

**Supplementary Table S3.** Distribution of SNPs identified in LUX annotated by SnpEff.

<b>Variants Type</b>	<b>Count</b>	<b>Percent</b>
3_prime_UTR_variant	648,748	0.783%
5_prime_UTR_premature_start_codon_gain_variant	25,965	0.031%
5_prime_UTR_variant	149,518	0.180%
downstream_gene_variant	4,169,606	5.031%
initiator_codon_variant	42	0.000%
intergenic_region	17,829,235	21.514%
intragenic_variant	277,815	0.335%
intron_variant	54,840,227	66.173%
missense_variant	239,036	0.288%
non_coding_transcript_exon_variant	243,335	0.294%
splice_acceptor_variant	1,075	0.001%
splice_donor_variant	1,401	0.002%
splice_region_variant	90,096	0.109%
start_lost	381	0.000%
start_retained_variant	53	0.000%
stop_gained	2,151	0.003%
stop_lost	298	0.000%
stop_retained_variant	384	0.000%
synonymous_variant	501,711	0.605%
upstream_gene_variant	3,852,636	4.649%

<b>Region Type</b>	<b>Count</b>	<b>Percent</b>
DOWNSTREAM	4,169,606	5.037%
EXON	974,840	1.178%
INTERGENIC	17,829,235	21.537%
INTRON	54,768,088	66.158%
SPLICE_SITE_ACCEPTOR	1,075	0.001%
SPLICE_SITE_DONOR	1,380	0.002%
SPLICE_SITE_REGION	85,324	0.103%
TRANSCRIPT	277,815	0.336%
UPSTREAM	3,852,636	4.654%
UTR_3_PRIME	648,748	0.784%
UTR_5_PRIME	175,483	0.212%