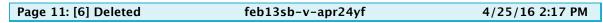
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(is robust the appropriate word to use)					
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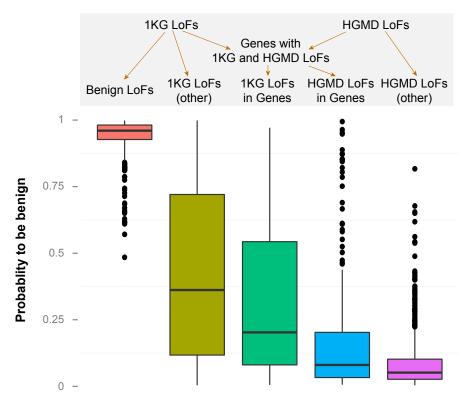


Figure 2 - ALoFT classification of 1000 Genomes and HGMD variants

Benign LoF score for premature stop variants in 1KGP1 and HGMD.

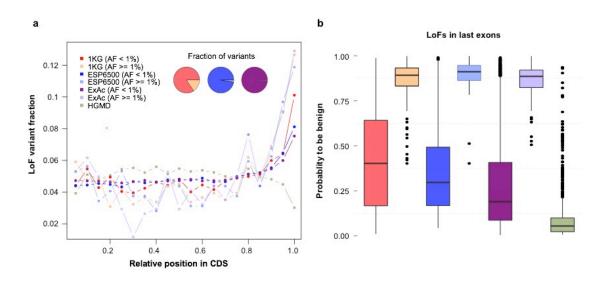
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The third (dark green) box plot pertains to premature stop variants in healthy 1KGP1 individuals occurring in disease-causing genes obtained from HGMD. The fourth (blue)

box plot pertains to LoF variants in the subset of HGMD genes where 1KGP1 LoFs are also seen. "1KGP1 LoFs in other" include variants in 1KGP1 in genes not in HGMD i.e.

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HGMD LoFs other" include variants in only those disease genes where 1KGP1 LoF variants are not seen.



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a) Position of premature stop variants in coding transcripts.

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, ESP6500 and ExAC variants are enriched in the last 5% of the coding sequence. "AF" stands for allele frequency. Variants at allele frequency less than 1% are considered to be rare variants. Variants with at least 1% allele frequency are considered as common.

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b) Predicted benign LoF scores for premature stop variants in the last coding exon.				
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LoF				
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LoF				
Page 12: [13] Deleted	feb13sb-v-apr24yf	4/25/16 2:17 PM		
LoF				
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LoF				
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LoF				
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LoF