

Supplementary Table 1. Sites where all Europeans and Africans are heterozygotes, allowing for up to two individuals with missing data. The position in the hg18 alignment is indicated. Regions containing these sites were excluded from analysis on the assumption that they could represent undocumented paralogs.

Genotypes	Chromosome	Site
YYYYYYYYYYY	1	12830424
YYYYYYYYYYY	1	12830472
NYYYYYYYYYY	1	143623590
MMMMMMMMMMM	1	143641953
YYYYYYYYYYY	1	143642297
YYYYYYYYYYY	1	143642687
RRRRRRRRRRR	1	143642749
YYYYYYYYYYY	1	143663577
MMMMMMMMMMM	1	143706015
SSSSSSSSSS	1	143787211
WWWWWWWNWW	1	246880675
RRRRRRRRRRR	2	112330900
NKKKKKKKKKK	3	75797027
RRRRRRRRRRR	3	75797392
RRRRRRRRRRR	3	75797588
YYNYYYYYYY	3	75797666
MMMNMMNMMM	4	9393640
RRRRRRRRRRR	4	9393648
RRRRRRRRRRR	4	104041853
RRRRRRRRRRR	4	191113198
RRRRRRNRRR	4	191113236
SSSSSSSSSS	4	191115648
RNRRRRRRRR	4	191120045
YYYYYYYYYYY	5	115276977
SSSNSSSSSN	5	140534190
YYYYYYYYYYY	5	156412146
RRKKRRKRRR	6	29516507
RRRRRRRRRRR	6	31718665
RRRRRRRRRRR	6	35863636
KKKKKKKKKKK	6	136624190
YYNYYYYYKY	6	136632306
MMMMMMMMMMM	6	136632333
NYYYYYYYYYY	6	136632391
YYYYYYYYYYY	6	136632405
NRRRRRRRRR	6	136638697
YYYYYYYYYYY	6	136638955
NWNWWWWWWW	6	136638974
SSSSSSSSSS	6	136641086
NYYYYYYYYYY	6	136641097
SSSSSSSSSS	6	136641515
YYNYYNYY	8	52895556

YYYYYYYYYYY	8	52895629
KKKKKKKKKK	8	52895681
YNYYYYNYYY	8	52895701
RRRRRRRRRR	8	52895781
RRRRNRRRRR	8	52895784
KKKNKKKKKK	9	33377047
NRRRRRRNR	9	33377073
SSSSSSSSSS	9	139064557
RRRRRRRRRR	10	46419005
RRRNRRRRRR	10	46419025
YYYYYYYNN	10	46419157
RRRRRRRRNR	10	46419471
KKKKKKKKKK	10	46419490
RRRRRRNR	10	46419738
YYYYYYYYYYY	10	46419753
YYYYYYYYYYY	10	46420085
SSSSSSSSSS	11	48303305
YYYYYYYYYYY	11	48303367
MMMMMMMMMM	11	48303398
YYYYYYYYYYY	11	48303419
YYYYYYYYYYY	11	48303843
KKKKKKKKKK	11	48303882
NRRRRRRNR	11	48303995
YYYYYYYYYYY	11	56224457
RRRRRRRRRR	11	56224502
YNYYYYYYYY	11	56224687
YYYYYYYYYYY	11	56224835
YYYYYYNYYY	11	56224944
WWNWWWWWW	12	40799177
YYNYYYYYYN	12	74711204
YYNYYYYYYY	12	74711207
YYNYYYYYYY	14	76563541
YYYYYYYYYYY	16	69409798
YYYYYYYYYYY	16	69409806
RRRRRRRRRR	16	69421221
YYYYYYYYYYY	16	69424261
WWWWWWWWWW	16	69425316
YYYYYYYYYYY	16	69425332
RRRRRRRRRR	16	69425563
YYYYYYYYYYY	16	69429102
SSSSSSSSSS	16	69429248
SSSSSSSSSS	16	69442025
WWWWWWWWWW	16	69442035
YYYYYYYNY	16	69451588
RRRRRRRRRR	16	69453619
SSSSSSSSSS	16	69454540

YYYYYYYYYYY	16	69460060
YYYYYYYYYYY	16	69460069
RRRRRRRRRR	16	69460184
RRRRRRRRRR	16	69466237
RRRRRRRRRR	16	69470887
RRRRRRRRRR	16	69475356
SSSSSSSSSS	16	69475432
MMMMMMMMMMM	16	69500189
YYYYYYYYYYY	16	69512014
YYYYYYYYYYY	16	69512107
WWWWWWWWW	16	69512446
SSSSSSSSSS	16	69530121
YYYYYYYYYYY	16	69533168
RRRRRRRRRR	16	69543981
YYYYYYYYYYY	16	69546800
RRRRRRRRRR	16	69546836
YYYYYYYYYYY	16	69565670
YYYYYYYYYYY	16	69570356
YYYYYYYYYYY	16	69582746
SSSSSSSSSS	16	69583577
YYYYYYYYYYY	16	69583599
YYYYYYYYYYY	16	69611679
RRRRRRRRRR	16	69618996
YYYYYYYYYYY	16	69656150
YYYYYYYYYYY	16	69658701
YYYYYYYYYYY	16	69658771
YYYYYYYYYYY	16	69660770
YYYYYYYYYYY	16	69721080
MMMNMMNMMM	17	16038595
MMMMMMMMMMM	17	21142784
SSSSSSSSSS	17	21142830
RRRNRRRRRR	17	21144850
YYYYYYYYYYY	17	21146053
YYYYYNYYNY	17	21156076
SSSSSSSSSS	17	21157439
RRRRRRRRRR	17	21259256
RRRRRRRRRR	17	21259375
RRRRRRRRRN	17	21259460
SSSSSSSSSS	17	21259490
RRRRRRRRRR	17	21259545
RNRRRRRRRN	17	21259600
SSNSSNSSSS	17	21259601
YYYYYYYYYYY	17	21259714
RRRNRRRRRR	17	21259764
SSSSSSSSSS	17	21259823
YYYYYYYYYYY	17	21259895

RRRRRRRRRR	17	21260066
YNNYYYYNYY	17	21260360
YNNYYYYYYY	17	21260378
MWYYYYYMY	17	21260453
NRRRRRRRRR	17	21260548
WWWWWWWWW	17	42569563
RRRRRRNRRR	17	42569681
RRRRRRNRRR	17	42569689
RRRNRRRRRR	17	42574298
SSSSSSSSSS	17	42589297
NMNMMMMMMM	17	42589359
NRRNRRRRRR	17	42602361
RNRNRRRRRR	17	42602380
NNKKKKKKKK	17	42604334
RRRRRRRRRR	17	71799189
YYYYYYYYYYY	19	452743
MMMMMMMMMMM	19	452786
RRRRRRRRRR	19	22155333
RRRRRRRRRR	19	22155348
SSSSSSSSSS	19	22155666
RRNRRRRRRN	19	22155684

Supplementary Table 2. SNPs with F_{ST} of one between African and European exomes. “CEU” and “YRI” refer to the frequency of the polymorphism in the HapMap populations of Europe and Africa, respectively; “na” indicates that the SNP was not included in the HapMap (The International HapMap Consortium 2005). “Site” indicates the position in the hg18 alignment.

Chromosome	Site	rsID	CEU	YRI	Type	Gene
1	1237357	12103	na	na	synonymous	<i>CPSF3L</i>
1	1239050	12142199	0.78	0.00	synonymous	<i>CPSF3L</i>
1	11010111	1782455	0.86	0.20	synonymous	<i>MASP2</i>
1	11013503	12711521	0.83	0.13	nonsynonymous	<i>MASP2</i>
2	39360921	3755176	0.84	0.19	synonymous	<i>MAP4K3</i>
2	74541058	8469	na	na	synonymous	<i>WBP1</i>
2	74543547	2268416	1.00	0.07	nonsynonymous	<i>GCSI</i>
2	74543886	1063588	0.91	0.13	nonsynonymous	<i>GCSI</i>
2	74553286	1047911	0.91	0.15	nonsynonymous	<i>MRPL53</i>
2	74563999	6707475	0.90	0.01	nonsynonymous	<i>TTC31</i>
2	74599830	6546909	0.88	0.16	synonymous	<i>DQX1</i>
4	38475043	5743618	na	na	nonsynonymous	<i>TLR1</i>
5	33987450	16891982	0.98	0.00	nonsynonymous	<i>SLC45A2</i>
6	133146813	6926101	0.95	0.32	nonsynonymous	<i>C6orf192</i>
7	98885914	883403	0.84	0.04	synonymous	<i>CPSF4</i>
7	98919666	6962772	0.82	0.04	nonsynonymous	<i>ZNF789</i>
7	98983781	10238965	0.84	0.03	synonymous	<i>C7orf38</i>
7	142279718	4987682	0.94	0.35	nonsynonymous	<i>TRPV6</i>
7	142280264	4987679	na	na	synonymous	<i>TRPV6</i>
7	142283030	4987667	0.94	0.36	nonsynonymous	<i>TRPV6</i>
7	142283385	4987665	0.94	0.39	synonymous	<i>TRPV6</i>
7	142285035	4987657	0.51	0.28	nonsynonymous	<i>TRPV6</i>
8	10517787	6601495	1.00	0.14	nonsynonymous	<i>RP1L1</i>
8	22329632	6558052	0.92	0.13	synonymous	<i>SLC39A14</i>
10	15178621	7896053	0.88	0.28	nonsynonymous	<i>C10orf111</i>
10	100138166	2147896	0.67	0.10	nonsynonymous	<i>C10orf33</i>
11	6869703	2741804	0.53	0.10	nonsynonymous	<i>OR2D2</i>
13	97627177	628778	na	na	synonymous	<i>RNF113B</i>
15	43179367	269868	0.98	0.17	nonsynonymous	<i>DUOX2</i>
15	43448970	1288775	0.83	0.12	nonsynonymous	<i>GATM</i>
15	43482987	1153849	0.83	0.12	synonymous	<i>SPATA5L1</i>
17	7532893	2287499	0.84	0.08	nonsynonymous	<i>WDR79</i>
17	45950987	8064455	0.83	0.31	nonsynonymous	<i>MYCBPAP</i>
18	66022323	3911730	0.89	0.07	nonsynonymous	<i>RTTN</i>
19	47084150	2288509	1.00	0.21	synonymous	<i>ARHGEF1</i>

Supplementary Table 3. Gene-based analysis of candidate selection targets, complementing the 100-kb region-based analysis discussed in the text. Overlap between previously identified candidate genes and extreme values in the exome data.

list of genes	# genes ^a	# polymorphic genes ^b	π (%) ^c	Tajima's D ^d	$\log(\pi_A/\pi_E)$ ^e
All E	14342	9972	0.040 ± 0.056	0.03 ± 1.05	0.26 ± 1.09
All A	14342	10689	0.051 ± 0.063	-0.18 ± 0.97	0.26 ± 1.09
Akey E	817	514	0.027*** ± 0.039	-0.11* ± 1.11	0.39* ± 1.22
Kelley E	118	65	0.015*** ± 0.026	-0.52*** ± 1.00	0.80*** ± 1.22
Williamson E	100	61	0.029* ± 0.043	-0.12 ± 1.05	0.52* ± 1.17
Voight E	172	111	0.027* ± 0.032	-0.06 ± 1.11	0.25 ± 1.07
Akey A	817	591	0.042*** ± 0.051	-0.19 ± 0.97	0.39* ± 1.22
Kelley A	91	65	0.045 ± 0.061	-0.66*** ± 0.87	0.02 ± 1.05
Williamson A	28	22	0.061 ± 0.054	-0.52 ± 1.07	-0.43* ± 1.19
Voight A	192	134	0.036* ± 0.042	-0.33 ± 0.99	0.25 ± 1.15

^anumber of genes analyzed, excluding all genes with 500 or fewer bp coding sequence

^bnumber of genes analyzed that harbored polymorphisms, allowing Tajima's D to be calculated

^cmean percentage value of π for each gene, $\pm$ standard deviation

^dmean value of Tajima's D for each polymorphic gene, $\pm$ standard deviation

^ethe log of π in Africa divided by π in Europe, $\pm$ standard deviation

*Wilcoxon rank-sum test, $p < 0.05$, Bonferroni corrected for three tests

**Wilcoxon rank-sum test, $p < 0.001$, Bonferroni corrected for three tests

***Wilcoxon rank-sum test, $p < 0.0001$, Bonferroni corrected for three tests

"E" and "A" refer to European and African samples, respectively. For each set of candidate genes, we tested whether each of three summary statistics was significantly different from the equivalent statistic calculated from all remaining genes.

Supplementary Table 4. Filtered list of candidate genes for Europe-specific selection. All 100 kb regions have been identified in a previous selection scan, have lower than median π_E (0.026%) and π_{ES} (0.044%), have nonpositive Tajima's D_E and Tajima's D_{ES} , and have higher than median $\log(\pi_A/\pi_E)$ (0.10). These statistics refer to the respective 100 kb region, not just the gene. Within these regions, candidate genes were identified as those having at least one nonsynonymous SNP with $F_{ST} > 0.5$ between the continents; for all SNPs meeting these criteria, the position in the hg18 alignment is indicated. The most specific Gene Ontology (GO) term, defined as that which is shared with the fewest other genes, is indicated; "na" indicates that no GO term shared by fewer than 100,000 genes is associated with the locus.

Chromosome	Gene	π_E (%)	Tajima's D_E	$\log(\pi_A/\pi_E)$	SNP(s)	Most specific GO term
1	<i>ANKRD45**</i>	0.000	0.00	2.29	171862880	na
2	<i>ADAM17</i>	0.015	-0.38	0.70	9585381	response to high density lipoprotein stimulus
2	<i>GALNT5</i>	0.004	-1.14	1.63	157849052	polypeptide N-acetylgalactosaminyltransferase activity
3	<i>IQCG</i>	0.000	0.00	3.00	199143557, 199149996,	na
3	<i>LMLN</i>	0.000	0.00	3.00	199186310	metalloendopeptidase activity
4	<i>CBR4</i>	0.023	-1.14	0.34	170165417	NADPH dehydrogenase (quinone) activity
5	<i>MYOZ3</i>	0.005	-0.19	1.42	150036500	Z disc
7	<i>ZNF789</i>	0.002	-1.14	0.72	98919666*	zinc ion binding
7	<i>CYP3A7</i>	0.006	-1.14	1.48	99144621	aromatase activity
7	<i>ZC3HAV1</i>	0.012	-1.45	1.10	138411574, 138414773	NAD+ ADP-ribosyltransferase activity
7	<i>TRPV6</i>	0.003	-1.14	2.17	142279718*, 142283030*, 142285035*	regulation of calcium ion-dependent exocytosis
7	<i>TAS2R40</i>	0.006	-1.14	0.84	142629853	sensory perception of taste
8	<i>TEX15</i>	0.022	-1.16	0.48	30822067, 30822144	regulation of double-strand break repair via homologous recombination
8	<i>TRIM55</i>	0.025	-1.35	0.79	67227208	microtubule
9	<i>ZNF782</i>	0.000	0.00	2.88	98621632	zinc ion binding
10	<i>COMMD3</i>	0.008	-1.14	0.86	22645404	protein binding
10	<i>SPAG6</i>	0.000	0.00	2.63	22715863	axoneme
11	<i>DAK</i>	0.004	-1.45	1.21	60865550	FAD-AMP lyase (cyclizing) activity
11	<i>SIAE</i>	0.008	-1.14	2.08	124044483	sialate O-acylesterase activity
12	<i>SSPN</i>	0.022	-1.14	1.93	26275101,	dystrophin-associated glycoprotein complex

14	<i>PPP2R5C</i>	0.016	-0.91	0.62	26275101 101461330	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
14	<i>PACS2</i>	0.000	0.00	2.89	104904724	endoplasmic reticulum lumen
15	<i>APBA2</i>	0.013	-0.19	0.98	27134311	multicellular organism growth
15	<i>SLC28A2</i>	0.024	-0.85	0.66	43332770, 43341559	purine nucleoside transport / nucleoside:sodium symporter activity
15	<i>GATM</i>	0.009	-0.19	1.32	43448970*	glycine amidinotransferase activity
15	<i>SLC24A5**</i>	0.000	0.00	1.75	46213776	melanosome
15	<i>MRPL46</i>	0.000	0.00	3.60	86809921	ribosome
15	<i>MRPS11</i>	0.000	0.00	3.60	86811980	DNA damage response, detection of DNA damage
16	<i>ZNF267</i>	0.000	0.00	2.09	31834120	zinc ion binding
16	<i>PLEKHG4</i>	0.008	-1.89	1.40	65873735, 65875743, 65877724	Rho guanyl-nucleotide exchange factor activity
16	<i>LRRC36</i>	0.007	-1.45	1.46	65955081, 65966681	response to stress
17	<i>POLG2</i>	0.016	-0.83	0.17	59923044	mitochondrial chromosome
17	<i>C17orf58</i>	0.000	0.00	1.89	63419510	protein binding
18	<i>MPPE1</i>	0.024	-0.85	0.31	11876563	integral to membrane
18	<i>RTTN**</i>	0.000	0.00	2.16	66022323*	determination of left/right symmetry
19	<i>NWD1</i>	0.022	-0.13	1.34	16751243, 16760865	ATP binding
20	<i>REM1</i>	0.018	-0.19	0.86	29527992	calmodulin binding
22	<i>CELSRI</i>	0.019	-1.89	1.72	45138750, 45140161, 45159185, 45164979, 45166358, 45166361	establishment of planar polarity

*nonsynonymous SNP with an F_{ST} of one between continents.

**100 kb region invariant in European exons and nonsynonymous SNP with an $F_{ST} > 0.78$ between continents

Supplementary Table 5. Filtered list of candidate genes for Africa-specific selection. All 100 kb regions have been identified in a previous selection scan, have lower than median π_A (0.037%) and π_{AS} (0.075%), have nonpositive Tajima's D_A and Tajima's D_{AS} , and have lower than median $\log(\pi_A/\pi_E)$ (0.10). These statistics refer to the respective 100 kb region, not just the gene. All listed genes have at least one nonsynonymous SNP with $F_{ST} > 0.5$ between the continents; for all SNPs meeting these criteria, the position in the hg18 alignment is indicated. The most specific Gene Ontology (GO) term, defined as that which is shared with the fewest other genes, is indicated; "na" indicates that no GO term shared by fewer than 100,000 genes is associated with the locus.

Chromosome	Gene	π_A (%)	Tajima's D_A	$\log(\pi_A/\pi_E)$	SNP(s)	Most specific GO term
1	<i>NADK</i>	0.000	0.00	-2.22	1675900	NAD+ kinase activity
1	<i>TMED5**</i>	0.000	0.00	-1.30	93392981	ER-Golgi intermediate compartment
1	<i>CCDC18</i>	0.034	-1.18	-0.36	93419006, 93445311, 93492741	na
1	<i>AP4B1</i>	0.004	-1.05	-0.70	114240474	clathrin adaptor complex
2	<i>RAD51AP2</i>	0.000	0.00	-1.90	17560054	na
2	<i>GCSI</i>	0.007	-0.81	-0.01	74543547*, 74543886*	mannosyl-oligosaccharide glucosidase activity
2	<i>MRPL53</i>	0.007	-0.81	-0.01	74553286*	ribosome
2	<i>TTC31</i>	0.007	-0.81	-0.01	74563999*	na
3	<i>ARHGEF3</i>	0.017	-1.05	-2.14	56746291	induction of apoptosis by extracellular signals
4	<i>SLC30A9**</i>	0.000	0.00	-2.15	41698428	zinc ion transport
4	<i>FLJ21511</i>	0.029	-1.05	-0.56	48683207	GPI anchor biosynthetic process
4	<i>SPATA18</i>	0.031	-1.31	0.05	52633000	spermatogenesis
7	<i>C7orf55</i>	0.016	-1.31	-0.19	138676692	mitochondrion
7	<i>TAS2R4</i>	0.029	-1.53	-0.97	141124777, 141125269	cilium membrane
7	<i>TAS2R5</i>	0.029	-1.53	-0.97	141136707	taste receptor activity
11	<i>LRP4</i>	0.029	-1.28	0.01	46849684, 46855347	endocytosis
15	<i>ZSCAN29</i>	0.021	-0.92	-0.35	41449094	transcription factor activity
15	<i>TP53BP1</i>	0.011	-1.31	-1.01	41511938, 41549488, 41555066	telomeric DNA binding

15	<i>MAP1A</i>	0.010	-1.23	-0.52	41605344	microtubule associated complex
16	<i>ACD</i>	0.000	0.00	-1.05	66249169	positive regulation of single-stranded telomeric DNA binding
17	<i>CD300A</i>	0.032	-1.45	-0.09	69981561	cell adhesion
18	<i>RTTN</i>	0.022	-1.31	-0.05	65869668	determination of left/right symmetry
22	<i>HMG2L1</i>	0.000	0.00	-2.20	33990875	endosome to lysosome transport
22	<i>FAM118A</i>	0.025	-1.60	-1.30	44102471, 44107034	integral to membrane

*nonsynonymous SNP with an F_{ST} of one between continents

**100 kb region invariant in African exons and nonsynonymous SNP with an $F_{ST} > 0.78$ between continents

Supplementary Table 6. Filtered list of candidate regions for selection that were not retained on the continent-specific lists (Supplementary Table 4; Supplementary Table 5), and thus show a more geographically ambiguous pattern. All regions have been identified in a previous selection scan (non- F_{ST} -based), have lower than median π and π_S both globally and locally in the original continent of identification (“continent” = E for Europe and/or A for Africa), have nonpositive Tajima’s D and Tajima’s D_S both globally and locally, and have π/d_H both globally and locally (d_H is human-specific divergence from the common ancestor with chimps).

Chromosome	Start	Global π (%)	Global Tajima’s D	d_H (%)	Continent
1	6500000	0.028	-0.73	0.38	A,E
1	13600000	0.000	0.00	0.70	A
1	33100000	0.020	-0.63	0.19	A
1	35400000	0.009	-1.51	0.25	E
1	35600000	0.010	-1.44	0.12	E
1	35700000	0.000	0.00	0.08	E
1	35800000	0.003	-1.16	0.20	E
1	36200000	0.008	-1.51	0.15	E
1	41200000	0.015	-1.36	0.20	A
1	53100000	0.015	-1.51	0.16	E
1	70500000	0.031	-1.41	0.37	A
1	77300000	0.000	0.00	0.24	E
1	108900000	0.000	0.00	0.07	E
1	114100000	0.014	-0.77	0.14	A
1	117800000	0.000	0.00	0.05	E
1	159600000	0.000	0.00	0.19	E
1	160700000	0.000	0.00	0.16	A
1	160800000	0.007	-1.16	0.13	A
1	196900000	0.012	-1.19	0.50	A
2	39200000	0.027	-1.51	0.40	E
2	47800000	0.018	-1.03	0.26	A
2	69400000	0.000	0.00	0.21	A
2	74600000	0.005	-1.64	0.25	E
2	84500000	0.000	0.00	0.10	E
2	84600000	0.024	-1.14	0.33	E
2	86500000	0.015	-1.26	0.18	A
2	88700000	0.000	0.00	0.21	A
2	99200000	0.000	0.00	0.49	A
2	108700000	0.027	-1.25	0.26	E
2	134800000	0.000	0.00	0.08	E
2	134900000	0.000	0.00	0.12	E
2	135300000	0.008	-1.16	0.24	E
2	135500000	0.023	-0.59	0.24	E
2	136400000	0.000	0.00	0.18	E
2	136500000	0.000	0.00	0.19	E
2	157800000	0.027	-0.35	0.28	E
2	157900000	0.000	0.00	0.11	E
2	162700000	0.000	0.00	0.18	E

2	170000000	0.009	-1.14	0.16	E
2	177700000	0.000	0.00	0.09	A
2	196200000	0.009	-1.51	0.09	E
2	200500000	0.005	-1.16	0.22	A
2	203000000	0.011	-1.16	0.11	A
2	203100000	0.000	0.00	0.19	A
2	203400000	0.007	-1.16	0.07	A
2	205700000	0.000	0.00	0.43	E
3	4400000	0.000	0.00	0.58	A
3	9600000	0.000	0.00	0.10	E
3	9700000	0.009	-0.76	0.12	E
3	46300000	0.000	0.00	0.28	A
3	123900000	0.020	-0.81	0.33	E
3	124000000	0.000	0.00	0.18	E
3	166300000	0.003	-1.16	0.10	A
3	199200000	0.000	0.00	0.29	E
4	41400000	0.022	-1.47	0.37	E
4	71700000	0.020	-0.69	0.27	E
4	71800000	0.000	0.00	0.16	E
4	77400000	0.013	-1.72	0.29	A
4	106800000	0.015	-1.44	0.15	E
4	115700000	0.012	-1.16	0.12	E
4	115800000	0.000	0.00	0.25	E
4	186300000	0.000	0.00	0.12	E
4	186400000	0.000	0.00	0.19	E
5	21800000	0.010	-1.16	0.10	E
5	37200000	0.027	-1.87	0.36	A
5	55000000	0.000	0.00	0.22	E
5	79700000	0.024	-0.42	0.37	E
5	79800000	0.013	-1.87	0.17	E
5	82500000	0.000	0.00	0.17	A
5	101800000	0.018	-1.41	0.16	A
5	121300000	0.034	-0.53	0.54	A,E
5	133900000	0.017	-1.64	0.21	E
5	138700000	0.007	-1.47	0.30	E
5	150000000	0.021	-0.95	0.19	E
5	157100000	0.000	0.00	0.23	E
6	15700000	0.000	0.00	0.22	E
6	27400000	0.009	-1.16	0.33	A
6	28900000	0.007	-1.09	0.06	A,E
6	34600000	0.011	-1.14	0.19	E
6	39600000	0.032	-0.81	0.53	A,E
6	43400000	0.014	-1.33	0.21	E
6	76000000	0.022	-1.34	0.16	E
6	105600000	0.014	-1.51	0.21	E
6	105700000	0.011	-1.16	0.11	E

6	130500000	0.000	0.00	0.41	A
7	31000000	0.000	0.00	0.29	E
7	65700000	0.000	0.00	0.21	A
7	65800000	0.000	0.00	0.21	A
7	65900000	0.000	0.00	0.47	A
7	66000000	0.019	-1.64	0.26	A
7	72400000	0.004	-1.16	1.17	A,E
7	87200000	0.000	0.00	0.33	E
7	98000000	0.015	-0.59	0.46	E
7	98700000	0.009	-1.16	0.37	E
7	99100000	0.028	-0.88	0.34	E
7	117100000	0.005	-1.16	0.09	A
7	120400000	0.000	0.00	0.26	E
7	142600000	0.016	-0.53	0.23	E
8	26400000	0.033	-0.44	0.21	A
8	54900000	0.000	0.00	0.42	E
8	68000000	0.000	0.00	0.44	E
8	68100000	0.014	-0.81	0.19	E
8	102600000	0.009	-1.16	0.28	E
8	102700000	0.020	-1.51	0.20	E
8	104900000	0.000	0.00	0.07	A
8	109300000	0.000	0.00	0.14	A
8	111000000	0.000	0.00	0.10	E
8	139600000	0.009	-1.16	0.67	E
9	12600000	0.000	0.00	0.19	E
9	122500000	0.000	0.00	0.07	A
9	127300000	0.000	0.00	0.18	E
10	38200000	0.007	-1.16	0.41	A
10	51200000	0.010	-0.09	0.20	A
10	59600000	0.010	-1.00	0.12	E
10	73700000	0.021	-1.44	0.33	E
10	74300000	0.000	0.00	0.11	E
10	74600000	0.007	-1.16	0.08	E
10	74900000	0.003	-1.51	0.08	E
10	75100000	0.003	-1.16	0.32	E
10	75200000	0.004	-1.14	0.16	E
10	83600000	0.015	-1.00	0.47	E
10	103500000	0.000	0.00	0.09	A
10	112800000	0.007	-1.16	0.35	E
10	118100000	0.000	0.00	0.19	E
10	121600000	0.017	-0.79	0.39	A,E
11	36400000	0.013	-1.72	0.13	E
11	46600000	0.015	-1.33	0.31	A
11	47500000	0.013	-0.09	0.24	A
11	60200000	0.000	0.00	0.42	E
11	67000000	0.031	-0.73	0.22	A

11	75200000	0.000	0.00	0.40	A
11	119500000	0.019	-1.72	0.19	E
12	2700000	0.005	-1.16	0.23	E
12	4500000	0.034	-1.85	0.36	E
12	18700000	0.007	-1.51	0.15	E
12	26100000	0.000	0.00	0.12	E
12	43000000	0.000	0.00	0.13	E
12	43800000	0.008	-1.16	0.56	A
12	45000000	0.000	0.00	0.07	A
12	54900000	0.014	-1.67	0.23	E
12	55000000	0.015	-1.73	0.13	E
12	55700000	0.004	-1.72	0.13	A,E
12	67300000	0.026	-1.19	0.33	A
12	67400000	0.013	-0.81	0.40	A
12	70300000	0.011	-0.99	0.10	E
12	70400000	0.015	-1.16	0.15	A,E
12	73700000	0.000	0.00	0.15	A
12	75300000	0.013	-1.51	0.09	E
12	78200000	0.000	0.00	0.13	A
12	78600000	0.000	0.00	0.39	A
12	87000000	0.000	0.00	0.21	E
12	87100000	0.000	0.00	0.23	E
12	87400000	0.000	0.00	0.12	E
12	90000000	0.014	-1.72	0.19	E
12	93900000	0.000	0.00	0.21	A
12	99100000	0.018	-0.81	0.46	E
12	99300000	0.007	-1.16	0.57	E
12	99400000	0.000	0.00	0.28	E
12	122400000	0.000	0.00	0.16	A
13	25800000	0.000	0.00	0.16	A
13	35900000	0.000	0.00	0.29	A
13	40500000	0.000	0.00	0.09	A
13	51900000	0.008	-1.51	0.23	A
13	56600000	0.000	0.00	1.39	A
13	75000000	0.000	0.00	0.09	A
14	31600000	0.002	-1.16	0.04	A
14	34500000	0.000	0.00	0.11	E
14	35000000	0.000	0.00	0.20	A
14	35100000	0.005	-1.09	0.09	A
14	35200000	0.021	-0.38	0.20	A
14	44400000	0.011	-1.72	0.15	E
14	44500000	0.020	-1.14	0.20	E
14	44600000	0.016	-0.29	0.17	E
14	54000000	0.000	0.00	0.14	A
14	60500000	0.027	-0.77	0.21	E
14	73100000	0.021	-1.87	0.47	A

14	80400000	0.024	-0.56	0.25	E
15	26500000	0.000	0.00	2.06	E
15	27800000	0.008	-1.51	0.15	E
15	32400000	0.024	-0.79	0.48	A
15	46400000	0.006	-1.16	0.13	E
15	54400000	0.010	-1.16	0.31	A
15	70200000	0.014	-1.64	0.26	E
15	70300000	0.003	-1.16	0.10	E
15	70400000	0.028	-1.59	0.27	E
15	72500000	0.008	-1.16	0.38	E
15	72700000	0.011	-1.72	0.14	E
15	73500000	0.000	0.00	0.12	A
15	89500000	0.013	-1.16	0.13	A
16	1600000	0.000	0.00	0.11	E
16	2600000	0.000	0.00	0.36	A
16	14600000	0.015	-0.09	0.16	A
16	22900000	0.023	-1.64	0.43	A
16	46100000	0.000	0.00	0.21	E
16	55000000	0.000	0.00	0.29	A
16	88400000	0.014	-1.73	0.59	A,E
16	88500000	0.025	-0.11	0.46	A,E
17	3600000	0.020	-0.79	0.25	A
17	60600000	0.007	-1.16	0.42	E
18	12000000	0.000	0.00	0.38	E
18	29700000	0.000	0.00	0.15	E
18	29900000	0.000	0.00	0.39	E
18	64500000	0.011	-1.16	0.33	E
18	65700000	0.000	0.00	0.62	E
18	65900000	0.003	-1.16	0.43	E
18	75700000	0.011	-1.51	0.59	A
18	75800000	0.008	-1.16	0.22	A
19	6300000	0.026	-1.26	0.53	A
19	42900000	0.029	-0.98	2.27	A
19	43500000	0.029	-1.59	0.32	A
19	45200000	0.024	-1.56	0.80	E
19	47100000	0.004	-1.51	0.49	A,E
19	47200000	0.003	-1.51	0.11	E
20	2000000	0.000	0.00	0.25	A
20	19600000	0.000	0.00	0.17	A
20	21400000	0.000	0.00	0.12	E
20	31400000	0.021	-0.44	0.25	A
20	33500000	0.008	-1.26	0.14	E
20	36500000	0.000	0.00	0.08	E
20	36700000	0.000	0.00	0.22	A
20	44000000	0.026	-1.32	0.22	A
20	57800000	0.007	-1.51	0.22	E

20	57900000	0.016	-1.80	0.40	E
21	36300000	0.022	-1.64	0.28	A
22	17700000	0.000	0.00	0.14	A
22	17800000	0.020	-0.76	0.33	A
22	25300000	0.007	-1.16	0.52	A
22	35000000	0.019	-1.96	0.28	A
