Table S24. Phenotypes of two selected regions including the protein-encoding genes of chitinases (*CHIs*) and ionotropic glutamate receptors (*GRIPs*).

Gene ID	Chromosome	Position	mutation type	Nucleotide change	Amino acid change	sites (S)	Sensistive		sites (R)	Resistant		π ratio	Fst	π_S	π_R
Cil_09G_00199V2	chr09	3163608	missense_variant	c.196C>G	p.Pro66Ala	112	C:0.803571	G:0.196429	60	C:0.833333	G:0.166667	1.128	-0.007	-	-
	chr09	3164389	missense_variant	c.769G>C	p.Glu257Gln	110	G:0.745455	C:0.254545	60	G:0.933333	C:0.066667	3.026	0.101	-	-
	chr09	3190099	missense_variant	c.230C>T	p.Ser77Phe	112	C:0.973214	T:0.026786	60	C:0.666667	T:0.333333	0.116	0.327	-	-
	chr09	3190114	missense_variant	c.245T>C	p.Leu82Ser	112	T:0.633929	C:0.366071	58	T:0.948276	C:0.051724	4.692	0.221	-	-
Cil_09G_00200V2	chr09	3190142	missense_variant	c.273C>A	p.His91Gln	110	C:0.363636	A:0.636364	60	C:0.033333	A:0.966667	7.127	0.248	-	-
	chr09	3190203	missense_variant	c.334G>A	p.Gly112Ser	112	G:0.946429	A:0.053571	60	G:0.616667	A:0.383333	0.213	0.315	-	-
	chr09	3190363	intron_variant	c.427+67C>T		110	C:0.472727	T:0.527273	60	C:0.683333	T:0.316667	1.143	0.080	-	-
	chr15	299519	missense_variant	c.3416C>T	p.Pro1139Leu	112	G:0.151786	A:0.848214	60	G:0.033333	A:0.966667	3.964	0.059	0.2 60	0.0 66
Cil_15G_00015V2	chr15	299557	synonymous_variant	c.3378C>T	p.Asp1126Asp	112	G:0.294643	A:0.705357	60	G:0.15	A:0.85	1.617	0.045	0.4 19	0.2 59
	chr15	299580	missense_variant	c.3355C>A	p.Pro1119Thr	112	G:0.294643	T:0.705357	60	G:0.15	T:0.85	1.617	0.045	0.4 19	0.2 59

chr15	299590	synonymous_variant	c.3345A>G	p.Leu1115Leu	112	T:0.678571	C:0.321429	60	T:0.95	C:0.05	4.556	0.183	0.440	0.097
chr15	299749	missense_variant	c.3186A>T	p.Arg1062Ser	112	T:0.883929	A:0.116071	60	T:0.916667	A:0.083333	1.333	-0.007	0.207	0.155
chr15	299769	missense_variant	c.3166G>A	p.Val1056Ile	112	C:0.294643	T:0.705357	60	C:0.15	T:0.85	1.617	0.045	0.419	0.259
chr15	299796	missense_variant	c.3139A>G	p.Lys1047Glu	112	T:0.883929	C:0.116071	60	T:0.916667	C:0.083333	1.333	-0.007	0.207	0.155
chr15	299874	missense_variant	c.3061C>G	p.Gln1021Glu	112	G:0.294643	C:0.705357	60	G:0.15	C:0.85	1.617	0.045	0.419	0.259
chr15	299909	missense_variant	c.3026T>A	p.Leu1009Gln	112	A:0.294643	T:0.705357	60	A:0.15	T:0.85	1.617	0.045	0.419	0.259
chr15	300794	downstream_gene_variant	c.*1765A>T		112	A:0.303571	T:0.696429	60	A:0.15	T:0.85	1.645	0.051	0.427	0.259
chr15	300842	downstream_gene_variant	c.*1813A>C		112	A:0.294643	C:0.705357	60	A:0.15	C:0.85	1.617	0.045	0.419	0.259
chr15	300882	downstream_gene_variant	c.*1853C>A		112	C:0.294643	A:0.705357	60	C:0.15	A:0.85	1.617	0.045	0.419	0.259
chr15	300951	downstream_gene_variant	c.*1922C>T		110	C:0.3	T:0.7	60	C:0.15	T:0.85	1.634	0.048	0.424	0.259
chr15	300993	downstream_gene_variant	c.*1964A>G		112	A:0.294643	G:0.705357	58	A:0.155172	G:0.844828	1.572	0.041	0.419	0.267
chr15	301095	missense_variant	c.2772G>C	p.Met924Ile	112	C:0.303571	G:0.696429	58	C:0.155172	G:0.844828	1.599	0.047	0.427	0.267

chr15	30112	missense_variant	c.2745C>G	p.His915Gln	110	G:0.881818	C:0.118182	60	G:0.916667	C:0.0833333	1.354	-0.007	0.210	0.155
chr15	30186	synonymous_variant	c.1935A>G	p.Thr645Thr	112	T:0.178571	C:0.821429	60	T:0.066667	C:0.933333	2.339	0.039	0.296	0.127
chr15	30223	downstream_gene_variant	c.*3205C>T		112	C:0.285714	T:0.714286	58	C:0.155172	T:0.844828	1.544	0.035	0.412	0.267
chr15	30251	downstream_gene_variant	c.*3222C>A		112	C:0.285714	A:0.714286	58	C:0.155172	A:0.844828	1.544	0.035	0.412	0.267
chr15	30238	downstream_gene_variant	c.*3351T>C		112	T:0.294643	C:0.705357	60	T:0.233333	C:0.766667	1.153	-0.002	0.419	0.364
chr15	30239	downstream_gene_variant	c.*3361G>C		112	G:0.178571	C:0.821429	60	G:0.066667	C:0.933333	2.339	0.039	0.296	0.127
chr15	30242	downstream_gene_variant	c.*3398A>G		112	A:0.294643	G:0.705357	60	A:0.15	G:0.85	1.617	0.045	0.419	0.259
chr15	30251	downstream_gene_variant	c.*3489C>T		112	C:0.294643	T:0.705357	60	C:0.15	T:0.85	1.617	0.045	0.419	0.259
chr15	30272	downstream_gene_variant	c.*3695A>C		112	A:0.910714	C:0.089286	60	A:0.966667	C:0.0333333	2.504	0.012	0.164	0.066
chr15	30273	downstream_gene_variant	c.*3707C>A		110	C:0.290909	A:0.709091	60	C:0.15	A:0.85	1.606	0.043	0.416	0.259
chr15	30277	downstream_gene_variant	c.*3748T>G		110	T:0.145455	G:0.854545	60	T:0.0333333	G:0.966667	3.828	0.054	0.251	0.066
chr15	30284	synonymous_variant	c.1878T>C	p.Val626Val	112	A:0.133929	G:0.866071	60	A:0.0166667	G:0.983333	7.022	0.068	0.234	0.033

Cil_15G_00016V2	chr15	303663	synonymous_variant	c.1146C>T	p.Thr382Thr	112	G:0.883929	A:0.116071	60	G:0.916667	A:0.083333	1.333	-0.007	0.207	0.155
	chr15	304146	synonymous_variant	c.663T>G	p.Ser221Ser	112	A:0.919643	C:0.0803571	60	A:0.95	C:0.05	1.544	-0.007	0.149	0.097
	chr15	304323	synonymous_variant	c.486T>C	p.Tyr162Tyr	112	A:0.294643	G:0.705357	60	A:0.15	G:0.85	1.617	0.045	0.419	0.259
	chr15	304776	missense_variant	c.171C>A	p.Asp57Glu	110	G:0.290909	T:0.709091	60	G:0.15	T:0.85	1.606	0.043	0.416	0.259
	chr15	304881	synonymous_variant	c.66T>C	p.Val22Val	112	A:0.294643	G:0.705357	60	A:0.15	G:0.85	1.617	0.045	0.419	0.259
	chr15	304893	synonymous_variant	c.54A>G	p.Ser18Ser	112	T:0.294643	C:0.705357	60	T:0.15	C:0.85	1.617	0.045	0.419	0.259
	chr15	307017	missense_variant	c.2632G>A	p.Val878Ile	112	C:0.303571	T:0.696429	58	C:0.189655	T:0.810345	1.364	0.022	0.427	0.313
	chr15	307019	missense_variant	c.2630G>T	p.Arg877Met	112	C:0.303571	A:0.696429	58	C:0.189655	A:0.810345	1.364	0.022	0.427	0.313
	chr15	307306	synonymous_variant	c.2343C>T	p.Leu781Leu	112	G:0.294643	A:0.705357	60	G:0.183333	A:0.816667	1.377	0.022	0.419	0.305
	chr15	307632	upstream_gene_variant	c.-2686C>T		112	G:0.625	A:0.375	60	G:0.283333	A:0.716667	1.145	0.198	0.473	0.413
	chr15	307649	upstream_gene_variant	c.-2703A>G		112	T:0.625	C:0.375	60	T:0.283333	C:0.716667	1.145	0.198	0.473	0.413
	chr15	307692	upstream_gene_variant	c.-2746A>G		110	T:0.627273	C:0.372727	60	T:0.283333	C:0.716667	1.143	0.200	0.472	0.413

chr15	307741	upstream_gene_variant	c.-2795A>G		112	T:0.625	C:0.375	60	T:0.283333	C:0.716667	1.145	0.198	0.473	0.413
chr15	308084	synonymous_variant	c.2157C>T	p.Asp719Asp	112	G:0.723214	A:0.276786	60	G:0.583333	A:0.416667	0.817	0.037	0.404	0.494
chr15	308448	upstream_gene_variant	c.-3502A>G		110	T:0.681818	C:0.318182	60	T:0.266667	C:0.733333	1.101	0.282	0.438	0.398
chr15	308484	upstream_gene_variant	c.-3538C>T		112	G:0.678571	A:0.321429	60	G:0.266667	A:0.733333	1.107	0.278	0.440	0.398
chr15	308662	upstream_gene_variant	c.-3716G>A		112	C:0.678571	T:0.321429	60	C:0.9	T:0.1	2.405	0.117	0.440	0.183
chr15	308959	synonymous_variant	c.1650C>T	p.Ser550Ser	112	G:0.410714	A:0.589286	60	G:0.15	A:0.85	1.883	0.138	0.488	0.259
chr15	309279	missense_variant	c.1499T>C	p.Leu500Ser	112	A:0.133929	G:0.866071	60	A:0.016667	G:0.983333	7.022	0.068	0.234	0.033
chr15	309340	missense_variant	c.1438C>A	p.Pro480Thr	112	G:0.678571	T:0.321429	60	G:0.266667	T:0.733333	1.107	0.278	0.440	0.398
chr15	309717	missense_variant	c.1061T>C	p.Ile354Thr	112	A:0.678571	G:0.321429	60	A:0.266667	G:0.733333	1.107	0.278	0.440	0.398
chr15	309729	missense_variant	c.1049T>C	p.Leu350Ser	112	A:0.678571	G:0.321429	58	A:0.275862	G:0.724138	1.083	0.267	0.407	0.407
chr15	309742	missense_variant	c.1036C>T	p.Arg346Cys	112	G:0.678571	A:0.321429	58	G:0.275862	A:0.724138	1.083	0.267	0.407	0.407
chr15	309839	synonymous_variant	c.939G>A	p.Gly313Gly	112	C:0.6875	T:0.3125	60	C:0.283333	T:0.716667	1.050	0.270	0.434	0.413
chr15	310067	missense_variant	c.797C>T	p.Ser266Phe	112	G:0.669643	A:0.330357	60	G:0.266667	A:0.733333	1.122	0.267	0.446	0.398

Cil_15G_00017V2	chr15	310138	missense_variant	c.726A>T	p.Glu242Asp	112	T:0.678571	A:0.321429	60	T:0.95	A:0.05	4.556	0.183	0.440	0.097
	chr15	310382	missense_variant	c.482G>A	p.Gly161Glu	112	C:0.669643	T:0.330357	60	C:0.266667	T:0.733333	1.122	0.267	0.446	0.398
	chr15	310443	synonymous_variant	c.421C>A	p.Arg141Arg	112	G:0.883929	T:0.116071	60	G:0.9	T:0.1	1.131	-0.012	0.207	0.183
	chr15	310669	intron_variant	c.259+34G>A		112	C:0.678571	T:0.321429	60	C:0.266667	T:0.733333	1.107	0.278	0.440	0.398
	chr15	310678	intron_variant	c.259+25A>T		112	T:0.678571	A:0.321429	60	T:0.916667	A:0.083333	2.833	0.137	0.440	0.155
	chr15	310683	intron_variant	c.259+20G>A		112	C:0.678571	T:0.321429	60	C:0.266667	T:0.733333	1.107	0.278	0.440	0.398
	chr15	310802	missense_variant	c.160C>G	p.His54Asp	112	G:0.669643	C:0.330357	60	G:0.266667	C:0.733333	1.122	0.267	0.446	0.398
	chr15	310900	missense_variant	c.62T>C	p.Val21Ala	112	A:0.133929	G:0.866071	60	A:0.0166667	G:0.983333	7.022	0.068	0.234	0.033
	chr15	322495	missense_variant	c.2631G>A	p.Met877Ile	110	C:0.836364	T:0.163636	60	C:0.333333	T:0.666667	0.611	0.420	0.276	0.452
	chr15	322572	missense_variant	c.2554C>A	p.Gln852Lys	112	G:0.839286	T:0.160714	60	G:0.95	T:0.05	2.818	0.045	0.272	0.097
	chr15	323615	splice_region_variant&intron_variant	c.1909+8T>A		112	A:0.330357	T:0.669643	60	A:0.133333	T:0.866667	1.899	0.088	0.446	0.235
	chr15	324197	intron_variant	c.1600-39T>C		112	A:0.330357	G:0.669643	60	A:0.15	G:0.85	1.722	0.072	0.446	0.259

	chr15	324470	missense_variant	c.1417G>A	p.Val473Ile	112	C:0.848214	T:0.151786	60	C:0.966667	T:0.033333	3.964	0.048	0.260	0.066
	chr15	325137	synonymous_variant	c.750C>T	p.Tyr250Tyr	112	G:0.160714	A:0.839286	60	G:0.083333	A:0.916667	1.752	0.015	0.272	0.155
	chr15	325497	synonymous_variant	c.390T>C	p.Pro130Pro	112	A:0.330357	G:0.669643	60	A:0.133333	G:0.866667	1.899	0.088	0.446	0.235
	chr15	325726	intron_variant	c.262+22A>G		112	T:0.133929	C:0.866071	60	T:0.05	C:0.95	2.423	0.026	0.234	0.097
	chr15	333618	synonymous_variant	c.2274T>C	p.Leu758Leu	112	A:0.473214	G:0.526786	60	A:0.133333	G:0.866667	2.140	0.214	0.503	0.235
	chr15	333822	intron_variant	c.2101-31C>A		112	G:0.473214	T:0.526786	60	G:0.15	T:0.85	1.940	0.193	0.503	0.259
	chr15	333998	intron_variant	c.2100+103G>A		112	C:0.375	T:0.625	60	C:0.083333	T:0.916667	3.044	0.187	0.473	0.155
	chr15	334058	intron_variant	c.2100+43T>C		112	A:0.473214	G:0.526786	60	A:0.183333	G:0.816667	1.652	0.155	0.503	0.305
Cil_15G_00018V2	chr15	334269	synonymous_variant	c.1932T>C	p.Leu644Leu	112	A:0.857143	G:0.142857	60	A:1	G:0	### #	0.104	0.247	0.000
	chr15	334520	intron_variant	c.1694-13T>C		112	A:0.133929	G:0.866071	60	A:0.05	G:0.95	2.423	0.026	0.234	0.097
	chr15	334770	intron_variant	c.1661+89A>G		112	T:0.875	C:0.125	60	T:0.366667	C:0.633333	0.467	0.449	0.221	0.472
	chr15	336314	synonymous_variant	c.300T>C	p.Asp100Asp	112	A:0.919643	G:0.080357	60	A:0.966667	G:0.033333	2.276	0.006	0.149	0.066
	chr15	336617	intron_variant	c.47-50G>C		112	C:0.473214	G:0.526786	60	C:0.133333	G:0.866667	2.140	0.214	0.503	0.235

Cil_15G_0 0019V2	chr15	3582 59	synonymous_variant	c.4338A> G	p.Gly144 6Gly	112	T:0.87 5	C:0.125	60	T:0.366 667	C:0.633 333	0.46 7	0.4 49	0.2 21	0.4 72
	chr15	3586 31	synonymous_variant	c.3966C> T	p.Ala132 2Ala	112	G:0.91 0714	A:0.089 2857	60	G:0.966 667	A:0.033 3333	2.50 4	0.0 12	0.1 64	0.0 66
	chr15	3588 65	intron_variant	c.3939+19 0G>A		112	C:0.87 5	T:0.125	60	C:0.366 667	T:0.633 333	0.46 7	0.4 49	0.2 21	0.4 72
	chr15	3591 19	missense_variant	c.3875T> C	p.Phe129 2Ser	110	A:0.91 8182	G:0.081 8182	60	A:0.966 667	G:0.033 3333	2.31 4	0.0 07	0.1 52	0.0 66
	chr15	3595 01	intron_variant	c.3533- 40A>G		112	T:0.83 9286	C:0.160 714	60	T:0.3	C:0.7	0.63 7	0.4 66	0.2 72	0.4 27
	chr15	3595 91	synonymous_variant	c.3522T> C	p.Phe117 4Phe	110	A:0.83 6364	G:0.163 636	60	A:0.3	G:0.7	0.64 7	0.4 61	0.2 76	0.4 27
	chr15	3599 85	synonymous_variant	c.3315C> A	p.Val110 5Val	112	G:0.91 0714	T:0.089 2857	60	G:0.966 667	T:0.033 3333	2.50 4	0.0 12	0.1 64	0.0 66
	chr15	3603 78	synonymous_variant	c.3019C> A	p.Arg100 7Arg	112	G:0.83 9286	T:0.160 714	60	G:0.316 667	T:0.683 333	0.61 8	0.4 47	0.2 72	0.4 40
	chr15	3604 19	missense_variant	c.2978A> C	p.Lys993 Thr	112	T:0.85 7143	G:0.142 857	60	T:1	G:0	### #	0.1 04	0.2 47	0.0 00
	chr15	3607 09	splice_region_variant& intron_variant	c.2779+4 G>A		112	C:0.91 9643	T:0.080 3571	60	C:1	T:0	### #	0.0 52	0.1 49	0.0 00
	chr15	3616 89	missense_variant	c.1900C> A	p.Pro634 Thr	112	G:0.85 7143	T:0.142 857	60	G:1	T:0	### #	0.1 04	0.2 47	0.0 00
	chr15	3618 17	missense_variant	c.1772T> C	p.Ile591 Thr	112	A:0.42 8571	G:0.571 429	60	A:0.1	G:0.9	2.70 0	0.2 16	0.4 94	0.1 83

chr15	362213	intron_variant	c.1709-333T>G	112	A:0.366071	C:0.633929	60	A:0.1	C:0.9	2.558	0.157	0.468	0.183
chr15	362226	intron_variant	c.1709-346G>A	112	C:0.571429	T:0.428571	60	C:0.883333	T:0.116667	2.358	0.195	0.494	0.210
chr15	362460	intron_variant	c.1709-580T>C	112	A:0.464286	G:0.535714	60	A:0.166667	G:0.833333	1.777	0.170	0.502	0.282
chr15	362481	intron_variant	c.1709-601G>A	112	C:0.839286	T:0.160714	60	C:0.316667	T:0.683333	0.618	0.447	0.272	0.440
chr15	362525	intron_variant	c.1709-645C>T	112	G:0.464286	A:0.535714	60	G:0.183333	A:0.816667	1.648	0.152	0.502	0.305
chr15	362550	intron_variant	c.1709-670G>T	112	C:0.857143	A:0.142857	60	C:1	A:0	###	0.104	0.247	0.000
chr15	362578	intron_variant	c.1709-698G>A	110	C:0.6	T:0.4	60	C:0.866667	T:0.133333	2.061	0.149	0.484	0.235
chr15	362584	intron_variant	c.1709-704A>G	112	T:0.535714	C:0.464286	60	T:0.833333	C:0.166667	1.777	0.170	0.502	0.282
chr15	362781	intron_variant	c.1709-901A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	362939	intron_variant	c.1709-1059A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	363042	intron_variant	c.1708+1098A>C	112	T:0.866071	G:0.133929	60	T:0.95	G:0.05	2.423	0.026	0.234	0.097
chr15	363244	intron_variant	c.1708+896T>C	112	A:0.428571	G:0.571429	60	A:0.116667	G:0.883333	2.358	0.195	0.494	0.210

chr15	363265	intron_variant	c.1708+875A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	363891	intron_variant	c.1708+249G>A	110	C:0.881818	T:0.118182	60	C:0.366667	T:0.633333	0.445	0.460	0.210	0.472
chr15	363919	intron_variant	c.1708+221C>G	112	G:0.875	C:0.125	60	G:0.383333	C:0.616667	0.459	0.430	0.221	0.481
chr15	363960	intron_variant	c.1708+180T>C	112	A:0.767857	G:0.232143	60	A:0.966667	G:0.0333333	5.489	0.126	0.360	0.066
chr15	363961	intron_variant	c.1708+179T>C	112	A:0.428571	G:0.571429	60	A:0.116667	G:0.883333	2.358	0.195	0.494	0.210
chr15	364122	intron_variant	c.1708+18G>T	112	C:0.464286	A:0.535714	60	C:0.166667	A:0.833333	1.777	0.170	0.502	0.282
chr15	364456	intron_variant	c.1592-200C>T	112	G:0.571429	A:0.428571	60	G:0.883333	A:0.116667	2.358	0.195	0.494	0.210
chr15	364486	intron_variant	c.1592-230T>C	112	A:0.428571	G:0.571429	58	A:0.0862069	G:0.913793	3.083	0.234	0.494	0.160
chr15	364607	intron_variant	c.1592-351A>G	112	T:0.366071	C:0.633929	60	T:0.1	C:0.9	2.558	0.157	0.468	0.183
chr15	364613	intron_variant	c.1592-357A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	364673	intron_variant	c.1592-417A>G	112	T:0.366071	C:0.633929	60	T:0.1	C:0.9	2.558	0.157	0.468	0.183
chr15	364731	intron_variant	c.1592-475A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210

chr15	364829	intron_variant	c.1591+508T>C		112	A:0.464286	G:0.535714	60	A:0.15	G:0.85	1.936	0.190	0.502	0.259
chr15	364837	intron_variant	c.1591+500A>G		112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	364859	intron_variant	c.1591+478T>G		112	A:0.866071	C:0.133929	60	A:0.95	C:0.05	2.423	0.026	0.234	0.097
chr15	364882	intron_variant	c.1591+455C>T		112	G:0.3125	A:0.6875	60	G:0.0333333	A:0.966667	6.616	0.199	0.434	0.066
chr15	364992	intron_variant	c.1591+345G>A		112	C:0.5	T:0.5	60	C:0.366667	T:0.633333	1.068	0.033	0.505	0.472
chr15	365048	intron_variant	c.1591+289G>A		110	C:0.645455	T:0.354545	60	C:0.9	T:0.1	2.523	0.147	0.462	0.183
chr15	365181	intron_variant	c.1591+156T>C		112	A:0.428571	G:0.571429	60	A:0.133333	G:0.866667	2.103	0.175	0.494	0.235
chr15	365269	intron_variant	c.1591+68C>T		112	G:0.839286	A:0.160714	60	G:0.333333	A:0.666667	0.602	0.428	0.272	0.452
chr15	365274	intron_variant	c.1591+63G>A		112	C:0.464286	T:0.535714	60	C:0.2	T:0.8	1.542	0.134	0.502	0.325
chr15	365279	intron_variant	c.1591+58G>A		112	C:0.571429	T:0.428571	60	C:0.883333	T:0.116667	2.358	0.195	0.494	0.210
chr15	365319	intron_variant	c.1591+18G>A		112	C:0.464286	T:0.535714	60	C:0.166667	T:0.833333	1.777	0.170	0.502	0.282
chr15	365459	missense_variant	c.1469C>T	p.Pro490Leu	112	G:0.428571	A:0.571429	60	G:0.116667	A:0.883333	2.358	0.195	0.494	0.210

chr15	365500	synonymous_variant	c.1428T>C	p.Asn476Asn	112	A:0.410714	G:0.589286	60	A:0.15	G:0.85	1.883	0.139	0.488	0.259
chr15	365576	intron_variant	c.1376-24T>C		112	A:0.428571	G:0.571429	60	A:0.116667	G:0.883333	2.358	0.195	0.494	0.210
chr15	365622	intron_variant	c.1375+23T>C		112	A:0.5625	G:0.4375	60	A:0.133333	G:0.866667	2.113	0.307	0.497	0.235
chr15	366319	intron_variant	c.1250-45A>C		110	T:0.854545	G:0.145455	60	T:0.45	G:0.55	0.498	0.319	0.251	0.503
chr15	366855	intron_variant	c.1114-57A>G		112	T:0.428571	C:0.571429	60	T:0.1	C:0.9	2.700	0.217	0.494	0.183
chr15	366857	intron_variant	c.1114-59C>T		112	G:0.473214	A:0.526786	60	G:0.25	A:0.75	1.319	0.095	0.503	0.381
chr15	366940	stop_gained	c.1090C>T	p.Gln364*	112	G:0.428571	A:0.571429	60	G:0.116667	A:0.883333	2.358	0.195	0.494	0.210
chr15	366960	splice_region_variant&intron_variant	c.1075-5A>G		112	T:0.428571	C:0.571429	60	T:0.1	C:0.9	2.700	0.216	0.494	0.183
chr15	366988	intron_variant	c.1075-33C>T		112	G:0.910714	A:0.0892857	60	G:0.966667	A:0.0333333	2.504	0.012	0.164	0.066
chr15	367070	intron_variant	c.1075-115G>A		112	C:0.464286	T:0.535714	60	C:0.166667	T:0.833333	1.777	0.170	0.502	0.282
chr15	367126	intron_variant	c.1075-171A>G		112	T:0.535714	C:0.464286	58	T:0.827586	C:0.172414	1.729	0.163	0.502	0.290
chr15	367279	intron_variant	c.1075-324T>C		112	A:0.464286	G:0.535714	58	A:0.189655	G:0.810345	1.605	0.145	0.502	0.313

chr15	367307	intron_variant	c.1075-352A>G	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	367555	intron_variant	c.1075-600G>C	112	C:0.866071	G:0.133929	60	C:0.95	G:0.05	2.423	0.026	0.234	0.097
chr15	367612	intron_variant	c.1075-657A>T	112	T:0.866071	A:0.133929	60	T:0.983333	A:0.0166667	7.022	0.068	0.234	0.033
chr15	367697	intron_variant	c.1075-742C>T	112	G:0.767857	A:0.232143	60	G:0.966667	A:0.0333333	5.489	0.126	0.360	0.066
chr15	367715	intron_variant	c.1075-760G>A	112	C:0.767857	T:0.232143	60	C:0.966667	T:0.0333333	5.489	0.126	0.360	0.066
chr15	368016	intron_variant	c.1075-1061G>T	110	C:0.954545	A:0.045454	60	C:1	A:0	###	0.023	0.088	0.000
chr15	368028	intron_variant	c.1075-1073T>C	110	A:0.954545	G:0.045454	60	A:1	G:0	###	0.023	0.088	0.000
chr15	368042	intron_variant	c.1075-1087A>G	112	T:0.3125	C:0.6875	60	T:0.05	C:0.95	4.488	0.174	0.434	0.097
chr15	368044	intron_variant	c.1075-1089C>T	112	G:0.857143	A:0.142857	60	G:1	A:0	###	0.104	0.247	0.000
chr15	368117	intron_variant	c.1074+1118A>G	112	T:0.428571	C:0.571429	58	T:0.0862069	C:0.913793	3.083	0.234	0.494	0.160
chr15	368281	intron_variant	c.1074+954C>A	112	G:0.857143	T:0.142857	60	G:1	T:0	###	0.104	0.247	0.000
chr15	368479	intron_variant	c.1074+756C>A	112	G:0.9375	T:0.0625	60	G:1	T:0	###	0.037	0.118	0.000

chr15	368492	intron_variant	c.1074+743T>C		112	A:0.428571	G:0.571429	58	A:0.103448	G:0.896552	2.618	0.211	0.494	0.189
chr15	368605	intron_variant	c.1074+630G>C		112	C:0.857143	G:0.142857	60	C:1	G:0	####	0.104	0.247	0.000
chr15	368634	intron_variant	c.1074+601A>G		112	T:0.571429	C:0.428571	60	T:0.883333	C:0.116667	2.358	0.195	0.494	0.210
chr15	368810	intron_variant	c.1074+425T>C		112	A:0.535714	G:0.464286	60	A:0.833333	G:0.166667	1.777	0.170	0.502	0.282
chr15	369605	intron_variant	c.924+29G>A		112	C:0.910714	T:0.0892857	60	C:0.966667	T:0.0333333	2.504	0.012	0.164	0.066
chr15	369863	missense_variant	c.829G>A	p.Gly277Ser	112	C:0.839286	T:0.160714	60	C:0.3	T:0.7	0.637	0.466	0.272	0.427
chr15	370007	missense_variant	c.685T>A	p.Cys229Ser	112	A:0.946429	T:0.0535714	60	A:1	T:0	####	0.030	0.102	0.000
chr15	370015	missense_variant	c.677G>A	p.Cys226Tyr	112	C:0.946429	T:0.0535714	60	C:1	T:0	####	0.030	0.102	0.000
chr15	370032	synonymous_variant	c.660A>G	p.Leu220Leu	112	T:0.946429	C:0.0535714	60	T:1	C:0	####	0.030	0.102	0.000
chr15	370053	intron_variant	c.654-15A>T		112	T:0.9375	A:0.0625	60	T:1	A:0	####	0.037	0.118	0.000
chr15	370057	intron_variant	c.654-19G>A		112	C:0.9375	T:0.0625	60	C:1	T:0	####	0.037	0.118	0.000
chr15	370062	intron_variant	c.654-24G>T		112	C:0.964286	A:0.0357143	60	C:1	A:0	####	0.015	0.069	0.000

chr15	37009	intron_variant	c.654-60G>C	110	C:0.945455	G:0.0545455	60	C:1	G:0	###	0.0	0.1	0.0
chr15	37014	intron_variant	c.654-102A>G	110	T:0.945455	C:0.0545455	60	T:1	C:0	###	0.0	0.1	0.0
chr15	37014	intron_variant	c.654-104C>T	112	G:0.946429	A:0.0535714	60	G:1	A:0	###	0.0	0.1	0.0
chr15	37020	intron_variant	c.654-165T>A	112	A:0.9375	T:0.0625	60	A:1	T:0	###	0.0	0.1	0.0
chr15	37020	intron_variant	c.654-170C>T	112	G:0.9375	A:0.0625	60	G:1	A:0	###	0.0	0.1	0.0
chr15	37022	intron_variant	c.654-185C>T	112	G:0.901786	A:0.0982143	60	G:0.966667	A:0.0333333	2.727	0.0	0.1	0.0
chr15	37022	intron_variant	c.654-189A>C	112	T:0.428571	G:0.571429	60	T:0.116667	G:0.883333	2.358	0.1	0.4	0.2
chr15	37025	intron_variant	c.654-212T>C	112	A:0.9375	G:0.0625	60	A:1	G:0	###	0.0	0.1	0.0
chr15	37026	intron_variant	c.654-227A>G	112	T:0.9375	C:0.0625	60	T:1	C:0	###	0.0	0.1	0.0
chr15	37026	intron_variant	c.654-228G>A	112	C:0.9375	T:0.0625	60	C:1	T:0	###	0.0	0.1	0.0
chr15	37035	intron_variant	c.654-314C>T	112	G:0.857143	A:0.142857	60	G:1	A:0	###	0.1	0.2	0.0
chr15	37049	intron_variant	c.654-452G>A	112	C:0.830357	T:0.169643	60	C:0.3	T:0.7	0.666	0.4	0.2	0.4

chr15	370877	intron_variant	c.653+73C>T		110	G:0.463636	A:0.536364	60	G:0.183333	A:0.816667	1.648	0.151	0.502	0.305
chr15	370912	intron_variant	c.653+38T>C		112	A:0.428571	G:0.571429	60	A:0.116667	G:0.883333	2.358	0.195	0.494	0.210
chr15	370982	synonymous_variant	c.621A>G	p.Arg207Arg	112	T:0.428571	C:0.571429	60	T:0.116667	C:0.883333	2.358	0.195	0.494	0.210
chr15	371001	missense_variant	c.602C>T	p.Ala201Val	112	G:0.464286	A:0.535714	60	G:0.15	A:0.85	1.936	0.190	0.502	0.259
chr15	371023	missense_variant	c.580A>C	p.Asn194His	112	T:0.428571	G:0.571429	60	T:0.116667	G:0.883333	2.358	0.195	0.494	0.210
chr15	371037	missense_variant	c.566C>A	p.Pro189Gln	112	G:0.625	T:0.375	60	G:0.883333	T:0.116667	2.256	0.145	0.473	0.210
chr15	371058	splice_region_variant&intron_variant	c.553-8C>T		112	G:0.964286	A:0.035714	60	G:0.966667	A:0.033333	1.060	-0.013	0.069	0.066
chr15	371496	intron_variant	c.366+57T>C		112	A:0.455357	G:0.544643	60	A:0.25	G:0.75	1.312	0.081	0.500	0.381
chr15	371537	intron_variant	c.366+16T>C		112	A:0.428571	G:0.571429	60	A:0.116667	G:0.883333	2.358	0.195	0.494	0.210
chr15	371577	synonymous_variant	c.342G>A	p.Leu114Leu	112	C:0.464286	T:0.535714	60	C:0.166667	T:0.833333	1.777	0.170	0.502	0.282