

Table S7 Functional annotation of stably inherited loci after filtering of parent-offspring shared loci

Type (alphabetical order)	Count	Percent
3_prime_UTR_variant	9,882	0.71%
5_prime_UTR_premature_start_codon_gain_variant	293	0.02%
5_prime_UTR_variant	2,080	0.15%
downstream_gene_variant	71,247	5.13%
initiator_codon_variant	3	0%
intergenic_region	384,995	27.73%
intragenic_variant	40	0.00%
intron_variant	820,235	59.09%
missense_variant	10,952	0.79%
non_coding_transcript_exon_variant	5,999	0.43%
splice_acceptor_variant	249	0.02%
splice_donor_variant	326	0.02%
splice_region_variant	2,266	0.16%
start_lost	12	0.00%
start_retained_variant	7	0.00%
stop_gained	536	0.04%
stop_lost	25	0.00%
stop_retained_variant	19	0.00%
synonymous_variant	8,501	0.61%
upstream_gene_variant	70,554	5.08%