

chrom	start	end	rsID	geneID	ancestral	derived
hg19	derived_AF_1kgp+sgdp		altai		vindija	chagyrskaya
denisovan	consequence		CADD			
1	105785758		105785758		.	A
G	G	1	A/A	A/A	A/A	A/A
	intergenic_variant		0.228			
1	105786065		105786065		.	A
T	T	1	A/A	A/A	A/A	A/A
	intergenic_variant		3.701			
1	105786884		105786884		rs1322471256	.
C	T	T	0.999968197430352		C/C	C/C
C/C	C/C	intergenic_variant	0.774			
1	105787270		105787270		.	T
C	C	1	T/T	T/T	T/T	T/T
	intergenic_variant		3.593			
1	105787399		105787399		.	T
C	C	1	T/T	T/T	T/T	T/T
	intergenic_variant		0.066			
1	105787498		105787498		.	G
A	A	1	G/G	G/G	G/G	G/G
	intergenic_variant		0.671			
1	106761082		106761082		rs745366988	.
G	A	A	1	G/G	G/G	G/G
	intergenic_variant		1.419			
1	106761085		106761085		rs1486654950	.
G	C	C	1	G/G	G/G	G/G
	intergenic_variant		0.872			
1	106761086		106761086		rs1250708304	.
T	A	A	1	T/T	T/T	T/T
	intergenic_variant		1.22			
1	106761089		106761089		rs367840139	.
T	A	A	1	T/T	T/T	T/T
	intergenic_variant		2.075			
1	107478164		107478164		rs4993710	.
T	A	A	1	T/T	T/T	T/T
	intergenic_variant		2.082			
1	107478166		107478166		rs4993712	.
T	A	A	1	T/T	T/T	T/T
	intergenic_variant		2.983			
1	107620703		107620703		rs181047315	.
G	A	A	0.995555837724589		G/G	G/G
G/G	G/G	intergenic_variant	7.905			
1	107622495		107622495		rs374125265	.
T	C	C	0.995547357038356		T/T	T/T
T/T	T/T	intergenic_variant	1.092			
1	107622509		107622509		rs536315227	.
G	A	A	0.995580005087764		G/G	G/G
G/G	G/G	intergenic_variant	0.915			
1	107633227		107633227		rs150376031	.
A	G	G	0.999397208121827		A/A	A/A
A/A	A/A	intergenic_variant	1.596			
1	107633232		107633232		rs138063315	.
G	T	T	0.999397399302252		G/G	G/G
G/G	G/G	intergenic_variant	0.504			

1	107645273		107645273		rs994714386	.	
T	C	C	0.999968270085036		T/T	T/T	
T/T	T/T		intergenic_variant		1.722		
1	107839978		107839978		rs142917715		
ENSG00000162631	G		A	A	0.997912920626766		
G/G	G/G	G/G	G/G				
			intron_variant,non_coding_transcript_variant		3.451		
1	107839978		107839978		rs142917715		
ENSG00000162631	G		A	A	0.997912920626766		
G/G	G/G	G/G	G/G		intron_variant	3.451	
1	108008477		108008477		rs149699743		
ENSG00000162631	C		G	G	0.996956439033669		
C/C	C/C	C/C	C/C		intron_variant	1.652	
1	108009374		108009374		rs141934558		
ENSG00000162631	T		C	C	0.998317994287528		
T/T	T/T	T/T	T/T		intron_variant	10.99	
1	108057244		108057244		.		C
T	T	1	C/C	C/C	C/C	C/C	
			regulatory_region_variant		4.31		
1	108057244		108057244		.		C
T	T	1	C/C	C/C	C/C	C/C	
			intergenic_variant		4.31		
1	108057720		108057720		.		T
C	C	1	T/T	T/T	T/T	T/T	
			intergenic_variant		2.369		
1	108062224		108062224		.		C
T	T	1	C/C	C/C	C/C	C/C	
			intergenic_variant		18.65		
1	108066006		108066006		.		C
T	T	1	C/C	C/C	C/C	C/C	
			regulatory_region_variant		3.029		
1	108066006		108066006		.		C
T	T	1	C/C	C/C	C/C	C/C	
			intergenic_variant		3.029		
1	108066132		108066132		rs1363971085		
T	C	C	1	T/T	T/T	T/T	T/T
			regulatory_region_variant		2.503		
1	108066132		108066132		rs1363971085		
T	C	C	1	T/T	T/T	T/T	T/T
			intergenic_variant		2.503		
1	108066451		108066451		.		C
A	A	1	C/C	C/C	C/C	C/C	
			regulatory_region_variant		12		
1	108066451		108066451		.		C
A	A	1	C/C	C/C	C/C	C/C	
			intergenic_variant		12		
1	108066747		108066747		.		C
T	T	1	C/C	C/C	C/C	C/C	
			regulatory_region_variant		14.02		
1	108066747		108066747		.		C
T	T	1	C/C	C/C	C/C	C/C	
			intergenic_variant		14.02		
1	108071115		108071115		.		C
A	A	1	C/C	C/C	C/C	C/C	

intergenic_variant					1.63	
1	108083704		108083704	rs376734938		.
C	T	T			0.999426751592357	C/C C/C
C/C	C/C		intergenic_variant			3.953
1	108179190		108179190	rs532263177		
ENSG00000134215	G	A	A	1	G/G	G/G
G/G	G/G		intron_variant,non_coding_transcript_variant			0.23
1	108179190		108179190	rs532263177		
ENSG00000134215	G	A	A	1	G/G	G/G
G/G	G/G		intron_variant			0.23
1	108179190		108179190	rs532263177		
ENSG00000134215	G	A	A	1	G/G	G/G
G/G	G/G		intron_variant,NMD_transcript_variant			0.23
1	108180336		108180336	rs530084164		
ENSG00000134215	A	C	C			0.999968282161888
A/A	A/A	A/A	A/A			
			intron_variant,non_coding_transcript_variant			6.623
1	108180336		108180336	rs530084164		
ENSG00000134215	A	C	C			0.999968282161888
A/A	A/A	A/A	A/A			intron_variant 6.623
1	108180336		108180336	rs530084164		
ENSG00000134215	A	C	C			0.999968282161888
A/A	A/A	A/A	A/A			
			intron_variant,NMD_transcript_variant			6.623
1	108180626		108180626	rs552314602		
ENSG00000134215	C	T	T	1	C/C	C/C
C/C	C/C		intron_variant,non_coding_transcript_variant			8.905
1	108180626		108180626	rs552314602		
ENSG00000134215	C	T	T	1	C/C	C/C
C/C	C/C		intron_variant			8.905
1	108180626		108180626	rs552314602		
ENSG00000134215	C	T	T	1	C/C	C/C
C/C	C/C		intron_variant,NMD_transcript_variant			8.905
1	108181025		108181025	rs1307969729		
ENSG00000134215	G	T	T	1	G/G	G/G
G/G	G/G		intron_variant,non_coding_transcript_variant			1.728
1	108181025		108181025	rs1307969729		
ENSG00000134215	G	T	T	1	G/G	G/G
G/G	G/G		intron_variant,NMD_transcript_variant			1.728
1	108182666		108182666	rs563452904		
ENSG00000134215	A	G	G	1	A/A	A/A
A/A	A/A		intron_variant,non_coding_transcript_variant			1.591
1	108182666		108182666	rs563452904		
ENSG00000134215	A	G	G	1	A/A	A/A
A/A	A/A		intron_variant			1.591
1	108182666		108182666	rs563452904		
ENSG00000134215	A	G	G	1	A/A	A/A

A/A	A/A	intron_variant,NMD_transcript_variant					1.591
1	108182666	108182666		rs563452904	.		
A	G	G	1	A/A	A/A	A/A	
regulatory_region_variant 1.591							
1	108183085	108183085		rs569780303			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant,non_coding_transcript_variant					
2.931							
1	108183085	108183085		rs569780303			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant					2.931
1	108183085	108183085		rs569780303			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant,NMD_transcript_variant					2.931
1	108183085	108183085		rs569780303	.		
G	A	A	1	G/G	G/G	G/G	
regulatory_region_variant 2.931							
1	108183085	108183085		rs569780303	.		
G	A	A	1	G/G	G/G	G/G	
TF_binding_site_variant 2.931							
1	108183659	108183659		rs1237578370			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant,non_coding_transcript_variant					
1.956							
1	108183659	108183659		rs1237578370			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant					1.956
1	108183659	108183659		rs1237578370			
ENSG00000134215	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant,NMD_transcript_variant					1.956
1	108183659	108183659		rs1237578370	.		
G	A	A	1	G/G	G/G	G/G	
regulatory_region_variant 1.956							
1	108183830	108183830			ENSG00000134215		
T	C	C	1	T/T	T/T	T/T	
intron_variant,non_coding_transcript_variant					3.145		
1	108183830	108183830			ENSG00000134215		
T	C	C	1	T/T	T/T	T/T	
intron_variant 3.145							
1	108183830	108183830			ENSG00000134215		
T	C	C	1	T/T	T/T	T/T	
intron_variant,NMD_transcript_variant					3.145		
1	108183910	108183910		rs982425828			
ENSG00000134215	C	T	T	1	C/C	C/C	
C/C	C/C	intron_variant,non_coding_transcript_variant					
4.218							
1	108183910	108183910		rs982425828			
ENSG00000134215	C	T	T	1	C/C	C/C	
C/C	C/C	intron_variant					4.218
1	108183910	108183910		rs982425828			
ENSG00000134215	C	T	T	1	C/C	C/C	
C/C	C/C	intron_variant,NMD_transcript_variant					4.218
1	108184312	108184312		rs564599021			
ENSG00000134215	C	T	T	1	C/C	C/C	

C/C	C/C	intron_variant,non_coding_transcript_variant						
4.417								
1	108184312		108184312		rs564599021			
ENSG00000134215	C	T	T	1	C/C	C/C		
C/C	C/C	intron_variant					4.417	
1	108184312		108184312		rs564599021			
ENSG00000134215	C	T	T	1	C/C	C/C		
C/C	C/C	intron_variant,NMD_transcript_variant					4.417	
1	108184312		108184312		rs564599021		.	
C	T	T	1	C/C	C/C	C/C	C/C	
regulatory_region_variant 4.417								
1	108188317		108188317			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						2.57		
1	108188317		108188317			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant						2.57		
1	108188317		108188317			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant						2.57		
1	108188345		108188345			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						13.62		
1	108188345		108188345			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant						13.62		
1	108188345		108188345			ENSG00000134215		
C	A	A	1	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant						13.62		
1	108192611		108192611			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						0.667		
1	108192611		108192611			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant						0.667		
1	108192611		108192611			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant						0.667		
1	108193856		108193856			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						1.278		
1	108193856		108193856			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant						1.278		
1	108193856		108193856			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant						1.278		
1	108194263		108194263			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						4.745		
1	108194263		108194263			ENSG00000134215		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant						4.745		
1	108194263		108194263			ENSG00000134215		

C	T	T	1	C/C	C/C	C/C	C/C
intron_variant,NMD_transcript_variant					4.745		
1	108211522		108211522			ENSG00000134215	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant,non_coding_transcript_variant					4.848		
1	108211522		108211522			ENSG00000134215	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant					4.848		
1	108211522		108211522			ENSG00000134215	
C	T	T	1	C/C	C/C	C/C	C/C
downstream_gene_variant					4.848		
1	108211522		108211522			ENSG00000134215	
C	T	T	1	C/C	C/C	C/C	C/C
non_coding_transcript_exon_variant					4.848		
1	108211522		108211522			ENSG00000134215	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant,NMD_transcript_variant					4.848		
1	108211522		108211522			.	C
T	T	1	C/C	C/C	C/C	C/C	
regulatory_region_variant					4.848		
1	110040454		110040454		rs2297795		
ENSG00000174151	C	T	T	1	C/C	C/C	
C/C	C/C	3_prime_UTR_variant		1.399			
1	110040454		110040454		rs2297795		
ENSG00000174151	C	T	T	1	C/C	C/C	
C/C	C/C	downstream_gene_variant		1.399			
1	110040454		110040454		rs2297795		
ENSG00000174151	C	T	T	1	C/C	C/C	
C/C	C/C	intron_variant	1.399				
1	110040454		110040454		rs2297795		.
C	T	T	1	C/C	C/C	C/C	C/C
regulatory_region_variant					1.399		
1	110304581		110304581		rs139058136		
ENSG00000198758	T	C	C	0.999617956064948			
T/T	T/T	T/T	T/T	intron_variant	8.877		
1	110304581		110304581		rs139058136		
ENSG00000134201	T	C	C	0.999617956064948			
T/T	T/T	T/T	T/T				
intron_variant,non_coding_transcript_variant					8.877		
1	110304581		110304581		rs139058136		
ENSG00000241720	T	C	C	0.999617956064948			
T/T	T/T	T/T	T/T				
intron_variant,non_coding_transcript_variant					8.877		
1	110304581		110304581		rs139058136		
ENSG00000198758	T	C	C	0.999617956064948			
T/T	T/T	T/T	T/T				
intron_variant,non_coding_transcript_variant					8.877		
1	110304581		110304581		rs139058136		
ENSG00000198758	T	C	C	0.999617956064948			
T/T	T/T	T/T	T/T	upstream_gene_variant	8.877		
1	110335251		110335251		rs960060994		.
T	C	C	0.999872789721409		T/T	T/T	
T/T	T/T	intergenic_variant	0.299				
1	110703152		110703152		rs920603708		

ENSG00000197106	C	A	A	0.999746337751284		
C/C	C/C	C/C	C/C	intron_variant	4.049	
1	110703152	110703152	rs920603708	.		
C	A	A	0.999746337751284	C/C	C/C	
C/C	C/C	regulatory_region_variant	4.049			
1	110769555	110769555	ENSG00000116396			
G	C	C	1	G/G	G/G	G/G G/G
intron_variant	0.496					
1	110769555	110769555	ENSG00000116396			
G	C	C	1	G/G	G/G	G/G G/G
intron_variant,non_coding_transcript_variant	0.496					
1	110769555	110769555	ENSG00000116396			
G	C	C	1	G/G	G/G	G/G G/G
intron_variant,NMD_transcript_variant	0.496					
1	110769555	110769555	ENSG00000116396			
G	C	C	1	G/G	G/G	G/G G/G
downstream_gene_variant	0.496					
1	110770422	110770422	rs114937306			
ENSG00000116396	A	G	G	0.995300990601981		
A/A	A/A	A/A	A/A	intron_variant	1.945	
1	110770422	110770422	rs114937306			
ENSG00000116396	A	G	G	0.995300990601981		
A/A	A/A	A/A	A/A			
intron_variant,non_coding_transcript_variant	1.945					
1	110770422	110770422	rs114937306			
ENSG00000116396	A	G	G	0.995300990601981		
A/A	A/A	A/A	A/A			
intron_variant,NMD_transcript_variant	1.945					
1	110770422	110770422	rs114937306			
ENSG00000116396	A	G	G	0.995300990601981		
A/A	A/A	A/A	A/A	downstream_gene_variant	1.945	
1	110778512	110778512	rs970979623			
ENSG00000116396	A	G	G	0.999968284173803		
A/A	A/A	A/A	A/A	downstream_gene_variant	2.042	
1	110778512	110778512	rs970979623			
ENSG00000116396	A	G	G	0.999968284173803		
A/A	A/A	A/A	A/A			
intron_variant,non_coding_transcript_variant	2.042					
1	110778512	110778512	rs970979623	.		
A	G	G	0.999968284173803	A/A	A/A	
A/A	A/A	regulatory_region_variant	2.042			
1	110778512	110778512	rs970979623	.		
A	G	G	0.999968284173803	A/A	A/A	
A/A	A/A	TF_binding_site_variant	2.042			
1	110887060	110887060	rs528599337			
ENSG00000162775	T	G	G	0.99987221263817	T/T	
T/T	T/T	T/T	intron_variant	11.56		
1	110887060	110887060	rs528599337			
ENSG00000162775	T	G	G	0.99987221263817	T/T	
T/T	T/T	T/T	downstream_gene_variant	11.56		
1	110887060	110887060	rs528599337	.		
T	G	G	0.99987221263817	T/T	T/T	T/T
T/T	regulatory_region_variant	11.56				
1	110888393	110888393	rs573099279			

ENSG00000162775	C	A	A	0.999872983614886
C/C	C/C	C/C	C/C	intron_variant 12.43
1	110888393	110888393	rs573099279	
ENSG00000162775	C	A	A	0.999872983614886
C/C	C/C	C/C	C/C	downstream_gene_variant 12.43
1	110889151	110889151	rs57552411	
ENSG00000162775	C	A	A	0.999873040055862
C/C	C/C	C/C	C/C	3_prime_UTR_variant 15.82
1	110889151	110889151	rs57552411	
ENSG00000162775	C	A	A	0.999873040055862
C/C	C/C	C/C	C/C	downstream_gene_variant 15.82
1	110893274	110893274	rs575988067	
ENSG00000162775	T	C	C	0.999873168875642
T/T	T/T	T/T	T/T	downstream_gene_variant 3.253
1	110899657	110899657	rs574922478	.
C	T	T	0.999873168875642	C/C C/C
C/C	C/C			regulatory_region_variant 1.633
1	110899657	110899657	rs574922478	.
C	T	T	0.999873168875642	C/C C/C
C/C	C/C			intergenic_variant 1.633
1	110908505	110908505	rs56786971	
ENSG00000168679	G	A	A	0.999333925399645
G/G	G/G	G/G	G/G	intron_variant 3.574
1	110908505	110908505	rs56786971	
ENSG00000168679	G	A	A	0.999333925399645
G/G	G/G	G/G	G/G	
1	110908505	110908505	rs56786971	
ENSG00000168679	G	A	A	0.999333925399645
G/G	G/G	G/G	G/G	intron_variant,NMD_transcript_variant 3.574
1	110908505	110908505	rs56786971	
ENSG00000273373	G	A	A	0.999333925399645
G/G	G/G	G/G	G/G	upstream_gene_variant 3.574
1	110915654	110915654	rs187764658	
ENSG00000168679	T	C	C	0.999872765443094
T/T	T/T	T/T	T/T	intron_variant 6.496
1	110915654	110915654	rs187764658	
ENSG00000168679	T	C	C	0.999872765443094
T/T	T/T	T/T	T/T	
1	110915654	110915654	rs187764658	
ENSG00000168679	T	C	C	0.999872765443094
T/T	T/T	T/T	T/T	intron_variant,NMD_transcript_variant 6.496
1	110915654	110915654	rs187764658	
ENSG00000168679	T	C	C	0.999872765443094
T/T	T/T	T/T	T/T	downstream_gene_variant 6.496
1	110915654	110915654	rs187764658	
ENSG00000273373	T	C	C	0.999872765443094
T/T	T/T	T/T	T/T	downstream_gene_variant 6.496
1	110917995	110917995	rs147951433	
ENSG00000168679	G	A	A	0.997811052598185
G/G	G/G	G/G	G/G	intron_variant 5.409
1	110917995	110917995	rs147951433	
ENSG00000168679	G	A	A	0.997811052598185
G/G	G/G	G/G	G/G	
1	110917995	110917995	rs147951433	
ENSG00000168679	G	A	A	0.997811052598185
G/G	G/G	G/G	G/G	3_prime_UTR_variant 5.409
1	110917995	110917995	rs147951433	

ENSG00000168679	G	A	A	0.997811052598185		
G/G	G/G	G/G	G/G	downstream_gene_variant	5.409	
1	110917995	110917995	rs147951433			
ENSG00000273373	G	A	A	0.997811052598185		
G/G	G/G	G/G	G/G	downstream_gene_variant	5.409	
1	110925242	110925242	rs568721418			
ENSG00000168679	T	C	C	0.999873096446701		
T/T	T/T	T/T	T/T	intron_variant	4.616	
1	110925242	110925242	rs568721418			
ENSG00000168679	T	C	C	0.999873096446701		
T/T	T/T	T/T	T/T			
intron_variant,NMD_transcript_variant				4.616		
1	110925242	110925242	rs568721418			
ENSG00000168679	T	C	C	0.999873096446701		
T/T	T/T	T/T	T/T	upstream_gene_variant	4.616	
1	110925242	110925242	rs568721418			
ENSG00000168679	T	C	C	0.999873096446701		
T/T	T/T	T/T	T/T			
intron_variant,non_coding_transcript_variant				4.616		
1	110925242	110925242	rs568721418			
ENSG00000224699	T	C	C	0.999873096446701		
T/T	T/T	T/T	T/T	upstream_gene_variant	4.616	
1	110928060	110928060	rs56738361			
ENSG00000168679	G	A	A	0.997651986292677		
G/G	G/G	G/G	G/G	intron_variant	4.137	
1	110928060	110928060	rs56738361			
ENSG00000168679	G	A	A	0.997651986292677		
G/G	G/G	G/G	G/G			
intron_variant,NMD_transcript_variant				4.137		
1	110928060	110928060	rs56738361			
ENSG00000168679	G	A	A	0.997651986292677		
G/G	G/G	G/G	G/G			
intron_variant,non_coding_transcript_variant				4.137		
1	110928060	110928060	rs56738361			
ENSG00000224699	G	A	A	0.997651986292677		
G/G	G/G	G/G	G/G			
intron_variant,non_coding_transcript_variant				4.137		
1	111032775	111032775	ENSG00000240194			
A	G	G	1	A/A	A/A	A/A
intron_variant,non_coding_transcript_variant				2.222		
1	111032775	111032775	ENSG00000235407			
A	G	G	1	A/A	A/A	A/A
non_coding_transcript_exon_variant				2.222		
1	111032775	111032775	ENSG00000240194			
A	G	G	1	A/A	A/A	A/A
downstream_gene_variant				2.222		
1	111071239	111071239	rs115007510			
C	T	T	0.999016372636121	C/C	C/C	
C/C				7.1		
1	112104164	112104164	ENSG00000116473			
A	G	G	1	A/A	A/A	A/A
intron_variant				3.876		
1	112104164	112104164	ENSG00000121933			
A	G	G	1	A/A	A/A	A/A

intron_variant 3.876							
1	112104164		112104164	.			A
G	G	1	A/A	A/A	A/A	A/A	
regulatory_region_variant 3.876							
1	112422674		112422674		rs148807299		
ENSG00000171385	A		G	G	0.99552437785678	A/A	
A/A	A/A	A/A	intron_variant 0.32				
1	112422674		112422674		rs148807299		.
A	G	G	0.99552437785678	A/A	A/A	A/A	
A/A	regulatory_region_variant 0.32						
1	112450488		112450488		rs180995412		
ENSG00000171385	C		G	G	0.999682861854624		
C/C	C/C	C/C	C/C	intron_variant 1.939			
1	112450488		112450488		rs180995412		
ENSG00000237556	C		G	G	0.999682861854624		
C/C	C/C	C/C	C/C	upstream_gene_variant 1.939			
1	113273321		113273321		rs571577120		
ENSG00000184599	T		C	C	0.999936309789185		
T/T	T/T	T/T	T/T	downstream_gene_variant 14.32			
1	113273321		113273321		rs571577120		.
T	C	C	0.999936309789185	T/T	T/T	T/T	
T/T	T/T	regulatory_region_variant 14.32					
1	113274744		113274744		ENSG00000184599		
A	G	G	1	A/A	A/A	A/A	A/A
downstream_gene_variant 1.833							
1	113274744		113274744		.		A
G	G	1	A/A	A/A	A/A	A/A	
regulatory_region_variant 1.833							
1	113429813		113429813		rs182867606		
ENSG00000228040	T		C	C	0.999872846334796		
T/T	T/T	T/T	T/T	downstream_gene_variant 3.045			
1	113431368		113431368		ENSG00000228040		
C	T	T	1	C/C	C/C	C/C	C/C
downstream_gene_variant 5.124							
1	113431378		113431378		rs1409991457		
ENSG00000228040	G		A	A	0.999968282161888		
G/G	G/G	G/G	G/G	downstream_gene_variant 3.697			
1	113431378		113431378		rs1409991457		.
G	A	A	0.999968282161888	G/G	G/G	G/G	
G/G	G/G	TF_binding_site_variant 3.697					
1	113432855		113432855		rs182388769		
ENSG00000228040	G		C	C	0.998921593504187		
G/G	G/G	G/G	G/G	downstream_gene_variant 1.528			
1	113432909		113432909		rs187367826		
ENSG00000228040	C		T	T	0.998922003804692		
C/C	C/C	C/C	C/C	downstream_gene_variant 3.426			
1	113439096		113439096		rs541465271		.
C	T	T	0.99891946863281	C/C	C/C	C/C	
C/C	intergenic_variant 5.416						
1	113447695		113447695		rs143992612		.
G	A	A	0.998445036811373	G/G	G/G	G/G	
G/G	G/G	regulatory_region_variant 5.961					
1	113447695		113447695		rs143992612		.
G	A	A	0.998445036811373	G/G	G/G	G/G	

G/G	G/G	intergenic_variant			5.961		
1	113453389		113453389			ENSG00000155380	
A	G	G	1	A/A	A/A	A/A	A/A
		downstream_gene_variant	0.152				
1	113453519		113453519			ENSG00000155380	
A	T	T	1	A/A	A/A	A/A	A/A
		downstream_gene_variant	2.207				
1	113461217		113461217			ENSG00000155380	
G	A	A	0.999587772704211			G/G	G/G
G/G	G/G	intron_variant	2.379				
1	113461217		113461217			ENSG00000229020	
G	A	A	0.999587772704211			G/G	G/G
G/G	G/G	upstream_gene_variant	2.379				
1	113461217		113461217			ENSG00000155380	
G	A	A	0.999587772704211			G/G	G/G
G/G	G/G	intron_variant,non_coding_transcript_variant					
			2.379				
1	113462236		113462236		rs186866669		
ENSG00000155380	T		C	C	0.999587798845837		
T/T	T/T	T/T	T/T	intron_variant	0.515		
1	113462236		113462236		rs186866669		
ENSG00000229020	T		C	C	0.999587798845837		
T/T	T/T	T/T	T/T	upstream_gene_variant	0.515		
1	113462236		113462236		rs186866669		
ENSG00000155380	T		C	C	0.999587798845837		
T/T	T/T	T/T	T/T				
		intron_variant,non_coding_transcript_variant				0.515	
1	113467737		113467737			ENSG00000155380	
T	A	A	1	T/T	T/T	T/T	T/T
		intron_variant	6.339				
1	113467737		113467737			ENSG00000229020	
T	A	A	1	T/T	T/T	T/T	T/T
		downstream_gene_variant	6.339				
1	113467737		113467737			ENSG00000155380	
T	A	A	1	T/T	T/T	T/T	T/T
		downstream_gene_variant	6.339				
1	113467737		113467737			ENSG00000155380	
T	A	A	1	T/T	T/T	T/T	T/T
		upstream_gene_variant	6.339				
1	113467737		113467737			.	T
A	A	1	T/T	T/T	T/T	T/T	
		regulatory_region_variant	6.339				
1	113469967		113469967			ENSG00000155380	
C	T	T	0.999549665465775			C/C	C/C
C/C	C/C	intron_variant	2.282				
1	113469967		113469967			ENSG00000229020	
C	T	T	0.999549665465775			C/C	C/C
C/C	C/C	downstream_gene_variant	2.282				
1	113469967		113469967			ENSG00000155380	
C	T	T	0.999549665465775			C/C	C/C
C/C	C/C	downstream_gene_variant	2.282				
1	113469967		113469967			ENSG00000155380	
C	T	T	0.999549665465775			C/C	C/C
C/C	C/C	upstream_gene_variant	2.282				

1	113470441		113470441			ENSG00000155380
A	C	C	0.99958764194633	A/A		A/A A/A
A/A	intron_variant		1.347			
1	113470441		113470441			ENSG00000229020
A	C	C	0.99958764194633	A/A		A/A A/A
A/A	downstream_gene_variant		1.347			
1	113470441		113470441			ENSG00000155380
A	C	C	0.99958764194633	A/A		A/A A/A
A/A	downstream_gene_variant		1.347			
1	113471026		113471026			ENSG00000155380
A	C	C	1	A/A	A/A	A/A A/A
	intron_variant		2.178			
1	113471026		113471026			ENSG00000229020
A	C	C	1	A/A	A/A	A/A A/A
	downstream_gene_variant		2.178			
1	113471026		113471026			ENSG00000155380
A	C	C	1	A/A	A/A	A/A A/A
	downstream_gene_variant		2.178			
1	113471302		113471302			ENSG00000155380
T	C	C	1	T/T	T/T	T/T T/T
	intron_variant		1.13			
1	113471302		113471302			ENSG00000229020
T	C	C	1	T/T	T/T	T/T T/T
	downstream_gene_variant		1.13			
1	113471302		113471302			ENSG00000155380
T	C	C	1	T/T	T/T	T/T T/T
	downstream_gene_variant		1.13			
1	113472055		113472055		rs546804901	
ENSG00000155380	G		A	A	0.999556006596473	
G/G	G/G	G/G	G/G		intron_variant	1.733
1	113472055		113472055		rs546804901	
ENSG00000155380	G		A	A	0.999556006596473	
G/G	G/G	G/G	G/G			
	intron_variant,non_coding_transcript_variant					1.733
1	113476228		113476228			ENSG00000155380
G	A	A	0.999587668104542			G/G G/G
G/G	G/G		intron_variant		2.27	
1	113476228		113476228			ENSG00000155380
G	A	A	0.999587668104542			G/G G/G
G/G	G/G		intron_variant,non_coding_transcript_variant			
			2.27			
1	113477600		113477600		rs536715661	
ENSG00000155380	G		C	C	0.999555696604253	
G/G	G/G	G/G	G/G		intron_variant	0.119
1	113477600		113477600		rs536715661	
ENSG00000155380	G		C	C	0.999555696604253	
G/G	G/G	G/G	G/G			
	intron_variant,non_coding_transcript_variant					0.119
1	113478773		113478773		rs553295987	
ENSG00000155380	G		C	C	0.999968278137292	
G/G	G/G	G/G	G/G		intron_variant	1.764
1	113478773		113478773		rs553295987	
ENSG00000155380	G		C	C	0.999968278137292	
G/G	G/G	G/G	G/G		upstream_gene_variant	1.764

1	113478773		113478773	rs553295987		
ENSG00000155380	G		C	C	0.999968278137292	
G/G	G/G	G/G	G/G			
intron_variant,non_coding_transcript_variant					1.764	
1	113487828		113487828	ENSG00000155380		
T	C	C	1	T/T	T/T	T/T
intron_variant					0.935	
1	113487828		113487828	ENSG00000155380		
T	C	C	1	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant					0.935	
1	113489721		113489721	ENSG00000155380		
T	C	C	0.999587824984147	T/T	T/T	
T/T	T/T	intron_variant		0.448		
1	113489721		113489721	ENSG00000155380		
T	C	C	0.999587824984147	T/T	T/T	
T/T	T/T	intron_variant,non_coding_transcript_variant		0.448		
1	113490956		113490956	rs553981737		
ENSG00000155380	A		G	G	0.998570339306138	
A/A	A/A	A/A	A/A	intron_variant		3.973
1	113490956		113490956	rs553981737		
ENSG00000155380	A		G	G	0.998570339306138	
A/A	A/A	A/A	A/A			
intron_variant,non_coding_transcript_variant					3.973	
1	113495474		113495474	rs574306252		
ENSG00000155380	C		T	T	0.998033618775769	
C/C	C/C	C/C	C/C	intron_variant		3.834
1	113495474		113495474	rs574306252		
ENSG00000226419	C		T	T	0.998033618775769	
C/C	C/C	C/C	C/C	upstream_gene_variant		3.834
1	113495474		113495474	rs574306252		
ENSG00000155380	C		T	T	0.998033618775769	
C/C	C/C	C/C	C/C			
intron_variant,non_coding_transcript_variant					3.834	
1	113495474		113495474	rs574306252		
C	T	T	0.998033618775769	C/C	C/C	
C/C	C/C	regulatory_region_variant		3.834		
1	113497757		113497757	rs551262547		
ENSG00000155380	G		A	A	0.999968286185462	
G/G	G/G	G/G	G/G	intron_variant		6.475
1	113497757		113497757	rs551262547		
ENSG00000226419	G		A	A	0.999968286185462	
G/G	G/G	G/G	G/G	upstream_gene_variant		6.475
1	113497757		113497757	rs551262547		
ENSG00000155380	G		A	A	0.999968286185462	
G/G	G/G	G/G	G/G			
intron_variant,non_coding_transcript_variant					6.475	
1	113497757		113497757	rs551262547		
G	A	A	0.999968286185462	G/G	G/G	
G/G	G/G	regulatory_region_variant		6.475		
1	113521180		113521180	rs114477819		
ENSG00000226419	T		C	C	0.995144090389742	
T/T	T/T	T/T	T/T			
intron_variant,non_coding_transcript_variant					1.116	

1	113525820		113525820		rs116266728		
ENSG00000226419	T		C	C	0.995143782136736		
T/T	T/T	T/T	T/T				
intron_variant,non_coding_transcript_variant					3.612		
1	113525820		113525820		rs116266728	.	
T	C	C		0.995143782136736	T/T	T/T	
T/T	T/T				regulatory_region_variant	3.612	
1	113526460		113526460		rs150481799		
ENSG00000226419	C		G	G	0.995142857142857		
C/C	C/C	C/C	C/C				
intron_variant,non_coding_transcript_variant					5.294		
1	113526460		113526460		rs150481799	.	
C	G	G		0.995142857142857	C/C	C/C	
C/C	C/C				regulatory_region_variant	5.294	
1	113527996		113527996		rs116484873		
ENSG00000226419	A		G	G	0.995147478591817		
A/A	A/A	A/A	A/A				
intron_variant,non_coding_transcript_variant					1.554		
1	113528483		113528483		rs138170925		
ENSG00000226419	C		A	A	0.995138226882745		
C/C	C/C	C/C	C/C				
intron_variant,non_coding_transcript_variant					3.057		
1	113528650		113528650		rs116001269		
ENSG00000226419	A		T	T	0.995145939086294		
A/A	A/A	A/A	A/A				
intron_variant,non_coding_transcript_variant					0.248		
1	113554161		113554161		rs562537743		
ENSG00000236066	A		G	G	0.999841219434741		
A/A	A/A	A/A	A/A				
intron_variant,non_coding_transcript_variant					12.49		
1	113554161		113554161		rs562537743		
ENSG00000238198	A		G	G	0.999841219434741		
A/A	A/A	A/A	A/A		downstream_gene_variant	12.49	
1	113554867		113554867		ENSG00000236066		
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant,non_coding_transcript_variant					0.876		
1	113554867		113554867		ENSG00000238198		
C	T	T	1	C/C	C/C	C/C	C/C
non_coding_transcript_exon_variant					0.876		
1	113554867		113554867		.	C	
T	T	1	C/C	C/C	C/C	C/C	
regulatory_region_variant					0.876		
1	113555008		113555008		ENSG00000236066		
C	A	A	1	C/C	C/C	C/C	C/C
intron_variant,non_coding_transcript_variant					7.447		
1	113555008		113555008		ENSG00000238198		
C	A	A	1	C/C	C/C	C/C	C/C
non_coding_transcript_exon_variant					7.447		
1	113555008		113555008		.	C	
A	A	1	C/C	C/C	C/C	C/C	
regulatory_region_variant					7.447		
1	113555404		113555404		ENSG00000236066		
T	C	C	1	T/T	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant					5.584		

1	113555404		113555404			ENSG00000238198	
T	C	C	1	T/T	T/T	T/T	T/T
non_coding_transcript_exon_variant						5.584	
1	113555404		113555404			.	T
C	C	1	T/T	T/T	T/T	T/T	
regulatory_region_variant						5.584	
1	113555706		113555706			ENSG00000236066	
C	A	A	1	C/C	C/C	C/C	C/C
intron_variant,non_coding_transcript_variant						15.56	
1	113555706		113555706			ENSG00000238198	
C	A	A	1	C/C	C/C	C/C	C/C
non_coding_transcript_exon_variant						15.56	
1	113555706		113555706			.	C
A	A	1	C/C	C/C	C/C	C/C	
regulatory_region_variant						15.56	
1	113559966		113559966			ENSG00000236066	
T	C	C	1	T/T	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant						2.314	
1	113559966		113559966			ENSG00000238198	
T	C	C	1	T/T	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant						2.314	
1	113562193		113562193		rs1402192100		
ENSG00000236066	C	T	T	1	C/C	C/C	C/C
C/C C/C intron_variant,non_coding_transcript_variant						6.919	
1	113562193		113562193		rs1402192100		
ENSG00000238198	C	T	T	1	C/C	C/C	C/C
C/C C/C intron_variant,non_coding_transcript_variant						6.919	
3	77759751	77759751	rs143136963		.	T	C
C	0.999492353575735		T/T	T/T	T/T	T/T	T/T
intergenic_variant						0.408	
3	77760672	77760672	rs181645774		.	C	T
T	0.999459699974574		C/C	C/C	C/C	C/C	C/C
intergenic_variant						0.77	
3	77897885	77897885	rs534760648		.	T	C
C	0.996280991735537		T/T	T/T	T/T	T/T	T/T
regulatory_region_variant						1.027	
3	77897885	77897885	rs534760648		.	T	C
C	0.996280991735537		T/T	T/T	T/T	T/T	T/T
intergenic_variant						1.027	
3	77898450	77898450	rs144453177		.	T	A
A	0.996384064053722		T/T	T/T	T/T	T/T	T/T
intergenic_variant						0.58	
3	77898497	77898497	rs190705776		.	A	G
G	0.99629345603272	A/A	A/A	A/A	A/A	A/A	
intergenic_variant						0.141	
3	77899201	77899201	rs76002741		.	A	G
G	0.996306908627826		A/A	A/A	A/A	A/A	A/A
intergenic_variant						0.775	
3	77899709	77899709	rs191659334		.	T	A
A	0.996319096274672		T/T	T/T	T/T	T/T	T/T
intergenic_variant						0.676	
3	77899717	77899717	rs184864418		.	C	A

A	0.99631746031746	C/C	C/C	C/C	C/C	
intergenic_variant	0.025					
3	77899903	77899903	rs184633895	.	A	G
G	0.996347583052785		A/A	A/A	A/A	A/A
intergenic_variant	1.376					
3	77900076	77900076	rs78782536	.	T	A
A	0.996317226490571		T/T	T/T	T/T	T/T
intergenic_variant	1.662					
3	77901839	77901839	rs151070706	.	T	G
G	0.996286185881158		T/T	T/T	T/T	T/T
intergenic_variant	3.135					
3	77902741	77902741	rs534189920	.	A	C
C	0.996199493265769		A/A	A/A	A/A	A/A
intergenic_variant	0.283					
3	77904239	77904239	rs115270105	.	A	C
C	0.996315822905418		A/A	A/A	A/A	A/A
intergenic_variant	0.718					
3	77906456	77906456	rs189385822	.	C	T
T	0.996309963099631		C/C	C/C	C/C	C/C
intergenic_variant	1.779					
3	77910070	77910070	rs183770514	.	T	A
A	0.996219101480587		T/T	T/T	T/T	T/T
intergenic_variant	0.951					
3	77911444	77911444	rs185489392	.	G	T
T	0.996375890132248		G/G	G/G	G/G	G/G
intergenic_variant	1.036					
3	77912617	77912617	rs558534876	.	G	A
A	0.996312074775863		G/G	G/G	G/G	G/G
intergenic_variant	1.164					
3	77918102	77918102	rs191656404	.	C	T
T	0.996284062758051		C/C	C/C	C/C	C/C
regulatory_region_variant	5.497					
3	77918102	77918102	rs191656404	.	C	T
T	0.996284062758051		C/C	C/C	C/C	C/C
intergenic_variant	5.497					
3	77919751	77919751	rs115617142	.	T	C
C	0.99629677336253		T/T	T/T	T/T	T/T
intergenic_variant	4.807					
3	77925389	77925389	rs183483553	.	C	T
T	0.99638003302426		C/C	C/C	C/C	C/C
intergenic_variant	1.238					
3	77928584	77928584	rs78462359	.	G	T
T	0.99634619050645		G/G	G/G	G/G	G/G
intergenic_variant	0.83					
3	77930441	77930441	rs189159259	.	C	T
T	0.99650394101195		C/C	C/C	C/C	C/C
intergenic_variant	1.006					
3	77932302	77932302	rs114300104	.	C	T
T	0.996463616668791		C/C	C/C	C/C	C/C
intergenic_variant	1.403					
3	77933266	77933266	rs570737472	.	T	C
C	0.99646766802444		T/T	T/T	T/T	T/T
intergenic_variant	0.805					
3	77933802	77933802	rs116709889	.	A	G

G	0.996469690223268	A/A	A/A	A/A	A/A
intergenic_variant	0.438				
3	77934007 77934007	rs115266291	.	G	C
C	0.996498822331148	G/G	G/G	G/G	G/G
intergenic_variant	1.331				
3	77935455 77935455	rs114551323	.	G	C
C	0.996469465648855	G/G	G/G	G/G	G/G
intergenic_variant	0.788				
3	78206212 78206212	rs142092751	ENSG00000222574	T	
C	C	0.995842061829493	T/T	T/T	T/T
T/T	upstream_gene_variant	4.545			
3	78229583 78229583	.	T	C	C
1	T/T	T/T	T/T	T/T	intergenic_variant
1.144					
3	78238598 78238598	.	T	C	C
1	T/T	T/T	T/T	T/T	intergenic_variant
0.239					
3	78240961 78240961	.	T	C	C
1	T/T	T/T	T/T	T/T	intergenic_variant
1.093					
3	78243673 78243673	.	C	T	T
1	C/C	C/C	C/C	C/C	intergenic_variant
1.159					
3	78551178 78551178	.	G	A	A
1	G/G	G/G	G/G	G/G	intergenic_variant
2.139					
3	78551359 78551359	rs148706404	.	C	T
T	0.996761699155502	C/C	C/C	C/C	C/C
intergenic_variant	4.76				
3	80485640 80485640	rs985978655	.	T	A
A	0.999936390814834	T/T	T/T	T/T	T/T
intergenic_variant	1.719				
3	80486948 80486948	rs968937659	ENSG00000242586	T	
A	A	0.999936475670182	T/T	T/T	T/T
T/T	upstream_gene_variant	0.579			
3	80487646 80487646	rs998365011	ENSG00000242586	G	
T	T	0.999936419125127	G/G	G/G	G/G
G/G	upstream_gene_variant	2.055			
3	80495637 80495637	rs953964470	ENSG00000242586	A	
C	C	0.99993624075491	A/A	A/A	A/A
downstream_gene_variant	3.798				
3	80497622 80497622	rs983875135	.	G	C
C	0.99993627326026	G/G	G/G	G/G	G/G
intergenic_variant	0.482				
3	80499599 80499599	rs1005083184	.	C	T
T	0.999936317901038	C/C	C/C	C/C	C/C
intergenic_variant	1.504				
3	80502916 80502916	rs1048474176	.	A	G
G	0.999936483739837	A/A	A/A	A/A	A/A
intergenic_variant	3.62				
3	81327602 81327602	rs73855076	ENSG00000241593	C	
T	T	0.995241418691707	C/C	C/C	C/C
C/C	intron_variant,non_coding_transcript_variant	4.867			
3	81336467 81336467	rs73855084	ENSG00000241593	G	

T	T	0.996413609242097		G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant					0.534
3	81427887	81427887	rs1047547836	.	T	C
C	0.999893624565634		T/T	T/T	T/T	T/T
intergenic_variant		0.889				
3	82290277	82290277		ENSG00000239440	T	C
C	1	T/T	T/T	T/T	T/T	
intron_variant,non_coding_transcript_variant					1.486	
3	82290400	82290400		ENSG00000239440	T	C
C	1	T/T	T/T	T/T	T/T	
intron_variant,non_coding_transcript_variant					2.397	
3	82291168	82291168	rs1187458759	ENSG00000239440	A	A
G	G	1	A/A	A/A	A/A	A/A
intron_variant,non_coding_transcript_variant					0.397	
3	82306878	82306878		ENSG00000239440	T	A
A	1	T/T	T/T	T/T	T/T	
intron_variant,non_coding_transcript_variant					1.862	
3	82609645	82609645	.	A	T	T
1	A/A	A/A	A/A	A/A	intergenic_variant	
1.647						
3	82612305	82612305	.	A	G	G
1	A/A	A/A	A/A	A/A	intergenic_variant	
12.59						
3	82616099	82616099	rs986262652	.	T	G
G	0.999968280149718		T/T	T/T	T/T	T/T
intergenic_variant		0.115				
3	85724355	85724355		ENSG00000175161	T	C
C	1	T/T	T/T	T/T	T/T	intron_variant
1.697						
3	85724497	85724497		ENSG00000175161	T	C
C	1	T/T	T/T	T/T	T/T	intron_variant
3.355						
3	85730015	85730015		ENSG00000175161	G	C
C	1	G/G	G/G	G/G	G/G	intron_variant
12.92						
3	85739412	85739412		ENSG00000175161	G	A
A	1	G/G	G/G	G/G	G/G	intron_variant
4.783						
3	85739540	85739540		ENSG00000175161	T	C
C	1	T/T	T/T	T/T	T/T	intron_variant
0.159						
3	85739753	85739753		ENSG00000175161	G	A
A	1	G/G	G/G	G/G	G/G	intron_variant
2.234						
3	85740645	85740645		ENSG00000175161	G	T
T	1	G/G	G/G	G/G	G/G	intron_variant
1.5						
3	85741302	85741302		ENSG00000175161	A	G
G	1	A/A	A/A	A/A	A/A	intron_variant
1.694						
3	85745914	85745914		ENSG00000175161	G	A
A	1	G/G	G/G	G/G	G/G	intron_variant
2.004						
3	85750144	85750144		ENSG00000175161	A	T

T	1	A/A	A/A	A/A	A/A	intron_variant
1.896						
3	85754604	85754604		ENSG00000175161	G	A
A	1	G/G	G/G	G/G	G/G	intron_variant
0.511						
3	85758716	85758716		ENSG00000175161	T	C
C	1	T/T	T/T	T/T	T/T	intron_variant
17.15						
3	85758716	85758716		.	T	C
1	T/T	T/T	T/T	T/T		C
17.15						
3	85759005	85759005		ENSG00000175161	A	G
G	1	A/A	A/A	A/A	A/A	intron_variant
14.93						
3	85759005	85759005		.	A	G
1	A/A	A/A	A/A	A/A		G
14.93						
3	85764213	85764213		ENSG00000175161	A	T
T	1	A/A	A/A	A/A	A/A	intron_variant
0.658						
3	85768437	85768437	rs570640547	ENSG00000175161		C
T	T	0.999714629970195		C/C	C/C	C/C
C/C		intron_variant	3.144			
3	85768826	85768826	rs555792645	ENSG00000175161		C
T	T	0.999713886063072		C/C	C/C	C/C
C/C		intron_variant	1.177			
3	85770231	85770231	rs559224401	ENSG00000175161		G
A	A	0.999714593771802		G/G	G/G	G/G
G/G		intron_variant	2.806			
3	85771043	85771043	rs547248737	ENSG00000175161		G
A	A	0.999714467005076		G/G	G/G	G/G
G/G		intron_variant	0.352			
3	85771043	85771043	rs547248737	ENSG00000175161		G
A	A	0.999714467005076		G/G	G/G	G/G
G/G		upstream_gene_variant	0.352			
3	85771043	85771043	rs547248737	.	G	A
A	0.999714467005076		G/G	G/G	G/G	G/G
		regulatory_region_variant	0.352			
3	85771202	85771202	rs577869200	ENSG00000175161		C
T	T	0.999714122355632		C/C	C/C	C/C
C/C		intron_variant	2.365			
3	85771202	85771202	rs577869200	ENSG00000175161		C
T	T	0.999714122355632		C/C	C/C	C/C
C/C		upstream_gene_variant	2.365			
3	85771202	85771202	rs577869200	.	C	T
T	0.999714122355632		C/C	C/C	C/C	C/C
		regulatory_region_variant	2.365			
3	85776502	85776502	rs575839778	ENSG00000175161		C
T	T	0.99971434012569	C/C	C/C	C/C	C/C
		intron_variant	3.663			
3	85782136	85782136	rs527265347	ENSG00000175161		A
G	G	0.999714467005076		A/A	A/A	A/A
A/A		intron_variant	0.783			
3	88741899	88741899	.	G	A	A

1	G/G	G/G	G/G	G/G		intergenic_variant		
2.034								
3	88990791	88990791	rs115824399	.	A	G		
G	0.995614313862582		A/A	A/A	A/A	A/A		
intergenic_variant			3.434					
7	110342115		110342115			ENSG00000184903		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant	0.414							
7	110342115		110342115			ENSG00000184903		
C	T	T	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant						0.414		
7	110411764		110411764		rs541017065			
ENSG00000184903	A	C	C		0.998283861946228			
A/A	A/A	A/A	A/A	intron_variant	5.102			
7	110411764		110411764		rs541017065			
ENSG00000184903	A	C	C		0.998283861946228			
A/A	A/A	A/A	A/A					
intron_variant,non_coding_transcript_variant						5.102		
7	110413080		110413080		rs189933685			
ENSG00000184903	T	C	C		0.998278719877598			
T/T	T/T	T/T	T/T	intron_variant	1.273			
7	110413080		110413080		rs189933685			
ENSG00000184903	T	C	C		0.998278719877598			
T/T	T/T	T/T	T/T					
intron_variant,non_coding_transcript_variant						1.273		
7	110484030		110484030		rs1478034051			
ENSG00000184903	A	C	C		0.999968272098483			
A/A	A/A	A/A	A/A	intron_variant	3.812			
7	110484030		110484030		rs1478034051			
ENSG00000184903	A	C	C		0.999968272098483			
A/A	A/A	A/A	A/A					
intron_variant,non_coding_transcript_variant						3.812		
7	110484030		110484030		rs1478034051	.		
A	C	C	0.999968272098483		A/A	A/A		
A/A	A/A	regulatory_region_variant	3.812					
7	110563788		110563788			ENSG00000184903		
T	A	A	1	T/T	T/T	T/T	T/T	
intron_variant	5.172							
7	110563788		110563788			ENSG00000221279		
T	A	A	1	T/T	T/T	T/T	T/T	
upstream_gene_variant	5.172							
7	110563788		110563788			ENSG00000184903		
T	A	A	1	T/T	T/T	T/T	T/T	
intron_variant,non_coding_transcript_variant						5.172		
7	110563788		110563788		.	T		
A	A	1	T/T	T/T	T/T	T/T		
regulatory_region_variant	5.172							
7	110563840		110563840			ENSG00000184903		
T	C	C	1	T/T	T/T	T/T	T/T	
intron_variant	1.079							
7	110563840		110563840			ENSG00000221279		
T	C	C	1	T/T	T/T	T/T	T/T	
upstream_gene_variant	1.079							
7	110563840		110563840			ENSG00000184903		

T	C	C	1	T/T	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant						1.079	
7	110563840		110563840			.	T
C	C	1	T/T	T/T	T/T	T/T	
regulatory_region_variant						1.079	
7	110568831		110568831			ENSG00000184903	
G	C	C	1	G/G	G/G	G/G	G/G
intron_variant						0.445	
7	110568831		110568831			ENSG00000221279	
G	C	C	1	G/G	G/G	G/G	G/G
downstream_gene_variant						0.445	
7	110568831		110568831			ENSG00000184903	
G	C	C	1	G/G	G/G	G/G	G/G
intron_variant,non_coding_transcript_variant						0.445	
7	110570282		110570282		rs549454303		
ENSG00000184903	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant		1.984			
7	110570282		110570282		rs549454303		
ENSG00000221279	T	C	C	1	T/T	T/T	
T/T	T/T	downstream_gene_variant		1.984			
7	110570282		110570282		rs549454303		
ENSG00000184903	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant,non_coding_transcript_variant		1.984			
7	113361210		113361210		rs147536214	.	
G	C	C	0.997742448330684		G/G	G/G	
G/G	G/G	intergenic_variant		0.58			
7	113390755		113390755		rs1035575193	.	
T	G	G	0.999968260013966		T/T	T/T	
T/T	T/T	intergenic_variant		7.414			
7	113734005		113734005		rs113204959		
ENSG00000128573	T	C	C	0.997617534942821			
T/T	T/T	T/T	T/T	intron_variant		0.736	
7	113734005		113734005		rs113204959		
ENSG00000128573	T	C	C	0.997617534942821			
T/T	T/T	T/T	T/T	intron_variant,NMD_transcript_variant		0.736	
7	113734005		113734005		rs113204959		
ENSG00000128573	T	C	C	0.997617534942821			
T/T	T/T	T/T	T/T	intron_variant,non_coding_transcript_variant		0.736	
7	114118906		114118906		rs894490018		
ENSG00000128573	C	A	A	0.999968211583699			
C/C	C/C	C/C	C/C	intron_variant		2.691	
7	114118906		114118906		rs894490018		
ENSG00000128573	C	A	A	0.999968211583699			
C/C	C/C	C/C	C/C	intron_variant,NMD_transcript_variant		2.691	
7	114118906		114118906		rs894490018		
ENSG00000128573	C	A	A	0.999968211583699			
C/C	C/C	C/C	C/C	intron_variant,non_coding_transcript_variant		2.691	
7	114310393		114310393		ENSG00000128573		
G	T	T	1	G/G	G/G	G/G	G/G

intron_variant		3.813					
7	114310393	114310393		ENSG00000128573			
G	T	T	1	G/G	G/G	G/G	
downstream_gene_variant		3.813					
7	114310393	114310393		ENSG00000128573			
G	T	T	1	G/G	G/G	G/G	
intron_variant,NMD_transcript_variant		3.813					
7	114345675	114345675		rs1037700010	.		
T	G	G	0.999936544196967	T/T	T/T		
T/T	T/T	intergenic_variant	2.393				
7	114460158	114460158		rs10264546	.		
G	T	T	0.997493654822335	G/G	G/G		
G/G	G/G	regulatory_region_variant	2.129				
7	114460158	114460158		rs10264546	.		
G	T	T	0.997493654822335	G/G	G/G		
G/G	G/G	intergenic_variant	2.129				
7	114462035	114462035		rs143871235	.		
G	A	A	0.997892359804291	G/G	G/G		
G/G	G/G	regulatory_region_variant	4.543				
7	114462035	114462035		rs143871235	.		
G	A	A	0.997892359804291	G/G	G/G		
G/G	G/G	intergenic_variant	4.543				
7	116948477	116948477		rs897147529			
ENSG00000105989	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant	16.48				
7	116948477	116948477		rs897147529			
ENSG00000238202	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant,non_coding_transcript_variant	16.48				
7	116948477	116948477		rs897147529			
ENSG00000105989	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant,NMD_transcript_variant	16.48				
7	117127856	117127856		rs543447891			
ENSG00000001626	A	G	G	0.999904707451877			
A/A	A/A	A/A	A/A	intron_variant	0.972		
7	117127856	117127856		rs543447891			
ENSG00000237974	A	G	G	0.999904707451877			
A/A	A/A	A/A	A/A	non_coding_transcript_exon_variant	0.972		
7	117127856	117127856		rs543447891			
ENSG00000001626	A	G	G	0.999904707451877			
A/A	A/A	A/A	A/A				
intron_variant,non_coding_transcript_variant		0.972					
7	117127856	117127856		rs543447891	.		
A	G	G	0.999904707451877	A/A	A/A		
A/A	A/A	regulatory_region_variant	0.972				
7	117207396	117207396		ENSG00000001626			
C	T	T	1	C/C	C/C	C/C	
intron_variant		3.172					
7	117207396	117207396		ENSG00000232661			
C	T	T	1	C/C	C/C	C/C	
upstream_gene_variant		3.172					
7	117207396	117207396		ENSG00000001626			
C	T	T	1	C/C	C/C	C/C	

intron_variant,non_coding_transcript_variant						3.172	
7	117213267		117213267			ENSG0000001626	
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant						10.65	
7	117213267		117213267			ENSG0000001626	
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant,non_coding_transcript_variant						10.65	
7	117223052		117223052			ENSG0000001626	
T	G	G	1	T/T	T/T	T/T	T/T
intron_variant						0.147	
7	117223052		117223052			ENSG00000234001	
T	G	G	1	T/T	T/T	T/T	T/T
downstream_gene_variant						0.147	
7	117223052		117223052			ENSG0000001626	
T	G	G	1	T/T	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant						0.147	
7	117707341		117707341			.	C
T	T	1	C/C	C/C	C/C	C/C	
intergenic_variant						5.714	
7	118260119		118260119		rs182463777	.	
T	C	C	0.997142131334942			T/T	T/T
T/T	T/T		intergenic_variant		4.068		
7	118324107		118324107			.	A
G	G	1	A/A	A/A	A/A	A/A	
intergenic_variant						2.043	
7	118816963		118816963		rs191997757		
ENSG00000270516	T		C	C	0.996605869445968		
T/T	T/T	T/T	T/T	downstream_gene_variant	1.56		
7	118818224		118818224		rs140961340		
ENSG00000270516	T		A	A	0.99682640431609	T/T	
T/T	T/T	T/T	downstream_gene_variant	6.843			
7	118818224		118818224		rs140961340	.	
T	A	A	0.99682640431609	T/T	T/T	T/T	
T/T	regulatory_region_variant		6.843				
7	119985611		119985611			ENSG00000184408	
C	G	G	1	C/C	C/C	C/C	C/C
intron_variant						0.114	
7	120148704		120148704			ENSG00000184408	
G	A	A	1	G/G	G/G	G/G	G/G
intron_variant						3.08	
7	120149721		120149721			ENSG00000184408	
T	C	C	1	T/T	T/T	T/T	T/T
intron_variant						0.209	
7	120150746		120150746			ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant						2.04	
7	120151290		120151290			ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant						4.852	
7	120151966		120151966			ENSG00000184408	
G	A	A	1	G/G	G/G	G/G	G/G
intron_variant						0.474	
7	120153608		120153608			ENSG00000184408	
A	T	T	1	A/A	A/A	A/A	A/A

intron_variant	3.171						
7	120154469	120154469				ENSG00000184408	
A	C	C	1	A/A	A/A	A/A	A/A
intron_variant	1.877						
7	120156003	120156003				ENSG00000184408	
G	A	A	1	G/G	G/G	G/G	G/G
intron_variant	0.621						
7	120156935	120156935				ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant	3.104						
7	120158468	120158468				ENSG00000184408	
C	G	G	1	C/C	C/C	C/C	C/C
intron_variant	0.133						
7	120159193	120159193				ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant	1.485						
7	120159269	120159269			rs1455833886		
ENSG00000184408	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant	3.989				
7	120161835	120161835				ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant	0.757						
7	120161857	120161857			rs939781521		
ENSG00000184408	T	C	C	1	T/T	T/T	
T/T	T/T	intron_variant	0.477				
7	120161864	120161864				ENSG00000184408	
C	T	T	1	C/C	C/C	C/C	C/C
intron_variant	5.761						
7	120162294	120162294				ENSG00000184408	
G	A	A	1	G/G	G/G	G/G	G/G
intron_variant	2.383						
7	120162440	120162440				ENSG00000184408	
C	G	G	1	C/C	C/C	C/C	C/C
intron_variant	9.967						
7	120164968	120164968			rs1292130440		
ENSG00000184408	T	G	G	0.999968260013966			
T/T	T/T	T/T	T/T	intron_variant	3.549		
7	120164968	120164968			rs1292130440		
T	G	G	0.999968260013966		T/T	T/T	
T/T	T/T	regulatory_region_variant	3.549				
7	120166540	120166540				ENSG00000184408	
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant	1.175						
7	120167630	120167630				ENSG00000184408	
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant	2.272						
7	120168173	120168173				ENSG00000184408	
T	C	C	1	T/T	T/T	T/T	T/T
intron_variant	13.08						
7	120168267	120168267				ENSG00000184408	
A	T	T	1	A/A	A/A	A/A	A/A
intron_variant	6.348						
7	120168513	120168513				ENSG00000184408	
A	C	C	1	A/A	A/A	A/A	A/A

intron_variant	1.34						
7	120168539	120168539			ENSG00000184408		
C	G	G	1	C/C	C/C	C/C	C/C
intron_variant	7.519						
7	120169201	120169201			ENSG00000184408		
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant	5.01						
7	120171648	120171648			ENSG00000184408		
C	G	G	1	C/C	C/C	C/C	C/C
intron_variant	0.374						
7	120172107	120172107			ENSG00000184408		
A	T	T	1	A/A	A/A	A/A	A/A
intron_variant	7.517						
7	120172456	120172456			ENSG00000184408		
G	A	A	1	G/G	G/G	G/G	G/G
intron_variant	1.292						
7	120172826	120172826			rs776503749		
ENSG00000184408	G	A	A	1	G/G	G/G	
G/G	G/G	intron_variant	0.251				
7	120173602	120173602			ENSG00000184408		
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant	1.946						
7	120173632	120173632			ENSG00000184408		
A	T	T	1	A/A	A/A	A/A	A/A
intron_variant	3.505						
7	120173902	120173902			ENSG00000184408		
A	G	G	1	A/A	A/A	A/A	A/A
intron_variant	1.96						
7	120643807	120643807			rs147322384		
ENSG00000106034	G	T	T	0.998218489533626			
G/G	G/G	G/G	G/G	intron_variant	0.604		
7	120643807	120643807			rs147322384		
ENSG00000106034	G	T	T	0.998218489533626			
G/G	G/G	G/G	G/G				
intron_variant,non_coding_transcript_variant					0.604		
7	120643807	120643807			rs147322384		
ENSG00000106034	G	T	T	0.998218489533626			
G/G	G/G	G/G	G/G				
intron_variant,NMD_transcript_variant					0.604		
7	120920628	120920628			rs530155400		
ENSG00000106034	A	G	G	0.999842022116904			
A/A	A/A	A/A	A/A	intron_variant	7.857		
7	121260396	121260396			rs75119578		
T	C	C	0.997138132790639		T/T	T/T	
T/T	T/T	intergenic_variant			13.08		
7	121756425	121756425			rs73426019		
ENSG00000008311	A	C	C	0.995937281787596			
A/A	A/A	A/A	A/A				
intron_variant,NMD_transcript_variant					4.646		
7	121756425	121756425			rs73426019		
ENSG00000008311	A	C	C	0.995937281787596			
A/A	A/A	A/A	A/A	intron_variant	4.646		
7	121756425	121756425			rs73426019		
ENSG00000008311	A	C	C	0.995937281787596			

A/A	A/A	A/A	A/A			
intron_variant,non_coding_transcript_variant				4.646		
7	121766397		121766397	rs560717101		
ENSG00000008311	A		G	G	0.999904840449153	
A/A	A/A	A/A	A/A			
intron_variant,NMD_transcript_variant				7.367		
7	121766397		121766397	rs560717101		
ENSG00000008311	A		G	G	0.999904840449153	
A/A	A/A	A/A	A/A	intron_variant	7.367	
7	121766397		121766397	rs560717101		
ENSG00000008311	A		G	G	0.999904840449153	
A/A	A/A	A/A	A/A			
intron_variant,non_coding_transcript_variant				7.367		
7	121770474		121770474	rs182276803		
ENSG00000008311	T		C	C	0.999904719557899	
T/T	T/T	T/T	T/T			
intron_variant,NMD_transcript_variant				1.197		
7	121770474		121770474	rs182276803		
ENSG00000008311	T		C	C	0.999904719557899	
T/T	T/T	T/T	T/T	intron_variant	1.197	
7	121770474		121770474	rs182276803		
ENSG00000008311	T		C	C	0.999904719557899	
T/T	T/T	T/T	T/T			
intron_variant,non_coding_transcript_variant				1.197		
7	121774214		121774214	rs185256474		
ENSG00000008311	G		A	A	0.999904834411877	
G/G	G/G	G/G	G/G	upstream_gene_variant	1.7	
7	121774214		121774214	rs185256474		
ENSG00000008311	G		A	A	0.999904834411877	
G/G	G/G	G/G	G/G	intron_variant	1.7	
7	121774214		121774214	rs185256474		
ENSG00000008311	G		A	A	0.999904834411877	
G/G	G/G	G/G	G/G			
intron_variant,non_coding_transcript_variant				1.7		
7	121804527		121804527	rs112994176		
ENSG00000226636	T		C	C	0.999587144308943	
T/T	T/T	T/T	T/T	downstream_gene_variant	2.481	
7	121809487		121809487	rs530050137	.	
G	A	A	0.999587380181553	G/G	G/G	
G/G	G/G	intergenic_variant	1.694			
7	121821520		121821520	rs113846478	.	
T	C	C	0.998158379373849	T/T	T/T	
T/T	T/T	intergenic_variant	0.65			
7	121830027		121830027	rs111808176	.	
A	G	G	0.999618950844659	A/A	A/A	
A/A	A/A	intergenic_variant	3.577			
7	121836335		121836335	rs112472232	.	
G	T	T	0.999587537280284	G/G	G/G	
G/G	G/G	intergenic_variant	4.613			
7	121837994		121837994	rs113607589	.	
C	A	A	0.999585168166443	C/C	C/C	
C/C	C/C	intergenic_variant	1.378			
7	121839092		121839092	rs112103683	.	
G	C	C	0.999587327788712	G/G	G/G	

G/G	G/G	intergenic_variant	1.503		
7	121839616	121839616	rs112284926	.	
C	A	A	0.999587563451777	C/C	C/C
C/C	C/C	intergenic_variant	0.457		
7	121839743	121839743	rs111852243	.	
A	T	T	0.999587091856181	A/A	A/A
A/A	A/A	intergenic_variant	4.621		
7	121853152	121853152	rs113970274		
ENSG00000234418	C	T	T	0.999587563451777	
C/C	C/C	C/C	C/C	upstream_gene_variant	3.879
7	121853152	121853152	rs113970274	.	
C	T	T	0.999587563451777	C/C	C/C
C/C	C/C	regulatory_region_variant	3.879		
7	121857718	121857718	rs111781481		
ENSG00000234418	T	G	G	0.999587432561092	
T/T	T/T	T/T	T/T		
intron_variant,non_coding_transcript_variant				0.815	
7	121857990	121857990	rs544707564		
ENSG00000234418	G	A	A	0.999587249174498	
G/G	G/G	G/G	G/G		
intron_variant,non_coding_transcript_variant				3.139	
7	122321984	122321984	rs890628037		
ENSG00000081803	T	C	C	0.998976877429916	
T/T	T/T	T/T	T/T	intron_variant	1.162
7	122321984	122321984	rs890628037		
ENSG00000235459	T	C	C	0.998976877429916	
T/T	T/T	T/T	T/T	downstream_gene_variant	1.162
7	122322345	122322345	rs186290371		
ENSG00000081803	T	A	A	0.999619289340101	
T/T	T/T	T/T	T/T	intron_variant	2.102
7	122322345	122322345	rs186290371		
ENSG00000235459	T	A	A	0.999619289340101	
T/T	T/T	T/T	T/T	downstream_gene_variant	2.102
7	122322522	122322522	rs377455979		
ENSG00000081803	C	T	T	0.999746225098338	
C/C	C/C	C/C	C/C	intron_variant	1.025
7	122322522	122322522	rs377455979		
ENSG00000235459	C	T	T	0.999746225098338	
C/C	C/C	C/C	C/C	downstream_gene_variant	1.025
7	122322665	122322665	rs1014792474		
ENSG00000081803	C	A	A	0.999936584437821	
C/C	C/C	C/C	C/C	intron_variant	0.76
7	122322665	122322665	rs1014792474		
ENSG00000235459	C	A	A	0.999936584437821	
C/C	C/C	C/C	C/C	downstream_gene_variant	0.76
7	122322980	122322980	rs897672672		
ENSG00000081803	G	A	A	0.999936560299435	
G/G	G/G	G/G	G/G	intron_variant	0.065
7	122322980	122322980	rs897672672		
ENSG00000235459	G	A	A	0.999936560299435	
G/G	G/G	G/G	G/G	downstream_gene_variant	0.065
7	122322980	122322980	rs897672672	.	
G	A	A	0.999936560299435	G/G	G/G
G/G	G/G	regulatory_region_variant	0.065		

7	122326774		122326774	rs1031892122		
ENSG00000081803	G		A	A	0.999936556274584	
G/G	G/G	G/G	G/G	intron_variant	0.307	
7	122326774		122326774	rs1031892122	.	
G	A	A	0.999936556274584	G/G	G/G	
G/G	G/G		regulatory_region_variant	0.307		
7	122327277		122327277	rs1003003894		
ENSG00000081803	C		T	T	0.999936560299435	
C/C	C/C	C/C	C/C	intron_variant	2.019	
7	122327277		122327277	rs1003003894	.	
C	T	T	0.999936560299435	C/C	C/C	
C/C	C/C		regulatory_region_variant	2.019		
7	122333281		122333281	rs891597926		
ENSG00000081803	C		A	A	0.999936592479868	
C/C	C/C	C/C	C/C	intron_variant	0.85	
7	122333281		122333281	rs891597926		
ENSG00000188050	C		A	A	0.999936592479868	
C/C	C/C	C/C	C/C	downstream_gene_variant	0.85	
7	122336571		122336571	rs200673307		
ENSG00000081803	T		A	A	0.998556240976506	
T/T	T/T	T/T	T/T	intron_variant	1.117	
7	122336571		122336571	rs200673307		
ENSG00000188050	T		A	A	0.998556240976506	
T/T	T/T	T/T	T/T	downstream_gene_variant	1.117	
7	122336571		122336571	rs200673307	.	
T	A	A	0.998556240976506	T/T	T/T	
T/T	T/T		regulatory_region_variant	1.117		
7	122336572		122336572	rs202028705		
ENSG00000081803	G		A	A	0.998425093510073	
G/G	G/G	G/G	G/G	intron_variant	0.382	
7	122336572		122336572	rs202028705		
ENSG00000188050	G		A	A	0.998425093510073	
G/G	G/G	G/G	G/G	downstream_gene_variant	0.382	
7	122336572		122336572	rs202028705	.	
G	A	A	0.998425093510073	G/G	G/G	
G/G	G/G		regulatory_region_variant	0.382		
7	122345008		122345008	rs926114634		
ENSG00000081803	G		A	A	0.999936451448907	
G/G	G/G	G/G	G/G	intron_variant	1.809	
7	122345008		122345008	rs926114634		
ENSG00000235631	G		A	A	0.999936451448907	
G/G	G/G	G/G	G/G	upstream_gene_variant	1.809	
7	122347267		122347267	rs924531760		
ENSG00000081803	A		C	C	0.999936431250397	
A/A	A/A	A/A	A/A	intron_variant	5.047	
7	122347267		122347267	rs924531760		
ENSG00000235631	A		C	C	0.999936431250397	
A/A	A/A	A/A	A/A	upstream_gene_variant	5.047	
7	122352810		122352810	rs1013076609		
ENSG00000081803	C		T	T	0.999936475670182	
C/C	C/C	C/C	C/C	intron_variant	1.342	
7	122354439		122354439	rs950726006		
ENSG00000081803	G		A	A	0.999936439331342	
G/G	G/G	G/G	G/G	intron_variant	1.938	

7	122355038		122355038	rs992732259	
ENSG00000081803	G		A	A	0.999936443371044
G/G	G/G	G/G	G/G	intron_variant	5.02
7	122355678		122355678	rs1055561320	
ENSG00000081803	T		C	C	0.999872765443094
T/T	T/T	T/T	T/T	intron_variant	1.755
7	122357339		122357339	rs762244065	
ENSG00000081803	T		C	C	0.999936507936508
T/T	T/T	T/T	T/T	intron_variant	4.667
7	122357610		122357610	rs888435065	
ENSG00000081803	C		T	T	0.999936515997969
C/C	C/C	C/C	C/C	intron_variant	5.114
7	122358644		122358644	rs990382537	
ENSG00000081803	C		T	T	0.999936511967494
C/C	C/C	C/C	C/C	intron_variant	1.864
7	122360587		122360587	rs1009976392	
ENSG00000081803	T		G	G	0.999935178583004
T/T	T/T	T/T	T/T	intron_variant	0.21
7	122365075		122365075	rs1016978637	
ENSG00000081803	G		T	T	0.999936475670182
G/G	G/G	G/G	G/G	intron_variant	1.52
7	122365223		122365223	rs914974856	
ENSG00000081803	G		C	C	0.999936427209154
G/G	G/G	G/G	G/G	intron_variant	0.866
7	122366091		122366091	rs914589336	
ENSG00000081803	C		G	G	0.999936317901038
C/C	C/C	C/C	C/C	intron_variant	0.755
7	122367415		122367415	rs976921451	
ENSG00000081803	C		A	A	0.999936386768448
C/C	C/C	C/C	C/C	intron_variant	6.46
7	122368148		122368148	rs1009823841	
ENSG00000081803	C		A	A	0.999936382721547
C/C	C/C	C/C	C/C	intron_variant	9.621
7	122368592		122368592	rs906886411	
ENSG00000081803	C		G	G	0.999936187862931
C/C	C/C	C/C	C/C	intron_variant	0.251
7	122368714		122368714	rs945461529	
ENSG00000081803	A		G	G	0.999936342224203
A/A	A/A	A/A	A/A	intron_variant	2.843
7	122368945		122368945	rs978163322	
ENSG00000081803	T		A	A	0.99993631384537
T/T	T/T	T/T	intron_variant	1.123	
7	122370430		122370430	rs927782270	
ENSG00000081803	G		A	A	0.999936334118546
G/G	G/G	G/G	G/G	intron_variant	3.262
7	122370675		122370675	rs914898364	
ENSG00000081803	A		T	T	0.999936378674132
A/A	A/A	A/A	A/A	intron_variant	5.408
7	122370925		122370925	rs960645080	
ENSG00000081803	A		C	C	0.999936216354127
A/A	A/A	A/A	A/A	intron_variant	5.366
7	122371219		122371219	rs1034685854	
ENSG00000081803	A		G	G	0.999936293559279
A/A	A/A	A/A	A/A	intron_variant	6.984

7	122371668		122371668	rs986864990		
ENSG00000081803	C		A	A	0.999936191934661	
C/C	C/C	C/C	C/C	intron_variant	2.83	
7	122373026		122373026	rs910902984		
ENSG00000081803	A		T	T	0.99993174527336	A/A
A/A	A/A	A/A		intron_variant	1.746	
7	122374819		122374819	rs900624027		
ENSG00000081803	C		T	T	0.999936524057382	
C/C	C/C	C/C	C/C	intron_variant	3.287	
7	122374819		122374819	rs900624027		.
C	T	T	0.999936524057382		C/C	C/C
C/C	C/C		regulatory_region_variant	3.287		
7	122375032		122375032	rs1038867554		
ENSG00000081803	C		A	A	0.99993653211475	C/C
C/C	C/C	C/C		intron_variant	10.68	
7	122375032		122375032	rs1038867554		.
C	A	A	0.99993653211475	C/C	C/C	C/C
C/C			regulatory_region_variant	10.68		
7	122375618		122375618	rs376859181		
ENSG00000081803	T		C	C	0.999904701397713	
T/T	T/T	T/T	T/T	intron_variant	1.297	
7	122375618		122375618	rs376859181		.
T	C	C	0.999904701397713		T/T	T/T
T/T	T/T		regulatory_region_variant	1.297		
7	122376412		122376412	rs939356162		
ENSG00000081803	G		T	T	0.999936398906061	
G/G	G/G	G/G	G/G	intron_variant	8.039	
7	122376412		122376412	rs939356162		.
G	T	T	0.999936398906061		G/G	G/G
G/G	G/G		regulatory_region_variant	8.039		
7	122379455		122379455	rs1048171682		
ENSG00000081803	C		A	A	0.99993653211475	C/C
C/C	C/C	C/C		intron_variant	0.976	
7	122379455		122379455	rs1048171682		.
C	A	A	0.99993653211475	C/C	C/C	C/C
C/C			regulatory_region_variant	0.976		
7	122464617		122464617	rs1032806413		
ENSG00000081803	T		C	C	0.999936487773896	
T/T	T/T	T/T	T/T	intron_variant	0.805	
7	122843099		122843099	rs114490038		
ENSG00000081800	G		A	A	0.998600330830895	
G/G	G/G	G/G	G/G	upstream_gene_variant	3.576	
7	122846638		122846638	rs147363973		.
C	T	T	0.998600686935504		C/C	C/C
C/C	C/C		intergenic_variant	1.502		
7	123093242		123093242	rs1007042563		
ENSG00000164675	G		A	A	0.999834885410475	
G/G	G/G	G/G	G/G	intron_variant	0.48	
7	123093242		123093242	rs1007042563		
ENSG00000207338	G		A	A	0.999834885410475	
G/G	G/G	G/G	G/G	downstream_gene_variant	0.48	
7	123093242		123093242	rs1007042563		
ENSG00000232524	G		A	A	0.999834885410475	
G/G	G/G	G/G	G/G	upstream_gene_variant	0.48	

7	123093242		123093242		rs1007042563		
ENSG00000164675	G		A	A	0.999834885410475		
G/G	G/G	G/G	G/G				
intron_variant,NMD_transcript_variant					0.48		
7	123467743		123467743		rs1002572610		
ENSG00000228211	T		C	C	0.999904828373834		
T/T	T/T	T/T	T/T				
intron_variant,non_coding_transcript_variant					6.481		
7	123467743		123467743		rs1002572610		
ENSG00000106302	T		C	C	0.999904828373834		
T/T	T/T	T/T	T/T	upstream_gene_variant	6.481		
7	123560416		123560416		rs116628859		
ENSG00000106304	T		G	G	0.996479766586325		
T/T	T/T	T/T	T/T	upstream_gene_variant	2.346		
7	123561763		123561763		rs950530868		
ENSG00000106304	A		G	G	0.999873152787467		
A/A	A/A	A/A	A/A	upstream_gene_variant	1.239		
7	123563658		123563658		rs115915636		
ENSG00000106304	A		G	G	0.996510152284264		
A/A	A/A	A/A	A/A	upstream_gene_variant	5.113		
7	123564360		123564360		rs116713900		
ENSG00000106304	A		G	G	0.996474623642254		
A/A	A/A	A/A	A/A	upstream_gene_variant	1.637		
8	54600149	54600149	rs1048482465	.	C	T	
T	1	C/C	C/C	C/C	C/C		
intergenic_variant					5.853		
8	54795353	54795353	rs1244741798		ENSG00000147509	C	
T	T	1	C/C	C/C	C/C	C/C	
intron_variant					8.014		
8	54795353	54795353	rs1244741798		ENSG00000244159	C	
T	T	1	C/C	C/C	C/C	C/C	
downstream_gene_variant					8.014		
8	54795353	54795353	rs1244741798		ENSG00000147509	C	
T	T	1	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant					8.014		
8	54795353	54795353	rs1244741798		ENSG00000147509	C	
T	T	1	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant					8.014		
8	54795353	54795353	rs1244741798	.	C	T	
T	1	C/C	C/C	C/C	C/C		
regulatory_region_variant					8.014		
8	54799827	54799827	rs868390536		ENSG00000147509	G	
C	C	0.999968280149718			G/G	G/G	G/G
G/G	intron_variant					8.368	
8	54799827	54799827	rs868390536		ENSG00000244159	G	
C	C	0.999968280149718			G/G	G/G	G/G
G/G	upstream_gene_variant					8.368	
8	54799827	54799827	rs868390536		ENSG00000147509	G	
C	C	0.999968280149718			G/G	G/G	G/G
G/G	intron_variant,NMD_transcript_variant					8.368	
8	54799827	54799827	rs868390536		ENSG00000147509	G	
C	C	0.999968280149718			G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant					8.368	
8	54799827	54799827	rs868390536	.	G	C	

C	0.999968280149718		G/G	G/G	G/G	G/G
regulatory_region_variant 8.368						
8	54801272	54801272	rs543933889	ENSG00000147509	A	
G	G	0.999936556274584		A/A	A/A	A/A
A/A intron_variant 2.724						
8	54801272	54801272	rs543933889	ENSG00000244159	A	
G	G	0.999936556274584		A/A	A/A	A/A
A/A upstream_gene_variant 2.724						
8	54801272	54801272	rs543933889	ENSG00000147509	A	
G	G	0.999936556274584		A/A	A/A	A/A
A/A intron_variant,NMD_transcript_variant 2.724						
8	54801272	54801272	rs543933889	ENSG00000147509	A	
G	G	0.999936556274584		A/A	A/A	A/A
A/A intron_variant,non_coding_transcript_variant 2.724						
8	54801272	54801272	rs543933889	.	A	G
G	0.999936556274584		A/A	A/A	A/A	A/A
regulatory_region_variant 2.724						
8	54807056	54807056	rs1336854780	ENSG00000147509	G	
C	C	1	G/G	G/G	G/G	G/G
intron_variant 0.72						
8	54807056	54807056	rs1336854780	ENSG00000147509	G	
C	C	1	G/G	G/G	G/G	G/G
intron_variant,NMD_transcript_variant 0.72						
8	54807056	54807056	rs1336854780	ENSG00000147509	G	
C	C	1	G/G	G/G	G/G	G/G
intron_variant,non_coding_transcript_variant 0.72						
8	54807056	54807056	rs1336854780	.	G	C
C	1	G/G	G/G	G/G	G/G	G/G
regulatory_region_variant 0.72						
8	54807771	54807771	rs1454468187	ENSG00000147509	C	
A	A	1	C/C	C/C	C/C	C/C
intron_variant 2.648						
8	54807771	54807771	rs1454468187	ENSG00000147509	C	
A	A	1	C/C	C/C	C/C	C/C
intron_variant,NMD_transcript_variant 2.648						
8	54807771	54807771	rs1454468187	ENSG00000147509	C	
A	A	1	C/C	C/C	C/C	C/C
intron_variant,non_coding_transcript_variant 2.648						
8	54853106	54853106	rs555606998	ENSG00000147509	T	
A	A	0.999334052134204		T/T	T/T	T/T
T/T intron_variant 0.047						
8	54853106	54853106	rs555606998	ENSG00000147509	T	
A	A	0.999334052134204		T/T	T/T	T/T
T/T upstream_gene_variant 0.047						
8	54853106	54853106	rs555606998	ENSG00000147509	T	
A	A	0.999334052134204		T/T	T/T	T/T
T/T intron_variant,NMD_transcript_variant 0.047						
8	54853106	54853106	rs555606998	ENSG00000147509	T	
A	A	0.999334052134204		T/T	T/T	T/T
T/T intron_variant,non_coding_transcript_variant 0.047						
8	54853881	54853881	rs879428238	ENSG00000147509	A	
C	C	1	A/A	A/A	A/A	A/A
intron_variant 0.908						
8	54853881	54853881	rs879428238	ENSG00000147509	A	

C	C	1	A/A	A/A	A/A	A/A	
upstream_gene_variant		0.908					
8	54853881	54853881	rs879428238		ENSG00000147509	A	
C	C	1	A/A	A/A	A/A	A/A	
intron_variant,NMD_transcript_variant		0.908					
8	54853881	54853881	rs879428238		ENSG00000147509	A	
C	C	1	A/A	A/A	A/A	A/A	
intron_variant,non_coding_transcript_variant		0.908					
8	54855162	54855162	rs553305739		ENSG00000147509	C	
T	T	0.99913726993865	C/C	C/C	C/C	C/C	
intron_variant		0.533					
8	54855162	54855162	rs553305739		ENSG00000147509	C	
T	T	0.99913726993865	C/C	C/C	C/C	C/C	
upstream_gene_variant		0.533					
8	54855162	54855162	rs553305739		ENSG00000147509	C	
T	T	0.99913726993865	C/C	C/C	C/C	C/C	
intron_variant,NMD_transcript_variant		0.533					
8	54855162	54855162	rs553305739		ENSG00000147509	C	
T	T	0.99913726993865	C/C	C/C	C/C	C/C	
intron_variant,non_coding_transcript_variant		0.533					
8	54856729	54856729		ENSG00000147509	T	C	
C	1	T/T	T/T	T/T	T/T	intron_variant	
0.88							
8	54856729	54856729		ENSG00000147509	T	C	
C	1	T/T	T/T	T/T	T/T		
upstream_gene_variant		0.88					
8	54856729	54856729		ENSG00000147509	T	C	
C	1	T/T	T/T	T/T	T/T		
intron_variant,NMD_transcript_variant		0.88					
8	54856729	54856729		ENSG00000147509	T	C	
C	1	T/T	T/T	T/T	T/T		
intron_variant,non_coding_transcript_variant		0.88					
8	54857308	54857308	rs575536717		ENSG00000147509	A	
G	G	0.999079598832043		A/A	A/A	A/A	
A/A intron_variant		3.04					
8	54857308	54857308	rs575536717		ENSG00000147509	A	
G	G	0.999079598832043		A/A	A/A	A/A	
A/A upstream_gene_variant		3.04					
8	54857308	54857308	rs575536717		ENSG00000147509	A	
G	G	0.999079598832043		A/A	A/A	A/A	
A/A intron_variant,NMD_transcript_variant		3.04					
8	54857308	54857308	rs575536717		ENSG00000147509	A	
G	G	0.999079598832043		A/A	A/A	A/A	
A/A intron_variant,non_coding_transcript_variant		3.04					
8	54857308	54857308	rs575536717		.	A	G
G	G	0.999079598832043	A/A	A/A	A/A	A/A	
regulatory_region_variant		3.04					
8	54857367	54857367	rs188963471		ENSG00000147509	G	
C	C	0.999080124341813		G/G	G/G	G/G	
G/G intron_variant		4.68					
8	54857367	54857367	rs188963471		ENSG00000147509	G	
C	C	0.999080124341813		G/G	G/G	G/G	
G/G upstream_gene_variant		4.68					
8	54857367	54857367	rs188963471		ENSG00000147509	G	

C	C	0.999080124341813	G/G	G/G	G/G
G/G	intron_variant,NMD_transcript_variant		4.68		
8	54857367	54857367	rs188963471	ENSG00000147509	G
C	C	0.999080124341813	G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant		4.68		
8	54857367	54857367	rs188963471	.	G
C	0.999080124341813	G/G	G/G	G/G	G/G
regulatory_region_variant 4.68					
8	54857367	54857367	rs188963471	.	G
C	0.999080124341813	G/G	G/G	G/G	G/G
TF_binding_site_variant 4.68					
8	54857941	54857941	rs186932892	ENSG00000147509	G
C	C	0.999080241040279	G/G	G/G	G/G
G/G	intron_variant		6.594		
8	54857941	54857941	rs186932892	ENSG00000147509	G
C	C	0.999080241040279	G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant		6.594		
8	54857941	54857941	rs186932892	ENSG00000147509	G
C	C	0.999080241040279	G/G	G/G	G/G
G/G	intron_variant,NMD_transcript_variant		6.594		
8	54857941	54857941	rs186932892	.	G
C	0.999080241040279	G/G	G/G	G/G	G/G
regulatory_region_variant 6.594					
8	54857941	54857941	rs186932892	.	G
C	0.999080241040279	G/G	G/G	G/G	G/G
TF_binding_site_variant 6.594					
8	54869580	54869580	rs116067708	ENSG00000147509	A
C	C	0.996829422954978	A/A	A/A	A/A
A/A	intron_variant		0.165		
8	54869580	54869580	rs116067708	ENSG00000147509	A
C	C	0.996829422954978	A/A	A/A	A/A
A/A	intron_variant,non_coding_transcript_variant		0.165		
8	54869580	54869580	rs116067708	ENSG00000147509	A
C	C	0.996829422954978	A/A	A/A	A/A
A/A	intron_variant,NMD_transcript_variant		0.165		
8	54869580	54869580	rs116067708	ENSG00000147509	A
C	C	0.996829422954978	A/A	A/A	A/A
A/A	downstream_gene_variant		0.165		
8	54871442	54871442	rs116129509	ENSG00000147509	T
G	G	0.996795278588653	T/T	T/T	T/T
T/T	3_prime_UTR_variant		4.763		
8	54871442	54871442	rs116129509	ENSG00000147509	T
G	G	0.996795278588653	T/T	T/T	T/T
T/T	downstream_gene_variant		4.763		
8	54871442	54871442	rs116129509	ENSG00000147509	T
G	G	0.996795278588653	T/T	T/T	T/T
T/T	3_prime_UTR_variant,NMD_transcript_variant		4.763		
8	54873711	54873711	rs115885996	ENSG00000147509	A
G	G	0.996217899822019	A/A	A/A	A/A
A/A	downstream_gene_variant		2.846		
8	54874154	54874154	rs193270084	ENSG00000147509	C
A	A	0.996823985263292	C/C	C/C	C/C
C/C	downstream_gene_variant		6.157		
8	54874154	54874154	rs193270084	ENSG00000187735	C

A	A	0.996823985263292			C/C	C/C	C/C
C/C	downstream_gene_variant 6.157						
8	54975904	54975904	rs145050847		ENSG00000120992		T
C	C	0.999968276124611			T/T	T/T	T/T
T/T	missense_variant 20.3						
8	54975904	54975904	rs145050847		ENSG00000120992		T
C	C	0.999968276124611			T/T	T/T	T/T
T/T	intron_variant 20.3						
8	54975904	54975904	rs145050847		ENSG00000120992		T
C	C	0.999968276124611			T/T	T/T	T/T
T/T	non_coding_transcript_exon_variant 20.3						
8	54975904	54975904	rs145050847		ENSG00000120992		T
C	C	0.999968276124611			T/T	T/T	T/T
T/T	intron_variant,non_coding_transcript_variant 20.3						
8	55010010	55010010	rs765394246		ENSG00000120992		T
C	C	1	T/T	T/T	T/T	T/T	
	intron_variant 4.533						
8	55010010	55010010	rs765394246		ENSG00000120992		T
C	C	1	T/T	T/T	T/T	T/T	
	intron_variant,non_coding_transcript_variant 4.533						
8	55010010	55010010	rs765394246		ENSG00000120992		T
C	C	1	T/T	T/T	T/T	T/T	
	downstream_gene_variant 4.533						
8	55124338	55124338	rs111247808		.	G	T
T	0.999904804214		G/G	G/G	G/G	G/G	
	intergenic_variant 1.535						
8	55125286	55125286	.		C	A	A
1	C/C	C/C	C/C	C/C			intergenic_variant
4.083							
8	55140175	55140175	.		C	T	T
1	C/C	C/C	C/C	C/C			intergenic_variant
5.662							
8	55266211	55266211	rs957272130		.	A	G
G	0.999968284173803		A/A	A/A	A/A	A/A	A/A
	intergenic_variant 1.954						
8	55488440	55488440	.		G	T	T
1	G/G	G/G	G/G	G/G			intergenic_variant
3.891							
8	55492421	55492421	.		G	T	T
1	G/G	G/G	G/G	G/G			intergenic_variant
0.973							
8	55508314	55508314	.		T	C	C
1	T/T	T/T	T/T	T/T			intergenic_variant
4.343							
8	55508363	55508363	.		G	A	A
1	G/G	G/G	G/G	G/G			intergenic_variant
1.819							
8	55509666	55509666	rs568366466		.	T	C
C	0.999684044233807		T/T	T/T	T/T	T/T	T/T
	intergenic_variant 2.42						
8	55510878	55510878	.		G	A	A
1	G/G	G/G	G/G	G/G			intergenic_variant
6.653							
8	60493199	60493199	rs371362758		ENSG00000253260		C

A	A	1	C/C	C/C	C/C	C/C		
intron_variant,non_coding_transcript_variant							2.598	
8	60503748	60503748	rs373614287		ENSG00000253260		G	
T	T	1	G/G	G/G	G/G	G/G		
intron_variant,non_coding_transcript_variant							0.604	
8	60513653	60513653	rs376901861		ENSG00000253879		A	
G	G	1	A/A	A/A	A/A	A/A		
upstream_gene_variant							6.107	
8	61811114	61811114	rs758053902		.	A	G	
G	0.999936592479868		A/A	A/A	A/A	A/A	A/A	
intergenic_variant							2.491	
8	61888297	61888297	rs376095310		.	C	T	
T	1	C/C	C/C	C/C	C/C			
regulatory_region_variant							1.826	
8	61888297	61888297	rs376095310		.	C	T	
T	1	C/C	C/C	C/C	C/C			
intergenic_variant							1.826	
8	62442948	62442948	rs144425520		ENSG00000198363		G	
C	C	0.999587615784799			G/G	G/G	G/G	
G/G	intron_variant 0.034							
8	62442948	62442948	rs144425520		ENSG00000198363		G	
C	C	0.999587615784799			G/G	G/G	G/G	
G/G	upstream_gene_variant 0.034							
8	62442948	62442948	rs144425520		.	G	C	
C	0.999587615784799		G/G	G/G	G/G	G/G	G/G	
regulatory_region_variant							0.034	
8	62443198	62443198	rs182928617		ENSG00000198363		C	
T	T	0.999587824984147			C/C	C/C	C/C	
C/C	intron_variant 1.274							
8	62443198	62443198	rs182928617		ENSG00000198363		C	
T	T	0.999587824984147			C/C	C/C	C/C	
C/C	upstream_gene_variant 1.274							
8	62443198	62443198	rs182928617		.	C	T	
T	0.999587824984147		C/C	C/C	C/C	C/C	C/C	
regulatory_region_variant							1.274	
8	62443586	62443586	rs571498754		ENSG00000198363		T	
G	G	0.999587537280284			T/T	T/T	T/T	
T/T	intron_variant 16.13							
8	62443586	62443586	rs571498754		ENSG00000198363		T	
G	G	0.999587537280284			T/T	T/T	T/T	
T/T	upstream_gene_variant 16.13							
8	62443879	62443879	rs185523507		ENSG00000198363		C	
T	T	0.999587668104542			C/C	C/C	C/C	
C/C	intron_variant 4.92							
8	62444135	62444135	rs142686683		ENSG00000198363		A	
G	G	0.999587196748381			A/A	A/A	A/A	
A/A	intron_variant 0.856							
8	62446039	62446039	rs149651805		ENSG00000198363		A	
G	G	0.999554452294571			A/A	A/A	A/A	
A/A	intron_variant 1.631							
8	62446413	62446413	rs367936870		ENSG00000198363		C	
A	A	0.999587720411011			C/C	C/C	C/C	
C/C	intron_variant 0.928							
8	62448108	62448108	rs143203536		ENSG00000198363		A	

G	G	0.99958764194633	A/A	A/A	A/A	A/A
intron_variant 0.895						
8	62454352	62454352	rs141905949	ENSG00000198363	C	
T	T	0.999587851119143		C/C	C/C	C/C
C/C intron_variant 3.512						
8	63312681	63312681	rs370118542	ENSG00000185942	G	
A	A	0.998359073359073		G/G	G/G	G/G
G/G intron_variant 1.151						
8	63312681	63312681	rs370118542	ENSG00000185942	G	
A	A	0.998359073359073		G/G	G/G	G/G
G/G intron_variant,non_coding_transcript_variant 1.151						
8	63313053	63313053	rs368239157	ENSG00000185942	T	
C	C	0.998313820310512		T/T	T/T	T/T
T/T intron_variant 3.843						
8	63313053	63313053	rs368239157	ENSG00000185942	T	
C	C	0.998313820310512		T/T	T/T	T/T
T/T intron_variant,non_coding_transcript_variant 3.843						
8	63314520	63314520	rs139239763	ENSG00000185942	A	
T	T	0.998382595458582		A/A	A/A	A/A
A/A intron_variant 2.359						
8	63314520	63314520	rs139239763	ENSG00000185942	A	
T	T	0.998382595458582		A/A	A/A	A/A
A/A intron_variant,non_coding_transcript_variant 2.359						
8	63314548	63314548	rs182152942	ENSG00000185942	G	
C	C	0.998413906864611		G/G	G/G	G/G
G/G intron_variant 0.06						
8	63314548	63314548	rs182152942	ENSG00000185942	G	
C	C	0.998413906864611		G/G	G/G	G/G
G/G intron_variant,non_coding_transcript_variant 0.06						
8	63315324	63315324	rs368706238	ENSG00000185942	A	
C	C	0.998382698040211		A/A	A/A	A/A
A/A intron_variant 1.081						
8	63315324	63315324	rs368706238	ENSG00000185942	A	
C	C	0.998382698040211		A/A	A/A	A/A
A/A intron_variant,non_coding_transcript_variant 1.081						
8	63317350	63317350	rs192481813	ENSG00000185942	C	
G	G	0.997558625120463		C/C	C/C	C/C
C/C intron_variant 0.852						
8	63317350	63317350	rs192481813	ENSG00000185942	C	
G	G	0.997558625120463		C/C	C/C	C/C
C/C intron_variant,non_coding_transcript_variant 0.852						
8	63317996	63317996	rs138181137	ENSG00000185942	A	
G	G	0.998381877022654		A/A	A/A	A/A
A/A intron_variant 1.26						
8	63317996	63317996	rs138181137	ENSG00000185942	A	
G	G	0.998381877022654		A/A	A/A	A/A
A/A intron_variant,non_coding_transcript_variant 1.26						
8	63317996	63317996	rs138181137	.	A	G
G	G	0.998381877022654	A/A	A/A	A/A	A/A
regulatory_region_variant 1.26						
8	63318895	63318895	rs185919990	ENSG00000185942	G	
A	A	0.998382185001903		G/G	G/G	G/G
G/G intron_variant 7.367						
8	63318895	63318895	rs185919990	ENSG00000185942	G	

A	A	0.998382185001903	G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant				7.367
8	63319394	63319394	rs150774281	ENSG00000185942	T
C	C	0.998381260712245	T/T	T/T	T/T
T/T	intron_variant 0.95				
8	63319394	63319394	rs150774281	ENSG00000185942	T
C	C	0.998381260712245	T/T	T/T	T/T
T/T	intron_variant,non_coding_transcript_variant				0.95
8	63321670	63321670	rs184657169	ENSG00000185942	C
A	A	0.997588373421337	C/C	C/C	C/C
C/C	intron_variant 1.963				
8	63321670	63321670	rs184657169	ENSG00000185942	C
A	A	0.997588373421337	C/C	C/C	C/C
C/C	intron_variant,non_coding_transcript_variant				1.963
8	63327074	63327074	rs151262744	ENSG00000185942	A
G	G	0.998000253936008	A/A	A/A	A/A
A/A	intron_variant 2.651				
8	63327074	63327074	rs151262744	ENSG00000185942	A
G	G	0.998000253936008	A/A	A/A	A/A
A/A	intron_variant,non_coding_transcript_variant				2.651
8	63327421	63327421	rs185643961	ENSG00000185942	G
A	A	0.998354307841239	G/G	G/G	G/G
G/G	intron_variant 1.416				
8	63327421	63327421	rs185643961	ENSG00000185942	G
A	A	0.998354307841239	G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant				1.416
8	63328760	63328760	rs374885803	ENSG00000185942	A
G	G	0.998381774336845	A/A	A/A	A/A
A/A	intron_variant 0.377				
8	63328760	63328760	rs374885803	ENSG00000185942	A
G	G	0.998381774336845	A/A	A/A	A/A
A/A	intron_variant,non_coding_transcript_variant				0.377
8	63334157	63334157	rs188953952	ENSG00000185942	G
A	A	0.998365594154596	G/G	G/G	G/G
G/G	intron_variant 0.043				
8	63334157	63334157	rs188953952	ENSG00000185942	G
A	A	0.998365594154596	G/G	G/G	G/G
G/G	intron_variant,non_coding_transcript_variant				0.043
8	63335621	63335621	rs148941104	ENSG00000185942	T
A	A	0.99838043823436	T/T	T/T	T/T
intron_variant 0.949					
8	63335621	63335621	rs148941104	ENSG00000185942	T
A	A	0.99838043823436	T/T	T/T	T/T
intron_variant,non_coding_transcript_variant				0.949	
8	63335621	63335621	rs148941104	.	A
A	0.99838043823436	T/T	T/T	T/T	
regulatory_region_variant 0.949					
13	54491995	54491995	rs75110386	.	T
T	0.995325914149444	C/C	C/C	C/C	C/C
intergenic_variant 1.026					
13	54493218	54493218	rs112363507	.	A
A	0.995326805696846	T/T	T/T	T/T	T/T
intergenic_variant 5.794					
13	58088276	58088276	rs188208514	.	C

C	0.999012738853503			T/T	T/T	T/T	T/T
intergenic_variant	6.536						
13	58091208	58091208		.	G	A	A
1	G/G	G/G	G/G	G/G	intergenic_variant		
0.569							
13	58091727	58091727		.	A	G	G
1	A/A	A/A	A/A	A/A	intergenic_variant		
11.67							
13	58092954	58092954		.	A	G	G
1	A/A	A/A	A/A	A/A	intergenic_variant		
1.708							
13	58095679	58095679		.	C	T	T
1	C/C	C/C	C/C	C/C	intergenic_variant		
0.193							
13	58116896	58116896		.	C	A	A
1	C/C	C/C	C/C	C/C	intergenic_variant		
0.802							
13	58120473	58120473	rs565828949	.	A		C
C	0.99900532631714	A/A	A/A	A/A	A/A	A/A	
intergenic_variant	2.685						
13	58124776	58124776		.	A	T	T
1	A/A	A/A	A/A	A/A	intergenic_variant		
4.677							
13	58125009	58125009		.	C	A	A
1	C/C	C/C	C/C	C/C	intergenic_variant		
2.836							
13	58126230	58126230		.	G	C	C
1	G/G	G/G	G/G	G/G	intergenic_variant		
0.618							
13	58127478	58127478		.	C	A	A
1	C/C	C/C	C/C	C/C	intergenic_variant		
5.577							
13	58130046	58130046		.	A	G	G
1	A/A	A/A	A/A	A/A	intergenic_variant		
1.759							
13	58130911	58130911	rs185680454	.	A		C
C	0.999048102551085	A/A	A/A	A/A	A/A	A/A	A/A
intergenic_variant	2.58						
13	58131337	58131337		.	T	C	C
1	T/T	T/T	T/T	T/T	intergenic_variant		
1.449							
13	58132252	58132252		.	C	G	G
1	C/C	C/C	C/C	C/C	regulatory_region_variant		
14.07							
13	58132252	58132252		.	C	G	G
1	C/C	C/C	C/C	C/C	intergenic_variant		
14.07							
13	58132620	58132620		.	C	G	G
1	C/C	C/C	C/C	C/C	regulatory_region_variant		
4.034							
13	58132620	58132620		.	C	G	G
1	C/C	C/C	C/C	C/C	intergenic_variant		
4.034							
13	58134194	58134194		.	C	G	G

1	C/C	C/C	C/C	C/C	intergenic_variant			
0.59								
13	58134524	58134524	rs1259332096	.	T	C		
C	1	T/T	T/T	T/T	T/T			
intergenic_variant			6.385					
13	58136210	58136210	.	T	C	C		
1	T/T	T/T	T/T	T/T	intergenic_variant			
2.242								
13	58142339	58142339	.	G	A	A		
1	G/G	G/G	G/G	G/G	intergenic_variant			
2.356								
13	58699811	58699811	rs146564147	.	A	T		
T	0.99930012088821	A/A	A/A	A/A	A/A			
intergenic_variant			0.572					
13	58701556	58701556	rs141081906	.	A	G		
G	0.999301498602997		A/A	A/A	A/A	A/A		
intergenic_variant			7.54					
13	58705454	58705454	rs376995582	.	C	A		
A	0.999301232371999		C/C	C/C	C/C	C/C		
intergenic_variant			1.927					
13	58711593	58711593	rs150261641	.	G	A		
A	0.999300965937977		G/G	G/G	G/G	G/G		
intergenic_variant			0.174					
13	58731244	58731244	rs760143858	.	T	C		
C	0.999936536142667		T/T	T/T	T/T	T/T		
intergenic_variant			1.067					
13	58733146	58733146	rs771153105	.	G	A		
A	0.999968266057375		G/G	G/G	G/G	G/G		
intergenic_variant			1.689					
13	58891013	58891013	rs974521894	.	A	G		
G	0.999841279918735		A/A	A/A	A/A	A/A		
intergenic_variant			1.407					