCTGTCCATAATGATCCTGCTT	TACACGTATGCTGTGTGTCTCCT	507
Siglec12_2	TGTCTCTCATTCAAGTTCTCGGT	TGAGGTTTGGACCAGTGTTAGTT	503
Siglec12_3	ACAGGAGTGGCATTTCCTAGAAT	GTGGAAGATGAGGTGATTCAAGAT	484
Siglec12_4	AACTAACACTGGTCCAAACCTCA	CAGCCAAGCAAGACAGATACTTT	486
Siglec12_5	ATCTGAATCACCTCATCTTCCAC	CAAGTCCAAGCCTAAGTCTTCCT	575
Siglec12_6	AAAGTATCTGTCTTGCTTGGCTG	CTTCTGGTCTTGTCTCAGGTCT	469
Siglec12_7	TATGGAGATGTTGAGGACTCTCG	GTGAAGAAATCTGAGAAGCTGGA	583
Siglec12_8	AGGGTCTCTTTGGAGGGTACTG	AAATATTTGAGCTGACGGATGTG	496
Siglec12_9	GATGCTGTAACTTATGGCCAAG	TCCTTTAGAATTAACAGCCCTCC	578
Siglec12_10	CAACACGGATGAACCTAGAGAAC	GAGGAAGGAGAGATCCAGTATGC	458
Siglec12_11	TAAGTTCTGATGTCCTGTTGCAC	CGCAGGGTACTTAACCATTCTA	588
Siglec12_12	GAATGGAGGAAGAGAAGGGAGT	TATTGCCACCTCCTTCAGTAAA	461
Siglec12_13	CATTAACCTCCAACAACAATTCCA	AGGTAACAGATCAACAGGTTCCA	519
Siglec12_14	TAACTGAAGGAGGTGGCAATAAA	TAAAGTTCTGAAGGTCACAAGCC	596
Siglec12_15	AGGAGGAGGGCATAGATAGATTG	AGATGTGGTGTGTGTGTGAATGT	458
Siglec12_16	GGCTTGTGACCTTCAGAACTTTA	GGAAGTCGTCAGTTTATTGATGG	581
Siglec12_17	GTCTTGCACTCTTCTCCTTCTTG	GAATTGCCAATAGATTGGGTGTA	529
Siglec12_18	GCCATCAATAAACTGACGACTTC	AGAAGTTGAGCCTGTGTGTGAAT	572
Siglec12_19	TACACCCAATCTATTGGCAATTC	TTAGTGATGTTTGAGCACAGGAA	491
Siglec12_20	TTAATCATGGTCTCTTGACAAAA	TCATTAAGGCTTTGATTTGCATT	513
Siglec12_21	GGAGTGCTCTTCAATCTCACAGT	TGGGTGTATATCCACAAGTAGGG	531
Siglec12_22	AATGCAAATCAAAGCCTTAATGA	CCACATTGTAAGGTGTGACAAGA	445
Siglec12_23	TGTGACATTTGTGGGAATGTAAA	ACATTGTTGAACAATAACTCCG	514
Siglec12_24	ATTCACAATAACCAAGAGGTGGA	CCATCCATCCAGCCATCTAC	455
Siglec12_25	GGGTGAACCTTGAGGATATTTGT	GTCTGTCCATCCATCCATCC	538
Siglec12_26	GTAGATGGCTGGATGGATGG	GATATGGCCAAACCAATCAACTA	553

STS_name	forward_primer	reverse_primer	STS_size
Siglec12_27	GGATGGATGGATGGACTGAC	CAGTGTCATCACCAACAAGGTTA	565
Siglec12_28	TGAATTAATGAATGAAGGGATGG	TCTCTCGAGTAGCTGGGATTACA	592
Siglec12_29	CAAATCTCAGCAATGAAGATGAA	TCAGCAGAGCACTGTCTACTAATC	446
Siglec12_30	GCTCGTGTATGTAATCCCAGCTA	GGGATTACTTCCTCACTGTCCTT	485
Siglec12_31	AACCCAGATTAGTGACAGTGCTC	ACTGAAAGGCTCTCTGGTCTCTT	481
Siglec12_32	GAAAGGAAGGACAGTGAGGAAGT	GGTCTTCCTGTACTTCTGCATCA	591
Siglec12_33	GTCTGAGGTTTGCCACAGACAT	TTTAAATAAAGGCAGACTGCACC	482
Siglec12_34	TGATGCAGAAGTACAGGAAGACC	CTGGACTAGTGTGAGGCAAGTG	442
Siglec12_35	ACAGAAAAGAACAAGGACGGAAG	AACGAGTACACAGGTGGGTAGG	476
Siglec12_36	GTTCTTAAATTGTGTGCCCAAAG	ACTTTGTCTCTCTGCCCCTTCT	580
Siglec12_37	CCTACCCACCTGTGTACTCGTT	TTATCCTACAGCACAAACACTGC	593
Siglec12_38	GGTTGTGGATGCTGTAGAGAAAG	GATCTCAGAGGTGGTTTGATGTC	453
Siglec12_39	ATATGCACGTTCACTGCTCACT	AGCTCAAGGATTTGAGGACTCTT	529
Siglec12_40	GAGGGTGCAAACAGTCTCACTAC	GAAC TTGACCATGACTGTCTTCC	525
Siglec12_41	ATAGGTGTGTGTGTGGAGGAGTT	CAACATATCCTGTGAGTTCTGGG	477
Siglec12_42	AGGAGGATCTGGAACAGAAAGAC	GAGGAGTAAGACCAGAGCCTGAG	594
Siglec12_43	ATCGAGGAGCGAGTGATAGTG	ACTACTCCAGGTGGAGAGAGGA	444
Siglec12_44	AGGCTCAGGCTCTGGTCTTACT	TCCCAGGACCTACTGTCAAGATA	521
Siglec12_45	CCTCTCTCCACCTGGAAGTAGTA	TGAGTTCCTATAGCATGTGGGTT	560
Siglec12_46	CCAGCCTGTATCTTGACAGTAGG	GTCCTCGGAGATCCACATTTAG	474
Siglec12_47	AAGAGAAACTGCAAACCCACAT	TTATCTCCACACATTGTCAAACG	444
Siglec12_48	CTAAATGTGGATCTCCGAGGAC	CAAATGTGATGAGGGCTTTAGG	556
MAGEE2_1	ATTTCAAAGAAATGGCTCTCAGG	TTATCATTCCAGGTGGTAAAGGA	555
MAGEE2_2	AAACTCTAAGGATGCCATGGCT	GGAGGATAGAGAAAGGGAAGACA	432
MAGEE2_3	ATCTCAGGGTGATCTCCTTTACC	AAGCAGACCTCAGTGTCTACAG	482
MAGEE2_4	CAATGGCTATTCTTGTGTCTTCC	GATTT CAGAACTGTGACCCAAAC	561
MAGEE2_5	ATTCTTGATGCACCTAAACCTCA	ATCTTTAGGAATTCTCTGCAGGC	516
MAGEE2_6	CAGCATTAAGTGGCCTAGAAAGA	TTTCAGGGATGAGTGGTTAGAAA	572
MAGEE2_7	AACCCTGTTCAACGAGAAATCTT	CATCAATGTCCACCAAGTATTGA	486
MAGEE2_8	TTTCTAACCACTCATCCCTGAAA	GAGTACTCCCATCCTTTAGGCAC	440
MAGEE2_9	TTCCATCTTCCAAATGAGTTCAC	GTATGCATTTCTGTCCAGTCTCC	562
MAGEE2_10	GGCTATTTCCCACTTCTGTTCTT	TGAGGCTTAACTAATATGCCCAA	490
MAGEE2_11	GGAGACTGGACAGAAATGCATAC	CTGGACAACGATGATCAATGTAA	430
MAGEE2_12	TGCAGCCTTTCTTTGTATATTCC	TGTGCTAAACAGCAATTCTCTCA	512
MAGEE2_13	ACAGTGCCTGACGCATATTTAGT	TACAGCCCAGTCTCAGTGATCTT	483
MAGEE2_14	TGAGAGAATTGCTGTTTAGCACA	CACTTATTACAGAGGGATGGCTG	562
MAGEE2_15	GAAACGATTGTGTCGTTCTCTTC	CTTTAAAGGAGGAGTGGGAGAAA	540
MAGEE2_16	GCAAACACTCACCTTAACAGCTT	GGCATAATAGGCATAAGCTCAGA	520
MAGEE2_17	GTCATAAAGCACATCTTGTCCTC	GATTGCTCTCCCTTTGTGTCTAC	502
MAGEE2_18	ATTGCTTGTTACTTCCATGAGC	AATTAGAATCCAGGTAGGGCTTG	565
MAGEE2_19	TTTGTTGTGTGTGTGTCATTGTT	CAGAACAATATAGGGAGGCTGTG	437
MAGEE2_20	CACAATTTGTACTTCCACACAA	AATCAGAGGAAGAGCAAGTGATG	539
MAGEE2_21	CTGGATTAGAGTAGGACAGTGGC	TTGGTCCAGTTGGCTATTAGTGT	430

STS_name	forward_primer	reverse_primer	STS_size
MAGEE2_22	CATCACTTGCTCTTCCTCTGATT	GAACACAAGGAACCTCCTCACTA	517
MAGEE2_23	AGTCAGGCTTCTTTCTTTGGTTT	GTTATTGATCCTCAGGCTGACAC	465
MAGEE2_24	CAGTAGTGAGGAGGTTCTTG TG	GACCCTCTAGAAGACAGGTCGAT	430
MAGEE2_25	GTGTCAGCCTGAGGATCAATAAC	CATGTCTCTGGTAAGCCAGAATG	459
MAGEE2_26	AATCGACCTGTCTTCTAGAGGGT	ATGAGAGACAAAGCATGGAAGAC	559
MAGEE2_27	AGAGACATGGTTCCAGGAGACAG	AATAATTCTAATCGTTAGCGCCC	566
MAGEE2_28	GAGAAGAGAATTGAGAAATGGA	ATGACCCAGTTTCCTCATCTGTA	511
MAGEE2_29	AAAGCTTCCATTCACTCAACAGA	ACTCCTTCTTGAGGCTTTATTGG	556
MAGEE2_30	TCCAAAGTCAAGCAGCAATAAAT	TGTCTAGCAACCTTCATCCTCAT	428
MAGEE2_31	CCAATAAAGCCTCAAGAAGGAGT	TGCAACCATCATAGTCTTCAACTT	484
MAGEE2_32	AGTATGTCAAAGCTTGTGTGGC	TTCTACCGTCTAGAACATGCACA	573
MAGEE2_33	TTCAGTAATCTTATGCCCTGGAA	GGAGGGAGTAGTAGGAGGTTCAA	495
MAGEE2_34	GTGTGGTTTGATGCTGATCCTT	TCAATATGGCCAGGAAGAAGATA	467
MAGEE2_35	TTGAACCTCCTACTACTCCCTCC	TGCTGTAATGGTCTGTTTCTTGA	549
MAGEE2_36	TCATGCTCTCCATTCTGAAC TTT	CAGTTGACAGGGTAAGTTGTGGT	495
MAGEE2_37	CAATCTCTTCCCACTCATTTGTC	GTGTGGACAAGAATACAGAGCAA	509
MAGEE2_38	CCACAACCTACCCTGTCAACTGT	ATTGTTTCCATCTCCTTCCATTT	520
MAGEE2_39	TTGCTCTGTATTCTTGTCCACAC	AATGTTCACTTGAGCACCAATCT	513
MAGEE2_40	AAATGGAAGGAGATGGAAACAAT	AAACAAATATCTCGGGTGGGT	535
MAGEE2_41	AGATTGGTGCTCAAGTGAACATT	GACAGAGGGTCTTCAAATGAGTG	511
MAGEE2_42	GAATATCCATGATTCCACCCAC	AAGCTATAAGGCAAACAATCGAA	448
MAGEE2_43	CATATTTGTATGACAAGCAGCCA	GACATGGAGAAACCAGAACTC	559
MAGEE2_44	CATTCGATTGTTTGCCTTATAGC	ATCCAAGTGGCTGATAAACACAT	441
MAGEE2_45	TTTGAAGAATTCCCAGAAGGAGT	GAAGGCACAGAAATACCTCATTG	540
MAGEE2_46	TTTGTCAAATATATGTACTGCAAATG	AAACAACCTGAGAAATGGAACAA	496
MAGEE2_47	GCCTTCTTCAAATACGATTTATTG	CCAAGGCTTCTCAAGTATGAATG	465
MAGEE2_48	AGCTTTCATCATGGCATTGTAGT	CCCTTTCACATCCACTTACTGAG	523

Appendix C

All scripts used are available on the accompanying CD.

Perl:

createfstinput

hgdp2sweep

merge_sts

pcroverlap

phase2fasta

phase2network

snptab2phase

Java:

DelimitedFileTransformer

InputFileTransformer

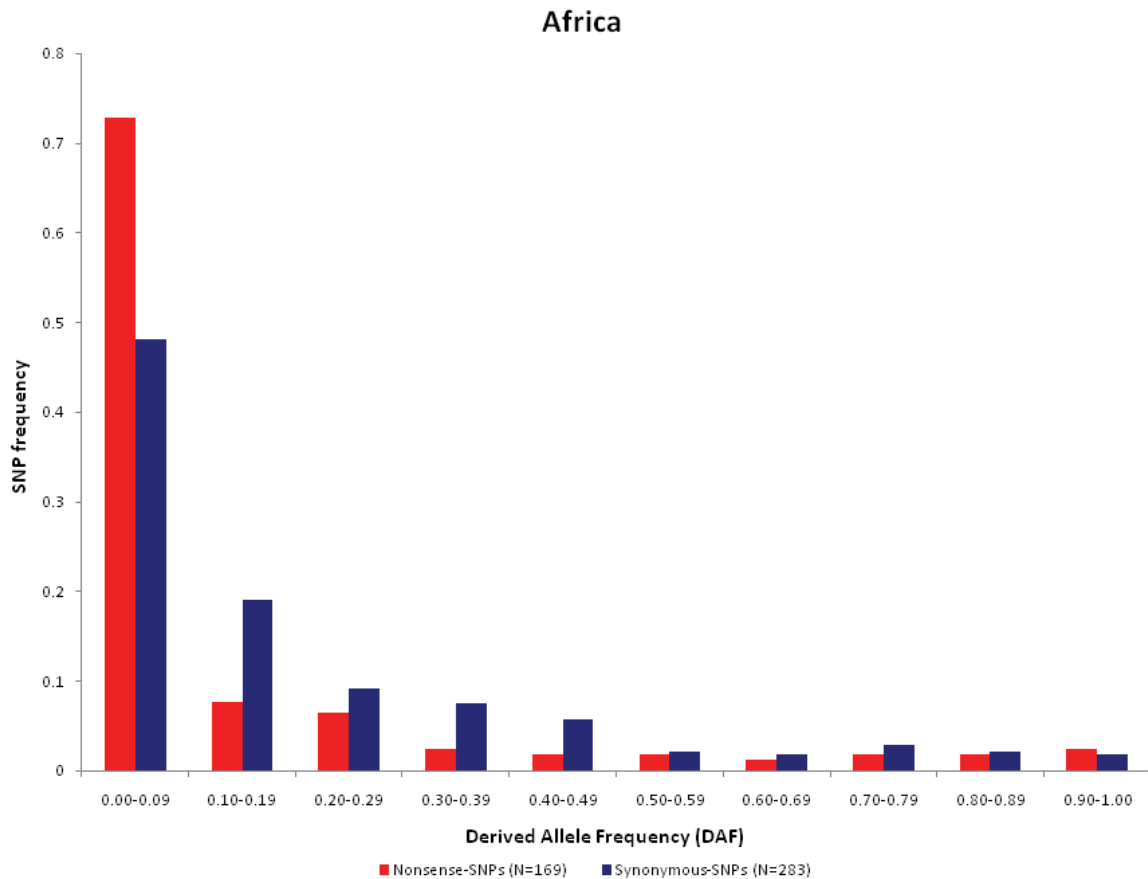
SweepFileConversion

Appendix D

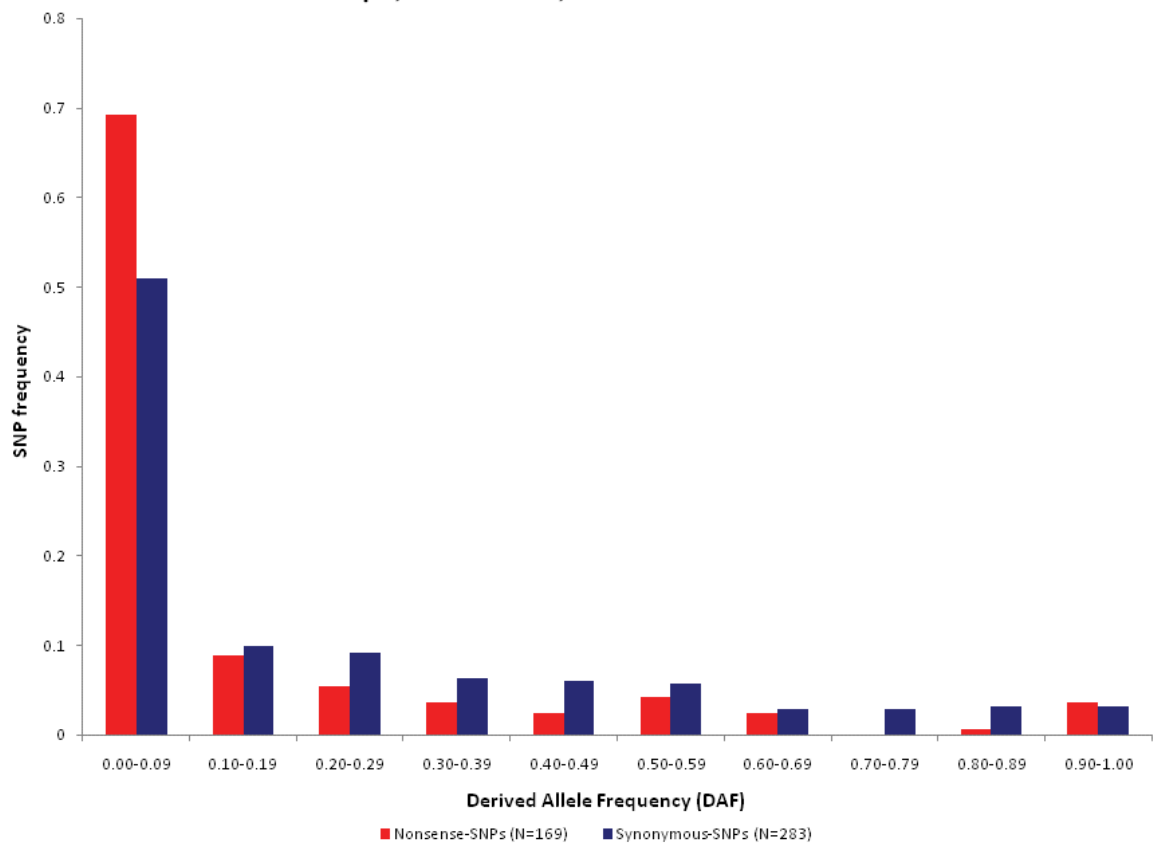
All genotype data is available in a tab delimited text file on the accompanying CD.

Appendix E

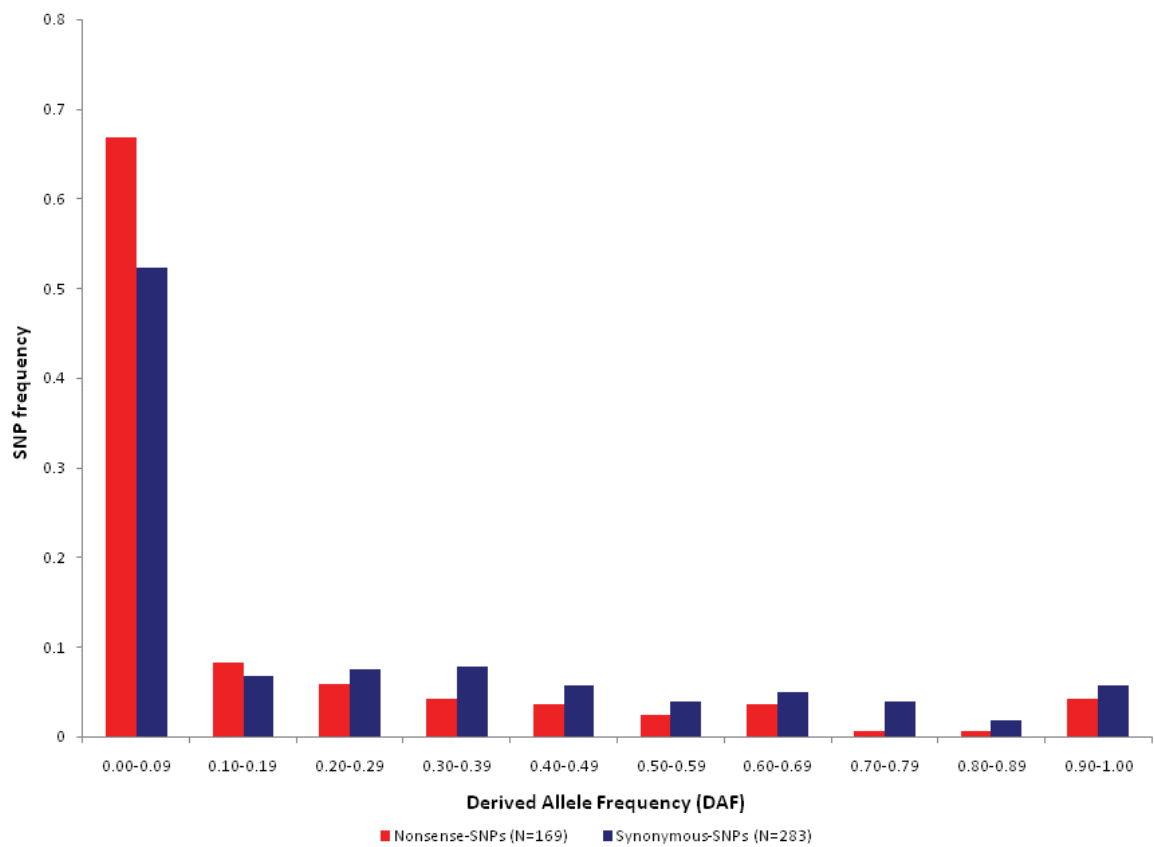
The derived allele frequency spectrum for the nonsense- and synonymous-SNPs plotted for the five populations (according to K=5 in Rosenberg et al. 2002) separately. The distribution was found to be similar to that of the combined populations.

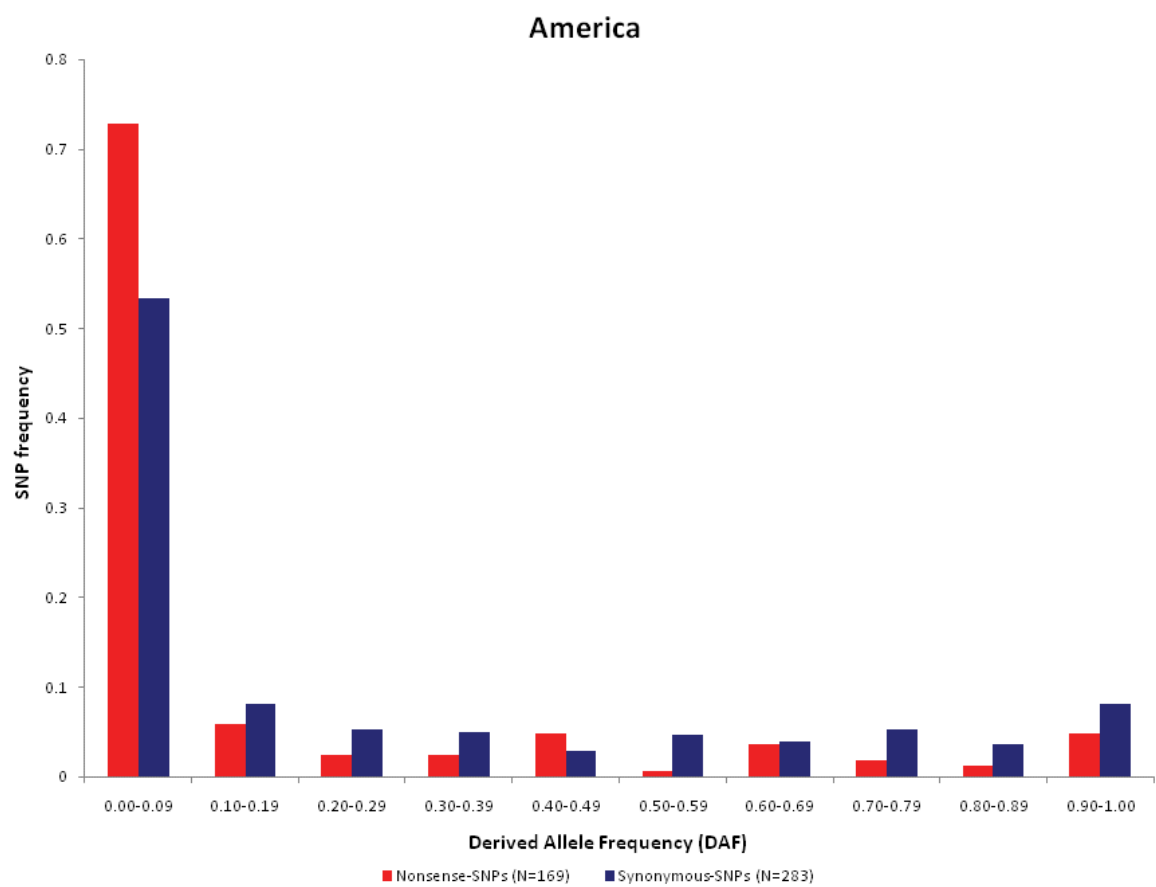
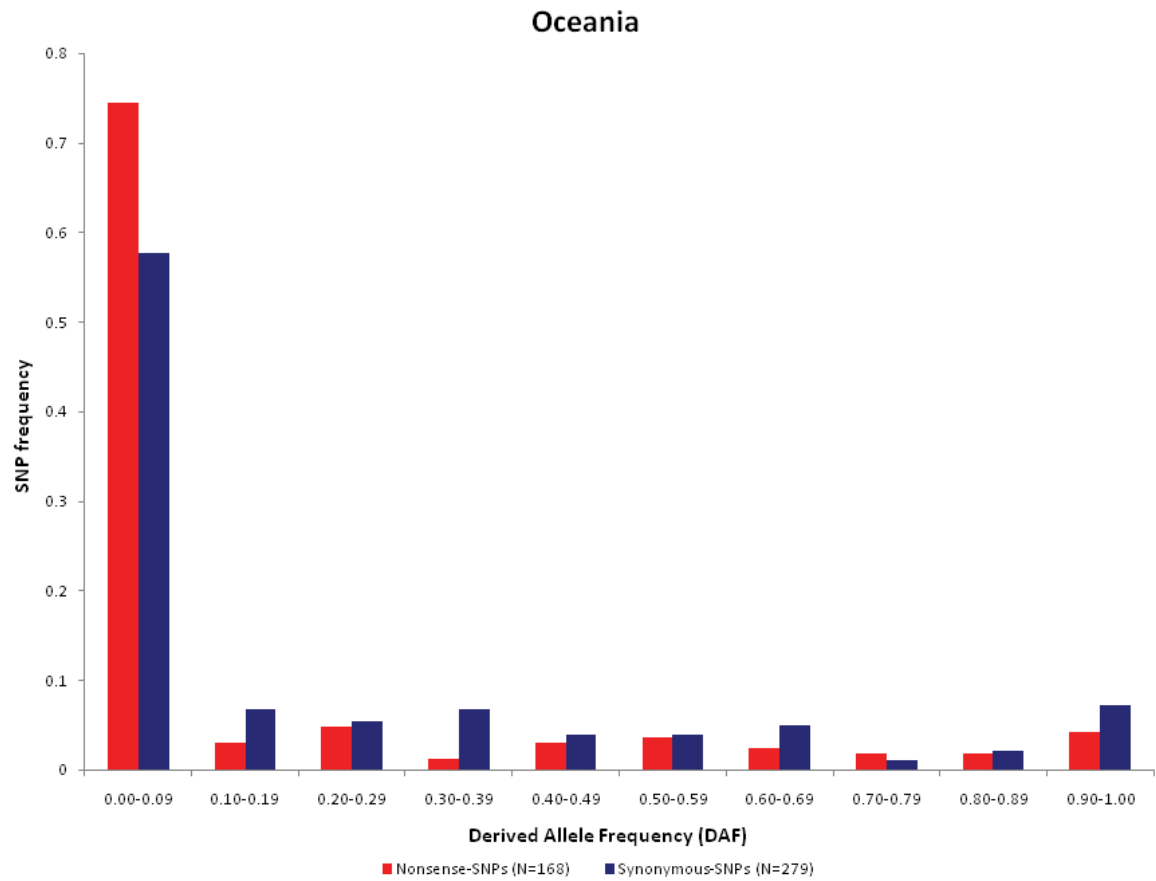


Europe, MiddleEast, Central and SouthAsia



East Asia





Appendix F

Summary of results from genome-wide survey of nonsense SNPs (also available on accompanying CD). The displayed includes: External Gene ID (normally from Hugo), the SNP ID, chromosome, chromosomal position (Build36), %truncated, prediction of whether NMD is triggered (YES/NO), heterozygosity calculated according to Nei (1987), the minor allele frequency (MAF) and the derived allele frequency (DAF), F_{ST} value calculated according to Weir and Cockerham (1984) across the combined 37 populations used in this study (HGDP-CEPH and HapMap), across the HGDP-CEPH populations divided into 5 geographical regions according to K=5 in Rosenberg et al (2002), and in the genotypes in the publicly available HapMap data (The International HapMap Consortium 2005). The table is sorted according to Gene ID.

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
	rs11727979	4	9014324	28.4	NO	0.01	0.01	0.02	0.01	0.01	
	rs34358	5	75000878	18.3	YES	0.47	0.53	0.09	0.50	0.06	0.07
	rs6997135	8	57125768	52.6	NO	0.01	0.01	0.08	0.02	0.09	0.09
ABCA10	rs10491178	17	64661568	14.4	YES	0.11	0.11	0.11	0.20	0.14	0.01
ADAM10	rs1801973	15	56689928	16.0	YES	0.00	0.00	0.00	0.00	0.00	
AKAP9	rs2285686	7	91525621	75.8	YES	0.00	0.00	0.00	0.00	0.00	
ALOX15	rs11870258	17	4488681	70.3	YES	0.00	0.00	0.00	0.00	0.00	0.00
AMPD1	rs17602729	1	115037580	98.4	YES	0.04	0.04	0.06	0.08	0.06	0.13
ANKRD1	rs1130407	10	92670013	89.4	YES	0.00	0.00	0.06	0.00	0.00	0.00
APOL3	rs11089781	22	34886714	85.6	YES	0.02	0.02	0.26	0.04	0.15	
ARHGEF19	rs12048007	1	16407971	93.0	YES	0.00	0.00	0.00	0.00	0.00	
ASCC1	rs11000217	10	73634249	80.7	YES	0.09	0.09	0.11	0.16	0.15	0.17

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
BARHL2	rs1335726	1	90952878	44.1	YES	0.00	0.00	0.00	0.00	0.00	0.00
BEX1	rs11550088	X	102204783	79.4	NO	0.00	0.00	0.01	0.00	0.00	0.00
BRCA2	rs11571833	13	31870626	2.7	NO	0.01	0.01	0.04	0.02	0.01	0.00
C14orf129	rs12435565	14	95918572	43.6	NO	0.00	0.00	0.00	0.00	0.00	0.00
C14orf149	rs3177474	14	59015670	37.7	YES	0.00	0.00	0.01	0.00	0.00	0.00
C16orf24	rs12931094	16	711847	55.5	YES	0.00	0.00	0.00	0.00	0.00	
C19orf44	rs3826726	19	16481328	40.7	YES	0.00	0.00	0.04	0.01	0.01	0.00
C1orf105	rs7532205	1	170688829	91.4	YES	0.04	0.04	0.26	0.09	0.25	
C1orf157	rs11803208	1	202273170	10.9	YES	0.01	0.01	0.00	0.01	0.00	0.00
C21orf111	rs12329656	21	45588725	10.9	NO	0.01	0.01	0.09	0.03	0.08	0.07
C4orf33	rs10009430	4	130250213	28.0	YES	0.01	0.01	0.04	0.01	0.02	0.07
C5orf20	rs12520799	5	134810349	52.2	NO	0.39	0.39	0.15	0.48	0.11	0.24
C6orf148	rs16883571	6	74076059	85.7	YES	0.04	0.04	0.04	0.08	0.02	0.02
C8orf49	rs809203	8	11656913	16.0	NO	0.27	0.27	0.11	0.40	0.10	0.14
CARD8	rs2043211	19	53429518	97.7	YES	0.34	0.34	0.06	0.45	0.07	0.07
CASP12	rs497116	11	104268327	63.7	YES	0.04	0.96	0.24	0.07	0.24	0.10
CD22	rs25677	19	40523826	54.2	YES	0.00	0.00	0.00	0.00	0.00	
CD2BP2	rs11547274	16	30273069	84.8	YES	0.00	0.00	0.00	0.00	0.00	0.01
CD36	rs3211938	7	80138385	31.3	YES	0.02	0.02	0.24	0.03	0.09	0.25
CD99	rs4268274	X	2647719	76.5	YES	0.00	0.00	0.00	0.00	0.00	
CDKL1	rs7148089	14	49872477	0.5	NO	0.41	0.59	0.03	0.48	0.02	0.03
CDKL1	rs11570829	14	49879445	22.5	YES	0.00	0.00	0.05	0.01	0.02	0.05
CEL	rs13287310	9	134936348	29.4	YES	0.00	0.00	0.00	0.00	0.00	
CLCA3	rs2292830	1	86873963	90.4	YES	0.45	0.55	0.08	0.50	0.08	0.12
CLEC7A	rs16910526	12	10162354	5.9	NO	0.05	0.05	0.03	0.09	0.04	0.06
CMA1	rs13306254	14	24046497	86.0	YES	0.00	0.00	0.01	0.01	0.02	0.00
CPN2	rs4974538	3	195543601	6.8	NO	0.20	0.20	0.06	0.32	0.02	0.00
CRHR2	rs8192492	7	30659687	7.0	NO	0.00	0.00	0.01	0.00	0.00	0.00

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
CST2	rs6049157	20	23753918	35.9	YES	0.01	0.01	0.10	0.01	0.08	0.00
CYFIP2	rs7705781	5	156700710	29.8	YES	0.00	0.00	0.02	0.01	0.03	0.00
DEPDC1	rs12759438	1	68717221	2.0	NO	0.09	0.09	0.04	0.16	0.04	0.03
DGCR8	rs2106143	22	18453499	99.4	YES	0.00	0.00	0.00	0.00	0.00	
DHDH	rs10423255	19	54137586	30.4	YES	0.04	0.04	0.01	0.08	0.00	0.00
DKC1	rs2853347	X	153647431	85.2	YES	0.00	0.00	0.00	0.00	0.00	0.00
DMN	rs5030689	15	97463526	87.2	YES	0.00	0.00	0.00	0.00	0.00	
DSCR8	rs2836172	21	38450325	13.3	NO	0.06	0.06	0.10	0.12	0.10	0.09
ELP4	rs3026403	11	31761622	1.9	NO	0.00	0.00	0.01	0.00	0.00	0.00
ENOPH1	rs11546516	4	83571058	93.1	YES	0.00	0.00	0.00	0.00	0.01	0.00
FAM19A5	rs3752466	22	47531852	77.2	NO	0.00	0.00	0.07	0.00	0.01	0.00
FCGR2A	rs9427397	1	159742828	80.4	YES	0.00	0.00	0.00	0.00	0.00	0.00
FCN3	rs15544	1	27573458	81.7	YES	0.00	0.00	0.01	0.00	0.00	
FLJ41766	rs12446322	16	21234774	87.3	NO	0.16	0.16	0.13	0.26	0.13	0.30
FMO2	rs2020866	1	169439745	47.2	YES	0.00	0.00	0.00	0.00	0.00	0.01
FMO2	rs6661174	1	169444714	11.8	YES	0.04	0.96	0.28	0.08	0.24	0.14
FMO6P	rs1736565	1	169379114	80.6	YES	0.36	0.64	0.08	0.46	0.10	0.13
FUT2	rs1800028	19	53898629	41.3	YES	0.00	0.00	0.00	0.00	0.00	
GLUD2	rs10657	X	120010633	15.6	NO	0.00	0.00	0.00	0.00	0.00	
GPNMB	rs11537976	7	23280348	1.1	NO	0.00	0.00	0.00	0.00	0.00	0.00
GRIK5	rs1143143	19	47201928	30.3	YES	0.00	0.00	0.00	0.00	0.00	
HERC6	rs4413373	4	89582627	0.2	NO	0.01	0.99	0.02	0.01	0.02	0.02
HPS4	rs3747129	22	25192041	53.5	YES	0.20	0.20	0.10	0.32	0.10	0.13
IDI2	rs1044261	10	1055710	36.8	NO	0.04	0.04	0.04	0.08	0.04	0.02
IL17RB	rs1043261	3	53874316	3.8	NO	0.15	0.15	0.04	0.25	0.03	0.01
INMT	rs6966017	7	30761567	53.4	NO	0.00	0.00	0.03	0.00	0.01	
KIAA0748	rs1801876	12	53630291	3.8	NO	0.36	0.36	0.24	0.46	0.22	0.40
KIAA1704	rs9567515	13	44461859	93.0	YES	0.00	0.00	0.00	0.00	0.00	0.00

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
KRT7	rs11558308	12	50913627	80.0	YES	0.00	0.00	0.00	0.00	0.00	
KRTAP13-1	rs1985418	21	30690365	73.7	NO	0.00	0.00	0.08	0.01	0.02	0.00
KRTAP13-2	rs877346	21	30665998	23.3	NO	0.28	0.72	0.06	0.41	0.09	0.09
LCE5A	rs2282298	1	150750869	33.6	NO	0.01	0.01	0.04	0.02	0.04	0.02
LCN10	rs9886752	9	138754316	21.3	YES	0.22	0.22	0.09	0.35	0.09	0.02
LGALS1	rs4887	22	36404553	49.3	YES	0.00	0.00	0.00	0.00	0.00	
LPL	rs328	8	19864004	0.4	NO	0.09	0.09	0.04	0.16	0.04	0.02
MAGEE2	rs1343879	X	74921254	77.1	NO	0.31	0.31	0.54	0.43	0.53	0.88
MATN4	rs2233091	20	43366762	91.2	YES	0.00	0.00	0.00	0.00	0.00	0.00
MCTP2	rs2289010	15	92712024	72.6	YES	0.00	0.00	0.00	0.00	0.00	0.00
MLLT11	rs11546017	1	149287905	6.4	NO	0.00	0.00	0.00	0.00	0.00	
MOBK2C	rs6671527	1	46853266	91.1	YES	0.34	0.34	0.15	0.45	0.12	0.24
MOSPD3	rs1053507	7	100048504	78.0	YES	0.00	0.00	0.01	0.00	0.00	
MS4A12	rs2298553	11	60021578	73.5	YES	0.50	0.50	0.03	0.50	0.02	0.03
MST1R	rs9819888	3	49910507	55.7	YES	0.00	0.00	0.00	0.00	0.01	
NAT1	rs5030839	8	18124395	35.7	NO	0.00	0.00	0.02	0.01	0.00	
NLRP8	rs306457	19	61191091	0.9	NO	0.25	0.25	0.05	0.38	0.03	0.01
NOP5_HUMAN	rs15160	2	202870470	24.7	YES	0.00	0.00	0.00	0.00	0.00	
NP_001073929.1	rs13062420	3	171023372	41.5	YES	0.00	0.00	0.01	0.00	0.00	
NP_064546.2	rs2176186	2	228184384	6.6	NO	0.33	0.67	0.07	0.44	0.04	0.05
NP_438169.2	rs1128610	13	31876483	68.1	NO	0.00	0.00	0.01	0.00	0.00	
NP_660151.2	rs11542462	16	80591311	92.4	NO	0.07	0.07	0.08	0.13	0.10	
NP_775760.2	rs1023840	5	41097472	88.0	YES	0.26	0.26	0.08	0.39	0.08	0.16
NP_899231.1	rs2407221	4	152432053	4.8	NO	0.20	0.20	0.19	0.32	0.24	0.09
NPPA	rs5065	1	11828655	0.7	NO	0.15	0.85	0.15	0.26	0.14	0.26
OR10X1	rs863362	1	156816116	84.2	NO	0.47	0.53	0.03	0.50	0.02	0.01
OR1B1	rs1476860	9	124431062	39.8	NO	0.40	0.40	0.21	0.48	0.25	0.26
OR2D2	rs16919417	11	6870116	79.3	NO	0.01	0.01	0.04	0.02	0.06	0.03

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
OR4C16	rs1459101	11	55096228	94.5	NO	0.33	0.33	0.12	0.44	0.16	0.05
OR4X1	rs10838851	11	48242807	10.8	NO	0.39	0.61	0.06	0.47	0.03	0.07
OR4X2	rs7120775	11	48223312	91.1	NO	0.16	0.16	0.04	0.26	0.03	0.06
OR5111	rs16930998	11	5419278	96.2	NO	0.13	0.13	0.15	0.22	0.17	0.25
OR5AK2	rs13343184	11	56512974	98.7	NO	0.00	0.00	0.00	0.01	0.00	
OR5D13	rs11230980	11	55297590	89.2	NO	0.00	0.00	0.00	0.00	0.00	0.01
OR7G3	rs17001893	19	9098263	61.0	NO	0.02	0.02	0.13	0.03	0.13	0.08
OVCH2	rs4509745	11	7669047	1.6	NO	0.49	0.51	0.12	0.50	0.13	0.23
PCDHB10	rs3733689	5	140552340	98.6	NO	0.00	0.00	0.01	0.00	0.00	0.00
PGAM2	rs10250779	7	44071421	69.3	YES	0.00	0.00	0.02	0.00	0.01	0.00
PKD1L3	rs4788587	16	70558637	54.4	YES	0.27	0.27	0.07	0.39	0.08	0.06
PKM2	rs11558352	15	70288149	79.8	YES	0.00	0.00	0.00	0.00	0.00	0.00
PLAT	rs1804182	8	42152676	0.5	NO	0.00	0.00	0.05	0.01	0.01	0.04
PML	rs11272	15	72122464	32.3	YES	0.00	0.00	0.01	0.00	0.00	0.01
PRL	rs6238	6	22398525	48.7	YES	0.00	0.00	0.01	0.00	0.00	0.00
PTPRE	rs3206183	10	129737879	89.3	YES	0.00	0.00	0.00	0.00	0.00	
Q2M2F3_HUMAN	rs7703216	5	177331574	32.3	NO	0.12	0.12	0.04	0.21	0.04	0.01
Q5R387_HUMAN	rs12139100	1	20374169	81.0	YES	0.21	0.21	0.05	0.33	0.05	0.04
Q5SVS6_HUMAN	rs9567547	13	44863210	80.6	NO	0.01	0.01	0.10	0.03	0.08	0.02
Q8IXR4_HUMAN	rs1001586	22	41000237	0.9	NO	0.17	0.17	0.07	0.28	0.09	0.00
Q8N7E8_HUMAN	rs16885508	5	55797209	6.5	NO	0.00	0.00	0.06	0.01	0.03	0.01
Q8N8G3_HUMAN	rs4723884	7	39615800	68.4	NO	0.22	0.22	0.23	0.35	0.26	0.18
Q8NH80_HUMAN	rs2512227	11	123561942	19.5	NO	0.50	0.50	0.07	0.50	0.08	
Q96NA9_HUMAN	rs2400941	14	100370320	96.6	YES	0.27	0.27	0.07	0.39	0.05	0.13
Q96NK0_HUMAN	rs13422553	2	201853604	40.0	NO	0.17	0.17	0.07	0.28	0.04	0.15
Q9H579-2	rs11539065	20	35241114	94.2	YES	0.00	0.00	0.01	0.00	0.00	
Q9UI72_HUMAN	rs642354	5	32185000	75.7	NO	0.01	0.01	0.10	0.03	0.11	0.09
RBPJ	rs5007634	4	26035389	71.6	YES	0.00	1.00	0.01	0.00	0.00	0.00

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
REG4	rs1052972	1	120138308	8.8	NO	0.49	0.49	0.21	0.50	0.27	0.24
ROBO1	rs1065217	3	78749727	20.1	YES	0.00	0.00	0.00	0.00	0.00	0.00
RORC	rs17582155	1	150070837	98.1	YES	0.00	0.00	0.00	0.00	0.00	0.00
RRM2	rs15516	2	10186932	2.6	NO	0.00	0.00	0.00	0.00	0.00	
SEMA4C	rs12471298	2	96890515	16.9	NO	0.04	0.04	0.47	0.08	0.52	
SEMG1	rs2233885	20	43270193	39.3	YES	0.00	0.00	0.00	0.00	0.00	0.00
SERPINA10	rs2232698	14	93826422	80.2	YES	0.02	0.02	0.03	0.04	0.03	0.00
SIGLEC12	rs16982743	19	56696715	95.1	YES	0.20	0.20	0.22	0.32	0.28	0.17
SLAIN1	rs17777179	13	77216390	89.3	NO	0.05	0.95	0.07	0.10	0.10	0.05
SLAMF8	rs10430458	1	158066432	77.3	YES	0.01	0.01	0.03	0.02	0.03	0.01
SLC17A4	rs2328894	6	25886161	13.1	YES	0.00	0.00	0.01	0.01	0.00	0.00
SLC22A10	rs1790218	11	62814501	82.3	YES	0.43	0.43	0.08	0.49	0.08	0.06
SLC25A5	rs11552294	X	118486534	96.7	YES	0.00	0.00	0.00	0.00	0.00	
SLC41A3	rs11543281	3	127269593	89.4	YES	0.00	0.00	0.00	0.00	0.00	
SLC7A8	rs17183863	14	22668816	41.1	YES	0.11	0.11	0.00	0.20	0.00	0.02
SOX13	rs3737659	1	202362310	15.8	YES	0.18	0.18	0.10	0.29	0.13	0.16
SPATA8	rs3812907	15	95128397	67.9	YES	0.12	0.12	0.10	0.22	0.11	0.05
SPG7	rs1057803	16	88143204	40.4	YES	0.00	0.00	0.00	0.00	0.00	0.00
SPTBN5	rs2271286	15	39972774	98.0	YES	0.01	0.01	0.03	0.02	0.04	0.03
SRD5A2	rs9332960	2	31659458	97.6	YES	0.00	0.00	0.00	0.00	0.00	
STARD6	rs17292725	18	50134887	91.4	YES	0.02	0.02	0.02	0.04	0.03	0.05
SURF4	rs2240173	9	135220580	1.1	NO	0.00	0.00	0.00	0.00	0.00	0.01
SYNE2	rs2781377	14	63629845	88.2	YES	0.09	0.09	0.00	0.16	0.00	0.00
TAAR2	rs8192646	6	132980535	59.9	NO	0.06	0.06	0.11	0.12	0.10	0.11
TALDO1	rs1804554	11	754350	11.2	YES	0.00	0.00	0.00	0.00	0.00	
TANC1	rs6755758	2	159794817	17.0	NO	0.00	0.00	0.00	0.00	0.00	
TBCA	rs1802165	5	77039855	60.6	YES	0.00	0.00	0.00	0.00	0.00	
TCP11L1	rs3758741	11	33063192	4.3	YES	0.27	0.27	0.09	0.40	0.08	0.11

Gene ID	SNP ID	Chr	Position (B36)	Truncated (%)	NMD	Heterozygosity	MAF	DAF	F_{ST} (37 pops in study)	F_{ST} (5 pop division)	F_{ST} (HapMap,4 pops)
THSD7B	rs12622896	2	137746704	52.6	YES	0.04	0.96	0.07	0.08	0.01	0.01
TLR4	rs5030720	9	119516006	29.4	NO	0.00	0.00	0.00	0.00	0.00	
TMEM143	rs16982007	19	53537872	62.8	YES	0.00	0.00	0.03	0.01	0.01	0.05
TMEM162	rs5411169	19	40410860	49.2	YES	0.32	0.32	0.07	0.43	0.06	0.01
TMPRSS7	rs340142	3	113263361	68.8	YES	0.01	0.01	0.08	0.01	0.07	0.05
TREM2	rs2234258	6	41234407	13.2	NO	0.00	0.00	0.03	0.01	0.01	
TRPM1	rs3784589	15	29082006	14.9	NO	0.07	0.07	0.06	0.13	0.05	0.01
TSNARE1	rs11988455	8	143308760	0.4	NO	0.01	0.01	0.17	0.01	0.05	0.04
UNC93A	rs2235197	6	167629692	67.0	YES	0.12	0.12	0.04	0.21	0.03	0.04
USP29	rs9973206	19	62334594	1.1	NO	0.04	0.04	0.09	0.08	0.05	0.15
UTS2D	rs16866426	3	192475738	7.5	NO	0.00	0.00	0.01	0.00	0.01	0.01
WDR37	rs10794716	10	1132208	5.3	NO	0.01	0.01	0.07	0.02	0.06	0.06
WRN	rs11574410	8	31150077	1.9	NO	0.00	0.00	0.00	0.01	0.00	0.00
XR_017624.1	rs17107991	14	70005689	2.9	NO	0.06	0.06	0.03	0.12	0.02	0.04
ZAN	rs2293766	7	100209294	33.0	YES	0.26	0.26	0.40	0.39	0.39	0.50
ZNF544	rs3745136	19	63465654	12.8	NO	0.00	0.00	0.00	0.00	0.00	0.00
ZSWIM3	rs11557696	20	43940042	31.1	NO	0.00	0.00	0.00	0.00	0.00	0.00

Appendix G

SNP variation data for the resequenced genes *MAGEE2* is available in tab delimited text files on the accompanying CD.