

## LEGEND OF SUPPLEMENTARY TABLES

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***Supplementary Table 1: GWAS candidate SNPs associated with diverticular disease (with CADD score, Regulome score and eQTL sigmoid colon annotation)***

This table shows diverticular disease candidate SNPs (SNPs which are in LD of any independent lead SNPs) mapped to genomic risk loci with a GWAS p-value  $<1.0 \times 10^{-5}$ , MAF  $>0.01$ . The table is sorted ascending by genomic risk loci and in descending order by Combined Annotation-Dependent Depletion (CADD) score as a potential indicator of functional implications. Correspondingly all exonic nonsynonymous SNPs and variant that affect gene expression of candidate genes in sigmoid colon tissue (FDR  $<0.05$ \_eQTL, GTEx\_V7) as a potential indicator of functional implications are shown. The following table headers are used: uniqID: Unique ID of SNPs consisting of chr:position:allele1:allele2 where alleles are alphabetically ordered; rsID : rsID based on dbSNP build 146; chr : chromosome; pos : position on hg19; effect\_allele : Effect/risk allele ; non\_effect\_allele : Non-effect/non-risk ; MAF : Minor allele frequency computed based on 1000G; gwasP : P-value provided in the input GWAS summary statistics file; r2 : The maximum r2 of the SNP with one of the independent significant SNPs; IndSigSNP: rsID of the independent significant SNP which has the maximum r2 with the SNP; Genomic locus : Index of the genomic risk loci matching with "Genomic risk loci" Supplementary Table 5; nearestGene: The nearest Gene of the SNP based on ANNOVAR annotations; ANNOVAR annotates "consequence" function by prioritizing the most deleterious annotation for SNPs which are locating a genomic region where multiple genes are overlapped. Genes are encoded in symbol, if it is available otherwise Ensembl ID. Genes include all transcripts from Ensembl gene build 85 including non-protein coding genes and RNAs. eQTL Gene 1 and 2: Genes affected in expression in sigmoid colon tissue (FDR  $<0.05$ \_eQTL, GTEx\_V7) by candidate SNPs; P\_eQTL: nominal p value for cis-eQTL variant. FDR\_eQTL: false discovery rate corrected p value for cis-eQTL variant; CADD: CADD score which is computed based on 63 annotations. The higher the score, the more deleterious the SNP is. 12.37 is the suggested threshold by Kircher et al (2014). RDB : RegulomeDB score which is a categorical score (from 1a to 7). 1a is the highest score for SNPs with the most biological evidence to be a regulatory element. minChrState : The minimum 15-core chromatin state across 127 tissue/cell type.

***References used in Supplementary Table 1:***

Kircher M, Witten DM, Jain P, O'Roak BJ, Cooper GM, Shendure J. A general framework for estimating the relative pathogenicity of human genetic variants. *Nat Genet.* 2014 Mar;46(3):310-5.

DiscoveryLocus	top_lead_SNP_uniqID	#candidate SNPs	chr	pos	non_effect_allele	effect_allele	MAF	gnasP	r2	IndelSNP	nearestGene (Ensembl)	AnnoType	Consequence	ConDetail	GeneName 2	AnnoType	Consequence	ConDetail	signifmod_colon_eqtMafPit	eQTL Gene 1	p_eQTL	FDR<0.05_eQTL	eQTL Gene 2	p_eQTL	FDR<0.05_eQTL	DiscoveryLocus	CADD	RDB	minChRate	CADD top (without pseudogenes)		
1	r51913166	2	144131821	G	A	0.2306	5.9e-09	0.897371	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0													
1	r50864317	2	144074015	C	A	0.3111	2.4e-26	0.937379	r51167960	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								top	2.24	7	5		
1	r5070973	2	144281919	T	A	0.1809	9.8e-54	0.972062	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								2.06	5	4			
1	214428109_TA_T	2	144281091	T	TA	0.1819	4.4e-53	0.979139	r6734367	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								19.79	NA	4			
1	r51148501	2	144180991	G	C	0.2306	3.2e-09	0.897371	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								2.06	29	1			
1	r50292184	A	0.2376	1.4e-09	0.942787	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0											18.55	4	4			
1	r50179961	2	144342061	T	C	0.1799	5.1e-54	0.910892	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								18.46	5	1			
1	r51211204	2	144178400	C	T	0.1797	3.4e-09	0.910892	r51211204	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								18.24	1				
1	2144437590_TAAAAAA	2	144437590	T	TAAAAAAA	0.1839	4.6e-12	1	2144437590_TAAAAAA	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0									17.58	NA	5		
1	r4662118	2	144280806	G	A	0.22485	5.6e-09	1	r4662118	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								16.75	5	1			
1	2144131721_TTAGA_T	2	144137071	T	TTAG	0.2375	1.1e-09	1	r51615162	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								16.64	1				
1	r50704060	2	144317029	T	A	0.2416	2.3e-09	0.952657	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								16.43	4	4			
1	r51312193	2	144343620	C	T	0.1405	1.0e-12	0.9608	r51402906	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								16.29	5	1			
1	r5050013	2	144180869	C	T	0.4433	1.4e-17	0.615162	r50516719	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								16.27	1				
1	r44146423	C	0.2247	1.3e-46	0.616181	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0											16.13	6	4			
1	r44321606	2	144332854	C	T	0.4085	7.4e-13	0.988232	r14029006	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								15.66	5	4			
1	r51340859	2	144463275	A	G	0.24374	6.4e-09	0.710917	r13883236	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								15.33	4				
1	r4611538	2	144198216	G	A	0.1561	6.9e-08	0.814491	r6723640	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								15.13	6	4			
1	r44233568	2	144233180	A	G	0.2227	8.0e-07	0.670343	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								14.84	6	4			
1	r512394189	2	144232064	T	C	0.2306	5.5e-09	0.897371	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								14.67	7	4			
1	r511898289	2	144347805	T	C	0.2316	4.5e-09	0.891938	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								14.48	7	4			
1	r50929186	2	144310402	A	G	0.2416	2.0e-09	0.952657	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								14.19	6	2			
1	r44662120	2	144384755	C	T	0.159	6.8e-06	0.808238	r6723640	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								13.82	29	5			
1	r510167657	2	144333705	G	C	0.2306	5.0e-09	0.897371	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								13.54	6	5			
1	r44146022	2	144378627	A	G	0.1465	3.3e-22	1	r446022	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								13.23	7	4			
1	r51083495	2	144323550	A	G	0.2347	1.3e-46	0.616181	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								12.62	5	4			
1	r512989517	2	144498931	G	C	0.3718	3.3e-22	0.818256	r51298858	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								12.34	7	2			
1	r50249597	2	144483781	T	A	0.3469	5.5e-08	0.738872	r10592197	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								12.33	5	4			
1	r42731563	C	0.2107	2.1e-09	0.970445	r51167960	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0											12.19	1				
1	r64217309	C	0.07753	2.3e-19	1	r64217309	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0												11.74	5	4		
1	r51018734	2	144330021	A	T	0.2316	5.6e-09	0.891938	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								11.22	5	4			
1	r50706216	2	144219957	T	C	0.2306	4.4e-09	0.897371	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								11.16	4				
1	r51001406	2	144352437	C	A	0.2316	8.4e-09	0.891938	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								11.08	5	4			
1	r50206067	2	144477751	A	G	0.4702	1.4e-15	1	r50206067	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								11.01	5	4			
1	r51341759	2	144316090	A	G	0.4215	1.1e-12	0.90154	r51402906	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								10.44	7	4			
1	r50223683	2	144479235	T	C	0.4146	8.9e-09	0.952657	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								9.98	5	4			
1	r5075423	2	144187417	G	A	0.1797	6.5e-08	0.973042	r12612084	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								9.88	3	5			
1	r50291823	2	144282635	T	C	0.2376	1.1e-09	0.942787	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								9.80	8	4			
1	2144483991_CA_C	2	144483991	C	CA	0.3509	8.9e-08	0.773433	r10592197	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								9.54	NA	1			
1	2144281782_AT_A	2	144281782	A	AT	0.1819	2.4e-51	0.979139	r6734367	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								9.51	NA	1			
1	r50593812	2	144423663	A	T	0.1562	9.0e-11	0.781334	r205945381	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								9.304	4				
1	2144349006_ACT_A	2	144349006	A	ACT	0.1789	6.3e-54	0.942787	r6734367	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0								9.15	NA	1			
1	r57412890	C	0.2883	4.4e-09	0.7958	r527110833	ARHGAP15	Transcript	INTRONIC	intron,feature_truncation	RP1-143622.1	Transcript	INTRONIC	intronic	intron,feature_truncation	0											8.92	NA	5			
1	r51092197	2	144491308	A	G	0.3966	2.4e-09	1	r51092197	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0									8.74	7	4		
1	r51300571	2	144490931	T	C	0.1708	4.4e-22	0.822517	r12608658	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								8.74	7	4			
1	r511477811	A	0.2883	4.2e-09	0.7958	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0											7.88	7	4			
1	r4561605	2	144272150	G	C	0.4493	1.1e-07	0.943893	r13032344	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								7.89	4	4			
1	r51342656	2	144318058	A	G	0.4085	6.8e-11	0.988271	r14029006	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0								7.65	1				
1	2142826162	G	0.2376	1.8e-09	0.942787	r51615162	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0											7.26	6	4			
1	r50929188	2	144352081	A	G	0.2247	1.1e-46	0.616181	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP1-143622.1	Transcript	INTRONIC	intronic	intron	0													

[illegible]

1	r55769935	2	14429912	A	G	0.2386	1.4e-09	0.95829	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.242	Transcript	INTRONIC	intron_cnc	0		1	0.880	7	4
1	r4278793	2	14429242	C	T	0.1789	1.1e-54		r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.243	Transcript	INTRONIC	intron_cnc	0		1	0.878	7	5
1	r520231726	1	14421708	T	C	0.1322	2e-21	0.1728234	r5202345381	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.244	Transcript	INTRONIC	intron_cnc	0		1	0.864	7	4
1	r51071589	1	14429240	C	A	0.1809	7.4e-54	0.986011	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.245	Transcript	INTRONIC	intron_cnc	0		1	0.844	5	4
1	r6727288	2	14427138	C	T	0.4423	4.1e-08	0.991473	r55508804	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.246	Transcript	INTRONIC	intron_cnc	0		1	0.834	4	4
1	2.144404928 TA, T	1	144404928	TA, T	G	0.9776	1e-24	1	2.144404928 TA, T	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.247	Transcript	INTRONIC	intron_cnc	0		1	0.841	NA	4
1	r4662124	1	14462124	T	G	0.2247	3.9e-08	1	r4662124	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.248	Transcript	INTRONIC	intron_cnc	0		1	0.799	7	4
1	2.144300304 AAT, A	2	144300304	AAT	AAT	0.4414	3.1e-11	1	2.144300304 AAT, A	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.249	Transcript	INTRONIC	intron_cnc	0		1	0.727	NA	5
1	r11157900	1	14417900	T	G	0.1301	1.2e-20	1	r11157900	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.250	Transcript	INTRONIC	intron_cnc	0		1	0.705	7	4
1	r11290195	1	14439585	A	G	0.2674	6.1e-09	0.99949	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.251	Transcript	INTRONIC	intron_cnc	0		1	0.692	6	5
1	r11889721	2	144327950	C	T	0.2316	6.0e-09	0.91838	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.252	Transcript	INTRONIC	intron_cnc	0		1	0.682	7	4
1	r51077079	1	14441987	T	G	0.2763	4.4e-08	0.939919	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.253	Transcript	INTRONIC	intron_cnc	0		1	0.674	6	5
1	r512211187	1	14448120	ATGTTG	A	0.804	1.1e-12	1	r512211187	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.254	Transcript	INTRONIC	intron_cnc	0		1	0.647	NA	4
1	r6217067	2	14426149	A	G	0.1779	2.8e-54	0.99298	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.255	Transcript	INTRONIC	intron_cnc	0		1	0.643	6	5
1	r62005177	2	144421627	A	G	0.2763	5.5e-08	0.939919	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.256	Transcript	INTRONIC	intron_cnc	0		1	0.571	7	5
1	r520231796	1	144441913	GGT	G	0.2763	5.5e-08	0.939919	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.257	Transcript	INTRONIC	intron_cnc	0		1	0.561	NA	4
1	r54010241	2	14428095	TTA	T	0.1352	9.4e-06	0.77917	r6273640	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.258	Transcript	INTRONIC	intron_cnc	0		1	0.541	NA	5
1	r54006062	2	14429934	A	G	0.4881	3.2e-21	0.905454	2.144305254 CT, C	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.259	Transcript	INTRONIC	intron_cnc	0		1	0.541	7	5
1	r1122115115	2	14443226	C	T	0.2773	8.2e-08	0.855139	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.260	Transcript	INTRONIC	intron_cnc	0		1	0.527	6	5
1	r510770378	2	14438078	T	C	0.2237	8.5e-47	0.65592	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.261	Transcript	INTRONIC	intron_cnc	0		1	0.509	5	5
1	r51019845	2	14446087	C	G	0.3539	2.7e-20	0.734837	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.262	Transcript	INTRONIC	intron_cnc	0		1	0.509	5	4
1	r57062381	1	14445243	AAT	A	0.3549	4.1e-20	0.739357	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.263	Transcript	INTRONIC	intron_cnc	0		1	0.475	NA	4
1	r556741473	2	144490479	GT	G	0.3509	6.1e-11	1	r556741473	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.264	Transcript	INTRONIC	intron_cnc	0		1	0.472	NA	5
1	r67355850	2	144345616	A	G	0.2806	3.4e-09	0.897371	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.265	Transcript	INTRONIC	intron_cnc	0		1	0.468	7	4
1	r54491526	1	14427756	C	G	0.4794	5.4e-08	0.959728	r55508804	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.266	Transcript	INTRONIC	intron_cnc	0		1	0.465	7	4
1	r5368217420	2	144349201	TC	T	0.1767	7.5e-32	1	r5368217420	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.267	Transcript	INTRONIC	intron_cnc	0		1	0.442	NA	4
1	r11839012	2	144274527	T	G	0.4903	1.4e-22	0.986169	2.144305254 CT, C	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.268	Transcript	INTRONIC	intron_cnc	0		1	0.436	6	4
1	r17364524	1	14427756	C	A	0.1728	1.6e-23	1	r17364524	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.269	Transcript	INTRONIC	intron_cnc	0		1	0.426	5	5
1	r10298176	2	144186113	T	G	0.1551	9.3e-06	0.821345	r6273640	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.270	Transcript	INTRONIC	intron_cnc	0		1	0.425	7	5
1	r42477108	2	14439018	C	A	0.4245	2.6e-14	0.880546	r6430036	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.271	Transcript	INTRONIC	intron_cnc	0		1	0.418	6	5
1	r11504125	2	144344913	T	G	0.2306	3.6e-09	0.897371	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.272	Transcript	INTRONIC	intron_cnc	0		1	0.395	6	4
1	r170031864	2	14419555	C	A	0.1581	6.1e-06	0.815	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.273	Transcript	INTRONIC	intron_cnc	0		1	0.354	6	5
1	r11892876	2	144326184	G	A	0.4533	1.8e-12	0.81341	r14409006	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.274	Transcript	INTRONIC	intron_cnc	0		1	0.353	7	4
1	r12691488	2	144412819	T	G	0.3072	1.9e-28	0.95751	r114379000	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.275	Transcript	INTRONIC	intron_cnc	0		1	0.353	5	4
1	r57294814	1	14441489	C	G	0.2761	4.5e-08	0.818515	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.276	Transcript	INTRONIC	intron_cnc	0		1	0.299	5	5
1	r6717024	2	14430870	G	C	0.1789	4.6e-55	1	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.277	Transcript	INTRONIC	intron_cnc	0		1	0.299	5	5
1	r11769792	2	14443071	G	A	0.3678	4.0e-22	0.707754	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.278	Transcript	INTRONIC	intron_cnc	0		1	0.272	6	4
1	r56516814	1	14429061	GT	G	0.4215	4.0e-14	0.793602	r4430036	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.279	Transcript	INTRONIC	intron_cnc	0		1	0.265	0	5
1	r57615295	2	144425178	T	G	0.1789	6.3e-12	1	r200345381	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.280	Transcript	INTRONIC	intron_cnc	0		1	0.260	6	5
1	r6459485	2	144347994	T	G	0.1789	3.0e-54	0.817042	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.281	Transcript	INTRONIC	intron_cnc	0		1	0.229	7	4
1	r57404480	2	14434847	AAT	A	0.0765	1.2e-23	0.91111	r63157684	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.282	Transcript	INTRONIC	intron_cnc	0		1	0.198	NA	4
1	r111878424	2	144461577	G	GA	0.1371	2.6e-09	1	r111878424	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.283	Transcript	INTRONIC	intron_cnc	0		1	0.185	NA	4
1	r59950149	2	144296927	GT	G	0.4811	2.5e-21	0.902024	2.144305254 CT, C	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.284	Transcript	INTRONIC	intron_cnc	0		1	0.183	NA	5
1	r5706665	2	14429411	C	G	0.4206	1.9e-09	0.958055	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.285	Transcript	INTRONIC	intron_cnc	0		1	0.177	6	5
1	r5774442620	2	144300226	A	ATT	0.0497	9.8e-16	1	r774442620	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.286	Transcript	INTRONIC	intron_cnc	0		1	0.176	NA	5
1	r4374318	2	144389671	C	G	0.1789	7.5e-11	1	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.287	Transcript	INTRONIC	intron_cnc	0		1	0.165	6	5
1	r565651196	2	144441839	GGCACACTCTGTAG	G	0.1789	1.6e-23	1	r774442620	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.288	Transcript	INTRONIC	intron_cnc	0		1	0.156	7	4
1	r5140478	2	144349478	T	G	0.1789	2.3e-54	0.917042	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.289	Transcript	INTRONIC	intron_cnc	0		1	0.137	6	4
1	r5131326	2	144170273	G	A	0.81	3.4e-20	0.818782	r527110833	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.290	Transcript	INTRONIC	intron_cnc	0		1	0.135	6	4
1	r11894956	2	144381312	A	T	0.1789	2.2e-51	0.917042	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.291	Transcript	INTRONIC	intron_cnc	0		1	0.132	7	4
1	r118341174	1	144421360	A	T	0.0946	1.9e-21	1	r118341174	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.292	Transcript	INTRONIC	intron_cnc	0		1	0.114	6	5
1	r5834868	2	144493827	AT	A	0.3489	3.1e-08	0.793312	r110928197	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.293	Transcript	INTRONIC	intron_cnc	0		1	0.113	NA	4
1	r10187118	2	14439126	C	G	0.2316	4.0e-09	0.918538	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.294	Transcript	INTRONIC	intron_cnc	0		1	0.082	5	2
1	r55688084	2	144271545	T	A	0.4408	3.4e-07	1	r55688084	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.295	Transcript	INTRONIC	intron_cnc	0		1	0.084	7	4
1	r5749183	2	14422081	T	C	0.1571	3.1e-08	0.807716	r6273640	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.296	Transcript	INTRONIC	intron_cnc	0		1	0.060	7	5
1	r54010551	2	144310137	G	T	0.1217	3.3e-08	0.845054	r6734367	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.297	Transcript	INTRONIC	intron_cnc	0		1	0.046	5	2
1	r5706254	2	14436816	G	A	0.1521	6.8e-08	0.846002	r6273640	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.298	Transcript	INTRONIC	intron_cnc	0		1	0.044	7	4
1	2.144341098 TG, T	2	144341098	TG	TG	0.2306	2.8e-09	0.897371	r56151632	ARHGAP15	Transcript	INTRONIC	intron	RP11-414621.299	Transcript	INTRONIC	intron_cnc	0		1	0.028	NA	5

3	r781764957	10	25821815 C	CAGCAGTCTTC0.4235	7.6e-19	0.898421	r77077800	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.361	Transcript	INTRONIC	intron,unc	1	GPRI58	3.95048e-06	1.51050e-05	GPRI58	3.95048e-06	1.51050e-05	3	8.004	NA	5	
3	10-23816032_CAT_C	10	25816032 C	CAT	0.4394	1.3e-22	0.972685	r77077800	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.364	Transcript	INTRONIC	intron,unc	1	GPRI58	3.62414e-08	1.51050e-05	GPRI58	3.62414e-08	1.51050e-05	3	7.997	NA	5
3	r14203126	10	25757981 T	C	0.4642	1.3e-08	0.843173	r8248489	GPRI58	Transcript	INTRONIC	intron	RP11-436023.365	Transcript	INTRONIC	intron,unc	1	GPRI58	6.25301e-07	1.51050e-05	GPRI58	6.25301e-07	1.51050e-05	3	7.772	NA	5
3	r5761925 C	A	0.16	1.2e-10	1	r577171310	GPRI58	Transcript	INTRONIC	intron	RP11-436023.366	Transcript	INTRONIC	intron,unc	0	GPRI58	2.52228e-07	1.51050e-05	GPRI58	2.52228e-07	1.51050e-05	3	7.999	7	5		
3	r4749043	10	25822360 G	A	0.3459	8.8e-11	0.792767	r4749042	GPRI58	Transcript	INTRONIC	intron	RP11-436023.367	Transcript	INTRONIC	intron,unc	0	GPRI58	2.52228e-07	1.51050e-05	GPRI58	2.52228e-07	1.51050e-05	3	7.557	7	5
3	r1414041	10	25851921 T	C	0.4076	8.7e-10	0.550347	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.368	Transcript	INTRONIC	intron,unc	0	GPRI58	1.83554e-07	1.51050e-05	GPRI58	1.83554e-07	1.51050e-05	3	7.446	NA	5
3	10-25820555_GTAT_G	10	25820555 C	GTAT	0.4274	6.7e-19	0.528023	r77077800	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.369	Transcript	INTRONIC	intron,unc	1	GPRI58	1.83554e-07	1.51050e-05	GPRI58	1.83554e-07	1.51050e-05	3	7.411	NA	5
3	r57329745	10	2579885 CT	C	0.136	6.0e-11	1	r577171310	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.370	Transcript	INTRONIC	intron,unc	0	GPRI58	7.234	NA	5						
3	r75504166	10	25850451 G	C	0.137	1.3e-06	0.72239	r7903204	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.371	Transcript	INTRONIC	intron,unc	0	GPRI58	1.34231e-09	1.51050e-05	GPRI58	1.34231e-09	1.51050e-05	3	7.087	NA	5
3	r4749051	10	25869789 CT	CTTAAATA	T	0.4473	2.4e-10	0.528023	r4749042	GPRI58	Transcript	INTRONIC	intron	RP11-436023.372	Transcript	INTRONIC	intron,unc	0	GPRI58	7.234	NA	5					
3	10-25698174_CTTG_C	10	25698174 C	CTTGG	0.1352	3.6e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.373	Transcript	INTRONIC	intron,unc	0	GPRI58	7.232	NA	7						
3	r75919158	10	25840529 A	C	0.1867	4.0e-12	0.811438	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.374	Transcript	INTRONIC	intron,unc	0	GPRI58	7.232	NA	7						
3	r15014057	10	25830127 G	A	0.4056	4.3e-06	0.740488	r1029179	GPRI58	Transcript	INTRONIC	intron	RP11-436023.375	Transcript	INTRONIC	intron,unc	0	GPRI58	7.232	NA	7						
3	r11818706	10	25883475 T	C	0.1799	3.7e-06	0.759262	r4749042	GPRI58	Transcript	INTRONIC	intron	RP11-436023.376	Transcript	INTRONIC	intron,unc	0	GPRI58	7.134	NA	6						
3	r11303614	10	25753801 A	C	0.1763	3.6e-07	0.861567	r8248489	GPRI58	Transcript	INTRONIC	intron	RP11-436023.377	Transcript	INTRONIC	intron,unc	0	GPRI58	1.34231e-09	1.51050e-05	GPRI58	1.34231e-09	1.51050e-05	3	6.952	6	9
3	r11014646	10	25716511 G	T	0.1352	4.8e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.378	Transcript	INTRONIC	intron,unc	0	GPRI58	5.08301e-09	1.51050e-05	GPRI58	5.08301e-09	1.51050e-05	3	6.828	NA	5
3	r15837174	10	25840529 A	C	0.137	2.1e-06	0.72239	r7903204	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.379	Transcript	INTRONIC	intron,unc	0	GPRI58	6.725	NA	7						
3	r11014610	10	25855809 A	T	0.4245	1.3e-11	0.964418	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.381	Transcript	INTRONIC	intron,unc	0	GPRI58	6.721	NA	5						
3	r11373212	10	25788138 CA	C	0.3748	4.1e-12	0.939739	r4749042	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.382	Transcript	INTRONIC	intron,unc	1	GPRI58	4.4196e-07	1.51050e-05	GPRI58	4.4196e-07	1.51050e-05	3	6.697	NA	5
3	r1524588	10	25752008 A	G	0.407	9.1e-09	0.564711	r8248489	GPRI58	Transcript	INTRONIC	intron	RP11-436023.383	Transcript	INTRONIC	intron,unc	0	GPRI58	2.15921e-07	1.51050e-05	GPRI58	2.15921e-07	1.51050e-05	3	6.627	NA	5
3	r150828830	10	25863763 A	G	0.4284	6.5e-09	0.592026	r34874972	GPRI58	Transcript	INTRONIC	intron	RP11-436023.384	Transcript	INTRONIC	intron,unc	0	GPRI58	6.620	NA	5						
3	r388833253	10	25863075 C	CAAAA	0.3151	1.7e-08	1	r38833253	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.385	Transcript	INTRONIC	intron,unc	0	GPRI58	6.608	NA	5						
3	r11014621	10	25855432 G	A	0.338	2.2e-06	0.755515	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.386	Transcript	INTRONIC	intron,unc	0	GPRI58	6.412	NA	7						
3	r11014654	10	25732995 G	T	0.165	1.0e-08	0.524635	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.387	Transcript	INTRONIC	intron,unc	0	GPRI58	6.239	NA	4						
3	r15773837	10	25766964 A	G	0.499	8.0e-09	0.594813	r8248489	GPRI58	Transcript	INTRONIC	intron	RP11-436023.388	Transcript	INTRONIC	intron,unc	1	GPRI58	9.56353e-08	1.51050e-05	GPRI58	9.56353e-08	1.51050e-05	3	5.867	7	5
3	r15703526	10	25764346 A	T	0.16	1.7e-10	1	r577171310	GPRI58	Transcript	INTRONIC	intron	RP11-436023.389	Transcript	INTRONIC	intron,unc	0	GPRI58	5.808	NA	7						
3	r150741092	10	25814527 T	G	0.3608	2.3e-13	0.898982	r4749042	GPRI58	Transcript	INTRONIC	intron	RP11-436023.390	Transcript	INTRONIC	intron,unc	1	GPRI58	1.05109e-08	1.51050e-05	GPRI58	1.05109e-08	1.51050e-05	3	5.716	7	5
3	r4749040	10	25787775 G	G	0.4364	1.4e-18	0.845856	r77077800	GPRI58	Transcript	INTRONIC	intron	RP11-436023.391	Transcript	INTRONIC	intron,unc	1	GPRI58	1.14208e-06	1.51050e-05	GPRI58	1.14208e-06	1.51050e-05	3	5.607	5	5
3	r150600135	10	25848080 A	C	0.4239	3.2e-06	0.718818	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.392	Transcript	INTRONIC	intron,unc	0	GPRI58	5.460	NA	5						
3	r150828808	10	25732083 A	A	0.161	3.3e-08	0.511558	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.393	Transcript	INTRONIC	intron,unc	0	GPRI58	5.457	NA	7						
3	r11014652	10	25732966 G	A	0.1412	4.0e-08	0.824647	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.394	Transcript	INTRONIC	intron,unc	0	GPRI58	5.453	NA	5						
3	r48030706	10	25767790 G	C	0.408	3.7e-09	0.838951	r8248489	GPRI58	Transcript	INTRONIC	intron	RP11-436023.395	Transcript	INTRONIC	intron,unc	0	GPRI58	5.450	NA	6						
3	r15605578	10	25851267 A	T	0.128	3.8e-08	0.820258	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.396	Transcript	INTRONIC	intron,unc	0	GPRI58	5.450	NA	6						
3	10-25791541_CA_C	10	25791541 C	CA	0.3718	7.4e-12	0.936418	r4749042	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.397	Transcript	INTRONIC	intron,unc	1	GPRI58	3.23567e-09	1.51050e-05	GPRI58	3.23567e-09	1.51050e-05	3	5.399	NA	5
3	r17474938	10	25814587 G	G	0.4801	2.8e-20	0.840593	r7902592	GPRI58	Transcript	INTRONIC	intron	RP11-436023.398	Transcript	INTRONIC	intron,unc	1	GPRI58	8.74988e-07	1.51050e-05	GPRI58	8.74988e-07	1.51050e-05	3	5.216	7	5
3	r57764895	10	25764006 T	C	0.1342	8.2e-08	0.813303	r577171310	GPRI58	Transcript	INTRONIC	intron	RP11-436023.399	Transcript	INTRONIC	intron,unc	1	GPRI58	2.38073e-06	1.51050e-05	GPRI58	2.38073e-06	1.51050e-05	3	5.066	NA	5
3	r138443630	10	25775741 CTT	C	0.5	1.6e-08	0.518256	r8248489	GPRI58	Transcript	INTRONIC	intron,feature_truncation	RP11-436023.400	Transcript	INTRONIC	intron,unc	0	GPRI58	5.066	NA	5						
3	r201594206	10	25779908 G	T	0.1581	3.2e-11	1	r20154206	GPRI58	Transcript	INTRONIC	intron	RP11-436023.401	Transcript	INTRONIC	intron,unc	0	GPRI58	5.062	NA	5						
3	r11014554	10	25724393	A	0.1352	6.7e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.402	Transcript	INTRONIC	intron,unc	0	GPRI58	4.967	NA	5						
3	r9299793	10	25875717 G	A	0.4722	2.6e-12	0.823293	r34874972	GPRI58	Transcript	INTRONIC	intron	RP11-436023.403	Transcript	INTRONIC	intron,unc	0	GPRI58	4.960	NA	8						
3	r67296777	10	25714319 G	C	0.1352	5.6e-06	0.740308	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.404	Transcript	INTRONIC	intron,unc	0	GPRI58	4.787	NA	7						
3	r67296777	10	25729679 T	C	0.1342	7.2e-09	0.833303	r577171310	GPRI58	Transcript	INTRONIC	intron	RP11-436023.405	Transcript	INTRONIC	intron,unc	0	GPRI58	4.760	NA	7						
3	r8074889	10	25786852 G	C	0.4503	5.7e-19	0.806503	r77077800	GPRI58	Transcript	INTRONIC	intron	RP11-436023.406	Transcript	INTRONIC	intron,unc	0	GPRI58	4.718	NA	5						
3	r11014565	10	25715319 A	G	0.2018	2.3e-06	0.786777	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-436023.407	Transcript	INTRONIC	intron,unc	0	GPRI58	4.687	NA	1						
3	r7903136	10	25847978	A	0.4006	7.8e-11	0.534773	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.408	Transcript	INTRONIC	intron,unc	0	GPRI58	4.683	NA	7						
3	r7100629	10	25834924 A	T	0.4205	3.4e-12	0.948192	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.409	Transcript	INTRONIC	intron,unc	0	GPRI58	4.672	NA	5						
3	r4749018	10	25769799 G	A	0.4513	1.3e-18	0.810639	r77077800	GPRI58	Transcript	INTRONIC	intron	RP11-436023.410	Transcript	INTRONIC	intron,unc	0	GPRI58	7.0251e-07	1.51050e-05	GPRI58	7.0251e-07	1.51050e-05	3	4.662	7	5
3	r15105086	10	25764521 A	T	0.16	1.4e-10	1	r577171310	GPRI58	Transcript	INTRONIC	intron	RP11-436023.411	Transcript	INTRONIC	intron,unc	0	GPRI58	4.662	NA	5						
3	r110082439	10	25832211 G	A	0.3976	1.4e-11	0.861839	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.412	Transcript	INTRONIC	intron,unc	0	GPRI58	4.550	NA	5						
3	r12780734	10	25847609 G	A	0.189	2.3e-06	0.788655	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.413	Transcript	INTRONIC	intron,unc	0	GPRI58	4.550	NA	5						
3	r7903204	10	25847680 A	C	0.1175	8.1e-11	1	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-436023.414	Transcript	INTRONIC	intron,unc	0	GPRI58	4.476	NA	5						
3	r4747524	10	25788015 C	A	0.4364	1.4e-18	0.845856	r77077800	GPRI58	Transcript	INTRON																

3	r1528865	10	25782764 C	T	0.4732	1.5e-08	0.75677	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	5.47339e-08	1.5105e-05	GPRI58	5.47339e-08	1.5105e-05	3	2.587	NA	1
3	r15101447	10	25717594 T	C	0.1352	6.4e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.560	6	9
3	r5784736	10	25821793 G	A	0.4235	6.8e-10	0.88642	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.550	6	9
3	r6482488	10	25796182 C	T	0.4821	1.1e-16	0.94204	r5708292	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	1.73728e-05	1.5105e-05	GPRI58	1.73728e-05	1.5105e-05	3	2.545	7	5
3	r57005382	10	25786532 A	G	0.4742	1.1e-08	0.75677	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	2.2660e-08	1.5105e-05	GPRI58	2.2660e-08	1.5105e-05	3	2.538	NA	5
3	r151015483	10	25713841 C	T	0.1352	3.3e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.524	NA	5
3	r15028450	10	25832059 A	T	0.3708	3.1e-10	0.72964	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.67232e-06	1.5105e-05	GPRI58	1.67232e-06	1.5105e-05	3	2.518	6	5
3	r980380	10	25827393 A	G	0.1311	1.3e-06	0.851269	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.67232e-06	1.5105e-05	GPRI58	1.67232e-06	1.5105e-05	3	2.440	NA	5
3	r1276816	10	25761511 T	T	0.1342	7.1e-09	0.813053	r57717130	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.67232e-06	1.5105e-05	GPRI58	1.67232e-06	1.5105e-05	3	2.430	6	7
3	r151014659	10	25731702 T	C	0.361	3.5e-08	0.911668	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.386	7	5
3	r12770990	10	25734142 C	T	0.36	1.6e-09	0.935356	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.306	6	9
3	r6484290	10	25821294 T	C	0.4235	4.3e-10	0.88642	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.275	6	9
3	r64545439	10	25743127 C	C	0.1322	1.9e-09	0.771189	r57717130	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.283	7	5
3	r10282807	10	25731823 T	C	0.361	3.5e-08	0.911668	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.267	7	9
3	r1512355	10	25781407 A	T	0.4742	2.1e-08	0.75677	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.183	NA	5
3	r7888963	10	25884742 G	A	0.1789	4.9e-06	0.751996	r12268257	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.167	6	5
3	r12018916	10	25831999 T	C	0.4205	3.6e-12	0.948182	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.162	7	5
3	r15121552	10	25735153 C	T	0.1403	8.8e-09	0.845532	r57717130	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.149	7	5
3	10-25911676_GT	10	25911676 G	GT	0.2356	1.6e-09	1	10-25911676_GT	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.085	NA	9
3	r83488146	10	25746371 CT	C	0.1372	3.9e-09	0.748853	r57717130	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	3.8564e-08	1.5105e-05	GPRI58	3.8564e-08	1.5105e-05	3	2.082	NA	5
3	r57048226	10	25772005 A	G	0.1581	5.6e-10	0.86871	r57721210	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.052	5	5
3	r5097800	10	25786532 G	A	0.4801	2.1e-13	0.936684	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	2.52567e-06	1.5105e-05	GPRI58	2.52567e-06	1.5105e-05	3	2.037	5	5
3	r12259686	10	25699841 C	T	0.1352	3.9e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	2.013	6	4
3	r25055658	10	25903965 C	A	0.1799	3.7e-06	0.759262	r12268257	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.969	NA	9
3	r5005591	10	25776176 G	A	0.492	1.3e-08	0.950244	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	2.1241e-07	1.5105e-05	GPRI58	2.1241e-07	1.5105e-05	3	1.968	NA	5
3	r50764543	10	25699291 C	T	0.1352	4.9e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.965	5	7
3	r150283816	10	25821273 G	A	0.4463	9.1e-12	1	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.1388e-07	1.5105e-05	GPRI58	1.1388e-07	1.5105e-05	3	1.917	29	5
3	r64747531	10	25865513 A	G	0.338	4.3e-06	0.704343	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.1388e-07	1.5105e-05	GPRI58	1.1388e-07	1.5105e-05	3	1.917	7	5
3	r25987363	10	25773608 A	G	0.5	1.6e-08	0.938256	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	1.47901e-07	1.5105e-05	GPRI58	1.47901e-07	1.5105e-05	3	1.903	6	5
3	r7089916	10	258219642	CT	0.4235	1.9e-09	0.86871	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	7.0997e-06	1.5105e-05	GPRI58	7.0997e-06	1.5105e-05	3	1.897	6	9
3	r15031889	10	25821234 TG	T	0.4463	1.2e-21	1	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	1.7746e-07	1.5105e-05	GPRI58	1.7746e-07	1.5105e-05	3	1.855	NA	5
3	r15135158	10	25838771 T	C	0.136	9.5e-07	0.759261	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.47901e-07	1.5105e-05	GPRI58	1.47901e-07	1.5105e-05	3	1.848	NA	5
3	r15130123	10	25773094 G	T	0.1	1.27e-08	0.748853	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.842	NA	5
3	r5708916	10	25815785 GA	G	0.4245	1.9e-10	0.86843	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.842	NA	5
3	r12334847	10	25699776 C	T	0.1352	3.1e-06	0.751895	r12764415	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.813	6	4
3	r7808793	10	25917499 G	A	0.1859	1.3e-06	0.731673	r12268257	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.810	7	5
3	r15040348	10	2574587 A	C	0.4897	6.1e-09	0.86871	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.808	NA	9
3	r7804979	10	25760600 A	G	0.16	1.7e-10	1	r57717130	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.798	6	5
3	r15101495	10	25810281 A	G	0.3777	1.7e-15	0.829634	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	2.41204e-09	1.5105e-05	GPRI58	2.41204e-09	1.5105e-05	3	1.794	7	5
3	r57279639	10	25861392 G	A	0.4294	5.5e-09	0.936624	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	2.41204e-09	1.5105e-05	GPRI58	2.41204e-09	1.5105e-05	3	1.794	7	5
3	r696296	10	25821826 G	A	0.4463	1.8e-21	1	r7077800	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	1	GPRI58	6.14784e-08	1.5105e-05	GPRI58	6.14784e-08	1.5105e-05	3	1.768	NA	5
3	r7913189	10	2584491 G	C	0.4225	1.1e-11	0.956265	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.748	7	5
3	r15140931	10	25874085 A	T	0.498	5.4e-09	0.936919	r824859	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	1.34261e-07	1.5105e-05	GPRI58	1.34261e-07	1.5105e-05	3	1.748	7	5
3	r10282818	10	25836095 T	C	0.4215	3.4e-12	0.95632	r7903204	GPRI58	Transcript	INTRONIC	intron	RP11-43621488	Transcript	INTRONIC	intronic	0	GPRI58	3.9004e-06	1.5105e-05	GPRI58	3.9004e-06	1.5105e-05	3	1.725	6	1
3	r1581117	10	25834481 C	T	0.4205	3.2e-12																					

[illegible]



5	rs7498797	2	56189500 T	C	0.1708	2.7e-06	0.758918	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.726	Transcript	INTRONIC	intronic	0				5	6.319	7	5				
5	rs1897478	2	56201771 T	C	0.3956	2.6e-06	0.839388	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.727	Transcript	INTRONIC	intronic	0				5	6.165	7	5				
5	rs7504347	2	56187437 G	T	0.3499	2.5e-06	0.84082	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.728	Transcript	INTRONIC	intronic	0				5	5.972	7	5				
5	2.56027013_CAAACA	2	56027013 C	CAAAACA	0.3588	3.7e-06	0.762261	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.730	Transcript	INTRONIC	intronic	0				5	5.763	NA	14				
5	rs1394045	2	56034835 G	A	0.2078	2.6e-06	0.818389	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.730	Transcript	INTRONIC	intronic	0				1	5.110	7	5				
5	rs6215788	2	56035186 A	C	0.2127	3.7e-06	0.805491	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.731	Transcript	INTRONIC	intronic	0				1	5.100	7	5				
5	rs233964	2	56134947 C	T	0.1083	3.7e-06	0.720693	2.56116193_TTGATCTCTGEEFMP1		Transcript	INTRONIC	intron	RP11-436021.732	Transcript	INTRONIC	intronic	0				5	4.926	7	4				
5	rs1897112	2	56115448 C	A	0.2127	2.7e-06	0.779177	rs5985551	EFEMP1	Transcript	INTRONIC	intron	RP11-436021.733	Transcript	INTRONIC	intronic	0				5	4.746	3a	5				
5	rs6082446	2	56021771 T	C	0.2087	2.0e-06	0.792713	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.734	Transcript	INTRONIC	intronic	0				1	5.100	7	5				
5	rs2009282	2	56012214 C	T	0.2107	5.2e-07	0.821888	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.735	Transcript	INTRONIC	intronic	0				1	4.504	7	5				
5	rs3972118	2	56131202 G	A	0.3499	3.6e-06	0.695824	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.736	Transcript	INTRONIC	intronic	0				5	4.465	6	5				
5	2.56042850_TTGAAA	2	56042850 T	TTGAAA	0.2028	2.5e-07	0.812969	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.737	Transcript	INTRONIC	intronic	0				5	4.448	6	5				
5	rs1727865	2	56095994 G	C	0.1759	1.4e-15	0.843053	rs1802575	EFEMP1	Transcript	INTRONIC	intron	RP11-436021.738	Transcript	INTRONIC	intronic	0				5	4.422	6	4				
5	rs1734934	2	56044936 G	A	0.07256	8.4e-11	1	rs1739379		Intergenic	INTERGENIC	intergenic	RP11-436021.739	Transcript	INTRONIC	intronic	0				5	4.382	5	5				
5	rs70321374	2	56003816 G	C	0.1243	1.7e-17	0.835609	rs1802575		Intergenic	INTERGENIC	intergenic	RP11-436021.740	Transcript	INTRONIC	intronic	0				5	4.136	7	5				
5	rs732132	2	56011881 T	C	0.2773	5.2e-08	0.801224	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.741	Transcript	INTRONIC	intronic	0				5	4.271	6	5				
5	rs6745113	2	56034076 C	T	0.3817	5.6e-06	0.905287	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.742	Transcript	INTRONIC	intronic	0				5	4.264	7	5				
5	rs14472359	2	56051245 T	C	0.1292	6.2e-10	1	rs7079392		Intergenic	INTERGENIC	intergenic	RP11-436021.743	Transcript	INTRONIC	intronic	0				5	4.221	7	5				
5	rs4671260	2	56026374 C	T	0.3579	2.8e-06	0.766554	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.744	Transcript	INTRONIC	intronic	0				5	4.168	6	14				
5	rs12472832	2	56200573 G	C	0.3956	1.7e-06	0.839388	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.745	Transcript	INTRONIC	intronic	0				5	4.124	7	5				
5	rs1432561	2	56138045 T	G	0.3499	2.5e-06	0.79072	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.746	Transcript	INTRONIC	intronic	0				5	4.064	NA	5				
5	rs113192127	2	55998449_CCA	C	0.2296	5.5e-09	1	rs113192127		Intergenic	INTERGENIC	intergenic	RP11-436021.747	Transcript	INTRONIC	intronic	0				5	4.031	NA	5				
5	rs4347871	2	56055825 G	C	0.2038	8.6e-07	0.839882	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.748	Transcript	INTRONIC	intronic	0				1	4.018	7	5				
5	rs6125349	2	56009405 T	A	0.2127	1.6e-06	0.799291	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.749	Transcript	INTRONIC	intronic	0				5	3.942	NA	5				
5	rs734540	2	56191794 G	A	0.3936	9.5e-07	0.854927	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.750	Transcript	INTRONIC	intronic	0				5	3.695	5	5				
5	rs6712017	2	56028444 C	T	0.3539	2.9e-06	0.79088	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.751	Transcript	INTRONIC	intronic	0				5	3.650	5	7				
5	rs1432560	2	56195816 T	G	0.3489	2.6e-06	0.837082	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.752	Transcript	INTRONIC	intronic	0				5	3.642	NA	5				
5	rs2052033	2	56028107 G	C	0.3588	2.7e-06	0.770217	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.753	Transcript	INTRONIC	intronic	0				5	3.527	3a	2				
5	rs3452760	2	56189053 G	A	0.1708	1.2e-06	0.758918	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.754	Transcript	INTRONIC	intronic	0				5	3.525	6	5				
5	rs6733889	2	56189052 G	A	0.1767	1.2e-06	0.758918	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.755	Transcript	INTRONIC	intronic	0				5	3.491	5	5				
5	rs6757057	2	56185138 A	G	0.1560	4.0e-06	0.793695	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.756	Transcript	INTRONIC	intronic	0				5	3.363	5	5				
5	rs7573721	2	56130598 C	T	0.1598	4.3e-06	0.773895	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.757	Transcript	INTRONIC	intronic	0				5	2.929	6	14				
5	rs1620305	2	56203065 A	G	0.1946	1.6e-06	0.818462	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.758	Transcript	INTRONIC	intronic	0				5	2.833	6	5				
5	rs1466485	2	56184741 A	G	0.1608	2.5e-06	0.793635	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.759	Transcript	INTRONIC	intronic	0				5	2.825	NA	5				
5	rs112481479	2	56010910 T	C	0.2038	6.7e-07	0.839882	rs5985551		RegulatoryFeature	REGULATORY	regulatory	RP11-436021.760	Transcript	INTRONIC	intronic	0				1	2.4491e-05	0.001485	RP527A	2.4491e-05	0.001485		
5	rs5802712	2	56021127 T	C	0.2107	2.2e-06	0.792103	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.761	Transcript	INTRONIC	intronic	1				1	RP527A	1.7356e-05	0.001485	RP527A	1.7356e-05	0.001485	
5	rs4991004	2	55994482 G	C	0.1091	2.0e-13	0.910513	rs1339578		Intergenic	INTERGENIC	intergenic	RP11-436021.762	Transcript	INTRONIC	intronic	0				5	2.785	4	2				
5	rs7885789	2	56135099 A	G	0.08151	2.5e-10	0.916129	2.56116193_TTGATCTCTGEEFMP1		Transcript	INTRONIC	intron	RP11-436021.763	Transcript	INTRONIC	intronic	0				5	2.749	7	5				
5	rs17047234	2	56015083 A	C	0.2286	2.1e-08	0.752588	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.764	Transcript	INTRONIC	intronic	1				1	RP527A	3.6799e-05	0.001485	RP527A	3.6799e-05	0.001485	
5	rs1318992	2	56021390 G	C	0.2426	2.6e-06	0.778181	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.765	Transcript	INTRONIC	intronic	0				5	2.437	6	5				
5	rs17360379	2	5592212 T	C	0.07256	8.2e-11	1	rs17360379		Intergenic	INTERGENIC	intergenic	RP11-436021.766	Transcript	INTRONIC	intronic	0				5	2.396	7	5				
5	rs1027129	2	56081813 C	T	0.0564	1.1e-10	1	rs10187129		Intergenic	INTERGENIC	intergenic	RP11-436021.767	Transcript	INTRONIC	intronic	0				5	2.391	7	5				
5	rs18164155	2	5608108 T	C	0.1274	6.2e-10	1	rs1802575		RegulatoryFeature	REGULATORY	regulatory	RP11-436021.768	Transcript	INTRONIC	intronic	0				5	2.365	3a	2				
5	rs20407878	2	56071109 T	C	0.1233	1.3e-17	0.943901	rs1802575		Intergenic	INTERGENIC	intergenic	RP11-436021.769	Transcript	INTRONIC	intronic	0				5	2.335	6	2				
5	rs1346790	2	56091871 T	C	0.1787	1.6e-06	0.841331	rs1125608	EFEMP1	Intergenic	DOWNSTREAM	downstream	RP11-436021.770	Transcript	INTRONIC	intronic	0				5	2.315	NA	4				
5	rs2868894	2	56151369 A	C	0.1916	3.2e-06	0.854927	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.771	Transcript	INTRONIC	intronic	0				5	2.191	5	5				
5	rs1682853	2	5618553 G	T	0.3489	3.3e-06	0.87082	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.772	Transcript	INTRONIC	intronic	0				5	2.188	4	5				
5	rs7074932	2	56081728 A	G	0.1292	6.2e-09	1	rs7074932		Intergenic	INTERGENIC	intergenic	RP11-436021.773	Transcript	INTRONIC	intronic	0				5	2.113	5	2				
5	rs6172916	2	56189501 G	A	0.1708	1.2e-06	0.758918	2.56191019_TA_T	RP11-48113.1	Transcript	INTRONIC	intronic	RP11-436021.774	Transcript	INTRONIC	intronic	0				5	2.110	5	5				
5	rs11891573	2	56007034 C	T	0.2058	3.6e-06	0.728776	rs5985551		RegulatoryFeature	REGULATORY	regulatory	RP11-436021.775	Transcript	INTRONIC	intronic	0				5	2.101	4	1				
5	rs7506567	2	56012652 T	C	0.2078	2.7e-06	0.818389	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.776	Transcript	INTRONIC	intronic	1				1	RP527A	1.06267e-05	0.001485	RP527A	1.06267e-05	0.001485	
5	rs1750458	2	56021098 T	C	0.3579	1.0e-06	0.774521	rs1125608		Intergenic	INTERGENIC	intergenic	RP11-436021.777	Transcript	INTRONIC	intronic	0				5	2.086	7	2				
5	rs1339578	2	56007636 T	C	0.1193	7.0e-10	1	rs1339578		Intergenic	INTERGENIC	intergenic	RP11-436021.778	Transcript	INTRONIC	intronic	0				5	1.980	7	2				
5	rs6724869	2	56034573 T	A	0.2078	2.6e-06	0.818389	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.779	Transcript	INTRONIC	intronic	1				1	RP527A	1.06267e-05	0.001485	RP527A	1.06267e-05	0.001485	
5	rs12490652	2	56010473 C	T	0.2127	3.4e-07	0.811617	rs5985551		Intergenic	INTERGENIC	intergenic	RP11-436021.780	Transcript	INTRONIC	intronic	0				5	1.954	7	5				
5	rs10180277	2	56181112 T	G	0.3808	1.0e-06	0.847432	2.56191019_TA_T	AC011306.2	Transcript	INTRONIC	intronic	RP11-436021.781	Transcript	INTRONIC	intronic	0			</								

6	11-2774893A.C	rs12288512	11	27747671 A	G	0.1799	1.1e-16	1	rs1730930	RP11-587021.4	Transcript	INTRONIC	intronic	RP11-43623.847	Transcript	INTRONIC	intronic	0	6	19.83	5	13	top
6		rs1730930	11	27748493 A	C	0.1799	6.8e-17	1	rs1730930	RP11-587021.4	Transcript	INTRONIC	intronic	RP11-43623.848	Transcript	INTRONIC	intronic	0	6	18.82	5	13	
6		rs1277363	11	27748503 C	T	0.1799	1.2e-16	1	rs1730930	RP11-587021.4	Transcript	INTRONIC	intronic	RP11-43623.849	Transcript	INTRONIC	intronic	0	6	17.94	4	5	top
6		rs1031019	11	2772810 A	G	0.2823	1.1e-16	0.999895	rnc62369	BNF	Transcript	INTRONIC	intron	RP11-43623.850	Transcript	INTRONIC	intronic	0	6	16.17	4	5	
6		rs1269837	11	27593570 G	A	0.2058	6.1e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.851	Transcript	INTRONIC	intronic	0	6	15.87	6	5	
6		rs16513711	11	2762334 A	G	0.2298	8.7e-15	0.75402352	r35288664	BNF-AS	Transcript	INTRONIC	intron	RP11-587021.4	Transcript	INTRONIC	intronic	0	6	15.30	6	5	
6		rs1515480	11	2767912 T	C	0.2952	1.3e-12	0.8602183	rnc62369	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.853	Transcript	INTRONIC	intronic	0	6	14.71	4	4	
6		rs1013402	11	27712381 G	A	0.2903	9.3e-15	0.954515	rnc62369	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.854	Transcript	INTRONIC	intronic	0	6	14.17	NA	5	
6		rs1571704A	11	2767780A A/C	C	0.2336	4.4e-07	0.8388	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.855	Transcript	INTRONIC	intronic	0	6	13.88	7	5	
6		rs1727239	11	27547379 C	A	0.2038	2.7e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.856	Transcript	INTRONIC	intronic	0	6	11.63	5	5	
6		rs1100102	11	27681596 G	C	0.2336	2.4e-14	0.738887	r1730930	BNF	Transcript	INTRONIC	intron	RP11-43623.857	Transcript	INTRONIC	intronic	0	6	11.41	7	4	
6		rs1688800	11	2772227 T	G	0.2286	7.6e-15	0.748074	r1730930	BNF	Transcript	INTRONIC	intronic	RP11-43623.858	Transcript	INTRONIC	intronic	0	6	10.73	20	1	
6		rs15288664	11	27595442 TA	A	0.2207	1.1e-03	0.73	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.859	Transcript	INTRONIC	intronic	0	6	10.31	NA	5	
6		rs944119	11	2772228 T	G	0.2873	5.2e-15	0.95139	rnc62369	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.860	Transcript	INTRONIC	intronic	0	6	9.509	4	1	
6		rs29619	11	2766702 G	T	0.2853	4.0e-14	0.906267	rnc62369	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.861	Transcript	INTRONIC	intronic	0	6	8.645	NA	5	
6		rs11503157	11	27704201 A	G	0.2298	9.5e-15	0.73812367	r1730930	BNF	Transcript	INTRONIC	intron	RP11-43623.862	Transcript	INTRONIC	intronic	0	6	8.032	7	5	
6		11-27579379 TA_T	11	27579379 TA	TA	0.2058	7.1e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.863	Transcript	INTRONIC	intronic	0	6	7.745	NA	5	
6		rs1517468	11	2768286 T	A	0.3032	1.7e-13	0.90496	rnc62369	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.864	Transcript	INTRONIC	intronic	0	6	7.089	7	5	
6		rs10707647	11	2764782 A	G	0.2038	1.5e-07	0.90208	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.865	Transcript	INTRONIC	intronic	0	6	6.479	5	5	
6		rs2353487	11	27603970 T	C	0.3072	1.2e-13	0.90496	rnc62369	BNF	Transcript	INTRONIC	intron	RP11-43623.866	Transcript	INTRONIC	intronic	0	6	6.355	7	5	
6		rs10835211	11	27701365 A	G	0.2276	9.1e-15	0.742163	r1730930	BNF	Transcript	INTRONIC	intron	RP11-43623.867	Transcript	INTRONIC	intronic	0	6	6.312	4	5	
6		rs11000057	11	27620932 T	C	0.2058	7.7e-08	0.912798	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.868	Transcript	INTRONIC	intronic	0	6	6.206	4	5	
6		rs12419402	11	27623309 A	G	0.2058	5.2e-08	0.903422	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.869	Transcript	INTRONIC	intronic	0	6	6.248	6	5	
6		rs11000088	11	27646247 A	G	0.2286	3.5e-13	0.729018	11-27670231_CT_C	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.870	Transcript	INTRONIC	intronic	0	6	5.972	5	4	
6		rs922454	11	2764219 G	A	0.2058	6.0e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.871	Transcript	INTRONIC	intronic	0	6	5.688	7	5	
6		11-27670231_CT_C	11	27670231 CT_C	CT	0.2813	4.2e-13	1	11-27670231_CT_C	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.872	Transcript	INTRONIC	intronic	0	6	4.974	NA	5	
6		11-27670234_CT_C	11	27670234 CT_C	CT	0.2734	1.8e-07	0.935699	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.873	Transcript	INTRONIC	intronic	0	6	4.791	NA	5	
6		11-27716133_CT_C	11	27716133 CT_C	CT	0.2614	8.2e-10	1	11-27716133_CT_C	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.874	Transcript	INTRONIC	intronic	0	6	4.544	NA	5	
6		rs6484386	11	27516703 C	T	0.2397	4.0e-06	0.873044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.875	Transcript	INTRONIC	intronic	0	6	4.057	6	2	
6		rs1038959	11	27549310 G	T	0.2286	9.4e-07	0.929209	r35288664	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.876	Transcript	INTRONIC	intronic	0	6	3.972	7	5	
6		rs1131924	11	27516709 T	C	0.2157	1.7e-07	0.830863	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.877	Transcript	INTRONIC	intronic	0	6	3.699	NA	5	
6		rs10707646	11	27507944 C	G	0.2387	2.7e-08	0.898613	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.878	Transcript	INTRONIC	intronic	0	6	3.484	5	5	
6		rs1100079	11	2762728 G	C	0.2197	1.2e-08	0.984392	r35288664	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.879	Transcript	INTRONIC	intronic	0	6	3.359	7	5	
6		rs448408	11	27521802 G	T	0.2038	2.9e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.880	Transcript	INTRONIC	intronic	0	6	3.356	6	4	
6		11-27681544_CTGT_T	11	27681544 CTGT_T	CTGT	0.3042	4.6e-13	0.901133	rnc62369	BNF	Transcript	INTRONIC	intronic	RP11-43623.881	Transcript	INTRONIC	intronic	0	6	3.289	4	5	
6		rs10707658	11	2767252 G	C	0.2853	4.5e-14	0.906267	rnc62369	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.882	Transcript	INTRONIC	intronic	0	6	3.172	5	5	
6		rs17989874	11	27667236 A	G	0.2346	2.9e-13	0.712727	11-27670231_CT_C	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.883	Transcript	INTRONIC	intronic	0	6	3.127	5	1	
6		rs12571588	11	27604518 C	T	0.2157	2.4e-08	0.929423	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.884	Transcript	INTRONIC	intronic	0	6	2.981	7	5	
6		rs11003121	11	27716207 T	C	0.2942	4.4e-15	0.948391	rnc62369	BNF	Transcript	INTRONIC	intron	RP11-43623.885	Transcript	INTRONIC	intronic	0	6	2.698	6	5	
6		rs4684311	11	2751374 A	G	0.2038	3.5e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.886	Transcript	INTRONIC	intronic	0	6	2.679	4	5	
6		rs10714393	11	27570090 G	C	0.2276	4.5e-07	0.904239	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.887	Transcript	INTRONIC	intronic	0	6	2.654	8	5	
6		rs7125904	11	27543003 G	T	0.2038	2.7e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.888	Transcript	INTRONIC	intronic	0	6	2.383	6	5	
6		rs10815201	11	27618265 G	A	0.2197	1.5e-08	0.994811	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.889	Transcript	INTRONIC	intronic	0	6	2.329	5	4	
6		rs1717507	11	27714884 C	T	0.3002	2.5e-13	0.916006	rnc62369	BNF-AS	Transcript	INTRONIC	intron	RP11-43623.890	Transcript	INTRONIC	intronic	0	6	2.246	6	3	
6		rs4681311	11	27583193 A	G	0.2058	4.6e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.891	Transcript	INTRONIC	intronic	0	6	2.182	7	5	
6		rs12786130	11	27505954 T	C	0.2167	5.4e-07	0.780802	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.892	Transcript	INTRONIC	intronic	0	6	2.173	7	5	
6		rs11001010	11	27606506 C	T	0.2486	1.7e-14	0.737467	r1730930	BNF	Transcript	INTRONIC	intronic	RP11-43623.893	Transcript	INTRONIC	intronic	0	6	2.172	5	5	
6		rs12361380	11	27615609 A	G	0.2058	7.8e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.894	Transcript	INTRONIC	intronic	0	6	2.095	6	5	
6		rs73430670	11	27615630 G	A	0.2296	2.0e-07	0.944813	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.895	Transcript	INTRONIC	intronic	0	6	1.998	5	5	
6		rs10875197	11	27607541 T	C	0.2058	9.0e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.896	Transcript	INTRONIC	intronic	0	6	1.970	6	5	
6		rs1071410	11	2751188 C	T	0.2028	2.3e-07	0.899123	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.897	Transcript	INTRONIC	intronic	0	6	1.925	6	5	
6		rs12842656	11	27601805 C	T	0.3091	3.9e-14	0.881357	rnc62369	BNF	Transcript	INTRONIC	intron	RP11-43623.898	Transcript	INTRONIC	intronic	0	6	1.873	6	5	
6		rs11001017	11	27604835 G	A	0.2346	2.4e-14	0.737467	r1730930	BNF	Transcript	INTRONIC	intronic	RP11-43623.899	Transcript	INTRONIC	intronic	0	6	1.828	20	2	
6		rs4922187	11	27607902 T	C	0.2177	6.7e-07	0.802017	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.900	Transcript	INTRONIC	intronic	0	6	1.802	6	5	
6		rs73430668	11	27613419 T	C	0.2058	8.7e-08	0.913788	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.901	Transcript	INTRONIC	intronic	0	6	1.650	7	5	
6		rs4684314	11	27505109 A	A	0.2038	2.6e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.902	Transcript	INTRONIC	intronic	0	6	1.586	6	5	
6		rs1038600	11	27549310 G	T	0.2038	2.6e-07	0.904044	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.903	Transcript	INTRONIC	intronic	0	6	1.585	6	5	
6		rs10851190	11	27546447 T	C	0.2286	9.5e-07	0.929209	r35288664	BNF-AS	Transcript	INTRONIC	intronic	RP11-43623.904	Transcript	INTRONIC	intronic	0	6	1.562	6	5	
6		rs1352479	11	27593899 T	A	0.2346	2.2e-07	0.912377	r35288664	BNF-AS	Transcript	INTRONIC											

7	rsl00026	19	7877437	A	G	0.4195	9.6e-08	r033829	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.968	Transcript	INTRONIC	intronic	1	PPP1814A	7.08536e-13	4.70966e-32	PPP1814A	7.08536e-13	4.70966e-32	7	1.471	6	4	
7	r7938509	19	7875586	A	G	0.159	1.9e-06	r074827	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.968	Transcript	INTRONIC	intronic	1	PPP1814A	6.71177e-07	4.70966e-32	PPP1814A	6.71177e-07	4.70966e-32	7	1.423	5	5	
7	r7231445	19	7875144	T	G	0.205	3.4e-08	r074827	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.970	Transcript	INTRONIC	intronic	1	PPP1814A	1.68318e-07	4.70966e-32	PPP1814A	1.68318e-07	4.70966e-32	7	1.146	11	10	
7	r5978203	19	7875120	A	C	0.2097	7.1e-08	r039463	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.971	Transcript	INTRONIC	intronic	1	PPP1814A	1.68191e-07	4.70966e-32	PPP1814A	1.68191e-07	4.70966e-32	7	1.119	5	1	
7	r5999125	19	7875143	A	G	0.4871	1.4e-06	r040029	r2752820	SPINT2	Intergenic	UPSTREAM	upstream	RP11-436202.972	Transcript	INTRONIC	intronic	1	PPP1814A	7.45001e-13	4.70966e-32	PPP1814A	7.45001e-13	4.70966e-32	7	1.049	6	5	
7	r5781820	19	7872676	A	A	0.4173	2.1e-08	r074827	r2752820	SPINT2	Intergenic	INTRONIC	intron	RP11-436202.973	Transcript	INTRONIC	intronic	1	PPP1814A	6.87226e-06	4.70966e-32	PPP1814A	6.87226e-06	4.70966e-32	7	0.475	4	2	
7	r11668070	19	7816993	A	G	0.4911	5.9e-16	r070572	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.974	Transcript	INTRONIC	intronic	1	PPP1814A	2.08633e-36	4.70966e-32	PPP1814A	2.08633e-36	4.70966e-32	7	0.830	6	5	
7	r8102476	19	7875613	T	C	0.5553	1.5e-13	r0804307	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.975	Transcript	INTRONIC	intronic	1	PPP1814A	6.71245e-27	4.70966e-32	PPP1814A	6.71245e-27	4.70966e-32	7	0.781	5	2	
7	r5099240	19	7874371	T	C	0.16	1.8e-06	r047914	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.976	Transcript	INTRONIC	intronic	1	PPP1814A	6.71177e-07	4.70966e-32	PPP1814A	6.71177e-07	4.70966e-32	7	0.475	4	2	
7	r11088450	19	7874239	C	T	0.4871	9.2e-16	r0562482	r4802297	SPINT2	Intergenic	UPSTREAM	upstream	RP11-436202.977	Transcript	INTRONIC	intronic	1	PPP1814A	1.18848e-26	4.70966e-32	PPP1814A	1.18848e-26	4.70966e-32	7	0.706	5	1	
7	r289100	19	7876710	C	T	0.4175	1.1e-07	r034295	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.978	Transcript	INTRONIC	intronic	1	PPP1814A	7.17338e-13	4.70966e-32	PPP1814A	7.17338e-13	4.70966e-32	7	0.674	7	4	
7	r11667258	19	7875104	T	A	0.185	3.9e-13	r058174	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.979	Transcript	INTRONIC	intronic	1	PPP1814A	6.71177e-07	4.70966e-32	PPP1814A	6.71177e-07	4.70966e-32	7	0.475	4	2	
7	r10562797	19	7874749	ATT	A	0.4722	1.7e-14	r0182963	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.980	Transcript	INTRONIC	intronic	0											
7	r1261109	19	7877281	C	T	0.4175	1.9e-07	r034295	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.981	Transcript	INTRONIC	intronic	1	PPP1814A	7.08536e-13	4.70966e-32	PPP1814A	7.08536e-13	4.70966e-32	7	0.537	4	4	
7	r1261109	19	7877281	C	T	0.4175	1.9e-07	r034295	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.982	Transcript	INTRONIC	intronic	1	PPP1814A	7.08536e-13	4.70966e-32	PPP1814A	7.08536e-13	4.70966e-32	7	0.537	4	4	
7	r34565749	19	7877726	T	T	0.4195	1.4e-07	r033829	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.983	Transcript	INTRONIC	intronic	1	PPP1814A	7.08536e-13	4.70966e-32	PPP1814A	7.08536e-13	4.70966e-32	7	0.415	6	4	
7	r8101462	19	7877371	C	T	0.4195	9.5e-08	r033829	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.984	Transcript	INTRONIC	intronic	1	PPP1814A	7.08536e-13	4.70966e-32	PPP1814A	7.08536e-13	4.70966e-32	7	0.533	7	4	
7	r21435250	19	7877259	A	C	0.16	1.8e-06	r0480432	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.985	Transcript	INTRONIC	intronic	1	PPP1814A	6.71177e-07	4.70966e-32	PPP1814A	6.71177e-07	4.70966e-32	7	0.475	4	2	
7	r12613084	19	7874672	C	A	0.497	1.2e-09	r045505	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.986	Transcript	INTRONIC	intronic	1	PPP1814A	8.06846e-30	4.70966e-32	PPP1814A	8.06846e-30	4.70966e-32	7	0.304	26	1	
7	r4803999	19	7879765	G	A	0.34	8.9e-06	r050002	r36035956	CTB_10215.4	Transcript	INTRONIC	intron	RP11-436202.987	Transcript	INTRONIC	intronic	1	PPP1814A	1.08228e-06	4.70966e-32	C10eF3	1.29823e-05	5.55572e-09	7	0.263	5	2	
7	r24023956	19	7879094	C	T	0.4944	6.1e-09	r01	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.988	Transcript	INTRONIC	intronic	1	PPP1814A	2.05986e-15	4.70966e-32	PPP1814A	2.05986e-15	4.70966e-32	7	0.204	4	1	
7	r4584930	19	7875309	A	G	0.159	1.8e-06	r074827	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.989	Transcript	INTRONIC	intronic	1	PPP1814A	6.71177e-07	4.70966e-32	PPP1814A	6.71177e-07	4.70966e-32	7	0.107	6	1	
7	r4802297	19	7878310	C	G	0.486	2.0e-16	r1	r4802297	SPINT2	Transcript	INTRONIC	intron	RP11-436202.990	Transcript	INTRONIC	intronic	1	PPP1814A	2.16735e-37	4.70966e-32	PPP1814A	2.16735e-37	4.70966e-32	7	0.049	3a	5	
7	r276887	19	7879385	C	T	0.4523	5.1e-09	r068046	r36035956	SPINT2	Transcript	INTRONIC	intron	RP11-436202.991	Transcript	INTRONIC	intronic	1	PPP1814A	2.18612e-19	4.70966e-32	PPP1814A	2.18612e-19	4.70966e-32	7	0.049	4	1	
7	r11208422	19	7874930	G	C	0.2097	7.3e-08	r058046	r2752345	SPINT2	Transcript	INTRONIC	intron	RP11-436202.992	Transcript	INTRONIC	intronic	1	PPP1814A	1.84648e-06	4.70966e-32	PPP1814A	1.84648e-06	4.70966e-32	7	0.034	7	5	
7	r3543012	19	7879063	C	A	0.3509	8.4e-07	r072205	r36035956	CTB_10215.4	Transcript	INTRONIC	intron	RP11-436202.993	Transcript	INTRONIC	intronic	1	PPP1814A	3.01962e-10	4.70966e-32	C10eF3	1.1182e-05	5.55572e-09	7	0.005	6	5	
7	r8176719	19	7861298	TC	C	0.3946	7.1e-12	r055449	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.994	Transcript	INTRONIC	intronic	1	ABO	4.50356e-12	4.38373e-09	ABO	4.50356e-12	4.38373e-09	8	10.58	NA	4	
7	r7821927	9	13613907	G	GAACATGCC	0.2823	4.3e-09	r062207	r055922	SPINT2	Transcript	INTRONIC	intron	RP11-436202.995	Transcript	INTRONIC	intronic	0											
7	r13615179	9	13615179	T	TGGTCGAGCCG	0.1859	5.3e-09	r1	r057666	RegulatoryFeature	REGULATORY	regulatory	RP11-436202.996	Transcript	INTRONIC	intronic	0												
7	r8151007	9	13615187	T	T	0.1137	7.1e-09	r0151795	r057666	ABO	C	INTRONIC	intronic	0															
7	r649129	9	13615190	T	C	0.2137	7.8e-09	r0151795	r057666	RegulatoryFeature	REGULATORY	regulatory	RP11-436202.997	Transcript	INTRONIC	intronic	0												
7	r614605	9	13614908	A	T	0.3966	4.2e-11	r031089	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.999	Transcript	INTRONIC	intronic	1	ABO	6.14605e-11	4.38373e-09	ABO	6.14605e-11	4.38373e-09	8	7.458	5	1	
7	r857123	9	13613206	A	C	0.2096	1.1e-14	r071464	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1000	Transcript	INTRONIC	intronic	1	ABO	1.78081e-09	4.38373e-09	ABO	1.78081e-09	4.38373e-09	8	7.114	NA	5	
7	r5151093	9	13614790	T	C	0.1489	6.1e-07	r0151797	r057666	ABO	Transcript	INTRONIC	intron	RP11-436202.1001	Transcript	INTRONIC	intronic	1	ABO	6.14605e-11	4.38373e-09	ABO	6.14605e-11	4.38373e-09	8	6.475	4	2	
7	r78182261	9	13614905	C	CA	0.3956	1.8e-14	r071464	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1002	Transcript	INTRONIC	intronic	1	ABO	6.14605e-11	4.38373e-09	ABO	6.14605e-11	4.38373e-09	8	6.576	NA	1	
7	r600008	9	13615186	C	T	0.2147	8.9e-09	r0151796	r057666	ABO	Intergenic	UPSTREAM	upstream	RP11-436202.1003	Transcript	INTRONIC	intronic	0											
7	r484242	9	13614518	T	C	0.3996	7.8e-15	r071464	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1004	Transcript	INTRONIC	intronic	0	ABO	1.78081e-09	4.38373e-09	ABO	1.78081e-09	4.38373e-09	8	6.180	NA	1	
7	r507666	9	13614939	A	G	0.1859	4.0e-09	r1	r057666	ABO	Transcript	INTRONIC	intron	RP11-436202.1005	Transcript	INTRONIC	intronic	0											
7	9-13614466_CAA_C	9	13614466	C	CAA	0.3837	1.1e-14	r0894748	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1006	Transcript	INTRONIC	intronic	0	ABO	2.3512e-11	4.38373e-09	ABO	2.3512e-11	4.38373e-09	8	4.444	4	1	
7	r8571236	9	13613706	A	C	0.34	1.2e-13	r072845	r58770723	ABO	Transcript	INTRONIC	intron	RP11-436202.1007	Transcript	INTRONIC	intronic	0	ABO	2.3512e-11	4.38373e-09	ABO	2.3512e-11	4.38373e-09	8	4.365	NA	5	
7	r641177	9	13614504	A	C	0.34	1.2e-13	r072845	r58770723	ABO	Transcript	INTRONIC	intron	RP11-436202.1008	Transcript	INTRONIC	intronic	0	ABO	2.3512e-11	4.38373e-09	ABO	2.3512e-11	4.38373e-09	8	4.329	3a	3	
7	r79209625	9	13614400	C	CA	0.3838	1.6e-12	r078813	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1009	Transcript	INTRONIC	intronic	0	ABO	1.48778e-11	4.38373e-09	ABO	1.48778e-11	4.38373e-09	8	1.737	NA	5	
7	r554883	9	13647460	T	C	0.2718	9.1e-15	r0584746	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1010	Transcript	INTRONIC	intronic	0	ABO	1.48778e-11	4.38373e-09	ABO	1.48778e-11	4.38373e-09	8	1.297	NA	4	
7	r641626	9	13614873	T	C	0.3708	1.0e-14	r058481	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1011	Transcript	INTRONIC	intronic	1	ABO	2.66939e-10	4.38373e-09	ABO	2.66939e-10	4.38373e-09	8	3.995	4	1	
7	r597988	9	13614284	A	T	0.3698	1.0e-14	r077064	r055922	ABO	Transcript	INTRONIC	intron	RP11-436202.1012	Transcript	INTRONIC	intronic	1	ABO	2.66939e-10	4.38373e-09	ABO	2.66939e-10	4.38373e-09	8	3.1			

9	r158193643	7	102010094	G	T	0.1392	2.2e-06	0.731687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1089	Transcript	INTRONIC	INTRONIC	0	7.286	3a	2
9	r10953380	7	102747149	G	C	0.3191	1.2e-07	0.674445	r142441296	NAPFLD	Transcript	INTRONIC	intron	RP11-43623.1090	Transcript	INTRONIC	INTRONIC	0	7.254	4	1
9	r13178117	7	102050113	G	T	0.1392	1.0e-06	0.731687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1091	Transcript	INTRONIC	INTRONIC	0	7.244	4	1
9	r133240483	7	102048043	G	T	0.2356	2.8e-11	r131242403	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1092	Transcript	INTRONIC	INTRONIC	0	7.052	6	4	
9	r10273949	7	102462636	G	T	0.3181	1.2e-14	0.968807	7102474902_T	FBXL13	CodingTranscript	SYNONYMOUS	synonymous	RP11-43623.1093	Transcript	INTRONIC	INTRONIC	0	6.931	2c	4
9	r14580325	7	102423025	G	T	0.1163	2.0e-05	0.545667	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1104	Transcript	INTRONIC	INTRONIC	0	6.903	7	4
9	r17789252	7	102624272	A	C	0.3062	1.6e-07	0.720127	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1105	Transcript	INTRONIC	INTRONIC	0	6.740	4	5
9	r17176090	7	102475673	A	G	0.1193	6.4e-09	0.518163	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1106	Transcript	INTRONIC	INTRONIC	0	6.621	2b	1
9	r171210195	7	102470002	G	T	0.3211	7.7e-15	r131242403	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1107	Transcript	INTRONIC	INTRONIC	0	6.584	3b	5	
9	r19601949	7	102425093	C	T	0.1163	3.3e-09	0.943657	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1108	Transcript	INTRONIC	INTRONIC	0	6.412	7	5
9	r16165167	7	102479719	C	C	0.1193	7.5e-09	0.518163	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1109	Transcript	INTRONIC	INTRONIC	0	6.289	6	5
9	r11184346	7	102479702	C	C	0.1362	2.8e-06	0.732073	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1110	Transcript	INTRONIC	INTRONIC	0	6.261	4	1
9	r15615624	7	102472408	C	T	0.1163	6.8e-09	0.943657	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1111	Transcript	INTRONIC	INTRONIC	0	6.146	5	5
9	r184748	7	10251580	T	C	0.3191	2.6e-10	0.897336	r142441296	URC17	Transcript	INTRONIC	intron	RP11-43623.1102	Transcript	INTRONIC	INTRONIC	0	6.137	7	1
9	r12518995	7	102416004	A	T	0.1163	6.3e-09	0.90895	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1103	Transcript	INTRONIC	INTRONIC	0	6.030	7	4
9	r4691288	7	102479510	A	T	0.1183	1.5e-09	0.731687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1104	Transcript	INTRONIC	INTRONIC	0	5.998	4	5
9	r154079580	7	102441168	GAAAC	G	0.1203	7.5e-09	0.910217	r2537428	FAM185A	Transcript	INTRONIC	intron,feature_elongation	RP11-43623.1105	Transcript	INTRONIC	INTRONIC	0	5.896	NA	5
9	r1100046	7	102540925	A	T	0.3201	2.7e-10	0.901907	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1106	Transcript	INTRONIC	INTRONIC	0	5.888	5	4
9	r1931360	7	102440016	A	T	0.1143	1.2e-09	0.764517	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1107	Transcript	INTRONIC	INTRONIC	0	5.798	NA	5
9	r6800434	7	102420701	T	A	0.3141	1.1e-13	0.92035	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1108	Transcript	INTRONIC	INTRONIC	0	5.660	5	4
9	r11983521	7	102498173	T	C	0.1362	1.3e-06	0.752073	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1109	Transcript	INTRONIC	INTRONIC	0	5.515	6	5
9	r17408280	7	10257190	C	C	0.1362	6.9e-06	0.721054	r2537428	URC17	Transcript	INTRONIC	intron	RP11-43623.1110	Transcript	INTRONIC	INTRONIC	0	5.483	5	2
9	r2411059	7	102594612	C	C	0.1402	8.3e-06	0.739495	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1111	Transcript	INTRONIC	INTRONIC	0	5.458	6	5
9	r13212185	7	102678422	C	C	0.3111	2.3e-07	0.72381	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1112	Transcript	INTRONIC	INTRONIC	0	5.305	5	1
9	r14782634	7	102435448	A	G	0.1213	1.1e-08	0.917123	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1113	Transcript	INTRONIC	INTRONIC	0	5.278	4	5
9	r6897771	7	102545179	C	T	0.1362	7.2e-06	0.721054	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1114	Transcript	INTRONIC	INTRONIC	0	5.263	6	5
9	r61679881	7	102509433	T	T	0.1392	3.1e-04	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1115	Transcript	INTRONIC	INTRONIC	0	5.192	4	5
9	r6877451	7	102504206	G	A	0.1292	2.2e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1116	Transcript	INTRONIC	INTRONIC	0	5.167	6	5
9	r5725366	7	10248664	T	C	0.1193	9.1e-09	0.918632	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1117	Transcript	INTRONIC	INTRONIC	0	5.090	5	4
9	r2411046	7	102419304	A	C	0.3141	1.6e-13	0.92035	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1118	Transcript	INTRONIC	INTRONIC	0	5.022	5	4
9	r1847658	7	102561544	A	T	0.1402	7.5e-06	0.739495	r2537428	URC17	Transcript	INTRONIC	intron	RP11-43623.1119	Transcript	INTRONIC	INTRONIC	0	4.984	NA	5
9	r13121394	7	102742554	A	C	0.3002	4.5e-08	0.720127	r142441296	NAPFLD	Transcript	INTRONIC	UTR	RP11-43623.1120	Transcript	INTRONIC	INTRONIC	0	4.957	6	4
9	r131770139	7	102770170	G	C	0.3191	1.2e-07	0.718031	r142441296	NAPFLD	Transcript	INTRONIC	intron	RP11-43623.1121	Transcript	INTRONIC	INTRONIC	0	4.933	5	5
9	r64645971	7	102441180	T	G	0.1181	1.1e-14	0.918632	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1122	Transcript	INTRONIC	INTRONIC	0	4.903	5	5
9	r11342493	7	102584013	G	A	0.1402	8.4e-06	0.739495	r2537428	URC17	Transcript	INTRONIC	intron	RP11-43623.1123	Transcript	INTRONIC	INTRONIC	0	4.865	5	1
9	r147068151	7	102497658	CACAAA	A	0.1362	2.4e-06	0.752073	r2537428	FBXL13	Transcript	INTRONIC	intron,feature_elongation	RP11-43623.1124	Transcript	INTRONIC	INTRONIC	0	4.673	NA	5
9	r57453534	7	102501273	A	G	0.1392	1.2e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1125	Transcript	INTRONIC	INTRONIC	0	4.656	4	5
9	r6804928	7	102589706	G	T	0.3211	4.8e-10	0.897336	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1126	Transcript	INTRONIC	INTRONIC	0	4.624	5	4
9	r7777618	7	102512122	G	C	0.1392	3.6e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1127	Transcript	INTRONIC	INTRONIC	0	4.406	7	4
9	r11973896	7	102498441	G	A	0.1372	1.9e-06	0.761256	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1128	Transcript	INTRONIC	INTRONIC	0	4.368	7	5
9	r57516389	7	102593073	T	C	0.1362	8.6e-06	0.721054	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1129	Transcript	INTRONIC	INTRONIC	0	4.307	5	5
9	r777619	7	10248906	G	C	0.3141	9.3e-14	0.924671	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1130	Transcript	INTRONIC	INTRONIC	0	4.285	5	5
9	r6849997	7	10261958	T	C	0.1402	8.3e-06	0.739495	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1131	Transcript	INTRONIC	INTRONIC	0	4.267	5	1
9	r1182880	7	102464020	G	T	0.1292	6.5e-09	0.918632	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1132	Transcript	INTRONIC	INTRONIC	0	4.218	6	5
9	r6861304	7	102483152	A	C	0.3718	2.3e-07	0.781433	r133232414	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1133	Transcript	INTRONIC	INTRONIC	0	4.135	6	5
9	r9778444	7	102425822	G	A	0.1163	4.2e-09	0.943657	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1134	Transcript	INTRONIC	INTRONIC	0	4.097	7	5
9	r10282345	7	102492378	A	C	0.4573	1.2e-07	0.721554	r133232414	FBXL13	Transcript	INTRONIC	intron,feature_elongation	RP11-43623.1135	Transcript	INTRONIC	INTRONIC	0	4.024	NA	5
9	r10206873	7	102476120	G	A	0.3191	2.1e-14	0.977011	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1136	Transcript	INTRONIC	INTRONIC	0	3.965	6	5
9	r1461704	7	102423618	A	G	0.1131	1.9e-09	0.971223	r2537428	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1137	Transcript	INTRONIC	INTRONIC	0	3.951	7	5
9	r168067024	7	102490724	A	G	0.1402	1.0e-06	0.739495	r2537428	URC17	Transcript	INTRONIC	intron	RP11-43623.1138	Transcript	INTRONIC	INTRONIC	0	3.922	5	5
9	r12519777	7	102519210	C	C	0.3201	1.2e-10	0.901907	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1139	Transcript	INTRONIC	INTRONIC	0	3.907	4	5
9	r1640579	7	10204773	G	A	0.1392	1.1e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1140	Transcript	INTRONIC	INTRONIC	0	3.881	7	4
9	r1266968	7	102471349	A	A	0.1183	6.4e-09	0.90895	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1141	Transcript	INTRONIC	INTRONIC	0	3.864	6	4
9	r11077157	7	102572915	G	C	0.34	8.1e-12	0.861093	7102474902_T	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1142	Transcript	INTRONIC	INTRONIC	0	3.798	5	4
9	r16465885	7	102574313	T	C	0.1362	9.4e-06	0.721054	r2537428	URC17	Transcript	INTRONIC	intron	RP11-43623.1143	Transcript	INTRONIC	INTRONIC	0	3.795	5	5
9	r12684814	7	10247674	A	G	0.1193	6.4e-09	0.918632	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1144	Transcript	INTRONIC	INTRONIC	0	3.722	6	4
9	r102501445	7	10201044	C	CAT	0.1392	2.5e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron,feature_truncation	RP11-43623.1145	Transcript	INTRONIC	INTRONIC	0	3.677	NA	5
9	r17456502	7	102596022	A	C	0.2944	6.3e-10	0.896029	r142441296	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1146	Transcript	INTRONIC	INTRONIC	0	3.639	6	5
9	r6404877	7	102504613	C	T	0.1392	1.3e-06	0.733687	r2537428	FBXL13	Transcript	INTRONIC	intron	RP11-43623.1147	Transcript	INTRONIC	INTRONIC	0	3.439	5	4
9	r102613174	7	102442173	A	C	0.3171	2.7e-14	0.964276	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1148	Transcript	INTRONIC	INTRONIC	0	3.409	5	5
9	r2430070	7	102420805	G	T	0.3131	8.1e-14	0.920502	7102474902_T	FAM185A	Transcript	INTRONIC	intron	RP11-43623.1149	Transcript	INTRONIC	INTRONIC	0	3.388	NA	5
9																					

[illegible]

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13	r6884008	10 101450604 G	A	0.1213 3.6e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1452	Transcript	INTRONIC	intronic	0	13	1.496	6	4	
13	r2300982	10 101454142 G	A	0.1213 4.0e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1453	Transcript	INTRONIC	intronic	0	13	1.490	5	2	
13	r4893382	10 101454900 C	T	0.1213 3.0e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1454	Transcript	INTRONIC	intronic	0	13	1.395	4	3	
13	r5708937	10 101454908 G	A	0.1203 3.7e-13 0.980842 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1455	Transcript	INTRONIC	intronic	0	13	1.368	7	5	
13	r4951983	10 101455100 A	T	0.1213 2.5e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1456	Transcript	INTRONIC	intronic	0	13	1.329	7	4	
13	r5707450	10 101394724 C	T	0.1203 1.2e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1457	Transcript	INTRONIC	intronic	0	13	1.242	3	3	
13	r5199941	10 101412471 G	A	0.1213 1.6e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1458	Transcript	INTRONIC	intronic	0	13	1.223	7	5	
13	r6844001	10 101388939 G	A	0.1203 1.0e-13 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1459	Transcript	INTRONIC	intronic	0	13	1.214	5	5	
13	r5707594	10 101391829 G	A	0.1203 1.4e-13 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1460	Transcript	INTRONIC	intronic	0	13	1.213	6	4	
13	r5718139	10 101465780 A	G	0.1213 3.2e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1461	Transcript	INTRONIC	intronic	0	13	1.170	6	4	
13	r4951980	10 101425578 C	A	0.1213 1.6e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1462	Transcript	INTRONIC	intronic	0	13	1.165	5	4	
13	r5135116	10 101381601 T	T	0.1203 2.1e-13 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1463	Transcript	INTRONIC	intronic	0	13	1.157	7	4	
13	r5663888	10 101402630 G	A	0.1213 1.8e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1464	Transcript	INTRONIC	intronic	0	13	1.028	6	5	
13	r2269194	10 101457155 G	A	0.1213 2.2e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1465	Transcript	INTRONIC	intronic	0	13	0.962	7	4	
13	r5663958	10 101401808 G	A	0.1213 1.9e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1466	Transcript	INTRONIC	intronic	0	13	0.953	7	5	
13	r5705415	10 101405244 A	G	0.1203 3.7e-13 0.980842 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1467	Transcript	INTRONIC	intronic	0	13	0.883	7	5	
13	r5103217	10 101386400 G	T	0.1233 3.3e-13 0.971763 r57089322	RP11-85A1.3	Transcript	INTRONIC	downstream	RP11-436021.1468	Transcript	INTRONIC	intronic	0	13	0.831	NA	5	
13	r5663384	10 101401622 C	T	0.1213 1.9e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1469	Transcript	INTRONIC	intronic	0	13	0.784	5	5	
13	r51088402	10 101426527 G	A	0.1213 2.1e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1470	Transcript	INTRONIC	intronic	0	13	0.675	6	4	
13	r511542	10 101433672 C	G	0.1213 5.5e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1471	Transcript	INTRONIC	intronic	0	13	0.638	5	4	
13	r51142827	10 101425013 GA	A	0.1202 1.5e-13 0.999542 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1472	Transcript	INTRONIC	intronic	0	13	0.627	NA	4	
13	r51193041	10 101437177 G	A	0.1213 2.1e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1473	Transcript	INTRONIC	intronic	0	13	0.627	7	4	
13	r5118001	10 101389084 C	T	0.1203 1.3e-13 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1474	Transcript	INTRONIC	intronic	0	13	0.545	4	1	
13	r51074787	10 101449597 G	A	0.1203 8.0e-13 0.980842 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1475	Transcript	INTRONIC	intronic	0	13	0.503	7	4	
13	r51999440	10 101412278 T	G	0.1213 9.8e-14 0.990447 r57089322	RP11-483F11.7	Transcript	INTRONIC	intron	RP11-436021.1476	Transcript	INTRONIC	intronic	0	13	0.491	7	5	
13	r51119038	10 101391648 T	A	0.1213 2.0e-13 0.951948 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1477	Transcript	INTRONIC	intronic	0	13	0.428	6	5	
13	r6858420	10 101481767 T	C	0.1213 2.3e-13 0.990447 r57089322	COX15	RegulatoryFeature	REGULATORY	intron	RP11-436021.1478	Transcript	INTRONIC	intronic	0	13	0.403	6	4	
13	r514717923	10 101414414 TAAc	T	0.1531 2.6e-13 0.765572 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1479	Transcript	INTRONIC	intronic	0	13	0.356	NA	2	
13	r4951979	10 101425468 T	C	0.1213 3.6e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1480	Transcript	INTRONIC	intronic	0	13	0.347	5	4	
13	r51430810	10 101391899 AATAG	A	0.1237 2.4e-13 0.971119 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1481	Transcript	INTRONIC	intronic	0	13	0.300	7	4	
13	r512181543	10 101367042 A	G	0.1153 3.8e-13 0.877874 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1482	Transcript	INTRONIC	intronic	0	13	0.277	6	5	
13	r5791939	10 101427983 C	T	0.1213 4.0e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1483	Transcript	INTRONIC	intronic	0	13	0.280	7	4	
13	r4918178	10 101418180 G	A	0.1203 7.6e-13 0.980842 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1484	Transcript	INTRONIC	intronic	0	13	0.226	6	4	
13	r5177144	10 101389700 A	A	0.1223 8.7e-14 0.981015 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1485	Transcript	INTRONIC	intronic	0	13	0.190	3a	3	
13	r5663403	10 101402896 C	T	0.1213 2.5e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1486	Transcript	INTRONIC	intronic	0	13	0.184	7	5	
13	r5790566	10 101405335 A	G	0.1213 1.8e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1487	Transcript	INTRONIC	intronic	0	13	0.162	7	5	
13	r51360921	10 101435311 G	A	0.1213 3.0e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1488	Transcript	INTRONIC	intronic	0	13	0.143	7	5	
13	r57717085	10 101401435 C	T	0.1213 1.8e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1489	Transcript	INTRONIC	intronic	0	13	0.110	6	5	
13	r57086162	10 101405998 A	G	0.1213 9.7e-14 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1490	Transcript	INTRONIC	intronic	0	13	0.087	6	5	
13	r5708086	10 101447258 T	A	0.1233 2.2e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1491	Transcript	INTRONIC	intronic	0	13	0.080	7	4	
13	r684296	10 101357014 T	A	0.1372 1.1e-13 0.729242 r57089322	intronic3	Intergenic	UPSTREAM	upstream	RP11-436021.1492	Transcript	INTRONIC	intronic	0	13	0.080	6	5	
13	r5185493	10 101987272 G	A	0.1203 6.5e-14 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1493	Transcript	INTRONIC	intronic	0	13	0.076	6	5	
13	r570979	10 101387058 G	A	0.1203 1.0e-13 1 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1494	Transcript	INTRONIC	intronic	0	13	0.076	6	5	
13	r2262278	10 101489868 C	COX15	Transcript	INTRONIC	intron	RP11-436021.1495	Transcript	INTRONIC	intronic	0	13	0.044	7	4			
13	r5556472	10 101400471 C	G	0.1213 1.9e-13 0.990447 r57089322	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1496	Transcript	INTRONIC	intronic	0	13	0.023	7	5	
13	r511782146	10 120411922 G	A	0.1849 7.1e-13 0.729943 r68089342	NOV	Transcript	INTRONIC	intron	RP11-436021.1497	Transcript	INTRONIC	intronic	NOV	2.9388e-11 5.0495e-07	NOV	2.9388e-11 5.0495e-07	NOV	2.9388e-11 5.0495e-07
13	r51178373	8 120434942 T	C	0.1839 1.8e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1498	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r57170783	8 120420884 T	A	0.1849 1.1e-13 0.789163 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1499	Transcript	INTRONIC	intronic	NOV	1.36347e-10 5.0495e-07	NOV	1.36347e-10 5.0495e-07	NOV	1.36347e-10 5.0495e-07
13	r511571242	8 120421447 T	A	0.1839 1.0e-13 0.786269 r68089342	NOV	Transcript	INTRONIC	intron	RP11-436021.1500	Transcript	INTRONIC	intronic	NOV	4.45041e-11 5.0495e-07	NOV	4.45041e-11 5.0495e-07	NOV	4.45041e-11 5.0495e-07
13	r51191747	8 120542085 A	G	0.2137 1.3e-13 1 r517191747	ENTP07	Transcript	INTRONIC	intron	RP11-436021.1501	Transcript	INTRONIC	intronic	NOV	3.6574e-07 5.0495e-07	NOV	3.6574e-07 5.0495e-07	NOV	3.6574e-07 5.0495e-07
13	r5105813	8 120575184 A	G	0.1948 2.5e-13 0.858811 r517191747	ENTP2	CodingTranscript	SYNONYMOUS	synonymous	RP11-436021.1502	Transcript	INTRONIC	intronic	NOV	4.7025e-07 5.0495e-07	NOV	4.7025e-07 5.0495e-07	NOV	4.7025e-07 5.0495e-07
13	r5106710	8 120624386 T	A	0.1216 4.2e-13 0.746421 G	ENTP2	Transcript	INTRONIC	intron	RP11-436021.1503	Transcript	INTRONIC	intronic	NOV	3.88677e-08 5.0495e-07	NOV	3.88677e-08 5.0495e-07	NOV	3.88677e-08 5.0495e-07
13	r5188962	8 120417690 C	T	0.1849 1.3e-13 0.729943 r68089342	ENTP2	Transcript	INTRONIC	intron	RP11-436021.1504	Transcript	INTRONIC	intronic	NOV	1.18715e-10 5.0495e-07	NOV	1.18715e-10 5.0495e-07	NOV	1.18715e-10 5.0495e-07
13	r5280831	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1505	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1506	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1507	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1508	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1509	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839 1.9e-13 0.786269 r68089342	RP11-77B515.2	Transcript	INTRONIC	intron	RP11-436021.1510	Transcript	INTRONIC	intronic	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07	NOV	8.92118e-10 5.0495e-07
13	r5188962	8 120404319 T	A	0.1839														

14	rs10503362	8	12044807	G	A	0.1839	1.7e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1573	Transcript	INTRONIC	intronic	1	NOV	1.50746e-07	5.04956e-07	NOV	1.50746e-09	5.04956e-07	14	2.720	7	5
14	rs7001817	8	12054622	G	A	0.1988	1.4e-10	0.846602	rs17191747	ENP2	Intergenic	DOWNSTREAM	downstream	RP11-436021.1574	Transcript	INTRONIC	intronic	1	NOV	8.79151e-07	5.04956e-07	NOV	8.79151e-07	5.04956e-07	14	2.637	7	5
14	rs10503363	8	12044622	G	A	0.1839	1.7e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1575	Transcript	INTRONIC	intronic	1	NOV	7.76521e-10	5.04956e-07	NOV	7.76521e-10	5.04956e-07	14	2.370	7	5
14	rs7349460	8	12034917	C	A	0.2018	5.7e-12	0.64049	rs60809342	ENP2	Intergenic	INTERGENIC	intergenic	RP11-436021.1576	Transcript	INTRONIC	intronic	1	NOV	9.04841e-09	5.04956e-07	NOV	9.04841e-09	5.04956e-07	14	2.484	7	9
14	rs10500357	8	12043706	G	T	0.1839	1.7e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1577	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.413	7	5
14	rs7350292	8	12054622	G	A	0.1988	2.3e-10	0.858811	rs17191747	ENP2	Intergenic	DOWNSTREAM	downstream	RP11-436021.1578	Transcript	INTRONIC	intronic	1	NOV	2.60797e-07	5.04956e-07	NOV	2.60797e-07	5.04956e-07	14	2.387	7	5
14	rs7342860	8	12034265	A	C	0.1829	1.4e-11	0.78305	rs60809342	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1579	Transcript	INTRONIC	intronic	1	NOV	2.79662e-08	5.04956e-07	NOV	2.79662e-08	5.04956e-07	14	2.376	7	4
14	rs1811834	8	120427603	G	A	0.2018	9.3e-10	0.809051	rs60809342	ENP2	Intergenic	DOWNSTREAM	downstream	RP11-436021.1580	Transcript	INTRONIC	intronic	1	NOV	1.28119e-08	5.04956e-07	NOV	1.28119e-08	5.04956e-07	14	2.348	5	2
14	rs1811835	8	120427603	G	A	0.2247	4.2e-12	0.789621	rs60809342	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1581	Transcript	INTRONIC	intronic	1	NOV	1.60899e-07	5.04956e-07	NOV	1.60899e-07	5.04956e-07	14	2.321	7	5
14	rs17801314	8	120573729	G	A	0.1948	2.7e-10	0.858811	rs17191747	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1582	Transcript	INTRONIC	intronic	1	NOV	2.60797e-07	5.04956e-07	NOV	2.60797e-07	5.04956e-07	14	2.320	7	4
14	rs107172213	8	120433320	G	A	0.1839	2.4e-11	0.783269	rs60809342	NOV	Transcript	INTRONIC	intronic	RP11-436021.1583	Transcript	INTRONIC	intronic	1	NOV	6.28574e-08	5.04956e-07	NOV	6.28574e-08	5.04956e-07	14	2.318	6	4
14	rs11780200	8	12045821	A	G	0.1839	1.6e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1584	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.317	7	5
14	rs11780200	8	12045821	A	G	0.1839	1.6e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1585	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.317	7	5
14	rs17317152	8	12043748	A	G	0.1839	1.6e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1586	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.319	5	2
14	rs10531540	8	12043751	G	C	0.1839	2.1e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1587	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.051	5	4
14	rs10575	8	12043640	T	C	0.1840	1.7e-11	0.729943	rs60809342	NOV	Transcript	SPRIME_UTR	3_prime_UTR	RP11-436021.1588	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	2.006	6	5
14	rs118040162	8	12042329	C	T	0.1839	1.2e-11	0.783269	rs60809342	NOV	Intergenic	INTERGENIC	intergenic	RP11-436021.1589	Transcript	INTRONIC	intronic	1	NOV	4.45041e-11	5.04956e-07	NOV	4.45041e-11	5.04956e-07	14	1.938	6	5
14	rs1243506	8	12043928	T	G	0.2018	9.3e-11	0.809051	rs60809342	NOV	Transcript	INTRONIC	intronic	RP11-436021.1590	Transcript	INTRONIC	intronic	1	NOV	4.42811e-09	5.04956e-07	NOV	4.42811e-09	5.04956e-07	14	1.895	3	1
14	rs1792171	8	12044376	C	T	0.1839	1.6e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1591	Transcript	INTRONIC	intronic	1	NOV	2.54886e-10	5.04956e-07	NOV	2.54886e-10	5.04956e-07	14	1.892	7	5
14	rs1791208	8	12043725	T	G	0.1839	1.6e-11	0.783269	rs60809342	NOV	Transcript	INTRONIC	intronic	RP11-436021.1592	Transcript	INTRONIC	intronic	1	NOV	3.00598e-10	5.04956e-07	NOV	3.00598e-10	5.04956e-07	14	1.756	7	1
14	rs6093389	8	12043702	T	G	0.2247	4.2e-12	0.789621	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1593	Transcript	INTRONIC	intronic	1	NOV	1.87621e-07	5.04956e-07	NOV	1.87621e-07	5.04956e-07	14	1.666	6	5
14	rs5532847	8	12058054	TA	T	0.3174	2.3e-10	1	rs532847	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1594	Transcript	INTRONIC	intronic	0	NOV	3.52663e-08	5.04956e-07	NOV	3.52663e-08	5.04956e-07	14	1.659	NA	4
14	rs67665719	8	12039596	G	A	0.2256	2.3e-10	0.75439	rs60809342	SNORA32	Intergenic	UPSTREAM	upstream	RP11-436021.1595	Transcript	INTRONIC	intronic	1	NOV	3.24688e-09	5.04956e-07	NOV	3.24688e-09	5.04956e-07	14	1.657	7	5
14	rs1738709	8	12043487	A	G	0.1839	1.7e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1596	Transcript	INTRONIC	intronic	1	NOV	1.729e-07	5.04956e-07	NOV	1.729e-07	5.04956e-07	14	1.657	7	5
14	rs1381338	8	120458587	T	C	0.2247	5.3e-12	0.798826	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1597	Transcript	INTRONIC	intronic	1	NOV	1.729e-07	5.04956e-07	NOV	1.729e-07	5.04956e-07	14	1.653	NA	5
14	rs68120708	8	120439009	A	T	0.2097	5.3e-12	0.78072	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1598	Transcript	INTRONIC	intronic	1	NOV	1.10774e-08	5.04956e-07	NOV	1.10774e-08	5.04956e-07	14	1.641	7	5
14	rs10505287	8	120430013	C	G	0.2247	4.9e-12	0.789626	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1599	Transcript	INTRONIC	intronic	0	NOV	1.65014e-07	5.04956e-07	NOV	1.65014e-07	5.04956e-07	14	1.469	4	1
14	8:120437457_C_A	8	120437457_C_A	CA	0.3082	1.1e-10	1	8:120437457_C_A	CA	0.3082	1.1e-10	1	8:120437457_C_A	CA	0.3082	1.1e-10	1	NOV	1.10774e-08	5.04956e-07	NOV	1.10774e-08	5.04956e-07	14	1.458	NA	5	
14	rs68089342	8	120456193	T	A	0.2276	4.4e-11	1	rs68089342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1601	Transcript	INTRONIC	intronic	0	NOV	1.86831e-07	5.04956e-07	NOV	1.86831e-07	5.04956e-07	14	1.450	5	5
14	rs10505337	8	120456193	T	A	0.1958	1.2e-10	0.846112	rs17191747	ENP2	Intergenic	DOWNSTREAM	downstream	RP11-436021.1602	Transcript	INTRONIC	intronic	0	NOV	4.45041e-11	5.04956e-07	NOV	4.45041e-11	5.04956e-07	14	1.382	7	4
14	rs5731327	8	120413952	C	G	0.1839	1.4e-11	0.752521	rs60809342	ENP2	Intergenic	INTERGENIC	intergenic	RP11-436021.1603	Transcript	INTRONIC	intronic	1	NOV	1.02101e-10	5.04956e-07	NOV	1.02101e-10	5.04956e-07	14	1.377	5	13
14	rs60246959	8	12046959	G	T	0.1839	1.9e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1604	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	1.373	7	5
14	rs12042728	8	12042728	A	G	0.1839	1.7e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1605	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	1.377	7	5
14	rs12042154	8	12042154	C	G	0.2276	4.1e-12	0.755051	rs60809342	ENP2	Intergenic	INTERGENIC	intergenic	RP11-436021.1606	Transcript	INTRONIC	intronic	1	NOV	2.17396e-08	5.04956e-07	NOV	2.17396e-08	5.04956e-07	14	1.372	7	5
14	rs11784229	8	120573597	A	G	0.1948	2.7e-10	0.858811	rs17191747	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1607	Transcript	INTRONIC	intronic	1	NOV	2.60797e-07	5.04956e-07	NOV	2.60797e-07	5.04956e-07	14	1.337	5	4
14	rs159966118	8	120456193	T	A	0.2008	8.2e-12	0.841983	rs17191747	ENP2	Transcript	INTRONIC	intronic	RP11-436021.1608	Transcript	INTRONIC	intronic	0	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	1.323	5	5
14	rs15511784	8	12044942	A	G	0.1839	1.8e-11	0.783269	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1609	Transcript	INTRONIC	intronic	1	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	1.317	7	5
14	rs12042053	C	T	0.1840	1.3e-11	0.729943	rs60809342	ENP2	Intergenic	INTERGENIC	intergenic	RP11-436021.1610	Transcript	INTRONIC	intronic	1	NOV	2.11531e-10	5.04956e-07	NOV	2.11531e-10	5.04956e-07	14	1.177	7	5		
14	rs1461693	8	120444158	T	C	0.2117	3.6e-12	0.78195	rs60809342	RP11-775815.2	Transcript	INTRONIC	intronic	RP11-436021.1611	Transcript	INTRONIC	intronic	1	NOV	3.17248e-08	5.04956e-07	NOV	3.17248e-08	5.04956e-07	14	1.176	7	5
14	rs73163608	8	12056284	G	C	0.1958	1.0e-10	0.84112	rs17191747	ENP2	Intergenic	INTERGENIC	intergenic	RP11-436021.1612	Transcript	INTRONIC	intronic	1	NOV	5.72258e-08	5.04956e-07	NOV	5.72258e-08	5.04956e-07	14	1.167	7	5
14	rs7014927	8	120431049	C	A	0.2266	4.6e-12	0.770744	rs60809342	NOV	Intergenic	INTERGENIC	intergenic	RP11-436021.1613	Transcript	INTRONIC	intronic	1	NOV	2.66973e-08	5.04956e-07	NOV	2.66973e-08	5.04956e-07	14	1.140	5	1
14	rs71700778	8	12043487	A	G	0.1849	1.6e-11	0.729943	rs60809342	NOV	Intergenic	INTERGENIC	intergenic	RP11-436021.1614	Transcript	INTRONIC	intronic	0	NOV	8.92118e-10	5.04956e-07	NOV	8.92118e-10	5.04956e-07	14	1.076	7	5
14	rs7341847	8	12043404	G																								





16	rs1208251	7	7341531 C	G	0.03678	1.7e-11	0.973125	rs12099918	Intergenic	INTRAGENIC	intergenic	RP11-43023.1815	Transcript	INTRONIC	intronic	0	16	0.209	3a	2
16	rs17140990	7	73438515 C	T	0.05169	2.7e-10	0.692238	rs12099918	ELN	Intergenic	UPSTREAM	upstream	RP11-43023.1816	Transcript	INTRONIC	intronic	0	16	0.022	5
16	rs3365312	7	73445902 C	G	0.05169	1.1e-10	0.692238	rs12099918	ELN	Intergenic	INTRONIC	intron	RP11-43023.1817	Transcript	INTRONIC	intronic	0	16	2.541	Na
16	rs303195	7	73452140 A	A	0.05169	3.8e-10	0.692238	rs12099918	ELN	Transcript	INTRONIC	intron	RP11-43023.1818	Transcript	INTRONIC	intronic	0	16	2.540	Na
16	rs74024	7	73447650 C	T	0.05169	1.6e-10	0.692238	rs12099918	ELN	Transcript	INTRONIC	intron	RP11-43023.1819	Transcript	INTRONIC	intronic	0	16	2.462	5
16	rs144049583	7	73450113 TA	A	0.05169	2.7e-10	0.692238	rs12099918	ELN	Intergenic	INTRONIC	intron	RP11-43023.1820	Transcript	INTRONIC	intronic	0	16	2.458	Na
16	rs19229261	7	7347875 A	T	0.1183	8.9e-06	0.757378	rs2855722	ELN	Transcript	INTRONIC	intron	RP11-43023.1821	Transcript	INTRONIC	intronic	0	16	2.318	6
16	rs120209918	7	73472600 T	A	0.03777	2.9e-12	1	rs12099918	RegulatoryFeature	REGULATORY	regulatory	RP11-43023.1822	Transcript	INTRONIC	intronic	0	16	2.081	2b	
16	rs6979609	7	73436068 C	G	0.05169	2.7e-10	0.692238	rs12099918	ELN	Intergenic	INTRONIC	intron	RP11-43023.1823	Transcript	INTRONIC	intronic	0	16	1.600	5
16	rs873647	7	73447506 A	A	0.05169	3.6e-10	0.692238	rs12099918	ELN	Transcript	INTRONIC	intron	RP11-43023.1824	Transcript	INTRONIC	intronic	0	16	1.764	Na
16	rs11807792	7	7351920 T	G	0.09046	2.5e-06	0.710196	rs2855722	Intergenic	INTRAGENIC	intergenic	RP11-43023.1825	Transcript	INTRONIC	intronic	0	16	1.690	7	
16	rs73141161	7	73544717 T	A	0.09046	1.6e-06	0.710196	rs2855722	Intergenic	INTRAGENIC	intergenic	RP11-43023.1826	Transcript	INTRONIC	intronic	0	16	1.657	Na	
16	rs11761821	7	73438135 A	G	0.05169	2.4e-10	0.692238	rs12099918	RegulatoryFeature	REGULATORY	regulatory	RP11-43023.1827	Transcript	INTRONIC	intronic	0	16	1.597	5	
16	rs1375784	7	73440096 A	C	0.05169	2.2e-10	0.692238	rs12099918	ELN	Intergenic	UPSTREAM	upstream	RP11-43023.1828	Transcript	INTRONIC	intronic	0	16	1.588	5
16	rs1895707	7	73470218 T	C	0.09145	1.7e-06	0.700181	rs2855722	LMK1	Intergenic	DOWNSTREAM	downstream	RP11-43023.1829	Transcript	INTRONIC	intronic	0	16	1.561	5a
16	rs1821878	7	73443420 A	A	0.05169	1.7e-10	0.692238	rs12099918	ELN	Transcript	INTRONIC	intron	RP11-43023.1830	Transcript	INTRONIC	intronic	0	16	1.500	5
16	rs56017804	7	73448994 C	T	0.05169	1.4e-10	0.692238	rs12099918	ELN	Transcript	INTRONIC	intron	RP11-43023.1831	Transcript	INTRONIC	intronic	0	16	1.433	7
16	rs6979291	7	73457027 G	A	0.05169	2.8e-10	0.692238	rs12099918	Intergenic	INTRAGENIC	intergenic	RP11-43023.1832	Transcript	INTRONIC	intronic	0	16	1.215	5	
16	rs7609981	7	73434586 C	T	0.05169	2.4e-10	0.692238	rs12099918	Intergenic	INTRAGENIC	intergenic	RP11-43023.1833	Transcript	INTRONIC	intronic	0	16	0.928	6	
16	rs55241353	7	73461430 GA	G	0.05368	2.2e-10	0.629145	rs12099918	ELN	Transcript	INTRONIC	intron,feature_elongation	RP11-43023.1834	Transcript	INTRONIC	intronic	0	16	0.822	Na
16	rs11183394	7	73546991 A	G	0.09046	2.6e-06	0.710196	rs2855722	Intergenic	INTRAGENIC	intergenic	RP11-43023.1835	Transcript	INTRONIC	intr					

18	rs934668	16	84938921	C	T	0.4185	4.1e-10	0.696361	rs7161253	CRNPLD2	Transcript	INTRONIC	intron	RP11-436021.1936	Transcript	INTRONIC	intronUnc	0	18	0.108	NA	4
18	rs478390	16	84884116	G	A	0.2813	2.6e-09	0.599218	rs1485701	CRNPLD2	Transcript	INTRONIC	intron	RP11-436021.1937	Transcript	INTRONIC	intronUnc	0	18	0.106	5	4
18	rs478386	16	84884201	C	T	0.3499	9.9e-08	0.656417	rs54472123	CRNPLD2	Transcript	INTRONIC	intron	RP11-436021.1938	Transcript	INTRONIC	intronUnc	0	18	0.087	20	4
18	rs2426304	16	84843611	G	A	0.1789	7.8e-08	0.593722	rs625882	CRNPLD2	Transcript	INTRONIC	intron	RP11-436021.1939	Transcript	INTRONIC	intronUnc	0	18	0.082	4	4
18	rs11746824	16	84925945	A	G	0.07504	1.8e-08	1	rs11746824	CRNPLD2	Transcript	INTRONIC	intron	RP11-436021.1940	Transcript	INTRONIC	intronUnc	0	18	0.062	7	4
18	rs6906737	6	98343581	A	T	0.4861	1.5e-07	0.63977	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1941	Transcript	INTRONIC	intronUnc	0	19	1.96	6	top
18	rs6839708	6	98361700	C	T	0.4861	1.4e-06	0.62025	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1942	Transcript	INTRONIC	intronUnc	0	19	17.75	5	
18	rs7393317	6	98390515	A	A	0.4453	2.3e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1943	Transcript	INTRONIC	intronUnc	0	19	17.27	5	7
18	rs12180979	6	98313409	A	G	0.4871	8.2e-08	0.64274	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1944	Transcript	INTRONIC	intronUnc	0	19	15.11	7	4
18	rs13215227	6	98502674	C	T	0.4056	7.4e-09	0.794279	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1945	Transcript	INTRONIC	intronUnc	0	19	15.08	3a	7
18	rs11394250	6	98494321	C	C	0.4404	1.5e-06	0.647878	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1946	Transcript	INTRONIC	intronUnc	0	19	14.61	7	5
18	6-98316220 GC_G	6	98316220	GC	GC	0.4891	7.8e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1947	Transcript	INTRONIC	intronUnc	0	19	14.02	6	4
18	rs9187845	6	98328963	A	C	0.4891	7.0e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1948	Transcript	INTRONIC	intronUnc	0	19	11.90	7	5
18	rs4240559	6	98437275	C	T	0.4433	4.7e-07	0.760566	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1949	Transcript	INTRONIC	intronUnc	0	19	11.16	7	5
18	rs71757867	6	98339496	G	A	0.486	3.2e-08	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1950	Transcript	INTRONIC	intronUnc	0	19	11.86	6	15
18	rs7757842	6	98332930	A	A	0.4891	6.4e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1951	Transcript	INTRONIC	intronUnc	0	19	11.71	7	5
18	rs9320747	6	98310291	G	T	0.4861	6.2e-08	0.641028	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1952	Transcript	INTRONIC	intronUnc	0	19	11.66	7	5
18	rs9316129	6	98309379	T	A	0.4016	8.2e-09	0.78648	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1953	Transcript	INTRONIC	intronUnc	0	19	11.61	7	5
18	rs938662	6	98489561	C	T	0.4414	1.6e-06	0.671551	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1954	Transcript	INTRONIC	intronUnc	0	19	11.59	5	1
18	rs938929	6	98326080	C	G	0.4891	7.2e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1955	Transcript	INTRONIC	intronUnc	0	19	11.17	6	5
18	rs6943784	6	98347395	C	A	0.486	2.3e-08	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1956	Transcript	INTRONIC	intronUnc	0	19	10.58	5	5
18	rs903628	6	98339377	G	C	0.4046	8.4e-09	0.7973	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1957	Transcript	INTRONIC	intronUnc	0	19	10.38	7	7
18	rs9401250	6	98316447	T	C	0.4891	8.9e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1958	Transcript	INTRONIC	intronUnc	0	19	9.838	7	5
18	rs12152382	6	98307633	C	T	0.4851	1.2e-06	0.673947	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1959	Transcript	INTRONIC	intronUnc	0	19	9.418	7	5
18	rs11515975	6	98368639	T	A	0.496	2.3e-06	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1960	Transcript	INTRONIC	intronUnc	0	19	9.081	6	5
18	rs6569189	6	98404383	C	A	0.4453	2.3e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1961	Transcript	INTRONIC	intronUnc	0	19	8.861	6	5
18	rs12205734	6	98321322	T	C	0.4891	6.7e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1962	Transcript	INTRONIC	intronUnc	0	19	8.801	7	5
18	rs6934796	6	98361813	A	G	0.4861	1.4e-06	0.62025	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1963	Transcript	INTRONIC	intronUnc	0	19	8.500	5	5
18	rs2032759	6	98331357	G	A	0.4891	6.2e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1964	Transcript	INTRONIC	intronUnc	0	19	7.676	7	5
18	rs1933712	6	98310223	G	A	0.4871	6.4e-08	0.64274	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1965	Transcript	INTRONIC	intronUnc	0	19	7.611	6	9
18	rs12176121	6	98529161	T	C	0.4046	7.9e-09	0.7973	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1966	Transcript	INTRONIC	intronUnc	0	19	7.115	6	9
18	rs4112207	6	98412756	A	G	0.4443	1.4e-07	0.764693	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1967	Transcript	INTRONIC	intronUnc	0	19	7.112	6	5
18	rs4824806	6	98349004	A	G	0.4046	8.5e-09	0.7973	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1968	Transcript	INTRONIC	intronUnc	0	19	6.807	7	9
18	rs10877213	6	98401271	T	T	0.496	2.4e-06	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1969	Transcript	INTRONIC	intronUnc	0	19	6.771	6	5
18	rs11513961	6	98348905	C	A	0.496	3.2e-06	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1970	Transcript	INTRONIC	intronUnc	0	19	6.637	6	15
18	rs9376255	6	98509056	G	T	0.4056	7.2e-09	0.794279	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1971	Transcript	INTRONIC	intronUnc	0	19	6.262	7	14
18	rs9387863	6	98421208	A	G	0.4433	1.5e-07	0.760566	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1972	Transcript	INTRONIC	intronUnc	0	19	5.486	7	5
18	6-98449775_TATA_T	6	98449775	T	TATA	0.4423	2.4e-06	0.763137	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1973	Transcript	INTRONIC	intronUnc	0	19	5.901	NA	5
18	rs2972186	6	98398087	C	T	0.4056	7.2e-09	0.794279	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1974	Transcript	INTRONIC	intronUnc	0	19	5.537	6	14
18	rs1266296	6	98321465	A	G	0.4891	7.0e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1975	Transcript	INTRONIC	intronUnc	0	19	5.486	7	5
18	rs490350	6	98457350	A	G	0.4423	1.6e-06	0.763137	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1976	Transcript	INTRONIC	intronUnc	0	19	5.460	6	14
18	rs7712104	6	98475100	A	A	0.4414	1.5e-06	0.671551	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1977	Transcript	INTRONIC	intronUnc	0	19	5.426	6	5
18	rs4246316	6	98442008	A	C	0.4433	3.8e-07	0.760566	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1978	Transcript	INTRONIC	intronUnc	0	19	5.136	7	5
18	6-98322714_ATATAT_A	6	98322714	ATATAT	ATATAT	0.4891	8.4e-08	0.650621	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1979	Transcript	INTRONIC	intronUnc	0	19	4.896	NA	5
18	rs7761851	6	98422438	T	T	0.4453	1.6e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1980	Transcript	INTRONIC	intronUnc	0	19	4.830	7	5
18	rs9006200	6	98401511	A	T	0.4453	2.1e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1981	Transcript	INTRONIC	intronUnc	0	19	4.829	3	5
18	rs72793867	6	98314763	A	AT	0.4881	8.8e-08	0.646659	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1982	Transcript	INTRONIC	intronUnc	0	19	4.765	NA	5
18	rs1154009	6	98398832	T	C	0.4453	1.6e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1983	Transcript	INTRONIC	intronUnc	0	19	4.765	NA	5
18	rs4153843	6	98401922	T	C	0.4531	1.5e-07	0.713882	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1984	Transcript	INTRONIC	intronUnc	0	19	4.441	7	4
18	rs4833939	6	98507832	C	A	0.4056	7.5e-09	0.794279	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1985	Transcript	INTRONIC	intronUnc	0	19	4.424	7	14
18	rs9805999	6	98403847	C	T	0.4453	2.4e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1986	Transcript	INTRONIC	intronUnc	0	19	4.072	7	5
18	rs4011601	6	98501713	C	T	0.4056	7.0e-09	0.794279	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1987	Transcript	INTRONIC	intronUnc	0	19	4.062	7	5
18	rs7772327	6	98404174	C	T	0.4453	2.1e-07	0.78877	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1988	Transcript	INTRONIC	intronUnc	0	19	3.828	6	5
18	rs4388816	6	98439152	A	T	0.4433	4.2e-07	0.760566	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1989	Transcript	INTRONIC	intronUnc	0	19	3.780	6	5
18	rs9482277	6	98351457	T	C	0.486	2.2e-08	0.650247	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1990	Transcript	INTRONIC	intronUnc	0	19	3.750	6	5
18	6-98373178_ATG_A	6	98373178	ATG	ATG	0.4891	2.2e-06	0.602431	rs4842094	RP11-436023.1	Transcript	INTRONIC	intronUnc	RP11-436021.1991	Transcript							

19	rs76112426	6	rs532427	G	T	0.4056	8.7e-09	0.793568	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.256	6	15	
19	rs2388151	6	rs361406	G	A	0.496	2.2e-06	0.650247	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.247	NA	5	
19	rs65020817	6	rs6348081	T	C	0.496	2.3e-06	0.650247	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.241	6	5	
19	rs7764648	6	rs5827416	C	T	0.3897	6.3e-09	0.751731	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.181	7	9	
19	rs121174762	6	rs5827741	C	C	0.4046	6.0e-09	0.7973	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.164	7	15	
19	rs9375068	6	rs485684	C	T	0.4423	1.6e-06	0.678377	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.118	14		
19	rs9372620	6	rs8330028	A	G	0.4851	6.1e-08	0.650621	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.103	6	5	
19	rs4904013	6	rs3619614	A	G	0.4453	2.0e-07	0.76877	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.082	3a	7	
19	rs65252431	6	rs8355221	C	C	0.496	2.5e-06	0.650247	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.063	7	5	
19	rs4849980	6	rs325541	G	C	0.4851	6.8e-08	0.650621	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.056	16	5	
19	rs148758237	6	rs397349	GGTGTGT	G	C	0.4583	1.2e-07	0.724808	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.031	NA	5
19	rs17604608	6	rs4906408	T	T	0.4443	1.4e-07	0.764693	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	1.031	NA	5	
19	rs1338640	6	rs3346803	A	A	0.4851	6.6e-06	0.611967	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.993	7	14	
19	rs601729	6	rs8351187	T	G	0.4861	1.7e-06	0.620225	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.984	7	9	
19	rs651405	6	rs4601808	C	T	0.4453	2.3e-07	0.76877	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.980	6	5	
19	rs1320821	6	rs4623117	C	T	0.4076	1.7e-09	0.673373	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.917	7	14	
19	rs61917247	6	rs4603317	G	C	0.4453	2.1e-07	0.76877	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.912	3a	5	
19	rs8177215	6	rs8177265	C	T	0.4026	1.5e-11	0.960226	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.865	5	7	
19	rs201030314	6	rs3236673	C	T	0.4851	7.4e-08	0.650621	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.860	6	5	
19	rs80147556	6	rs5324484	G	A	0.4036	6.2e-09	0.792949	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.846	7	15	
19	rs6524808	6	rs3858575	A	G	0.496	2.4e-06	0.650247	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.828	6	5	
19	rs4644073	6	rs4829064	C	T	0.4443	2.1e-07	0.764693	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.817	6	5	
19	rs10872224	6	rs485125	T	G	0.4085	2.0e-09	0.837727	rs482094	RP11-436021.1	Transcript	INTRONIC	INTRONIC	0	19	0.807	7	14	
19	rs13216075	6	rs5																

[illegible]



22	rs1874431	11	15083132	G	A	0.2376	2.0e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron				22	4.042	6	7
22	rs10741663		15133753	G	A	0.2594	7.2e-10	0.870542	rs75091118		Intergenic	INTERGENIC	intergenic				22	3.985	7	7
22	rs4648224		15100701	T	C	0.2594	7.2e-10	0.870542	rs75091118		Intergenic	INTERGENIC	intergenic				22	3.847	6	5
22	11:15103357_CAT_C		15103357	C	CAT	0.2594	1.4e-09	0.870542	rs75091118	CALCB	Transcript	SPRIME_UTR	3_prime_UTR,feature_truncation				22	3.812	NA	5
22	rs12274061		15102897	T	C	0.2376	2.1e-10	0.882722	rs75091118		Transcript	INTRONIC	intron				22	3.744	6	13
22	rs12226508		15084344	T	C	0.2376	2.2e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron				22	3.636		
22	rs1023400	11	14987728	A	G	0.2913	3.4e-07	0.795576	rs03808	CALCB	Transcript	INTRONIC	intron	CALCA	RegulatoryFeature	REGULATORY	regulatory	0		
22	rs7040031	11	15015501	CTT	C	0.2535	1.8e-10	0.890315	rs75091118	CALCB	Transcript	INTRONIC	intron,feature_elongation	RP11-7020.4	Intergenic	UPSTREAM	upstream	0		
22	rs4050613		15011300	T	C	0.2475	1.1e-10	0.918217	rs75091118	CALCB	Transcript	INTRONIC	intron	RP11-7020.4	Intergenic	UPSTREAM	upstream	0		
22	rs41213873		15080244	CT	C	0.2326	1.4e-10	0.826914	rs75091118	CALCB	Transcript	INTRONIC	intron,feature_elongation				22	3.309	NA	13
22	rs10430834		15105688	A	C	0.3469	3.4e-07	0.739151	rs03808		Intergenic	DOWNTSTREAM	downstream				22	3.305	6	14
22	rs75091118	11	15045210	CT	C	0.2366	1.2e-11			CALCB	Transcript	INTRONIC	intron,feature_elongation				22	3.276	NA	14
22	rs1540148	11	15091140	T	G	0.2609	1.1e-09	0.876383	rs75091118	CALCB	Transcript	SPRIME_UTR	3_prime_UTR				22	3.220	4	9
22	rs10813265	11	15104089	A	G	0.2594	8.1e-10	0.870642	rs75091118	CALCB	Intergenic	DOWNTSTREAM	downstream				22	3.219	5	5
22	rs1021422	11	15087909	C	A	0.2376	2.1e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron				22	3.130	6	9
22	rs4121974	11	15057907	G	A	0.2495	5.1e-10	0.918217	rs75091118	CALCB	Transcript	INTRONIC	intron				22	3.081	5	
22	rs794520	11	15093381	T	C	0.2505	4.9e-10	0.903528	rs75091118	CALCB	Intergenic	UPSTREAM	upstream				22	2.949	5	5
22	rs1021428	11	15116717	A	G	0.3509	9.6e-07	0.719578	rs03808		Intergenic	INTERGENIC	intergenic				22	2.924	7	5
22	11:15108645_ATTOT_A		15108645	ATTOT	ATTOT	0.2376	1.5e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron,feature_truncation				22	2.913	NA	
22	11:15119869_CCATATT1		15119869	CCATATT1	CCATATTTTG	0.2634	6.8e-09	0.852884	rs75091118		Intergenic	INTERGENIC	intergenic				22	2.815	NA	5
22	rs10832347	11	15071674	T	C	0.2376	3.1e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron				22	2.806	7	9
22	rs12285663	11	15061287	T	C	0.2376	3.0e-10	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron				22	2.648	5	9
22	11:15025884_AAATG_A		15025884	AAATG	AAATG	0.2376	7.6e-11	0.882722	rs75091118	CALCB	Transcript	INTRONIC	intron,feature_truncation				22	2.553	NA	5
22	rs12286051	11	14980848	T	C															

1	110832350	11	15082063 A	G	0.2376	3.3e-10	0.582722	r51599118	CALCB	Transcript	INTRONIC	intron			0				22	0.004	7	14			
2	r5687635	1	15138805 C	T	0.3171	4.0e-09	0.587457	r51481883		Intergenic	INTERGENIC	intergenic			1	THEM4	6.48806e-06	4.42843e-06	S100A10	2.7844e-06	0.0017914	23	13.56	5	
3	r4688874	1	15193140 A	G	0.2783	2.5e-10	0.912504	r51854883		RegulatoryFeature	REGULATORY	regulatory			1	THEM4	8.3849e-06	4.42843e-06	S100A10	3.06265e-05	0.0017914	23	14.82	11	
4	r5671174	1	15193086 B	A	0.2793	4.3e-10	0.879383	r51854883		Intergenic	INTERGENIC	intergenic			1	THEM4	5.1621e-06	4.42843e-06	THEM4	8.1621e-06	4.42843e-06	23	13.70	7	
5	r5687632	1	15193122 A	A	0.2793	4.4e-10	0.879383	r51854883		Intergenic	INTERGENIC	intergenic			1	THEM4	1.2785e-06	4.42843e-06	THEM4	1.2785e-06	4.42843e-06	23	13.51	7	
6	r53791153	1	151958144 G	A	0.2863	3.6e-11	0.999515	r51854883		Transcript	INTRONIC	intron			1	S100A10	1.51883e-06	0.0017914	S100A10	1.51883e-06	0.0017914	23	13.10	N/A	top
7	r56899129	1	15196091 A	A	0.2823	3.5e-10	0.864945	r51854883	S100A10	Intergenic	INTERGENIC	intergenic			1	THEM4	1.27756e-06	4.42843e-06	THEM4	1.27756e-06	4.42843e-06	23	13.51	7	
8	r112770825	1	151366607 G	A	0.2863	3.3e-11	1	r51854883		Transcript	INTRONIC	intron			1	S100A10	3.74259e-06	0.0017914	S100A10	3.74259e-06	0.0017914	23	10.29	20	1
9	r51817720	1	151907457 G	A	0.2793	3.3e-10	0.879383	r51854883		Intergenic	INTERGENIC	intergenic			1	THEM4	1.2785e-06	4.42843e-06	THEM4	1.2785e-06	4.42843e-06	23	10.27	7	
10	r5687632	1	15193122 A	A	0.2793	4.3e-10	0.912504	r51854883		RegulatoryFeature	REGULATORY	regulatory			1	THEM4	1.38426e-05	4.42843e-06	0.0017914	23	10.27	7			
11	r23176815	1	151923917 C	C	0.3052	8.8e-09	0.791727	r51854883	KRTBP28	Intergenic	UPSTREAM	upstream			1	THEM4	3.92686e-07	4.42843e-06	THEM4	3.92686e-07	4.42843e-06	23	10.11	6	
12	r751402717	1	151926354 T	TTTAA	0.3042	8.8e-09	0.802322	r51854883	KRTBP28	Intergenic	UPSTREAM	upstream			1	THEM4	4.83454e-07	4.42843e-06	THEM4	4.83454e-07	4.42843e-06	23	9.878	N/A	
13	1151930185 ET C	1	151930185 ET C	C	0.3072	7.7e-10	0.740102	r51854883		Intergenic	INTERGENIC	intergenic			0							23	9.426	1	
14	r12566232	1	151936612 G	A	0.2833	1.5e-10	0.831864	r51854883		RegulatoryFeature	REGULATORY	regulatory			0							23	9.426	1	
15	r58807484	1	151879919 T	C	0.2843	2.7e-10	0.856592	r51854883	THEM4	Transcript	INTRONIC	intron			1	THEM4	4.42843e-06	4.42843e-06	THEM4	4.42843e-06	4.42843e-06	23	9.342	4	
16	r51753163	1	151928432 C	A	0.3042	3.5e-10	0.879383	r51854883		Intergenic	INTERGENIC	intergenic			1	THEM4	7.72004e-07	4.42843e-06	THEM4	7.72004e-07	4.42843e-06	23	9.342	4	
17	r72084048	1	151905083 A	T	0.2793	4.3e-10	0.879383	r51854883		Intergenic	INTERGENIC	intergenic			1	THEM4	6.16709e-06	4.42843e-06	THEM4	6.16709e-06	4.42843e-06	23	9.143	6	
18	r4689124	1	151926762 T	A	0.3042	8.2e-09	0.802322	r51854883	KRTBP28	Intergenic	UPSTREAM	upstream			1	THEM4	3.81424e								



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35	rs9916089	17	7685259	C	A	0.1899	4.9e-08	0.962175	rs1973212	TIMP2	Transcript	INTRONIC	intron	RP11-323N12.5	Intergenic	DOWNSTREAM	downstream	0	35	0.983	6	4
35	rs895419	17	7686014	G	A	0.1958	4.1e-06	0.806416	rs1973212	RP19P29	Intergenic	DOWNSTREAM	downstream	USP36	Intergenic	UPSTREAM	upstream	0	35	0.905	5	5
35	rs6501254	17	7684253	A	A	0.1948	1.0e-06	0.812032	rs1973212	TIMP3	Intergenic	DOWNSTREAM	downstream	USP36	Intergenic	UPSTREAM	upstream	0	35	0.068	5	5
36	rs740722	11	7004096	A	G	0.1252	9.2e-07	0.760705	rs781659	AN01-AS1	Transcript	INTRONIC	intron,nc	AN01	CodingTranscript	NON_SYNONYMOUS	missense	0	36	22.9	NA	4 top
36	rs710595	11	7000331	A	C	0.4851	4.3e-09	1	rs875107	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	2.541	2b	2 top
36	11-7001192 CA_C	11	7001192	C	C	0.1352	4.9e-08	1	rs781659	AN01	Transcript	INTRONIC	intron,feature_truncation	AN01	Intergenic	DOWNSTREAM	downstream	0	36	1.015	NA	4
36	rs5917526	11	7000218	AT	A	0.2005	3.1e-06	0.668962	rs875107	AN01	Transcript	INTRONIC	intron,feature_truncation	AN01	Intergenic	DOWNSTREAM	downstream	0	36	6.234	NA	2
36	rs272609	11	70007562	A	C	0.1352	4.2e-08	1	rs781659	AN01	Transcript	INTRONIC	intron	AN01-AS1	Intergenic	UPSTREAM	upstream	0	36	6.204	5	4
36	rs17131347	11	7004854	T	C	0.1252	1.9e-07	0.760705	rs781659	AN01	Transcript	INTRONIC	intron	AN01-AS1	Intergenic	UPSTREAM	upstream	0	36	6.181	NA	4
36	rs14212765	11	7000711	A	C	0.1352	3.9e-08	1	rs781659	AN01	Transcript	INTRONIC	intron	AN01-AS1	Intergenic	UPSTREAM	upstream	0	36	5.652	5	2
36	rs15400958	11	7000184	T	CT	0.2783	2.4e-08	0.734076	rs34094842	AN01	Transcript	INTRONIC	intron,feature_truncation	AN01	Intergenic	DOWNSTREAM	downstream	0	36	3.396	NA	2
36	rs1720811	11	6998206	T	C	0.1431	1.7e-07	0.812032	rs781659	AN01	Transcript	INTRONIC	intron	RP11-805U14.3	Transcript	INTRONIC	intron,nc	0	36	1.747	3b	5
36	11-7001509 C_C	11	7001509	C	CTA	0.1272	1.4e-06	0.778339	rs781659	AN01	Transcript	INTRONIC	intron,feature_truncation	AN01	Intergenic	DOWNSTREAM	downstream	0	36	4.956	NA	4
36	rs875107	11	70005174	A	C	0.4851	3.7e-09	1	rs875107	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	4.675	NA	4
36	rs15531507	11	7001824	T	C	0.1252	9.4e-07	0.760705	rs781659	AN01	Transcript	INTRONIC	intron	AN01-AS1	Intergenic	DOWNSTREAM	downstream	0	36	4.049	4	4
36	rs17444388	11	7001720	A	T	0.1262	1.2e-06	0.752088	rs781659	AN01	Transcript	INTRONIC	intron	AN01-AS1	Intergenic	UPSTREAM	upstream	0	36	3.748	3b	5
36	rs1781658	11	7000287	A	G	0.4145	1.5e-06	0.677001	rs875107	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	3.609	NA	4
36	rs175108	11	7000641	A	C	0.4851	1.2e-09	1	rs875107	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	3.378	NA	2
36	rs55714726	11	7002431	T	C	0.1262	1.9e-06	0.768838	rs781659	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	3.314	4	1
36	rs12806297	11	7000117	T	C	0.1352	5.1e-08	1	rs781659	AN01	Transcript	INTRONIC	intron	AN01	RegulatoryFeature	REGULATORY	regulatory	0	36	3.091	5	4
36	rs12420027	11	7001889	A	G	0.1272	1.1e-06	0.778339	rs781659	AN01	Transcript	INTRONIC	in									

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40	rs4303974	4	rs157598A	A	C	0.2744	1.6e-08	0.98975	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.871	7	1
40	rs3564937	4	rs1549877A	G	A	0.2724	1.3e-08	0.93937	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-46564.1	Transcript	INTRONIC	intronic	0	4.810	7	5
40	rs432788	4	rs1536357	A	C	0.2763	1.3e-08	0.94027	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.810	7	5
40	rs1312790	4	rs1556795 G	A	A	0.2744	9.6e-08	0.94847	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Intergenic	DOWNSTREAM	downstream	0	4.582	5	5
40	rs4420978	4	rs157828A	G	G	0.3628	1.4e-06	0.65216	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.453	7	5
40	rs6403237	4	rs1557017 G	G	G	0.3618	1.7e-06	0.658287	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Intergenic	DOWNSTREAM	downstream	0	4.272	5	5
40	rs999460	4	rs1574135 C	T	T	0.2753	2.2e-08	0.946427	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.266	7	5
40	rs4623443	4	rs1585866 T	C	C	0.3628	1.4e-06	0.65216	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.193	5	5
40	rs15384029 CA_C	4	rs15384029 CA_C	CA	CA	0.3648	1.1e-06	0.652163	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	4.193	5	5
40	rs4320053	4	rs1570073 G	C	C	0.2744	1.5e-08	0.979493	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-46564.1	Regulatory/feature	REGULATORY	regulatory	0	3.994	5	5
40	rs4641135	4	rs1591784 G	A	A	0.3648	3.6e-06	0.646331	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.852	7	5
40	rs10030738	4	rs155496A	G	G	0.3608	3.0e-06	0.614778	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Intergenic	DOWNSTREAM	downstream	0	3.841	5	5
40	rs4467406	4	rs1558915 A	G	G	0.3618	1.7e-06	0.658287	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.809	7	5
40	rs4698878	4	rs1588800 G	C	C	0.3638	3.6e-06	0.649239	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.466	5	5
40	rs4698973	4	rs1568962 G	C	C	0.3618	2.3e-06	0.617737	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.446	7	5
40	rs4645128	4	rs1570127 G	G	G	0.3598	1.7e-06	0.651388	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.404	7	5
40	rs4346643	4	rs1572744 C	T	T	0.3618	2.3e-06	0.617737	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.276	7	5
40	rs13861047	4	rs1593835 A	G	G	0.3628	1.3e-06	0.642594	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	3.074	4	5
40	rs6852633	4	rs1554453 C	T	T	0.3618	1.7e-06	0.658287	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-46564.1	Transcript	INTRONIC	intronic	0	2.987	5	2
40	rs13139185	4	rs1582335 A	G	G	0.3638	3.6e-06	0.649239	rs432788	CLOUTNF7	Transcript	INTRONIC	intron	RP11-48402.1	Transcript	INTRONIC	intronic	0	2.941	7	5
40	rs4698972	4	rs1568972 A	G	G	0.3579	5.4e-06	0.615771	rs432788	CLOUTNF7											









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50	rs10924249	1	24570642	T	G	0.2117	1.0e-06	0.830572	rs12041565	KIF26B	Transcript	INTRONIC	intron	0				50	3.170	5	1
51	rs12549788	8	11653907	A	G	0.4394	4.9e-07	0.862341	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	20.4	4	5
51	rs10576621	8	11657662	T	C	0.4225	1.3e-06	0.938423	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	25.65	5	1
51	rs3808428	8	11651979	G	C	0.4394	3.6e-07	0.855319	rs2049865	TP53	Transcript	INTRONIC	intron	0				AF178030.2	Intergenic	UPSTREAM	upstream
51	rs1569364	8	11662974	T	C	0.4254	7.4e-07	0.797031	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	16.42	4	1
51	rs3205424	8	11655442	G	A	0.4324	1.3e-06	0.894906	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	14.18	7	1
51	rs800878	8	11648149	C	G	0.4394	6.2e-06	0.817199	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	13.94	5	5
51	rs1963767	8	11658380	A	G	0.4225	1.6e-06	0.938423	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	13.73	7	5
51	rs3265036	8	11656037	G	A	0.4324	1.3e-06	0.894906	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	13.38	5	1
51	rs3808459	8	11659190	C	T	0.4215	1.6e-06	0.942214	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	12.43	7	5
51	rs1028274	8	11658351	G	T	0.4225	1.9e-06	0.938423	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	12.01	7	5
51	rs2393897	8	11659199	G	T	0.4365	2.6e-07	0.932226	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	11.47	20	1
51	rs2717216	8	11663007	T	A	0.4225	6.4e-07	0.805189	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	11.34	4	1
51	rs1180624	8	11647811	C	T	0.4604	4.2e-06	0.815252	rs2049865	TP53	Transcript	INTRONIC	intron	0				RegulatoryFeature	REGULATORY	regulatory	0
51	rs97906	8	11661931	T	C	0.4314	1.2e-06	0.863193	rs2049865	TP53	Transcript	INTRONIC	intron	0				RegulatoryFeature	REGULATORY	regulatory	0
51	rs2409844	8	11648834	A	C	0.4205	1.3e-06	0.946022	rs2049865	TP53	Transcript	INTRONIC	intron	0				RegulatoryFeature	REGULATORY	regulatory	0
51	rs12114740	8	116481700	C	T	0.4394	6.1e-06	0.817199	rs2049865	TP53	Transcript	INTRONIC	intron	0				RegulatoryFeature	REGULATORY	regulatory	0
51	rs1481582	8	116480713	A	G	0.4394	6.1e-06	0.817199	rs2049865	TP53	Transcript	INTRONIC	intron	0				RegulatoryFeature	REGULATORY	regulatory	0
51	rs3028461	8	116597716	T	C	0.4395	1.2e-07	0.934021	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	9.08	7	2
51	rs11659497	TA, T	8	116595497	T	TA	0.4205	1.1e-06	0.930388	rs2049865	TP53	Transcript	INTRONIC	intron,feature_truncation	0			51	8.86	6	5
51	rs1384810	8	116486106	T	C	0.4394	5.7e-06	0.817199	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	8.85	NA	2
51	rs3808449	8	116576978	A	G	0.4225	1.6e-06	0.938423	rs2049865	TP53	Transcript	INTRONIC	intron	0				51	8.316	NA	5
51	rs800910	8	116496984	A	T	0.4384	2.0e-07	0.858827	rs2049865	TP53	Transcript	INTRONIC	intron								

51	rs1079822	8	116525324	T	C	0.4394	3.9e-07	0.855319	r2049865	TRPS1	Transcript	INTRONIC	intron	AF178030.2	Intergenic	DOWNSTREAM	downstream	0		51	1.359	NA	4	
51	rs2721954	8	116405103	T	C	0.4175	2.8e-07	0.917766	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.320	7	4	
51	rs1380648	8	116471025	T	G	0.4404	5.5e-06	0.815252	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.318	NA	5	
51	rs2358019	8	116565968	G	C	0.4215	1.1e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.318	6	4	
51	rs1178504	8	116591288	G	A	0.4215	1.6e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.309	5	5	
51	rs12056626	8	116557955	G	C	0.4344	2.4e-06	0.887707	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.291	6	5	
51	8:116592145_GA_G	8	116592145	G	GA	0.4215	1.5e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron,feature_truncation					0		51	1.287	NA	5	
51	rs2178947	8	116537530	C	A	0.4374	5.4e-07	0.861783	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.234	8	5	
51	rs800381	8	116506134	T	G	0.4374	2.8e-07	0.854215	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.241	NA	2	
51	rs10505258	8	116602855	C	T	0.4145	2.8e-07	0.906179	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.188	5	4	
51	rs2178946	8	116537058	A	G	0.4384	4.9e-07	0.858258	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.184	6	5	
51	rs11602499	8	116602795	C	T	0.4175	2.7e-07	0.917766	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.183	5	4	
51	rs1483589	8	116564796	G	A	0.4215	1.2e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.167	5	4	
51	rs800369	8	116480905	C	T	0.4404	6.4e-06	0.82282	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.160	NA	5	
51	rs2625674	8	11649221	A	G	0.4374	1.6e-07	0.814808	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.150	NA	5	
51	rs6991253	8	116593107	C	T	0.4195	1.5e-06	0.93384	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	1.056	7	5	
51	rs35864552	8	116499483	GA	G	0.4294	1.1e-06	0.783911	r2049865	TRPS1	Transcript	INTRONIC	intron,feature_elongation					0		51	1.052	NA	4	
51	rs2737305	8	116610180	C	T	0.4205	1.6e-06	0.824609	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.937	6	4	
51	rs800880	8	116508132	C	T	0.4404	5.1e-07	0.852425	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.935	NA	5	
51	rs7823575	8	116551546	G	A	0.4384	4.9e-07	0.865856	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.917	5	4	
51	rs1905176	8	116537058	G	A	0.4374	5.5e-07	0.861783	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.827	NA	4	
51	8:116499624_AC_A	8	116499624	A	AC	0.4384	2.3e-07	0.858827	r2049865	TRPS1	Transcript	INTRONIC	intron,feature_truncation					0		51	0.741	NA	4	
51	rs2049867	8	116588570	C	T	0.4205	1.2e-06	0.946032	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.734	3a	1	
51	rs2737312	8	116621214	T	C	0.4334	1.5e-06	0.855032	r2049865	TRPS1	Transcript	INTRONIC	intron			RegulatoryFeature	REGULATORY	regulatory	0		51	0.690	7	5
51	rs809623	8	116499185	A	G	0.4394	2.9e-07	0.855319	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.665	NA	4	
51	rs808418	8	116491594	G	T	0.4374	2.0e-07	0.854808	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.616	3a	1	
51	rs2625675	8	116499086	T	A	0.4384	2.2e-07	0.858827	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.616	7	4	
51	rs4326410	8	116593582	T	C	0.4185	1.2e-06	0.937673	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.588	7	5	
51	rs9643105	8	116542967	C	T	0.4384	3.1e-07	0.865856	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.585	7	4	
51	rs11267515	8	116602676	A	G	0.4185	2.7e-07	0.912089	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.572	4	4	
51	rs1180647	8	116472478	T	C	0.4404	5.5e-06	0.815252	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.460	7	5	
51	rs800887	8	116460882	G	A	0.4404	4.4e-06	0.815252	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.457	NA	5	
51	rs2625676	8	114951133	C	T	0.4374	1.9e-07	0.814808	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.412	NA	5	
51	rs1160133	8	116480724	G	T	0.4215	1.2e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.407	6	5	
51	rs803220	8	116505452	A	G	0.4215	1.1e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.388	6	4	
51	rs2721933	8	116827175	C	T	0.4245	8.2e-07	0.86584	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.359	2b	2	
51	rs1531144	8	116564879	C	A	0.4225	1.0e-06	0.938423	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.230	6	4	
51	rs824200	8	116531797	A	G	0.4384	5.4e-07	0.858258	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.213	6	5	
51	rs12148221	8	116512403	T	C	0.4394	5.4e-07	0.855319	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.171	7	5	
51	rs13360941	8	116535753	C	T	0.4374	5.4e-07	0.861783	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.163	7	5	
51	8:116476308_TA_T	8	116476308	T	TA	0.4404	4.7e-06	0.815252	r2049865	TRPS1	Transcript	INTRONIC	intron,feature_truncation					0		51	0.051	NA	5	
51	rs2737217	8	116583511	G	A	0.4225	8.9e-07	0.805189	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.035	7	3	
51	rs2070481	8	116585157	T	C	0.4215	1.4e-06	0.942214	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.031	6	4	
51	rs2737206	8	116611902	C	T	0.4294	7.9e-07	0.862291	r2049865	TRPS1	Transcript	INTRONIC	intron					0		51	0.025	6	4	
51	rs1384812	8	116519075	G	T	0.4384	3.5e-07	0.858827	r2049865	TRPS1	Transcript	INTRONIC	intron		AF178030.2	Intergenic	UPSTREAM	upstream	0		51	0.016	7	5
51	rs3808425	8	116515643	A	G	0.4394	3.8e-07	0.855319	r2049865	TRPS1	Transcript	INTRONIC	intron		AF178030.2	Intergenic	UPSTREAM	upstream	0		51	0.004	7	5
51	rs3808426	8	116518834	T	A	0.4384	2.9e-07	0.858827	r2049865	TRPS1	Transcript	INTRONIC	intron		AF178030.2	Intergenic	UPSTREAM	upstream	0		51	0.004	5	5

***Supplementary Table 2: Genes implicated by positional, eQTL, or chromatin interaction mapping of SNPs associated with diverticular disease by FUMA***

To link the associated variants to genes, we applied three gene-mapping strategies as implemented in FUMA. Positional gene mapping aligned SNPs to 176 genes by genomic location located at the identified 51 distinct genomic risk loci for diverticulosis, by eQTL gene mapping matched with cis-eQTL SNPs to 269 genes whose expression levels they influence, and by chromatin interaction mapping annotated SNPs to 977 genes on the basis of 3D DNA–DNA interactions. This resulted in 1080 unique mapped genes, 176 of which were implicated by at least two mapping strategies and 97 of which were implicated by all three. The majority of these mapped genes are protein coding genes (n=657, 61%), while 39% are RNA genes (n=302) and pseudogenes (n=121). Loci for genes mapped by two genomic risk loci are listed as locus1:locus2. Abbreviations used in the column headers are coded as follows: pLI = probability of loss of function mutation intolerance (higher scores indicate higher probability); ncRVIS : Non-coding residual variation intolerance score. The higher the score is, the more intolerant to noncoding variants the gene is; posMapSNPs = SNPs mapped to this gene by positional mapping; eqtlMapSNPs = SNPs mapped to this gene by expression quantitative trait locus mapping; eqtlMapminP = minimum P value of eQTL association for the mapped gene; eqtlMapminQ = minimum false discovery rate Q value of eQTL association for the mapped gene; Tissues = tissues in which the significant eQTL association or chromatin interaction was observed; eqtlDirection = direction of association of eQTL SNP with expression levels (upregulation or downregulation); ciMap = chromatin interaction mapping; minGwasP = minimum GWAS P value of SNP(s) implicating the gene.





1	ENSG00000003970	SPY11	SETP11	10041936	3	15080728	15080717	8.4e-11	NA	NA	39	0	11.3102146	7.52967e-12	NA	NA	Yes	NSC-Mycophenyl Stem Cell ARS018-04228 Transposon
2	ENSG00001188271	SP787	OPR87	508187	3	15010181	15010740	protein coding	1.7e-11	0.29054804899993	0.1737777332	50	61	1.11012146	7.52967e-12	NA	Yes	NSC-Mycophenyl Stem Cell ARS018-04228 Transposon
3	ENSG00001081651	SP711	TS113	518213	3	15104410	15104106	protein coding	1.7e-11	0.1710312361051	0.140094349	20	68	1.13086126	5.60376e-17	NA	Yes	NSC-Mycophenyl Stem Cell ARS018-04228 Transposon
GRC_HiSeq_v2, v3, v4, v5, v6, v7, v8, v9, v10, v11, v12, v13, v14, v15, v16, v17, v18, v19, v20, v21, v22, v23, v24, v25, v26, v27, v28, v29, v30, v31, v32, v33, v34, v35, v36, v37, v38, v39, v40, v41, v42, v43, v44, v45, v46, v47, v48, v49, v50, v51, v52, v53, v54, v55, v56, v57, v58, v59, v60, v61, v62, v63, v64, v65, v66, v67, v68, v69, v70, v71, v72, v73, v74, v75, v76, v77, v78, v79, v80, v81, v82, v83, v84, v85, v86, v87, v88, v89, v90, v91, v92, v93, v94, v95, v96, v97, v98, v99, v100, v101, v102, v103, v104, v105, v106, v107, v108, v109, v110, v111, v112, v113, v114, v115, v116, v117, v118, v119, v120, v121, v122, v123, v124, v125, v126, v127, v128, v129, v130, v131, v132, v133, v134, v135, v136, v137, v138, v139, v140, v141, v142, v143, v144, v145, v146, v147, v148, v149, v150, v151, v152, v153, v154, v155, v156, v157, v158, v159, v160, v161, v162, v163, v164, v165, v166, v167, v168, v169, v170, v171, v172, v173, v174, v175, v176, v177, v178, v179, v180, v181, v182, v183, 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[illegible]

[illegible]

1	ENSG00000204832	STES46.AS1	STES46.AS1	100126088	10	17438915	1745550	2.76e-10	NA	0	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal Stem Cell-Mesenchymal
1	ENSG0000025852	SPFB2A2	SPFB2A2	100131947	10	17619381	17620313	psaeglucan	2.76e-10	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal Stem Cell-Mesenchymal
1	ENSG0000025853	SPFB2A2	SPFB2A2	100131948	10	17619388	17620303	psaeglucan	2.76e-10	0.2768823155538	NA	0	0	NA	NA	NA	YES	NCSC-Mesenchymal Stem Cell-Mesenchymal
1	ENSG00000260589	SP1A.9004A.5	SP1A.AS1	100272196	10	17602833	17608477	arntanase	2.76e-10	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000261728	STAM	STAM	8057	10	17680124	17737953	protein	2.76e-10	0.902276080804	0.025607004	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000261828	SC3B1.1	SC3B1.1	20075	10	18020785	18032223	protein	2.76e-10	0.002090585133897	0.126473059	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000262083	SC3B1A2.1	SC3B1A2.1	100129213	10	18020755	18238491	arntanase	2.76e-10	NA	0	28	1.50464e-15	1.81105e-15	NA	NA	YES	NCSC-Mesenchymal Stem Cell-Mesenchymal
1	ENSG00000262473	ITIFB2P	ITIFB2P	100126337	10	21117028	21139721	psaeglucan	3e-09	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000262514	MRP12A.2	MRP12A.2	100841617	10	23881314	23881314	protein	4.0e-10	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000262512	OTUD1	OTUD1	220313	10	23737018	23731308	protein	4.0e-10	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000262649	KIAA1237	KIAA1237	56243	10	23093835	23480772	protein	4.0e-13	0.014367094373996	-0.482447167	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000270793	KRIB2	KRIB2	2464214	10	2464214	2464210	protein	4.0e-13	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000270863	AHRHA2P1	AHRHA2P1	17584	10	24871538	25012397	protein	4.0e-13	0.99944672007151	0.427480786	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000270957	NTVTC2	NTVTC2	2137375	10	2137375	2137375	protein	4.0e-13	0.718324481820	0.6486641	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000271023	FNOL3	FNOL3	219670	10	25170059	25105099	protein	4.0e-13	0.960084042081106	0.547300545	0	0	NA	NA	NA	YES	NCSC-Trophoblast
1	ENSG00000271847	THN3L1	THN3L1	78996	10	25105147	25115593	protein	4.0e-13	5.6183088219396	1.59221866	0	0	NA	NA	NA	YES	NCSC-Trophoblast
1	ENSG00000272422	FNOL3	FNOL3	219670	10	25170059	25105099	protein	4.0e-13	0.960084042081106	0.547300545	0	0	NA	NA	NA	YES	NCSC-Trophoblast
1	ENSG00000273162	GNP13A.AS1	GNP13A.AS1	100138131	10	25470061	25463205	arntanase	4.0e-10	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000273232	SPR12	SPR12	21512	10	25480911	25811215	protein	4.0e-10	0.1650083438113	0.1802111	0.11	5.38339e-10	0.10506e-05	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000274220	NR750P.20	NR750P.20	100480005	10	25604266	25627733	mRNA	6e-09	NA	0	0	NA	NA	NA	NA	YES	NCSC-Mesenchymal Stem Cell-Artery-Mesenchymal
1	ENSG00000272740	GP2P1	GP2P1	100103589	10	25934909	25937033	psaeglucan	7.0e-22	NA	2	0	0	NA	NA	NA	YES	NCSC-Mesenchymal
1	ENSG00000272753	HRAP1	HRAP1	19822545	10	25904046	25912552	psaeglucan	7.0e-22	NA	0	0	NA	NA	NA	NA	YES	





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**Supplementary Table 3: Identification of curated lead candidate gene(s) (CCG) at the identified genomic risk locations for diverticular disease**

The table provides a per locus account of the manually curated selection of CCGs. The top two rows of the table provide the selection criteria used. For each locus, one row indicates the lead variant data (denoted as **L**) in column 3. If an additional proxy variant (denoted as **P**) in LD to the lead variant was utilized for selection of the CCG, a second row with the respective information was inserted. The decision criterion is noted in the row with the variant on which the decision was based. The decision criterion in the manually curated selection process is provided in Column 8. The criteria were traversed hierarchically from 1 to 6 as follows: **Criterion 1:** For lead variants located intronic, exonic, in the 3' or 5'UTR to a single annotated gene, the respective gene was identified as the CCG (30 out of 51 loci). **Criterion 2:** For variants located upstream or downstream to a single annotated gene, this gene was assigned as the CCG (12 out of 51 loci) if a variant in the CCG had at least an  $r^2 > 0.5$  to the lead variant at the locus. **Criterion 3:** For loci, where variants in more than one neighbouring or overlapping transcript showed significant LD ( $r^2 > 0.5$ ) to the lead variant, the transcript with higher expression in the tissue of interest (columns 14-16) was selected as the CCG (3 out of 51 loci). **Criterion 4:** For loci, where variants in more than one neighbouring or overlapping transcript showed significant LD ( $r^2 > 0.5$ ) to the lead variant and no clear differences in expression were evident, the CCG was selected if additional regulatory evidence was present, i.e. an eQTL in a tissue of interest according to GTEx\_v7 (column 12, 13) or a chromatin interaction (column 14) pointed to a particular gene (1 out of 51 loci). **Criterion 5:** If the lead variant was not located in a gene region and did not show significant LD to a variant in a neighbouring transcript, the impact of the lead variant and the variants in LD to the lead variant on regulatory elements (eQTLs or chromatin interaction) was evaluated. If such elements were identified, the closest respective gene was annotated as the CCG (4 out of 51 loci). **Criterion 6:** For the remaining loci, the closest transcript to the lead variant was annotated as a CCG if the distance to the variant was less than 1MB (1 out of 51 loci). Gene annotation are based on RefSeq Curated gene predictions from NCBI (pseudogenes were excluded from annotation) as implemented in UCSC Genome Browser (Ref. 6).

Risk locus					CCG			<u>Decision criterion</u>	cis-eQTL	cis-eQTL	3D chromatin interaction	mRNA expression normal sigmoid colon		Protein expression	
Locus	Chr	Position (hg19)	Variant	R <sup>2</sup> to lead	P value discovery	CCG	Gene, Biotype	Variant location	Decision criterion	Lead/proxy variant affects gene expression of CCG in sigmoid colon	Lead/proxy variant affects gene expression of CCG in other tissue (most sign. tissue shown)	Lead variant/proxy variant chromatin interaction with gene (FUMA; HiC; GSE87112)	mRNA expression in normal sigmoid colonic epithelium (SAGE tags/tissue) (Genecards, Ref. 1,6)	mRNA expression in muscularis propria of normal sigmoid colon (RNA-seq 100xFPKM) <sup>1/2</sup> (GTEx_v7, Ref. 1,2)	Colon- estimated protein expression log10(ppm) iBAQ <sup>DB</sup>   annotated protein expression <sup>§</sup> , single antibody staining <sup>AB</sup> , Endothelial cells  Glandular cells  Peripheral nerve/ganglion
1	2	144314247	rs6734367(L)	1	4.4 × 10 <sup>-55</sup>	ARHGAP15 (CCG)	protein-cod.	intron	1	no	no		0	2	4
2	1	234352899	rs4333882(L)	1	2.5 × 10 <sup>-24</sup>	SLC35F3 (CCG)	protein-cod.	intron	1	no	no		n/a	0.6	35 <sup>DB</sup>   med   high   med <sup>AB</sup>



3	10	25819228	rs7077800(L)	1	$1.7 \times 10^{-22}$	<i>GPR158</i> (CCG)	protein-cod.	intron	1	<i>GPR158</i> Colon – Sigmoid P=1.1e-6	<i>GPR158</i> Esophagus – Muscularis P=2.5e-7	0	0.3	low low low <sup>AB</sup>	
4	3	15502681	rs7609897(L)	1	$5.6 \times 10^{-22}$	<i>COLQ</i> (CCG)	protein-cod.	intron	1	no	no	0	5	n/a	
5	2	56093204	rs1802575(L)	1	$3.7 \times 10^{-19}$	<i>EFEMP1</i> (CCG)	protein-cod.	3_prime_UTR	1	no	<i>EFEMP1</i> Skin P=8.0e-7	0	46	colon (med) <sup>DB</sup>	
6	11	27748493	rs17309930(L)	1	$6.8 \times 10^{-17}$	<i>BDNF</i> (CCG)	protein-cod.	upstream (5kb)		no	no	0	0.3	nd low low <sup>AB</sup>	
6	11	27723334	rs56133711(P)	0.75	$8.7 \times 10^{-15}$	<i>BDNF</i> (CCG)	protein-cod.	intron	2	no	no				
7	19	38738130	rs4802297(L)	1	$2.0 \times 10^{-16}$	<i>PPP1R14A</i> (CCG)	protein-cod.	downstream (4 kb)		<i>PPP1R14A</i> Colon – Sigmoid P= 2.2e-37	<i>PPP1R14A</i> Esophagus – Muscularis P= 5.1e-47	0	292	med nd low <sup>S</sup>	
7	19	38746567	rs4803934(P)	0.92	$4.8 \times 10^{-16}$	<i>PPP1R14A</i> (CCG)	protein-cod.	intron	2						
8	9	136149229	rs505922(L)	1	$4.5 \times 10^{-15}$	<i>ABO</i> (CCG)	protein-cod.	intron	1	<i>ABO</i> Colon – Sigmoid P= 2.0e-13	<i>ABO</i> Esophagus – Mucosa P=1.2e-44	7	1	colonic epith. cell (high) <sup>DB</sup>	
9	7	102474903	rs72221075(L)	1	$7.7 \times 10^{-15}$	<i>FBXL13</i> (CCG)	protein-cod.	intron	1	no	no	0	0.3	high low low <sup>S</sup>	
10	13	107897823	rs9520339(L)	1	$1.1 \times 10^{-14}$	<i>FAM155A_1</i> (CCG)	protein-cod.	intron	1	no	no	n/a	1	-  mod  -	
11	13	108215404	rs9555371(L)	1	$1.2 \times 10^{-13}$	<i>FAM155A_2</i> (CCG)	protein-cod.	intron	1	no	no	n/a	1	-  mod  -	
12	1	219294570	rs61823192(L)	1	$4.6 \times 10^{-14}$	<i>LYPLAL1-ASI</i>	antisense	intron	1	no	no	n/a	n/a		
13	10	101391169	rs7098322(L)	1	$9.2 \times 10^{-14}$	<i>SLC25A28</i> (CCG)	protein-cod.	upstream(11kb)	3	no	<i>SLC25A28</i> Adrenal Gland P=6.9e-7	<i>SLC25A28</i> Mesenchymal_Stem_Cell P=3.09e-127 (rs2300979 r2=0.99)	3	97	n/a
13	10	101379280	rs11190190(P)	1	$1.2 \times 10^{-13}$	<i>SLC25A28</i> (CCG)	protein-cod.	intron							
13	10	101391169	rs7098322(L)	1	$9.2 \times 10^{-14}$	<i>ENTPD7</i>	protein-cod.	upstream(28kb)		no	<i>ENTPD7</i> Cells - Transformed fibroblasts P=1.2e-10,	<i>ENTPD7</i> Mesenchymal_Stem_Cell P=7.09e-31	n/a	2	nd low nd <sup>S</sup>
13	10	101422423	rs753642536(P)	0.99	$8.3 \times 10^{-14}$	<i>ENTPD7</i>	protein-cod.	intron							
14	8	120456193	rs60869342(L)	1	$4.4 \times 10^{-13}$	<i>NOV</i> (CCG)	protein-cod.	downstream (20kb)		no	no	<i>NOV</i> Mesenchymal_Stem_Cell P=1.45e-38 (rs2085905 r2=0.75)	0	10	nd nd nd <sup>S</sup>
14	8	120435812	rs2071518(P)	0.79	$5.8 \times 10^{-12}$	<i>NOV</i> (CCG)	protein-cod.	3_prime_UTR	2	<i>NOV</i> Colon – Sigmoid P=1.7e-7	<i>NOV</i> Esophagus – Muscularis P=2.3e-12				
15	21	47399453	rs111316530(L)	1	$4.8 \times 10^{-13}$	<i>COL6A1</i> (CCG)	protein-cod.	upstream (2kb)		no	no	3	1915	med  nd  nd <sup>S</sup>	

15	21	47403155	rs9974290(P)	0.95	$2.4 \times 10^{-12}$	COL6A1 (CCG)	protein-cod.	intron	2	no	no					
16	7	73427600	rs112609918(L)	1	$2.9 \times 10^{-12}$	ELN (CCG)	protein-cod.	upstream(15kb)		no	no	ELN IMR90 P= 1.20e-18	0	68	colon	(med) <sup>DB</sup>
16	7	73443245	rs3823878(P)	0.69	$1.7 \times 10^{-10}$	ELN (CCG)	protein-cod.	intron	2	no	no					
17	16	86233413	rs2280028(L)	1	$4.1 \times 10^{-12}$	LINC01082 (CCG)	lncRNA	downstream (87bp)	2	no	no	no	n/a	17		
18	16	84857378	rs2131755(L)	1	$1.5 \times 10^{-11}$	CRISPLD2 (CCG)	protein-cod.	intron	1	no	CRISPLD2 Cells - Transformed fibroblasts P=8.2e-16		n/a	95	low med med <sup>S</sup>	
19	6	98364895	rs9482094(L)	1	$1.6 \times 10^{-11}$	LOC101927314 (CCG)	lincRNA	intron	1	no	no		n/a	n/a		
20	3	151074941	rs3732760(L)	1	$1.7 \times 10^{-11}$	P2RY12 (CCG)	protein-cod.	intron	4	no	P2RY12 Brain - basal ganglia P=1.1e-5	P2RY12 Mesenchymal_Stem_Cell P=3.09e-37	0	2	low med low <sup>AB</sup>	
20	3	151074941	rs3732760(L)	1	$1.7 \times 10^{-11}$	MED12L	protein-cod.	intron		no	no	no	3	0.2	nd  nd  low <sup>S</sup>	
21	5	64295363	rs10471645(L)	1	$2.1 \times 10^{-11}$	CWC27 (CCG)	protein-cod.	intron	1	no	no		0	18	med high med <sup>S</sup>	
22	11	15065235	rs575909118(L)	1	$2.8 \times 10^{-11}$	CALCB (CCG)	protein-cod.	upstream (30kb)		no	no	CALCB Mesendoderm P=3.09e-37	0	0.6	n/a	
22	11	15098067	rs1894128(P)	0.87	$7.9 \times 10^{-10}$	CALCB (CCG)	protein-cod.	intron	2	no	no					
23	1	151970629	rs61814883(L)	1	$3.2 \times 10^{-11}$	S100A10 (CCG)	protein-cod.	upstream (4kb)		S100A10 Colon – Sigmoid P=2.9e-6	S100A10 Brain – Cerebellum P=7.2e-11		690	152	high med high <sup>S</sup>	
23	1	151962689	rs12083193(P)	1	$3.6 \times 10^{-11}$	S100A10 (CCG)	protein-cod.	intron	2							
24	5	37772780	rs10472291(L)	1	$3.8 \times 10^{-11}$	WDR70	protein-cod.	downstream (19kb)		no	no	WDR70 Mesenchymal_Stem_Cell P= 9.53e-24, IMR90 P=3.69e-21	3	22	nd  nd  nd <sup>S</sup>	
24	5	37772780	rs10472291(L)	1	$3.8 \times 10^{-11}$	GDNF (CCG)	protein-cod.	downstream (40kb)	5	GDNF Colon – Sigmoid P=0.008	GDNF Brain - Cerebellum P=6.0e-6	GDNF Mesenchymal_Stem_Cell P=1.17e-25, IMR90 P=5.62e-15	n/a	12	nd  nd  nd <sup>S</sup>	
25	15	40649609	rs71472433(L)	1	$6.1 \times 10^{-11}$	PHGR1 (CCG)	protein-cod.	downstream (1kb)	3	PHGR1 Colon – Sigmoid P=1.8e-3	PHGR1/Skin - Sun Exposed P=3.1e-7	PHGR1 IMR90 P=7.84e-135	3299	7	nd  high  nd <sup>S</sup>	
25	15	40645098	rs7164581(P)	0.96	$1.7 \times 10^{-10}$	PHGR1 (CCG)	protein-cod.	intron								
25	15	40649609	rs71472433(L)	1	$6.1 \times 10^{-11}$	DISP2 (CCG)	protein-cod.	upstream (1kb)	3	DISP2 Colon – Sigmoid P=5.2e-23	DISP2 Skin - Sun Exposed P=1.7e-43	DISP2 IMR90 P= 7.84e-135	7	0.9	nd  nd  nd <sup>S</sup>	
25	15	40655444	rs12913300(P)	0.9	$1.6 \times 10^{-10}$	DISP2 (CCG)	protein-cod.	intron								
26	17	7372637	rs12942267(L)	1	$6.7 \times 10^{-11}$	ZBTB4 (CCG)	protein-	intron	1	ZBTB4 Colon –	ZBTB4 Esophagus		3	95	low low low <sup>S</sup>	

cod.															Sigmoid P 0.02		– Mucosa P=5.4e-8	
27	15	76826003	rs2056544(L)	1	9.8 × 10 <sup>-11</sup>	SCAPER (CCG)	protein-cod.	intron	1	no	no	0	9	low med med <sup>§</sup>				
28	7	96078564	rs3113037(L)	1	1.0 × 10 <sup>-11</sup>	SEM1(C7orf76) (CCG )	protein-cod.	downstream (13kb)		no	no	SEM1 (C7orf76) hESC cells P=5.05e-94	n/a	49	low med med <sup>§</sup>			
28	7	96115099	rs10281460(P)	0.93	2.0 × 10 <sup>-9</sup>	SEM1(C7orf76) (CCG )	protein-cod.	intron	2	no	no							
29	18	20028737	rs9960286(L)	1	2.3 × 10 <sup>-10</sup>	CTAGE1 (CCG)	protein-cod.	intergenic 31kb upstream of gene	5	no	no	CTAGE1 IMR90 P=1.42e-282	0	1	low med nd <sup>AB</sup>			
30	17	42312778	rs8074740(L)	1	2.4 × 10 <sup>-10</sup>	SLC4A1	protein-cod.	downstream (13kb)		no	no	3	0.02	nd nd nd <sup>§</sup>				
30	17	42326258	rs5033(P)	0.92	3.6 × 10 <sup>-9</sup>	SLC4A1	protein-cod.	3_prime_UTR		no	no							
30	17	42312778	rs8074740(L)	1	2.4 × 10 <sup>-10</sup>	UBTF (CCG)	protein-cod.	upstream(14kb)	3	no	no	17	49	high high nd <sup>§</sup>				
30	17	42292476	rs778428825(P)	0.98	2.4 × 10 <sup>-9</sup>	UBTF (CCG)	protein-cod.	intron		no	no							
31	10	18440444	rs1888693(L)	1	2.7 × 10 <sup>-10</sup>	CACNB2 (CCG)	protein-cod.	intron	1	no	no	0	20	nd low med <sup>AB</sup>				
32	4	95821419	rs3775010(L)	1	6.8 × 10 <sup>-10</sup>	BMPR2 (CCG)	protein-cod.	intron	1	no	no	0	1	n/a <sup>§</sup>				
33	8	122259074	rs4871180(L)	1	1.1 × 10 <sup>-9</sup>	HAS2 (CCG)	protein-cod.	intergenic (366kb downstream from gene)	5	no	no	HAS2 Mesenchymal_Stem_Cell P=4.78e-46 ;	0	2	n/a <sup>§</sup>			
33	8	122259074	rs4871180(L)	1	1.1 × 10 <sup>-9</sup>	SNTB1	protein-cod.	intergenic (435kb upstream from gene)	3	no	no	0	5	nd nd n/a <sup>§</sup>				
34	9	78739440	rs147496465(L)	1	1.2 × 10 <sup>-9</sup>	PCSK5 (CCG)	protein-cod.	intron	1	no	no	0	4	nd med nd <sup>§</sup>				
35	17	76856966	rs1973232(L)	1	2.9 × 10 <sup>-9</sup>	TIMP2 (CCG)	protein-cod.	intron	1	no	no	7	315	med low low <sup>§</sup>				
36	11	70005374	rs875107(L)	1	3.7 × 10 <sup>-9</sup>	ANO1 (CCG)	protein-cod.	intron	1	no	no	3	16	nd med nd <sup>§</sup>				
37	22	40695172	rs6001870(L)	1	4.3 × 10 <sup>-9</sup>	TNRC6B (CCG)	protein-cod.	intron	1	no	no	n/a	7	low med nd <sup>§</sup>				
38	20	37493576	rs208814(L)	1	9.0 × 10 <sup>-9</sup>	PPP1R16B (CCG)	protein-cod.	intron	1	no	no	0	3	n/a <sup>§</sup>				
39	2	18937283	rs62125298(L)	1	1.0 × 10 <sup>-8</sup>	NT5C2 (CCG)	protein-cod.	intergenic (166kb upstream from gene)	5	no	no	NT5C2 IMR90 P=3.63e-16	n/a	0.12	low high nd <sup>AB</sup>			
39	2	18937283	rs62125298(L)	1	1.0 × 10 <sup>-8</sup>	RDH14	protein-cod.	(195kb upstream from gene)		no	no	RDH14 IMR90 P=1.49e-16	3	31	med high high <sup>§</sup>			
40	4	15386383	rs4132788(L)	1	1.1 × 10 <sup>-8</sup>	CIQTNF7 (CCG)	protein-cod.	intron	3	CIQTNF7 Colon – Sigmoid P=0.0007	CIQTNF7 Testis P=1.1e-7	CIQTNF7 Mesenchymal_Stem_Cell P=8.31e-141	3	10	med high nd <sup>AB</sup>			
40	4	15386383	rs4132788(L)	1	1.1 × 10 <sup>-8</sup>	LOC101929095	antisense	intron		no	no	n/a	n/a					

41	5	122329729	rs34126945(L)	1	$1.2 \times 10^{-8}$	<i>SNX24</i> (CCG)	protein-cod.	intron	1	no	no	n/a	6	nd med nd <sup>§</sup>
42	6	32609965	rs7990(L)	1	$1.4 \times 10^{-8}$	<i>HLA-DQA1</i> (CCG)	protein-cod.	exon	1	no	<i>HLA-DQA1</i> Skin P=1.2e-9	0	7	colonic epithelial cell (med) <sup>DB</sup>
43	10	124168942	rs139760870(L)	1	$1.4 \times 10^{-8}$	<i>PLEKHA1</i> (CCG)	protein-cod.	intron	1	no	no	0	27	med high low <sup>§</sup>
44	10	105670849	rs3752946(L)	1	$1.8 \times 10^{-8}$	<i>STN1</i> (CCG)	protein-cod.	intron	1	<i>STN1</i> Colon – Sigmoid P=0.01	<i>STN1</i> Muscle – Skeletal P= 1.0e-5	n/a	19	n/a <sup>§</sup>
45	1	221066373	rs2784255(L)	1	$2.0 \times 10^{-8}$	<i>HLX</i> (CCG)	protein-cod.	intergenic 8kb upstream of gene		no	no	7	41	nd nd low <sup>§</sup>
45	1	221081261	rs2784272 (P)	0.98	$2.8 \times 10^{-8}$	<i>HLX</i> (CCG)	protein-cod.	intergenic 23kb upstream	5	no	no	<i>HLX</i> Mesenchymal_Stem_Cell P=1.56e-67; IMR90 P=3.19e-42		
46	3	5843836	rs7624168(L)	1	$2.3 \times 10^{-8}$	<i>EDEMI</i>	protein-cod.	intergenic (582kb downstream from gene)	6	no	no	14	14	low med nd <sup>§</sup>
47	2	33361425	rs6714546(L)	1	$2.4 \times 10^{-8}$	<i>LTBP1</i> (CCG)	protein-cod.	intron	1	<i>LTBP1</i> Colon – Sigmoid P= 0.03	<i>LTBP1</i> Thyroid P=7.9e-10	0	33	nd low nd <sup>§</sup>
48	13	33727605	rs1473813(L)	1	$2.9 \times 10^{-8}$	<i>STARD13</i> (CCG)	protein-cod.	intron	1	no	no	0	35	low high low <sup>§</sup>
49	15	68238462	rs387505(L)	1	$2.9 \times 10^{-8}$	<i>PIAS1</i> (CCG)	protein-cod.	intergenic (108kb upstream from gene)	5	<i>PIAS1</i> Colon – Sigmoid P=2.1e-3	<i>PIAS1</i> Esophagus – Muscularis P=2.7e-11	<i>PIAS1</i> Mesenchymal_Stem_Cell P= 7.74e-98		high high med <sup>§</sup>
49	15	68238462	rs387505(L)	1	$2.9 \times 10^{-8}$	<i>SKOR1</i>	protein-cod.	intergenic 112kb downstream from gene		no	no	n/a	1	nd n/a n/a <sup>§</sup>
50	1	245773041	rs12041565(L)	1	$3.0 \times 10^{-8}$	<i>KIF26B</i> (CCG)	protein-cod.	intron	1	no	no	3	1	med med nd <sup>§</sup>
51	8	116588546	rs2049865(L)	1	$4.9 \times 10^{-8}$	<i>TRPS1</i> (CCG)	protein-cod.	intron	1	no	no	0	9	n/a <sup>§</sup>

§knowledge-based protein expression level<sup>§</sup> (nd –not detected, low, medium, high) or level of single antibody<sup>AB</sup> staining (nd –not detected, low, medium, high) observed in the annotated cell types from Human Protein Atlas database ([www.proteinatlas.org](http://www.proteinatlas.org), [Ref. 4](#)), if gene is not listed in Human Protein Atlas median protein expression level from Proteomics<sup>DB</sup> ([www.proteomicsdb.org](http://www.proteomicsdb.org), [Ref. 5](#)) is given. Fragments Per Kilobase of exon per Million fragments mapped (FPKM); log 10 normalized protein levels (‘intensity-based absolute quantification (iBAQ (Ref. 8) (data obtained from <https://www.genecards.org>, [Ref. 6](#)) n/a: no data available

### Cited Literature for Supplementary Table 3

Ref. 1: GTEx Consortium. The Genotype-Tissue Expression (GTEx) project. Nat Genet. 2013; 45(6):580-5.

Ref. 2: [https://biospecimens.cancer.gov/resources/sops/docs/GTEX\\_SOPs/](https://biospecimens.cancer.gov/resources/sops/docs/GTEX_SOPs/)

Ref. 3: Zhang L et al. Gene expression profiles in normal and cancer cells. *Science*. 1997; 276(5316):1268-72.

Ref. 4: Uhlén M et al. Tissue-based map of the human proteome. *Science*. 2015;347(6220):1260419.

Ref. 5: Schmidt T et al. ProteomicsDB. *Nucleic Acids Research*, Volume 46, Issue D1, 4 January 2018, Pages D1271–D1281

Ref. 6: Stelzer G. et al. The GeneCards Suite: From Gene Data Mining to Disease Genome Sequence Analysis, *Current Protocols in Bioinformatics* (2016), 54:1.30.1 - 1.30.33

Ref. 7: Veyrieras JB et al. High-resolution mapping of expression-QTLs yields insight into human gene regulation. *PLoS Genet*. 2008; 4(10):e1000214.

Ref. 8: Schwanhäusser B et al. Global quantification of mammalian gene expression control. *Nature*. 2011;473(7347):337-42

Ref. 9: Casper J et al. The UCSC Genome Browser database: 2018 update. *Nucleic Acids Res*. 2018;46(D1):D762-D769

***Supplementary Table 4: Results of GWAS analysis in diverticular disease present study in comparison to Maguire et al. (2018[1]).***

Results of GWAS and differentiation analyses in diverticular disease. Results are ordered by the *P*-value in the replication analysis for diverticular disease in European cohorts (column Q, present study). The gene annotation corresponds to the curated candidate gene, which selection is described in the Results and Supplementary Table 5.

***Reference for Supplementary Table 4:***

- 1 Maguire LH, Handelman SK, Du X, *et al.* Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. *Nat Genet* Published Online First: 2018. doi:10.1038/s41588-018-0203-z

Supplementary Table 4. Results of GWAS analysis in diverticular disease present study in comparison to Maguire et al. (2018[1]).

current study Chr	current study Position	current study rsID	current study curated candidate gene	current study OR direction	current study GWAS p- value	current study P value replication	current study Benjamini- Hochberg Adjusted P value	current study Significant using an FDR of 0.1	risk differentiation current study p-value diverticulitis vs. diverticulosis	risk differentiation current study OR [CI 95%] diverticulitis vs. diverticulosis	Maguire et al. GWAS p- value	MGI replication p-value diverticulosis	MGI replication p-value diverticulitis	MGI replication Significant using an FDR of 0.1
2	144314247	rs6734367	<u>ARHGAP15</u>	consistent	$4.4 \times 10^{-55}$	$1.5 \times 10^{-7}$	7.65E-06	YES	0.160387	1.11 [0.96-1.29]	4.29E-44	0.0033	0.0669	YES
8	120456193	rs60869342	NOV	consistent	$4.4 \times 10^{-13}$	$3.0 \times 10^{-4}$	8.93E-06	YES	0.991565	1.00 [0.86-1.16]	1.91E-10	0.7440	0.6200	
7	102474903	rs72221075	FBXL13	consistent	$7.7 \times 10^{-15}$	$3.9 \times 10^{-4}$	4.97E-03	YES	0.744793	1.02 [0.91-1.15]	3.74E-14	0.1920	0.4680	
13	108215404	rs9555371	<u>FAM155A_2*</u>	consistent	$1.2 \times 10^{-13}$	$3.5 \times 10^{-7}$	5.10E-03	YES	<b>0.014783</b>	<b>1.21 [1.04-1.42]</b>	1.70E-09	0.0056	0.0242	YES
11	70005374	rs875107	ANO1	consistent	$3.7 \times 10^{-9}$	<b>0.001</b>	1.02E-02	YES	0.139587	1.09 [0.97-1.23]	2.33E-09	0.0005	0.1010	YES
1	151970629	rs61814883	S100A10	consistent	$3.2 \times 10^{-11}$	<b>0.003</b>	1.70E-02	YES	<b>0.016011</b>	<b>1.17 [1.03-1.33]</b>	2.05E-10	0.4700	0.5980	
18	20028737	rs9960286	CTAGE1	consistent	$2.3 \times 10^{-10}$	<b>0.002</b>	1.70E-02	YES	0.834603	1.01 [0.89-1.15]	6.64E-08	0.0129	0.1990	
10	25819228	rs7077800	GPR158	consistent	$1.7 \times 10^{-22}$	<b>0.003</b>	1.91E-02	YES	0.583504	1.03 [0.92-1.16]	5.37E-16	0.1980	0.7650	
7	73427600	rs112609918	ELN	consistent	$2.9 \times 10^{-12}$	<b>0.004</b>	2.04E-02	YES	0.225221	1.23 [0.88-1.72]	2.63E-09	0.0032	0.8440	YES
10	18440444	rs1888693	CACNB2	consistent	$2.7 \times 10^{-10}$	<b>0.003</b>	2.19E-02	YES	0.115518	1.10 [0.98-1.25]	3.58E-09	0.0679	0.4290	
15	68238462	rs387505	PIAS1	consistent	$2.9 \times 10^{-8}$	<b>0.009</b>	3.53E-02	YES	0.053776	1.12 [1.00-1.26]	2.55E-07	0.5530	0.6820	
21	47399453	rs111316530	COL6A1	consistent	$4.8 \times 10^{-13}$	<b>0.009</b>	3.83E-02	YES	0.185996	0.89 [0.76-1.06]	4.90E-11	0.3620	0.9210	
9	136149229	rs505922	ABO	consistent	$4.5 \times 10^{-15}$	<b>0.011</b>	4.01E-02	YES	0.956971	1.00 [0.88-1.13]	1.55E-11	0.1490	0.0010	YES
3	15502681	rs7609897	<u>COLQ</u>	consistent	$5.6 \times 10^{-22}$	<b>0.009</b>	4.17E-02	YES	0.197669	0.91 [0.79-1.05]	2.72E-18	0.0858	0.0085	
15	40649609	rs71472433	PHGR1/DISP2	consistent	$6.1 \times 10^{-11}$	<b>0.014</b>	4.76E-02	YES	<b>0.001127</b>	<b>1.32 [1.12-1.56]</b>	8.90E-11	0.6400	0.8250	
1	221066373	rs2784255	HLX	consistent	$2.0 \times 10^{-8}$	<b>0.023</b>	5.33E-02	YES	0.518459	1.04 [0.93-1.17]	1.06E-08	0.9420	0.5870	
6	98364895	rs9482094	LOC101927314	consistent	$1.6 \times 10^{-11}$	<b>0.022</b>	5.34E-02	YES	0.575298	1.04 [0.92-1.17]	1.62E-10	0.8820	0.2610	
4	95821419	rs3775010	BMPR1B	consistent	$6.8 \times 10^{-10}$	<b>0.021</b>	5.36E-02	YES	0.433669	0.95 [0.84-1.08]	5.74E-09	0.0276	0.0006	YES
11	15065235	rs575909118	CALCB	consistent	$2.8 \times 10^{-11}$	<b>0.020</b>	5.37E-02	YES	0.013948	1.17 [1.03-1.33]	6.20E-10	0.3630	0.4640	
4	15386383	rs4132788	C1QTNF7	consistent	$1.1 \times 10^{-8}$	<b>0.019</b>	5.38E-02	YES	0.166202	0.91 [0.80-1.04]	2.26E-07	0.0792	0.9660	
3	151074941	rs3732760	P2RY12	consistent	$1.7 \times 10^{-11}$	<b>0.026</b>	5.53E-02	YES	0.803750	1.02 [0.90-1.15]	8.80E-11	0.1420	0.8330	
22	40695172	rs6001870	TNRC6B	consistent	$4.3 \times 10^{-9}$	<b>0.025</b>	5.54E-02	YES	0.996879	1.00 [0.89-1.13]	1.30E-06	0.4190	0.6240	
16	86233413	rs2280028	LINC01082	consistent	$4.1 \times 10^{-12}$	<b>0.019</b>	5.70E-02	YES	0.574601	1.05 [0.88-1.25]	7.05E-11	0.7390	0.0990	
13	107897823	rs9520339	FAM155A_1	consistent	$1.1 \times 10^{-14}$	<b>0.018</b>	5.74E-02	YES	0.058384	1.14 [1.00-1.31]	5.23E-12	0.0908	0.3550	
19	38738130	rs4802297	PPP1R14A	consistent	$2.0 \times 10^{-16}$	<b>0.029</b>	5.92E-02	YES	0.714050	0.98 [0.87-1.10]	1.24E-14	0.1030	0.0809	
3	5843836	rs7624168	EDEM1	consistent	$2.3 \times 10^{-8}$	<b>0.036</b>	7.06E-02	YES	0.542684	1.05 [0.91-1.21]	4.51E-08	0.9930	0.2040	
15	76826003	rs2056544	SCAPER	consistent	$9.8 \times 10^{-11}$	<b>0.039</b>	7.37E-02	YES	0.739139	1.02 [0.91-1.15]	1.01E-07	0.9960	0.0780	
7	96078564	rs3113037	SEM1	consistent	$1.0 \times 10^{-11}$	0.070	1.28E-01	No	0.225644	1.09 [0.95-1.25]	2.52E-10	0.0055	0.0041	YES
5	122329729	rs34126945	SNX24	consistent	$1.2 \times 10^{-8}$	0.079	1.30E-01	No	0.514753	0.96 [0.85-1.09]	5.56E-08	0.0163	0.0349	
17	42312778	rs8074740	UBTF	consistent	$2.4 \times 10^{-10}$	0.077	1.31E-01	No	0.311022	1.07 [0.94-1.21]	2.34E-10	0.9160	0.1100	
1	219294570	rs61823192	LYPLAL1-AS1	consistent	$4.6 \times 10^{-14}$	0.082	1.31E-01	No	0.872225	1.04 [0.68-1.58]	1.15E-13	0.2010	0.0260	
10	101391169	rs7098322	SLC25A28	consistent	$6.0 \times 10^{-14}$	0.076	1.34E-01	No	0.171771	1.13 [0.95-1.36]	9.94E-12	0.6770	0.3220	
16	84857378	rs2131755	CRISPLD2	consistent	$1.5 \times 10^{-11}$	0.095	1.47E-01	No	0.567328	0.97 [0.86-1.09]	1.50E-10	0.0442	0.5450	
1	234352899	rs4333882	SLC35F3	consistent	$2.5 \times 10^{-24}$	0.106	1.59E-01	No	0.925027	0.99 [0.86-1.14]	4.44E-22	0.0010	0.1540	YES
2	56093204	rs1802575	EFEMP1	consistent	$3.7 \times 10^{-19}$	0.111	1.62E-01	No	0.442844	0.93 [0.77-1.12]	7.71E-16	0.0136	0.0004	
5	37772780	rs10472291	GDNF	consistent	$3.8 \times 10^{-11}$	0.143	2.03E-01	No	0.927492	1.01 [0.89-1.14]	1.01E-11	0.2270	0.9180	
10	124168942	rs139760870	PLEKHA1	consistent	$1.4 \times 10^{-8}$	0.318	4.27E-01	No	0.722197	1.05 [0.79-1.40]	1.57E-07	0.4070	0.5370	

11	27748493	rs17309930	BDNF	consistent	$6.8 \times 10^{-17}$	0.335	4.38E-01	No	0.851469	1.01 [0.88-1.16]	2.16E-14	0.0235	0.0598
8	122259074	rs4871180	HAS2	consistent	$1.1 \times 10^{-9}$	0.364	4.64E-01	No	0.742496	1.02 [0.90-1.16]	4.15E-09	0.7000	0.8070
13	33727605	rs1473813	STARD13	consistent	$2.9 \times 10^{-8}$	0.507	6.16E-01	No	0.603133	1.03 [0.92-1.16]	6.89E-07	0.4530	0.5200
2	33361425	rs6714546	LTBP1	consistent	$2.4 \times 10^{-8}$	0.552	6.40E-01	No	0.209217	0.92 [0.80-1.05]	1.60E-06	0.2590	0.5890
8	116588546	rs2049865	TRPS1	consistent	$4.9 \times 10^{-8}$	0.550	6.52E-01	No	0.778372	1.02 [0.90-1.14]	5.54E-09	0.6000	0.5220
5	64295363	rs10471645	CWC27	consistent	$2.1 \times 10^{-11}$	0.579	6.56E-01	No	0.123085	1.13 [0.97-1.33]	3.03E-09	0.0409	0.0098
20	37493576	rs208814	PPP1R16B	consistent	$9.0 \times 10^{-9}$	0.637	7.06E-01	No	0.832557	1.01 [0.90-1.15]	9.75E-07	0.0906	0.5900
2	18937283	rs62125298	NT5C1B	consistent	$1.0 \times 10^{-8}$	0.714	7.59E-01	No	0.739499	1.03 [0.88-1.19]	3.77E-08	0.6840	0.2470
6	32609965	rs7990	HLA-DQA1	consistent	$1.4 \times 10^{-8}$	0.739	7.69E-01	No	0.455626	1.06 [0.91-1.23]	N/A	N/A	N/A
17	76856966	rs1973232	TIMP2	consistent	$2.9 \times 10^{-9}$	0.764	7.79E-01	No	0.964098	1.00 [0.87-1.16]	1.24E-07	0.8900	0.3440
9	78739440	rs147496465	PCSK5	consistent	$1.2 \times 10^{-9}$	0.818	8.18E-01	No	0.533972	1.04 [0.92-1.17]	1.54E-08	0.8340	0.3650
1	245773041	rs12041565	KIF26B	<b>opposite</b>	$3.0 \times 10^{-8}$	0.495	6.16E-01	No	N/A	N/A	1.46E-07	0.0350	0.1490
10	105670849	rs3752946	STN1	<b>opposite</b>	$1.8 \times 10^{-8}$	0.668	7.25E-01	No	N/A	N/A	2.60E-06	0.3110	0.8420
17	7372637	rs12942267	ZBTB4	<b>opposite</b>	$6.7 \times 10^{-11}$	0.175	2.41E-01	No	N/A	N/A	2.55E-08	0.0357	0.6970



## SUPPLEMENTARY TABLES

### Supplementary Table 5: GWAS lead variants and replication results

Results of GWAS analysis in diverticular disease. Results are ordered by the nominal P-value in the discovery analysis. The gene annotation corresponds to the candidate gene, which selection is described in the Methods and Supplementary Table 3. Rs-IDs of replication SNP which are proxies for the discovery variant are marked with an asterisk (\*) and pairwise LD ( $r^2$ ) to the discovery variant is provided. SNPs genotyped by TaqMan rather than iPLEX are indicated by a pound (#) sign. Variants at the *FAM155A-1* and *FAM155A-2* were in low LD ( $r^2=0.0043$ ) and thus considered as individual loci. In 48 out of 51 loci, the odds ratio direction was consistent between the discovery and replication cohorts. The 27 out of 51 loci which replicate at a nominal  $p<0.05$  are indicated by a bold gene name and replication P value. Odds ratios are based on the reference allele. The positions of lead variants were annotated according to Genome Reference Consortium Human Build 37 patch release 13 (GRCh37.p13).

Discovery GWAS in UK Biobank									Replication in European samples							
locus	Chr	Position	rsID	Gene	P value	OR [CI 95%]	Alt/Ref	MAF%	rsID	Ref	Alt	r <sup>2</sup>	P value	OR	OR direction	I2
1	2	144314247	rs6734367	<i>ARHGAP15</i>	4.4 × 10 <sup>-55</sup>	1.17 [1.15-1.19]	G/T	20.1/17.8	rs6734367#	T	G	1	<b>1.5 × 10<sup>-7</sup></b>	1.29 [1.17-1.42]	consistent	0
2	1	234352899	rs4333882	<i>SLC35F3</i>	2.5 × 10 <sup>-24</sup>	1.10 [1.08-1.13]	A/G	20.7/19.2	rs4333882	G	A	1	0.106	1.08 [0.98-1.17]	consistent	28
3	10	25819228	rs7077800	<i>GPR158</i>	1.7 × 10 <sup>-22</sup>	0.93 [0.91-0.94]	C/T	45.7/47.6	rs7086249*	C	T	1	<b>0.003</b>	0.90 [0.83-0.96]	consistent	0
4	3	15502681	rs7609897	<i>COLQ</i>	5.6 × 10 <sup>-22</sup>	0.91 [0.89-0.93]	G/T	19.9/21.4	rs7609897#	T	G	1	<b>0.009</b>	0.89 [0.81-0.97]	consistent	24
5	2	56093204	rs1802575	<i>EFEMP1</i>	3.7 × 10 <sup>-19</sup>	1.11 [1.08-1.13]	G/C	14.5/13.3	rs1802575	C	G	1	0.111	1.10 [0.98-1.25]	consistent	47
6	11	27748493	rs17309930	<i>BDNF</i>	6.8 × 10 <sup>-17</sup>	0.92 [0.91-0.94]	C/A	19.5/20.8	rs962369*#	C	T	0.50	0.335	0.96 [0.88-1.04]	consistent	0
7	19	38738130	rs4802297	<i>PPP1R14A</i>	2.0 × 10 <sup>-16</sup>	1.06 [1.05-1.08]	C/G	49.8/48.2	rs12976534*#	G	A	1	<b>0.029</b>	1.08 [1.01-1.17]	consistent	15
8	9	136149229	rs505922	<i>ABO</i>	4.5 × 10 <sup>-15</sup>	0.94 [0.92-0.95]	T/C	30.2/31.8	rs687621*	G	A	0.96	<b>0.011</b>	0.91 [0.84-0.98]	consistent	0
9	7	102474903	rs72221075	<i>FBXL13</i>	7.7 × 10 <sup>-15</sup>	1.07 [1.05-1.08]	TA/-	35.2/33.6	rs10257317*#	C	T	0.93	<b>3.9 × 10<sup>-4</sup></b>	1.14 [1.06-1.23]	consistent	0
10	13	107897823	rs9520339	<i>FAM155A_1</i>	1.1 × 10 <sup>-14</sup>	0.93 [0.92-0.95]	C/T	22.7/24.0	rs9520344*#	A	T	1	<b>0.018</b>	0.90 [0.83-0.98]	consistent	0
11	13	108215404	rs9555371	<i><u>FAM155A_2</u>*</i>	1.2 × 10 <sup>-13</sup>	0.93 [0.91-0.95]	A/G	18.7/19.8	rs9555371#	G	A	1	<b>3.5 × 10<sup>-7</sup></b>	0.79 [0.72-0.87]	consistent	55
12	1	219294570	rs61823192	<i>LYPLAL1-AS1</i>	4.6 × 10 <sup>-14</sup>	0.84 [0.80-0.88]	C/T	2.5/3.0	rs61823192#	T	C	1	0.082	0.80 [0.62-1.03]	consistent	63

13	10	101391169	rs7098322	<i>SLC25A28</i>	$6.0 \times 10^{-14}$	1.09 [1.07-1.12]	T/C	13.4/12.5	rs7091203*	A	G	1	0.076	1.11 [0.99-1.25]	consistent	33
14	8	120456193	rs60869342	<i>NOV</i>	$4.4 \times 10^{-13}$	0.94 [0.92-0.96]	A/T	23.0/24.2	rs1381335*#	T	C	0.61	$3.0 \times 10^{-4}$	0.85 [0.78-0.93]	consistent	21
15	21	47399453	rs111316530	<i>COL6A1</i>	$4.8 \times 10^{-13}$	1.08 [1.06-1.10]	GTGTGTCA/-	15.5/14.5	rs7281388*	A	C	0.96	<b>0.009</b>	1.16 [1.04-1.30]	consistent	0
16	7	73427600	rs112609918	<i>ELN</i>	$2.9 \times 10^{-12}$	1.14 [1.10-1.18]	A/T	5.2/4.6	rs112609918*	T	A	1	<b>0.004</b>	1.39 [1.11-1.74]	consistent	0
17	16	86233413	rs2280028	<i>LINC01082</i>	$4.1 \times 10^{-12}$	0.93 [0.91-0.95]	G/A	13.2/14.2	rs2280028	A	G	1	<b>0.019</b>	0.88 [0.79-0.98]	consistent	0
18	16	84857378	rs2131755	<i>CRISPLD2</i>	$1.5 \times 10^{-11}$	1.06 [1.04-1.07]	A/G	42.1/40.7	rs2131755	G	A	1	0.095	1.07 [0.99-1.15]	consistent	0
19	6	98364895	rs9482094	<i>LOC101927314</i>	$1.6 \times 10^{-11}$	0.95 [0.93-0.96]	G/A	35.9/37.2	rs4839715*#	A	G	1	<b>0.022</b>	0.91 [0.85-0.99]	consistent	0
20	3	151074941	rs3732760	<i>P2RY12</i>	$1.7 \times 10^{-11}$	1.06 [1.04-1.07]	A/C	38.7/37.3	rs3732760	C	A	1	<b>0.026</b>	1.09 [1.01-1.18]	consistent	0
21	5	64295363	rs10471645	<i>CWC27</i>	$2.1 \times 10^{-11}$	1.07 [1.05-1.09]	C/T	17.5/16.5	rs2968205*	A	G	1	0.579	1.03 [0.93-1.14]	consistent	0
22	11	15065235	rs575909118	<i>CALCB</i>	$2.8 \times 10^{-11}$	1.06 [1.04-1.08]	-/T	28.6/27.5	rs12293178*	A	G	0.95	<b>0.020</b>	1.10 [1.02-1.19]	consistent	27
23	1	151970629	rs61814883	<i>S100A10</i>	$3.2 \times 10^{-11}$	0.95 [0.93-0.96]	G/A	28.6/29.9	rs61814883	A	G	1	<b>0.003</b>	0.89 [0.82-0.96]	consistent	0
24	5	37772780	rs10472291	<i>GDNF</i>	$3.8 \times 10^{-11}$	1.06 [1.04-1.07]	C/A	34.6/33.2	rs10472291#	A	C	1	0.143	1.06 [0.98-1.14]	consistent	33
25	15	40649609	rs71472433	<i>PHGR1/DISP2</i>	$6.1 \times 10^{-11}$	1.07 [1.05-1.09]	A/C	17.6/16.6	rs71472433	C	A	1	<b>0.014</b>	1.14 [1.03-1.27]	consistent	0
26	17	7372637	rs12942267	<i>ZBTB4</i>	$6.7 \times 10^{-11}$	0.95 [0.93-0.96]	T/C	34.9/36.1	rs9217*#	C	T	1	0.175	1.05 [0.98-1.14]	<b>opposite</b>	29
27	15	76826003	rs2056544	<i>SCAPER</i>	$9.8 \times 10^{-11}$	0.95 [0.94-0.96]	A/G	41.2/42.3	rs12443137*	G	T	1	<b>0.039</b>	0.93 [0.86-1.00]	consistent	43
28	7	96078564	rs3113037	<i>SEMI</i>	$1.0 \times 10^{-11}$	1.06 [1.04-1.08]	C/T	24.4/23.2	rs3113037	T	C	1	0.070	1.08 [0.99-1.18]	consistent	50
29	18	20028737	rs9960286	<i>CTAGE1</i>	$2.3 \times 10^{-10}$	1.06 [1.04-1.08]	A/G	25.4/24.4	rs2009593*	G	C	0.97	<b>0.002</b>	1.14 [1.05-1.24]	consistent	0
30	17	42312778	rs8074740	<i>UBTF</i>	$2.4 \times 10^{-10}$	1.05 [1.04-1.07]	G/A	33.4/32.1	rs4793086*	C	T	0.98	0.077	1.07 [0.99-1.16]	consistent	38
31	10	18440444	rs1888693	<i>CACNB2</i>	$2.7 \times 10^{-10}$	0.95 [0.94-0.97]	G/A	33.2/34.3	rs1888693	A	G	1	<b>0.003</b>	0.89 [0.82-0.96]	consistent	0
32	4	95821419	rs3775010	<i>BMPRI1B</i>	$6.8 \times 10^{-10}$	1.05 [1.03-1.07]	T/C	37.0/35.8	rs972409*#	T	C	1	<b>0.021</b>	1.10 [1.01-1.19]	consistent	0
33	8	122259074	rs4871180	<i>HAS2</i>	$1.1 \times 10^{-9}$	1.06 [1.04-1.07]	C/T	25.6/24.4	rs4871180	T	C	0.97	0.364	1.04 [0.96-1.13]	consistent	4
34	9	78739440	rs147496465	<i>PCSK5</i>	$1.2 \times 10^{-9}$	0.95 [0.94-0.97]	TCAGGAGG/-	45.6/46.9	rs7035893*	C	T	0.98	0.818	0.99 [0.92-1.07]	consistent	31
35	17	76856966	rs1973232	<i>TIMP2</i>	$2.9 \times 10^{-9}$	1.06 [1.04-1.08]	A/G	19.3/18.5	rs9909232	A	C	0.92	0.764	1.01 [0.92-1.11]	consistent	0
36	11	70005374	rs875107	<i>ANO1</i>	$3.7 \times 10^{-9}$	1.05 [1.03-1.06]	A/C	49.6/48.2	rs2276068*#	C	G	1	<b>0.001</b>	1.14 [1.05-1.23]	consistent	0
37	22	40695172	rs6001870	<i>TNRC6B</i>	$4.3 \times 10^{-9}$	1.05 [1.03-1.07]	A/C	36.1/35.1	rs5995842*#	G	C	0.98	<b>0.025</b>	1.09 [1.01-1.18]	consistent	2
38	20	37493576	rs208814	<i>PPP1R16B</i>	$9.0 \times 10^{-9}$	1.05 [1.03-1.06]	G/A	36.6/35.5	rs208814#	A	G	1	0.637	1.02 [0.94-1.10]	consistent	0
39	2	18937283	rs62125298	<i>NT5C1B</i>	$1.0 \times 10^{-8}$	0.94 [0.92-0.96]	G/T	16.1/17.0	rs4832619*#	G	T	1	0.714	0.98 [0.90-1.08]	consistent	15
40	4	15386383	rs4132788	<i>CIQTNF7</i>	$1.1 \times 10^{-8}$	1.05 [1.03-1.07]	C/T	27.0/26.0	rs4515160*#	G	C	1	<b>0.019</b>	1.10 [1.02-1.20]	consistent	35
41	5	122329729	rs34126945	<i>SNX24</i>	$1.2 \times 10^{-8}$	0.96 [0.94-0.97]	A/G	32.3/33.5	rs34126945	G	A	1	0.079	0.93 [0.86-1.01]	consistent	47

42	6	32609965	rs7990	<i>HLA-DQAI</i>	$1.4 \times 10^{-8}$	1.07 [1.05-1.09]	C/A	10.5/9.9	rs2395163*#	C	T	0.25	0.739	1.02 [0.92-1.12]	consistent	59
43	10	124168942	rs139760870	<i>PLEKHA1</i>	$1.4 \times 10^{-8}$	0.91 [0.88-0.94]	G/A	5.4/5.9	rs117811194*	A	G	1	0.318	0.91 [0.76-1.09]	consistent	0
44	10	105670849	rs3752946	<i>STN1</i>	$1.8 \times 10^{-8}$	1.04 [1.03-1.06]	T/A	49.5/48.6	rs10748858*#	A	G	0.84	0.668	0.98[0.88-1.09]	<b>opposite</b>	1
45	1	221066373	rs2784255	<i>HLX</i>	$2.0 \times 10^{-8}$	0.96 [0.94-0.97]	T/C	47.3/48.5	rs2784255	C	T	1	<b>0.023</b>	0.92 [0.85-0.99]	consistent	0
46	3	5843836	rs7624168	<i>EDEMI</i>	$2.3 \times 10^{-8}$	0.95 [0.93-0.97]	G/A	21.5/22.6	rs4684509*	G	C	1	<b>0.036</b>	0.91 [0.83-0.99]	consistent	8
47	2	33361425	rs6714546	<i>LTBP1</i>	$2.4 \times 10^{-8}$	1.05 [1.03-1.07]	G/A	30.1/29.1	rs6714546#	A	G	1	0.552	1.03 [0.94-1.11]	consistent	0
48	13	33727605	rs1473813	<i>STARD13</i>	$2.9 \times 10^{-8}$	0.96 [0.94-0.97]	G/A	38.0/39.2	rs1473813#	A	G	1	0.507	0.98 [0.90-1.05]	consistent	34
49	15	68238462	rs387505	<i>PIASI</i>	$2.9 \times 10^{-8}$	1.04 [1.03-1.06]	C/T	44.9/43.8	rs387505#	T	C	1	<b>0.009</b>	1.10 [1.02-1.18]	consistent	0
50	1	245773041	rs12041565	<i>KIF26B</i>	$3.0 \times 10^{-8}$	1.06 [1.04-1.08]	C/T	19.0/18.1	rs12041565#	T	C	1	0.495	0.97 [0.88-1.06]	<b>opposite</b>	0
51	8	116588546	rs2049865	<i>TRPS1</i>	$4.9 \times 10^{-8}$	0.96 [0.94-0.97]	A/C	41.0/42.1	rs6469600*#	C	T	1	0.550	0.98 [0.91-1.05]	consistent	20

## SUPPLEMENTARY TABLES

**Supplementary Table 6: Replicating loci ordered by discovery p-value**

Replicating risk loci for diverticular disease sorted by the discovery P-value. The data for the presented 27 loci that replicate in European colonoscopy cohorts.

Discovery GWAS in UK Biobank								Replication in European colonoscopy samples							
Chr	Position	rsID	Gene(s)	P value	OR [CI 95%]	Alt/Ref	MAF%	rsID	Ref	Alt	r <sup>2</sup>	P value	OR	OR-dir	I2
2	144314247	rs6734367	<u>ARHGAP15</u>	4.4 × 10-55	1.17 [1.15-1.19]	G/T	20.1/17.8	rs6734367	T	G	1	1.5 × 10-7	1.29 [1.17-1.42]	consistent	0
10	25819228	rs7077800	GPR158	1.7 × 10-22	0.93 [0.91-0.94]	C/T	45.7/47.6	rs7086249*	C	T	1	0.003	0.90 [0.83-0.96]	consistent	0
3	15502681	rs7609897	<u>COLO</u>	5.6 × 10-22	0.91 [0.89-0.93]	G/T	19.9/21.4	rs7609897	T	G	1	0.009	0.89 [0.81-0.97]	consistent	24
19	38738130	rs4802297	PPP1R14A	2.0 × 10-16	1.06 [1.05-1.08]	C/G	49.8/48.2	rs12976534*	G	A	1	0.029	1.08 [1.01-1.17]	consistent	15
9	136149229	rs505922	ABO	4.5 × 10-15	0.94 [0.92-0.95]	T/C	30.2/31.8	rs687621*	G	A	0.96	0.011	0.91 [0.84-0.98]	consistent	0
7	102474903	rs72221075	FBXL13	7.7 × 10-15	1.07 [1.05-1.08]	TA/-	35.2/33.6	rs10257317*	C	T	0.93	3.9 × 10-4	1.14 [1.06-1.23]	consistent	0
13	107897823	rs9520339	FAM155A_1	1.1 × 10-14	0.93 [0.92-0.95]	C/T	22.7/24.0	rs9520344*	A	T	1	0.018	0.90 [0.83-0.98]	consistent	0
13	108215404	rs9555371	<u>FAM155A_2*</u>	1.2 × 10-13	0.93 [0.91-0.95]	A/G	18.7/19.8	rs9555371	G	A	1	3.5 × 10-7	0.79 [0.72-0.87]	consistent	55
8	120456193	rs60869342	NOV	4.4 × 10-13	0.94 [0.92-0.96]	A/T	23.0/24.2	rs1381335*	T	C	0.61	3.0 × 10-4	0.85 [0.78-0.93]	consistent	21
21	47399453	rs111316530	COL6A1	4.8 × 10-13	1.08 [1.06-1.10]	GTGTGTCA/-	15.5/14.5	rs7281388*	A	C	0.96	0.009	1.16 [1.04-1.30]	consistent	0
7	73427600	rs112609918	ELN	2.9 × 10-12	1.14 [1.10-1.18]	A/T	5.2/4.6	rs112609918*	T	A	1	0.004	1.39 [1.11-1.74]	consistent	0
16	86233413	rs2280028	LINC01082	4.1 × 10-12	0.93 [0.91-0.95]	G/A	13.2/14.2	rs2280028	A	G	1	0.019	0.88 [0.79-0.98]	consistent	0
6	98364895	rs9482094	LOC101927314	1.6 × 10-11	0.95 [0.93-0.96]	G/A	35.9/37.2	rs4839715*	A	G	1	0.022	0.91 [0.85-0.99]	consistent	0
3	151074941	rs3732760	P2RY12	1.7 × 10-11	1.06 [1.04-1.07]	A/C	38.7/37.3	rs3732760	C	A	1	0.026	1.09 [1.01-1.18]	consistent	0
11	15065235	rs575909118	CALCB	2.8 × 10-11	1.06 [1.04-1.08]	-/T	28.6/27.5	rs12293178*	A	G	0.95	0.020	1.10 [1.02-1.19]	consistent	27
1	151970629	rs61814883	S100A10	3.2 × 10-11	0.95 [0.93-0.96]	G/A	28.6/29.9	rs61814883	A	G	1	0.003	0.89 [0.82-0.96]	consistent	0
15	40649609	rs71472433	PHGR1/DISP2	6.1 × 10-11	1.07 [1.05-1.09]	A/C	17.6/16.6	rs71472433	C	A	1	0.014	1.14 [1.03-1.27]	consistent	0
15	76826003	rs2056544	SCAPER	9.8 × 10-11	0.95 [0.94-0.96]	A/G	41.2/42.3	rs12443137*	G	T	1	0.039	0.93 [0.86-1.00]	consistent	43
18	20028737	rs9960286	CTAGE1	2.3 × 10-10	1.06 [1.04-1.08]	A/G	25.4/24.4	rs2009593*	G	C	0.97	0.002	1.14 [1.05-1.24]	consistent	0

10	18440444	rs1888693	<i>CACNB2</i>	$2.7 \times 10^{-10}$	0.95 [0.94-0.97]	G/A	33.2/34.3	rs1888693	A	G	1	0.003	0.89 [0.82-0.96]	consistent	0
4	95821419	rs3775010	<i>BMPRI1B</i>	$6.8 \times 10^{-10}$	1.05 [1.03-1.07]	T/C	37.0/35.8	rs972409*	T	C	1	0.021	1.10 [1.01-1.19]	consistent	0
11	70005374	rs875107	<i>ANO1</i>	$3.7 \times 10^{-9}$	1.05 [1.03-1.06]	A/C	49.6/48.2	rs2276068*	C	G	1	0.001	1.14 [1.05-1.23]	consistent	0
22	40695172	rs6001870	<i>TNRC6B</i>	$4.3 \times 10^{-9}$	1.05 [1.03-1.07]	A/C	36.1/35.1	rs5995842*	G	C	0.98	0.025	1.09 [1.01-1.18]	consistent	2
4	15386383	rs4132788	<i>CIQTNF7</i>	$1.1 \times 10^{-8}$	1.05 [1.03-1.07]	C/T	27.0/26.0	rs4515160*	G	C	1	0.019	1.10 [1.02-1.20]	consistent	35
1	221066373	rs2784255	<i>HLX</i>	$2.0 \times 10^{-8}$	0.96 [0.94-0.97]	T/C	47.3/48.5	rs2784255	C	T	1	0.023	0.92 [0.85-0.99]	consistent	0
3	5843836	rs7624168	<i>EDEM1</i>	$2.3 \times 10^{-8}$	0.95 [0.93-0.97]	G/A	21.5/22.6	rs4684509*	G	C	1	0.036	0.91 [0.83-0.99]	consistent	8
15	68238462	rs387505	<i>PIAS1</i>	$2.9 \times 10^{-8}$	1.04 [1.03-1.06]	C/T	44.9/43.8	rs387505	T	C	1	0.009	1.10 [1.02-1.18]	consistent	0

***Supplementary Table 7: Characteristics of patients used for RT-PCR of curated candidate transcripts in colon tissue***

The analyses for layer-specific and disease-specific expression in colonic anatomic layers were each performed in on the same PCR-plate to avoid batch- and plate effects. Thus, for each type of experiments, a respective set of patients was defined. The characteristics of the patient samples are provided below.

**Supplementary Table 7a:** Patients used for layer specific expression analysis in controls by RT-PCRs (mucosa, submucosa, muscle layer)

<b>Patient group</b>	<b>Number of patients</b>	<b>Mean age [years]</b>	<b>Gender distribution</b>
Control	7	75,1	5 women, 2 men

**Supplementary Table 7b:** Patients used for disease- and layer-specific expression analysis by RT-PCRs (mucosa, submucosa, muscle layer)

<b>Patient group</b>	<b>Number of patients</b>	<b>Mean age [years]</b>	<b>Gender distribution</b>
Control	20	71,3	11 women, 9 men
Diverticulitis	21	60,8	13 women, 8 men
Diverticulosis	13	71,9	5 women, 8 men

**Supplementary Table 8: Primer sequences used for real time (RT) PCR of colon tissue**

RT-PCR was performed for the top 20 replicating risk loci as shown in Supplementary Table 6. Pre-validated TaqMan® Assays (with the Applied Biosystems ID provided in the able) were used for RT-PCR in colonic tissue. For the remaining three transcripts, assays were designed manually.

Risk locus	Gene	Assay	Forward primer (5'-3')	Reverse primer (5'-3')	Probe (5'-3')
ARHGAP15	<i>ARHGAP15</i>		AGGAGCTGTGCAAATGAGAATCA	TGAATGATTCTTCTGTGTCTGGAT	AGCCACCATGACAGGCTCAGCCAAAGTA
GPR158	<i>GPR158</i>		ACATCCGATCACCTCATCTTCAATA	CGATGGGACTGTCCGCAC	TGCCTCATTGACCGCTGGGACTACATG
COLQ	<i>COLQ</i>	Hs01552912_m1			
PPP1R14A	<i>PPP1R14A</i>	Hs00264434_m1			
ABO	<i>ABO</i>	Hs00220850_m1			
FBXL13	<i>FBXL13</i>	Hs00376683_m1			
FAM155A	<i>FAM155A</i>		GGCCTCTCCAGTTTCATCTGTACA	TCCCTTTGGATGGGTTATTGA	TGAACCAGAATGCTGTGACGTCAGGAGAGA
NOV	<i>NOV</i>	Hs00159631_m1			
COL6A1	<i>COL6A1</i>	Hs01095585_m1			
ELN	<i>ELN</i>	Hs00355783_m1			
LINC01082	<i>LINC01082</i>	Hs01388639_m1			
LOC101927314	<i>LOC101927314</i>	Hs01384818_m1			
P2RY12	<i>P2RY12</i>	Hs00224470_m1			
CALCB	<i>CALCB</i>	Hs01119333_gH			
S100A10	<i>S100A10</i>	Hs00237010_m1			
PHGR1:DISP2	<i>PHGR1</i>	Hs04188719_m1			
PHGR1:DISP2	<i>DISP2</i>	Hs00394338_m1			
SCAPER	<i>SCAPER</i>	Hs01065655_m1			
CTAGE1	<i>CTAGE1</i>	Hs00535737_s1			
CACNB2	<i>CACNB2</i>	Hs01100744_m1			
BMPRI1B	<i>BMPRI1B</i>	Hs01010965_m1			
Housekeeping gene	<i>HPRT</i>		TGAACGTCTTGCTCGAGATGTG	CCAGCAGGTCAGCAAAGAATT	TGGGAGGCCATCACATTGTAGCC

**Supplementary Table 9: Results of differential expression analysis in controls**

Sigmoid colon layer specific expression of transcripts encoded by the curated candidate genes at top 20 replicating diverticular disease risk associated loci ranked by discovery p-value. Relative gene expression values are provided normalized to reference gene Hypoxanthine Phosphoribosyltransferase 1 (*HPRT1*). Median values with lower and upper quartile ranges shown in round brackets. The number of patients utilized after quality control is provided in square brackets. Nominal significant ( $p < 0.05$ ) differences in layer specific expression are marked in bold print. A graphical representation of the data is provided in Supplementary Figure 3.

Gene	Mucosa	Submucosa	Muscularis	P value (Kruskal-Wallis)
<i>ARHGAP15</i>	0.326 (0.224 - 0.437) [6]	0.415 (0.361 - 0.443) [7]	0.103 (0.093 - 0.172) [4]	0.0620
<i>GPR158</i>	0.003 (0.002 - 0.003) [4]	0.033 (0.027 - 0.041) [7]	0.012 (0.005 - 0.013) [5]	<b>0.0014</b>
<i>COLO</i>	0.020 (0.008 - 0.074) [6]	0.133 (0.116 - 0.188) [7]	0.044 (0.022 - 0.077) [5]	<b>0.0357</b>
<i>PPP1R14A</i>	3.548 (1.459 - 8.882) [7]	10.56 (7.577 - 11.355) [7]	49.21 (42.91 - 67.08) [6]	<b>0.0053</b>
<i>ABO</i>	3.963 (1.460 - 5.905) [7]	0.417 (0.404 - 0.552) [7]	0.282 (0.217 - 0.446) [6]	<b>0.0025</b>
<i>FBXL13</i>	0.069 (0.055 - 0.164) [5]	0.154 (0.136 - 0.192) [6]	0.114 (0.106 - 0.127) [4]	0.3072
<i>FAM155A</i>	0.013 (0.007 - 0.019) [4]	0.241 (0.180 - 0.302) [7]	0.067 (0.056 - 0.077) [4]	<b>0.0024</b>
<i>NOV</i>	0.610 (0.440 - 2.605) [7]	1.959 (1.523 - 2.435) [7]	1.170 (1.006 - 1.423) [6]	0.2256
<i>COL6A1</i>	1.120 (0.712 - 3.765) [7]	10.171 (6.650 - 12.323) [7]	4.504 (4.104 - 4.545) [5]	<b>0.0286</b>
<i>ELN</i>	0.067 (0.032 - 0.160) [7]	0.705 (0.436 - 0.803) [7]	0.422 (0.187 - 0.573) [6]	<b>0.0097</b>
<i>LINC01082</i>	2.027 (1.766 - 4.925) [7]	2.070 (1.407 - 3.063) [7]	1.921 (1.655 - 1.962) [6]	0.7073
<i>P2RY12</i>	0.365 (0.211 - 0.457) [7]	1.198 (0.975 - 1.291) [7]	1.058 (0.930 - 1.226) [6]	<b>0.0111</b>
<i>CALCB</i>	0.006 (0.004 - 0.009) [3]	0.023 (0.018 - 0.029) [4]	0.292 (0.213 - 0.338) [4]	<b>0.0116</b>
<i>S100A10</i>	45.44 (32.55 - 50.99) [7]	117.49 (94.67 - 129.63) [7]	10.47 (10.20 - 12.92) [5]	<b>0.0008</b>
<i>PHGR1</i>	932.71 (475.52 - 1370.90) [7]	104.95 (66.49 - 158.94) [7]	97.02 (56.99 - 142.13) [6]	<b>0.0026</b>



<i>DISP2</i>	0.024 (0.015 - 0.053) [5]	0.098 (0.091 - 0.223) [7]	0.020 (0.020 - 0.035) [5]	<b>0.0029</b>
<i>SCAPER</i>	1.281 (0.831 - 4.077) [6]	2.435 (2.005 - 2.729) [6]	1.564 (1.469 - 1.884) [5]	0.2296
<i>CACNB2</i>	0.699 (0.501 - 1.579) [7]	1.051 (0.920 - 1.600) [7]	4.443 (3.355 - 5.274) [6]	0.0552
<i>BMPRI1B</i>	0.024 (0.012 - 0.073) [7]	0.223 (0.191 - 0.230) [7]	0.364 (0.245 - 0.440) [6]	<b>0.0093</b>
<i>CTAGE1</i>	low expression	low expression	low expression	N/A
<i>LOC101927314</i>	low expression	low expression	low expression	N/A

**Supplementary Table 10: Results of phenotype-specific expression analysis in anatomical layers of the colon**

Disease and layer specific expression of diverticular disease risk associated genes. Relative gene expression values in the mucosal, submucosal and muscularis layer are shown as median values with lower and upper quartile ranges in round brackets for the inflamed (diverticulitis) and non-inflamed (diverticulosis) disease stage and diverticula-free controls. Number of patients utilized after quality control is provided in square brackets. Relative gene expression values were normalized to housekeeping gene *HPRT1*. All expression values were normalized to the median of control individuals. Nominal significant ( $p < 0.05$ ) differences are marked in bold print. \*Diverticula (presence of diverticula); \*\* unpaired two-samples Wilcoxon test; \*\*\* global Kruskal-Wallis test by ranks

Layer (sigmoid colon)	Gene	Control /no diverticula/ (n)	Diverticula* /D-itis & D-osis/ (n)	Control   Diverticula P **	Diverticulitis /D-itis/ (n)	Diverticulosis /D-osis/ (n)	D-itis   D-osis P **	Control   D-itis   D-osis (global) P ***	Control   D-itis P **	Control   D-osis P **
Mucosa	<i>ARHGAP15</i>	1.00 (0.89 - 1.78) [12]	1.75 (1.15 - 2.36) [25]	0.095	2.02 (1.31 - 3.87) [13]	1.58 (0.99 - 1.89) [12]	0.29	0.141	0.06	0.34
Submucosa	<i>ARHGAP15</i>	1.00 (0.76 - 1.07) [16]	0.97 (0.77 - 1.12) [24]	0.879	0.95 (0.84 - 1.03) [15]	1.07 (0.70 - 1.87) [9]	0.81	0.921	0.95	0.67
Muscularis	<i>ARHGAP15</i>	1.00 (0.84 - 1.34) [9]	1.96 (1.23 - 2.66) [25]	<b>0.019</b>	1.81 (1.15 - 2.52) [16]	2.19 (1.39 - 3.05) [9]	0.35	<b>0.039</b>	0.07	<b>0.02</b>
Mucosa	<i>GPR158</i>	1.00 (0.70 - 1.43) [8]	0.87 (0.69 - 1.05) [16]	0.520	0.81 (0.64 - 0.96) [7]	0.90 (0.77 - 1.13) [9]	0.60	0.686	0.45	0.74
Submucosa	<i>GPR158</i>	1.00 (0.88 - 1.43) [16]	1.43 (0.98 - 1.96) [23]	0.236	1.59 (1.03 - 2.20) [15]	1.07 (0.88 - 1.58) [8]	0.32	0.289	0.14	0.83
Muscularis	<i>GPR158</i>	1.00 (0.75 - 1.14) [3]	0.61 (0.40 - 1.21) [18]	0.451	0.76 (0.39 - 1.17) [11]	0.46 (0.44 - 1.10) [7]	0.86	0.714	0.53	0.49
Mucosa	<i>COLQ</i>	1.00 (0.62 - 2.15) [8]	2.46 (0.78 - 8.60) [23]	0.232	3.09 (1.11 - 19.43) [14]	0.61 (0.58 - 6.63) [9]	0.10	0.077	<b>0.04</b>	0.81
Submucosa	<i>COLQ</i>	1.00 (0.62 - 1.51) [16]	0.88 (0.54 - 1.63) [23]	0.721	0.88 (0.65 - 1.54) [15]	0.82 (0.43 - 2.56) [8]	0.97	0.925	0.68	0.93
Muscularis	<i>COLQ</i>	1.00 (0.56 - 2.88) [12]	0.91 (0.57 - 1.63) [24]	0.725	1.37 (0.70 - 2.14) [15]	0.68 (0.57 - 0.89) [9]	0.14	0.404	1.00	0.46
Mucosa	<i>PPP1R14A</i>	1.00 (0.70 - 1.59) [16]	1.20 (0.73 - 4.55) [28]	0.289	1.77 (0.76 - 6.69) [15]	1.16 (0.72 - 2.16) [13]	0.38	0.419	0.24	0.55

Submucosa	<i>PPP1R14A</i>	1.00 (0.73 - 1.73) [16]	1.08 (0.68 - 1.98) [23]	0.830	1.30 (0.73 - 1.96) [14]	0.77 (0.66 - 1.91) [9]	0.59	0.847	0.69	0.93
Muscularis	<i>PPP1R14A</i>	1.00 (0.65 - 1.42) [11]	0.56 (0.37 - 0.70) [28]	<b>0.041</b>	0.58 (0.37 - 0.74) [16]	0.49 (0.38 - 0.66) [12]	0.56	0.096	0.13	<b>0.03</b>
Mucosa	<i>ABO</i>	1.00 (0.31 - 2.49) [16]	0.53 (0.29 - 0.93) [28]	0.360	0.37 (0.26 - 0.96) [15]	0.56 (0.45 - 0.66) [13]	0.33	0.345	0.15	0.98
Submucosa	<i>ABO</i>	1.00 (0.62 - 1.93) [16]	0.90 (0.42 - 2.74) [23]	0.989	0.86 (0.36 - 1.45) [15]	2.71 (0.55 - 6.74) [8]	0.23	0.419	0.54	0.37
Muscularis	<i>ABO</i>	1.00 (0.51 - 1.69) [10]	0.53 (0.20 - 0.74) [23]	0.057	0.47 (0.16 - 0.71) [13]	0.71 (0.25 - 0.88) [10]	0.56	0.127	<b>0.04</b>	0.24
Mucosa	<i>FBXL13</i>	1.00 (0.94 - 1.87) [8]	0.89 (0.62 - 1.56) [23]	0.289	0.95 (0.85 - 1.16) [10]	0.83 (0.49 - 3.46) [13]	0.60	0.471	0.56	0.23
Submucosa	<i>FBXL13</i>	1.00 (0.88 - 1.43) [16]	1.43 (0.98 - 1.96) [23]	0.236	1.59 (1.03 - 2.20) [15]	1.07 (0.88 - 1.58) [8]	0.32	0.289	0.14	0.83
Muscularis	<i>FBXL13</i>	1.00 (0.76 - 1.51) [9]	0.98 (0.61 - 1.94) [26]	0.748	1.40 (0.55 - 2.33) [16]	0.89 (0.65 - 1.13) [10]	0.41	0.637	0.98	0.44
Mucosa	<i>FAM155A</i>	1.00 (0.84 - 1.72) [7]	1.07 (0.79 - 1.53) [21]	0.791	1.33 (0.90 - 1.54) [11]	0.96 (0.65 - 1.29) [10]	0.38	0.686	1.00	0.66
Submucosa	<i>FAM155A</i>	1.00 (0.68 - 1.20) [16]	0.97 (0.50 - 1.40) [23]	0.743	1.22 (0.94 - 1.53) [15]	0.50 (0.39 - 0.69) [8]	<b>0.02</b>	0.015	0.26	<b>0.01</b>
Muscularis	<i>FAM155A</i>	1.00 (0.72 - 2.26) [7]	1.54 (1.10 - 1.85) [23]	0.590	1.20 (0.96 - 1.58) [14]	1.81 (1.64 - 2.27) [9]	0.07	0.275	0.74	0.53
Mucosa	<i>NOV</i>	1.00 (0.56 - 1.66) [15]	0.76 (0.52 - 2.20) [26]	0.989	0.77 (0.54 - 3.45) [13]	0.72 (0.47 - 1.41) [13]	0.36	0.627	0.65	0.61
Submucosa	<i>NOV</i>	1.00 (0.55 - 1.29) [16]	0.76 (0.51 - 0.88) [23]	0.134	0.78 (0.55 - 0.91) [15]	0.63 (0.32 - 0.87) [8]	0.50	0.219	0.37	0.07
Muscularis	<i>NOV</i>	1.00 (0.78 - 1.63) [11]	0.77 (0.47 - 1.37) [26]	0.189	0.96 (0.50 - 1.50) [16]	0.69 (0.49 - 1.15) [10]	0.62	0.333	0.42	0.11
Mucosa	<i>COL6A1</i>	1.00 (0.66 - 1.85) [12]	0.60 (0.34 - 2.85) [27]	0.704	0.83 (0.57 - 7.57) [14]	0.46 (0.26 - 0.91) [13]	0.07	0.157	0.59	0.20
Submucosa	<i>COL6A1</i>	1.00 (0.23 - 1.70) [16]	1.16 (0.78 - 1.59) [24]	0.400	1.39 (1.01 - 1.61) [15]	0.83 (0.46 - 1.57) [9]	0.40	0.519	0.31	0.80
Muscularis	<i>COL6A1</i>	1.00 (0.67 - 1.85) [12]	0.82 (0.50 - 1.36) [25]	0.446	0.95 (0.63 - 1.40) [15]	0.72 (0.44 - 1.00) [10]	0.33	0.467	0.75	0.28
Mucosa	<i>ELN</i>	1.00 (0.74 - 1.54) [11]	0.75 (0.64 - 1.31) [20]	0.421	0.77 (0.64 - 3.00) [11]	0.73 (0.65 - 0.78) [9]	0.76	0.560	0.95	0.17
Submucosa	<i>ELN</i>	1.00 (0.07 - 1.34) [16]	0.85 (0.46 - 1.17) [24]	0.751	1.09 (0.85 - 1.39) [15]	0.47 (0.40 - 0.63) [9]	<b>0.03</b>	0.186	0.42	0.63
Muscularis	<i>ELN</i>	1.00 (0.82 - 2.56) [10]	0.93 (0.81 - 2.23) [25]	0.898	1.11 (0.87 - 2.58) [15]	0.85 (0.73 - 1.44) [10]	0.21	0.452	0.76	0.47

Mucosa	<i>LINC01082</i>	1.00 (0.70 - 2.12) [13]	1.18 (0.82 - 1.95) [26]	0.846	1.25 (0.81 - 2.28) [13]	1.09 (0.85 - 1.44) [13]	0.44	0.686	0.54	0.80
Submucosa	<i>LINC01082</i>	1.00 (0.87 - 1.18) [16]	1.05 (0.73 - 1.40) [23]	0.432	1.27 (0.96 - 1.54) [15]	0.72 (0.62 - 1.11) [8]	<b>0.04</b>	0.080	0.11	0.44
Muscularis	<i>LINC01082</i>	1.00 (0.66 - 1.96) [12]	1.18 (0.63 - 1.43) [28]	0.779	1.34 (0.95 - 1.43) [16]	1.13 (0.62 - 1.45) [12]	0.76	0.910	0.91	0.71
Mucosa	<i>LOC101927314</i>	1.00 (1.00 - 1.00) [1]	1.33 (0.41 - 1.94) [9]	1.000	1.39 (1.10 - 1.58) [4]	0.81 (0.26 - 3.27) [5]	0.90	0.911	0.72	1.00
Submucosa	<i>LOC101927314</i>	1.00 (0.95 - 2.34) [9]	1.05 (0.65 - 1.58) [16]	0.552	1.05 (0.71 - 1.67) [10]	1.17 (0.67 - 1.48) [6]	0.96	0.824	0.54	0.77
Muscularis	<i>LOC101927314</i>	1.00 (0.98 - 1.02) [2]	3.20 (3.06 - 3.33) [2]	0.245	3.47 (3.47 - 3.47) [1]	2.93 (2.93 - 2.93) [1]	1.00	0.259	0.54	0.54
Mucosa	<i>P2RY12</i>	1.00 (0.40 - 1.54) [13]	0.72 (0.59 - 1.48) [23]	0.921	0.65 (0.52 - 1.24) [11]	0.87 (0.62 - 1.61) [12]	0.56	0.867	0.95	0.81
Submucosa	<i>P2RY12</i>	1.00 (0.80 - 1.07) [16]	1.03 (0.56 - 1.47) [23]	0.786	1.16 (0.69 - 1.49) [14]	0.72 (0.56 - 0.91) [9]	0.27	0.264	0.20	0.25
Muscularis	<i>P2RY12</i>	1.00 (0.91 - 1.11) [11]	0.91 (0.60 - 1.14) [26]	0.344	0.73 (0.47 - 1.16) [16]	0.95 (0.84 - 1.12) [10]	0.41	0.474	0.29	0.65
Mucosa	<i>CALCB</i>	low expression	low expression	N/A	low expression	low expression	N/A	N/A	N/A	N/A
Submucosa	<i>CALCB</i>	1.00 (0.42 - 1.27) [14]	1.13 (0.41 - 2.46) [22]	0.465	1.56 (0.62 - 2.87) [14]	0.49 (0.39 - 1.43) [8]	0.29	0.371	0.22	0.81
Muscularis	<i>CALCB</i>	1.00 (0.97 - 1.73) [3]	0.13 (0.12 - 0.27) [12]	<b>0.012</b>	0.12 (0.11 - 0.32) [7]	0.14 (0.13 - 0.17) [5]	1.00	<b>0.034</b>	<b>0.02</b>	<b>0.04</b>
Mucosa	<i>S100A10</i>	1.00 (0.73 - 1.33) [16]	0.84 (0.63 - 1.40) [27]	0.606	0.90 (0.69 - 1.41) [14]	0.84 (0.60 - 1.23) [13]	0.94	0.856	0.79	0.55
Submucosa	<i>S100A10</i>	1.00 (0.73 - 1.20) [16]	1.21 (1.00 - 1.48) [23]	<b>0.047</b>	1.37 (1.13 - 1.55) [14]	1.01 (0.57 - 1.21) [9]	0.07	<b>0.013</b>	<b>0.003</b>	0.98
Muscularis	<i>S100A10</i>	1.00 (0.77 - 1.74) [13]	1.40 (1.11 - 1.95) [26]	0.125	1.52 (1.31 - 1.86) [14]	1.29 (1.05 - 2.01) [12]	0.66	0.272	0.13	0.29
Mucosa	<i>PHGR1</i>	1.00 (0.66 - 2.21) [13]	0.99 (0.65 - 1.43) [29]	0.624	0.87 (0.52 - 1.20) [16]	1.07 (0.85 - 2.62) [13]	0.12	0.231	0.23	0.64
Submucosa	<i>PHGR1</i>	1.00 (0.17 - 3.03) [16]	2.03 (0.57 - 8.57) [23]	0.134	1.78 (0.59 - 7.04) [14]	3.33 (0.59 - 8.63) [9]	0.59	0.276	0.27	0.15
Muscularis	<i>PHGR1</i>	1.00 (0.48 - 2.90) [12]	1.21 (0.40 - 2.05) [25]	0.685	1.28 (0.31 - 1.81) [15]	1.13 (0.83 - 1.92) [10]	0.93	0.850	0.45	0.87
Mucosa	<i>DISP2</i>	1.00 (0.41 - 1.15) [12]	0.66 (0.38 - 1.19) [20]	0.425	0.51 (0.36 - 0.99) [10]	0.74 (0.53 - 1.45) [10]	0.47	0.564	0.34	0.72

Submucosa	<i>DISP2</i>	1.00 (0.82 - 1.71) [16]	1.36 (0.74 - 1.73) [23]	0.875	1.37 (0.63 - 1.73) [15]	1.35 (1.22 - 1.71) [8]	0.63	0.736	0.77	0.41
Muscularis	<i>DISP2</i>	1.00 (0.57 - 1.92) [10]	0.43 (0.28 - 0.74) [16]	<b>0.016</b>	0.53 (0.30 - 0.79) [8]	0.43 (0.28 - 0.70) [8]	0.79	<b>0.049</b>	0.08	<b>0.02</b>
Mucosa	<i>SCAPER</i>	1.00 (0.53 - 2.24) [12]	0.72 (0.47 - 2.10) [26]	0.695	1.19 (0.69 - 2.51) [13]	0.57 (0.33 - 1.19) [13]	0.10	0.232	0.68	0.26
Submucosa	<i>SCAPER</i>	1.00 (0.67 - 1.24) [16]	1.14 (0.57 - 1.60) [23]	0.764	1.11 (0.64 - 1.26) [14]	1.60 (0.45 - 1.73) [9]	0.51	0.878	0.79	0.84
Muscularis	<i>SCAPER</i>	1.00 (0.71 - 1.07) [11]	0.78 (0.57 - 1.28) [28]	0.564	1.02 (0.63 - 1.80) [16]	0.73 (0.49 - 0.80) [12]	0.20	0.258	0.75	0.12
Mucosa	<i>CACNB2</i>	1.00 (0.65 - 1.21) [13]	0.73 (0.53 - 1.12) [24]	0.556	0.68 (0.46 - 1.13) [11]	0.77 (0.56 - 1.09) [13]	0.82	0.802	0.52	0.72
Submucosa	<i>CACNB2</i>	1.00 (0.72 - 1.18) [16]	0.78 (0.60 - 1.44) [23]	0.617	0.77 (0.60 - 1.30) [15]	0.83 (0.59 - 1.89) [8]	0.63	0.770	0.51	0.98
Muscularis	<i>CACNB2</i>	1.00 (0.78 - 1.48) [12]	0.96 (0.54 - 1.76) [24]	0.700	1.21 (0.52 - 1.86) [14]	0.92 (0.58 - 1.25) [10]	0.58	0.738	1.00	0.45
Mucosa	<i>BMPR1B</i>	1.00 (0.78 - 1.02) [7]	0.43 (0.26 - 0.65) [14]	<b>0.010</b>	0.57 (0.26 - 0.71) [8]	0.35 (0.27 - 0.46) [6]	0.75	<b>0.032</b>	<b>0.02</b>	<b>0.04</b>
Submucosa	<i>BMPR1B</i>	1.00 (0.52 - 1.46) [16]	0.66 (0.45 - 1.28) [23]	0.353	0.79 (0.54 - 1.28) [15]	0.60 (0.36 - 1.22) [8]	0.63	0.591	0.46	0.41
Muscularis	<i>BMPR1B</i>	1.00 (0.67 - 1.43) [8]	0.49 (0.41 - 1.08) [23]	0.055	0.46 (0.40 - 0.97) [13]	0.69 (0.46 - 1.18) [10]	0.28	0.088	<b>0.04</b>	0.23

**Supplementary Table 11: Gene set enrichment analysis (GSEA) for GO: Biological Process Ontology using the 48 curated candidate genes for diverticular disease**

The table shows the results of GSEA with gene sets derived from the MSigDB GO Biological Process Ontology (4436 gene sets) according to Subramanian et al., PNAS 2005 (full reference provided below the table). K is the number of genes in the set from The Molecular Signatures Database (MSigDB v6.1). k is the number of genes in the intersection of the query set with a set from MSigDB. \* p-value: hypergeometric distribution (k, K, n, N), Genes in Comparison (n=45 with HUGO gene symbols), Genes in Universe (all known human gene symbols) (N=45956); \*\* q-values significant at FDR (p < 0.05)

Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p-value*	FDR q-value**	Genes in Overlap (diverticular disease risk associated genes )
GO_REGULATION_OF_CELL_DIFFERENTIATION	1492	11	0.0074	1.5E-7	6.64E-4	<i>BMPRI1B; TRPS1; GDNF; EFEMP1; HLX; TIMP2; BDNF; P2RY12; HAS2; NOV; S100A10</i>
GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1672	11	0.0066	4.64E-7	1.03E-3	<i>BMPRI1B; TRPS1; GDNF; EFEMP1; HLX; TIMP2; BDNF; P2RY12; PPP1R16B; COLQ; STARD13</i>
GO_ORGAN_MORPHOGENESIS	841	8	0.0095	1.44E-6	2.13E-3	<i>BMPRI1B; TRPS1; GDNF; EFEMP1; HLX; HAS2; PLEKHA1; ELN;</i>
GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	46	3	0.0652	1.29E-5	5.46E-3	<i>BMPRI1B; EFEMP1; TRPS1</i>
GO_SYNAPSE_ORGANIZATION	145	4	0.0276	1.28E-5	5.46E-3	<i>GDNF; BDNF; COLQ; CACNB2</i>
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	304	5	0.0164	1.21E-5	5.46E-3	<i>HAS2; ELN; TIMP2; COL6A1; CRISPLD2</i>
GO_SKELETAL_SYSTEM_DEVELOPMENT	455	6	0.0132	5.35E-6	5.46E-3	<i>BMPRI1B; TRPS1; HAS2; PLEKHA1; NOV; PCSK5</i>
GO_TUBE_DEVELOPMENT	552	6	0.0109	1.6E-5	5.46E-3	<i>GDNF; HLX; TRPS1; STARD13; CRISPLD2; PCSK5</i>

GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	823	7	0.0085	1.45E-5	5.46E-3	<i>BMPR1B; GDNF; HAS2; HLX; BDNF; TIMP2; S100A10</i>
GO_REGULATION_OF_CELL_DEVELOPMENT	836	7	0.0084	1.6E-5	5.46E-3	<i>GDNF; HAS2; BDNF; TIMP2; S100A10; EFEMP1; P2RY12</i>
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	1142	8	0.0070	1.35E-5	5.46E-3	<i>BMPR1B; GDNF; BDNF; HAS2; TIMP2; HLX; PPP1R16B; S100A10</i>
GO_REGULATION_OF_CELL_PROLIFERATION	1496	9	0.0060	1.23E-5	5.46E-3	<i>HAS2; TIMP2; BMPR1B; NOV; GDNF; EFEMP1; HLX; PPP1R16B; PIAS1</i>
GO_TISSUE_DEVELOPMENT	1518	9	0.0059	1.38E-5	5.46E-3	<i>BMPR1B; GDNF; HAS2; HLX; PPP1R16B; TRPS1; NOV; COL6A1; STARD13</i>
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	162	4	0.0247	1.98E-5	6.28E-3	<i>GDNF; HAS2; BDNF; S100A10</i>
GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	63	3	0.0476	3.34E-5	9.89E-3	<i>TRPS1; EFEMP1; BMPR1B</i>
GO_ENTERIC_NERVOUS_SYSTEM_DEVELOPMENT	11	2	0.1818	5.13E-5	1.4E-2	<i>GDNF; HLX</i>
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	1021	7	0.0069	5.69E-5	1.4E-2	<i>S100A10; GDNF; HAS2; BDNF; STARD13; PPP1R16B; ARHGAP15</i>
GO_PROTEIN_LOCALIZATION	1805	9	0.0050	5.37E-5	1.4E-2	<i>TRPS1; S100A10; PCSK5; COLQ; CACNB2; PLEKHA1; SNX24; GPR158; LTBP1</i>
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	1929	9	0.0047	8.95E-5	2.09E-2	<i>BDNF; PLEKHA1; HLX; BMPR1B; TIMP2; NOV; HLA-DQA1; ANO1; EDEM1</i>
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	472	5	0.0106	9.74E-5	2.16E-2	<i>BDNF; TIMP2; S100A10; GDNF; HAS2</i>

**Reference for Supplementary Table 11:**

Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES, Mesirov JP. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A*. 2005 Oct 25;102(43):15545-50.

***Supplementary Table 12: Gene set enrichment analysis (GSEA) for CP: Canonical pathways Ontology using the 48 curated candidate genes for diverticular disease***

The table shows the results of GSEA with gene sets derived from curated gene sets for CP: Canonical pathways (1329 gene sets) according to Subramanian et al., PNAS 2005 (full reference provided below the table). These gene sets are canonical representations of a biological process compiled by domain experts. Table headings match headings in Supplementary Table 11.

Gene Set Name (Reference)	# Genes in Gene Set (K)	Description	# Genes in Overlap (k)	k/K	FDR q-value**	Genes in Overlap (diverticular disease risk associated genes )
NABA_MATRISOME (Naba et al.)	1028	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	13	0.0126	8.51E-9	<i>COLQ; LTBP; ELN; EFEMP1; NOV; CRISPLD2; COL6A1; GDNF; BDNF; TIMP2; S100A10; PCSK5; C1QTNF7</i>
NABA_CORE_MATRISOME (Naba et al.)	275	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	7	0.0255	4.53E-6	<i>COLQ; LTBP; ELN; EFEMP1; NOV; CRISPLD2; COL6A1</i>
NABA_ECM_GLYCOPROTEINS (Naba et al.)	196	Genes encoding structural ECM glycoproteins	6	0.0306	1.32E-5	<i>COLQ; LTBP; ELN; EFEMP1; NOV; CRISPLD2</i>
NABA_MATRISOME_ASSOCIATED (Naba et al.)	753	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	6	0.0080	2.29E-2	<i>GDNF; BDNF; TIMP2; S100A10; PCSK5; C1QTNF7</i>

**Reference for Supplementary Table 12:**



Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES, Mesirov JP. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A*. 2005 Oct 25;102(43):15545-50.

Naba A, Clauser KR, Hoersch S, Liu H, Carr SA, Hynes RO. The matrisome: in silico definition and in vivo characterization by proteomics of normal and tumor extracellular matrices. *Mol Cell Proteomics*. 2012 Apr;11(4):M111.014647. doi: 10.1074/mcp.M111.014647.

### ***Supplementary Table 13: VEGAS2PathwayAnalysis***

We performed pathway analysis on Diverticular Disease GWAS summary data to assign gene-based test statistics to a pathway using the VEGAS2-Pathway approach (Mirsha et al., 2017). The analysis was performed on 6,212 gene-sets, including 18,399 genes with 511,336 annotations. An empirical p-value for each pathway was computed by comparing the summed set score against that of replicates of the same size obtained through resampling of gene-based test statistics. Supplementary Table 13 shows the top five pathways observed in pathway analysis. Two pathways reached the genome-wide, pathway-based significant p value of  $p < 1.00 \times 10^{-5}$ , which are GO:0045596\_negative\_regulation\_of\_cell\_differentiation and GO:0031012\_extracellular\_matrix, both pathways are highlighted in grey shading. The full analysis is provided in Supplementary Table 14.

#	Pathway ID	Pathway size (number of genes )	Empirical p value
1	<a href="#">GO:0045596_negative_regulation_of_cell_differentiation</a>	176	$4.00 \times 10^{-06}$
2	<a href="#">GO:0031012_extracellular_matrix</a>	248	$8.00 \times 10^{-06}$
3	<a href="#">GO:0051093_negative_regulation_of_developmental_process</a>	209	$1.80 \times 10^{-05}$
4	<a href="#">GO:0007517_muscle_organ_development</a>	191	$2.06 \times 10^{-04}$
5	<a href="#">GO:0045595_regulation_of_cell_differentiation</a>	368	$2.24 \times 10^{-04}$

### ***Literature cited in Supplementary Table 13:***

Mishra A, MacGregor S. A Novel Approach for Pathway Analysis of GWAS Data Highlights Role of BMP Signalling and Muscle Cell Differentiation in Colorectal Cancer Susceptibility. *Twin Res Hum Genet.* 2017;20(1):1-9.

***Supplementary Table 14: VEGAS2 pathway analysis of gene-based test statistics using summary data from the UK Biobank GWAS analysis for diverticular disease.***

Supplementary 14 shows the top 100 results of the VEGAS2 pathway analysis approach (Mishra *et al.*) based on gene-based test statistics of diverticular disease GWAS summary data. All together, the analysis was performed on 6,212 gene-sets, including 18,399 genes with 511,336 annotations. An empirical p value for each pathway was computed by comparing the summed set score against that of replicates of the same size obtained through resampling of gene-based test statistics.

***Reference for Supplementary Table 14:***

Mishra A, MacGregor S. A Novel Approach for Pathway Analysis of GWAS Data Highlights Role of BMP Signaling and Muscle Cell Differentiation in Colorectal Cancer Susceptibility. *Twin Res Hum Genet.* 2017;20(1):1-9.



[illegible]

[illegible]



	PC_Proteoglycan_syndecan-mediated_signaling_events	2.788279801350416-4	0.0035	579
72	PC_Serotonin_receptors	7.90966697953674e-20	0.0035	117
74	GO:0030203_glycosaminoglycan_metabolic_process	2.46812379001373e-12	0.0035	43
75	GO:0010717_regulation_of_epithelial_to_mesenchymal_transition	6.20765172992516e-08	0.0035	11
76	GO:0005518_collagen_binding	7.65742720684874e-11	0.0036	31
77	GO:0048738_cardiac_muscle_development	1.92747055717248e-12	0.0039	46
78	GO:0005501_ventricular_cardiac_muscle_morphogenesis	3.58753563385671e-09	0.0039	19
79	GO:0022607_cellular_component_assembly	2.78771260324077e-50	0.0041	528
80	PANTHER_BIOLOGICAL_PROCESS_Cell_cycle_control	1.11914555385854e-32	0.0042	286
81	GO:0044451_nucleoplasm_part	1.31812730670233e-42	0.0043	414
82	PC_RhoA_signaling_pathway	3.21733847959749e-21	0.0043	146
83	PC_G-protein_beta:gamma_signalling	9.41117507039735e-16	0.0044	81
84	PANTHER_BIOLOGICAL_PROCESS_Tumor_suppression	1.56280979446776e-14	0.0044	67



[illegible]

**Supplementary Table 15: GWAS analysis of regulatory and functional information enrichment with LD correction (GARFIELD)**

Functional enrichment analysis of diverticular disease variants in DNaseI Hypersensitive sites from ENCODE and Roadmap Epigenomics data. The table is sorted ascending by the enrichment P value up to a multiple testing adjusted P value threshold of  $P_{adj} < 9.5194e-05$  based on the estimated effective number of enrichment annotations ( $M_{eff} N = 525.24$ ). Fold enrichment of the respective tissue type at GWAS variant significance cutoff of  $p < 1e-08$  is expressed as odds ratio (OR) with lower and upper 95% confidence interval. Celltype specifies the cell type of annotation. Tissue count (%) shows the observed frequency of the respective tissue type at top 20 and total observations.

TOP	Tissue	Celltype	$P_{enrich}$	$OR_{enrich}$	Tissue count (%) Top 20	Tissue count (%) total	Annotation *.twopass.merge150.wgt10.zgt2.wig
1	brain	SK-N-SH	1.36e-07	6.24 [3.16-12.32]	1 (5%)	2 (3%)	SKNSH-DS8482*
2	epithelium	HAEPiC	3.52e-07	6.57 [3.19-13.57]	1 (5%)	2 (3%)	HAEPiC-DS12663*
3	fibroblast	Fibroblasts_Fetal_Skin_Scalp	3.60e-07	6.41 [3.13-13.11]	<b>5 (25%)</b>	<b>13 (22%)</b>	UW.Fibroblasts_Fetal_Skin_Scalp.CA.H-24259.DS19444*
4	gingival	AG09319	3.90e-07	6.17 [3.05-12.46]	1 (5%)	1 (2%)	AG09319-DS12291*
5	skin	AG10803	7.43e-07	5.94 [2.93-12.03]	1 (5%)	4 (7%)	AG10803-DS12384*
6	lung	HPF	1.15e-06	5.75 [2.84-11.64]	1 (5%)	2 (3%)	HPF-DS13390*
7	fibroblast	Fibroblasts_Fetal_Skin_Biceps_Right	1.46e-06	5.78 [2.83-11.81]			UW.Fibroblasts_Fetal_Skin_Biceps_Right.CA.H-24259.DS19761*
8	fibroblast	Fibroblasts_Fetal_Skin_Back	1.88e-06	5.58 [2.75-11.33]			UW.Fibroblasts_Fetal_Skin_Back.CA.H-24218.DS19233*
9	blood_vessel	AoSMC	1.90e-06	5.97 [2.86-12.46]	2 (10%)	3 (5%)	wgEncodeOpenChromDnaseAosmcSerumfreeAlnAllReps.30000000*
10	fetal_muscle	Fetal_Muscle_Back	2.01e-06	6.01 [2.87-12.60]	2 (10%)	6 (10%)	UW.Fetal_Muscle_Back.CA.H-24218.DS19117*
11	blood_vessel	AoAF	3.02e-06	5.36 [2.65-10.84]			AoAF-DS13523*
12	fetal_muscle	Fetal_Muscle_Arm	3.22e-06	5.96 [2.81-12.65]			UW.Fetal_Muscle_Arm.CA.H-24218.DS19053*
13	connective	HVMF	3.97e-06	5.25 [2.60-10.62]	1 (5%)	1 (2%)	HVMF-DS13981*

14	fibroblast	Fibroblasts_Fetal_Skin_Biceps_Left	4.07e-06	5.29 [2.60-10.74]			UW.Fibroblasts_Fetal_Skin_Biceps_Left.CA.H-24259.DS19867*
15	embryonic_lung	WI-38	4.16e-06	5.14 [2.56-10.33]	1 (5%)	1 (2%)	WI_38-DS14315*
16	es_cell	H1_Derived_Mesenchymal_Stem_Cells	4.43e-06	5.17 [2.56-10.42]	2 (10%)	2 (3%)	UW.H1_Derived_Mesenchymal_Stem_Cells.CA.DS20671*
17	es_cell	H1_Derived_Mesenchymal_Stem_Cells	5.59e-06	5.12 [2.53-10.37]			UW.H1_Derived_Mesenchymal_Stem_Cells.CA.DS21042*
18	fetal_stomach	Fetal_Stomach	6.19e-06	5.30 [2.57-10.92]	1 (5%)	4 (7%)	UW.Fetal_Stomach.CA.H-23589.DS16530*
19	breast	HMF	6.49e-06	4.99 [2.48-10.04]	1 (5%)	2 (3%)	HMF-DS13363*
20	fibroblast	Fibroblasts_Fetal_Skin_Biceps_Right	7.64e-06	4.93 [2.45-9.93]			UW.Fibroblasts_Fetal_Skin_Biceps_Right.CA.H-24259.DS19745*
21	fibroblast	Fibroblasts_Fetal_Skin_Scalp	8.75e-06	4.86 [2.42-9.74]			UW.Fibroblasts_Fetal_Skin_Scalp.CA.H-24259.DS19449*
22	fetal_muscle	Fetal_Muscle_Back	9.78e-06	5.48 [2.58-11.65]			UW.Fetal_Muscle_Back.CA.H-24297.DS19648*
23	brain	BE2_C	1.07e-05	4.78 [2.38-9.58]			BE_2_C-DS14625*
24	muscle	SKMC	1.09e-05	4.87 [2.41-9.87]		1 (2%)	SkMC-DS11949*
25	fetal_lung	Fetal_Lung_Right	1.41e-05	5.20 [2.47-10.94]		6 (10%)	UW.Fetal_Lung_Right.CA.H-23604.DS16566*
26	fetal_lung	Fetal_Lung	1.41e-05	4.92 [2.40-10.10]			UW.Fetal_Lung.CA.H-23365.DS15227*
27	blood	Mobilized_CD34_Primary_Cells	1.41e-05	4.65 [2.32-9.31]		2 (3%)	UW.Mobilized_CD34_Primary_Cells.CA.RO_01492.DS14206*
28	foreskin	HFF-Myc	1.49e-05	4.96 [2.40-10.24]		2 (3%)	HFF_MyC-DS15079*
29	fibroblast	Fibroblasts_Fetal_Skin_Quadriceps_Right	1.55e-05	4.67 [2.32-9.38]			UW.Fibroblasts_Fetal_Skin_Quadriceps_Right.CA.H-24259.DS19943*
30	fetal_renal_pelvis	Fetal_Renal_Pelvis	1.61e-05	4.55 [2.29-9.05]		1 (2%)	UW.Fetal_Renal_Pelvis.CA.H-24005.DS18088*
31	breast	Breast_vHMEC	1.76e-05	4.75 [2.33-9.67]			UW.Breast_vHMEC.CA.RM035.DS18406*
32	heart	HCM	1.81e-05	4.64 [2.30-9.37]		2 (3%)	HCM-DS12599*
33	fetal_lung	Fetal_Lung	1.93e-05	4.93 [2.37-10.25]			UW.Fetal_Lung.CA.H-23266.DS14751*
34	brain_hippocampus	HA-h	2.17e-05	4.94 [2.36-10.34]		1 (2%)	HAh-DS15192*
35	fetal_lung	Fetal_Lung_Right	2.22e-05	4.89 [2.35-10.17]			UW.Fetal_Lung_Right.CA.H-24005.DS17954*
36	fetal_muscle	Fetal_Muscle_Back	2.61e-05	4.83 [2.32-10.06]			UW.Fetal_Muscle_Back.CA.H-24111.DS18468*
37	skin	BJ	2.61e-05	4.43 [2.21-8.86]			BJ-DS10081*
38	skin	AG09309	2.64e-05	4.49 [2.23-9.06]			AG09309-DS12352*
39	fibroblast	Fibroblasts_Fetal_Skin_Biceps_Left	2.76e-05	4.50 [2.23-9.08]			UW.Fibroblasts_Fetal_Skin_Biceps_Left.CA.H-24259.DS19857*

40	fibroblast	Fibroblasts_Fetal_Skin_Upper_Back	2.76e-05	4.48 [2.22-9.03]			UW.Fibroblasts_Fetal_Skin_Upper_Back.CA.H-24259.DS19696*
41	fibroblast	Fibroblasts_Fetal_Skin_Upper_Back	2.94e-05	4.51 [2.22-9.14]			UW.Fibroblasts_Fetal_Skin_Upper_Back.CA.H-24259.DS19706*
42	blood	Mobilized_CD4_Primary_Cells	3.67e-05	4.28 [2.15-8.54]			UW.Mobilized_CD4_Primary_Cells.CA.RO_01701.DS17175*
43	fetal_lung	Fetal_Lung_Left	3.75e-05	4.74 [2.26-9.92]			UW.Fetal_Lung_Left.CA.H-24089.DS18421*
44	fibroblast	Penis_Foreskin_Fibroblast_Primary_Cells	3.91e-05	4.33 [2.15-8.70]			UW.Penis_Foreskin_Fibroblast_Primary_Cells.CA.skin02.DS18252*
45	fetal_lung	Fetal_Lung_Left	4.59e-05	4.28 [2.13-8.61]			UW.Fetal_Lung_Left.CA.H-23887.DS17674*
46	heart	HCFAa	4.68e-05	4.37 [2.15-8.89]			HCFAa-DS13480*
47	skin	NHDF-Ad	4.75e-05	4.32 [2.13-8.75]			NHDF_Ad-DS12863*
48	blood_vessel	HPAF	4.88e-05	4.23 [2.11-8.48]			HPAF-DS13411*
49	fetal_muscle_trunk	Fetal_Muscle_Trunk	5.69e-05	4.31 [2.11-8.76]		1 (2%)	UW.Fetal_Muscle_Trunk.CA.H-24507.DS20544*
50	foreskin	HFF	5.71e-05	4.23 [2.09-8.53]			HFF-DS15115*
51	fetal_muscle	Fetal_Muscle_Leg	5.96e-05	4.39 [2.13-9.04]			UW.Fetal_Muscle_Leg.CA.H-24089.DS18456*
52	fetal_stomach	Fetal_Stomach	6.13e-05	4.07 [2.05-8.10]			UW.Fetal_Stomach.CA.H-23769.DS17325*
53	colon	Caco-2	6.23e-05	3.88 [2.00-7.53]		1 (2%)	CACO2-DS8235*
54	fetal_stomach	Fetal_Stomach	6.42e-05	4.26 [2.09-8.66]			UW.Fetal_Stomach.CA.H-24005.DS17963*
55	fetal_muscle	Fetal_Muscle_Arm	6.43e-05	4.20 [2.08-8.49]			UW.Fetal_Muscle_Arm.CA.H-24297.DS19646*
56	fibroblast	Fibroblasts_Fetal_Skin_Abdomen	6.44e-05	4.14 [2.06-8.32]			UW.Fibroblasts_Fetal_Skin_Abdomen.CA.H-24259.DS19561*
57	fetal_stomach	Fetal_Stomach	7.16e-05	4.26 [2.08-8.71]			UW.Fetal_Stomach.CA.H-24401.DS20349*
58	epithelium	HPdLF	9.00e-05	4.01 [2.00-8.05]			HPdLF-DS13573*
59	lung	IMR90	9.02e-05	4.00 [2.00-8.00]			UW.IMR90.CA.DS13229*
60	fibroblast	Fibroblasts_Fetal_Skin_Quadriceps_Left	9.27e-05	4.02 [2.00-8.09]			UW.Fibroblasts_Fetal_Skin_Quadriceps_Left.CA.H-24259.DS20046*

## SUPPLEMENTARY TABLES

***Supplementary Table 16: Overview of the study populations included in risk differentiation of diverticulitis versus diverticulosis***

The following European sample collections were utilized for the subphenotype analysis comparing uncomplicated diverticulosis and diverticulitis. All quantitative measures are shown as medians with interquartile ranges provided in brackets. Body mass index (BMI) and age at the time point of inclusion in the study are included. Patients diagnosed with colorectal cancer, ulcerative colitis or Crohn's disease were excluded from analyses.

Variable	Germany (North) (n=1411)		Germany (West) (n=227)		Austria (Vienna) (n=419)		Austria (Oberndorf) (n=387)		Lithuania (n=479)	
	D-itis (n=728)	D-osis (n=683)	D-itis (n=86)	D-osis (n=141)	D-itis (n=212)	D-osis (n=207)	D-itis (n=98)	D-osis (n=289)	D-itis (n=43)	D-osis (n=436)
Gender (% male)	45	57	84	140	55.2	58.0	58.2	57.1	41.9	43.1
Age (years )	64 (56-72)	72 (65-77)	64 (54-72)	68 (62-77)	65 (56-72)	71 (65-76)	61 (51-69)	66 (59-73)	63 (57-72)	68 (62-74)
BMI	27.0 (24.6-30.0)	26.7 (24.4-29.9)	27.2 (23.9-30.1)	26.8 (24.2-31.0)	28.4 (26.1-32.6)	27.4 (25.5-30.4)	28.0(23.0-32.9)	26.1(21.7-30.5)	27.2 (25.6-31.6)	28.7 (26.1-32.3)

**Supplementary Table 17: Results of comparison of diverticulitis versus diverticulosis risk**

The relative genetic effect of the 27 replicating loci on diverticulitis versus diverticulosis risk was assessed in European cohorts (Supplementary Table 1). Reference allele frequencies for diverticulitis and diverticulosis are shown for the largest (n=1411) differentiation cohort. Loci are ordered by odds ratio obtained from the metanalysis of the European cohorts. To harmonize the directionality of diverticulitis risk increment for all 27 loci, the OR in Figure 1(B) is based on the reference allele (Ref) in Supplementary Table 17. The reference allele was chosen as the risk increasing allele - the allele observed more common in diverticular disease cases as compared to diverticula-free controls.

Chr	Position	rsID	Gene(s)	European cohorts			Germany (Northern Germany) cohort		
				P value	OR [CI 95%] **	OR-comparison	Ref	Ref (%) Diverticulitis (n=728) ***	Ref (%) Diverticulosis (n=683)
15	40649609	rs71472433	<i>PHGR1/ISP2</i>	<b>0.001</b>	1.32 [1.12-1.56]	<b>ITIS&gt;OSIS</b>	C	18.7	14.4
7	73427600	rs112609918*	<i>ELN</i>	0.225	1.23 [0.88-1.72]	<b>ITIS&gt;OSIS</b>	T	3.9	2.8
13	108215404	rs9555371	<i>FAM155A 2</i>	<b>0.015</b>	1.21 [1.04-1.42]	<b>ITIS&gt;OSIS</b>	A	83.9	81.5
11	15014179	rs12293178*	<i>CALCB</i>	<b>0.014</b>	1.17 [1.03-1.33]	<b>ITIS&gt;OSIS</b>	A	33.4	28.2
1	151970629	rs61814883	<i>SI00A10</i>	<b>0.016</b>	1.17 [1.03-1.33]	<b>ITIS&gt;OSIS</b>	G	73.8	68.4
13	107902770	rs9520344*	<i>FAM155A 1</i>	0.058	1.14 [1.00-1.31]	<b>ITIS&gt;OSIS</b>	T	78.5	75.0
15	68238462	rs387505	<i>PIASI</i>	0.054	1.12 [1.00-1.26]	<b>ITIS&gt;OSIS</b>	T	46.9	45.4
2	144314247	rs6734367	<i>ARHGAP15</i>	0.160	1.11 [0.96-1.29]	ITIS±OSIS	T	20.9	18.5
10	18440444	rs1888693	<i>CACNB2</i>	0.116	1.10 [0.98-1.25]	ITIS±OSIS	G	68.7	65.1
11	70007484	rs2276068*	<i>ANO1</i>	0.140	1.09 [0.97-1.23]	ITIS±OSIS	C	49.7	46.6
16	86233413	rs2280028	<i>LINC01082</i>	0.575	1.05 [0.88-1.25]	ITIS±OSIS	G	86.5	86.0
3	5846159	rs4684509*	<i>EDEMI</i>	0.543	1.05 [0.91-1.21]	ITIS±OSIS	C	80.7	78.5

1	221066373	rs2784255	<i>HLX</i>	0.518	1.04 [0.93-1.17]	ITIS±OSIS	C	53.2	52.9
6	98365289	rs4839715*	<i>LOC101927314</i>	0.575	1.04 [0.92-1.17]	ITIS±OSIS	G	67.1	66.6
10	25811435	rs7086249*	<i>GPR158</i>	0.584	1.03 [0.92-1.16]	ITIS±OSIS	T	58.2	56.8
15	76840832	rs12443137*	<i>SCAPER</i>	0.739	1.02 [0.91-1.15]	ITIS±OSIS	T	55.9	55.6
7	102447056	rs10257317*	<i>FBXL13</i>	0.745	1.02 [0.91-1.15]	ITIS±OSIS	C	36.8	35.2
3	151074941	rs3732760	<i>P2RY12</i>	0.804	1.02 [0.90-1.15]	ITIS±OSIS	C	39.9	36.7
18	20011920	rs2009593*	<i>CTAGE1</i>	0.835	1.01 [0.89-1.15]	ITIS±OSIS	G	31.0	28.7
8	120427648	rs1381335*	<i>NOV</i>	0.992	1.00 [0.86-1.16]	ITIS±OSIS	C	80.2	79.2
22	40679362	rs5995842*	<i>TNRC6B</i>	0.997	1.00 [0.89-1.13]	ITIS±OSIS	G	38.7	39.2
9	136137065	rs687621*	<i>ABO</i>	0.957	1.00 [0.88-1.13]	ITIS±OSIS	A	64.8	64.7
19	38743962	rs12976534*	<i>PPP1R14A</i>	0.714	0.98 [0.87-1.10]	ITIS±OSIS	G	49.5	50.4
4	95832551	rs972409*	<i>BMPRI1B</i>	0.434	0.95 [0.84-1.08]	ITIS±OSIS	T	33.2	34.6
4	15384544	rs4515160*	<i>CIQTNF7</i>	0.166	0.91 [0.80-1.04]	ITIS±OSIS	G	28.3	29.8
3	15502681	rs7609897	<i>COLQ</i>	0.198	0.91 [0.79-1.05]	ITIS±OSIS	T	79.3	80.3
21	47398647	rs7281388*	<i>COL6A1</i>	0.186	0.89 [0.76-1.06]	ITIS±OSIS	A	13.8	15.8

\* proxy SNP for GWAs lead SNP; \*\* OR adjusted for gender and age; \*\*\*allele frequency of risk increasing allele (Ref Allele) in German differentiation cohort (North)

**Supplementary Table 18: Genetic overlap with Mendelian diseases (OMIM- Online Mendelian Inheritance in Man)**

Direct overlap of the curated candidate genes at diverticular disease associated risk loci with genes causal for monogenic Mendelian diseases. \*Phenotype MIM number from OMIM. \*\*Inheritance AR autosomal recessive, AD autosomal dominant.

Genomic risk locus	plausible candidate gene at locus	OMIM gene.map search (genomic region, hg38)	Genomic coordinates (From NCBI/GRCh38)	Gene/Locus MIM number	Gene/Locus (OMIM)	Phenotype MIM number*	Phenotype	Inheritance**
4	<i>COLQ</i>	chr1:14961174-15961174	3:15450132-15521750	603033	<i>COLQ, EAD, CMS5</i>	603034	Myasthenic syndrome, congenital, 5	AR
5	<i>EFEMP1</i>	chr2:55366068-56366069	2:55865961-55924162	601548	<i>EFEMP1, FBNL, DHRD</i>	126600	Doyle honeycomb degeneration of retina	AD
15	<i>COL6A1</i>	chr21:45479539-46479540	21:45981748-46005048	120220	<i>COL6A1, BTHLM1, UCHMD1</i>	158810	Bethlem myopathy 1	AR; AD
15	<i>COL6A1</i>	chr21:45479539-46479540	21:45981748-46005048	120220	<i>COL6A1, BTHLM1, UCHMD1</i>	254090	Ullrich congenital muscular dystrophy 1	AR; AD
16	<i>ELN</i>	chr7:73513270-74513270	7:74027771-74069906	130160	<i>ELN, SVAS, ADCLI</i>	185500	Supravalvar aortic stenosis	AD
16	<i>ELN</i>	chr7:73513270-74513270	7:74027771-74069906	130160	<i>ELN, SVAS, ADCLI</i>	123700	Cutis laxa, AD	AD
20	<i>P2RY12</i>	chr3:150857154-151857153	3:151336842-151384811	600515	<i>P2RY12, P2Y12, BDPLT8</i>	609821	Bleeding disorder, platelet-type, 8	AR
21	<i>CWC27</i>	chr5:64499536-65499536	5:64768917-65018762	617170	<i>CWC27, SDCCAG10, RPSKA</i>	250410	Retinitis pigmentosa with or without skeletal anomalies	AR
24	<i>GDNF</i>	chr5:37272678-38272678	5:37812676-37840043	600837	<i>GDNF, HSCR3</i>	613711	Hirschsprung disease, susceptibility to, 3	AD
24	<i>GDNF</i>	chr5:37272678-38272678	5:37812676-37840043	600837	<i>GDNF, HSCR3</i>	209880	Central hypoventilation syndrome	AD
28	<i>SEMI</i>	chr7:95949252-96949252	7:91500000-98400000	183600	<i>SEMI, SHFD1, SHSF1</i>	183600	Split hand/foot malformation 1	AD
30	<i>UBTF</i>	chr17:43735410-44735410	17:44205032-44221625	600673	<i>UBTF, UBF, CONDBA</i>	617672	Neurodegeneration, childhood-onset, with brain atrophy	AD
31	<i>CACNB2</i>	chr10:17651515-18651515	10:18140559-18545880	600003	<i>CACNB2</i>	611876	Brugada syndrome 4	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDA1D</i>	112600	Brachydactyly, type A2	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDA1D</i>	616849	Brachydactyly, type A1, D	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDA1D</i>	609441	Acromesomelic dysplasia, Demirhan type	AR
51	<i>TRPS1</i>	chr8:115076317-116076321	8:115408495-115669636	604386	<i>TRPS1</i>	190351	Trichorhinophalangeal syndrome, type III	AD
51	<i>TRPS1</i>	chr8:115076317-116076321	8:115408495-115669636	604386	<i>TRPS1</i>	190350	Trichorhinophalangeal syndrome, type I	AD



**Supplementary Table 19: Genetic overlap with Mendelian diseases (OMIM- Online Mendelian Inheritance in Man) - 500 kilo-base (kb) window**

Genetic overlap of diverticular disease associated genomic risk loci with genes causal for monogenic Mendelian diseases. Genes with a transcript start within 500kb on either side of the respective lead variant at genomic risk locus are considered. A direct overlap of the curated candidate gene at genomic risk locus with OMIM annotated genes is highlighted in bold print (OMIM overlap with candidate gene). \*Phenotype MIM number from OMIM. \*\*Inheritance AR autosomal recessive, AD autosomal dominant. The table was assembled as follows: Diverticular disease risk loci with consistency in odds ratio direction between discovery and replication cohorts (n=48, Table 2,3) were analysed for overlap with autosomal dominant and autosomal recessive inherited Mendelian diseases cataloged in OMIM. For this analysis we converted the genomic locations of diverticular disease-associated lead variants from hg19 (GRCh37) to the hg38 (GRCh38) human genome build using the software liftOver which is integrated in the UCSC genome browser. Next we retrieved the gene annotations (July 15, 2018) that lie within a 500 kilo-base (kb) window on either side of the lead variant from OMIM by using "Advanced Search" (gene <https://www.omim.org/search/advanced/geneMap>). Overlapping phenotypes and associated genes are listed.

Genomic risk locus	curated candidate gene at locus	OMIM gene.map search (genomic region, hg38)	OMIM overlap with candidate gene	Cytogenetic location	Genomic coordinates (From NCBI/GRCh38)	Gene/Locus MIM number	Gene/Locus	Phenotype MIM number*	Phenotype	Inheritance **
1	<i>ARHGAP15</i>	chr2:143056678-144056680		2p12-q22	2:74800000-147900000	139900	<i>HSR</i>	139900	Handedness	AD
1	<i>ARHGAP15</i>	chr2:143056678-144056680		2q	2:93900000-242193529	606053	<i>AUTS5</i>	606053	Autism susceptibility 5	AR; AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q31-q42	1:185800000-236400000	145260	<i>PHA2A, PHA2</i>	145260	Pseudohypoaldosteronism, type IIA	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q41-q44	1:214400000-248956422	615589	<i>OTSC10</i>	615589	Otosclerosis 10	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42	1:223900000-236400000	606554	<i>EA3</i>	606554	Episodic ataxia, type 3	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42	1:223900000-236400000	604801	<i>MDC1B</i>	604801	Muscular dystrophy, congenital, 1B	AR
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42.2-q43	1:230500000-243500000	602759	<i>PCAP</i>	176807	Prostate cancer, susceptibility to	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42.2-q43	1:230500000-243500000	119100	<i>SHFL1, SHFLD</i>	119100	Split-hand/foot malformation with long bone deficiency 1	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42.2	1:234373436-234384048	614772	<i>COA6, CEMCOX4, C1orf31</i>	616501	Cardioencephalomyopathy, fatal infantile, due to cytochrome c oxidase deficiency 4	AR
2	<i>SLC35F3</i>	chr1:233717153-234717152		1q42.3	1:234604268-234609524	615332	<i>IRF2BP2, CIVD14</i>	617765	Immunodeficiency, common variable, 14	AD
2	<i>SLC35F3</i>	chr1:233717153-234717152		Chr.1		108420	<i>SPGF2, ASG</i>	108420	Spermatogenic failure 2	AD

3	<i>GPR158</i>	chr10:25030299-26030299		10p12.1	10:25934072-26212535	606808	<i>MYO3A, DFNB30</i>	607101	Deafness, autosomal recessive 30	AR
4	<i>COLQ</i>	chr3:14961174-15961174	yes	3p25.1	3:15450132-15521750	603033	<i>COLQ, EAD, CMS5</i>	603034	Myasthenic syndrome, congenital, 5	AR
4	<i>COLQ</i>	chr3:14961174-15961174		3pter-p25		613792	<i>DEL3pterp25, C3DELpterp25</i>	613792	3p- syndrome	AD
4	<i>COLQ</i>	chr3:14961174-15961174		3p26-p24.2		252350	<i>MYMY1, MYMY</i>	252350	Moyamoya disease	AR
4	<i>COLQ</i>	chr3:14961174-15961174		3p25.1-p23	3:13200000-32000000	613530	<i>LGMD1H</i>	613530	Muscular dystrophy, limb-girdle, type 1H	AD
4	<i>COLQ</i>	chr3:14961174-15961174		3p25.1	3:15601351-15653710	609019	<i>BTB</i>	253260	Biotinidase deficiency	AR
5	<i>EFEMP1</i>	chr2:55366068-56366069	yes	2p16.1	2:55865961-55924162	601548	<i>EFEMP1, FBNL, DHRD</i>	126600	Doyne honeycomb degeneration of retina	AD
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p25-p12		101850	<i>PPKP3</i>	101850	Keratoderma, palmoplantar, punctate type 3	AD
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p21-p12	2:41500000-83100000	615654	<i>DFNA58</i>	615654	Deafness, AD 58	AD
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p21-p13	2:41500000-74800000	608703	<i>SCA25</i>	608703	Spinocerebellar ataxia 25	AD
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p16.1	2:54700000-61000000	142335	<i>HBQTL5</i>	142335	Fetal hemoglobin QTL5	AD
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p16.1	2:55287816-55419920	609736	<i>CCDC88A, KIAA1212, HKRP1, GIRDIN, APE, GIV, PEHOL</i>	617507	PEHO syndrome-like	AR
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p16.1	2:55634062-55693909	610316	<i>PNPT1, OLD35, COXPD13, DFNB70</i>	614934	Deafness, autosomal recessive 70	AR
5	<i>EFEMP1</i>	chr2:55366068-56366069		2p16.1	2:55634062-55693909	610316	<i>PNPT1, OLD35, COXPD13, DFNB70</i>	614932	Combined oxidative phosphorylation deficiency 13	AR
6	<i>BDNF</i>	chr11:27226946-28226946		11p15-p14		606528	<i>DEL11p15p14, C11DELp15p14</i>	606528	Chromosome 11p15-p14 deletion syndrome	AR
6	<i>BDNF</i>	chr11:27226946-28226946		11p		600165	<i>NNO1</i>	600165	Nanophthalmos-1	AD
6	<i>BDNF</i>	chr11:27226946-28226946		11p14.2-q12.3	11:26200000-63600000	612642	<i>DFNA59</i>	612642	Deafness, AD 59	AD
6	<i>BDNF</i>	chr11:27226946-28226946		11p14.1-p11.2	11:27200000-48800000	613364	<i>SPG41</i>	613364	Spastic paraplegia 41, AD	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q	19:26200000-58617616	601764	<i>BFIS1, BFIC1</i>	601764	Seizures, benign familial infantile, 1	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q	19:26200000-58617616	607592	<i>HPCQTL19</i>	176807	Prostate cancer aggressiveness QTL	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13	19:31900000-58617616	100070	<i>AAA1, AAA</i>	100070	Aortic aneurysm, familial abdominal 1	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13	19:31900000-58617616	609376	<i>CTRCT35, CATCN1</i>	609376	Cataract 35, congenital nuclear	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13	19:31900000-58617616	611907	<i>EA7</i>	611907	Episodic ataxia, type 7	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13	19:31900000-58617616	600757	<i>OFC3</i>	600757	Orofacial cleft-3	AD

7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.1-q13.2	19:37906821-38208371	616655	<i>SIPA1L3, SPAL3, SPAR3, KIAA0545, CTRCT45</i>	616851	Cataract 45	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2-q13.3	19:38200000-50900000	611097	<i>MRT11</i>	611097	Mental retardation, autosomal recessive, 11	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38200000-42900000	227050	<i>TEC</i>	227050	Transient erythroblastopenia of childhood	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38264457-38292613	605124	<i>SPINT2, HAI2, DIAR3</i>	270420	Diarrhea 3, secretory sodium, congenital, syndromic	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38433699-38587563	180901	<i>RYR1, MHS, CCO</i>	145600	Malignant hyperthermia susceptibility 1	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38433699-38587563	180901	<i>RYR1, MHS, CCO</i>	117000	Neuromuscular disease, congenital, with uniform type 1 fiber	AR; AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38433699-38587563	180901	<i>RYR1, MHS, CCO</i>	255320	Minicore myopathy with external ophthalmoplegia	AR
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38433699-38587563	180901	<i>RYR1, MHS, CCO</i>	145600	King-Denborough syndrome	AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38433699-38587563	180901	<i>RYR1, MHS, CCO</i>	117000	Central core disease	AR; AD
7	<i>PPP1R14A</i>	chr19:37747491-38747490		19q13.2	19:38647615-38730531	604638	<i>ACTN4, FSGS1, FSGS</i>	603278	Glomerulosclerosis, focal segmental, 1	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q	9:43000000-138394717	607152	<i>SPG19</i>	607152	Spastic paraplegia 19, AD	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q31-q34	9:99800000-138394717	183840	<i>SPDA2</i>	183840	Spondyloarthropathy, susceptibility to, 2	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34	9:127500000-138394717	614623	<i>KTCN6</i>	614623	Keratoconus 6	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34.13	9:131100000-133100000	171720	<i>ALPQTL1</i>	171720	Alkaline phosphatase, plasma level of, QTL1	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34.13	9:132891347-132945268	605284	<i>TSC1, LAM</i>	191100	Tuberous sclerosis-1	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34.13	9:132945544-132991696	604383	<i>GF11B, BDPLT17</i>	187900	Bleeding disorder, platelet-type, 17	AR; AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34.13	9:133061977-133071862	114840	<i>CEL, BSSL, CELL, MODY8</i>	609812	Maturity-onset diabetes of the young, type VIII	AD
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133351804-133356484	185620	<i>SURF1, CMT4K</i>	616684	Charcot-Marie-Tooth disease, type 4K	AR
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133414338-133459402	604134	<i>ADAMTS13, VWFCP, TTP</i>	274150	Thrombotic thrombocytopenic purpura, familial	AR
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133514585-133524945	615345	<i>MYMK, TMEM8C</i>	254940	Carey-Fineman-Ziter syndrome	AR
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133532163-133575518	612277	<i>ADAMTSL2, KIAA0605, GPHYSD1</i>	231050	Geleophysic dysplasia 1	AR
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133636362-133659343	609312	<i>DBH</i>	223360	Dopamine beta-hydroxylase deficiency	AR
8	<i>ABO</i>	chr9:132773842-133784107		9q34.2	9:133663073-133739957	604455	<i>SARDH, SARD, SAR</i>	268900	Sarcosinemia	AR
9	<i>FBXL13</i>	chr7:102334488-103334456		7q	7:60100000-159345973	252270	<i>MLSM7, DEL7q, C7DELq</i>	252270	Myelodysplasia and leukemia syndrome with monosomy 7	AR
9	<i>FBXL13</i>	chr7:102334488-103334456		7q21-q22	7:77900000-107800000	154276	<i>MHS3</i>	154276	Malignant hyperthermia susceptibility 3	AD
9	<i>FBXL13</i>	chr7:102334488-103334456		7q22-qter	7:98400000-159345973	162820	<i>NM, NCR</i>	162820	Neutrophil chemotactic response, abnormal	AD
9	<i>FBXL13</i>	chr7:102334488-103334456		7q22-q32	7:98400000-132900000	607458	<i>SCA18, SMNA</i>	607458	Spinocerebellar ataxia 18	AD

9	<i>FBXL13</i>	chr7:102334488-103334456		7q22.1	7:103297425-103329901	603131	<i>PMPCB, MPPB</i>	617954	Multiple mitochondrial dysfunctions syndrome 6	AR
10	<i>FAM155A</i>	chr13:107063056-108063056'		13	13:78500000-109600000	193003	<i>NYS4</i>	193003	Nystagmus 4, congenital, AD	AD
11	<i>FAM155A</i>	chr13:107063056-108063056'		13	13:78500000-109600000	193003	<i>NYS4</i>	193003	Nystagmus 4, congenital, AD	AD
12	<i>LYPLAL1-AS1</i>	chr1:218621228-219621228		1	1:185800000-236400000	145260	<i>PHA2A, PHA2</i>	145260	Pseudohypoaldosteronism, type IIA	AD
12	<i>LYPLAL1-AS1</i>	chr1:218621228-219621228		1	1:214400000-248956422	615589	<i>OTSC10</i>	615589	Otosclerosis 10	AD
12	<i>LYPLAL1-AS1</i>	chr1:218621228-219621228		1	1:214400000-223900000	600332	<i>RMD1</i>	600332	Rippling muscle disease-1	AD
12	<i>LYPLAL1-AS1</i>	chr1:218621228-219621228		1		108420	<i>SPGF2, ASG</i>	108420	Spermatogenic failure 2	AD
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q22-q24	10:68800000-104000000	608583	<i>ATFB1</i>	608583	Atrial fibrillation, familial, 1	AD
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24.1-q25.1	10:95300000-110100000	606483	<i>CMTDIA</i>	606483	Charcot-Marie-Tooth disease, dominant intermediate A	AD
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24	10:95300000-104000000	246560	<i>SHFM3, SHSF3, DUP10q24, C10DUPq24</i>	246560	Split-hand/foot malformation 3, gene duplication syndrome	AD
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24.2	10:98457076-99235874	613469	<i>HPSE2, HPA2, UFS1</i>	236730	Urofacial syndrome 1	AR
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24.2	10:99694792-99732665	603646	<i>COX15, CEMCOX2</i>	615119	Cardioencephalomyopathy, fatal infantile, due to cytochrome c oxidase deficiency 2	AR
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24.2	10:99782597-99853740	601107	<i>ABCC2, CMOAT</i>	237500	Dubin-Johnson syndrome	AR
13	<i>SLC25A28</i>	chr10:99131412-100131412		10q24.2	10:100042307-100081884	603103	<i>CPN1, SCPN, CPN</i>	212070	Carboxypeptidase N deficiency	AR
14	<i>NOV</i>	chr8:118943954-119943953		8q	8:45200000-145138636	600668	<i>CCAL1</i>	600668	Chondrocalcinosis with early-onset osteoarthritis	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q23-q24	8:105100000-145138636	140300	<i>HT</i>	140300	Hashimoto thyroiditis	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q23-q24	8:105100000-145138636	611376	<i>MGS</i>	611376	Mungan syndrome	AR
14	<i>NOV</i>	chr8:118943954-119943953		8q24	8:116700000-145138636	600131	<i>ECA1</i>	600131	Epilepsy, childhood absence, 1	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q24	8:116700000-145138636	600669	<i>EIG1</i>	600669	Epilepsy, idiopathic generalized, susceptibility to, 1	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q24	8:116700000-145138636	601068	<i>FAME1, BAFME1, MEBA</i>	601068	Epilepsy, myoclonic, familial adult, 1	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q24.1	8:116700000-126300000	275220	<i>THM</i>	275220	Tibial hemimelia	AR
14	<i>NOV</i>	chr8:118943954-119943953		8q24.11-q24.13	8:116700000-126300000	150230	<i>TRPS2, LGCR, LGS</i>	150230	Trichorhinophalangeal syndrome, type II	AD
14	<i>NOV</i>	chr8:118943954-119943953		8q24.12	8:118923556-118952143	602643	<i>TNFRSF11B, OCIF, PDB5, OPG</i>	239000	Paget disease of bone 5, juvenile-onset	AR
14	<i>NOV</i>	chr8:118943954-119943953		8q24.12	8:118952166-119108454	607620	<i>COLEC10, CLL1, 3MC3</i>	248340	3MC syndrome 3	AR
14	<i>NOV</i>	chr8:118943954-119943953		8q24.12	8:119730772-119832857	604912	<i>TAF2, TAF2B, TAFII150, CIF150, MRT40</i>	615599	Mental retardation, autosomal recessive 40	AR

15	<i>COL6A1</i>	chr21:45479539-46479540	yes	21q22.3	21:45981748-46005048	120220	<i>COL6A1, BTHLMI, UCHMD1</i>	158810	Bethlem myopathy 1	AR; AD
15	<i>COL6A1</i>	chr21:45479539-46479540	yes	21q22.3	21:45981748-46005048	120220	<i>COL6A1, BTHLMI, UCHMD1</i>	254090	Ullrich congenital muscular dystrophy 1	AR; AD
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22	21:30200000-46709983	609428	<i>TUKLS</i>	609428	Tukel syndrome	AR
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:41200000-46709983	236100	<i>HPE1</i>	236100	Holoprosencephaly 1	AD
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:45405136-45513719	120328	<i>COL18A1, KNO1</i>	267750	Knobloch syndrome, type 1	AR
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46098070-46132848	120240	<i>COL6A2, BTHLMI, UCMD1</i>	255600	Myosclerosis, congenital	AR
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46098070-46132848	120240	<i>COL6A2, BTHLMI, UCMD1</i>	158810	Bethlem myopathy 1	AR; AD
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46098070-46132848	120240	<i>COL6A2, BTHLMI, UCMD1</i>	254090	Ullrich congenital muscular dystrophy 1	AR; AD
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46135980-46156481	606806	<i>FTCD</i>	229100	Glutamate formiminotransferase deficiency	AR
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46188445-46228823	600909	<i>LSS, OSC, CTCT44</i>	616509	Cataract 44	AR
15	<i>COL6A1</i>	chr21:45479539-46479540		21q22.3	21:46324121-46445768	605925	<i>PCNT, PCNT2, KEN, SCKL4, MOPD2</i>	210720	Microcephalic osteodysplastic primordial dwarfism, type II	AR
16	<i>ELN</i>	chr7:73513270-74513270	yes	7q11.23	7:74027771-74069906	130160	<i>ELN, SVAS, ADCL1</i>	185500	Supravalvar aortic stenosis	AD
16	<i>ELN</i>	chr7:73513270-74513270	yes	7q11.23	7:74027771-74069906	130160	<i>ELN, SVAS, ADCL1</i>	123700	Cutis laxa, AD	AD
16	<i>ELN</i>	chr7:73513270-74513270		7p12.1-q21	7:50500000-98400000	614676	<i>CMH21</i>	614676	Cardiomyopathy, hypertrophic, 21	AD
16	<i>ELN</i>	chr7:73513270-74513270		7p11-q21	7:53900000-98400000	608658	<i>HPC4</i>	176807	Prostate cancer, susceptibility to, 4	AD
16	<i>ELN</i>	chr7:73513270-74513270		7q	7:60100000-159345973	252270	<i>MLSM7, DEL7q, C7DELq</i>	252270	Myelodysplasia and leukemia syndrome with monosomy 7	AR
16	<i>ELN</i>	chr7:73513270-74513270		7q11.2	7:62100000-77900000	105800	<i>ANIB1</i>	105800	Aneurysm, intracranial berry, 1	AD
16	<i>ELN</i>	chr7:73513270-74513270		7q11.2-q21.3	7:62100000-98400000	129900	<i>EEC1</i>	129900	EEC syndrome-1	AD
16	<i>ELN</i>	chr7:73513270-74513270		7q11.23	7:72700000-77900000	609757	<i>DUP7q11.23, C7DUPq11.23</i>	609757	Chromosome 7q11.23 duplication syndrome	AD
16	<i>ELN</i>	chr7:73513270-74513270		7q11.23	7:72700000-77900000	194050	<i>WBS, WMS, WS, DEL7q11, C7DELq11</i>	194050	Williams-Beuren syndrome	AD
17	<i>LINC01082</i>	chr16:85699807-86699807		16q	16:36800000-90338345	194090	<i>WT3</i>	194090	Wilms tumor, type 3	AD
17	<i>LINC01082</i>	chr16:85699807-86699807		16q24.1	16:85899167-85922605	601565	<i>IRF8, ICSBP1, IMD32A, IMD32B</i>	614893	Immunodeficiency 32A, mycobacteriosis, AD	AD
17	<i>LINC01082</i>	chr16:85699807-86699807		16q24.1	16:85899167-85922605	601565	<i>IRF8, ICSBP1, IMD32A, IMD32B</i>	226990	Immunodeficiency 32B, monocyte and dendritic cell deficiency, autosomal recessive	AR
17	<i>LINC01082</i>	chr16:85699807-86699807		16q24.1	16:86510526-86514463	601089	<i>FOXF1, FKHL5, ACDMPV</i>	265380	Alveolar capillary dysplasia with misalignment of pulmonary veins	AD
17	<i>LINC01082</i>	chr16:85699807-86699807		16q24.1	16:86567250-86568932	602402	<i>FOXC2, FKHL14, MFH1</i>	153400	Lymphedema-distichiasis syndrome with renal disease and diabetes mellitus	AD

17	<i>LINC01082</i>	chr16:85699807-86699807		16q24.1	16:86567250-86568932	602402	<i>FOXC2, FKHL14, MFH1</i>	153400	Lymphedema-distichiasis syndrome	AD
18	<i>CRISPLD2</i>	chr16:84323772-85323772		16q	16:36800000-90338345	194090	<i>WT3</i>	194090	Wilms tumor, type 3	AD
19	<i>LOC101927314</i>	chr6:97417019-98417019		6q	6:59800000-170805979	193007	<i>BPPV</i>	193007	Vestibulopathy, familial	AD
19	<i>LOC101927314</i>	chr6:97417019-98417019		6q13-q16.1	6:69200000-98900000	611572	<i>OTSC7</i>	611572	Otosclerosis 7	AD
19	<i>LOC101927314</i>	chr6:97417019-98417019		6q13-q26	6:69200000-164100000	603175	<i>SCZD5</i>	181500	Schizophrenia	AD
19	<i>LOC101927314</i>	chr6:97417019-98417019		6q14-q16.2	6:75200000-100000000	600790	<i>PBCRA, CRAPB</i>	600790	Chorioretinal atrophy, progressive bifocal	AD
20	<i>P2RY12</i>	chr3:150857154-151857153	yes	3q25.1	3:151336842-151384811	600515	<i>P2RY12, P2Y12, BDPLT8</i>	609821	Bleeding disorder, platelet-type, 8	AR
20	<i>P2RY12</i>	chr3:150857154-151857153		3q25.1	3:150926162-150972998	606397	<i>CLRN1, USH3A, USH3, RP61</i>	276902	Usher syndrome, type 3A	AR
21	<i>CWC27</i>	chr5:64499536-65499536	yes	5q12.3	5:64768917-65018762	617170	<i>CWC27, SDCCAG10, RPSKA</i>	250410	Retinitis pigmentosa with or without skeletal anomalies	AR
21	<i>CWC27</i>	chr5:64499536-65499536		5q12	5:59600000-67400000	615668	<i>DEL5q12, C5DELq12</i>	615668	Chromosome 5q12 deletion syndrome	AD
21	<i>CWC27</i>	chr5:64499536-65499536		5q12-q14	5:59600000-93000000	611364	<i>EJM4</i>	611364	Myoclonic epilepsy, juvenile, 4	AD
22	<i>CALCB</i>	chr11:14543689-15543689		11p15-p14		606528	<i>DEL11p15p14, C11DELp15p14</i>	606528	Chromosome 11p15-p14 deletion syndrome	AR
22	<i>CALCB</i>	chr11:14543689-15543689		11p15		235000	<i>IH, HHP</i>	235000	Hemihypertrophy	AD
22	<i>CALCB</i>	chr11:14543689-15543689		11p		600165	<i>NNO1</i>	600165	Nanophthalmos-1	AD
22	<i>CALCB</i>	chr11:14543689-15543689		11p15.2	11:14878004-14898914	608713	<i>CYP2R1</i>	600081	Rickets due to defect in vitamin D 25-hydroxylation	AR
23	<i>SI00A10</i>	chr1:151498153-152498153		1p21.1-q21.3	1:101800000-155100000	612841	<i>HYPT5, MUHH2</i>	612841	Hypotrichosis 5	AD
23	<i>SI00A10</i>	chr1:151498153-152498153		1q12-q24	1:125100000-173000000	605549	<i>CORD8</i>	605549	Cone-rod dystrophy 8	AR
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21-q23	1:143200000-165500000	608372	<i>DFNA49</i>	608372	Deafness, AD 49	AD
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21-q23	1:143200000-165500000	601412	<i>DFNA7</i>	601412	Deafness, AD 7	AD
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21	1:143200000-155100000	161900	<i>RFH1, AORF</i>	161900	Nephropathy-hypertension	AD
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21.3	1:150600000-155100000	139450	<i>HRM2</i>	139450	Hair, curly	AD
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21.3	1:151806070-151832450	602943	<i>RORC, RORG, RZRG, IMD42</i>	616622	Immunodeficiency 42	AR
23	<i>SI00A10</i>	chr1:151498153-152498153		1q21.3	1:152106316-152115453	190370	<i>TCHH, THH, THL, TRHY, UHS3</i>	617252	Uncombable hair syndrome 3	AR

[illegible]

28	<i>SEMI</i>	chr7:95949252-96949252	yes	7q21.2-q21.3	7:91500000-98400000	183600	<i>SEMI, SHFD1, SHSF1</i>	183600	Split hand/foot malformation 1	AD
28	<i>SEMI</i>	chr7:95949252-96949252		7p12.1-q21	7:50500000-98400000	614676	<i>CMH21</i>	614676	Cardiomyopathy, hypertrophic, 21	AD
28	<i>SEMI</i>	chr7:95949252-96949252		7p11-q21	7:53900000-98400000	608658	<i>HPC4</i>	176807	Prostate cancer, susceptibility to, 4	AD
28	<i>SEMI</i>	chr7:95949252-96949252		7q	7:60100000-159345973	252270	<i>MLSM7, DEL7q, C7DELq</i>	252270	Myelodysplasia and leukemia syndrome with monosomy 7	AR
28	<i>SEMI</i>	chr7:95949252-96949252		7q11.2-q21.3	7:62100000-98400000	129900	<i>EEC1</i>	129900	EEC syndrome-1	AD
28	<i>SEMI</i>	chr7:95949252-96949252		7q21-q22	7:77900000-107800000	154276	<i>MHS3</i>	154276	Malignant hyperthermia susceptibility 3	AD
28	<i>SEMI</i>	chr7:95949252-96949252		7q21.3	7:96120219-96322146	603859	<i>SLC25A13, CTLN2</i>	603471	Citrullinemia, adult-onset type II	AR
28	<i>SEMI</i>	chr7:95949252-96949252		7q21.3	7:96120219-96322146	603859	<i>SLC25A13, CTLN2</i>	605814	Citrullinemia, type II, neonatal-onset	AR
29	<i>CTAGE1</i>	chr18:21948776-22948774		18p11.23-q12.2	18:7200000-39500000	107200	<i>ANIC</i>	107200	Anosmia, isolated congenital	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q	18:18500000-80373285	601808	<i>DEL18q</i>	601808	Chromosome 18q deletion syndrome	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q	18:18500000-80373285	143850	<i>OHDS</i>	143850	Orthostatic hypotensive disorder of Streeten	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2-q12.2	18:21500000-39500000	613930	<i>APMR3</i>	613930	Alopecia-mental retardation syndrome 3	AR
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22169436-22202527	601656	<i>GATA6, AVSD5, ASD9, PACHD</i>	614475	Atrial septal defect 9	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22169436-22202527	601656	<i>GATA6, AVSD5, ASD9, PACHD</i>	614474	Atrioventricular septal defect 5	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22169436-22202527	601656	<i>GATA6, AVSD5, ASD9, PACHD</i>	600001	Pancreatic agenesis and congenital heart defects	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22169436-22202527	601656	<i>GATA6, AVSD5, ASD9, PACHD</i>	187500	Tetralogy of Fallot	AD
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22914120-23026485	604124	<i>RBBP8, RIM, SCKL2, JWDS</i>	251255	Jawad syndrome	AR
29	<i>CTAGE1</i>	chr18:21948776-22948774		18q11.2	18:22914120-23026485	604124	<i>RBBP8, RIM, SCKL2, JWDS</i>	606744	Seckel syndrome 2	AR
30	<i>UBTF</i>	chr17:43735410-44735410	yes	17q21.31	17:44205032-44221625	600673	<i>UBTF, UBF, CONDBA</i>	617672	Neurodegeneration, childhood-onset, with brain atrophy	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q11.2-q24	17:27400000-72900000	154275	<i>MHS2</i>	154275	Malignant hyperthermia susceptibility 2	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q12-q21	17:33500000-52100000	601363	<i>WT4</i>	601363	Wilms tumor, type 4	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21-q22	17:39800000-59500000	608474	<i>MYP5</i>	608474	Myopia 5	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21-q22	17:39800000-59500000	168860	<i>PTLAH, FPAH</i>	168860	Patella aplasia or hypoplasia	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31-q22	17:42800000-59500000	615162	<i>MRT35</i>	615162	Mental retardation, autosomal recessive 35	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:43753730-43758787	605740	<i>SOST, VBCH, CDD, SOST1</i>	122860	Craniodiaphyseal dysplasia, AD	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:43753730-43758787	605740	<i>SOST, VBCH, CDD, SOST1</i>	269500	Sclerosteosis 1	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:43753730-43758787	605740	<i>SOST, VBCH, CDD</i>	239100	Van Buchem disease	AR



							<i>SOST1</i>			
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44004545-44009067	608300	<i>NAGS</i>	237310	N-acetylglutamate synthase deficiency	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44070699-44076343	611045	<i>G6PC3, UGRP, SCN4</i>	612541	Dursun syndrome	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44070699-44076343	611045	<i>G6PC3, UGRP, SCN4</i>	612541	Neutropenia, severe congenital 4, autosomal recessive	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44248389-44268160	109270	<i>SLC4A1, AE1, EPB3, SPH4, SAO, CHC</i>	185020	Cryohydrocytosis	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44248389-44268160	109270	<i>SLC4A1, AE1, EPB3, SPH4, SAO, CHC</i>	166900	Ovalocytosis, SA type	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44248389-44268160	109270	<i>SLC4A1, AE1, EPB3, SPH4, SAO, CHC</i>	179800	Renal tubular acidosis, distal, AD	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44248389-44268160	109270	<i>SLC4A1, AE1, EPB3, SPH4, SAO, CHC</i>	611590	Renal tubular acidosis, distal, AR	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44248389-44268160	109270	<i>SLC4A1, AE1, EPB3, SPH4, SAO, CHC</i>	612653	Spherocytosis, type 4	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44345085-44353105	138945	<i>GRN, CLN11</i>	607485	Aphasia, primary progressive	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44345085-44353105	138945	<i>GRN, CLN11</i>	614706	Ceroid lipofuscinosis, neuronal, 11	AR
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44345085-44353105	138945	<i>GRN, CLN11</i>	607485	Frontotemporal lobar degeneration with ubiquitin-positive inclusions	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44372180-44389600	607759	<i>ITGA2B, GP2B, CD41B, GT, BDPLT2, BDPLT16</i>	187800	Bleeding disorder, platelet-type, 16, AD	AD
30	<i>UBTF</i>	chr17:43735410-44735410		17q21.31	17:44372180-44389600	607759	<i>ITGA2B, GP2B, CD41B, GT, BDPLT2, BDPLT16</i>	273800	Glanzmann thrombasthenia	AR
31	<i>CACNB2</i>	chr10:17651515-18651515	yes	10p12.33-p12.31	10:18140559-18545880	600003	<i>CACNB2</i>	611876	Brugada syndrome 4	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	yes	4q22.3	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDAID</i>	112600	Brachydactyly, type A2	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	yes	4q22.3	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDAID</i>	616849	Brachydactyly, type A1, D	AD
32	<i>BMPR1B</i>	chr4:94400268-95400268	yes	4q22.3	4:94757976-95158452	603248	<i>BMPR1B, ALK6, AMDD, BDA2, BDAID</i>	609441	Acromesomelic dysplasia, Demirhan type	AR
32	<i>BMPR1B</i>	chr4:94400268-95400268		4q21-q23	4:75300000-100100000	609566	<i>PFM3</i>	609566	Parietal foramina 3	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q	8:45200000-145138636	600668	<i>CCAL1</i>	600668	Chondrocalcinosis with early-onset osteoarthritis	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q23-q24	8:105100000-145138636	140300	<i>HT</i>	140300	Hashimoto thyroiditis	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q23-q24	8:105100000-145138636	611376	<i>MGS</i>	611376	Mungan syndrome	AR
33	<i>HAS2</i>	chr8:120746834-121746834		8q24	8:116700000-145138636	600131	<i>ECA1</i>	600131	Epilepsy, childhood absence, 1	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q24	8:116700000-145138636	600669	<i>EIG1</i>	600669	Epilepsy, idiopathic generalized, susceptibility to, 1	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q24	8:116700000-145138636	601068	<i>FAME1, BAFME1, MEBA</i>	601068	Epilepsy, myoclonic, familial adult, 1	AD

33	<i>HAS2</i>	chr8:120746834-121746834		8q24.1	8:116700000-126300000	275220	<i>THM</i>	275220	Tibial hemimelia	AR
33	<i>HAS2</i>	chr8:120746834-121746834		8q24.11-q24.13	8:116700000-126300000	150230	<i>TRPS2, LGCR, LGS</i>	150230	Trichorhinophalangeal syndrome, type II	AD
33	<i>HAS2</i>	chr8:120746834-121746834		8q24.13-q24.21	8:121500000-130400000	614936	<i>PPKP1B</i>	614936	Keratoderma, palmoplantar, punctate type IB	AD
34	<i>PCSK5</i>	chr9:75624524-76624524		9q	9:43000000-138394717	607152	<i>SPG19</i>	607152	Spastic paraplegia 19, AD	AD
34	<i>PCSK5</i>	chr9:75624524-76624524		9q13-q21	9:61500000-87800000	190100	<i>GSM1, GSP</i>	190100	Geniospasm	AD
34	<i>PCSK5</i>	chr9:75624524-76624524		9q21-q22	9:65000000-99800000	611631	<i>ETL4, ETOLM</i>	611631	Epilepsy, familial temporal lobe, 4	AD
35	<i>TIMP2</i>	chr17:78360885-79360884		17q25	17:72900000-83257441	614163	<i>DSPS</i>	614163	Delayed sleep phase syndrome, susceptibility to	AD
35	<i>TIMP2</i>	chr17:78360885-79360884		17q25.1-q25.3	17:72900000-83257441	614149	<i>NDNC9</i>	614149	Nail disorder, nonsyndromic congenital, 9	AR
35	<i>TIMP2</i>	chr17:78360885-79360884		17q25.3	17:78991715-79009816	613165	<i>CANT1, SCAN1, DBQD1, EDM7</i>	617719	Epiphyseal dysplasia, multiple, 7	AR
35	<i>TIMP2</i>	chr17:78360885-79360884		17q25.3	17:78991715-79009816	613165	<i>CANT1, SCAN1, DBQD1, EDM7</i>	251450	Desbuquois dysplasia 1	AR
36	<i>ANO1</i>	chr11:69659268-70659268		11p13-q14.1	11:31000000-85900000	614344	<i>MRT23</i>	614344	Mental retardation, autosomal recessive 23	AR
36	<i>ANO1</i>	chr11:69659268-70659268		11q13	11:63600000-77400000	166750	<i>OTDD, C11DELq13, DEL11q13</i>	166750	Otodental dysplasia chromosome deletion syndrome	AD
36	<i>ANO1</i>	chr11:69659268-70659268		11q13	11:63600000-77400000	607088	<i>SMAR</i>	607088	Spinal muscular atrophy, chronic distal, autosomal recessive	AR
36	<i>ANO1</i>	chr11:69659268-70659268		11q13.3	11:69809967-69819423	164950	<i>FGF3, INT2</i>	610706	Deafness, congenital with inner ear agenesis, microtia, and microdontia	AR
36	<i>ANO1</i>	chr11:69659268-70659268		11q13.3	11:70203162-70207401	602457	<i>FADD</i>	613759	Infections, recurrent, with encephalopathy, hepatic dysfunction, and cardiovascular malformations	AR
37	<i>TNRC6B</i>	chr22:39799167-40799168		22q12-q13	22:25500000-50818468	603116	<i>CDAGS</i>	603116	CDAGS syndrome	AR
37	<i>TNRC6B</i>	chr22:39799167-40799168		22q12.3-q13.1	22:31800000-40600000	613689	<i>MDNS</i>	613689	Mammary-digital-nail syndrome	AD
37	<i>TNRC6B</i>	chr22:39799167-40799168		22q13.1	22:40346499-40387407	608222	<i>ADSL</i>	103050	Adenylosuccinase deficiency	AR
38	<i>PPP1R16B</i>	chr20:38364922-39364933		20p11.2-q13.12	20:17900000-47800000	612406	<i>DYT17</i>	612406	Dystonia-17, primary torsion	AR
38	<i>PPP1R16B</i>	chr20:38364922-39364933		20q11-q13	20:28100000-64444167	608029	<i>SCAR6, CLA3</i>	608029	Spinocerebellar ataxia, autosomal recessive 6	AR
38	<i>PPP1R16B</i>	chr20:38364922-39364933		20q12-q13.1	20:39000000-51200000	603694	<i>NIDDM3</i>	125853	Diabetes mellitus, noninsulin-dependent	AD
39	<i>NT5C1B</i>	chr2:18256017-19237522		2pter-p24		115800	<i>CTRCT29</i>	115800	Cataract 29, coralliform	AD
39	<i>NT5C1B</i>	chr2:18256017-19237522		2p25-p22		602134	<i>ETM2, ETM</i>	602134	Essential tremor, hereditary, 2	AD

39	<i>NT5C1B</i>	chr2:18256017-19237522		2p25-p12		101850	<i>PPKP3</i>	101850	Keratoderma, palmoplantar, punctate type 3	AD
39	<i>NT5C1B</i>	chr2:18256017-19237522		2p24	2:12000000-23800000	609800	<i>GEFSP4</i>	609800	Epilepsy, generalized, with febrile seizures plus, type 4	AD
40	<i>C1QTNF7</i>	chr4:14884759-15884760		4p16-p15		612335	<i>SPG38</i>	612335	Spastic paraplegia 38, AD	AD
40	<i>C1QTNF7</i>	chr4:14884759-15884760		4p15.3	4:11300000-21300000	604802	<i>HDL3, HLN2</i>	604802	Huntington disease-like 3	AR
40	<i>C1QTNF7</i>	chr4:14884759-15884760		4p15.32	4:15468659-15601970	612013	<i>CC2D2A, KIAA1345, MKS6</i>	612284	Meckel syndrome 6	AR
40	<i>C1QTNF7</i>	chr4:14884759-15884760		4p15.32	4:15468659-15601970	612013	<i>CC2D2A, KIAA1345, MKS6</i>	612285	Joubert syndrome 9	AR
40	<i>C1QTNF7</i>	chr4:14884759-15884760		4p15.32	4:15468659-15601970	612013	<i>CC2D2A, KIAA1345, MKS6</i>	216360	COACH syndrome	AR
41	<i>SNX24</i>	chr5:122494034-123494035		5q21.3-q33.2	5:105100000-156300000	608970	<i>MDBS2</i>	608970	Macular dystrophy, butterfly-shaped pigmentary, 2	AD
41	<i>SNX24</i>	chr5:122494034-123494035		5q22.1-q32	5:110200000-150400000	610535	<i>GLC1M</i>	610535	Glaucoma 1, open angle, M	AD
41	<i>SNX24</i>	chr5:122494034-123494035		5q23-q35	5:115900000-181538259	181510	<i>SCZD1</i>	181500	Schizophrenia	AD
41	<i>SNX24</i>	chr5:122494034-123494035		5q23.2	5:123089102-123194265	616982	<i>PRDM6, PRISM, PDA3</i>	617039	Patent ductus arteriosus 3	AD
41	<i>SNX24</i>	chr5:122494034-123494035		5q23.2	5:123344884-123423591	613446	<i>CEP120, CCDC100, SRTD13, JBTS31</i>	617761	Joubert syndrome 31	AR
41	<i>SNX24</i>	chr5:122494034-123494035		5q23.2	5:123344884-123423591	613446	<i>CEP120, CCDC100, SRTD13, JBTS31</i>	616300	Short-rib thoracic dysplasia 13 with or without polydactyly	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p23-p21	6:13400000-46200000	271250	<i>SCAR3, SCABD</i>	271250	Spinocerebellar ataxia, autosomal recessive 3	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p22-p21	6:15200000-46200000	600202	<i>DYX2</i>	600202	Dyslexia, susceptibility to, 2	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p22.3-p21.3	6:15200000-36600000	608244	<i>OTSC3</i>	608244	Otosclerosis 3	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	107320	<i>ATPLS</i>	107320	Antiphospholipid syndrome, familial	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	608645	<i>DFNA31</i>	608645	Deafness, AD 31	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	222100	<i>IDDM1</i>	222100	Diabetes mellitus, insulin-dependent-1	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3-p21.2	6:30500000-40500000	150270	<i>LAP</i>	150270	Laryngeal adductor paralysis	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	600089	<i>PBCA</i>	600089	Diabetes mellitus, insulin-dependent, neonatal	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	179450	<i>RWS</i>	179450	Ragweed sensitivity	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	193200	<i>VAMAS6</i>	193200	Vitiligo-associated multiple autoimmune disease susceptibility 6	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.3	6:30500000-36600000	153600	<i>WMI</i>	153600	Macroglobulinemia, Waldenstrom, susceptibility to, 1	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32393338-32408878	606000	<i>BTNL2, SS2</i>	612387	Sarcoidosis, susceptibility to, 2	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32578768-32589835	142857	<i>HLA-DRB1, SS1</i>	181000	Sarcoidosis, susceptibility to, 1	AD

42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32659463-32666688	604305	<i>HLA-DQB1, CELIAC1</i>	123400	Creutzfeldt-Jakob disease, variant, resistance to	AD
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32821832-32838822	170261	<i>TAP2, ABCB3, PSF2, RING11</i>	604571	Bare lymphocyte syndrome, type 1, due to TAP2 deficiency	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32840716-32844934	177046	<i>PSMB8, LMP7, RING10, JMP, NKJO, ALDD</i>	256040	Autoinflammation, lipodystrophy, and dermatosis syndrome	AR
42	<i>HLA-DQA1</i>	chr6:32142188-33142188		6p21.32	6:32845208-32853970	170260	<i>TAP1, ABCB2, RING4, PSF1</i>	604571	Bare lymphocyte syndrome, type 1	AR
43	<i>PLEKHA1</i>	chr10:121909427-122909426		10q26	10:117300000-133797422	615163	<i>CORD17</i>	615163	Cone-rod dystrophy 17	AD
43	<i>PLEKHA1</i>	chr10:121909427-122909426		10q26	10:117300000-133797422	609625	<i>DEL10q26, C10q26DEL</i>	609625	Chromosome 10q26 deletion syndrome	AD
43	<i>PLEKHA1</i>	chr10:121909427-122909426		10q26.13	10:122461524-122514907	602194	<i>HTRA1, PRSSI1, ARMD7, CARASIL, CADASIL2</i>	600142	CARASIL syndrome	AR
43	<i>PLEKHA1</i>	chr10:121909427-122909426		10q26.13	10:122461524-122514907	602194	<i>HTRA1, PRSSI1, ARMD7, CARASIL, CADASIL2</i>	616779	Cerebral arteriopathy, AD, with subcortical infarcts and leukoencephalopathy, type 2	AD
45	<i>HLX</i>	chr1:220393031-221393031		1q31-q42	1:185800000-236400000	145260	<i>PHA2A, PHA2</i>	145260	Pseudohypoaldosteronism, type IIA	AD
45	<i>HLX</i>	chr1:220393031-221393031		1q41-q44	1:214400000-248956422	615589	<i>OTSC10</i>	615589	Otosclerosis 10	AD
45	<i>HLX</i>	chr1:220393031-221393031		1q41	1:214400000-223900000	600332	<i>RMD1</i>	600332	Rippling muscle disease-1	AD
45	<i>HLX</i>	chr1:220393031-221393031		Chr.1		108420	<i>SPGF2, ASG</i>	108420	Spermatogenic failure 2	AD
46	<i>EDEMI</i>	chr3:5302151-6302149		3pter-p25		613792	<i>DEL3pterp25, C3DELpterp25</i>	613792	3p- syndrome	AD
46	<i>EDEMI</i>	chr3:5302151-6302149		3p26		609299	<i>HPC5</i>	176807	Prostate cancer, hereditary, 5	AD
46	<i>EDEMI</i>	chr3:5302151-6302149		3p26-p24.2		252350	<i>MYMY1, MYMY</i>	252350	Moyamoya disease	AR
47	<i>LTBP1</i>	chr2:32636358-33636358		2p25-p22		602134	<i>ETM2, ETM</i>	602134	Essential tremor, hereditary, 2	AD
47	<i>LTBP1</i>	chr2:32636358-33636358		2p25-p12		101850	<i>PPKP3</i>	101850	Keratoderma, palmoplantar, punctate type 3	AD
47	<i>LTBP1</i>	chr2:32636358-33636358		2p22.3-p21	2:31800000-47500000	114580	<i>CANDFI, CMCT</i>	114580	Candidiasis, familial, 1, AD	AD
48	<i>STARD13</i>	chr13:32653468-33653468		13q13-q14.3	13:31600000-54700000	600631	<i>ENURI</i>	600631	Enuresis, nocturnal, 1	AD
48	<i>STARD13</i>	chr13:32653468-33653468		13q13.1	13:31600000-33400000	612089	<i>HPRHP</i>	612089	Hypophosphatemic rickets and hyperparathyroidism	AD
49	<i>PLASI</i>	chr15:67446124-68446123		15q	15:19000000-101991189	214900	<i>LCSI, CHLS</i>	214900	Cholestasis-lymphedema syndrome	AR
49	<i>PLASI</i>	chr15:67446124-68446123		15q23	15:68206991-68229741	606725	<i>CLN6, CLN4A</i>	204300	Ceroid lipofuscinosis, neuronal, Kufs type, adult onset	AR
49	<i>PLASI</i>	chr15:67446124-68446123		15q23	15:68206991-68229741	606725	<i>CLN6, CLN4A</i>	601780	Ceroid lipofuscinosis, neuronal, 6	AR

51	<i>TRPS1</i>	chr8:115076317-116076321	<b>yes</b>	8q23.3	8:115408495-115669636	604386	<i>TRPS1</i>	190351	Trichorhinophalangeal syndrome, type III	AD
51	<i>TRPS1</i>	chr8:115076317-116076321	<b>yes</b>	8q23.3	8:115408495-115669636	604386	<i>TRPS1</i>	190350	Trichorhinophalangeal syndrome, type I	AD
51	<i>TRPS1</i>	chr8:115076317-116076321		8q	8:45200000-145138636	600668	<i>CCAL1</i>	600668	Chondrocalcinosis with early-onset osteoarthritis	AD
51	<i>TRPS1</i>	chr8:115076317-116076321		8q13-q23	8:65100000-116700000	607731	<i>CMT2H</i>	607731	Charcot-Marie-Tooth disease, axonal, type 2H	AR
51	<i>TRPS1</i>	chr8:115076317-116076321		8q23-q24	8:105100000-145138636	140300	<i>HT</i>	140300	Hashimoto thyroiditis	AD
51	<i>TRPS1</i>	chr8:115076317-116076321		8q23-q24	8:105100000-145138636	611376	<i>MGS</i>	611376	Mungan syndrome	AR

### Supplementary Table 20: eQTL analysis

This table shows diverticular disease candidate SNPs (SNPs which are in LD of any independent lead SNPs) with a GWAS p-value  $<1.0 \times 10^{-5}$ ,  $MAF > 0.01$  that affect gene expression of candidate genes in sigmoid colon tissue (FDR  $< 0.05$  eQTL, GTEx\_V7 database) as a potential indicator of functional implications. The following table headers are used: DiscoveryLocus: risk locus assignment as in Supplementary Table 1; rsID : rsID based on dbSNP build 146; chr : chromosome; pos : position on hg19; effect\_allele : Effect/risk allele; MAF : Minor allele frequency computed based on 1000G; gwasP : P-value from BOLT GWAS summary statistics; Gene expression of eQTL Genes marked with an asterisk were analysed for differential expression in controls (Supplementary Table 9) and for phenotype-specific expression in anatomical layers of the colon (Supplementary Table 10).

DiscoveryLocus	rsID	chr	pos	effect_allele	MAF	gwasP	eQTL Genes	p_eQTL	FDR<0.05_eQTL
3	rs10828815	10	25811764	T	0.3608	6.8e-13	<i>GPR158*</i>	8.58539e-10	1.5105e-05
5	rs1946545	2	56036435	A	0.2078	2.0e-06	<i>RPS27A</i>	1.06267e-05	0.0081485
7	rs12976534	19	38743962	A	0.495	2.3e-16	<i>PPP1R14A*</i>	5.45618e-39	4.70966e-32
7	rs35436012	19	38790635	A	0.3509	8.4e-07	<i>C19orf33</i>	1.1182e-05	5.55572e-09
8	rs505922	9	136149229	T	0.3678	4.5e-15	<i>ABO*</i>	1.99858e-13	4.33873e-09
14	rs34112166	8	120400532	G	0.1839	2.6e-11	<i>NOV*</i>	2.26152e-11	5.04956e-07
23	rs6684114	1	151928715	A	0.3052	8.4e-09	<i>THEM4</i>	1.35854e-07	4.42843e-06
23	rs3791153	1	151958144	A	0.2863	3.9e-11	<i>S100A10*</i>	1.51883e-06	0.00173914
25	rs2289328	15	40705417	G	0.1491	7.5e-11	<i>DISP2*</i>	3.74554e-25	3.49097e-19
26	rs9217	17	7363088	T	0.3419	2.2e-10	<i>CHRNBI</i>	2.61112e-09	5.01543e-12
27	rs2120109	15	76900654	C	0.3042	6.9e-07	<i>SCAPER*</i>	7.58033e-18	1.3597e-12
27	rs2120109	15	76900654	C	0.3042	6.9e-07	<i>RP11-593F23.1</i>	8.83622e-07	2.03633e-06
30	rs228768	17	42191893	G	0.2992	6.2e-06	<i>ASB16-AS1</i>	8.99607e-06	0.0239413
38	rs208817	20	37492316	C	0.4672	1.3e-06	<i>FAM83D</i>	4.37967e-06	2.96537e-19
41	rs62377399	5	122324679	G	0.3191	4.8e-08	<i>RN7SL689P (pseudogene)</i>	1.02254e-10	5.28914e-07
42	rs9268614	6	32402778	T	0.2018	9.5e-08	<i>HLA-DRB6</i>	1.6391e-15	1.21805e-26
42	rs1281935	6	32583820	G	0.05268	1.9e-06	<i>HLA-DQA2</i>	5.40847e-07	1.5472e-31
42	rs3997872	6	32580617	T	0.1551	1.6e-06	<i>HLA-DRB1</i>	8.83716e-07	5.66271e-06
42	rs7990	6	32609965	C	0.06859	1.4e-08	<i>BAG6</i>	3.96831e-05	1.68144e-07
42	rs1281947	6	32592009	A	0.1551	1.3e-06	<i>HLA-DOB</i>	2.69839e-05	9.2768e-19
45	rs2738750	1	221050400	G	0.4722	5.1e-07	<i>RP11-295M18.2</i>	1.03776e-05	7.18793e-16

***Supplementary Table 21: Potential functional implications of candidate SNPs associated with diverticular disease (by CADD score >12.37 in descending order)***

This table shows diverticular disease candidate SNPs (SNPs which are in LD of any independent lead SNPs) with a GWAS p-value  $<1.0 \times 10^{-5}$ , MAF>0.01 and CADD score >12.37 in descending order by Combined Annotation-Dependent Depletion (CADD) score as a potential indicator of functional implications, correspondingly all exonic nonsynonymous SNPs are shown. The following table headers are used: uniqID: Unique ID of SNPs consisting of chr:position:allele1:allele2 where alleles are alphabetically ordered; rsID : rsID based on dbSNP build 146; chr : chromosome; pos : position on hg19; effect\_allele : Effect/risk allele ; non\_effect\_allele : Non-effect/non-risk ; MAF : Minor allele frequency computed based on 1000G; gwasP : P-value provided in the input GWAS summary statistics file; r2 : The maximum r2 of the SNP with one of the independent significant SNPs; IndSigSNP: rsID of the independent significant SNP which has the maximum r2 with the SNP; Genomic locus : Index of the genomic risk loci matching with "Genomic risk loci" Supplementary Table 5; nearestGene: The nearest Gene of the SNP based on ANNOVAR annotations; ANNOVAR annotates "consequence" function by prioritizing the most deleterious annotation for SNPs which are locating a genomic region where multiple genes are overlapped. Genes are encoded in symbol, if it is available otherwise Ensembl ID. Genes include all transcripts from Ensembl gene build 85 including non-protein coding genes and RNAs. CCG: manually selected curated candidate gene at risk locus (NCBI RefSeq annotation); CCG (replicating): nominal replication ( $P<0.05$ ) of lead SNP from PCG in European replication cohorts; dist : Distance to the nearest gene. SNPs which are locating in the gene body or 1kb up- or down-stream of TSS or TES have 0. func: Functional consequence of the SNP on the gene obtained from ANNOVAR. For exonic SNPs, detailed annotation (e.g. non-synonymous, stop gain and so on) is available in the ANNOVAR table (annov.txt). CADD: CADD score which is computed based on 63 annotations. The higher the score, the more deleterious the SNP is. 12.37 is the suggested threshold by Kircher et al (2014). RDB : RegulomeDB score which is a categorical score (from 1a to 7). 1a is the highest score for SNPs with the most biological evidence to be a regulatory element. minChrState : The minimum 15-core chromatin state across 127 tissue/cell type.

***References used in Supplementary Table 21***

Kircher M, Witten DM, Jain P, O'Roak BJ, Cooper GM, Shendure J. A general framework for estimating the relative pathogenicity of human genetic variants. *Nat Genet.* 2014 Mar;46(3):310-5.

DiscoveryLocus	top_lead_SNP_uniqid	unqid	#candidate SNPs	unqid	chr	pos	non_effect_allele	effect_allele	MAF	gwasP	r2	IndigSNP	nearestGene (Ensembl/Genecode annotation)	CCG	CCG (replication)	dist	func	exonic_function	CADD	RDB	minChrState
15	21:47545768.A.G	n1024731		21:47545768.A.G	21	47545768	A	G	0.4901	1.6e-08	0.944457	n108443991	COL4A2	COL4A2	0	exonic	nononymous SNV	25.8	4	3	
16	7:73474825.C.G	n17034066		7:73474825.C.G	7	73474825	C	G	0.09145	2.6e-06	0.7485771	n10851722	ELN	ELN	0	exonic	nononymous SNV	23.2	2b	2	
15	11:70034096.A.G	n1740722		11:70034096.A.G	11	70034096	A	G	0.2152	9.2e-07	0.760705	n1781659	ANO1	ANO1	0	exonic	nononymous SNV	22.9	NA	4	
30	17:42254417.A.G	n1721884		17:42254417.A.G	17	42254417	A	G	0.2714	1.3e-07	0.780694	17:42260315	AT A	ASB16	0	exonic	nononymous SNV	22.8	4	4	
1	2:44313821.A.G	n14313821		2:44313821.A.G	2	44313821	A	G	0.2406	5.9e-09	0.892071	n15651342	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	21.4	7	1
32	4:95747824.C.CAG	n15717456		4:95747824.C.CAG	4	95747824	C	CAG	0.4344	1.1e-07	0.720994	n12023834	BMPR1B	BMPR1B	0	intronic	NA	22.2	NA	5	
29	18:20037597.A.G	n1811327		18:20037597.A.G	18	20037597	A	G	0.2813	1.1e-08	0.89517	n19960286	CTAGE1	CTAGE1	0	intronic	NA	21.6	6	2	
1	3:14316027.C.T	n11113111		3:14316027.C.T	3	14316027	C	T	0.5111	1.4e-07	0.93422	n17632242	COL4	COL4	0	intronic	downstream	NA	21.4	7	1
1	2:14440711.C.CAG	n18084337		2:14440711.C.CAG	2	14440711	C	CAG	0.3111	2.6e-28	0.957179	n1179600	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	21.3	NA	4
15	15:7647155.A.G	n1259378		15:7647155.A.G	15	7647155	A	G	0.4563	5.4e-07	0.648184	n167306087	SCAPER	SCAPER	0	intronic	NA	21.1	4	5	
19	15:82829047.C.T	n18202423		15:82829047.C.T	15	82829047	C	T	0.327	6.82e-09	0.92722	n158816702	PIAS1	PIAS1	0	ncRNA	intronic	NA	19.79	NA	4
1	2:14428793.C.T	n17607879		2:14428793.C.T	2	14428793	C	T	0.1809	9.8e-54	0.972062	n17833637	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	20.6	5	4
34	9:78729313.C.T	n1571791		9:78729313.C.T	9	78729313	C	T	0.4066	1.6e-07	0.658707	n147466465	PCSK5	PCSK5	0	intronic	NA	20.5	4	2b	
16	7:73474811.C.T	n17034169		7:73474811.C.T	7	73474811	C	T	0.09149	1.1e-10	0.692238	n112620918	ELN	ELN	0	intronic	intergenic	NA	20.4	5	2
22	11:15066117.C.T	n17482964		11:15066117.C.T	11	15066117	C	T	0.2386	2.0e-10	0.977352	n157909118	CALCB	CALCB	0	intronic	NA	20.4	5	7	
15	8:11633907.A.G	n1254798		8:11633907.A.G	8	11633907	A	G	0.4394	4.9e-07	0.862341	n12049865	TRP51	TRP51	0	intronic	NA	20.4	4	5	
39	2:18800499.A.G	n1761186		2:18800499.A.G	2	18800499	A	G	0.4561	1.1e-07	0.895951	n161125298	NTSC1	NTSC1	0	intronic	intergenic	NA	20.4	5	2
10	13:10790049.A.G	n11636947		13:10790049.A.G	13	10790049	A	G	0.2326	2.3e-14	0.94039	n19520339	FAM155A	FAM155A_1	0	intronic	NA	19.98	6	5	
15	15:76513004.A.G	n1291602		15:76513004.A.G	15	76513004	A	G	0.4672	2.4e-07	0.697262	n17306087	SCAPER	SCAPER	0	intronic	intergenic	NA	19.85	5	2
7	11:27747671.A.G	n12288512		11:27747671.A.G	11	27747671	A	G	0.1799	1.3e-16	1	n17309930	BDNF	BDNF	0	ncRNA	intronic	NA	19.83	5	13
1	2:144281981.T.A	2:144281981.T.A		2:144281981.T.A	2	144281981	T	A	0.3819	4.4e-53	0.979119	n16734367	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	19.79	NA	4
11	11:5081335.A.G	n1082349		11:5081335.A.G	11	5081335	A	G	0.2376	2.0e-10	0.98272	n157909118	CALCB	CALCB	0	intronic	NA	19.67	5	13	
51	8:116576827.C.T	n1808448		8:116576827.C.T	8	116576827	C	T	0.4225	1.8e-06	0.938423	n12049865	TRP51	TRP51	0	intronic	NA	19.65	5	1	
1	2:14433991.C.G	n11685583		2:14433991.C.G	2	14433991	C	G	0.2036	3.7e-09	0.897371	n156151621	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	19.29	6	1
5	2:56196423.C.T	n1672496		2:56196423.C.T	2	56196423	C	T	0.3767	1.3e-06	0.789972	2:56191019	TA T	EFEMP1	0	ncRNA	intronic	NA	19.13	5	5
19	6:98345853.A.T	n16006737		6:98345853.A.T	6	98345853	A	T	0.4861	1.5e-07	0.663977	n19482094	RPL13A3023.1	LOC101927314 (RPL13A3023.1)	0	ncRNA	intronic	NA	19.06	6	14
5	5:15227293.C.G	n19004		5:15227293.C.G	5	15227293	C	G	0.3191	7.9e-08	0.958361	n15651342	SNQ2	SNQ2	0	intronic	NA	18.94	7	2	
5	2:56004219.G.T	n1675291		2:56004219.G.T	2	56004219	G	T	0.2157	8.3e-06	0.681429	n15985553	PMP1	EFEMP1	0	intronic	NA	18.85	5	5	
6	11:27748493.A.C	n17309930		11:27748493.A.C	11	27748493	A	C	0.1799	6.8e-17	1	n17309930	BDNF	BDNF	0	ncRNA	intronic	NA	18.82	5	13
21	5:6811896.C.T	n15111833		5:6811896.C.T	5	6811896	C	T	0.4541	1.98e-07	0.901349	n158816702	CWC27	CWC27	0	intronic	intergenic	NA	18.8	6	5
18	18:20037576.A.G	n1811326		18:20037576.A.G	18	20037576	A	G	0.2714	6.5e-10	0.979309	n19960286	CTAGE1	CTAGE1	0	intronic	NA	18.8	6	2	
19	8:120419182.G.T	n1370146		8:120419182.G.T	8	120419182	G	T	0.2849	1.3e-11	0.729943	n108089342	NOV	NOV	0	intronic	NA	18.75	7	2	
34	17:4236442.C.T	n11080007		17:4236442.C.T	17	4236442	C	T	0.2714	1.3e-07	0.780694	17:42260315	AT A	UHRF1	0	intronic	NA	18.7	11	1	
40	9:78729176.A.T	n17037190		9:78729176.A.T	9	78729176	A	T	0.4066	1.3e-07	0.658707	n147466465	PCSK5	PCSK5	0	intronic	NA	18.7	9	5	
44	10:105615074.C.T	n105615074		10:105615074.C.T	10	105615074	C	T	0.3082	2.1e-07	0.617447	n13752946	SHPRX2A	SHPRX2A	0	UTRS	NA	18.66	4	1	
21	5:64322590.A.G	n1271000		5:64322590.A.G	5	64322590	A	G	0.2008	1.2e-09	0.915996	n10471561	CWC27	CWC27	0	intronic	intergenic	NA	18.59	5	2
17	17:42426033.C.T	n1207464		17:42426033.C.T	17	42426033	C	T	0.2992	8.0e-09	0.901349	17:42260315	AT A	ARHGAP15	0	ncRNA	intronic	NA	18.59	11	1
1	2:144281981.A.C	n10928184		2:144281981.A.C	2	144281981	A	C	0.2376	1.4e-09	0.942787	n15651342	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	18.55	4	4
5	2:56176031.C.T	n1422809		2:56176031.C.T	2	56176031	C	T	0.3648	2.0e-06	0.737992	2:56191019	TA T	EFEMP1	0	intronic	NA	18.53	5	1	
1	8:1165197691.C.G	n1808428		8:1165197691.C.G	8	1165197691	C	G	0.1904	1.9e-07	0.855119	n12049865	TRP51	TRP51	0	intronic	intergenic	NA	18.1	6	5
7	7:102574999.T.TGAA	n102574999		7:102574999.T.TGAA	7	102574999	T	TGAA	0.3602	4.1e-06	0.739485	n12531428	FBX13	FBX13	0	exonic	nonframeshift substitution	18.49	NA	1	
1	2:144342661.C.T	n10179961		2:144342661.C.T	2	144342661	C	T	0.3799	5.1e-54	0.910202	n16734367	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	18.46	5	4
1	5:122301079.C.T	n19001		5:122301079.C.T	5	122301079	C	T	0.3191	1.6e-08	0.958361	n15651342	SNQ2	SNQ2	0	intronic	NA	18.4	7	2	
1	2:144178400.C.T	n12612084		2:144178400.C.T	2	144178400	C	T	0.1797	1.4e-08	1	n12612084	ARHGAP15	ARHGAP15	0	ncRNA	intronic	NA	18.34	5	4
13	8:12043892.C.T	n17188373		8:12043892.C.T	8	12043892	C	T	0.1839	1.8e-11	0.738269	n108089342	NOV	NOV	0	ncRNA	intronic	NA	18.22	5	5
42	6:12349086.C.T	n1204865		6:12349086.C.T	6	12349086	C	T	0.3208	8.0e-07	0.859362	6:12327713	GGA4A_G	HC23	0	intronic	intergenic	NA	18.01	6	5
33	8:12259446.C.G	n1870765		8:12259446.C.G	8	12259446	C	G	0.2744	1.9e-09	0.959159	n1871180	HAS2	HAS2	0	intronic	NA	18.09	4	5	
14	8:12042084.A.T	n17307983		8:12042084.A.T	8	12042084	A	T	0.1849	1.1e-11	0.729943	n108089342	NOV	NOV	0	intronic	NA	18.07	6	5	
3	10:15797906.C.G	n1478908		10:15797906.C.G	10	15797906	C	G	0.2518	1.2e-12	0.696320	n1514942	GPR158	GPR158	0	intronic	NA	17.95	8	2	
3	17:42287519.C.T	n1071167		17:42287519.C.T	17	42287519	C	T	0.2416	9.2e-08	0.606127	17:42260315	AT A	UHRF1	0	exonic	synonymous SNV	17.93	NA	2	
44	10:10564370.T.TC	n1760414699		10:10564370.T.TC	10	10564370	T	TC	0.4622	8.6e-07	0.781138	n13752946	OBFC1	STN1 (OBFC1)	0	intronic	NA	17.91	NA	4	
15	15:82829047.C.T	n18202423		15:82829047.C.T	15	82829047	C	T	0.4712	1.4e-06	0.816743	n1873055	PIAS1	PIAS1	0	intronic	NA	17.87	12	1	
49	6:98361770.C.T	n1693598		6:98361770.C.T	6	98361770	C	T	0.4861	1.4e-06	0.620257	n19482094	RPL13A3023.1	LOC101927314 (RPL13A3023.1)	0	ncRNA	intronic	NA	17.85	NA	4
13	13:108216200.A.G	n1697078		13:108216200.A.G	13	108216200	A	G	0.1909	3.7e-13	0.925441	n19555371	FAM155A	FAM155A_2*	0	intronic	NA	17.74	4	4	
28	7:96171818.C.G	n1671920		7:96171818.C.G	7	96171920	C	G	0.3539	3.6e-08	1	n14752920	SCAPER	SCAPER	0	intronic	NA	17.74	6	14	
41	5:122146272.C.T	n12821387		5:122146272.C.T	5	122146272	C	T	0.46175	1.3e-06	0.91324965	SNQ2	SNQ2	0	intronic	NA	17.74	6	14		
1	2:144337590.C.T	n102574999		2:144337590.C.T	2	144337590	C	T	0.1839	4.6e-12	1	2:144437590	TAAAGAAAAA	EFEMP1	0	ncRNA	intronic	NA	17.58	NA	5
40	1:415379502.C.T	n1455387		1:415379502.C.T	4	15379502	C	T	0.2744	1.6e-08	0.889751	n14321788	C12orf77	C12orf77	0	ncRNA	intronic	NA	17.42	5	1
1	22:40951312.A.T	n12821387		22:40951312.A.T	22	40951312	A	T	0.3161	1.4e-07	0.900372	n1606103	TNRC8	TNRC8	0	intronic	intergenic	NA	17.42	5	1
6	11:27748493.C.T	n17309930		11:27748493.C.T	11	27748493	C	T	0.1799	1.2e-16	1	n17309930	BDNF	BDNF	0	nc					



13	10.101382252-A.C	rs4919369	10.101382252-A.C	10	10138252-A	C	0.1203	1.2e-13	1	rs709832	ENSG00000260475	SUC2A28	LOC101927314 (RP11-436023.1)	0	downstream	NA	14.62	5	1			
14	6.9849418-C.T	rs11194230	6.9849418-C.T	6	9849418-T	T	0.4404	1.5e-06	0.6678	rs0482094				0	ncRNA, intronic	NA	14.61	7	5			
15	10.124070803-C.T	rs7081388	10.124070803-C.T	10	12407083-T	C	0.0646	3.7e-06	0.6948	rs12416882	TTATGATGGAGATAA T	P2RY12	LOC101927314 (RP11-436023.1)	0	ncRNA, intronic	NA	14.61	7	5			
19	3.15100558-A.G	rs859584	3.15100558-A.G	3	15100558-A	A	0.1879	4.5e-10	0.99345	3.1510061411_ACAT_A	MDJL2	P2RY12	LOC101927314 (RP11-436023.1)	0	intronic	NA	14.56	7	5			
21	2.14434705-C.T	rs11892829	2.14434705-C.T	2	14437805-T	T	0.2316	4.5e-09	0.89138	rs06151632	ARRGAP15	ARRGAP15		0	ncRNA, intronic	NA	14.48	7	4			
22	8.122205445-G.T	rs122205445-G.T	8.122205445-G.T	8	12220544-G	G	0.2074	1.1e-09	0.8717	rs0471180	HA2			0	intronic	NA	14.47	7	4			
15	2.14745426-C.T	rs13046626	2.14745426-C.T	21	4745426-T	C	0.4891	1.8e-08	0.94107	rs108443991	COL6A2	COL6A1	LOC101927314 (RP11-436023.1)	0	exonic	synonymous SNV	14.44	5	3			
40	4.15372325-A.G	rs4076789	4.15372325-A.G	4	15372325-A	A	0.2744	2.3e-08	0.959335	rs4132788	C10TNF7	C10TNF7		0	ncRNA, intronic	NA	14.42	6	5			
9	7.10259417-C.T	rs10620124	7.10259417-C.T	7	10259417-T	T	0.3191	2.1e-10	0.8191	rs142441296	FBXL3	FBXL3		0	intronic	NA	14.39	7	4			
30	17.42191893-G.T	rs272878	17.42191893-G.T	17	42191893-T	C	0.2992	6.2e-06	0.62877	rs176816	URF1	URF1		0	intronic	NA	14.35	NA	4			
32	4.9585396-C.T	rs1775209	4.9585396-C.T	4	9585396-T	T	0.4496	6.2e-06	0.766329	rs2023834	BMPRI8	BMPRI8		0	intronic	NA	14.24	4	2			
42	6.12349772-C.T	rs1304855	6.12349772-C.T	6	1234977-T	C	0.3108	6.5e-06	0.85086	6.12349773_GAAA_G	HC23	HC23		0	intronic	NA	14.22	5	5			
1	2.14431002-A.G	rs1092186	2.14431002-A.G	2	14431002-A	G	0.2416	2.0e-09	0.95267	rs05161632	ARRGAP15	ARRGAP15		0	ncRNA, intronic	NA	14.19	6	2			
51	8.116559435-A.G	rs1808434	8.116559435-A.G	8	116559435-G	A	0.4324	1.8e-06	0.89406	rs2049865	TRPS1	TRPS1		0	intronic	NA	14.18	7	4			
15	11.71711381-A.G	rs10114814	11.71711381-A.G	11	71711381-A	A	0.2903	3.8e-05	0.76615	rs0621269	BMP6	BMP6	LOC101927314 (RP11-436023.1)	0	ncRNA, intronic	NA	14.17	NA	4			
17	15.76609733-C.T	rs17669733-C.T	15.76609733-C.T	15	76609733-C	CT	0.4732	6.9e-08	0.64508	rs2056544	SCAPER	SCAPER		0	intronic	NA	14.16	NA	4			
51	5.122224118-A.ACA	rs174811825	5.122224118-A.ACA	5	122224118-A	A	ACATTCTGTGGCTG	0.3201	1.4e-07	0.959971	rs14120495	SNZ24		0	intronic	NA	14.15	NA	1			
41	2.3381425-A.G	rs1745466	2.3381425-A.G	2	3381425-G	A	0.2932	2.4e-08	1	rs0714546	URF1	URF1		0	intronic	NA	14.12	5	1			
5	2.56029071-A.C	rs1344732	2.56029071-A.C	2	56029071-A	C	0.2734	8.2e-08	0.61728	rs0989551	EFEMP1	EFEMP1		0	intronic	NA	14.09	7	5			
27	17.42229015-A.G	rs255918	17.42229015-A.G	17	42229015-A	G	0.2406	3.0e-07	0.60172	17.42236016_AT_A			ENSG00000067394	0	ncRNA, intronic	NA	14.08	NA	3			
27	15.7678314-A.C	rs17012597	15.7678314-A.C	15	7678314-A	C	0.327	9.4e-08	0.667499	rs2056544	SCAPER	SCAPER		0	intronic	NA	14.06	6	4			
27	15.76601871-A.G	rs1786126	15.76601871-A.G	15	76601871-G	A	0.4602	3.3e-07	0.684584	rs07380897	ETFA	SCAPER		0	intronic	NA	14.03	7	5			
19	6.98326220-GC	rs08326220-GC	6.98326220-GC	6	98326220-G	GC	0.4891	7.8e-08	0.650261	rs0482094	TRPS1	TRPS1	LOC101927314 (RP11-436023.1)	0	ncRNA, intronic	NA	14.02	NA	5			
51	8.116481498-C.G	rs1080878	8.116481498-C.G	8	116481498-C	G	0.4584	6.2e-06	0.81799	rs2049865	TRPS1	TRPS1	LOC101927314 (RP11-436023.1)	0	intronic	NA	13.94	5	5			
19	6.9832682-A.C	rs0832682-A.C	6.9832682-A.C	6	9832682-A	C	0.4891	7.0e-08	0.650261	rs0482094	TRPS1	TRPS1	LOC101927314 (RP11-436023.1)	0	ncRNA, intronic	NA	13.9	7	5			
38	20.37493576-A.G	rs208814	20.37493576-A.G	20	37493576-G	A	0.3827	5.0e-09	1	rs208814	PPP1R16B	PPP1R16B		0	intronic	NA	13.86	NA	2			
17	15.77082234-A.T	rs15710279	15.77082234-A.T	15	77082234-A	T	0.3052	5.8e-07	0.60706	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.85	6	4			
8	8.120542085-A.G	rs120542085-A	8.120542085-A.G	8	120542085-A	G	0.2137	1.3e-11	1	rs12171427	NOV	NOV		0	intronic	NA	13.83	6	5			
1	2.144186475-C.T	rs4662330	2.144186475-C.T	2	144186475-T	T	0.159	6.8e-06	0.80828	rs0736460	ARRGAP15	ARRGAP15		0	ncRNA, intronic	NA	13.82	2b	5			
1	15.7713322-A.C	rs1633869	15.7713322-A.C	15	7713322-C	A	0.3101	4.3e-07	0.625162	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.79	17	4			
16	17.7392141-A.G	rs1168077	17.7392141-A.G	17	7392141-A	G	0.3187	6.1e-09	0.81887	rs1204287	CALCB	CALCB		0	intronic	NA	13.79	7	4			
13	8.116381869-A.G	rs1963677	8.116381869-A.G	8	116381869-A	G	0.4225	1.6e-06	0.93823	rs2048065	TRPS1	TRPS1		0	intronic	NA	13.73	7	5			
10	10.10138191-A.T	rs1033214	10.10138191-A.T	10	10138191-T	A	0.1103	1.0e-13	1	rs709832	SUC2A28			6516	intronic	NA	13.72	6	5			
13	1.151160384-A.G	rs17011374	1.151160384-A.G	1	151160384-G	A	0.2799	4.3e-10	0.879183	rs16314883	STROBP3	STROBP3	S100A10	0	intronic	NA	13.71	7	5			
27	15.76404151-A.G	rs7161397	15.76404151-A.G	15	7640415-G	A	0.496	1.7e-08	0.72856	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.7	7	5			
20	3.151070692-C.T	rs10915839	3.151070692-C.T	3	151070692-T	C	0.3688	8.6e-11	0.974163	rs1723760	MDJL2.P2RY12	P2RY12		0	intronic	NA	13.69	7	5			
41	4.1538354-C.T	rs1488081	4.1538354-C.T	4	1538354-T	C	0.3628	2.4e-06	0.65216	rs1432788	C10TNF7	C10TNF7		0	ncRNA, intronic	NA	13.69	5	5			
22	11.15094191-C.T	rs1540139	11.15094191-C.T	11	1509419-T	C	0.2994	1.0e-09	0.87062	rs275909118	CALCB	CALCB		0	intronic	NA	13.6	2b	5			
31	10.18431986-A.G	rs1547776	10.18431986-A.G	10	18431986-A	G	0.2913	3.0e-09	0.682766	rs1888693	CANCR2	CANCR2		0	intronic	NA	13.67	4	4			
27	15.76531588-A.G	rs2020246	15.76531588-A.G	15	76531588-A	G	0.2465	1.3e-07	0.86267	rs2398697	TYROBP	SCAPER		0	ncRNA, exonic	NA	13.67	5	4			
27	2.22104985-A.T	rs22104985-A.T	2.22104985-A.T	2	22104985-T	T	0.3999	2.2e-07	0.74908	rs26216188	TM6B	TM6B		0	intronic	NA	13.66	5	5			
23	2.18690155-A.C	rs4832623	2.18690155-A.C	2	18690155-A	C	0.1441	4.3e-07	0.80856	rs62121298	NTS1B	NTS1B		0	downstream	NA	13.57	5	4			
18	18.20015171-C.T	rs12607091	18.20015171-C.T	18	20015171-T	C	0.2614	5.4e-10	0.99503	rs0960286	CTAGE1	CTAGE1		0	intronic	NA	13.56	2a	5			
18	18.20021891-C.T	rs0962129	18.20021891-C.T	18	2002189-T	C	0.2614	5.4e-10	0.99503	rs0960286	CTAGE1	CTAGE1		0	intronic	NA	13.54	2a	5			
1	2.14433705-C.G	rs10167657	2.14433705-C.G	2	14433705-T	C	0.2806	5.0e-09	0.807371	rs06151632	ARRGAP15	ARRGAP15		0	ncRNA, intronic	NA	13.54	6	5			
23	1.151911254-A.G	rs0687632	1.151911254-A.G	1	151911254-G	A	0.2793	4.4e-10	0.879183	rs06151632	KRTBP28	S100A10		10745	intronic	NA	13.51	7	5			
8	8.120517384-A.G	rs1058193	8.120517384-A.G	8	120517384-G	A	0.2148	2.3e-10	0.85811	rs17317427	NOV	NOV		0	intronic	synonymous SNV	13.46	NA	4			
18	18.20015273-C.T	rs2728667	18.20015273-C.T	18	20015273-T	C	0.2614	5.3e-10	0.99503	rs0960286	CTAGE1	CTAGE1		0	intronic	NA	13.43	4	5			
17	15.7714295-C.T	rs2592686	15.7714295-C.T	15	7714295-T	C	0.3101	4.7e-07	0.625162	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.43	7	4			
5	2.56138091-A.C	rs1790640	2.56138091-A.C	2	56138091-A	C	0.2449	1.7e-10	0.974073	2.56138103_TTGATCTGGGCTCCCTCC-T	EFEMP1	EFEMP1		0	intronic	NA	13.4	7	4			
51	8.116560967-A.G	rs1808436	8.116560967-A.G	8	116560967-G	A	0.4324	1.9e-06	0.89406	rs2048065	TRPS1	TRPS1		0	intronic	NA	13.38	6	4			
4	3.15502681-G.T	rs7609987	3.15502681-G.T	3	15502681-T	G	0.2416	5.6e-22	1	rs7609987	COLQ	COLQ		0	intronic	NA	13.37	4	4			
41	5.12234920-A.G	rs0591618	5.12234920-A.G	5	12234920-G	A	0.339	2.7e-06	0.873483	rs14120495	SNZ24	SNZ24		0	intronic	NA	13.37	7	5			
8	7.10250063-C.T	rs1254384	7.10250063-C.T	7	10250063-T	C	0.1392	2.9e-07	0.78767	rs2573428	FBXL3	FBXL3		0	intronic	NA	13.33	6	5			
15	15.7680083-C.T	rs204856	15.7680083-C.T	15	7680083-T	C	0.3489	1.8e-08	0.931394	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.28	NA	5			
22	11.5306582-A.TT	rs115306582-A.TT	11.5306582-A.TT	11	5306582-A	T	0.2425	2.8e-10	0.95461	rs75999118	CALCB	CALCB		0	intronic	NA	13.27	NA	14			
22	15.7716461-C.T	rs4122776	15.7716461-C.T	15	7716461-T	C	0.3162	6.6e-07	0.840761	rs2056544	SCAPER	SCAPER		0	intronic	NA	13.27	NA	14			
1	2.144379627-A.G	rs14617927	2.144379627-A.G	2	144379627-A	G	0.165	3.2e-12	1	rs1440022	ARRGAP15	ARRGAP15		0	intronic	NA	13.23	7	4			
20	3.15100841-A.C	rs7617077	3.15100841-A.C	3	15100841-A	C	0.4751	6.6e-10	0.91288	rs1065374	MDJL2	P2RY12		0	intronic	NA	13.2	6	5			
41	5.122327780-A.G	rs1362166	5.122327780-A.G	5	122327780-G	A	0.3591	5.8e-08	0.85811	rs06151632	SNZ24	SNZ24		0	intronic	NA	13.14	7	5			
16	15.68282309-G.T	rs0200246	15.68282309-G.T	15	68282309-T	T	0.337	2.4e-06	0.615484	rs428022			ENSG00000061009	PIA81	PIA81		3683	intronic	NA	13.18	5	5
26	17.74345395-CACA	rs177434539	17.74345395-CACA	17	74345395																	