Supplemental Table 1: List of large-insert clones (BACs and fosmids) sequenced at 8p23.1

*All PacBio sequenced clones can be found under BioProject ID: PRJNA306877 (http://www.ncbi.nlr

**BACs that solely underwent capillary sequencing were publically available sequences used in our a

Species	Clone ID	chr	GenBank
Human	CH17-315P16	chr8	AC243982.3
Orangutan	CH276-173C3	chr8	AC205861.3
Orangutan	CH276-204E18	chr8	AC275324.1/AC206098.6
Orangutan	CH276-328I17	chr8	AC206038.3/AC275326.1
Orangutan	CH276-222M18	chr8	AC206339.2
Orangutan	CH276-244L10	chr8	AC206445.3
Orangutan	CH276-490J7	chr8	AC206546.3
Orangutan	CH276-43O14	chr8	AC206556.3
Orangutan	CH276-327M11	chr8	AC206707.3/AC275395.1
Orangutan	CH276-480A19	chr8	AC206881.3
Orangutan	CH276-245P17	chr8	AC206882.3
Orangutan	CH276-458F1	chr8	AC207005.3
Orangutan	CH276-289K21	chr8	AC207014.4
Orangutan	CH276-236D24	chr8	AC207519.3
Orangutan	CH276-500A7	chr8	AC207782.6
Orangutan	CH276-107A5	chr8	AC212986.3
Human	CH17-276F21	chr8	AC245425.2
Human	CH17-322E21	chr8	AC246795.2
Human	CH17-106K1	chr8	AC270275
Human	CH17-10F5	chr8	AC270267
Human	CH17-145N17	chr8	AC275404
Human	CH17-168C14	chr8	AC270299
Human	CH17-172D3	chr8	AC270273
Human	CH17-174O18	chr8	AC270297
Human	CH17-175G16	chr8	AC275369
Human	CH17-180K5	chr8	AC270248
Human	CH17-183D12	chr8	AC275401
Human	CH17-183F15	chr8	AC275362
Human	CH17-189E11	chr8	AC270270
Human	CH17-194A21	chr8	AC270265
Human	CH17-195A22	chr8	AC270260
Human	CH17-196E9	chr8	AC270259
Human	CH17-196K11	chr8	AC270252
Human	CH17-203J21	chr8	AC270274
Human	CH17-206L7	chr8	AC270291
Human	CH17-20H22	chr8	AC275331
Human	CH17-214M14	chr8	AC270253
Human	CH17-21L15	chr8	AC270257
Human	CH17-221K15	chr8	AC270262
Human	CH17-231D4	chr8	AC270268
Human	CH17-238C3	chr8	AC270271
Human	CH17-241F1	chr8	AC270296
Human	CH17-245C6	chr8	AC275360
Human	CH17-251L15	chr8	AC270255
Human	CH17-278K24	chr8	AC270263
Human	CH17-281O3	chr8	AC270264
Human	CH17-287B5	chr8	AC270285

Human	CH17-28E6	chr8	AC275485
Human	CH17-294L6	chr8	AC270292
Human	CH17-302E9	chr8	AC270284
Human	CH17-305H6	chr8	AC270289
Human	CH17-306H24	chr8	AC270251
Human	CH17-30L14	chr8	AC270300
Human	CH17-312D18	chr8	AC270295
Human	CH17-33D7	chr8	AC270290
Human	CH17-347E16	chr8	AC270277
Human	CH17-349F14	chr8	AC275317
Human	CH17-352N3	chr8	AC275411
Human	CH17-354E2	chr8	AC270287
Human	CH17-35D22	chr8	AC270249
Human	CH17-365F15	chr8	AC270281
Human	CH17-371B8	chr8	AC270293
Human	CH17-376D14	chr8	AC270302
Human	CH17-377H11	chr8	AC270258
Human	CH17-385L20	chr8	AC270283
Human	CH17-395B1	chr8	AC275307
Human	CH17-401E19	chr8	AC270298
Human	CH17-418E9	chr8	AC270269
Human	CH17-423H5	chr8	AC270288
Human	CH17-423O10	chr8	AC270254
Human	CH17-435C19	chr8	AC270282
Human	CH17-435N6	chr8	AC270286
Human	CH17-436E1	chr8	AC270261
Human	CH17-449G4	chr8	AC270266
Human	CH17-465H18	chr8	AC270279
Human	CH17-477A15	chr8	AC270301
Human	CH17-51L18	chr8	AC270276
Human	CH17-54J21	chr8	AC270280
Human	CH17-56I4	chr8	AC270256
Human	CH17-67G5	chr8	AC270250
Human	CH17-76E23	chr8	AC275403
Human	CH17-82E17	chr8	AC270272
Human	CH17-90D10	chr8	AC275349
Human	CH17-99L5	chr8	AC270472
Human	ABC10_000044083200_P10	chr8	AC275322
Human	ABC10_000044495400_N18	chr8	AC275344
Human	ABC10_000044511300_H10	chr8	AC275316
Human	ABC10_000044516000_K3	chr8	AC275408
Human	ABC10_000044516400_C11	chr8	AC275407
Human	ABC10_000044587800_H4	chr8	AC275365
Human	ABC10_000044638200_G16	chr8	AC275346
Human	ABC10_000044679400_G1	chr8	AC275426
Human	ABC10_000045494800_D1	chr8	AC275329
Human	ABC10_000045517500_H16	chr8	AC275348
Human	ABC10_000045522900_D13	chr8	AC275368
Human	ABC10_000046314100_G4	chr8	AC275339
Human	ABC12_000046335100_A4	chr8	AC275377
Human	ABC12_000047032800_E10	chr8	AC275364
Human	ABC12_46356100_G21	chr8	AC275378

Human	ABC12_46656500_L6	chr8	AC275419
Human	ABC12_46660700_B3	chr8	AC275312
Human	ABC12_46665700_H21	chr8	AC275350
Human	ABC12_46790000_K10	chr8	AC275345
Human	ABC12_46839700_P7	chr8	AC275425
Human	ABC12_46849200_N24	chr8	AC275342
Human	ABC12_46988000_J13	chr8	AC275393
Human	ABC12_47012300_E16	chr8	AC275383
Human	ABC12_47044200_J6	chr8	AC275353
Human	ABC12_49053100_C11	chr8	AC275409
Human	ABC12_49055700_O16	chr8	AC275385
Human	ABC12_49081200_C3	chr8	AC275336
Human	ABC12_49093000_L15	chr8	AC275355
Human	ABC12_49214600_E16	chr8	AC275398
Human	ABC12_7920449_H21	chr8	AC275400
Human	ABC9_41250000_B13	chr8	AC275361
Human	ABC9_41290200_F3	chr8	AC275367
Human	ABC9_43350400_G19	chr8	AC275351
Human	ABC9_43833900_G24	chr8	AC275333
Human	ABC9_43849300_F17	chr8	AC275340
Human	ABC9_43866900_B10	chr8	AC275413
Human	ABC9_43874200_G15	chr8	AC275402
Human	ABC9_44001300_J5	chr8	AC275347
Human	ABC9_44019600_P10	chr8	AC275373
Human	ABC9_44026100_F7	chr8	AC275422
Human	ABC9_44033500_J6	chr8	AC275334
Human	ABC9_45365100_H16	chr8	AC275379
Human	ABC9_45920200_O18	chr8	AC275341
Human	ABC9_46009100_E2	chr8	AC275308
Human	ABC9_46272700_P10	chr8	AC275354
Chimpanzee	CH251-16F3	chr8	AC275315
Chimpanzee	CH251-189O20	chr8	AC275318
Chimpanzee	CH251-206K8	chr8	AC275382
Chimpanzee	CH251-231A21	chr8	AC275337
Chimpanzee	CH251-25J11	chr8	AC275321
Chimpanzee	CH251-268A17	chr8	AC275357
Chimpanzee	CH251-316J16	chr8	AC275392
Chimpanzee	CH251-329P19	chr8	AC275352
Chimpanzee	CH251-351I24	chr8	AC275376
Chimpanzee	CH251-3A13	chr8	AC275372
Chimpanzee	CH251-434L13	chr8	AC275418
Chimpanzee	CH251-4G1	chr8	AC275391
Chimpanzee	CH251-553E24	chr8	AC275309
Chimpanzee	CH251-67O17	chr8	AC275421
Orangutan	CH276-114M21	chr8	AC275406
Orangutan	CH276-247O4	chr8	AC275311
Orangutan	CH276-324M13	chr8	AC275388
Orangutan	CH276-364C1	chr8	AC275359
Orangutan	CH276-403I6	chr8	AC275323
Orangutan	CH276-48G19	chr8	AC275314
Orangutan	CH276-501K8	chr8	AC275325
Orangutan	CH276-60F1	chr8	AC275386

Orangutan	CH276-72N9	chr8	AC275335
Orangutan	CH276-87C11	chr8	AC275424
Orangutan	CH276-277M12	chr8	AC275310
Gorilla	CH277-15E23	chr8	AC275371
Gorilla	CH277-160N5	chr8	AC275363
Gorilla	CH277-192L15	chr8	AC275410
Gorilla	CH277-199N4	chr8	AC275387
Gorilla	CH277-208E13	chr8	AC275375
Gorilla	CH277-264M10	chr8	AC275427
Gorilla	CH277-272C3	chr8	AC275420
Gorilla	CH277-275M15	chr8	AC275358
Gorilla	CH277-331A9	chr8	AC275319
Gorilla	CH277-400C12	chr8	AC275415
Gorilla	CH277-459J15	chr8	AC275328
Gorilla	CH277-51F5	chr8	AC275399
Gorilla	CH277-574K7	chr8	AC275381
Gorilla	CH277-65O2	chr8	AC275414
Gorilla	CH277-98D3	chr8	AC275416
Gorilla	CH277-14C13	chr8	AC275412
Gorilla	CH277-230O4	chr8	AC275405
Gorilla	CH277-237N5	chr8	AC275338
Gorilla	CH277-502K16	chr8	AC275313
Gorilla	CH277-531L7	chr8	AC275374
Gorilla	CH277-69O14	chr8	AC275327
Human	RP11-257J3	chr8	AC275356
Human	RP11-957L3	chr8	AC275428
Human	RP11-158L15	chr8	AC275394
Human	RP11-980I9	chr8	AC275330

n.nih.gov/bioproject/).
analyses and not redundantly submitted as part of this BioProject.

PacBio Sequence	Capillary Sequence	insert size (kbp)
-	Finished	207
-	Finished	125
Finished	Finished	194
ogress, 2 ordered p	Finished	235
-	Finished	196
-	Finished	214
-	Finished	215
-	Finished	223
Finished	Finished	203
-	Finished	187
-	Finished	150
-	Finished	191
-	Finished	202
-	Finished	172
-	Finished	197
-	Finished	205
-	Finished	216
-	Finished	199
Finished	-	200
Finished	-	237
Finished	-	230
Finished	-	201
Finished	-	216
Finished	-	223
Finished	-	207
Finished	-	239
Finished	-	206
Collapsed	-	200
Finished	-	44
Finished	-	205
Collapsed	-	186
Finished	-	187
Finished	-	192
Finished	-	207
Finished	-	216
Collapsed	-	164
Finished	-	199
Finished	-	216
Finished	-	103
Finished	-	75
Finished	-	211
Finished	-	244
ollapsed Fragment	-	211
Finished	-	215
Finished	-	202
Finished	-	203
Finished	-	211

Collapsed	-	158
Finished	-	218
Finished	-	226
Finished	-	224
Finished	-	196
Finished	-	214
Finished	-	218
Finished	-	216
Finished	-	218
Finished	-	208
Finished	-	214
Finished	-	193
Finished	-	196
Finished	-	208
Finished	-	199
Collapsed	-	198
Finished	-	195
Finished	-	215
Fragmented	-	227
Finished	-	173
Finished	-	36
Finished	-	193
Finished	-	202
Finished	-	205
Finished	-	202
Finished	-	205
Finished	-	231
Finished	-	210
Finished	-	215
Finished	-	208
Finished	-	215
Finished	-	198
Finished	-	239
Fragmented	-	238
Finished	-	256
Collapsed	-	198
Finished	-	214
Finished	-	42
Finished	-	41
Finished	-	39
Finished	-	34
Finished	-	43
Finished	-	38
Finished	-	39
Finished	-	42
Finished	-	41
Finished	-	41
Finished	-	40
Finished	-	42
Finished	-	40
Finished	-	39
Finished	-	38

Finished	-	36
Finished	-	40
Finished	-	40
Finished	-	35
Finished	-	38
Finished	-	38
Finished	-	40
Finished	-	41
Finished	-	39
Finished	-	38
Finished	-	40
Finished	-	41
Finished	-	41
Finished	-	39
Finished	-	40
Finished	-	37
Finished	-	36
Finished	-	46
Finished	-	38
Finished	-	36
Finished	-	37
Finished	-	39
Finished	-	40
Finished	-	39
Finished	-	37
Finished	-	39
Finished	-	33
Finished	-	38
Finished	-	36
Finished	-	42
Finished	-	169
Finished	-	185
Finished	-	118
Finished	-	167
Collapsed	-	169
Finished	-	151
Collapsed	-	148
Finished	-	202
Collapsed	-	116
Finished	-	182
Finished	-	180
Finished	-	155
Finished	-	174
Finished	-	178
Finished	-	201
Finished	-	220
Finished	-	182
Finished	-	197
Finished	-	186
Finished	-	206
Finished	-	196
Finished	-	216

Finished	-	207
Finished	-	208
Collapsed	-	189
Finished	-	168
Finished	-	160
Finished	-	184
Finished	-	136
Finished	-	229
Finished	-	157
Finished	-	172
Finished	-	206
Finished	-	179
Finished	-	190
Finished	-	149
Finished	-	139
Finished	-	161
Finished	-	153
Finished	-	176
apsed and Fragme	-	-
Collapsed	-	56
Collapsed	-	93
Collapsed	-	70
Collapsed	-	118
Fragmented	-	-
Finished	-	179
Finished	-	185
Finished	-	157
Finished	-	161

Supplemental Table 2: Clone end mapping statistics used to assess the accuracy of the 8p23.1 ha

Sample	Sample Genotype	Reference Haplotype	Bases without concordance
CHM1	Homozygous H2	H2	0
NA19240	Homozygous H2	H2	51,045
NA12878	Homozygous H2	H2	89,377
NA18956	Homozygous H1	H2	62,914
NA18947	Homozygous H1	H2	89,879

plotype

Discordant end cluster bases	High quality base matches	High quality bases
118,741	236,284	236,311
705,938	1,380,370	1,381,508
673,369	1,793,307	1,794,274
780,691	1,305,298	1,306,268
780,795	678,908	679,400

% identity of	high quality bases	Insert size mean	Insert size std dev	Pairs	Concord Matches
0.9999	209,408	19,016	249	220,534	
0.9992	41,033	1,678	1,249	1,323,455	
0.9995	39,796	1,226	1,668	1,740,398	
0.9993	39,662	2,209	1,107	1,239,213	
0.9993	38,481	1,680	736	633,769	

ant pairs			Discordant pairs					Singletons	
Bases	Identity	Pairs	Matches	Bases	Identity	Clones	Matches	Bases	Identity
220,560	0.9999	6	6,535	6,535	1.0000	22	9,215	9,216	0.9999
1,324,542	0.9992	43	42,243	42,288	0.9989	32	15,696	15,704	0.9995
1,741,319	0.9995	49	42,015	42,055	0.9990	29	10,894	10,900	0.9994
1,240,127	0.9993	45	47,138	47,184	0.9990	38	20,881	20,893	0.9994
634,238	0.9993	16	23,205	23,221	0.9993	60	22,743	22,751	0.9996

Internal clones
7
20
17
27
51

Supplemental Table 3: Structural variation >50 bp called by

Assembly	SV Start (H2)	SV End (H2)	SV Type	SV Size
H2	2066984	2067034	deletion	50
H2	5467427	5467477	insertion	50
H2	3479379	3479430	insertion	51
H2	5230651	5230702	insertion	51
H2	4864433	4864485	deletion	52
H2	5199469	5199525	deletion	56
H2	4056767	4056827	insertion	60
H2	5517748	5517808	deletion	60
H2	274916	274979	insertion	63
H2	988946	989010	deletion	64
H2	1082864	1082933	deletion	69
H2	5569136	5569214	deletion	78
H2	5528593	5528672	insertion	79
H2	1141538	1141618	deletion	80
H2	957968	958053	deletion	85
H2	4914204	4914296	deletion	92
H2	5545540	5545644	insertion	104
H2	2634357	2634462	insertion	105
H2	4029939	4030044	deletion	105
H2	2540913	2541028	deletion	115
H2	2475144	2475272	insertion	128
H2	3495760	3495901	insertion	141
H2	6186436	6186593	deletion	157
H2	3417946	3418112	deletion	166
H2	4532526	4532692	deletion	166
H2	1853454	1853623	deletion	169
H2	5505054	5505258	deletion	204
H2	1125001	1125221	deletion	220
H2	2282172	2282395	deletion	223
H2	5438396	5438712	insertion	316
H2	1226712	1227034	insertion	322
H2	4250709	4251033	deletion	324
H2	3359658	3359984	deletion	326
H2	1853696	1854023	deletion	327
H2	5798682	5799009	insertion	327
H2	5768735	5769068	deletion	333
H2	3502213	3502550	deletion	337
H2	1168487	1168825	deletion	338
H2	3037163	3037512	deletion	349
H2	1166005	1166510	deletion	505
H2	5504188	5504693	insertion	505
H2	1124264	1124988	deletion	724
H2	54246	55146	deletion	900
H2	3159162	3160180	deletion	1018
H2	4737213	4738549	deletion	1336
H2	5464039	5465629	deletion	1590
H2	1920403	1922052	insertion	1649
H2	3538773	3541297	deletion	2524
H2	4881869	4886395	insertion	4526

H2	1167245	1171975	insertion	4730
H2	5177291	5183262	insertion	5971
H2	1286012	1292118	deletion	6106
H2	903207	910829	insertion	7622
H2	913943	921566	insertion	7623
H2	635039	642684	insertion	7645
H2	629532	637186	insertion	7654
H2	912162	927406	insertion	15244
H2	5288314	5303609	insertion	15295
H2	5295935	5318888	insertion	22953

y the SMRT SV pipeline in the H2 haplotype

Sequence	Repeat
GGCTCCAACAAAGATCACAAGGCAAAGGGCAAAAGCAGAACTACTGATA	NONE
CTTGCAATCCTGTCAAGATAATAGGATTTTCCATTTATAGTGTAATCTGA	NONE
ATGTCCACTAGAGGTCAGCACCTACTTCCGTGTAGAGCTGTATTGCTACAC	NONE
TGCAACCTGCTCCTCACTACAACCTCCTCCTCACTGCAACCTCCTCCTCAC	NONE
AAATGCAATGCCTCTTCAAAACTCTCATCCATTCCAGTGTCTGCATCCAGA	NONE
acatatatacacgtatgtgtacatatacacgtatgtgtacatatatacacgtatgt	(TA)n:FULL
AagagagagaaagagagagaaagagagagaaagagagagaaagagagagaaagagagaA	(GA)n:FULL
TTCTtttctttctttctttctctttctctttctttctttctttctttctttctttc	(TTTC)n:FULL
tatattatatatattatattatatattatatattatattatatattatatatattatatta	(TTATA)n:FULL
GCGTGtatatatgtacacatatacgtgtatatgtacacatacgtgtatatatgtacacataCGT	(TA)n:FULL
CGTCTGTCTGagctgagactagatatgaatctttcaccataaaaatgttaaaagatatgaag	HERVK-int:INC
Gtatgtgtgtatatatacacatatatacatgtatatatgtatatacacacatacatatatacataca	(TA)n:FULL
TTAATATCCTTTTCTATACTCTAGTTCTGAATTTAAAGAAAGAAAAAGGTA	NONE
AATAGAAATAGCTGATACCTATATTTGCTAACCTACCTTTTTCTTTCTTTAA	NONE
GCAGTGAGGAGGAGGTTGCAGTGAGGAGGAGGTCGCAGTGAGGAGGAC	NONE
CTTctcccctcttctcccctcctcctcccccctcctctcccctcctcctcccccctcctctcccctcctcct	none
GGGATGTGGCAGCTGCAGCGGGCTTGGCTTTGTGAGGAACCGAGTGTGT	NONE
GGTGTGATATGGGGGTTGCAGGGCATGATATGGGGGCTACAGGGTGTGC	NONE
aaggaaaggaaaggaaaggaaaggaaaggaaaggaaaggaaaggaaaggaaaggaaaggaaagg	(GGAAA)n:FULL
TGTGGCTGTGAGGGTGCCTGGTCACCGAGCCTGTCTCTGTGTGGCTGTGA	NONE
GTCATTCTTCTCCAGCCTCCCGCACCCCAGTCGTCATTCTTCTCCAGCCTCC	NONE
GGGAGAGGAGAGGGGAgaggggagaggagaggggaggggagaggagaggagagag	GA-rich:FULL
ACCTTAATTACAATGAAGGAGAAACATACTTTGTGAGCATTTGGAGTTGA	NONE
ATATATTATAAAATATATtatatattatatatattatatatatattttatatatattatatata	(TA)n:FULL
CAcaccgatcagcaccctgtgtctagctcagggtttgtgaatgcaccagtcgacactgtatctagc	LTR12E:INC
CACAGCAAGGCAACCACCCAACACTCACATACCCCCAGCAGGGCAACCAC	NONE
ctcactgtgtccttgtttcctcagtgttcaactttcacttattagtgagaacatgcggtatttgtttttt	L1PA8A:INC
aattgtcttgtgaccctgacacatccccctctttgagaaacacccacagatgatcaataaatacta	LTR5_Hs:INC
TAGTAGGCAACGCCATtaagagtttagtaggctagaccatctaggtgtgtagtaggctaga	Tigger3a:INC;Tigger
CTATGGGTGAGttttttttttttttttttttttttttgagacggagtctcgctctgtcgcccaggctgg	AluY:FULL
ttttttttttttttttttttttttttttgagacggagtctcgctctgtcgcccaggctggagtgcagtggcgc	AluY:FULL
ttttttttttttttttttttttttttgagacggagtctcgctctgtcgcccaggtcggactgcggactgcag	AluY:FULL
ttttttttttttttttttttttttttttgagacggagtctcgctctgtcgctcaggccagactgcggactgc	AluY:FULL
ACTCACACTCACAGCAAGGCAACCACCCCCCACACTCACACTCACACTCAC	NONE
TTGGAGCCAAATCttttttttttttttttttttttttttttttgagacggagtctcgctctgtcgcccag	AluY:FULL
GTGGGGTGGGGGCAGACAAGCGGGTAGGGGCTGGACCCCCCAGGACAC	L1ME4b:INC
GCCAGTGAAGATCTTCTTTttttttttttttttttttttttttttttttttgagacggagtctcgctct	AluY:FULL
GTTTCATGTTTTCTTTCTTTttttttttttttttttttttttttttttttgagacggggtctcgctct	AluY:FULL
ATTATGTCACTATTTACTTATATTTTACAATCTGCATAATTTCTAGAAAGAT	L1MC5a:INC
TTTCTTGCAGTCATAACTTCGGTGGATGTCATCAATTAGTCTCCGGGTTAT	L1M2:INC
AGTGTATTTGTGTGTTTGTTTCTGGATGTGTGTGTATGCCTTGAGAAGTAC	L1M2:INC
tgtggggaaaagcaagagagatcagattgttactgtgtctgtgtagaaagaagtagacataggag	LTR5_Hs:INC
GAgagggaaggaaggaaggaaggagggagggagggagggagagagggaaggaaggaagg	(GGGA)n:FULL;(GGA
CTAACAACAACAAAAATTCTTACAAGAAATAGCATGAACATTATGGGCTCC	MIRc:INC
CTCAGTAGACTGGCCCCCTGAATCTCCAGACAACCAATATCACTTAAATAA	NONE
tgcaaataatgctataataaatatatgagtgcacacatctttatggtagaacaatttatttttcttttg	L1P4:INC;THE1-int:I
CTTGGGGTCCAGGGTCCTCTGCTTTCTGACCAGAGCTGAGGACCTGCTTG	Charlie4z:INCTC
cctccctctctcactctgcccctctccctccctccctctcactctctccctctgcctcccccctctccctc	C-rich:FULL;CT-rich:
TAATCAGcagtggttcccaaactttagcttgtgcaagaatcacctgggattccataaaagatgc	MER5A:INC;AluSx:I

AGAGAGAAACGATTGTGGAGAATGGCCCCTTACTTTTGTATATTTGCTGAT	(CA)n:FULL;(CA)n:FU
aatccacgttcttctgtcatggcttcagccggtccctctgtttggggtcccgacttcccgcaacatct	MER11C:INC;HERVK
CACAGCCTCTAAGTTGGATACCCTGAATTTAAATCTCAACATGGCCATTTTC	ERVL-B4-int:INC;MI
CGGCCTCTTACAGGTTGTGTGGACCGGCATTGGCCCCCTTGCAACCTGAAA	L1MB3:INC;LTR5A:F
TTACACGTCTACTTTCTTTCCCAGGCTGGCGCTGAGATGGGCAGGTGCTGC	L1MB3:INC;LTR5A:F
TGGACCCTGTCCTCGCTGATCGCTCCGCAACTGAAATGTCTGGCAGGGGC	LTR5A:FULL;L1MB3
ctttaacatcccacgaggccatatttcagactgttacatggggagaaaccttggacaataacctgc	LTR5A:INC;L1MB3:I
CCCGGGGCTTCCATGGTTTCAGGTTTTCCTTCCCTTCCTTTTTCCCCAAGGTC	L1MB3:INC;LTR5A:F
GAACCAGGCAGAGTTTCACTGGCCAAATAGACCCCAGCAAAGCTGAAGTT	L1MB3:INC;(CAAAA
GTGAAGTGGCTTCCGGATGTGCGAAGGAACCAGGCAGAGTTTCACTGGC	L1MB3:INC;(CAAAA

Repeat Unit	SV Start (H1)	SV End (H1)	Identity
no_tsd	8925475	8925525	0
CTTGCAATC	7801643	7801693	0
ATGTCCACTAGAGGTCAGC	10335773	10335824	0
TGCAACCTGCTCCTCACTA	7527848	7527899	0
no_tsd	11716251	11716303	0
no_tsd	12417687	12417743	1
GAGAGAGAAAGAGAGA	10910452	10910512	0.95
no_tsd	7852340	7852400	0.93
TATTATATATATTATATTA	6756268	6756331	1
no_tsd	12368061	12368125	0.88
no_tsd	7943057	7943126	0.86
no_tsd	12306579	12306657	0.99
ATTA	7863144	7863223	0
no_tsd	8000823	8000903	0
no_tsd	12337051	12337136	0
no_tsd	11770467	11770559	0.97
GGGATGTGGCAGCTGCAGC	12282881	12282985	0
GGTGTGATATGGGGGTTGC	9492469	9492574	0
no_tsd	10883676	10883781	1
no_tsd	9399156	9399271	0
GTCATTCTTCTCCAGCCTC	9333220	9333348	0
AGAGGAGAGGGGAG	10352208	10352349	0.89
no_tsd	12916691	12916848	0
no_tsd	10274517	10274683	0.85
no_tsd	11385823	11385989	0.99
no_tsd	8710737	8710906	0
no_tsd	7839838	7840042	1
no_tsd	7984499	7984719	1
no_tsd	9140503	9140726	0.9
CTATGGGTGAGTTTT	7773854	7774170	0.97
TTTCCCAGGTTTTT	8089858	8090180	0.95
no_tsd	11104356	11104680	0.96
no_tsd	10216580	10216906	0.97
no_tsd	8710810	8711137	0
TGAGCC	12528701	12529028	0.96
no_tsd	12499025	12499358	0.43
no_tsd	10358798	10359135	0.94
no_tsd	7942551	8032295	0.94
no_tsd	9895437	9895786	0.82
no_tsd	8025241	8025746	0.43
no_tsd	7838977	7524650.43	
no_tsd	7984483	7985207	1
no_tsd	6536464	6537364	0.97
no_tsd	10017089	10018107	0.09
no_tsd	11590378	11591714	0
no_tsd	7799842	7801432	0.67
no_tsd	8777261	8778910	0.05
no_tsd	10395040	10397564	0.8
CCA	11733641	11738167	0.49

ATTGTGG	7941952	8030703	0.03
no_tsd	12389514	12395485	1
no_tsd	8149478	8155584	0.4
notsd	7392295	7399917	0.15
CTACTTTCTTT	7425898	7433521	0.17
GTCCTCGCTGA	7116493	7124138	0.17
TCCCA	7103339	7110993	0.16
notsd	7408873	7424117	0.17
notsd	7585577	7600872	0.18
GTGAAGTGGCTTCCGGATG	7608494	7631447	0.17

Supplemental Table 4: Sequence coordinates of inversion associated repeats (IARs) with the GRCh37 r

Cytogenetic Position	Size	Orientation	Chromosome	Core Start
3p12.3	68635	+	chr3	75555226
3q21.2	61252	-	chr3	125498819
3q22.1	30022	+	chr3	129901597
4p16.3	58788	+	chr4	4038030
4p16.1_A	62796	-	chr4	9015707
4p16.1_B	63322	-	chr4	9547140
7q21.3	54064	+	chr7	97503239
8p23.1_A	68690	+	chr8	7004876
8p23.1_B	68633	-	chr8	7936497
8p23.1_C	69918	+	chr8	12383473
8p23.1_D	36207	+	chr8	12467539
11p15.4	52719	+	chr11	3536646
11q13.2	62202	+	chr11	67655605
11q13.4	62332	-	chr11	71363639
12p13.31	67638	+	chr12	8476130
16p13.3	56354	-	chr16	5303454

eference assembly

Core End	Core % Repeat
75615948	74
125552157	68
129931618	80
4096189	73
9071498	69
9602843	68
97545411	67
7066068	71
7997226	71
12445578	72
12503746	66
3589365	67
67710213	69
71418407	69
8530078	67
5345789	64

Supplemental Table 5: List of inter and intrachromosomal SDs in the H2 haplotype

chrom	chromSta	chromEnc	name	score	strand	otherChr	otherStart	otherEnd	otherSize
H2	0	653973	chr8:648	0	+	chr8	6482282	7135400	653118
H2	350306	369425	EntireDEI	0	+	EntireDEI	369425	388548	19123
H2	369425	388548	EntireDEI	0	+	EntireDEI	350306	369425	19119
H2	440927	458210	chr12:52	0	+	chr12	52489027	52499504	10477
H2	441009	445902	EntireDEI	0	+	EntireDEI	1392737	1397493	4756
H2	441039	450599	EntireDEI	0	_	EntireDEI	5826890	5836243	9353
H2	444666	455884	chr3:873	0	+	chr3	8731715	8735690	3975
H2	444666	457278	chr4:895	0	+	chr4	8953210	8958574	5364
H2	451257	458245	chr21:33	0	+	chr21	33985908	33991844	5936
H2	451933	472450	EntireDEI	0	_	EntireDEI	600766	621731	20965
H2	451933	472450	EntireDEI	0	+	EntireDEI	924120	945049	20929
H2	451933	472450	EntireDEI	0	+	EntireDEI	1270779	1291771	20992
H2	451933	458219	EntireDEI	0	+	EntireDEI	1381933	1387229	5296
H2	451933	472450	EntireDEI	0	_	EntireDEI	5243551	5264500	20949
H2	451933	472450	EntireDEI	0	_	EntireDEI	5782638	5803405	20767
H2	451933	458220	chr10:15	0	_	chr10	15043678	15048954	5276
H2	451933	522402	chr11:35	0	_	chr11	3550163	3619969	69806
H2	451933	486757	chr11:67	0	_	chr11	67704795	67740808	36013
H2	451933	522409	chr11:71	0	+	chr11	71332979	71404199	71220
H2	451933	457278	chr11:71	0	+	chr11	71306361	71311690	5329
H2	451933	458246	chr11:71	0	+	chr11	71606367	71612648	6281
H2	451933	472450	chr12:85	0	_	chr12	8545865	8566481	20616
H2	451933	458220	chr12:85	0	_	chr12	8582808	8589102	6294
H2	451933	458220	chr13:42	0	_	chr13	42007941	42012743	4802
H2	451933	458249	chr13:68	0	+	chr13	68478253	68483551	5298
H2	451933	458247	chr14:52	0	_	chr14	52232314	52237599	5285
H2	451933	458249	chr3:753	0	_	chr3	75399481	75404749	5268
H2	451933	488330	chr3:756	0	_	chr3	75609150	75646900	37750
H2	451933	522409	chr3:125	0	+	chr3	125467839	125537625	69786
H2	451933	458247	chr3:125	0	+	chr3	125424100	125429407	5307
H2	451933	458217	chr3:125	0	+	chr3	125445242	125451501	6259
H2	451933	472177	chr3:129	0	_	chr3	129717908	129739498	21590
H2	451933	521917	chr4:405	0	_	chr4	4057594	4127438	69844
H2	451933	457278	chr4:415	0	_	chr4	4151981	4157315	5334
H2	451933	486757	chr4:898	0	+	chr4	8985046	9021140	36094
H2	451933	522409	chr4:951	0	+	chr4	9516435	9588264	71829
H2	451933	458220	chr4:946	0	+	chr4	9462865	9469139	6274
H2	451933	457278	chr4:948	0	+	chr4	9487267	9492598	5331
H2	451933	457278	chr7:689	0	_	chr7	6899607	6905389	5782
H2	451933	522415	chr7:975	0	_	chr7	97512684	97575397	62713
H2	451933	458248	chr9:935	0	_	chr9	93507293	93512597	5304
H2	451933	481307	chrUn_gl	0	+	chrUn_gl	155871	186860	30989
H2	451934	458247	chr2:712	0	+	chr2	71257937	71263264	5327
H2	451935	457278	chr11:67	0	_	chr11	67483701	67489027	5326
H2	451936	458026	EntireDEI	0	_	EntireDEI	5819013	5822296	3283
H2	451936	458219	chr4:417	0	_	chr4	4178397	4183651	5254
H2	451942	458247	chr2:159	0	+	chr2	159712005	159717290	5285
H2	451943	459019	chr4:388	0	_	chr4	3883075	3890123	7048
H2	452867	458249	chr9:929	0	+	chr9	92972358	92976713	4355

H2	452892	456019	chr2:712	0	+	chr2	71236039	71239179	3140
H2	454670	458220	chr11:34	0	_	chr11	3414589	3418128	3539
H2	454670	458246	chr3:754	0	_	chr3	75422094	75425663	3569
H2	454682	458246	chr11:67	0	_	chr11	67505586	67509145	3559
H2	454682	458220	chr4:390	0	_	chr4	3905853	3909389	3536
H2	454682	458249	chr4:975	0	+	chr4	9751351	9754913	3562
H2	454682	458220	chr7:692	0	_	chr7	6921813	6925357	3544
H2	454693	458246	chr3:129	0	_	chr3	129755909	129759465	3556
H2	455540	456956	chr2:135	0	+	chr2	135723991	135725426	1435
H2	458015	465668	chr16:52	0	+	chr16	5256075	5263442	7367
H2	465123	522415	EntireDEI	0	_	EntireDEI	544135	600934	56799
H2	465123	522415	EntireDEI	0	+	EntireDEI	944881	1002533	57652
H2	465123	522415	EntireDEI	0	_	EntireDEI	5185972	5243719	57747
H2	465123	522415	EntireDEI	0	_	EntireDEI	5666855	5724530	57675
H2	465123	518196	EntireDEI	0	_	EntireDEI	5730203	5782806	52603
H2	465126	474755	EntireDEI	0	+	EntireDEI	1291606	1300939	9333
H2	465126	522409	chr12:84	0	_	chr12	8490294	8546030	55736
H2	465641	472450	EntireDEI	0	_	EntireDEI	5724362	5730204	5842
H2	465667	522415	chr16:52	0	+	chr16	5287439	5341897	54458
H2	471816	486757	chr3:151	0	+	chr3	15164115	15171944	7829
H2	487885	522409	chr11:67	0	_	chr11	67670378	67704962	34584
H2	487885	503971	chr3:151	0	+	chr3	15171777	15187934	16157
H2	487885	522415	chr4:902	0	+	chr4	9020973	9056263	35290
H2	491086	522081	chr3:755	0	_	chr3	75568768	75600000	31232
H2	503987	522408	chr3:129	0	_	chr3	129916066	129931618	15552
H2	523442	646586	EntireDEI	0	_	EntireDEI	899282	1023316	124034
H2	523442	907030	EntireDEI	0	+	EntireDEI	5171228	5539949	368721
H2	523442	606602	EntireDEI	0	+	EntireDEI	5646085	5730204	84119
H2	523442	578055	chr11:67	0	+	chr11	67655591	67704923	49332
H2	523442	600934	chr11:71	0	_	chr11	71347642	71418428	70786
H2	523442	623591	chr12:84	0	+	chr12	8476116	8568331	92215
H2	523442	543393	chr3:755	0	+	chr3	75555204	75569026	13822
H2	523442	562560	chr3:129	0	+	chr3	129901553	129931616	30063
H2	523442	543378	chr4:403	0	+	chr4	4038009	4057673	19664
H2	523445	600934	chr11:35	0	+	chr11	3536630	3605317	68687
H2	523469	600934	chr3:125	0	_	chr3	125482435	125552149	69714
H2	523477	578055	chr4:902	0	_	chr4	9021012	9071481	50469
H2	524270	529182	chr7:703	0	+	chr7	7031699	7039851	8152
H2	524722	539541	chr16:52	0	+	chr16	5208315	5216111	7796
H2	525828	600934	chr4:953	0	_	chr4	9531072	9600000	68928
H2	535180	600923	chr7:975	0	+	chr7	97503238	97560612	57374
H2	540673	577002	chr16:53	0	_	chr16	5310865	5345785	34920
H2	544135	600934	EntireDEI	0	_	EntireDEI	465123	522415	57292
H2	544481	575559	chr3:755	0	+	chr3	75568781	75599999	31218
H2	544481	600931	chr4:405	0	+	chr4	4057444	4112178	54734
H2	548367	623591	EntireDEI	0	+	EntireDEI	5730203	5805255	75052
H2	562577	578055	chr3:151	0	_	chr3	15171816	15187934	16118
H2	577642	600934	chr3:756	0	+	chr3	75609150	75632299	23149
H2	577954	600444	chr16:52	0	_	chr16	5287439	5310140	22701
H2	579225	600934	chr11:67	0	+	chr11	67704797	67726104	21307
H2	579225	594361	chr3:151	0	_	chr3	15164140	15171942	7802
H2	579225	600924	chr4:899	0	_	chr4	8999626	9021138	21512

H2	584606	600934	chrUn_gl	0	_	chrUn_gl	170476	186861	16385
H2	591452	621496	EntireDEI	0	_	EntireDEI	1271009	1300939	29930
H2	593761	600760	EntireDEI	0	+	EntireDEI	600766	606944	6178
H2	594032	600934	chr3:129	0	+	chr3	129717908	129724801	6893
H2	600766	621731	EntireDEI	0	_	EntireDEI	451933	472450	20517
H2	600766	606944	EntireDEI	0	+	EntireDEI	593761	600760	6999
H2	600766	623591	chr11:67	0	+	chr11	67718978	67742658	23680
H2	600766	628661	chr11:71	0	_	chr11	71322016	71354828	32812
H2	600766	623591	chr3:756	0	+	chr3	75625138	75648757	23619
H2	600766	623591	chr3:125	0	_	chr3	125465987	125489962	23975
H2	600766	623591	chr4:410	0	+	chr4	4105035	4129287	24252
H2	600766	623591	chr7:975	0	+	chr7	97554254	97577231	22977
H2	600766	623591	chrUn_gl	0	_	chrUn_gl	154014	177635	23621
H2	600834	623591	chr11:35	0	+	chr11	3598231	3621829	23598
H2	600834	606576	chr16:52	0	_	chr16	5287439	5294041	6602
H2	600834	623591	chr4:898	0	_	chr4	8983189	9006732	23543
H2	600834	623591	chr4:951	0	_	chr4	9514587	9538172	23585
H2	601038	623591	chr3:129	0	+	chr3	129717908	129741353	23445
H2	606575	615677	chr16:52	0	_	chr16	5256075	5263442	7367
H2	614666	623591	chr4:388	0	+	chr4	3883064	3891984	8920
H2	615446	623591	chr13:68	0	_	chr13	68476400	68483551	7151
H2	615446	623591	chr3:753	0	+	chr3	75399481	75406591	7110
H2	615446	620798	chr9:929	0	_	chr9	92972358	92976713	4355
H2	615447	623591	chr9:935	0	+	chr9	93507293	93514452	7159
H2	615448	622933	chr14:52	0	+	chr14	52232314	52238808	6494
H2	615448	623591	chr2:712	0	_	chr2	71256071	71263264	7193
H2	615448	623591	chr2:159	0	_	chr2	159710131	159717290	7159
H2	615448	623591	chr3:125	0	_	chr3	125422231	125429407	7176
H2	615449	618958	chr11:67	0	+	chr11	67505586	67509076	3490
H2	615449	623591	chr11:71	0	_	chr11	71604522	71612648	8126
H2	615449	623591	chr12:85	0	+	chr12	8582782	8590951	8169
H2	615449	623590	chr13:42	0	+	chr13	42007915	42014927	7012
H2	615449	618955	chr3:754	0	+	chr3	75422094	75425579	3485
H2	615449	623591	chr3:125	0	_	chr3	125443392	125451530	8138
H2	615449	619010	chr3:129	0	+	chr3	129755909	129759465	3556
H2	615449	618959	chr4:390	0	+	chr4	3905827	3909321	3494
H2	615449	618987	chr7:692	0	+	chr7	6921787	6925323	3536
H2	615450	621767	chr21:33	0	_	chr21	33986538	33991844	5306
H2	615472	619010	chr11:34	0	+	chr11	3414586	3418105	3519
H2	615621	621740	chr12:52	0	_	chr12	52494243	52499379	5136
H2	615623	623591	EntireDEI	0	_	EntireDEI	1380070	1387093	7023
H2	615623	623591	chr10:15	0	+	chr10	15043815	15050811	6996
H2	615623	622237	chr4:417	0	+	chr4	4178533	4184174	5641
H2	615623	618958	chr4:975	0	_	chr4	9751420	9754747	3327
H2	615638	623591	chr4:946	0	_	chr4	9461014	9468986	7972
H2	615673	623511	EntireDEI	0	+	EntireDEI	5819020	5824072	5052
H2	616435	623591	chr11:67	0	+	chr11	67483715	67490885	7170
H2	616435	623591	chr11:71	0	_	chr11	71304509	71311676	7167
H2	616435	623587	chr4:415	0	+	chr4	4151995	4159156	7161
H2	616435	623591	chr4:895	0	_	chr4	8951384	8958560	7176
H2	616435	623591	chr4:948	0	_	chr4	9485419	9492584	7165
H2	616435	623591	chr7:689	0	+	chr7	6899621	6907240	7619

H2	616742	618169	chr2:135	0	_	chr2	135723991	135725426	1435
H2	617691	620783	chr2:712	0	_	chr2	71236033	71239179	3146
H2	617826	623591	chr3:872	0	_	chr3	8729890	8735690	5800
H2	620100	623591	chr3:112	0	+	chr3	112240477	112243986	3509
H2	620544	623591	chr14:52	0	_	chr14	52223747	52226782	3035
H2	620799	623591	chr9:929	0	_	chr9	92994449	92997250	2801
H2	620845	623591	chr2:159	0	_	chr2	159731220	159734000	2780
H2	624772	628665	chr13:41	0	+	chr13	41995535	41999418	3883
H2	625853	628657	chr10:15	0	+	chr10	15022511	15025310	2799
H2	629419	638666	EntireDEI	0	+	EntireDEI	644725	653973	9248
H2	631187	638937	chr12:83	0	_	chr12	8371420	8379161	7741
H2	631187	638937	chr4:917	0	+	chr4	9173170	9180894	7724
H2	631191	638937	EntireDEI	0	+	EntireDEI	1130188	1137911	7723
H2	631191	638937	EntireDEI	0	_	EntireDEI	5532225	5539952	7727
H2	638835	646592	chr12:83	0	_	chr12	8371414	8379161	7747
H2	638839	646592	EntireDEI	0	+	EntireDEI	1130188	1137917	7729
H2	644725	653973	EntireDEI	0	+	EntireDEI	629419	638666	9247
H2	779279	780407	chr12:81	0	+	chr12	8169318	8170451	1133
H2	779279	781477	chr12:56	0	_	chr12	56904775	56906973	2198
H2	779279	781477	chr4:145	0	_	chr4	145766767	145768973	2206
H2	779283	780471	chr2:198	0	+	chr2	198351307	198353944	2637
H2	779290	781477	chr5:218	0	_	chr5	21882685	21884875	2190
H2	819365	854060	chr11:71	0	_	chr11	71515828	71552097	36269
H2	819380	833006	EntireDEI	0	_	EntireDEI	1200000	1212103	12103
H2	819380	870149	chr4:935	0	_	chr4	9357888	9408758	50870
H2	827527	856330	chr12:83	0	+	chr12	8315368	8346215	30847
H2	857316	907030	chr4:917	0	_	chr4	9173177	9223055	49878
H2	857316	870149	chr4:922	0	_	chr4	9224402	9237288	12886
H2	857316	870149	chr4:925	0	_	chr4	9257628	9270522	12894
H2	857316	870149	chr4:932	0	_	chr4	9329415	9342306	12891
H2	860259	864976	EntireDEI	0	+	EntireDEI	864978	869712	4734
H2	862031	907030	EntireDEI	0	_	EntireDEI	1130191	1175675	45484
H2	864978	869712	EntireDEI	0	+	EntireDEI	860259	864976	4717
H2	873265	907030	chr12:83	0	+	chr12	8345181	8379154	33973
H2	899282	1023316	EntireDEI	0	_	EntireDEI	523442	646586	123144
H2	899282	906931	EntireDEI	0	+	EntireDEI	906935	914553	7618
H2	899282	988647	EntireDEI	0	_	EntireDEI	5200002	5289351	89349
H2	906929	914659	chr12:83	0	+	chr12	8371414	8379161	7747
H2	906935	914553	EntireDEI	0	+	EntireDEI	899282	906931	7649
H2	917806	954344	EntireDEI	0	+	EntireDEI	1268930	1300939	32009
H2	917806	930215	EntireDEI	0	+	EntireDEI	1380072	1387093	7021
H2	917806	998252	EntireDEI	0	_	EntireDEI	5730244	5805253	75009
H2	917806	930165	EntireDEI	0	_	EntireDEI	5819020	5824145	5125
H2	917806	930215	chr10:15	0	_	chr10	15043815	15050809	6994
H2	917806	945049	chr11:35	0	_	chr11	3598163	3621827	23664
H2	917806	929404	chr11:67	0	_	chr11	67483714	67490883	7169
H2	917806	945049	chr11:67	0	_	chr11	67718978	67742656	23678
H2	917806	945049	chr11:71	0	+	chr11	71331130	71354828	23698
H2	917806	929404	chr11:71	0	+	chr11	71304511	71311677	7166
H2	917806	930390	chr11:71	0	+	chr11	71604524	71612648	8124
H2	917806	1163923	chr12:83	0	_	chr12	8345181	8568329	223148
H2	917806	930390	chr12:85	0	_	chr12	8582782	8590949	8167

H2	917806	930390	chr13:42(	0	_	chr13	42007915	42014926	7011
H2	917806	930393	chr13:68-	0	+	chr13	68476402	68483551	7149
H2	917806	925625	chr2:962:	0	+	chr2	96212349	96215766	3417
H2	917806	930391	chr2:159'	0	+	chr2	159710133	159717290	7157
H2	917806	928012	chr3:872!	0	+	chr3	8729892	8735690	5798
H2	917806	930393	chr3:753!	0	_	chr3	75399481	75406589	7108
H2	917806	945049	chr3:756:	0	_	chr3	75625138	75648755	23617
H2	917806	925745	chr3:112:	0	_	chr3	112240477	112243984	3507
H2	917806	942033	chr3:125-	0	+	chr3	125465989	125485752	19763
H2	917806	930391	chr3:125-	0	+	chr3	125422233	125429407	7174
H2	917806	930390	chr3:125-	0	+	chr3	125443394	125451530	8136
H2	917806	942033	chr3:129'	0	_	chr3	129721540	129741351	19811
H2	917806	931140	chr4:388:	0	_	chr4	3883082	3891982	8900
H2	917806	945049	chr4:410!	0	_	chr4	4105035	4129285	24250
H2	917806	945049	chr4:898:	0	+	chr4	8983191	9006800	23609
H2	917806	929404	chr4:895:	0	+	chr4	8951386	8958561	7175
H2	917806	944981	chr4:951-	0	+	chr4	9514589	9538172	23583
H2	917806	930390	chr4:946:	0	+	chr4	9461016	9469165	8149
H2	917806	929404	chr4:948!	0	+	chr4	9485421	9492585	7164
H2	917806	929404	chr7:689!	0	_	chr7	6899620	6907238	7618
H2	917806	945049	chr7:975!	0	_	chr7	97554254	97577229	22975
H2	917806	930392	chr9:935(	0	_	chr9	93507293	93514450	7157
H2	917806	945049	chrUn_gl(	0	+	chrUn_gl(	154016	177635	23619
H2	922260	925301	chr14:52:	0	+	chr14	52223747	52226782	3035
H2	922260	930391	chr2:712!	0	+	chr2	71256071	71263264	7193
H2	922260	925064	chr2:712(	0	+	chr2	71282334	71285141	2807
H2	922260	925007	chr2:159'	0	+	chr2	159731220	159734007	2787
H2	922260	925046	chr9:929!	0	+	chr9	92994449	92997250	2801
H2	922271	929404	chr4:415:	0	_	chr4	4151994	4159149	7155
H2	922918	930391	chr14:52:	0	_	chr14	52232314	52238808	6494
H2	923614	930215	chr4:417(	0	_	chr4	4178533	4184174	5641
H2	924106	930217	chr12:52-	0	+	chr12	52494238	52499379	5141
H2	924120	945049	EntireDEI	0	+	EntireDEI	451933	472450	20517
H2	924129	930389	chr21:33!	0	+	chr21	33986583	33991844	5261
H2	925047	930393	chr9:929'	0	+	chr9	92972358	92976713	4355
H2	925062	928147	chr2:712:	0	+	chr2	71236033	71239179	3146
H2	926834	930367	chr11:34:	0	_	chr11	3414586	3418105	3519
H2	926834	930390	chr3:129'	0	_	chr3	129755909	129759465	3556
H2	926857	930390	chr7:692:	0	_	chr7	6921787	6925323	3536
H2	926885	930390	chr4:390!	0	_	chr4	3905827	3909321	3494
H2	926886	930390	chr11:67!	0	_	chr11	67505586	67509076	3490
H2	926886	930393	chr4:975:	0	+	chr4	9751420	9754913	3493
H2	926889	930390	chr3:754:	0	_	chr3	75422094	75425579	3485
H2	927672	929096	chr2:135'	0	+	chr2	135723991	135725426	1435
H2	930161	939247	chr16:52!	0	+	chr16	5256075	5263442	7367
H2	939062	945049	EntireDEI	0	+	EntireDEI	945196	952034	6838
H2	939220	1175675	EntireDEI	0	_	EntireDEI	5495314	5730204	234890
H2	939246	944981	chr16:52(	0	+	chr16	5287439	5294041	6602
H2	944881	1002533	EntireDEI	0	+	EntireDEI	465123	522415	57292
H2	944881	1130175	chr11:34:	0	_	chr11	3424931	3605317	180386
H2	944881	966597	chr11:67'	0	_	chr11	67704797	67726104	21307
H2	944881	1078850	chr11:71:	0	+	chr11	71347642	71475118	127476

H2	944881	968169	chr3:756(	0	_	chr3	75609150	75632299	23149
H2	944881	1127758	chr3:125-	0	+	chr3	125482435	125651040	168605
H2	944881	951763	chr3:129	0	_	chr3	129717908	129724801	6893
H2	944881	1040556	chr4:953	0	+	chr4	9531072	9620276	89204
H2	944881	961218	chrUn_gl(	0	+	chrUn_gl	170476	186860	16384
H2	944884	1002200	chr4:405	0	_	chr4	4057431	4112178	54747
H2	944891	966597	chr4:899	0	+	chr4	8999626	9021138	21512
H2	945196	952034	EntireDEI	0	+	EntireDEI	939062	945049	5987
H2	945371	967861	chr16:52	0	+	chr16	5287439	5310136	22697
H2	949016	979312	chr7:975	0	_	chr7	97527271	97557285	30014
H2	951441	966597	chr3:151(	0	+	chr3	15164147	15171942	7795
H2	967756	1071845	chr11:67(	0	_	chr11	67605062	67704931	99869
H2	967756	983202	chr3:151	0	+	chr3	15171808	15187934	16126
H2	967756	1175675	chr4:902	0	+	chr4	9021004	9218308	197304
H2	968809	1006455	chr16:53	0	+	chr16	5310865	5345782	34917
H2	970225	1002200	chr3:755(	0	_	chr3	75568768	75600000	31232
H2	983218	1096686	chr3:129	0	_	chr3	129835893	129931618	95725
H2	988550	1130175	EntireDEI	0	_	EntireDEI	5071463	5199975	128512
H2	989306	1011954	chr7:975(	0	_	chr7	97503238	97525961	22723
H2	1003303	1130175	chr3:754(	0	_	chr3	75466171	75569026	102855
H2	1003318	1130175	chr4:393	0	_	chr4	3939122	4057673	118551
H2	1007600	1039533	chr16:51	0	_	chr16	5196791	5216116	19325
H2	1012455	1075302	chr7:698(	0	_	chr7	6980380	7039856	59476
H2	1044445	1108046	chr16:51	0	_	chr16	5153835	5191969	38134
H2	1074095	1130175	chr11:67	0	_	chr11	67554688	67605143	50455
H2	1093283	1129113	chr11:71	0	+	chr11	71475864	71515825	39961
H2	1107149	1130162	chr3:129	0	_	chr3	129812065	129835894	23829
H2	1108382	1130175	chr16:51	0	_	chr16	5129857	5152101	22244
H2	1108382	1130160	chr4:968	0	+	chr4	9689736	9710463	20727
H2	1115798	1130175	chr7:696	0	_	chr7	6965390	6980342	14952
H2	1130188	1137911	EntireDEI	0	+	EntireDEI	631191	638937	7746
H2	1130188	1137917	EntireDEI	0	+	EntireDEI	638839	646592	7753
H2	1130188	1137911	EntireDEI	0	+	EntireDEI	5281605	5289351	7746
H2	1130191	1175675	EntireDEI	0	_	EntireDEI	862031	907030	44999
H2	1166942	1170962	EntireDEI	0	+	EntireDEI	1172186	1175675	3489
H2	1167256	1277087	chr4:936	0	+	chr4	9362633	9469143	106510
H2	1167256	1175675	chr4:923	0	+	chr4	9238633	9246782	8149
H2	1167256	1175675	chr4:925	0	+	chr4	9257628	9265775	8147
H2	1167256	1175675	chr4:922	0	+	chr4	9224402	9232544	8142
H2	1167256	1175675	chr4:933	0	+	chr4	9338908	9347051	8143
H2	1167256	1175675	chr4:932	0	+	chr4	9329415	9337561	8146
H2	1172186	1175675	EntireDEI	0	+	EntireDEI	1166942	1170962	4020
H2	1176663	1203917	chr12:83	0	_	chr12	8315368	8346215	30847
H2	1178932	1277099	chr11:71	0	+	chr11	71515828	71612638	96810
H2	1200000	1212103	EntireDEI	0	_	EntireDEI	819380	833006	13626
H2	1200000	1212103	EntireDEI	0	_	EntireDEI	5452716	5466347	13631
H2	1254916	1260235	EntireDEI	0	+	EntireDEI	1300967	1306283	5316
H2	1260245	1276135	chr11:71	0	+	chr11	71295844	71311685	15841
H2	1260253	1276137	chr4:947(	0	+	chr4	9476734	9492595	15861
H2	1260259	1277112	chr3:753	0	_	chr3	75399481	75416300	16819
H2	1260269	1274720	chr3:872	0	+	chr3	8723366	8735688	12322
H2	1260294	1291771	chr3:125-	0	+	chr3	125457373	125489962	32589

H2	1260294	1277087	chr3:125	0	+	chr3	125434740	125451508	16768
H2	1260312	1276135	chr7:689	0	_	chr7	6899612	6916070	16458
H2	1260343	1277106	chr2:712	0	+	chr2	71246456	71263260	16804
H2	1260368	1269478	chr10:15	0	_	chr10	15028873	15037996	9123
H2	1260371	1277874	chr4:388	0	_	chr4	3883081	3899999	16918
H2	1260374	1300939	EntireDEI	0	_	EntireDEI	5773283	5813699	40416
H2	1260374	1291499	chr3:129	0	_	chr3	129717908	129749922	32014
H2	1260384	1300941	chr12:85	0	_	chr12	8536578	8576796	40218
H2	1260400	1276137	chr4:415	0	_	chr4	4151984	4167608	15624
H2	1260410	1276137	chr11:67	0	_	chr11	67483704	67499404	15700
H2	1260851	1277082	EntireDEI	0	+	EntireDEI	1371030	1387229	16199
H2	1260851	1277092	EntireDEI	0	_	EntireDEI	5818925	5835374	16449
H2	1260851	1291771	chr11:67	0	_	chr11	67718978	67750637	31659
H2	1260851	1277087	chr12:85	0	_	chr12	8582804	8596965	14161
H2	1260851	1271964	chr14:52	0	+	chr14	52214682	52226779	12097
H2	1260851	1271681	chr2:159	0	+	chr2	159722070	159734019	11949
H2	1260851	1291771	chr3:756	0	_	chr3	75625138	75657897	32759
H2	1260851	1291704	chr4:897	0	+	chr4	8974119	9006733	32614
H2	1260851	1276137	chr4:894	0	+	chr4	8943472	8958571	15099
H2	1260851	1268842	chr7:687	0	_	chr7	6877635	6886701	9066
H2	1260851	1271708	chr9:929	0	+	chr9	92985302	92997250	11948
H2	1260851	1277111	chr9:935	0	_	chr9	93507293	93522171	14878
H2	1260851	1291771	chrUn_gl	0	+	chrUn_gl	144874	177635	32761
H2	1260853	1291771	chr4:410	0	_	chr4	4105035	4136766	31731
H2	1260853	1291771	chr7:975	0	_	chr7	97554254	97585324	31070
H2	1260854	1277099	chr3:125	0	+	chr3	125412309	125429396	17087
H2	1260855	1291771	chr11:71	0	+	chr11	71322016	71354828	32812
H2	1260855	1291743	chr4:950	0	+	chr4	9508108	9538212	30104
H2	1263008	1277090	chr13:42	0	_	chr13	42007934	42016686	8752
H2	1266877	1291705	chr11:35	0	_	chr11	3598229	3623878	25649
H2	1267574	1272299	chr2:962	0	+	chr2	96210892	96215743	4851
H2	1267574	1277106	chr2:159	0	+	chr2	159708796	159717286	8490
H2	1267574	1272443	chr3:112	0	_	chr3	112240477	112245343	4866
H2	1267578	1276938	chr10:15	0	_	chr10	15043815	15052176	8361
H2	1268847	1277104	chr13:68	0	+	chr13	68476319	68483543	7224
H2	1268930	1300939	EntireDEI	0	+	EntireDEI	917806	954344	36538
H2	1268930	1300939	EntireDEI	0	_	EntireDEI	5234274	5270815	36541
H2	1269586	1277090	chr14:52	0	_	chr14	52232334	52238808	6474
H2	1270283	1277082	chr4:417	0	_	chr4	4178397	4184174	5777
H2	1270775	1276945	chr12:52	0	+	chr12	52494248	52499384	5136
H2	1270779	1291771	EntireDEI	0	+	EntireDEI	451933	472450	20517
H2	1270790	1277106	chr21:33	0	+	chr21	33986585	33991842	5257
H2	1271009	1300939	EntireDEI	0	_	EntireDEI	591452	621496	30044
H2	1271735	1277112	chr9:929	0	+	chr9	92972380	92976713	4333
H2	1271743	1274854	chr2:712	0	+	chr2	71236048	71239176	3128
H2	1273540	1277086	chr11:34	0	_	chr11	3414586	3418105	3519
H2	1273540	1277106	chr11:67	0	_	chr11	67505589	67509134	3545
H2	1273540	1277090	chr3:754	0	_	chr3	75422113	75425640	3527
H2	1273540	1277099	chr3:129	0	_	chr3	129755919	129759465	3546
H2	1273540	1277087	chr4:390	0	_	chr4	3905849	3909378	3529
H2	1273540	1277090	chr4:975	0	+	chr4	9751362	9754891	3529
H2	1273540	1277086	chr7:692	0	_	chr7	6921810	6925346	3536

H2	1274382	1275819	chr2:135	0	+	chr2	135723991	135725426	1435
H2	1276884	1285988	chr16:525	0	+	chr16	5256075	5263442	7367
H2	1285443	1291606	EntireDEI	0	+	EntireDEI	1291606	1298588	6982
H2	1285961	1300939	EntireDEI	0	_	EntireDEI	5715066	5730204	15138
H2	1285987	1291704	chr16:528	0	+	chr16	5287439	5294042	6603
H2	1291603	1300968	chr4:410	0	_	chr4	4102700	4112181	9481
H2	1291606	1300939	EntireDEI	0	+	EntireDEI	465126	474755	9629
H2	1291606	1298588	EntireDEI	0	+	EntireDEI	1285443	1291606	6163
H2	1291606	1300968	chr11:359	0	_	chr11	3595829	3605314	9485
H2	1291606	1300939	chr11:67	0	_	chr11	67716679	67726101	9422
H2	1291606	1300968	chr11:713	0	+	chr11	71347645	71357158	9513
H2	1291606	1300968	chr3:756	0	_	chr3	75622802	75632296	9494
H2	1291606	1300968	chr3:125	0	+	chr3	125482438	125492294	9856
H2	1291606	1298481	chr3:129	0	_	chr3	129717908	129724798	6890
H2	1291606	1300968	chr4:953	0	+	chr4	9531075	9540578	9503
H2	1291606	1300968	chrUn_gl	0	+	chrUn_gl	170479	179971	9492
H2	1291613	1300939	chr4:899	0	+	chr4	8999626	9009113	9487
H2	1291614	1300968	chr7:975	0	_	chr7	97551931	97560612	8681
H2	1292093	1300968	chr16:528	0	+	chr16	5287439	5296430	8991
H2	1298158	1300679	chr3:151	0	+	chr3	15164147	15166658	2511
H2	1300967	1306283	EntireDEI	0	+	EntireDEI	1254916	1260235	5319
H2	1300967	1306286	chr11:715	0	+	chr11	71590538	71595845	5307
H2	1300967	1306286	chr4:944	0	+	chr4	9447298	9452478	5180
H2	1370981	1389697	chr3:125	0	+	chr3	125412257	125431837	19580
H2	1370982	1374895	EntireDEI	0	+	EntireDEI	1393583	1397493	3910
H2	1370982	1387093	chr11:713	0	+	chr11	71321964	71339127	17163
H2	1370982	1387085	chr4:412	0	_	chr4	4120986	4136816	15830
H2	1370982	1387093	chr4:897	0	+	chr4	8974071	8991208	17137
H2	1370982	1386030	chr4:894	0	+	chr4	8943424	8957307	13883
H2	1370982	1387093	chr7:975	0	_	chr7	97569272	97585374	16102
H2	1370982	1382882	chr9:929	0	+	chr9	92985254	92997250	11996
H2	1370982	1389697	chr9:935	0	_	chr9	93504859	93522219	17360
H2	1370989	1387085	chr4:950	0	+	chr4	9508063	9522579	14516
H2	1371010	1387093	chr11:67	0	_	chr11	67734662	67750657	15995
H2	1371030	1387229	EntireDEI	0	+	EntireDEI	1260851	1277082	16231
H2	1371030	1386284	chr11:674	0	_	chr11	67483701	67498962	15261
H2	1371030	1386031	chr11:712	0	+	chr11	71296449	71310423	13974
H2	1371030	1389697	chr3:753	0	_	chr3	75397073	75415700	18627
H2	1371030	1387093	chr3:129	0	_	chr3	129733366	129749445	16079
H2	1371030	1387093	chr4:388	0	_	chr4	3884018	3899519	15501
H2	1371030	1389697	chr4:945	0	+	chr4	9453011	9471633	18622
H2	1371033	1386284	chr7:689	0	_	chr7	6899607	6915523	15916
H2	1371065	1386030	chr4:947	0	+	chr4	9477372	9491333	13961
H2	1374181	1389697	chr12:858	0	_	chr12	8580333	8596339	16006
H2	1375887	1380620	chr10:150	0	_	chr10	15028873	15033492	4619
H2	1375887	1389697	chr11:710	0	+	chr11	71600466	71615089	14623
H2	1375887	1385895	chr3:872	0	+	chr3	8724850	8735690	10840
H2	1375887	1389697	chr3:125	0	+	chr3	125439326	125453993	14667
H2	1375891	1383137	chr14:522	0	+	chr14	52221844	52226782	4938
H2	1375892	1389697	chr10:150	0	_	chr10	15041195	15055945	14750
H2	1377923	1387093	chr11:361	0	_	chr11	3613832	3623875	10043
H2	1378732	1389697	chr2:159	0	+	chr2	159708763	159719709	10946

H2	1378736	1387093	chr3:756	0	_	chr3	75640767	75650139	9372
H2	1378736	1387093	chrUn_gl	0	+	chrUn_gl	152632	162010	9378
H2	1378745	1383486	chr2:962	0	+	chr2	96210872	96215766	4894
H2	1378745	1383606	chr3:112	0	_	chr3	112240478	112245363	4885
H2	1378806	1389697	chr13:42	0	_	chr13	42005475	42016194	10719
H2	1379989	1389697	chr13:68	0	+	chr13	68476319	68486004	9685
H2	1380070	1387093	EntireDEI	0	_	EntireDEI	615623	623591	7968
H2	1380072	1387093	EntireDEI	0	+	EntireDEI	917806	930215	12409
H2	1380072	1387093	EntireDEI	0	_	EntireDEI	5258405	5270815	12410
H2	1380728	1389697	chr14:52	0	_	chr14	52229887	52238808	8921
H2	1381425	1389697	chr4:417	0	_	chr4	4176123	4184174	8051
H2	1381897	1389697	chr21:33	0	+	chr21	33986538	33994262	7724
H2	1381933	1387229	EntireDEI	0	+	EntireDEI	451933	458219	6286
H2	1381933	1389697	chr12:52	0	+	chr12	52494252	52501971	7719
H2	1382883	1389697	chr9:929	0	+	chr9	92972358	92979164	6806
H2	1382898	1386266	chr2:712	0	+	chr2	71236033	71239408	3375
H2	1384699	1389697	chr11:34	0	_	chr11	3412115	3418105	5990
H2	1384699	1389697	chr4:975	0	+	chr4	9751362	9757353	5991
H2	1386912	1389697	chr7:687	0	_	chr7	6874529	6877633	3104
H2	1392737	1397493	EntireDEI	0	+	EntireDEI	441009	445902	4893
H2	1393583	1397493	EntireDEI	0	+	EntireDEI	1370982	1374895	3913
H2	1395182	1402492	chr2:159	0	+	chr2	159736971	159742065	5094
H2	1516396	1519352	chr5:326	0	_	chr5	32601108	32604185	3077
H2	1549643	1550779	chr8:125	0	_	chr8	125438030	125439169	1139
H2	1652059	1685045	chr7:624	0	+	chr7	62477674	62508810	31136
H2	1976246	1978115	chr18:11	0	_	chr18	11608833	11610689	1856
H2	1976258	1977518	chr17:73	0	_	chr17	7384658	7386386	1728
H2	1976258	1979118	chr17:33	0	+	chr17	33520243	33523023	2780
H2	2801850	2804038	chr3:174	0	+	chr3	174190661	174192855	2194
H2	5068367	5120436	chr11:67	0	+	chr11	67551070	67605143	54073
H2	5068367	5069481	chr21:33	0	_	chr21	33800462	33801600	1138
H2	5068367	5190337	chr3:129	0	+	chr3	129808964	129920422	111458
H2	5068367	5152393	chr4:963	0	_	chr4	9630530	9713810	83280
H2	5068368	5079260	chr7:696	0	+	chr7	6961770	6980378	18608
H2	5068376	5198991	chr11:34	0	+	chr11	3421627	3563162	141535
H2	5068376	5185189	chr4:393	0	+	chr4	3935814	4057673	121859
H2	5069118	5185204	chr3:754	0	+	chr3	75463606	75569026	105420
H2	5069118	5071946	chr3:125	0	_	chr3	125650944	125654010	3066
H2	5069492	5086672	chr16:51	0	+	chr16	5127891	5152101	24210
H2	5071462	5200000	EntireDEI	0	+	EntireDEI	5539964	5680845	140881
H2	5071462	5199166	chr12:83	0	+	chr12	8379169	8503441	124272
H2	5071462	5157475	chr4:907	0	_	chr4	9079830	9173162	93332
H2	5071463	5199975	EntireDEI	0	_	EntireDEI	988550	1130175	141625
H2	5072470	5101266	chr11:71	0	_	chr11	71475864	71515825	39961
H2	5073056	5104213	chr3:125	0	_	chr3	125601691	125644535	42844
H2	5087008	5150090	chr16:51	0	+	chr16	5153835	5191969	38134
H2	5115409	5199156	chr3:125	0	_	chr3	125524394	125599996	75602
H2	5115677	5243719	chr11:71	0	_	chr11	71347642	71475118	127476
H2	5119229	5176591	chr7:698	0	+	chr7	6980380	7039851	59471
H2	5122691	5199164	chr11:67	0	+	chr11	67605062	67683492	78430
H2	5153979	5199187	chr4:957	0	_	chr4	9575085	9620276	45191
H2	5155002	5180951	chr16:51	0	+	chr16	5196791	5216116	19325

H2	5162948	5199395	chr4:904	0	_	chr4	9042803	9079871	37068
H2	5171228	5539949	EntireDEI	0	+	EntireDEI	523442	907030	383588
H2	5176603	5199162	chr7:975	0	+	chr7	97503238	97525927	22689
H2	5182096	5219867	chr16:53	0	_	chr16	5310865	5345782	34917
H2	5185972	5243719	EntireDEI	0	_	EntireDEI	465123	522415	57292
H2	5186316	5199137	chr3:755	0	+	chr3	75568779	75581662	12883
H2	5186471	5199157	chr4:405	0	+	chr4	4057595	4070311	12716
H2	5190252	5266361	EntireDEI	0	+	EntireDEI	5730244	5805255	75011
H2	5200002	5289351	EntireDEI	0	_	EntireDEI	899282	988647	89365
H2	5200002	5249405	EntireDEI	0	+	EntireDEI	5680813	5730204	49391
H2	5200012	5243716	chr4:407	0	+	chr4	4070697	4112178	41481
H2	5200182	5243719	chr4:953	0	_	chr4	9531072	9575106	44034
H2	5200189	5220921	chr4:902	0	_	chr4	9021004	9042325	21321
H2	5200195	5218450	chr3:755	0	+	chr3	75581707	75599999	18292
H2	5200211	5243719	chr11:35	0	+	chr11	3563326	3605317	41991
H2	5200211	5220921	chr11:67	0	+	chr11	67683551	67704931	21380
H2	5200211	5266361	chr12:85	0	+	chr12	8503537	8568331	64794
H2	5200211	5243719	chr3:125	0	_	chr3	125482435	125524290	41855
H2	5200211	5205455	chr3:129	0	+	chr3	129926296	129931618	5322
H2	5205471	5220921	chr3:151	0	_	chr3	15171808	15187934	16126
H2	5209357	5243708	chr7:975	0	+	chr7	97527271	97560612	33341
H2	5220507	5243719	chr3:756	0	+	chr3	75609150	75632299	23149
H2	5220812	5243229	chr16:52	0	_	chr16	5287439	5310140	22701
H2	5222082	5243719	chr11:67	0	+	chr11	67704797	67726104	21307
H2	5222082	5237177	chr3:151	0	_	chr3	15164147	15171942	7795
H2	5222082	5243709	chr4:899	0	_	chr4	8999626	9021138	21512
H2	5227458	5243719	chrUn_gl	0	_	chrUn_gl	170476	186861	16385
H2	5234274	5270815	EntireDEI	0	_	EntireDEI	1268930	1300939	32009
H2	5236584	5243545	EntireDEI	0	+	EntireDEI	5243551	5249746	6195
H2	5236855	5243719	chr3:129	0	+	chr3	129717908	129724801	6893
H2	5243551	5264500	EntireDEI	0	_	EntireDEI	451933	472450	20517
H2	5243551	5249746	EntireDEI	0	+	EntireDEI	5236584	5243545	6961
H2	5243551	5266361	chr11:35	0	+	chr11	3598163	3621829	23666
H2	5243551	5271440	chr11:67	0	+	chr11	67718978	67750637	31659
H2	5243551	5271436	chr11:71	0	_	chr11	71322016	71354828	32812
H2	5243551	5266361	chr3:756	0	+	chr3	75625138	75648757	23619
H2	5243551	5266361	chr4:410	0	+	chr4	4105035	4129287	24252
H2	5243551	5271440	chr4:897	0	_	chr4	8974119	9006800	32681
H2	5243551	5271438	chr7:975	0	+	chr7	97554254	97585324	31070
H2	5243551	5266361	chrUn_gl	0	_	chrUn_gl	154014	177635	23621
H2	5243619	5249379	chr16:52	0	_	chr16	5287439	5294041	6602
H2	5243619	5266361	chr4:951	0	_	chr4	9514587	9538172	23585
H2	5246592	5266361	chr3:125	0	_	chr3	125465987	125485752	19765
H2	5246592	5266361	chr3:129	0	+	chr3	129721540	129741353	19813
H2	5249378	5258459	chr16:52	0	_	chr16	5256075	5263442	7367
H2	5257464	5266361	chr4:388	0	+	chr4	3883064	3891984	8920
H2	5258228	5266361	chr13:68	0	_	chr13	68476400	68483551	7151
H2	5258228	5266361	chr3:753	0	+	chr3	75399481	75406591	7110
H2	5258228	5261734	chr4:975	0	_	chr4	9751420	9754913	3493
H2	5258228	5263573	chr9:929	0	_	chr9	92972358	92976713	4355
H2	5258229	5266361	chr9:935	0	+	chr9	93507293	93514452	7159
H2	5258230	5265703	chr14:52	0	+	chr14	52232314	52238808	6494

H2	5258230	5266361	chr2:712	0	_	chr2	71256071	71263264	7193
H2	5258230	5266361	chr2:159	0	_	chr2	159710131	159717290	7159
H2	5258230	5266361	chr3:125	0	_	chr3	125422231	125429407	7176
H2	5258231	5261734	chr11:67	0	+	chr11	67505586	67509076	3490
H2	5258231	5266361	chr11:71	0	_	chr11	71604522	71612648	8126
H2	5258231	5266361	chr12:85	0	+	chr12	8582782	8590951	8169
H2	5258231	5266360	chr13:42	0	+	chr13	42007915	42014927	7012
H2	5258231	5261731	chr3:754	0	+	chr3	75422094	75425579	3485
H2	5258231	5266361	chr3:125	0	_	chr3	125443392	125451530	8138
H2	5258231	5261786	chr3:129	0	+	chr3	129755909	129759465	3556
H2	5258231	5261735	chr4:390	0	+	chr4	3905827	3909321	3494
H2	5258231	5266361	chr4:946	0	_	chr4	9461014	9469165	8151
H2	5258231	5261763	chr7:692	0	+	chr7	6921787	6925323	3536
H2	5258232	5264536	chr21:33	0	_	chr21	33986538	33991844	5306
H2	5258254	5261786	chr11:34	0	+	chr11	3414586	3418105	3519
H2	5258403	5264509	chr12:52	0	_	chr12	52494243	52499379	5136
H2	5258405	5270815	EntireDEI	0	_	EntireDEI	1380072	1387093	7021
H2	5258405	5266361	chr10:15	0	+	chr10	15043815	15050811	6996
H2	5258405	5265007	chr4:417	0	+	chr4	4178533	4184174	5641
H2	5258455	5266281	EntireDEI	0	+	EntireDEI	5819020	5824072	5052
H2	5259216	5266361	chr11:67	0	+	chr11	67483714	67490885	7171
H2	5259216	5266361	chr11:71	0	_	chr11	71304509	71311677	7168
H2	5259216	5266350	chr4:415	0	+	chr4	4151994	4159149	7155
H2	5259216	5266361	chr4:895	0	_	chr4	8951384	8958561	7177
H2	5259216	5266361	chr4:948	0	_	chr4	9485419	9492585	7166
H2	5259216	5266361	chr7:689	0	+	chr7	6899620	6907240	7620
H2	5259524	5260948	chr2:135	0	_	chr2	135723991	135725426	1435
H2	5260473	5263558	chr2:712	0	_	chr2	71236033	71239179	3146
H2	5260608	5266361	chr3:872	0	_	chr3	8729890	8735690	5800
H2	5262875	5266361	chr3:112	0	+	chr3	112240477	112243986	3509
H2	5263319	5266361	chr14:52	0	_	chr14	52223747	52226782	3035
H2	5263574	5266361	chr9:929	0	_	chr9	92994449	92997250	2801
H2	5263613	5266361	chr2:159	0	_	chr2	159731220	159734007	2787
H2	5267542	5271440	chr13:41	0	+	chr13	41995535	41999418	3883
H2	5268623	5271432	chr10:15	0	+	chr10	15022511	15025310	2799
H2	5272194	5281432	EntireDEI	0	+	EntireDEI	5287490	5296727	9237
H2	5281432	5289080	EntireDEI	0	+	EntireDEI	5289080	5296727	7647
H2	5281601	5289351	chr12:83	0	_	chr12	8371420	8379161	7741
H2	5281601	5289351	chr4:917	0	+	chr4	9173170	9180894	7724
H2	5281605	5289351	EntireDEI	0	+	EntireDEI	1130188	1137911	7723
H2	5281605	5289351	EntireDEI	0	_	EntireDEI	5532225	5539952	7727
H2	5287490	5296727	EntireDEI	0	+	EntireDEI	5272194	5281432	9238
H2	5289080	5296727	EntireDEI	0	+	EntireDEI	5281432	5289080	7648
H2	5412593	5413722	chr12:81	0	+	chr12	8169318	8170452	1134
H2	5412593	5414801	chr12:56	0	_	chr12	56904765	56906973	2208
H2	5412593	5414824	chr4:145	0	_	chr4	145766734	145768973	2239
H2	5412597	5413785	chr2:198	0	+	chr2	198351307	198353944	2637
H2	5412604	5414791	chr5:218	0	_	chr5	21882685	21884875	2190
H2	5452701	5487343	chr11:71	0	_	chr11	71515828	71552097	36269
H2	5452716	5466347	EntireDEI	0	_	EntireDEI	1200000	1212103	12103
H2	5452716	5503451	chr4:935	0	_	chr4	9357882	9408758	50876
H2	5460869	5489615	chr12:83	0	+	chr12	8315368	8346215	30847

H2	5490583	5632341	chr4:907	0	_	chr4	9079830	9223072	143242
H2	5490583	5503451	chr4:922	0	_	chr4	9224396	9237305	12909
H2	5490583	5503451	chr4:925	0	_	chr4	9257622	9270539	12917
H2	5490583	5503451	chr4:933	0	_	chr4	9334155	9347068	12913
H2	5493387	5498118	EntireDEI	0	+	EntireDEI	5498124	5502852	4728
H2	5495314	5730204	EntireDEI	0	_	EntireDEI	939220	1175675	236455
H2	5495314	6261457	chr8:122	0	+	chr8	12231878	12998535	766657
H2	5498124	5502852	EntireDEI	0	+	EntireDEI	5493387	5498118	4731
H2	5506265	5599972	chr12:83	0	+	chr12	8345181	8429635	84454
H2	5532225	5539952	EntireDEI	0	_	EntireDEI	631191	638937	7746
H2	5532225	5539952	EntireDEI	0	_	EntireDEI	5281605	5289351	7746
H2	5539964	5680845	EntireDEI	0	+	EntireDEI	5071462	5200000	128538
H2	5539964	5724530	chr11:34	0	+	chr11	3424930	3605317	180387
H2	5539964	5595342	chr11:67	0	+	chr11	67554687	67605143	50456
H2	5539964	5560713	chr16:51	0	+	chr16	5129856	5152101	22245
H2	5539964	5666087	chr3:754	0	+	chr3	75466170	75569026	102856
H2	5539964	5599980	chr4:393	0	+	chr4	3939121	3999843	60722
H2	5539964	5553367	chr7:696	0	+	chr7	6965389	6980378	14989
H2	5539978	5561950	chr3:129	0	+	chr3	129812065	129835894	23829
H2	5539980	5627262	chr4:963	0	_	chr4	9630530	9710463	79933
H2	5541031	5576150	chr11:71	0	_	chr11	71475864	71515825	39961
H2	5542377	5579082	chr3:125	0	_	chr3	125601691	125651040	49349
H2	5561053	5624959	chr16:51	0	+	chr16	5153839	5191969	38130
H2	5572753	5671220	chr3:129	0	+	chr3	129835893	129920422	84529
H2	5590314	5599959	chr3:125	0	_	chr3	125590687	125599996	9309
H2	5590583	5724530	chr11:71	0	_	chr11	71347642	71475118	127476
H2	5594135	5602995	chr7:698	0	+	chr7	6980380	6988875	8495
H2	5597587	5701710	chr11:67	0	+	chr11	67605062	67704931	99869
H2	5600003	5724530	chr3:125	0	_	chr3	125482435	125590638	108203
H2	5600031	5730204	chr12:84	0	+	chr12	8429698	8551716	122018
H2	5600143	5666072	chr4:400	0	+	chr4	4000000	4057673	57673
H2	5628848	5724530	chr4:953	0	_	chr4	9531072	9620276	89204
H2	5629871	5661813	chr16:51	0	+	chr16	5196791	5216116	19325
H2	5637808	5701710	chr4:902	0	_	chr4	9021004	9079871	58867
H2	5646085	5730204	EntireDEI	0	+	EntireDEI	523442	606602	83160
H2	5657456	5680078	chr7:975	0	+	chr7	97503238	97525961	22723
H2	5662958	5700655	chr16:53	0	_	chr16	5310865	5345782	34917
H2	5666855	5724530	EntireDEI	0	_	EntireDEI	465123	522415	57292
H2	5667188	5699233	chr3:755	0	+	chr3	75568768	75599999	31231
H2	5667188	5724527	chr4:405	0	+	chr4	4057431	4112178	54747
H2	5671135	5730204	EntireDEI	0	+	EntireDEI	5730244	5788477	58233
H2	5680813	5730204	EntireDEI	0	+	EntireDEI	5200002	5249405	49403
H2	5681014	5686266	chr3:129	0	+	chr3	129926296	129931618	5322
H2	5686282	5701710	chr3:151	0	_	chr3	15171808	15187934	16126
H2	5690162	5720398	chr7:975	0	+	chr7	97527271	97557285	30014
H2	5701295	5724530	chr3:756	0	+	chr3	75609150	75632299	23149
H2	5701601	5724040	chr16:52	0	_	chr16	5287439	5310140	22701
H2	5702869	5724530	chr11:67	0	+	chr11	67704797	67726104	21307
H2	5702869	5717969	chr3:151	0	_	chr3	15164147	15171942	7795
H2	5702869	5724520	chr4:899	0	_	chr4	8999626	9021138	21512
H2	5708260	5724530	chrUn_gl	0	_	chrUn_gl	170476	186861	16385
H2	5715066	5730204	EntireDEI	0	_	EntireDEI	1285961	1300939	14978

H2	5717376	5724066	EntireDEI	0	+	EntireDEI	5724362	5730204	5842
H2	5717647	5724530	chr3:129	0	+	chr3	129717908	129724801	6893
H2	5724362	5730204	EntireDEI	0	_	EntireDEI	465641	472450	6809
H2	5724362	5730204	EntireDEI	0	+	EntireDEI	5717376	5724066	6690
H2	5724362	5730188	chr11:35	0	+	chr11	3598163	3604838	6675
H2	5724362	5730204	chr11:67	0	+	chr11	67718978	67725641	6663
H2	5724362	5730204	chr11:71	0	_	chr11	71348105	71354828	6723
H2	5724362	5730204	chr3:756	0	+	chr3	75625138	75631835	6697
H2	5724362	5730204	chr4:410	0	+	chr4	4105035	4111710	6675
H2	5724362	5730204	chr4:900	0	_	chr4	9000080	9006800	6720
H2	5724362	5730204	chr7:975	0	+	chr7	97554254	97560096	5842
H2	5724362	5730204	chrUn_gl	0	_	chrUn_gl	170940	177635	6695
H2	5724390	5730204	chr4:953	0	_	chr4	9531546	9538212	6666
H2	5724430	5730178	chr16:52	0	_	chr16	5287439	5294041	6602
H2	5727390	5730204	chr3:125	0	_	chr3	125482952	125485752	2800
H2	5727390	5730204	chr3:129	0	+	chr3	129721540	129724337	2797
H2	5730203	5782806	EntireDEI	0	_	EntireDEI	465123	518196	53073
H2	5730203	5805255	EntireDEI	0	+	EntireDEI	548367	623591	75224
H2	5730203	5782806	chr11:35	0	+	chr11	3554379	3605317	50938
H2	5730203	5759888	chr11:67	0	+	chr11	67674609	67704931	30322
H2	5730203	5782806	chr11:71	0	_	chr11	71347642	71399957	52315
H2	5730203	5832255	chr12:84	0	+	chr12	8494525	8596339	101814
H2	5730203	5757363	chr3:755	0	+	chr3	75572680	75599999	27319
H2	5730203	5782806	chr3:125	0	_	chr3	125482435	125533392	50957
H2	5730203	5782803	chr4:406	0	+	chr4	4061339	4112178	50839
H2	5730203	5759888	chr4:902	0	_	chr4	9021004	9052028	31024
H2	5730203	5782806	chr4:953	0	_	chr4	9531072	9584025	52953
H2	5730203	5778662	chr7:975	0	+	chr7	97516928	97557285	40357
H2	5730205	5758816	chr16:53	0	_	chr16	5310865	5337673	26808
H2	5730244	5805253	EntireDEI	0	_	EntireDEI	917806	998252	80446
H2	5730244	5805255	EntireDEI	0	+	EntireDEI	5190252	5266361	76109
H2	5730244	5788477	EntireDEI	0	+	EntireDEI	5671135	5730204	59069
H2	5733280	5744403	chr3:129	0	+	chr3	129920418	129931618	11200
H2	5744469	5759888	chr3:151	0	_	chr3	15171808	15187869	16061
H2	5759456	5782806	chr3:756	0	+	chr3	75609150	75632299	23149
H2	5759779	5782316	chr16:52	0	_	chr16	5287439	5310140	22701
H2	5761054	5782806	chr11:67	0	+	chr11	67704797	67726104	21307
H2	5761054	5776227	chr3:151	0	_	chr3	15164115	15171942	7827
H2	5761054	5782796	chr4:899	0	_	chr4	8999626	9021138	21512
H2	5766763	5782806	chrUn_gl	0	_	chrUn_gl	170476	186861	16385
H2	5773283	5813699	EntireDEI	0	_	EntireDEI	1260374	1300939	40565
H2	5775593	5782632	EntireDEI	0	+	EntireDEI	5782638	5788817	6179
H2	5775866	5782806	chr3:129	0	+	chr3	129717908	129724801	6893
H2	5782638	5803405	EntireDEI	0	_	EntireDEI	451933	472450	20517
H2	5782638	5788817	EntireDEI	0	+	EntireDEI	5775593	5782632	7039
H2	5782638	5807201	chr11:35	0	+	chr11	3598163	3623874	25711
H2	5782638	5813222	chr11:67	0	+	chr11	67718978	67750637	31659
H2	5782638	5813218	chr11:71	0	_	chr11	71322016	71354828	32812
H2	5782638	5813222	chr3:756	0	+	chr3	75625138	75657897	32759
H2	5782638	5813220	chr4:410	0	+	chr4	4105035	4136766	31731
H2	5782638	5813222	chr4:897	0	_	chr4	8974119	9006800	32681
H2	5782638	5818515	chr7:975	0	+	chr7	97554254	97597457	43203

H2	5782638	5813222	chrUn_gl	0	_	chrUn_gl	144874	177635	32761
H2	5782706	5788451	chr16:52	0	_	chr16	5287439	5294041	6602
H2	5782706	5813218	chr4:950	0	_	chr4	9508108	9538172	30064
H2	5785676	5821454	chr3:129	0	+	chr3	129721544	129759465	37921
H2	5785680	5832255	chr3:125	0	_	chr3	125435928	125485744	49816
H2	5788450	5797566	chr16:52	0	_	chr16	5256075	5263442	7367
H2	5796574	5821454	chr4:388	0	+	chr4	3883081	3909378	26297
H2	5797337	5802453	chr9:929	0	_	chr9	92972380	92976713	4333
H2	5797359	5806506	chr13:42	0	+	chr13	42007934	42016283	8349
H2	5797359	5804597	chr14:52	0	+	chr14	52232334	52238808	6474
H2	5797359	5803396	chr21:33	0	_	chr21	33986583	33991826	5243
H2	5797363	5800911	chr11:34	0	+	chr11	3414586	3418105	3519
H2	5797510	5809684	chr11:71	0	_	chr11	71600000	71612487	12487
H2	5797510	5803410	chr12:52	0	_	chr12	52494247	52499379	5132
H2	5797512	5805337	chr13:68	0	_	chr13	68476318	68483384	7066
H2	5797512	5815072	chr2:712	0	_	chr2	71245095	71263100	18005
H2	5797512	5821477	chr3:753	0	+	chr3	75399647	75425663	26016
H2	5797512	5800911	chr4:975	0	_	chr4	9751362	9754747	3385
H2	5797512	5813222	chr9:935	0	+	chr9	93507458	93522171	14713
H2	5797527	5813699	chr4:945	0	_	chr4	9452534	9468986	16452
H2	5797557	5814993	EntireDE	0	+	EntireDE	5819015	5837431	18416
H2	5798314	5821454	chr11:67	0	+	chr11	67483704	67509134	25430
H2	5798314	5822800	chr4:415	0	+	chr4	4151984	4184174	32190
H2	5798314	5813222	chr4:894	0	_	chr4	8943472	8958571	15099
H2	5798314	5813663	chr4:947	0	_	chr4	9476897	9492595	15698
H2	5798316	5813695	chr11:71	0	_	chr11	71295976	71311685	15709
H2	5798316	5821454	chr7:689	0	+	chr7	6899612	6925346	25734
H2	5798632	5800066	chr2:135	0	_	chr2	135723991	135725426	1435
H2	5799594	5802445	chr2:712	0	_	chr2	71236048	71239176	3128
H2	5799730	5806507	chr3:872	0	_	chr3	8728543	8735686	7143
H2	5802009	5806506	chr3:112	0	+	chr3	112240477	112245342	4865
H2	5802197	5806506	chr2:962	0	_	chr2	96210893	96215446	4553
H2	5802224	5813222	chr14:52	0	_	chr14	52214682	52226779	12097
H2	5802462	5806506	chr2:712	0	_	chr2	71280960	71285141	4181
H2	5802480	5821611	chr9:929	0	_	chr9	92974019	92997250	23231
H2	5802507	5830468	chr2:159	0	_	chr2	159703461	159734019	30558
H2	5804704	5825127	chr10:15	0	+	chr10	15028872	15051795	22923
H2	5805341	5813222	chr7:687	0	+	chr7	6877635	6886701	9066
H2	5808771	5825127	chr11:71	0	_	chr11	71603556	71623368	19812
H2	5809939	5821454	chr4:975	0	_	chr4	9751362	9764736	13374
H2	5813190	5825127	chr13:42	0	+	chr13	42001671	42015894	14223
H2	5813190	5840026	chr2:712	0	_	chr2	71239539	71269062	29523
H2	5813191	5824201	chr13:68	0	_	chr13	68476346	68489527	13181
H2	5813814	5816922	chr13:47	0	_	chr13	47034805	47037907	3102
H2	5813814	5816923	chr13:64	0	_	chr13	64316486	64319587	3101
H2	5813814	5816923	chr13:64	0	+	chr13	64408465	64411573	3108
H2	5813814	5823498	chr14:52	0	+	chr14	52227175	52238808	11633
H2	5813949	5817546	chr13:42	0	_	chr13	42016699	42026163	9464
H2	5814909	5822317	chr12:52	0	_	chr12	52494234	52503581	9347
H2	5814909	5822290	chr21:33	0	_	chr21	33986583	33995813	9230
H2	5814938	5832255	chr7:687	0	+	chr7	6872947	6886085	13138
H2	5815268	5832255	chr9:935	0	+	chr9	93503611	93521548	17937

H2	5815495	5835374	chr4:945	0	_	chr4	9453011	9472656	19645
H2	5818925	5835374	EntireDEI	0	_	EntireDEI	1260851	1277092	16241
H2	5818925	5825127	chr11:36	0	+	chr11	3613673	3622796	9123
H2	5818925	5836225	chr11:67	0	+	chr11	67734510	67751480	16970
H2	5818925	5832255	chr7:975	0	+	chr7	97569113	97584705	15592
H2	5819013	5822296	EntireDEI	0	_	EntireDEI	451936	458026	6090
H2	5819014	5836243	chr11:71	0	_	chr11	71321148	71339083	17935
H2	5819014	5832255	chr3:756	0	+	chr3	75640811	75657276	16465
H2	5819014	5832255	chrUn_gl	0	_	chrUn_gl	145495	161966	16471
H2	5819015	5837431	EntireDEI	0	+	EntireDEI	5797557	5814993	17436
H2	5819020	5824072	EntireDEI	0	+	EntireDEI	615673	623511	7838
H2	5819020	5824145	EntireDEI	0	_	EntireDEI	917806	930165	12359
H2	5819020	5824072	EntireDEI	0	+	EntireDEI	5258455	5266281	7826
H2	5819058	5836212	chr4:897	0	_	chr4	8973289	8991121	17832
H2	5819769	5832255	chr11:71	0	_	chr11	71297065	71311690	14625
H2	5819787	5821611	chr2:712	0	_	chr2	71237680	71239408	1728
H2	5820026	5835643	chr4:894	0	_	chr4	8943202	8957307	14105
H2	5820026	5832213	chr4:947	0	_	chr4	9478001	9491333	13332
H2	5820161	5830110	chr3:872	0	_	chr3	8723573	8735690	12117
H2	5821378	5832255	chr14:52	0	_	chr14	52215304	52226511	11207
H2	5821378	5825178	chr2:962	0	_	chr2	96211324	96215152	3828
H2	5821378	5826920	chr3:112	0	+	chr3	112241211	112247292	6081
H2	5821378	5832255	chr9:929	0	_	chr9	92985924	92997235	11311
H2	5821586	5833276	chr2:712	0	_	chr2	71272994	71284901	11907
H2	5826890	5836243	EntireDEI	0	_	EntireDEI	441039	450599	9560

uid	posBases	alignL	indelN	indelS	alignB	matchB	mismatch	transition	transvers	fracMatch
645	1000	654415	210	1741	652594	650707	1887	1099	788	0.99711
1	1000	19126	7	10	19116	19006	110	69	41	0.99425
1	1000	19126	7	10	19116	19006	110	69	41	0.99425
175	1000	17347	58	6934	10413	9577	836	471	365	0.91972
2	1000	5045	16	441	4604	4188	416	222	194	0.90964
3	1000	9596	28	279	9317	8485	832	454	378	0.9107
337	1000	11236	13	7279	3957	3610	347	193	154	0.91231
463	1000	12631	14	7286	5345	4899	446	241	205	0.91656
328	1000	7016	22	1108	5908	5482	426	273	153	0.92789
4	1000	22023	65	2564	19459	18178	1281	695	586	0.93417
5	1000	21135	61	1717	19418	18176	1242	661	581	0.93604
6	1000	21134	59	1693	19441	18195	1246	661	585	0.93591
7	1000	6339	19	1096	5243	4798	445	254	191	0.91512
8	1000	21135	61	1697	19438	18192	1246	658	588	0.9359
9	1000	21180	65	1959	19221	17990	1231	678	553	0.93596
67	1000	6316	19	1069	5247	4742	505	285	220	0.90375
78	1000	72335	193	4399	67936	64625	3311	1924	1387	0.95126
79	1000	36509	110	2181	34328	32320	2008	1204	804	0.94151
80	1000	72434	200	3172	69262	65784	3478	2017	1461	0.94978
81	1000	5360	15	46	5314	4883	431	231	200	0.91889
82	1000	6337	16	80	6257	5739	518	275	243	0.91721
176	1000	21190	65	2122	19068	17865	1203	646	557	0.93691
177	1000	6329	18	77	6252	5754	498	262	236	0.92035
211	1000	6324	20	1559	4765	4335	430	240	190	0.90976
212	1000	6356	23	1098	5258	4788	470	263	207	0.91061
233	1000	6348	18	1097	5251	4782	469	260	209	0.91068
338	1000	6339	18	1094	5245	4736	509	296	213	0.90296
339	1000	38433	134	2719	35714	33524	2190	1308	882	0.93868
340	1000	70572	228	3128	67444	63668	3776	2195	1581	0.94401
341	1000	6348	16	1075	5273	4816	457	264	193	0.91333
342	1000	6316	17	89	6227	5745	482	260	222	0.9226
343	1000	21850	67	1866	19984	18671	1313	748	565	0.9343
464	1000	71191	234	4515	66676	62786	3890	2176	1714	0.94166
465	1000	5370	16	61	5309	4885	424	232	192	0.92014
466	1000	36556	121	2194	34362	32137	2225	1315	910	0.93525
467	1000	72530	253	2755	69775	65499	4276	2439	1837	0.93872
468	1000	6316	19	71	6245	5720	525	277	248	0.91593
469	1000	5365	17	54	5311	4851	460	245	215	0.91339
603	1000	5832	16	537	5295	4894	401	223	178	0.92427
604	1000	63845	202	3378	60467	57350	3117	1773	1344	0.94845
774	1000	6361	24	1103	5258	4791	467	267	200	0.91118
796	1000	31414	111	2465	28949	27127	1822	1075	747	0.93706
285	1000	6366	17	1092	5274	4810	464	266	198	0.91202
83	1000	5368	15	67	5301	4898	403	221	182	0.92398
10	1000	6217	11	3061	3156	2861	295	149	146	0.90653
470	1000	6329	17	1121	5208	4755	453	247	206	0.91302
286	1000	6330	14	1070	5260	4751	509	279	230	0.90323
471	1000	7103	22	82	7021	6525	496	281	215	0.92935
775	1000	5414	17	1091	4323	3940	383	217	166	0.9114

287	1000	3160	10	53	3107	2859	248	148	100	0.92018
84	1000	3572	11	55	3517	3249	268	145	123	0.9238
344	1000	3598	11	51	3547	3263	284	165	119	0.91993
85	1000	3587	13	51	3536	3258	278	154	124	0.92138
472	1000	3561	9	48	3513	3233	280	155	125	0.9203
473	1000	3589	12	49	3540	3256	284	161	123	0.91977
605	1000	3565	13	48	3517	3239	278	148	130	0.92096
345	1000	3581	10	53	3528	3240	288	156	132	0.91837
288	1000	1441	6	31	1410	1293	117	57	60	0.91702
248	1000	7753	28	486	7267	6772	495	303	192	0.93188
11	1000	57968	177	1845	56123	52864	3259	1875	1384	0.94193
12	1000	58904	197	2864	56040	52830	3210	1882	1328	0.94272
13	1000	57956	203	1934	56022	52838	3184	1874	1310	0.94317
14	1000	58922	202	2877	56045	52844	3201	1878	1323	0.94289
15	1000	53739	145	1802	51937	49528	2409	1362	1047	0.95362
16	1000	9655	31	348	9307	8763	544	310	234	0.94155
178	1000	57685	180	2351	55334	52525	2809	1616	1193	0.94924
17	1000	5930	13	102	5828	5451	377	204	173	0.93531
249	1000	57662	218	4118	53544	50066	3478	2013	1465	0.93504
346	1000	7919	23	117	7802	7431	371	233	138	0.95245
86	1000	34732	90	356	34376	33105	1271	723	548	0.96303
347	1000	16182	30	121	16061	15520	541	314	227	0.96632
474	1000	35537	115	1254	34283	32387	1896	1083	813	0.9447
348	1000	31396	102	565	30831	29137	1694	977	717	0.94506
349	1000	18553	32	3133	15420	14864	556	329	227	0.96394
18	1000	125005	236	2832	122092	118463	3629	2057	1572	0.97028
19	1000	384949	398	18654	366198	360410	5788	3304	2484	0.98419
20	1000	85010	209	2741	82269	79198	3071	1767	1304	0.96267
87	1000	56909	178	9873	47036	44539	2497	1489	1008	0.94691
88	1000	78617	229	8956	69661	65786	3875	2268	1607	0.94437
179	1000	102003	311	11642	90361	85057	5304	3043	2261	0.9413
350	1000	20988	61	8203	12785	11963	822	524	298	0.93571
351	1000	40322	110	11463	28859	27377	1482	876	606	0.94865
475	1000	21020	59	2440	18580	17801	779	443	336	0.95807
89	1000	79123	214	12072	67051	63355	3696	2175	1521	0.94488
352	1000	77691	243	10447	67244	63615	3629	2170	1459	0.94603
476	1000	56757	159	8467	48290	45784	2506	1444	1062	0.94811
606	1000	8157	12	3250	4907	4735	172	97	75	0.96495
250	1000	14934	31	7253	7681	7152	529	310	219	0.93113
477	1000	76699	221	9364	67335	63253	4082	2366	1716	0.93938
607	1000	58003	178	1759	56244	53467	2777	1621	1156	0.95063
251	1000	36977	142	2705	34272	31912	2360	1330	1030	0.93114
11	1000	57968	177	1845	56123	52864	3259	1875	1384	0.94193
353	1000	31321	93	346	30975	29378	1597	925	672	0.94844
478	1000	55370	175	1579	53791	50881	2910	1624	1286	0.9459
21	1000	75924	193	1572	74352	70842	3510	1969	1541	0.95279
354	1000	16194	37	792	15402	14636	766	459	307	0.95027
355	1000	23802	75	1163	22639	21308	1331	796	535	0.94121
252	1000	23075	83	959	22116	20732	1384	827	557	0.93742
90	1000	21845	61	674	21171	19968	1203	740	463	0.94318
356	1000	7840	23	88	7752	7331	421	261	160	0.94569
479	1000	21888	64	565	21323	20027	1296	778	518	0.93922

797	1000	16795	50	877	15918	14992	926	552	374	0.94183
22	1000	30197	75	420	29777	28119	1658	926	732	0.94432
23	1000	7076	15	975	6101	5842	259	152	107	0.95755
357	1000	6918	13	41	6877	6479	398	235	163	0.94213
4	1000	22023	65	2564	19459	18178	1281	695	586	0.93417
23	1000	7076	15	975	6101	5842	259	152	107	0.95755
91	1000	22982	69	350	22632	21326	1306	763	543	0.94229
92	1000	28095	88	416	27679	25843	1836	1035	801	0.93367
358	1000	22970	75	386	22584	21124	1460	844	616	0.93535
359	1000	23238	60	561	22677	21392	1285	701	584	0.94333
480	1000	23591	75	1002	22589	21172	1417	794	623	0.93727
608	1000	23147	66	492	22655	21465	1190	656	534	0.94747
798	1000	22973	75	390	22583	21124	1459	844	615	0.93539
93	1000	22896	65	330	22566	21276	1290	745	545	0.94283
253	1000	5770	20	84	5686	5331	355	206	149	0.93757
481	1000	22928	67	446	22482	20966	1516	854	662	0.93257
482	1000	22904	66	357	22547	21135	1412	788	624	0.93738
360	1000	22732	64	357	22375	21044	1331	768	563	0.94051
254	1000	9154	29	1839	7315	6817	498	285	213	0.93192
483	1000	8976	27	107	8869	8399	470	254	216	0.94701
213	1000	8223	35	1150	7073	6474	599	297	302	0.91531
361	1000	8207	33	1159	7048	6366	682	345	337	0.90323
776	1000	5415	20	1123	4292	3896	396	197	199	0.90774
777	1000	8230	35	1157	7073	6465	608	308	300	0.91404
234	1000	7561	30	1143	6418	5862	556	265	291	0.91337
289	1000	8241	29	1146	7095	6475	620	323	297	0.91261
290	1000	8213	25	1124	7089	6517	572	285	287	0.91931
362	1000	8227	27	1135	7092	6494	598	307	291	0.91568
94	1000	3513	9	27	3486	3211	275	152	123	0.92111
95	1000	8192	24	116	8076	7528	548	294	254	0.93214
180	1000	8208	23	105	8103	7615	488	244	244	0.93978
214	1000	8537	33	1921	6616	6042	574	289	285	0.91324
363	1000	3511	10	31	3480	3225	255	148	107	0.92672
364	1000	8196	22	112	8084	7568	516	270	246	0.93617
365	1000	3577	10	37	3540	3259	281	137	144	0.92062
484	1000	3516	9	28	3488	3223	265	142	123	0.92403
609	1000	3555	13	36	3519	3248	271	141	130	0.92299
329	1000	6374	26	1125	5249	4832	417	232	185	0.92056
96	1000	3549	12	41	3508	3249	259	136	123	0.92617
181	1000	6186	28	1117	5069	4684	385	209	176	0.92405
24	1000	8056	25	1121	6935	6397	538	280	258	0.92242
68	1000	8038	30	1112	6926	6337	589	306	283	0.91496
485	1000	6712	27	1169	5543	5026	517	255	262	0.90673
486	1000	3340	10	18	3322	3066	256	134	122	0.92294
487	1000	8008	24	91	7917	7407	510	270	240	0.93558
25	1000	7970	22	3050	4920	4454	466	221	245	0.90528
97	1000	7217	23	108	7109	6677	432	240	192	0.93923
98	1000	7204	23	85	7119	6687	432	222	210	0.93932
488	1000	7208	25	103	7105	6660	445	226	219	0.93737
489	1000	7207	20	82	7125	6665	460	241	219	0.93544
490	1000	7208	27	95	7113	6655	458	229	229	0.93561
610	1000	7674	22	573	7101	6688	413	218	195	0.94184

291	1000	1442	5	22	1420	1320	100	56	44	0.92958
292	1000	3163	14	88	3075	2817	258	134	124	0.9161
366	1000	5829	22	93	5736	5268	468	235	233	0.91841
367	1000	3535	14	70	3465	3132	333	171	162	0.9039
235	1000	3054	9	26	3028	2870	158	82	76	0.94782
778	1000	2812	12	31	2781	2557	224	114	110	0.91945
293	1000	2784	10	42	2742	2542	200	99	101	0.92706
215	1000	3921	14	66	3855	3597	258	155	103	0.93307
69	1000	2812	10	21	2791	2523	268	133	135	0.90398
26	1000	9261	7	27	9215	9055	160	75	85	0.98264
182	1000	7771	9	51	7707	7355	352	185	167	0.95433
491	1000	7768	14	62	7693	7329	364	197	167	0.95268
27	1000	7771	13	73	7685	7369	316	161	155	0.95888
28	1000	7767	9	61	7693	7357	336	186	150	0.95632
183	1000	7778	10	52	7661	7330	331	172	159	0.95679
29	1000	7778	14	74	7640	7339	301	151	150	0.9606
26	1000	9261	7	27	9215	9055	160	75	85	0.98264
184	1000	1152	8	43	1109	1004	105	60	45	0.90532
185	1000	2229	15	62	2167	1985	182	108	74	0.91601
492	1000	2228	13	52	2176	1967	209	118	91	0.90395
294	1000	2661	9	1497	1164	1080	84	47	37	0.92784
600	1000	2216	9	55	2161	1987	174	104	70	0.91948
99	1000	36359	73	1754	34605	33494	1111	670	441	0.96789
30	1000	13761	33	1793	11968	11584	384	215	169	0.96791
493	1000	51058	114	477	50581	48224	2357	1252	1105	0.9534
186	1000	30912	46	2174	28738	27864	874	522	352	0.96959
494	1000	50251	114	910	49341	46800	2541	1307	1234	0.9485
495	1000	12901	19	83	12818	11827	991	459	532	0.92269
496	1000	12907	18	87	12820	11848	972	456	516	0.92418
497	1000	12903	16	82	12821	11856	965	459	506	0.92473
31	1000	4734	4	17	4717	4491	226	112	114	0.95209
32	1000	45701	93	919	44782	42827	1955	1007	948	0.95634
31	1000	4734	4	17	4717	4491	226	112	114	0.95209
187	1000	34189	68	640	33549	32168	1381	782	599	0.95884
18	1000	125005	236	2832	122092	118463	3629	2057	1572	0.97028
33	1000	7662	6	57	7605	7355	250	134	116	0.96713
34	1000	89494	39	274	89199	88722	477	249	228	0.99465
188	1000	7775	9	73	7702	7358	344	180	164	0.95534
33	1000	7662	6	57	7605	7355	250	134	116	0.96713
35	1000	36733	78	4919	31814	30106	1708	956	752	0.94631
36	1000	12507	28	5584	6923	6395	528	269	259	0.92373
37	1000	81271	205	7087	74184	70604	3580	2010	1570	0.95174
38	1000	12503	24	7522	4981	4517	464	214	250	0.90685
70	1000	12492	32	5581	6911	6327	584	296	288	0.9155
100	1000	27394	63	4772	22622	21351	1271	725	546	0.94382
101	1000	11659	23	4551	7108	6685	423	226	197	0.94049
102	1000	27421	65	4812	22609	21341	1268	733	535	0.94392
103	1000	27412	59	4773	22639	21314	1325	765	560	0.94147
104	1000	11652	25	4540	7112	6686	426	210	216	0.9401
105	1000	12641	26	4574	8067	7534	533	276	257	0.93393
189	1000	250576	645	31887	218689	207983	10706	6192	4514	0.95104
190	1000	12653	23	4555	8098	7627	471	226	245	0.94184

216	1000	12988	34	6381	6607	6043	564	277	287	0.91464
217	1000	12668	35	5600	7068	6476	592	288	304	0.91624
295	1000	7888	14	4540	3348	3059	289	141	148	0.91368
296	1000	12663	27	5584	7079	6509	570	278	292	0.91948
368	1000	10274	24	4544	5730	5270	460	223	237	0.91972
369	1000	12649	33	5603	7046	6374	672	337	335	0.90463
370	1000	27411	74	4852	22559	21125	1434	819	615	0.93643
371	1000	7983	14	4520	3463	3137	326	163	163	0.90586
372	1000	24332	49	4674	19658	18590	1068	575	493	0.94567
373	1000	12675	27	5591	7084	6494	590	298	292	0.91671
374	1000	12645	23	4570	8075	7573	502	255	247	0.93783
375	1000	24414	57	4790	19624	18469	1155	664	491	0.94114
498	1000	13403	28	4572	8831	8364	467	243	224	0.94712
499	1000	28029	76	5462	22567	21188	1379	764	615	0.93889
500	1000	27431	69	4900	22531	21045	1486	831	655	0.93405
501	1000	11656	22	4539	7117	6669	448	224	224	0.93705
502	1000	27338	68	4809	22529	21162	1367	764	603	0.93932
503	1000	12644	25	4555	8089	7557	532	270	262	0.93423
504	1000	11660	29	4558	7102	6650	452	218	234	0.93636
611	1000	12119	23	5022	7097	6688	409	205	204	0.94237
612	1000	27585	61	4952	22633	21475	1158	637	521	0.94884
779	1000	12679	35	5615	7064	6468	596	295	301	0.91563
799	1000	27416	75	4860	22556	21123	1433	817	616	0.93647
236	1000	3047	9	18	3029	2879	150	73	77	0.95048
297	1000	8240	30	1156	7084	6476	608	306	302	0.91417
298	1000	2831	13	51	2780	2503	277	141	136	0.90036
299	1000	2791	10	48	2743	2551	192	92	100	0.93
780	1000	2810	12	33	2777	2557	220	107	113	0.92078
505	1000	7194	26	100	7094	6656	438	213	225	0.93826
237	1000	7559	31	1151	6408	5857	551	257	294	0.91401
506	1000	6703	27	1164	5539	5022	517	245	272	0.90666
191	1000	6188	29	1124	5064	4686	378	199	179	0.92536
5	1000	21135	61	1717	19418	18176	1242	661	581	0.93604
330	1000	6323	25	1125	5198	4797	401	219	182	0.92285
781	1000	5410	19	1119	4291	3896	395	194	201	0.90795
300	1000	3160	15	89	3071	2812	259	127	132	0.91566
106	1000	3544	11	36	3508	3258	250	129	121	0.92873
376	1000	3575	11	38	3537	3263	274	131	143	0.92253
613	1000	3555	13	41	3514	3247	267	138	129	0.92402
507	1000	3513	9	27	3486	3224	262	142	120	0.92484
107	1000	3510	9	26	3484	3212	272	147	125	0.92193
508	1000	3515	12	30	3485	3193	292	149	143	0.91621
377	1000	3509	11	32	3477	3231	246	139	107	0.92925
301	1000	1439	5	19	1420	1319	101	54	47	0.92887
255	1000	9155	28	1857	7298	6818	480	282	198	0.93423
39	1000	6880	15	935	5945	5627	318	174	144	0.94651
40	1000	237394	275	3443	233951	230240	3711	2153	1558	0.98414
256	1000	5767	18	85	5682	5336	346	197	149	0.93911
12	1000	58904	197	2864	56040	52830	3210	1882	1328	0.94272
108	1000	191575	560	20584	170991	162193	8798	5193	3605	0.94855
109	1000	21871	69	719	21152	19948	1204	744	460	0.94308
110	1000	136964	381	12483	124481	118172	6309	3731	2578	0.94932

378	1000	23826	83	1215	22611	21271	1340	809	531	0.94074
379	1000	196419	591	46692	149727	140859	8868	5425	3443	0.94077
380	1000	6906	17	37	6869	6481	388	233	155	0.94351
509	1000	98144	355	11431	86713	81425	5288	3141	2147	0.93902
800	1000	16824	55	927	15897	14975	922	550	372	0.942
510	1000	55669	173	1297	54372	51916	2456	1407	1049	0.95483
511	1000	21912	68	606	21306	19995	1311	791	520	0.93847
39	1000	6880	15	935	5945	5627	318	174	144	0.94651
257	1000	23098	90	1009	22089	20716	1373	826	547	0.93784
614	1000	30498	80	686	29812	28561	1251	751	500	0.95804
381	1000	7836	26	96	7740	7297	443	276	167	0.94276
111	1000	109170	312	14382	94788	90174	4614	2782	1832	0.95132
382	1000	16197	45	822	15375	14659	716	439	277	0.95343
512	1000	207510	480	15323	192187	183596	8591	4902	3689	0.9553
258	1000	37911	148	3259	34652	32351	2301	1300	1001	0.9336
383	1000	32257	105	1307	30950	29338	1612	944	668	0.94792
384	1000	116473	286	23753	92720	88347	4373	2617	1756	0.95284
41	1000	135330	117	7113	128217	126651	1566	968	598	0.98779
615	1000	22839	55	307	22532	21930	602	330	272	0.97328
385	1000	131793	370	33859	97934	91945	5989	3659	2330	0.93885
513	1000	131820	378	18232	113588	107706	5882	3448	2434	0.94822
259	1000	33451	95	15652	17799	16535	1264	728	536	0.92898
616	1000	66810	144	11297	55513	52808	2705	1594	1111	0.95127
260	1000	64258	149	26781	37477	35035	2442	1496	946	0.93484
112	1000	58117	163	12796	45321	42654	2667	1563	1104	0.94115
113	1000	38591	104	4552	34039	31950	2089	1234	855	0.93863
386	1000	24906	56	2970	21936	20977	959	556	403	0.95628
261	1000	23626	72	3215	20411	19272	1139	689	450	0.9442
514	1000	22080	67	3246	18834	17655	1179	726	453	0.9374
617	1000	16178	53	3027	13151	12257	894	527	367	0.93202
27	1000	7771	13	73	7685	7369	316	161	155	0.95888
29	1000	7778	14	74	7640	7339	301	151	150	0.9606
42	1000	7771	13	73	7695	7380	315	162	153	0.95906
32	1000	45701	93	919	44782	42827	1955	1007	948	0.95634
43	1000	4025	7	541	3484	3193	291	133	158	0.91648
515	1000	111935	289	7529	104406	99132	5274	2762	2512	0.94949
516	1000	8488	10	408	8080	7483	597	284	313	0.92611
517	1000	8487	11	408	8079	7483	596	279	317	0.92623
518	1000	8482	11	403	8079	7473	606	280	326	0.92499
519	1000	8482	10	402	8080	7487	593	284	309	0.92661
520	1000	8485	10	405	8080	7488	592	283	309	0.92673
43	1000	4025	7	541	3484	3193	291	133	158	0.91648
192	1000	30927	55	3753	27174	26357	817	484	333	0.96993
114	1000	101613	281	8253	93360	89026	4334	2302	2032	0.95358
30	1000	13761	33	1793	11968	11584	384	215	169	0.96791
44	1000	13762	29	1790	11972	11653	319	176	143	0.97335
45	1000	5328	15	21	5307	5171	136	80	56	0.97437
115	1000	15923	41	115	15808	14825	983	518	465	0.93782
521	1000	15937	48	129	15808	14682	1126	585	541	0.92877
387	1000	17942	55	2212	15730	14447	1283	685	598	0.91844
388	1000	15489	39	4205	11284	10346	938	500	438	0.91687
389	1000	31893	82	607	31286	29575	1711	921	790	0.94531

390	1000	16845	38	129	16716	15672	1044	558	486	0.93754
618	1000	16550	41	819	15731	14729	1002	535	467	0.9363
302	1000	17941	48	2315	15626	14330	1296	682	614	0.91706
71	1000	9133	20	33	9100	8563	537	284	253	0.94099
522	1000	17530	47	639	16891	15843	1048	577	471	0.93796
46	1000	40883	96	785	40098	37955	2143	1192	951	0.94656
391	1000	31340	85	426	30914	29120	1794	1018	776	0.94197
193	1000	40878	102	981	39897	37845	2052	1150	902	0.94857
523	1000	15770	43	179	15591	14580	1011	533	478	0.93515
116	1000	15766	40	105	15661	14703	958	523	435	0.93883
47	1000	18996	44	5562	13434	12369	1065	559	506	0.92072
48	1000	19609	63	6528	13081	11810	1271	650	621	0.90284
117	1000	31077	108	460	30617	28616	2001	1115	886	0.93464
194	1000	16819	44	3241	13578	12683	895	459	436	0.93408
238	1000	12240	38	1270	10970	10140	830	429	401	0.92434
303	1000	11973	34	1167	10806	9998	808	424	384	0.92523
392	1000	32146	106	1497	30649	28577	2072	1125	947	0.9324
524	1000	32058	107	1533	30525	28316	2209	1191	1018	0.92763
525	1000	15333	38	281	15052	14111	941	506	435	0.93748
619	1000	9090	29	1123	7967	7249	718	356	362	0.90988
782	1000	11976	33	1147	10829	10032	797	422	375	0.9264
783	1000	16351	53	1564	14787	13601	1186	647	539	0.91979
801	1000	32143	103	1489	30654	28589	2065	1118	947	0.93264
526	1000	31681	103	1641	30040	27985	2055	1100	955	0.93159
620	1000	31258	90	528	30730	28920	1810	980	830	0.9411
393	1000	18189	53	3046	15143	13913	1230	662	568	0.91877
118	1000	32131	95	1469	30662	28687	1975	1087	888	0.93559
527	1000	31026	94	1994	29032	27101	1931	1043	888	0.93349
218	1000	14464	47	6094	8370	7577	793	409	384	0.90526
119	1000	24938	67	292	24646	23285	1361	785	576	0.94478
304	1000	4889	17	202	4687	4260	427	219	208	0.9089
305	1000	9578	21	1134	8444	7768	676	354	322	0.91994
394	1000	4918	22	101	4817	4366	451	225	226	0.90637
72	1000	9425	27	1129	8296	7584	712	370	342	0.91418
219	1000	8309	30	1137	7172	6546	626	325	301	0.91272
35	1000	36733	78	4919	31814	30106	1708	956	752	0.94631
49	1000	36744	81	4938	31806	30090	1716	956	760	0.94605
239	1000	7558	25	1138	6420	5850	570	276	294	0.91121
528	1000	6873	25	1170	5703	5155	548	275	273	0.90391
195	1000	6204	22	1102	5102	4695	407	222	185	0.92023
6	1000	21134	59	1693	19441	18195	1246	661	585	0.93591
331	1000	6343	23	1113	5230	4818	412	234	178	0.92122
22	1000	30197	75	420	29777	28119	1658	926	732	0.94432
784	1000	5407	17	1104	4303	3894	409	211	198	0.90495
306	1000	3149	11	59	3090	2822	268	142	126	0.91327
120	1000	3552	11	39	3513	3231	282	150	132	0.91973
121	1000	3577	14	43	3534	3234	300	167	133	0.91511
395	1000	3555	9	33	3522	3222	300	163	137	0.91482
396	1000	3575	11	45	3530	3232	298	149	149	0.91558
529	1000	3558	9	40	3518	3212	306	164	142	0.91302
530	1000	3559	12	39	3520	3217	303	152	151	0.91392
621	1000	3564	13	46	3518	3225	293	153	140	0.91671

307	1000	1442	5	12	1430	1323	107	53	54	0.92517
262	1000	9153	32	1835	7318	6825	493	287	206	0.93263
50	1000	7060	16	975	6085	5789	296	168	128	0.95136
51	1000	15179	32	242	14937	14177	760	438	322	0.94912
263	1000	5768	22	98	5670	5368	302	159	143	0.94674
531	1000	9549	31	252	9297	8738	559	315	244	0.93987
16	1000	9655	31	348	9307	8763	544	310	234	0.94155
50	1000	7060	16	975	6085	5789	296	168	128	0.95136
122	1000	9519	26	191	9328	8865	463	273	190	0.95036
123	1000	9493	25	231	9262	8794	468	290	178	0.94947
124	1000	9547	25	219	9328	8817	511	307	204	0.94522
397	1000	9554	35	252	9302	8800	502	302	200	0.94603
398	1000	9885	28	552	9333	8871	462	277	185	0.9505
399	1000	6907	15	49	6858	6514	344	204	140	0.94984
532	1000	9550	30	235	9315	8753	562	325	237	0.93967
802	1000	9552	35	250	9302	8800	502	303	199	0.94603
533	1000	9509	22	205	9304	8740	564	333	231	0.93938
622	1000	8709	27	274	8435	8040	395	228	167	0.95317
264	1000	9068	32	270	8798	8313	485	287	198	0.94487
400	1000	2523	7	14	2509	2377	132	92	40	0.94739
45	1000	5328	15	21	5307	5171	136	80	56	0.97437
125	1000	5325	13	24	5301	5138	163	94	69	0.96925
534	1000	5333	19	167	5166	4980	186	106	80	0.964
401	1000	21462	58	4628	16834	15687	1147	653	494	0.93186
52	1000	3960	16	97	3863	3576	287	166	121	0.92571
126	1000	19850	51	6426	13424	12328	1096	566	530	0.91836
535	1000	19226	59	6519	12707	11631	1076	560	516	0.91532
536	1000	19811	53	6374	13437	12350	1087	563	524	0.9191
537	1000	16804	41	4677	12127	11191	936	496	440	0.92282
623	1000	18919	53	5625	13294	12259	1035	559	476	0.92215
785	1000	14624	34	5352	9272	8608	664	358	306	0.92839
786	1000	20483	48	4891	15592	14548	1044	595	449	0.93304
538	1000	18897	51	7182	11715	10757	958	487	471	0.91822
127	1000	18887	58	5696	13191	12156	1035	543	492	0.92154
47	1000	18996	44	5562	13434	12369	1065	559	506	0.92072
128	1000	18031	45	5547	12484	11574	910	491	419	0.92711
129	1000	16749	45	4523	12226	11302	924	499	425	0.92442
402	1000	21355	61	5416	15939	14600	1339	735	604	0.91599
403	1000	18850	49	5558	13292	12266	1026	574	452	0.92281
539	1000	18823	49	6082	12741	11729	1012	539	473	0.92057
540	1000	21472	60	5655	15817	14518	1299	676	623	0.91787
624	1000	18718	50	6269	12449	11503	946	514	432	0.92401
541	1000	16736	49	4546	12190	11185	1005	530	475	0.91756
196	1000	17055	59	2588	14467	13295	1172	579	593	0.91899
73	1000	4749	14	146	4603	4350	253	135	118	0.94504
130	1000	14881	49	1329	13552	12540	1012	531	481	0.92532
404	1000	10926	32	1004	9922	9318	604	353	251	0.93913
405	1000	14885	46	1293	13592	12583	1009	543	466	0.92577
240	1000	7261	29	2338	4923	4484	439	222	217	0.91083
74	1000	14837	42	1119	13718	12690	1028	534	494	0.92506
131	1000	10224	26	1235	8989	8358	631	341	290	0.9298
308	1000	11038	25	165	10873	10112	761	410	351	0.93001

406	1000	9455	27	1181	8274	7643	631	343	288	0.92374
803	1000	9456	26	1177	8279	7648	631	347	284	0.92378
309	1000	4940	17	245	4695	4270	425	221	204	0.90948
407	1000	4948	24	150	4798	4383	415	216	199	0.91351
220	1000	11258	38	906	10352	9575	777	407	370	0.92494
221	1000	9744	27	95	9649	9094	555	314	241	0.94248
24	1000	8056	25	1121	6935	6397	538	280	258	0.92242
36	1000	12507	28	5584	6923	6395	528	269	259	0.92373
53	1000	12507	27	5583	6924	6393	531	274	257	0.92331
241	1000	8982	20	74	8908	8345	563	300	263	0.9368
542	1000	8318	28	313	8005	7383	622	328	294	0.9223
332	1000	7811	28	98	7713	7145	568	319	249	0.92636
7	1000	6339	19	1096	5243	4798	445	254	191	0.91512
197	1000	7792	35	101	7691	7128	563	323	240	0.9268
787	1000	6840	21	60	6780	6392	388	230	158	0.94277
310	1000	3393	12	43	3350	3108	242	136	106	0.92776
132	1000	6042	23	1096	4946	4506	440	234	206	0.91104
543	1000	6029	17	1069	4960	4568	392	214	178	0.92097
625	1000	3117	10	345	2772	2555	217	110	107	0.92172
2	1000	5045	16	441	4604	4188	416	222	194	0.90964
52	1000	3960	16	97	3863	3576	287	166	121	0.92571
311	1000	7468	14	2532	4936	4487	449	267	182	0.90904
601	1000	3115	22	197	2918	2758	160	95	65	0.94517
722	1000	1151	8	27	1124	1018	106	63	43	0.90569
626	1000	32837	159	3370	29467	27085	2382	1529	853	0.91916
284	1000	1869	2	13	1856	1778	78	47	31	0.95797
282	1000	1728	1	468	1260	1220	40	24	16	0.96825
283	1000	2901	8	162	2739	2615	124	79	45	0.95473
408	1000	2199	5	16	2183	2118	65	44	21	0.97022
133	1000	52802	144	9853	42949	40458	2491	1517	974	0.942
333	1000	1144	7	36	1108	1021	87	52	35	0.92148
409	1000	114989	289	13855	101134	96450	4684	2797	1887	0.95369
544	1000	83327	225	11328	71999	67884	4115	2501	1614	0.94285
627	1000	11450	36	693	10757	10040	717	460	257	0.93335
134	1000	133771	411	6494	127277	120897	6380	3779	2601	0.94987
545	1000	126245	348	21030	105215	99749	5466	3205	2261	0.94805
410	1000	119447	353	24661	94786	88935	5851	3621	2230	0.93827
411	1000	3077	9	260	2817	2643	174	110	64	0.93823
265	1000	17237	56	237	17000	16062	938	595	343	0.94482
54	1000	135605	119	7358	128247	126553	1694	1042	652	0.98679
198	1000	130498	348	14542	115956	110298	5658	3343	2315	0.95121
546	1000	87695	200	3342	84353	80374	3979	2321	1658	0.95283
41	1000	135330	117	7113	128217	126651	1566	968	598	0.98779
135	1000	29613	80	1084	28529	26713	1816	1126	690	0.93635
412	1000	40475	110	10014	30461	28543	1918	1233	685	0.93703
266	1000	63702	148	26188	37514	35083	2431	1512	919	0.9352
413	1000	87093	303	14837	72256	67831	4425	2693	1732	0.93876
136	1000	130051	389	5646	124405	118113	6292	3718	2574	0.94942
628	1000	61322	143	5811	55511	52815	2696	1593	1103	0.95143
137	1000	80718	249	6533	74185	70578	3607	2176	1431	0.95138
547	1000	46711	209	3045	43666	40888	2778	1646	1132	0.93638
267	1000	27474	97	9684	17790	16524	1266	736	530	0.92884

548	1000	37201	101	887	36314	34943	1371	789	582	0.96225
19	1000	384949	398	18654	366198	360410	5788	3304	2484	0.98419
629	1000	22762	57	276	22486	21877	609	338	271	0.97292
268	1000	36695	150	2051	34644	32348	2296	1308	988	0.93373
13	1000	57956	203	1934	56022	52838	3184	1874	1310	0.94317
414	1000	12988	52	272	12716	11972	744	425	319	0.94149
549	1000	12750	30	98	12652	12264	388	202	186	0.96933
55	1000	75913	212	1712	74201	70631	3570	2007	1563	0.95189
34	1000	89494	39	274	89199	88722	477	249	228	0.99465
56	1000	49472	33	150	49322	49031	291	184	107	0.9941
550	1000	41984	131	807	41177	39192	1985	1149	836	0.95179
551	1000	44536	149	1501	43035	40526	2509	1501	1008	0.9417
552	1000	21472	53	891	20581	19679	902	538	364	0.95617
415	1000	18360	52	173	18187	17341	846	514	332	0.95348
138	1000	44450	133	3403	41047	38866	2181	1331	850	0.94687
139	1000	21558	72	1026	20532	19572	960	583	377	0.95324
199	1000	67259	217	3574	63685	59996	3689	2101	1588	0.94207
416	1000	42541	141	1990	40551	38436	2115	1287	828	0.94784
417	1000	5346	19	126	5220	4980	240	160	80	0.95402
418	1000	16207	45	838	15369	14660	709	433	276	0.95387
630	1000	33771	94	742	33029	31583	1446	860	586	0.95622
419	1000	23765	87	1169	22596	21273	1323	814	509	0.94145
269	1000	23047	92	976	22071	20700	1371	831	540	0.93788
140	1000	21800	70	656	21144	19940	1204	750	454	0.94306
420	1000	7835	27	96	7739	7297	442	282	160	0.94289
553	1000	21844	70	549	21295	19983	1312	797	515	0.93839
804	1000	16761	57	876	15885	14966	919	559	360	0.94215
49	1000	36744	81	4938	31806	30090	1716	956	760	0.94605
57	1000	7077	17	998	6079	5749	330	181	149	0.94571
421	1000	6907	19	57	6850	6470	380	229	151	0.94453
8	1000	21135	61	1697	19438	18192	1246	658	588	0.9359
57	1000	7077	17	998	6079	5749	330	181	149	0.94571
141	1000	22954	62	325	22629	21355	1274	724	550	0.9437
142	1000	30136	87	2489	27647	25896	1751	990	761	0.93667
143	1000	28080	82	396	27684	25873	1811	1006	805	0.93458
422	1000	22966	72	393	22573	21127	1446	829	617	0.93594
554	1000	23587	75	1009	22578	21196	1382	767	615	0.93879
555	1000	28107	90	506	27601	25619	1982	1095	887	0.92819
631	1000	28250	76	536	27714	26077	1637	889	748	0.94093
805	1000	22972	73	403	22569	21125	1444	828	616	0.93602
270	1000	5774	18	74	5700	5348	352	193	159	0.93825
556	1000	22901	67	366	22535	21158	1377	762	615	0.9389
423	1000	19874	46	214	19660	18584	1076	577	499	0.94527
424	1000	19957	55	332	19625	18462	1163	669	494	0.94074
271	1000	9152	28	1856	7296	6816	480	280	200	0.93421
557	1000	8967	28	117	8850	8383	467	243	224	0.94723
222	1000	8214	34	1144	7070	6478	592	288	304	0.91627
425	1000	8195	32	1147	7048	6374	674	339	335	0.90437
558	1000	3514	12	29	3485	3195	290	148	142	0.91679
788	1000	5409	19	1118	4291	3896	395	194	201	0.90795
789	1000	8224	34	1157	7067	6469	598	297	301	0.91538
242	1000	7558	31	1149	6409	5857	552	257	295	0.91387

312	1000	8239	30	1154	7085	6475	610	310	300	0.9139
313	1000	8208	26	1126	7082	6512	570	278	292	0.91951
426	1000	8221	27	1135	7086	6497	589	296	293	0.91688
144	1000	3509	9	25	3484	3213	271	148	123	0.92222
145	1000	8187	25	118	8069	7539	530	273	257	0.93432
200	1000	8199	22	99	8100	7629	471	226	245	0.94185
223	1000	8532	33	1923	6609	6044	565	280	285	0.91451
427	1000	3508	11	31	3477	3233	244	139	105	0.92982
428	1000	8191	22	114	8077	7575	502	258	244	0.93785
429	1000	3574	11	37	3537	3264	273	131	142	0.92282
559	1000	3512	9	26	3486	3226	260	141	119	0.92542
560	1000	8190	24	99	8091	7559	532	271	261	0.93425
632	1000	3554	13	40	3514	3249	265	138	127	0.92459
334	1000	6367	25	1124	5243	4832	411	223	188	0.92161
146	1000	3543	11	35	3508	3259	249	129	120	0.92902
201	1000	6183	29	1124	5059	4681	378	196	182	0.92528
53	1000	12507	27	5583	6924	6393	531	274	257	0.92331
75	1000	8038	31	1124	6914	6328	586	300	286	0.91524
561	1000	6703	27	1163	5540	5022	518	246	272	0.9065
58	1000	7966	20	3054	4912	4454	458	216	242	0.90676
147	1000	7206	22	96	7110	6688	422	224	198	0.94065
148	1000	7199	24	85	7114	6689	425	210	215	0.94026
562	1000	7195	26	101	7094	6657	437	211	226	0.9384
563	1000	7203	21	84	7119	6672	447	225	222	0.93721
564	1000	7207	28	103	7104	6653	451	216	235	0.93651
633	1000	7666	22	567	7099	6691	408	205	203	0.94253
314	1000	1439	5	19	1420	1320	100	53	47	0.92958
315	1000	3160	15	89	3071	2813	258	126	132	0.91599
430	1000	5821	23	89	5732	5272	460	223	237	0.91975
431	1000	3529	13	63	3466	3138	328	164	164	0.90537
243	1000	3048	9	19	3029	2877	152	76	76	0.94982
790	1000	2810	12	32	2778	2556	222	110	112	0.92009
316	1000	2791	10	47	2744	2550	194	93	101	0.9293
224	1000	3926	14	71	3855	3605	250	149	101	0.93515
76	1000	2812	9	16	2796	2525	271	132	139	0.90308
59	1000	9239	3	3	9218	9100	118	56	62	0.9872
60	1000	7649	3	3	7642	7564	78	39	39	0.98979
202	1000	7771	9	51	7717	7372	345	184	161	0.95529
565	1000	7768	14	62	7703	7345	358	197	161	0.95352
42	1000	7771	13	73	7695	7380	315	162	153	0.95906
61	1000	7767	9	61	7703	7370	333	186	147	0.95677
59	1000	9239	3	3	9218	9100	118	56	62	0.9872
60	1000	7649	3	3	7642	7564	78	39	39	0.98979
203	1000	1153	8	43	1110	1007	103	62	41	0.90721
204	1000	2239	15	62	2177	1993	184	112	72	0.91548
566	1000	2261	13	52	2209	1997	212	125	87	0.90403
317	1000	2661	9	1497	1164	1083	81	48	33	0.93041
602	1000	2216	9	55	2161	1989	172	106	66	0.92041
149	1000	36357	76	1803	34554	33449	1105	658	447	0.96802
44	1000	13762	29	1790	11972	11653	319	176	143	0.97335
567	1000	51005	111	399	50606	48205	2401	1296	1105	0.95256
205	1000	30907	50	2221	28686	27810	876	518	358	0.96946

568	1000	146078	321	7197	138881	132359	6522	3727	2795	0.95304
569	1000	12921	20	65	12856	11831	1025	503	522	0.92027
570	1000	12926	19	67	12859	11856	1003	499	504	0.922
571	1000	12922	17	63	12859	11857	1002	504	498	0.92208
62	1000	4737	7	15	4722	4491	231	125	106	0.95108
40	1000	237394	275	3443	233951	230240	3711	2153	1558	0.98414
742	1000	767937	353	3078	764859	762182	2677	1567	1110	0.9965
62	1000	4737	7	15	4722	4491	231	125	106	0.95108
206	1000	94553	197	10947	83606	80342	3264	1949	1315	0.96096
28	1000	7767	9	61	7693	7357	336	186	150	0.95632
61	1000	7767	9	61	7703	7370	333	186	147	0.95677
54	1000	135605	119	7358	128247	126553	1694	1042	652	0.98679
150	1000	190967	561	20144	170823	162118	8705	5175	3530	0.94904
151	1000	57431	159	12127	45304	42721	2583	1543	1040	0.94299
272	1000	22595	76	2196	20399	19263	1136	703	433	0.94431
432	1000	131056	363	33171	97885	91931	5954	3671	2283	0.93917
572	1000	62151	174	3564	58587	55576	3011	1790	1221	0.94861
634	1000	15260	56	2128	13132	12277	855	525	330	0.93489
433	1000	24005	66	2209	21796	20758	1038	625	413	0.95238
573	1000	88115	238	13756	74359	70043	4316	2616	1700	0.94196
152	1000	37939	97	3967	33972	31940	2032	1242	790	0.94019
434	1000	47861	128	12733	35128	32967	2161	1361	800	0.93848
273	1000	64464	141	26965	37499	35043	2456	1518	938	0.9345
435	1000	101258	241	19569	81689	77905	3784	2238	1546	0.95368
436	1000	9710	34	466	9244	8655	589	360	229	0.93628
153	1000	136937	397	12491	124446	118144	6302	3740	2562	0.94936
635	1000	8906	28	501	8405	7943	462	286	176	0.94503
154	1000	109200	318	14456	94744	90141	4603	2781	1822	0.95142
437	1000	126833	417	23201	103632	97665	5967	3650	2317	0.94242
207	1000	133746	418	15301	118445	112023	6422	3771	2651	0.94578
574	1000	68824	207	14046	54778	51872	2906	1683	1223	0.94695
575	1000	98166	361	11468	86698	81398	5300	3155	2145	0.93887
274	1000	33456	96	15655	17801	16531	1270	734	536	0.92866
576	1000	65336	166	7903	57433	55069	2364	1403	961	0.95884
20	1000	85010	209	2741	82269	79198	3071	1767	1304	0.96267
636	1000	22819	56	293	22526	21907	619	340	279	0.97252
275	1000	37972	152	3330	34642	32341	2301	1317	984	0.93358
14	1000	58922	202	2877	56045	52844	3201	1878	1323	0.94289
438	1000	32338	107	1400	30938	29321	1617	950	667	0.94773
577	1000	55667	174	1274	54393	51951	2442	1398	1044	0.9551
63	1000	59776	170	2250	57526	54831	2695	1529	1166	0.95315
56	1000	49472	33	150	49322	49031	291	184	107	0.9941
439	1000	5353	19	132	5221	4972	249	165	84	0.95231
440	1000	16198	44	842	15356	14646	710	435	275	0.95376
637	1000	30437	82	624	29813	28568	1245	754	491	0.95824
441	1000	23776	87	1168	22608	21292	1316	810	506	0.94179
276	1000	23032	91	924	22108	20733	1375	828	547	0.93781
155	1000	21819	73	670	21149	19952	1197	753	444	0.9434
442	1000	7854	28	119	7735	7297	438	280	158	0.94337
578	1000	21855	69	547	21308	20005	1303	789	514	0.93885
806	1000	16755	57	855	15900	14987	913	552	361	0.94258
51	1000	15179	32	242	14937	14177	760	438	322	0.94912

64	1000	6722	13	912	5810	5515	295	158	137	0.94923
443	1000	6908	17	40	6868	6483	385	233	152	0.94394
17	1000	5930	13	102	5828	5451	377	204	173	0.93531
64	1000	6722	13	912	5810	5515	295	158	137	0.94923
156	1000	5836	16	64	5772	5426	346	200	146	0.94006
157	1000	5841	14	68	5773	5423	350	210	140	0.93937
158	1000	5858	12	41	5817	5444	373	221	152	0.93588
444	1000	5863	21	77	5786	5416	370	212	158	0.93605
579	1000	5846	17	72	5774	5384	390	217	173	0.93246
580	1000	5854	11	36	5818	5419	399	233	166	0.93142
638	1000	5854	11	24	5830	5519	311	179	132	0.94666
807	1000	5862	21	77	5785	5414	371	214	157	0.93587
581	1000	5831	13	73	5758	5358	400	231	169	0.93053
277	1000	5769	17	76	5693	5340	353	198	155	0.93799
445	1000	2817	4	20	2797	2629	168	89	79	0.93994
446	1000	2816	4	21	2795	2612	183	97	86	0.93453
15	1000	53739	145	1802	51937	49528	2409	1362	1047	0.95362
21	1000	75924	193	1572	74352	70842	3510	1969	1541	0.95279
159	1000	53668	170	3799	49869	47159	2710	1601	1109	0.94566
160	1000	30633	102	1259	29374	27875	1499	858	641	0.94897
161	1000	53112	172	1306	51806	49086	2720	1565	1155	0.9475
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447	1000	27403	83	327	27076	25707	1369	760	609	0.94944
448	1000	51828	168	2345	49483	46951	2532	1500	1032	0.94883
582	1000	51530	158	1634	49896	47566	2330	1293	1037	0.9533
583	1000	31214	88	1719	29495	28181	1314	723	591	0.95545
584	1000	53684	182	1812	51872	48841	3031	1756	1275	0.94157
639	1000	40953	118	1034	39919	38305	1614	945	669	0.95957
278	1000	28786	104	2153	26633	24800	1833	986	847	0.93118
37	1000	81271	205	7087	74184	70604	3580	2010	1570	0.95174
55	1000	75913	212	1712	74201	70631	3570	2007	1563	0.95189
63	1000	59776	170	2250	57526	54831	2695	1529	1166	0.95315
449	1000	11320	43	317	11003	10442	561	326	235	0.94901
450	1000	16138	38	796	15342	14607	735	436	299	0.95209
451	1000	23894	86	1289	22605	21320	1285	795	490	0.94315
279	1000	23240	89	1242	21998	20632	1366	841	525	0.9379
162	1000	21911	65	763	21148	20046	1102	698	404	0.94789
452	1000	8216	23	440	7776	7414	362	234	128	0.95345
585	1000	22048	69	842	21206	19926	1280	791	489	0.93964
808	1000	16544	58	660	15884	14956	928	571	357	0.94158
46	1000	40883	96	785	40098	37955	2143	1192	951	0.94656
65	1000	7105	20	992	6113	5754	359	205	154	0.94127
453	1000	6957	16	81	6876	6474	402	243	159	0.94154
9	1000	21180	65	1959	19221	17990	1231	678	553	0.93596
65	1000	7105	20	992	6113	5754	359	205	154	0.94127
163	1000	24994	62	609	24385	23023	1362	782	580	0.94415
164	1000	31076	99	794	30282	28328	1954	1081	873	0.93547
165	1000	32129	86	1764	30365	28462	1903	1030	873	0.93733
454	1000	32131	96	1803	30328	28299	2029	1099	930	0.9331
586	1000	31679	96	1922	29757	27723	2034	1089	945	0.93165
587	1000	32101	95	1821	30280	28104	2176	1158	1018	0.92814
640	1000	43457	115	7834	35623	33232	2391	1247	1144	0.93288

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280	1000	5774	20	83	5691	5370	321	180	141	0.9436
588	1000	31000	85	2307	28693	26806	1887	1015	872	0.93423
455	1000	38247	95	2795	35452	32901	2551	1349	1202	0.92804
456	1000	50849	130	5307	45542	42134	3408	1759	1649	0.92517
281	1000	9160	28	1837	7323	6829	494	282	212	0.93254
589	1000	27069	80	2961	24108	22134	1974	1025	949	0.91812
791	1000	5397	14	1345	4052	3689	363	190	173	0.91041
225	1000	9639	34	1782	7857	7146	711	343	368	0.90951
244	1000	7548	21	1384	6164	5624	540	267	273	0.91239
335	1000	6314	21	1348	4966	4597	369	210	159	0.92569
166	1000	3555	11	43	3512	3235	277	147	130	0.92113
167	1000	12557	33	453	12104	11357	747	402	345	0.93828
209	1000	6187	21	1342	4845	4480	365	208	157	0.92466
226	1000	8130	24	1369	6761	6218	543	285	258	0.91969
318	1000	19136	55	2707	16429	15005	1424	711	713	0.91332
457	1000	27256	81	4531	22725	20673	2052	1046	1006	0.9097
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792	1000	16100	49	1777	14323	13203	1120	606	514	0.9218
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66	1000	21381	64	6910	14471	13070	1401	690	711	0.90319
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319	1000	1442	6	15	1427	1319	108	51	57	0.92432
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458	1000	7183	24	446	6737	6180	557	296	261	0.91732
459	1000	4901	24	440	4461	4061	400	202	198	0.91033
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245	1000	12234	37	1373	10861	10083	778	384	394	0.92837
322	1000	4202	19	179	4023	3639	384	204	180	0.90455
793	1000	23384	60	4406	18978	17553	1425	741	684	0.92491
323	1000	31786	88	5053	26733	24605	2128	1123	1005	0.9204
77	1000	23057	55	2768	20289	18855	1434	744	690	0.92932
642	1000	9088	26	1229	7859	7179	680	321	359	0.91347
170	1000	20081	68	3994	16087	14505	1582	783	799	0.90166
595	1000	13539	44	2189	11350	10305	1045	540	505	0.90793
227	1000	14403	44	2646	11757	10724	1033	511	522	0.91214
324	1000	32704	84	9049	23655	21587	2068	1056	1012	0.91258
228	1000	13360	38	2529	10831	9982	849	454	395	0.92161
229	1000	3108	4	6	3102	2882	220	128	92	0.92908
230	1000	3109	6	8	3101	2879	222	122	100	0.92841
231	1000	3112	5	7	3105	2885	220	120	100	0.92915
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643	1000	13186	33	1018	12168	11038	1130	626	504	0.90713
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10	1000	6217	11	3061	3156	2861	295	149	146	0.90653
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66	1000	21381	64	6910	14471	13070	1401	690	711	0.90319
25	1000	7970	22	3050	4920	4454	466	221	245	0.90528
38	1000	12503	24	7522	4981	4517	464	214	250	0.90685
58	1000	7966	20	3054	4912	4454	458	216	242	0.90676
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325	1000	1851	10	150	1701	1553	148	67	81	0.91299
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247	1000	11371	36	658	10713	9755	958	529	429	0.91058
326	1000	3852	13	76	3776	3421	355	186	169	0.90599
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0.93614	0.06351	0.06369
0.93942	0.05959	0.05977
0.94545	0.0533	0.05345
0.94001	0.0592	0.05943
0.94642	0.05248	0.05262

0.9373	0.06174	0.06196
0.93707	0.0617	0.06193
0.94119	0.05873	0.05892
0.93519	0.06361	0.06383
0.93875	0.06036	0.06057
0.9518	0.04659	0.04669
0.93548	0.0642	0.06445
0.94413	0.05549	0.05561
0.93404	0.06489	0.06513
0.95547	0.04318	0.04329
0.93961	0.05954	0.05978
0.9482	0.05033	0.05047
0.95065	0.04808	0.04822
0.95292	0.04609	0.04618
0.92963	0.06953	0.06974
0.94471	0.05398	0.05413
0.94991	0.04871	0.04884
0.98689	0.01231	0.01232
0.97091	0.02721	0.02723
0.93531	0.06379	0.06404
0.94507	0.05366	0.05381
0.92405	0.07461	0.07487
0.94881	0.05038	0.05051
0.93114	0.06817	0.06846
0.93778	0.06128	0.06148
0.93577	0.06403	0.06425
0.95385	0.04504	0.04514
0.94088	0.05799	0.05819
0.93408	0.06537	0.06564
0.92828	0.07126	0.07153
0.95726	0.04229	0.04233
0.95885	0.04047	0.04051
0.95745	0.0421	0.04214
0.95436	0.04498	0.04503
0.91464	0.08855	0.08865
0.94686	0.0523	0.05238
0.92497	0.07778	0.07789
0.92497	0.07766	0.07775
0.92373	0.07903	0.07912
0.92546	0.07723	0.07734
0.92559	0.0771	0.0772
0.91464	0.08855	0.08865
0.96798	0.03068	0.03073
0.95072	0.04792	0.04799
0.96525	0.03279	0.03284
0.971	0.02713	0.02716
0.97163	0.02607	0.02611
0.93539	0.06491	0.06504
0.92596	0.07484	0.075
0.91524	0.08635	0.0866
0.91372	0.0881	0.08836
0.94284	0.05679	0.05689

0.93542	0.06521	0.06535
0.93387	0.06656	0.06671
0.91425	0.08789	0.08813
0.93893	0.06146	0.06158
0.93535	0.06476	0.06492
0.9443	0.05544	0.05557
0.93939	0.0604	0.06056
0.94615	0.05328	0.0534
0.93258	0.06782	0.06796
0.93644	0.06381	0.06396
0.91772	0.08379	0.084
0.89851	0.10406	0.10435
0.93136	0.06838	0.06857
0.93107	0.06899	0.06912
0.92115	0.07976	0.07993
0.92232	0.07877	0.07896
0.92918	0.07085	0.07103
0.92439	0.0761	0.0763
0.93512	0.06528	0.06542
0.90658	0.09601	0.09622
0.92359	0.07746	0.07766
0.91651	0.08483	0.0851
0.92951	0.07058	0.07076
0.92841	0.07173	0.0719
0.93835	0.06134	0.06147
0.91557	0.08597	0.08623
0.9327	0.06735	0.06752
0.93047	0.06965	0.06982
0.9002	0.10128	0.10157
0.94222	0.05736	0.05752
0.90561	0.09713	0.09739
0.91766	0.08466	0.08488
0.90225	0.10001	0.10024
0.91121	0.09115	0.09139
0.90891	0.09279	0.09304
0.944	0.05571	0.05583
0.94364	0.05599	0.05612
0.90768	0.0945	0.09467
0.89997	0.10283	0.10308
0.91628	0.08434	0.08461
0.93308	0.067	0.06714
0.91719	0.08323	0.08354
0.94195	0.05786	0.05799
0.90139	0.10164	0.10193
0.91003	0.09217	0.09245
0.91686	0.0849	0.08514
0.9115	0.09009	0.09043
0.91249	0.09042	0.09072
0.91274	0.08956	0.08975
0.91069	0.09245	0.09275
0.91082	0.09143	0.09163
0.91334	0.08828	0.08852

0.92195	0.07883	0.07896
0.92857	0.07059	0.07084
0.94886	0.05029	0.0504
0.94709	0.05269	0.05282
0.94308	0.05525	0.05534
0.93675	0.06267	0.06284
0.93842	0.06085	0.06102
0.94886	0.05029	0.0504
0.94772	0.05135	0.05149
0.94692	0.05231	0.05249
0.94269	0.05689	0.05707
0.94249	0.05601	0.05619
0.94766	0.05121	0.05136
0.94777	0.05192	0.05206
0.93665	0.0629	0.06309
0.94249	0.05601	0.05619
0.93716	0.06321	0.06342
0.95013	0.04835	0.04846
0.94145	0.05726	0.05743
0.94475	0.05455	0.05486
0.97163	0.02607	0.02611
0.96688	0.0314	0.03144
0.96046	0.0369	0.03696
0.92866	0.07143	0.07166
0.92189	0.07824	0.07854
0.91488	0.08644	0.08665
0.91109	0.08985	0.09009
0.91549	0.0856	0.08581
0.91971	0.08145	0.08166
0.91848	0.0822	0.08244
0.92499	0.07527	0.07546
0.93018	0.07014	0.07036
0.91424	0.08659	0.08678
0.9175	0.08288	0.08309
0.91772	0.08379	0.084
0.92378	0.07668	0.07689
0.92103	0.07966	0.07989
0.9125	0.0891	0.0894
0.91942	0.08146	0.08174
0.91704	0.08396	0.08419
0.9144	0.08698	0.0872
0.92031	0.08012	0.08036
0.91388	0.08734	0.08758
0.91526	0.08573	0.08589
0.94217	0.05708	0.05719
0.92199	0.07866	0.07885
0.93611	0.06349	0.06369
0.92264	0.07817	0.07838
0.90549	0.09494	0.09516
0.92224	0.07895	0.07913
0.92712	0.0737	0.07389
0.92788	0.07347	0.07366

0.92073	0.08043	0.08066
0.92089	0.08037	0.08062
0.9062	0.09647	0.09674
0.90896	0.0919	0.09215
0.92156	0.07908	0.07927
0.93985	0.05984	0.06
0.91911	0.08189	0.08208
0.92001	0.08043	0.0806
0.91972	0.0809	0.08108
0.9347	0.06602	0.06617
0.91908	0.08203	0.08224
0.92301	0.07751	0.07777
0.91182	0.09007	0.09046
0.9226	0.07703	0.07731
0.93986	0.05953	0.05972
0.92445	0.07596	0.07621
0.90682	0.0947	0.09499
0.91782	0.08351	0.08378
0.9184	0.08268	0.08285
0.90649	0.09628	0.09659
0.92189	0.07824	0.07854
0.90646	0.09697	0.09751
0.9381	0.05694	0.05712
0.89929	0.10078	0.10137
0.91423	0.08553	0.08611
0.95694	0.04325	0.04336
0.96749	0.03244	0.0325
0.95195	0.0467	0.04686
0.96801	0.03038	0.03047
0.93885	0.06036	0.06059
0.9157	0.08294	0.08334
0.95097	0.04781	0.04793
0.93991	0.05945	0.05966
0.93023	0.0698	0.07018
0.94682	0.05188	0.05202
0.94492	0.05384	0.05399
0.93479	0.06442	0.06469
0.93524	0.06446	0.06476
0.94172	0.05731	0.05755
0.98588	0.01333	0.01334
0.94836	0.05045	0.05059
0.95058	0.04872	0.04884
0.98689	0.01231	0.01232
0.93373	0.06652	0.06681
0.93366	0.06577	0.0661
0.93152	0.06777	0.06808
0.93484	0.06389	0.06414
0.94646	0.05236	0.05251
0.94899	0.05021	0.05034
0.9482	0.05027	0.05042
0.93192	0.06648	0.06672
0.9238	0.07477	0.07505

0.95958	0.03874	0.03881
0.98313	0.01597	0.01599
0.97046	0.02758	0.02761
0.9297	0.06939	0.06961
0.93976	0.0591	0.05929
0.93766	0.06092	0.06109
0.96704	0.03131	0.03134
0.94918	0.04973	0.04983
0.99422	0.00537	0.00537
0.99344	0.00592	0.00593
0.94878	0.04983	0.04994
0.93845	0.06069	0.0609
0.95372	0.04516	0.04527
0.95076	0.04802	0.04816
0.94381	0.05511	0.0553
0.94991	0.04828	0.04842
0.93888	0.06028	0.06045
0.94456	0.05406	0.05424
0.95056	0.04745	0.04764
0.95108	0.04761	0.04775
0.95351	0.04511	0.04522
0.93784	0.06096	0.0612
0.93399	0.06484	0.06509
0.93995	0.05922	0.05946
0.93961	0.05941	0.05967
0.93531	0.06429	0.06454
0.93878	0.06021	0.06043
0.94364	0.05599	0.05612
0.94308	0.05635	0.05647
0.94191	0.05763	0.05783
0.93297	0.06701	0.06715
0.94308	0.05635	0.05647
0.94112	0.05852	0.05868
0.93373	0.06617	0.06636
0.93182	0.06845	0.06864
0.93297	0.06696	0.06717
0.93568	0.06385	0.06401
0.92517	0.07548	0.07571
0.93836	0.06152	0.06166
0.933	0.06688	0.06709
0.93529	0.06445	0.0646
0.93611	0.06374	0.0639
0.94306	0.05683	0.05694
0.93811	0.06173	0.06191
0.93064	0.06886	0.0691
0.94424	0.05472	0.0548
0.91188	0.08879	0.08894
0.90028	0.1023	0.10256
0.91364	0.0882	0.08841
0.90394	0.09821	0.09842
0.911	0.08978	0.08996
0.90947	0.09149	0.09161

0.91005	0.09145	0.09167
0.91615	0.08514	0.08528
0.9134	0.0881	0.08828
0.91984	0.08212	0.08237
0.93143	0.06874	0.06887
0.9393	0.06053	0.06059
0.90997	0.09077	0.09095
0.92689	0.07368	0.07393
0.9353	0.06488	0.06499
0.91995	0.08145	0.08157
0.92303	0.07856	0.07878
0.93148	0.06881	0.06893
0.92118	0.07948	0.07966
0.91724	0.0828	0.08305
0.92612	0.07457	0.07472
0.92001	0.07871	0.07888
0.91972	0.0809	0.08108
0.91116	0.08994	0.09016
0.9021	0.09986	0.10003
0.90308	0.09957	0.09973
0.93775	0.06183	0.06195
0.9371	0.06226	0.06234
0.93497	0.06428	0.06435
0.93445	0.06557	0.06568
0.93284	0.06633	0.06641
0.93962	0.05979	0.05988
0.92632	0.07395	0.07412
0.91154	0.0891	0.08926
0.91607	0.08488	0.08502
0.90198	0.10116	0.1014
0.947	0.05194	0.052
0.91613	0.0845	0.08466
0.92593	0.07426	0.07435
0.93177	0.06783	0.06809
0.90018	0.10378	0.104
0.98688	0.01291	0.01291
0.9894	0.01028	0.01028
0.95418	0.04609	0.04616
0.95179	0.04798	0.04806
0.95745	0.0421	0.04214
0.95565	0.04453	0.04461
0.98688	0.01291	0.01291
0.9894	0.01028	0.01028
0.90072	0.09906	0.09965
0.90922	0.08967	0.09018
0.89874	0.10269	0.10328
0.92327	0.07303	0.07332
0.91659	0.08414	0.08461
0.9659	0.03268	0.03274
0.971	0.02713	0.02716
0.95047	0.04901	0.04909
0.96778	0.03118	0.03123

0.95084	0.0485	0.0486
0.91884	0.08429	0.08444
0.92064	0.08236	0.08251
0.92086	0.08227	0.08244
0.94967	0.05059	0.05068
0.98298	0.01603	0.01604
0.99604	0.00351	0.00351
0.94967	0.05059	0.05068
0.9587	0.04009	0.04018
0.95521	0.045	0.04508
0.95565	0.04453	0.04461
0.98588	0.01333	0.01334
0.94593	0.05277	0.05292
0.93969	0.0593	0.0595
0.94081	0.05786	0.05808
0.9357	0.06344	0.0637
0.9458	0.05324	0.05339
0.93092	0.06811	0.06841
0.9495	0.0492	0.04934
0.93895	0.06041	0.06063
0.93751	0.06233	0.06258
0.93507	0.06419	0.06448
0.931	0.06853	0.06884
0.95087	0.04781	0.04794
0.93285	0.06659	0.06686
0.94634	0.05243	0.05258
0.94189	0.05709	0.0573
0.94823	0.05023	0.05038
0.93864	0.05991	0.06013
0.94245	0.05628	0.05644
0.94338	0.05502	0.05517
0.93498	0.06377	0.06399
0.92367	0.07497	0.07525
0.95608	0.04233	0.04243
0.96023	0.03829	0.03836
0.97011	0.028	0.02802
0.9295	0.06955	0.06977
0.9395	0.05941	0.05959
0.94447	0.05418	0.05433
0.95206	0.0463	0.04639
0.95034	0.04838	0.04848
0.99344	0.00592	0.00593
0.94885	0.04928	0.04948
0.95104	0.04772	0.04786
0.95561	0.04297	0.04308
0.93818	0.06059	0.06083
0.93396	0.06493	0.06517
0.94016	0.05885	0.05909
0.93997	0.05888	0.05914
0.93582	0.06379	0.06403
0.93921	0.05974	0.05995
0.94709	0.05269	0.05282

0.94711	0.05257	0.05267
0.94161	0.05826	0.05846
0.93323	0.06765	0.06781
0.94711	0.05257	0.05267
0.93746	0.06248	0.06266
0.9371	0.06322	0.06345
0.93395	0.06703	0.06728
0.93267	0.06684	0.06705
0.92972	0.07078	0.07099
0.92966	0.07192	0.07219
0.94487	0.05534	0.05548
0.93248	0.06704	0.06726
0.92844	0.0729	0.07316
0.9352	0.06472	0.0649
0.93859	0.06261	0.06273
0.93319	0.06851	0.06866
0.95096	0.04788	0.04798
0.95033	0.04876	0.04886
0.94244	0.05641	0.05658
0.94568	0.05285	0.05298
0.94436	0.05443	0.05457
0.93093	0.06902	0.06918
0.94654	0.05235	0.05245
0.94562	0.053	0.05315
0.95029	0.04821	0.0483
0.95261	0.04593	0.04601
0.93828	0.06083	0.06101
0.95674	0.04156	0.04165
0.92755	0.07219	0.07237
0.94912	0.04988	0.04998
0.94918	0.04973	0.04983
0.95034	0.04838	0.04848
0.94532	0.0528	0.05294
0.94974	0.04951	0.04964
0.93958	0.05912	0.05934
0.93412	0.06482	0.06509
0.94499	0.05401	0.05422
0.95063	0.04806	0.04824
0.93659	0.06293	0.06319
0.93815	0.06082	0.06106
0.9443	0.05544	0.05557
0.9382	0.06115	0.06132
0.93935	0.06087	0.06109
0.9328	0.06695	0.06712
0.9382	0.06115	0.06132
0.94175	0.05804	0.0582
0.93242	0.06747	0.06765
0.93468	0.06544	0.0656
0.93015	0.07008	0.07025
0.92865	0.07167	0.07184
0.92523	0.07554	0.07573
0.92988	0.07032	0.07046

0.93055	0.06967	0.06985
0.94029	0.05864	0.05878
0.93148	0.06883	0.06899
0.92556	0.07565	0.07583
0.92253	0.07883	0.07901
0.92899	0.07069	0.07092
0.91508	0.08671	0.08692
0.90728	0.0954	0.09568
0.90559	0.09643	0.09661
0.9093	0.09316	0.09335
0.9218	0.07825	0.07853
0.91825	0.08334	0.08356
0.93573	0.0644	0.06454
0.92067	0.07939	0.07968
0.91643	0.08495	0.08517
0.91028	0.09211	0.0923
0.90647	0.09621	0.09646
0.91701	0.08429	0.08451
0.91866	0.08258	0.08282
0.93315	0.06766	0.06778
0.89921	0.10366	0.10389
0.91779	0.08366	0.08384
0.9251	0.07567	0.07582
0.93644	0.06405	0.06416
0.92878	0.07182	0.07194
0.93647	0.06344	0.06356
0.91451	0.08735	0.08752
0.92045	0.07978	0.07988
0.91532	0.08659	0.08678
0.91407	0.0876	0.08785
0.90546	0.0955	0.09572
0.90882	0.09361	0.09388
0.92522	0.07529	0.07541
0.9003	0.1021	0.10244
0.922	0.07912	0.0793
0.91738	0.08415	0.08437
0.92681	0.07423	0.07439
0.91046	0.09194	0.09207
0.89786	0.10541	0.10566
0.90442	0.09823	0.09851
0.90874	0.09345	0.09364
0.90935	0.09295	0.09318
0.91839	0.08279	0.08302
0.92788	0.0745	0.07478
0.92662	0.07524	0.07546
0.92765	0.07443	0.07463
0.91664	0.08524	0.08546
0.90589	0.09679	0.09719
0.9093	0.0927	0.09299
0.90757	0.09489	0.09515
0.90468	0.09914	0.09954
0.91662	0.08447	0.08477

0.89705	0.10651	0.10679
0.89851	0.10406	0.10435
0.90395	0.0985	0.09869
0.90409	0.09799	0.09827
0.90308	0.09946	0.09978
0.90338	0.09983	0.10008
0.91045	0.09145	0.09168
0.90681	0.09539	0.0957
0.90697	0.09512	0.09543
0.89921	0.10366	0.10389
0.90125	0.10125	0.10143
0.9025	0.09947	0.09961
0.90308	0.09957	0.09973
0.90312	0.09931	0.09963
0.90448	0.09745	0.09774
0.90766	0.09248	0.09259
0.90383	0.09856	0.0988
0.89666	0.10616	0.10644
0.91602	0.08518	0.08544
0.90753	0.09522	0.09559
0.90288	0.10045	0.10076
0.90199	0.09958	0.09996
0.91631	0.08559	0.08587
0.90153	0.10114	0.10154
0.90797	0.09508	0.09542

Supplemental Table 6: Details of congenital

Individual ID	Type	Population
GC36743	Patient	unk
GC25092	Parent	unk
GC11200	Patient	unk
GC28058	Patient	unk
GC42961	Patient	unk
GC27175	Patient	unk
GC3746	Patient	unk
GM10932	Patient	unk
GC58789	Patient	unk
GC72100	Patient	unk
GM23831	Patient	unk
GC48867	Patient	unk
GC92095	Patient	unk
GC59139	Patient	unk
NA18517	Control	YRI
NA18523	Control	YRI
NA18502	Control	YRI
HG01500	Control	IBS
HG01597	Control	IBS
HG01503	Control	IBS
NA20502	Control	TSI
NA20504	Control	TSI
NA20505	Control	TSI
HG00096	Control	GBR
HG00097	Control	GBR
HG00098	Control	GBR
HG00099	Control	GBR
HG00100	Control	GBR
NA12046	Control	CEPH
NA12005	Control	CEPH
NA07056	Control	CEPH
NA10851	Control	CEPH
NA12814	Control	CEPH
NA12234	Control	CEPH
NA12156	Control	CEPH
NA10847	Control	CEPH
NA11840	Control	CEPH

heart defect patients with 8p23.1 microdeletions and normal HapMap control individuals

Phenotype
Developmental Delay, Hypotonia, Gross Motor Delay
Included for parental study
Multiple Congenital Anomalies
Coarctation of Aorta, Dysmorphia
Developmental Delay, Multiple Congenital Anomalies
Dysmorphic Features, Congenital Heart Defect
Developmental Delay, Dysmorphic Features
Congenital Heart Defect
Multiple Congenital Anomalies
Abnormal Ultrasound, Diaphragmatic Hernia, Heart Defect, Possible Abnormal Karyotype Invc
Congenital Heart Defect
Heart defect
Amnio shows possible abnormal 8p
Developmental Delay, Dysmorphic Features, Multiple Congenital Anomalies
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A
N/A

Rearrangements	GRCh37 coordinates		
~94 Kbp deletion	chr8	11629883	11723588
~329 Kbp deletion	chr8	8,421,932	8,751,479
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~3.6 Mbp deletion	chr8	8,099,443	11699630
~2.7 Mbp deletion	chr8	8165331	10889421
~3.0 Mbp deletion	chr8	8801117	11756687
~2.3 Mbp deletion	chr8	9441379	11762989
~725 Kbp deletion	chr8	11034866	11761806
~225 Kbp deletion	chr8	11538763	11765512

Supplemental Table 7: Statistical pairwise comparison of predicted copy number depletions for deletio

Model	NoDel	SD19	SD20	SD21	SD25	SD41
NoDel	-	0	0	0	0	0
SD19		-	1.20E-165	1.20E-165	6.20E-168	2.20E-211
SD20			-	1	0.04038	6.00E-202
SD21				-	0.04038	6.00E-202
SD25					-	9.10E-204
SD41						-

ns mediated by each SD pair; p-values are from paired t-tests and corrected for 15 comparisons

Supplemental Table 8: Residual standard errors for pairwise comparison of predicted copy number deple

Model	NoDel	SD19	SD20	SD21	SD25	SD41
SD19	0.977	0	0.381	0.381	0.383	0.419
SD20	1.188	0.381	0	0	0.042	0.775
SD21	1.188	0.381	0	0	0.042	0.775
SD25	1.189	0.383	0.042	0.042	0	0.776
SD41	0.866	0.419	0.775	0.775	0.776	0

ɛtions for deletions mediated by each SD

Supplemental Table 9: Prediction of CNV type by residual standard errors for H2 copy number maps comp

SampleNames	NoDel	SD19	SD20/21	SD25	SD41	Prediction
HG01500	0.457	1.028	1.203	1.203	0.973	No Deletion
HG01503	1.084	1.366	1.497	1.494	1.305	No Deletion
HG01507	0.827	1.208	1.367	1.37	1.143	No Deletion
NA20502	1.784	1.921	1.994	1.993	1.921	No Deletion
NA20504	0.828	1.027	1.072	1.071	1.132	No Deletion
NA20505	0.498	1.142	1.347	1.348	0.997	No Deletion
HG00096	0.844	1.268	1.414	1.415	1.233	No Deletion
HG00097	0.485	1.091	1.264	1.266	1.034	No Deletion
HG00098	0.568	1.234	1.453	1.455	1.085	No Deletion
HG00099	0.378	1.019	1.187	1.187	0.969	No Deletion
HG00100	0.422	1.192	1.412	1.413	1.038	No Deletion
ABC14	0.859	1.354	1.588	1.586	1.156	No Deletion
ABC18	1.065	1.569	1.834	1.832	1.311	No Deletion
ABC22	1.123	1.59	1.805	1.804	1.411	No Deletion
NA12046	0.835	1.321	1.555	1.553	1.125	No Deletion
NA12005	1.439	1.877	2.061	2.064	1.733	No Deletion
NA07056	0.609	1.144	1.32	1.322	1.075	No Deletion
NA10851	1.184	1.734	1.87	1.873	1.657	No Deletion
NA12814	1.134	1.679	1.835	1.837	1.59	No Deletion
NA12234	1.284	1.696	1.793	1.796	1.679	No Deletion
GC36743	1.011	1.305	1.417	1.416	1.286	No Deletion
GC25092	1.216	1.359	1.446	1.444	1.361	No Deletion
GC11200	1.809	1.387	1.431	1.428	1.442	SD19
GC28058	1.849	1.465	1.516	1.514	1.51	SD19
GC42961	1.733	1.381	1.458	1.457	1.399	SD19
GC27175	1.884	1.439	1.429	1.428	1.548	SD20/21
GC3746	1.971	1.561	1.544	1.542	1.678	SD20/21
GM10932	1.996	1.509	1.439	1.438	1.695	SD20/21
GC58789	1.912	1.43	1.339	1.339	1.631	SD20/21

ıared to expected copy number models for deletions mediated by large directly oriented SDs

Supplemental Table 10: Timing duplication expansion of IARs

IAR Phylogeny Node	Timing Estimate	Error
A	0.42	0.14
B	0.55	0.14
C	0.86	0.36
D	0.99	0.19
E	2.4	0.57
F	7.2	0.58
G	8.4	1.4
H	8.7	0.57
I	11	0.72
J	12	0.85
K	12	1.3
L	13	1.4
M	15	1.7
N	19	0.69
O	19	2

***see Figure 3A for phylogeny**

Supplemental Table 11: Pairwise list of SDs at 8p23.1 for the H1 haplotype

Haplotype	ID	SD1 Start	SD1 End	Orientati	SD2 Start	SD2 End	Alignment Length	Percent Identity (Indels Included)
H1	1	6839960	6859070	+	6859070	6878169	19110	0.995027
H1	2	6922487	6932047	-	12564249	12573597	9596	0.907816
H1	3	6933358	6953891	+	7451369	7472338	21167	0.931453
H1	4	6933359	6953891	-	7082237	7103248	22062	0.929946
H1	5	6933381	6953891	-	7540833	7561770	21145	0.930222
H1	6	6933381	6953891	+	7899388	7920339	21135	0.932085
H1	7	6933381	6956196	-	11866167	11890233	24373	0.933295
H1	8	6933381	6939670	-	11779873	11785171	6342	0.910161
H1	9	6933381	6953891	-	12519641	12540754	21503	0.934342
H1	10	6933384	6939474	-	12556362	12559656	6228	0.902747
H1	11	6946564	7003835	-	7025560	7082405	58028	0.938034
H1	12	6946564	6962729	-	7524649	7541001	16555	0.938468
H1	13	6946564	6949153	+	7472170	7474649	2590	0.931562
H1	14	6946564	7003835	+	7920171	7976966	57982	0.938634
H1	15	6946564	7003835	-	12404192	12461833	58905	0.939441
H1	16	6946564	6999576	-	12467544	12519809	53376	0.95072
H1	17	6947082	6953891	-	12461665	12467505	5931	0.930834
H1	18	7005690	7135647	-	7866864	7999583	133405	0.986837
H1	19	7005690	7088082	+	12381111	12467505	87343	0.960073
H1	20	7029792	7105095	+	12467504	12542604	76009	0.950326
H1	21	7066062	7141383	+	7524649	7599999	75420	0.993916
H1	22	7072932	7082405	+	11866167	11875567	9552	0.942934
H1	23	7075241	7082231	+	7082237	7088424	7068	0.959007
H1	24	7075241	7078259	-	7469329	7472338	3021	0.961819
H1	25	7079924	7150644	-	7403845	7474649	70888	0.983904
H1	26	7082237	7105095	+	11868353	11892081	22972	0.939741
H1	27	7096974	7105095	+	11779873	11787032	8210	0.915892
H1	28	7097171	7105015	+	12556369	12561432	7990	0.90079
H1	29	7110934	7133810	+	7133810	7156664	22877	0.989807
H1	29	7133810	7156664	+	7110934	7133810	22877	0.989807
H1	30	7110934	7126188	+	7126188	7141432	15255	0.993703
H1	31	7110934	7118566	+	7118566	7126188	7633	0.99095
H1	32	7110934	7143022	+	7600048	7632239	32202	0.984731
H1	33	7120308	7128031	-	12269593	12277323	7768	0.955674
H1	34	7120309	7128031	-	12027274	12035003	7767	0.955278
H1	35	7127951	7143178	+	7143195	7158430	15247	0.981536
H1	36	7135552	7143275	-	12269593	12277323	7768	0.955284
H1	37	7143195	7150800	+	7150817	7158430	7625	0.967224
H1	38	7150796	7195814	-	12231878	12277323	45729	0.954244
H1	39	7150797	7238459	-	11949217	12035003	88216	0.967896
H1	40	7188125	7192866	+	7192867	7197587	4741	0.953208
H1	41	7200000	7436083	-	7600000	7825413	236649	0.990911
H1	42	7200000	7238459	-	12195464	12232403	38642	0.9656
H1	43	7403845	7420740	+	7426796	7443689	16915	0.982121
H1	44	7403845	7411500	+	7411500	7419150	7661	0.99268

H1	45	7411223	7418977	+	12269593	12277326	7777	0.953244
H1	46	7411223	7418973	+	12027274	12035003	7773	0.952572
H1	47	7413138	7474649	-	7538520	7600000	61577	0.984789
H1	48	7418879	7474649	+	7866864	7922650	55831	0.98958
H1	49	7426519	7434273	+	12269593	12277326	7776	0.954281
H1	50	7426519	7434269	+	12027274	12035003	7772	0.95335
H1	51	7445068	7472338	-	11868353	11892079	27418	0.94092
H1	52	7445068	7457638	-	11779873	11787030	12664	0.916808
H1	53	7445068	7474649	-	12517329	12542602	30032	0.948356
H1	54	7465989	7468521	+	7472170	7474649	2534	0.936393
H1	55	7466505	7474649	-	12459354	12467505	8152	0.994598
H1	56	7469327	7472338	-	12512591	12515658	3069	0.923434
H1	57	7469327	7472338	-	12454675	12457694	3022	0.958845
H1	58	7469329	7472338	+	7924312	7927347	3039	0.964464
H1	59	7472170	7474649	-	11873029	11875567	2539	0.940371
H1	60	7524649	7594262	-	7866864	7936502	69760	0.982758
H1	61	7524649	7563640	+	12503740	12542604	39540	0.943636
H1	62	7524649	7546652	+	12445572	12467505	22046	0.976777
H1	63	7531528	7541001	+	11866167	11875567	9552	0.943041
H1	64	7533844	7540839	+	7540840	7547005	7053	0.95719
H1	65	7540833	7563640	+	11868353	11892081	22953	0.939615
H1	66	7555518	7563640	+	11779873	11787032	8211	0.915751
H1	67	7555715	7563560	+	12556369	12561432	7990	0.90081
H1	68	7569473	7584704	+	7584753	7599999	15257	0.989622
H1	69	7569473	7577105	+	7577105	7584753	7658	0.985049
H1	70	7569473	7600000	+	7600048	7630601	30565	0.99122
H1	71	7571225	7578972	-	12269593	12277323	7768	0.955676
H1	72	7571226	7578972	-	12027274	12035003	7767	0.955023
H1	73	7584237	7591885	+	7591885	7599532	7648	0.998954
H1	74	7586516	7594268	-	12269593	12277326	7773	0.954528
H1	75	7586520	7594268	-	12027274	12035003	7769	0.954375
H1	76	7600000	7615296	+	7615296	7630601	15307	0.992221
H1	77	7600048	7624854	-	7866864	7891681	24839	0.979757
H1	78	7609459	7617211	-	12269593	12277326	7773	0.954398
H1	79	7609463	7617211	-	12027274	12035003	7769	0.954245
H1	80	7616934	7624583	+	7624583	7632239	7659	0.984446
H1	81	7788474	7874612	+	11949217	12035003	86640	0.969783
H1	82	7788474	7832954	+	12195464	12240266	44914	0.977868
H1	83	7827824	7832546	+	7832547	7837292	4745	0.948382
H1	84	7866880	7876379	+	7882180	7891681	9524	0.967949
H1	85	7876899	7884025	+	7884547	7891681	7136	0.984145
H1	86	7882158	7889909	+	12269593	12277326	7773	0.953756
H1	87	7893060	7920339	-	11868353	11892079	27432	0.940993
H1	88	7893060	7905635	-	11779873	11787030	12668	0.916126
H1	89	7893060	7972733	-	12467504	12542602	80429	0.951219
H1	90	7913977	7920171	+	7920171	7927179	7095	0.944816
H1	91	7914493	8096968	-	12277338	12467505	185176	0.975737
H1	92	7920171	7929656	-	11866167	11875567	9575	0.945778
H1	93	8046345	8096968	-	12035019	12091854	51337	0.970923
H1	94	11766330	11773531	+	11791219	11796120	7258	0.92148
H1	95	11779873	11792921	+	11883925	11899536	15838	0.920289
H1	96	11860820	11866139	+	11900773	11906094	5330	0.970329

H1	97	11860820	11866139	+	12147338	12152658	5330	0.973897
H1	98	11866167	11875567	+	12510281	12519809	9607	0.936022
H1	99	11866167	11875567	+	12452365	12461833	9556	0.943641
H1	100	11868353	11900637	+	12519641	12551048	31854	0.943621
H1	101	11868353	11875044	+	12461665	12467505	5845	0.939384
H1	102	11883915	11900160	+	12556274	12572728	19619	0.897444
H1	103	11895289	11993727	+	12141854	12240266	98848	0.986805
H1	104	11988415	11993164	+	11993170	11997894	4753	0.951132
H1	105	12000004	12091854	+	12242319	12334342	92173	0.99284
H1	106	12231878	12235253	+	12236595	12240297	3711	0.916642
H1	107	12408472	12467505	+	12467544	12525492	59454	0.950305
H1	108	12454675	12461369	+	12461665	12467505	6720	0.945417
H1	109	12512591	12519635	+	12519641	12525832	7110	0.938467
H1	110	12534906	12549944	+	12556364	12569614	16018	0.906324

Supplemental Table 12: GMAP-based gene annotation of the H2 haplotype

Sequence	Exon Star	Exon End	Gene Na	Score	Direction	Start Cod	End Codo	Number of Exons
H2	246757	254181	DEFB1	40	-	246757	254181	2
H2	300763	302145	DEFA6	40	-	300763	302145	2
H2	311891	314333	DEFA4	40	-	311891	314333	3
H2	326783	327657	DEFA8P	40	-	326783	327657	2
H2	335344	336217	DEFA9P	40	-	335344	336217	2
H2	344195	345168	DEFA10P	40	-	344195	345168	2
H2	353706	356150	DEFA1	3	-	353706	356150	3
H2	353706	356143	DEFA3	3	-	353706	356143	3
H2	353706	356150	DEFA1B	3	-	353706	356150	3
H2	363242	365784	DEFT1P	40	-	363242	365784	3
H2	372825	375268	DEFA1/D	40	-	372825	375268	3
H2	372825	375268	DEFA1B	40	-	372825	375268	3
H2	372825	375268	DEFA3	40	-	372825	375268	3
H2	382362	384904	DEFT1P	40	-	382362	384904	3
H2	382362	384904	DEFT1P2	40	-	382362	384904	3
H2	391934	394371	DEFA1	3	-	391934	394371	3
H2	391934	394364	DEFA3	3	-	391934	394364	3
H2	391934	394371	DEFA1B	3	-	391934	394371	3
H2	404670	405559	DEFA11P	40	-	404670	405559	2
H2	431378	432810	DEFA5	40	-	431378	432810	2
H2	574507	574656	MIR548I3	40	+	574507	574656	1
H2	633543	636508	FAM90A7	40	+	633543	636508	3
H2	641189	651805	FAM90A7	40	+	641189	651805	3
H2	644300	647196	LINC0096	40	-	644300	647196	1
H2	648838	650568	FAM90A1	40	+	648838	650568	3
H2	657846	660669	PRR23D2	40	-	657846	660669	4
H2	657846	660670	PRR23D1	40	-	657846	660670	4
H2	690989	704452	DEFB107	3	-	690989	704452	2
H2	710745	712576	DEFB105	3	-	710745	712576	3
H2	713909	717793	DEFB106	3	+	713909	717793	2
H2	725212	729986	DEFB104	3	+	725212	729986	2
H2	736622	749732	SPAG11B	0	+	736622	749732	3
H2	736622	749732	SPAG11B	0	+	736622	749732	4
H2	747928	749732	SPAG11B	0	+	747928	749732	2
H2	747928	749732	SPAG11B	0	+	747928	749732	3
H2	769962	771343	DEFB103	3	+	769962	771343	2
H2	770150	771424	DEFB103	3	+	770150	771424	2
H2	783448	785464	DEFB4A	40	+	783448	785464	2
H2	783479	785457	DEFB4B	40	+	783479	785457	2
H2	837354	842346	ZNF705G	40	+	837354	842346	5
H2	844967	898695	FAM66B	40	+	844967	898695	7
H2	857050	867937	LOC3921	0	-	857050	867937	2
H2	866344	867937	USP17L1	40	-	866344	867937	1
H2	866344	867937	USP17L4	40	-	866344	867937	1
H2	880357	887462	DEFB109	40	-	880357	887462	2
H2	880357	887462	DEFB109	40	-	880357	887462	2
H2	906324	909198	LINC0096	40	+	906324	909198	1
H2	998166	1012164	LOC7297	0	+	998166	1012164	7
H2	998166	1112045	LOC1005	0	-	998166	1112045	7

H2	1112674	1124674	FAM86B1	0	-	1112674	1124674	6
H2	1113021	1134222	FAM90A2	0	-	1113021	1134222	5
H2	1139000	1188029	FAM66A	40	-	1139000	1188029	5
H2	1169786	1171378	USP17L2		-	1169786	1171378	
H2	1149700	1156754	DEFB109I	40	+	1149700	1156754	2
H2	1170259	1170782	LOC6493	40	+	1170259	1170782	1
H2	1174500	1175869	USP17L7		-	1174500	1175869	
H2	1188294	1214475	ZNF705D	40	-	1188294	1214475	7
H2	1231746	1239100	DEFB130	40	+	1231746	1239100	2
H2	1313327	1315600	DEFB134	40	+	1313327	1315600	2
H2	1324989	1327259	DEFB135	40	-	1324989	1327259	2
H2	1334984	1335647	DEFB136	40	+	1334984	1335647	2
H2	1441483	1467132	CTSB	40	+	1441483	1467132	10
H2	1441483	1467132	CTSB	40	+	1441483	1467132	11
H2	1441483	1467132	CTSB	40	+	1441483	1467132	12
H2	1470325	1506973	FDFT1	40	-	1470325	1506973	8
H2	1522313	1540000	NEIL2	40	-	1522313	1540000	4
H2	1522313	1540000	NEIL2	40	-	1522313	1540000	5
H2	1546417	1548390	C8orf49	40	-	1546417	1548390	1
H2	1549645	1605438	GATA4	40	-	1549645	1605438	7
H2	1728367	1733185	LINC002C	40	-	1728367	1733185	3
H2	1745117	1815671	BLK	40	-	1745117	1815671	13
H2	1842923	1888712	FAM167A	40	+	1842923	1888712	3
H2	1871512	1940052	C8orf12	40	-	1871512	1940052	7
H2	1940001	1968811	TDH	40	-	1940001	1968811	9
H2	1976261	1977462	SLC35G5	40	-	1976261	1977462	1
H2	1977515	2023963	MTMR9	40	-	1977515	2023963	11
H2	2107170	2412723	XKR6	0	+	2107170	2412723	1
H2	2273334	2273431	MIR598	40	+	2273334	2273431	1
H2	2462388	2468869	LOC1019	40	+	2462388	2468869	
H2	2468994	2543872	PINX1	40	+	2468994	2543872	6
H2	2468994	2543872	PINX1	40	+	2468994	2543872	7
H2	2483319	2483390	MIR1322	40	+	2483319	2483390	1
H2	2578239	2585046	SOX7	40	+	2578239	2585046	2
H2	2608235	2636108	C8orf74	40	-	2608235	2636108	4
H2	2653607	2702326	RP1L1	40	-	2653607	2702326	
H2	2754520	2783139	PRSS55	40	-	2754520	2783139	5
H2	2826689	2834053	LINCR-00	40	+	2826689	2834053	
H2	2879774	3214500	MSRA	40	-	2879774	3214500	6
H2	2879774	3214500	MSRA	40	-	2879774	3214500	7
H2	2879774	3255733	MSRA	40	-	2879774	3255733	5
H2	2879774	3255733	MSRA	40	-	2879774	3255733	6
H2	3406897	3406982	MIR124-1	40	+	3406897	3406982	1
H2	3407040	3410561	LINC005S	40	+	3407040	3410561	4
H2	3528365	3757190	TNKS	40	-	3528365	3757190	27
H2	3571455	3571552	MIR597	40	-	3571455	3571552	1
H2	3978095	3988135	LOC1572	40	-	3978095	3988135	3
H2	4110375	4124232	LOC1019	40	+	4110375	4124232	
H2	4161644	4177034	PPP1R3B	40	+	4161644	4177034	2
H2	4265120	4265194	MIR4660	40	-	4265120	4265194	1
H2	4280300	4310802	ERI1	40	-	4280300	4310802	7
H2	4420016	4529179	MFHAS1	40	+	4420016	4529179	3

H2	4609688	4611640	CLDN23	40	-	4609688	4611640	1
H2	4929129	4993145	SGK223	40	+	4929129	4993145	5
H2	5066043	5082340	FAM86B3	40	-	5066043	5082340	9
H2	5070878	5082340	FAM86B3	40	-	5070878	5082340	6
H2	5071983	5082340	FAM86B3	40	-	5071983	5082340	8
H2	5276307	5293332	FAM90A1	0	+	5276307	5293332	3
H2	5291603	5294569	FAM90A7	0	+	5291603	5294569	3
H2	5300601	5303423	PRR23D2	0	-	5300601	5303423	4
H2	5300601	5303424	PRR23D1	0	-	5300601	5303424	4
H2	5333752	5337755	DEFB107	3	-	5333752	5337755	2
H2	5344046	5345877	DEFB105	3	-	5344046	5345877	3
H2	5347210	5351132	DEFB106	3	+	5347210	5351132	2
H2	5358549	5363322	DEFB104	3	+	5358549	5363322	2
H2	5369958	5383068	SPAG11B	40	+	5369958	5383068	3
H2	5369958	5383068	SPAG11B	40	+	5369958	5383068	4
H2	5369958	5385874	SPAG11B	3	+	5369958	5385874	3
H2	5369958	5385874	SPAG11B	40	+	5369958	5385874	4
H2	5369958	5385875	SPAG11A	0	+	5369958	5385875	4
H2	5381264	5383068	SPAG11B	40	+	5381264	5383068	3
H2	5403285	5404666	DEFB103	3	+	5403285	5404666	2
H2	5403473	5404747	DEFB103	3	+	5403473	5404747	2
H2	5416759	5418794	DEFB4A	0	+	5416759	5418794	2
H2	5416790	5418787	DEFB4B	0	+	5416790	5418787	2
H2	5448096	5475636	ZNF705B	0	+	5470645	5475636	5
H2	5478259	5531635	FAM66E	40	+	5478259	5513657	6
H2	5490338	5491778	LOC3921	40	-	5490338	5491778	1
H2	5494899	5496492	USP17L7	40	-	5494899	5496492	1
H2	5494899	5501225	USP17L4	0	-	5494899	5501225	2
H2	5494899	5501225	USP17L8	40	-	5494899	5501225	2
H2	5499632	5501225	USP17L1	0	-	5499632	5501225	1
H2	5499632	5501225	USP17L2	40	-	5499632	5501225	1
H2	5499632	5501225	USP17L3	0	-	5499632	5501225	1
H2	5513357	5520457	DEFB109	40		5513357	5520457	
H2	5534655	5538167	FAM90A2	40	-	5534655	5538167	4
H2	5535907	5539721	FAM90A2	40	-	5535907	5539721	5
H2	5545677	5556403	FAM86B2	40	-	5545677	5556403	8
H2	5557074	5671221	LOC1005	40	+	5557074	5671221	7
H2	5657246	5786105	LOC7297	40	-	5657246	5786105	9
H2	5839283	5839351	MIR5692	40	-	5839283	5839351	1
H2	5842044	5875647	LONRF1	40	-	5842044	5875647	12
H2	5847380	5847453	MIR3926	40	-	5847380	5847453	1
H2	5847385	5847448	MIR3926	40	+	5847385	5847448	1
H2	5886200	5931576	LOC3403	40	-	5886200	5931576	4
H2	5914410	5938469	LINC0068	40	+	5914410	5938469	2
H2	6065902	6150014	KIAA145	40	+	6065902	6150014	5

Exon Sizes	Exon Star	% identity with mRNA RefSeq
256,211	0,7213	0.99143469
234,234	0,1148	1
319,184,39	0,905,240	1
113,172	0,702	1
113,172	0,701	1
107,184	0,789	0.996563574
231,187,80	0,811,236	1
231,187,73	0,811,236	1
231,187,80	0,811,236	1
246,187,63	0,921,247	0.989919355
231,187,80	0,881,236	0.9902
231,187,73	0,811,236	0.9902
231,187,80	0,811,236	0.9902
246,187,63	0,921,247	0.9903
246,187,63	0,921,247	0.9903
231,187,80	0,811,235	1
231,187,73	0,811,235	1
231,187,80	0,811,235	1
128,173	0,716	0.996677741
237,212	0,1220	1
149	0	0.993288591
210,109,1525	0,8317,90	0.9845
210,109,1525	0,8317,90	0.989154013
2,874	0	0.9776
210,109,288	0,668,144	0.986820428
1203,68,62,254	0,1431,17	0.997479521
1203,68,62,255	0,1431,17	0.997479521
231,158	0,13305	1
125,42,70	0,1374,17	1
54,249	0,3635	1
72,209	0,4565	1
228,153,337	0,811,127	0.998677249
228,153,76,337	0,811,124	0.998677249
107,337	0,1467	0.998677249
107,76,337	0,1168,14	0.998677249
276,161	0,1220	1
88,242	0,1032	1
94,242	0,1774	0.99702381
63,235	0,1743	0.993288591
34,127,96,83,585	0,1732,26	0.993513514
44,64,62,68,68,65,561	0,6211,30	1
1365,82	0,10805	0.985487215
1593	0	0.98430634
1593	0	0.981795355
206,58	0,7047	0.996212121
206,58	0,7047	0.996212121
2874	0	0.996172582
5,68,241,131,217,1989	0,464,612	0.993220339
39,267,139,93,348,698	0,20048,5	0.980919612

		0.95
		0.98
37,68,62,64,544	0,22703,2	0.997419355
		0.98
58,131	0,6923	0.996212121
523	0	0.988527725
		0.98
3,83,96,127,83,45,306	0,3997,46	0.997013304
58,182	0,7172	1
58,143	0,2130	1
170,64	0,2206	1
49,188	0,475	1
,86,144,117,129,2699	0,14672,1	0.997092255
,86,144,117,129,2699	0,3675,14	0.997092255
,86,144,117,129,2699	0,3675,66	0.997092255
77,192,129,184,98,251	0,7664,89	0.999525166
1385,197,353,129	0,3948,73	0.997731397
1,385,197,353,129	0,3948,15	0.997731397
1973	0	0.995438419
49,88,126,167,1073,97	0,2917,48	0.998532864
872,272,790	0,2700,40	0.994312306
,104,99,94,52,124,580	0,1489,31	0.998455598
1427,783,171	0,22438,4	0.998289763
71,273,216,100,189,51	0,447,355	0.997545008
,173,150,71,43,187,83	0,2664,34	0.997545008
1201	0	1
##################	0,2791,11	0.999461207
789	0	0.997471555
97	0	1
		0.998
162,110,93,79,93,956	0,5116,67	0.999330208
2,110,93,79,93,77,956	0,5116,67	0.999330208
71	0	1
3,792,899	0,3908	0.998779744
359,407,193,77	0,2592,25	1
		0.997
224,143,251,193,194	0,21120,2	0.99800995
		0.997
44,107,105,120,69,488	0,108926,	0.998533724
107,105,120,69,75,488	0,108926,	0.998533724
744,107,105,69,339	0,108926,	0.998533724
44,107,105,120,69,339	0,108926,	0.998533724
85	0	1
2641,58,223,20	0,2717,30	0.999660095
7,95,76,37,96,225,678	0,14591,1	0.999791645
97	0	1
2,677,402,363	0,8776,96	0.997966299
		0.998
2965415	0,9975	0.999820241
74	0	1
15,110,84,211,179,368	0,12860,1	0.99805026
35611,27,1569	0,96157,1	0.999048887

1952	0	0.999487705
301,832,158,752,1561	0,3666,42	0.997841571
268,134,102,81,63,131	0,543,759	1
404,150,134,81,63,228	0,2756,40	1
268,134,102,81,63,228	0,1651,26	1
210,109,288	0,8316,16	0.989154013
2,101,091,525	0,668,144	0.989154013
1202,68,62,254	0,1430,17	0.997479521
1202,68,62,255	0,1430,17	0.997479521
231,158	0,3845	1
125,42,70	0,1374,17	1
54,249	0,3673	1
72,209	0,4564	1
228,153,337	0,811,127	0.998677249
228,153,76,337	0,811,124	0.998677249
228,153,296	0,811,156	0.998677249
228,153,78,296	0,811,127	0.998677249
228,153,78,297	0,811,127	0.998677249
107,76,337	0,1168,14	0.992443325
276,161	0,1220	1
88,242	0,1032	1
94,242	0,1793	0.99702381
63,235	0,1762	0.993288591
34,127,96,83,585	0,1731,26	0.97864
542,64,124,62,84,193	0,6208,29	0.97389
1440	0	0.985487215
1593	0	0.997489014
5,881,007	0,5319	0.981818182
4,181,176	0,5150	0.981806775
1593	0	0.981795355
1593	0	0.998116761
1593	0	0.98430634
7170		0.95
1522,109,200,65	0,2186,27	0.997890295
270,109,200,179,32	0,934,150	1
,266,134,102,81,63,96	0,2039,30	0.992902208
698,348,93,139,267,89	0,1151,39	0.980919612
1987,217,131,241,68,2	0,43768,4	0.993220339
		1
7,241,150,123,119,784	0,3830,70	0.999441964
73	0	1
63	0	1
534,103,113,22	0,12219,2	0.998704663
175,329	0,23730	1
2931,981,551,74,8778	0,45160,6	0.995832465

Supplemental Table 13: Pairwise list of SDs at 8p23.1 for the H2 haplotype that flank this disease-ass

Haplotype	ID	SD1 Start	SD1 End	Orientation	SD2 Start	SD2 End
H2	1	350306	369425	+	369425	388548
H2	2	441009	445902	+	1392737	1397493
H2	3	441039	450599	_	5826890	5836243
H2	4	451933	472450	_	600766	621731
H2	5	451933	472450	+	924120	945049
H2	6	451933	472450	+	1270779	1291771
H2	7	451933	458219	+	1381933	1387229
H2	8	451933	472450	_	5243551	5264500
H2	9	451933	472450	_	5782638	5803405
H2	10	451936	458026	_	5819013	5822296
H2	11	465123	522415	_	544135	600934
H2	12	465123	522415	+	944881	1002533
H2	13	465123	522415	_	5185972	5243719
H2	14	465123	522415	_	5666855	5724530
H2	15	465123	518196	_	5730203	5782806
H2	16	465126	474755	+	1291606	1300939
H2	17	465641	472450	_	5724362	5730204
H2	18	523442	646586	_	899282	1023316
H2	19	523442	907030	+	5171228	5539949
H2	20	523442	606602	+	5646085	5730204
H2	21	548367	623591	+	5730203	5805255
H2	22	591452	621496	_	1271009	1300939
H2	23	593761	600760	+	600766	606944
H2	24	615623	623591	_	1380070	1387093
H2	25	615673	623511	+	5819020	5824072
H2	26	629419	638666	+	644725	653973
H2	27	631191	638937	+	1130188	1137911
H2	28	631191	638937	_	5532225	5539952
H2	29	638839	646592	+	1130188	1137917
H2	30	819380	833006	_	1200000	1212103
H2	31	860259	864976	+	864978	869712
H2	32	862031	907030	_	1130191	1175675
H2	33	899282	906931	+	906935	914553
H2	34	899282	988647	_	5200002	5289351
H2	35	917806	954344	+	1268930	1300939
H2	36	917806	930215	+	1380072	1387093
H2	37	917806	998252	_	5730244	5805253
H2	38	917806	930165	_	5819020	5824145
H2	39	939062	945049	+	945196	952034
H2	40	939220	1175675	_	5495314	5730204
H2	41	988550	1130175	_	5071463	5199975
H2	42	1130188	1137911	+	5281605	5289351
H2	43	1166942	1170962	+	1172186	1175675
H2	44	1200000	1212103	_	5452716	5466347
H2	45	1254916	1260235	+	1300967	1306283

H2	46	1260374	1300939	_	5773283	5813699
H2	47	1260851	1277082	+	1371030	1387229
H2	48	1260851	1277092	_	5818925	5835374
H2	49	1268930	1300939	_	5234274	5270815
H2	50	1285443	1291606	+	1291606	1298588
H2	51	1285961	1300939	_	5715066	5730204
H2	52	1370982	1374895	+	1393583	1397493
H2	53	1380072	1387093	_	5258405	5270815
H2	54	5071462	5200000	+	5539964	5680845
H2	55	5190252	5266361	+	5730244	5805255
H2	56	5200002	5249405	+	5680813	5730204
H2	57	5236584	5243545	+	5243551	5249746
H2	58	5258455	5266281	+	5819020	5824072
H2	59	5272194	5281432	+	5287490	5296727
H2	60	5281432	5289080	+	5289080	5296727
H2	61	5281605	5289351	_	5532225	5539952
H2	62	5493387	5498118	+	5498124	5502852
H2	63	5671135	5730204	+	5730244	5788477
H2	64	5717376	5724066	+	5724362	5730204
H2	65	5775593	5782632	+	5782638	5788817
H2	66	5797557	5814993	+	5819015	5837431

ociated critical region

Alignment Length	Percent Identity (Indels Included)
19126	0.993881713
5045	0.906493506
9596	0.907972178
22023	0.931059209
21135	0.933107449
21134	0.933076923
6339	0.911820601
21135	0.932970922
21180	0.932800996
6217	0.903378592
57968	0.938969805
58904	0.93941711
57956	0.939759893
58922	0.939498996
53739	0.950961945
9655	0.938423645
5930	0.933230611
125005	0.968404617
384949	0.983125839
85010	0.960231819
75924	0.950325307
30197	0.941946938
7076	0.955199477
8056	0.919109195
7970	0.901254553
9261	0.98189113
7771	0.957261626
7767	0.95520644
7778	0.958845048
13761	0.965252896
4734	0.951281508
45701	0.954362117
7662	0.966364472
89494	0.99421771
36733	0.943998495
12507	0.920011509
81271	0.949118821
12503	0.902497502
6880	0.944127517
237394	0.982982248
135330	0.986885782
7771	0.957446809
4025	0.91463764
13762	0.971002416
5328	0.971627208

40883	0.944295168
18996	0.917717762
19609	0.898508825
36744	0.943644746
7060	0.948860842
15179	0.947090654
3960	0.921887084
12507	0.919723781
135605	0.985876322
75913	0.949175547
49472	0.993435316
7077	0.943077428
7966	0.903081914
9239	0.986877779
7649	0.98940484
7767	0.955653527
4737	0.949672235
59776	0.950343178
6722	0.947106303
7105	0.938203163
21381	0.899208806

Supplemental Table 14: Regions of sequence diversity detected between H1 and H2 haplotypes

build	chromosome	start	end	RefSeq intersect	
GRCh37	chr8	6601826	6632110	AGPAT5	diversity region_A
GRCh37	chr8	9000840	9011530		high % sequence identity
GRCh37	chr8	9169786	9200289	LOC157273	diversity region_B
GRCh37	chr8	9305044	9322780		diversity region_C
GRCh37	chr8	9316473	9331693		high % sequence identity
GRCh37	chr8	9351253	9361566		high % sequence identity
GRCh37	chr8	9608235	9614492	TNKS	high % sequence identity
GRCh37	chr8	10041750	10052547	MRSA	high % sequence identity
GRCh37	chr8	10380699	10409897	PRSS55	diversity region_D
GRCh37	chr8	10814979	10839875	XKR6	diversity region_E
GRCh37	chr8	11145823	11174759	MTMR9	high % sequence identity
GRCh37	chr8	11382685	11408097	BLK	diversity region_F
GRCh37	chr8	12765713	12786672		diversity region_G