

Supplementary Table 3. Classification of SNPs based on genome location.

Type	Number of SNPs	percentage	Impact
Intergenic	7,176,639	72.418292%	MODIFIER
Intron	832,336	8.398967%	MODIFIER
Upstream	827,769	8.352882%	MODIFIER
Downstream	727,361	7.339681%	MODIFIER
Non-synonymous-coding	158,107	1.595432%	MODERATE
Synonymous-coding	96,541	0.974179%	LOW
UTR-3-prime	46,628	0.470516%	MODIFIER
UTR-5-prime	26,265	0.265036%	MODIFIER
Stop-gained	6,833	0.068951%	HIGH
Start-gained	4,190	0.042281%	LOW
Stop-lost	4,005	0.040414%	HIGH
Synonymous-stop	1394	0.014067%	LOW
Splice-site-acceptor	857	0.008648%	HIGH
Splice-site-donor	609	0.006145%	HIGH
Start-lost	384	0.003875%	HIGH
Non-synonymous-start	63	0.000636%	LOW