

Table S6 Functional annotation of shared loci

Type	Number	Percent
3_prime_UTR_variant	19776	0.00713
5_prime_UTR_premature_start_cod	485	0.00017
5_prime_UTR_variant	4117	0.00149
bidirectional_gene_fusion	6	0
conservative_inframe_deletion	204	0.00007
conservative_inframe_insertion	205	0.00007
disruptive_inframe_deletion	254	0.00009
disruptive_inframe_insertion	131	0.00005
downstream_gene_variant	140581	0.05072
frameshift_variant	5870	0.00212
initiator_codon_variant	5	0
intergenic_region	782206	0.28221
intragenic_variant	68	0.00002
intron_variant	1626347	0.58676
missense_variant	18155	0.00655
non_coding_transcript_exon_variant	11792	0.00425
non_coding_transcript_variant	8	0
splice_acceptor_variant	526	0.00019
splice_donor_variant	642	0.00023
splice_region_variant	4576	0.00165
start_lost	46	0.00002
start_retained_variant	13	0
stop_gained	1105	0.0004
stop_lost	58	0.00002
stop_retained_variant	33	0.00001
synonymous_variant	14085	0.00508
upstream_gene_variant	140457	0.05067