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Category	Count	Consequences (all)	
Variants processed	774		intron_variant: 39% intergenic_variant: 18%
Variants filtered out	0		downstream_gene_variant: 14% missense_variant: 11%
Novel / existing variants	773 (99.9) / 1 (0.1)		synonymous_variant: 6%
Overlapped genes	557		3_prime_UTR_variant: 5% upstream_gene_variant: 4%
Overlapped transcripts	589		splice_region_variant: 1%
Overlapped regulatory features	-		stop_gained: 0% Others

