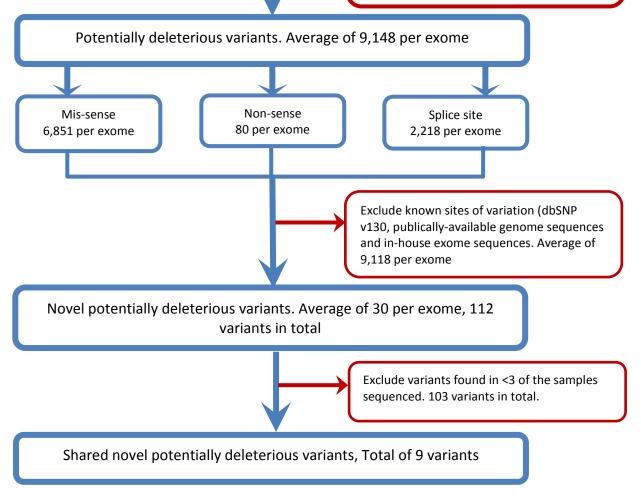


Figure S1 – A flow diagram showing the filtering of the exome data.

High quality reads. Average of 36,105 per exome.

Exclude nongenic, intronic (other than canonical splice sites) and synonymous variants. Average of 26,597 variants per exome



Blue boxes show each filter step and red boxes describe exclusion criteria involved in each

step