

Determining the impact of putative loss-of-function variants in protein-coding genes

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_____ Variants predicted to result in the loss of function (LoF) of human genes have recently attracted considerable interest both because of their clinical impact as well as their surprising prevalence in seemingly healthy humans. To better understand the impact of putative LoF variants (pLoF), we developed ALoFT (Annotation of Loss-of-Function Transcripts), to annotate and predict the deleteriousness (disease-causing potential) of LoF variants. Our method is able to distinguish between pLoF variants discovered by Mendelian studies, that are deleterious as heterozygotes or just in the homozygote state. Investigation of variants discovered in >1,000 healthy human genome sequences suggests that each individual carries about two heterozygous premature stop alleles that could potentially lead to disease if present as homozygotes. When applied to *de novo* pLoF variants in autism-affected families, ALoFT predicts that the variants are more deleterious in patients than in unaffected siblings. Finally, analysis of > 6,500 cancer exomes shows that somatic premature stop variants predicted to be deleterious by ALoFT are enriched in known cancer driver genes.

One of the most notable findings from personal genomics studies is that all individuals harbor loss-of-function variants in some of their genes¹. A systematic study of

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pLoF variants from [the 1000 Genomes](#) revealed that there are over 100 putative LoF variants in each individual²⁴. Recently, a larger study aimed at elucidating rare LoF events in 2,636 Icelanders generated a catalog of 1,171 genes that contain either homozygous or compound heterozygous LoF variants with a minor allele frequency less than 2%³. Thus, several genes are knocked out either completely or in an isoform-specific manner in apparently healthy individuals. Remarkably, recent studies have led to the discovery of protective LoF variants associated with beneficial traits. The potential of pLoF variants to identify valuable drug targets has fueled an increased interest in a more thorough understanding of putative LoF variants. For example, nonsense variants in *PCSK9* are associated with low LDL levels^{6,7} which has prompted the active pursuit of the inhibition of *PCSK9* as a potential therapeutic for hypercholesterolemia⁸. Other examples include nonsense and splice mutations in *APOC3* associated with low levels of circulating triglycerides, a nonsense mutation in *SLC30A8* resulting in about 65% reduction in risk for Type II diabetes, two splice variants in the Finnish population in *LPA* that protect against coronary heart disease, and two [LoF-producing](#) splice variants and a nonsense mutation in *HAL* associated with increased blood histidine levels and reduced risk of coronary heart disease⁹⁻¹³.

About 12% of known disease-causing mutations in the Human Gene Mutation Database (HGMD) are due to nonsense mutations¹⁴. pLoF variants are also prioritized in cancer studies where various filtration schemes are used to narrow down causal mutations^{15,16}. Even though premature stop variants often lead to loss of function and are thus deleterious, predicting the functional impact of premature stop codons is not straightforward. Aberrant transcripts containing premature stop codons are typically removed by nonsense-mediated decay (NMD), an mRNA surveillance mechanism¹⁷. However, a recent large-scale expression analysis demonstrated that 68% of predicted NMD events due to premature stop variants are unsupported by [RNA-Seq](#) analyses¹⁸. A study aimed at understanding disease mutations using a 3D structure-based interaction network suggests that truncating mutations can give rise to functional protein products¹⁹. Moreover, premature stop codons in the last exon are [generally](#) not subject to NMD. Further, when a variant affects only some isoforms of a gene, it is difficult to infer its impact on gene function without the knowledge of the isoforms that are expressed in the tissue of interest and how their levels of expression affect gene function. Finally, loss-of-function of a gene might not have any impact on the fitness of the organism.

We have developed a pipeline called ALoFT (**A**nnotation of **L**oss-of-**F**unction **T**ranscripts), to provide extensive annotation of putative LoF variants. In this study, we include premature stop-causing ([nonsense](#)) SNPs, frameshift-causing indels and variants affecting canonical splice sites as putative LoF variants, also referred to as premature truncating variants. An overview of the pipeline is shown in Supplementary Figure 1. The main features of ALoFT include (1) [functional domain](#) annotations; (2) evolutionary conservation; and (3) biological [networks](#). For comprehensive functional annotation, we integrated several annotation resources such as PFAM and SMART functional domains^{20,21}, signal peptide and transmembrane annotations, post-translational modification sites, NMD prediction^{22,23}, and structure-based features such as SCOP domains and disordered residues. For evolutionary conservation, ALoFT outputs variant position-specific GERP scores, which is a measure of evolutionary conservation²⁴ and dN/dS values (ratio of missense to synonymous substitution rates) for macaque and mouse that are computed from human-macaque and human-mouse orthologous alignments, respectively. In addition, we evaluate if the region removed due to the truncation of the coding sequence is evolutionarily conserved based on

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constrained elements²⁵. ALoFT includes network features shown to be important in disease prediction algorithms: a proximity parameter that gives the number of disease genes connected to a gene in a protein-protein interaction network and the shortest path to the nearest disease gene^{2,26}. The pipeline also includes features to help identify erroneous LoF calls, potential mismapping, and annotation errors, because LoF variant calls have been shown to be enriched for annotation and sequencing artifacts². A detailed description of all the annotations provided by ALoFT is included in the Online Methods (Supplementary Table 1). [Documentation](#) and github link to source code can be found at aloft.gersteinlab.org.

To understand the impact of pLoF variants on gene function we developed a prediction method to differentiate between disease-causing and benign variants. While there are several algorithms to predict the effect of missense coding variants on protein function, there is a paucity of methods that are applicable to nonsense variants²⁷⁻³⁰. Additionally, current prediction methods that infer the pathogenicity of variants do not take into account the zygosity of the variant^{31,32}. The majority of pLoF variants in healthy population cohorts are heterozygous. It is likely that a subset of these variants will cause disease [as homozygotes](#). Therefore, we developed a prediction model to classify premature stop causing variants into [three classes](#) that are benign, that lead to recessive disease ([disease-causing only when homozygous](#)) and that lead to dominant disease ([disease-causing as heterozygotes](#)) using the annotations output by ALoFT as predictive features (Fig. 1, Online Methods).

To build the ALoFT classifier, we used three classes of [premature stop](#) variants as training data: benign variants, dominant [disease-causing](#) and recessive [disease-causing variants](#). The benign set includes homozygous premature stop variants discovered in a cohort of [1,092](#) healthy people, Phase1 1000 Genomes data ([1KG](#)). Homozygous premature stop mutations from HGMD that lead to recessive disease and heterozygous premature stop variants in haplo-insufficient genes that lead to dominant disease represent the two disease classes^{3,26}. In addition to [loss-of-function](#) effects, truncating mutations can also lead to gain of function. However, gain of function mutations are difficult to model systematically as the effect of variant is very context dependent depending on the biology [of](#) the gene and can vary widely for different genes and gene classes. In order to minimize errors that might arise due to inadequate modeling of gain-of-function effects and focus only on LoF, we only use predicted haploinsufficient genes as the training data for dominant model. We built the ALoFT classifier to distinguish among the three classes using a random forest algorithm³³. [For each mutation, ALoFT provides three class probability estimates, and we obtain good discrimination between each class](#). The average multiclass test AUC (area under the curve) with 10-fold cross-validation is 0.97. The precision for the three classes are as follows: Dominant=0.86, Recessive=0.86, Benign=0.96. The classifier is robust to the choice of training data sets and performs well with different training data sets (Supplementary Table 4, Supplementary Fig. 2). The prediction output provides three scores for each pLoF variant that correspond to the probability of the pLoF being benign, dominant or recessive disease-causing allele. In addition, ALoFT also provides the predicted pathogenicity. The pathogenic effect of pLoF variant is assigned to the class that corresponds to the maximum [score](#). [Though trained with premature stop SNVs, our method is also applicable to frameshift indels. 99.4% of HGMD disease-causing \('DM'\) frameshift indels are predicted as pathogenic based on the maximum score.](#)

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We analyzed the importance of the various features to the classification (Supplementary Fig. 3). The global allele frequency of variants in the Exome Aggregation Consortium, a dataset comprised of sequence variations obtained from analysis of unrelated 60,706 individuals of diverse ethnicities (ExAC, <http://exac.broadinstitute.org>), appears to be the most important feature for the classification. When we removed this feature and other features related to allele frequency (ie both ExAC and ESP) and retrained the random forest model, the classifier still performs well with an average multiclass test AUC of 0.93. (The precision for the three classes are as follows: Dominant=0.84, Recessive=0.80, and Benign=0.75). We also systematically evaluated the classifier using models trained on various specific sets of features (Supplementary Table 5). Overall, we find that classifier is not driven by any single feature and integrating many features improves prediction accuracy.

Validation of classifier

We applied ALoFT to elucidate the pathogenicity of pLoF variants in various disease scenarios. Using case studies, we show that ALoFT provides robust predictions for the effect of pLoFs.

Case study 1: Application of ALoFT to understand pLOFs in Mendelian disease

We evaluated ALoFT by predicting the effect of known disease-causing premature stop mutations from ClinVar³⁴ (details in Methods) and predicted the mode of inheritance and pathogenicity of all of the truncating variants (Fig. 2a). ALoFT is clearly able to distinguish between pLoFs that possibly lead to disease in a heterozygous state versus those that do so only in a homozygous state. Our method shows that heterozygous disease-causing variants have significantly higher dominant disease-causing scores than the homozygous disease-causing variants (p-value: 1.3e-13; Wilcoxon rank-sum test). We used two other measures, GERP score, which is a measure of evolutionary conservation, and CADD score, which gives a measure of pathogenicity, to classify recessive versus dominant pLoF variants³⁵. Both CADD (p-value: 0.13) and GERP (p-value: 0.49) scores are not able to discriminate between recessive and dominant disease-causing mutations (Fig. 2a). We also tested our method on a smaller dataset from the Center For Mendelian Genomics studies (<http://data.mendelian.org/CMG/>) and was able to correctly recapitulate the pathogenic effect of pLoF variants and their inheritance pattern (Supplementary figure 4).

Case study 2: Application of ALoFT to understand de novo pLoFs implicated in autism

De novo pLoF SNPs have been implicated in autism based on analysis of sporadic or simplex families (families with no prior history of autism)³⁶⁻³⁹. We applied our method to de novo pLoF mutations discovered in these studies. Our method also shows that the proportion of dominant disease-causing de novo LoF events is significantly higher in autism patients versus siblings (Fig. 2b; p-value: 8.4e-4; Wilcoxon rank-sum test).

Autism spectrum disorder is known to be four times more prevalent in males than females suggesting a protective effect in females. Previous studies show that there is a higher mutational burden for non-synonymous mutations in females ascertained for

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autism spectrum disorder⁴⁰. Therefore, we investigated the differences in [the impact of *de novo* pLoF variants](#) in male versus female autism patients. We also observe a similar pattern for pLoF mutations [as has been found for missense variants](#) – female probands have a higher proportion of predicted deleterious *de novo* pLoF variants than male probands (Fig. 2b; p-value: 0.03). A recent study based on exome sequencing of 3,871 autism cases delineated 33 risk genes at FDR < 0.1⁴¹. We observe that the *de novo* pLoF mutations in the autism patients in the 33 risk genes have higher dominant disease causing score than the *de novo* pLoF variants in other genes (Supplementary Fig. 5; p-value: 5e-3). Supplementary Table 9 includes the ALoFT predictions for *de novo* pLoF variants. Thus, ALoFT predictions corroborate the role of *de novo* pLoF variants in autism as shown by others using entirely different approaches.

Case Study 3: Identification of pathogenic somatic pLoF variants in cancer

We applied our prediction method to infer the effect of somatic premature stop variants (somatic pLoFs) from a compilation of 6,535 cancer exomes⁴². As shown in Figure 2c, somatic pLoFs are enriched in known cancer driver genes compared to randomly sampled genes of matched lengths. Moreover, deleterious somatic LoFs are strongly enriched in driver genes and depleted in LoF-tolerant genes (genes that contain at least one homozygous LoF variant in the 1KG population). To classify driver genes as tumor suppressors, Vogelstein proposed a “20/20” rule where a gene is classified as a tumor suppressor if > 20% of the observed mutations in that gene are LoF mutations⁴³. Considering the fact that loss-of-function of tumor suppressor genes can lead to oncogenesis, ALoFT can be used to identify [cancer-related pLoFs](#), especially those in tumor suppressors.

Case study 4: Distinguishing between benign and pathogenic pLoFs

Finally, we applied ALoFT to predict the effect of premature stop variants in the final exons of protein-coding genes. It is often assumed that premature stop variants in the last coding exon are likely to be benign because they [could](#) escape NMD; as a result, in many cases the effect will be the expression of a truncated protein rather than a complete loss of function. However, examples of disease-causing mutations in the last exon are also known⁴⁴. Therefore, we applied ALoFT to see if we could distinguish between benign and disease-causing LoF variants in the last coding exon. To this end, we applied ALoFT to understand the effect of pLoF variants in ESP6500, ExAC and HGMD datasets. A higher proportion of rare variants are observed in ESP6500 and ExAC cohort due to its larger sample size and higher sequencing depth (Fig. 3a). A large number of both common and rare premature stop variants are seen at the end of the coding genes in the 1KG, ESP6500 and ExAC datasets. In contrast, fewer disease-causing HGMD variants are seen at the ends of coding genes (Fig. 3a). ALoFT predicts that both common and rare premature stop variants in the last coding exon in the 1KG, ESP6500 and ExAC cohort are likely to be benign, whereas HGMD mutations [in the last coding exon](#) tend to be disease-causing (Fig. 3b). Thus, ALoFT is able to differentiate between rare but benign premature stop variants seen in healthy individuals and the rare disease-causing HGMD alleles.

Application to [personal genomes](#): Estimating the number of pathogenic pLoFs in a healthy genome or understanding pLoFs in an individual genome

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The above case studies clearly illustrate the validity of ALoFT score in elucidating the effect of pLoF variants. In order to estimate the number of pLoF disease alleles in a healthy individual, we applied ALoFT to 5,495 premature stop variants from the [1KG](#) dataset (Online Methods). The predicted benign LoF score for pLoFs in this population cohort have a wide range of values (Fig. 4, Supplementary Table 6,7). On average, each individual is a carrier of two rare heterozygous premature stop alleles that are predicted to be disease-causing in the homozygous state (Online Methods, Supplementary Table 7). Current estimates of the genetic burden of disease alleles (all types of variations, including LoFs) in an individual vary widely, ranging from 1.1 recessive alleles per individual to 31 deleterious alleles.⁴⁵⁻⁴⁹ In connection with this, it should be noted that disease databases include incorrect disease annotations and common variants and about 27% of variants were excluded by Bell *et al.* in their estimate of carrier burden for severe recessive diseases⁴⁵. The estimation and disease-causing potential of deleterious premature stop alleles can be affected by a number of confounding factors that include incomplete penetrance of disease alleles, variable expressivity, compensatory mutations, marginal variant calls and imperfect training datasets. [\[to add ExAC calculation ... \]](#)

Next, we looked at premature stop variants in the [1KG](#) cohort in known disease-causing genes. We find that variants in [1KG](#) are more likely to be benign compared to known disease-causing mutations in the same genes (Fig. 4; green vs. blue boxes, p-value: 6.9e-9). Our results provide a possible rationale for this observation. Firstly, variants predicted to be benign in [1KG](#) often affect isoforms that are different from the isoforms containing the disease-causing HGMD variant. This suggests that LoFs in healthy individuals may affect minor isoforms. About 12.4% of premature stop variants in the presumed healthy [1KG](#) individuals in known disease genes and the disease-causing variants in the same genes are on different isoforms. Secondly, some variants predicted to be benign in [1KG](#) occur in the last exon or later in the protein-coding transcript relative to the disease-causing variant in the same transcript. The effect of such variants is possibly the production of truncated proteins that are functional. Lastly, a majority of [1KG](#) variants seen in the disease genes are predicted to be disease-causing only if they are homozygous. However, they occur as rare heterozygous variants in the [1KG](#) cohort.

In summary, we describe a tool for predicting the impact of pLoF variants in the context of a diploid model, i.e. discriminating whether premature stop variants are likely to lead to recessive or dominant disease. Better identification and characterization of pLoF variants has both diagnostic and therapeutic implications. ALoFT allows for the identification and prioritization of high impact putative disease-causing pLoF variants in individual genomes. Integrating benign LoF variants with phenotypic information will help us to identify protective variants which are valuable drug targets^{50,51}. Gene functions important for species propagation might actually be deleterious as one ages; thus, LoF variants in such genes provide an intriguing avenue to discover targets for aging-related diseases⁵². Lastly, diseases caused by LoF variants provide opportunities for targeted therapy using drugs that either enable read-through of the premature stop, thus restoring the function of the mutant protein, or NMD inhibitors that prevents degradation of the LoF-containing transcript by NMD⁵³⁻⁵⁹. This is especially useful in the context of rare diseases where targeting the same molecular phenotype leading to different diseases alleviates the need to design a new drug for each individual disease. Further work will be needed both to correlate the predictions of ALoFT with experimental assays of protein

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loss of function, and to study the phenotypic impact of heterozygous and homozygous LoF variants in large clinical cohorts.

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Acknowledgments

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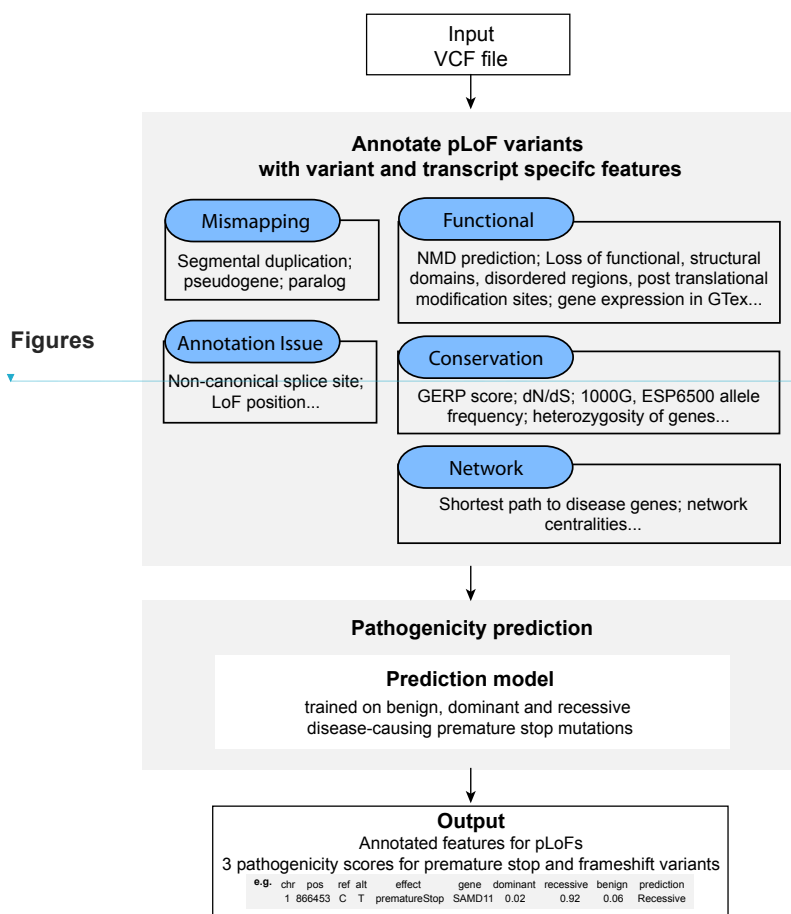
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Figures

Figure 1 - Schematic workflow.

ALoFT uses a VCF file as input and annotates premature [stop](#), frameshift-causing indel and canonical splice-site mutations with functional, conservation, network features. ALoFT also flags potential mismatching and annotation errors. Using the annotation features, ALoFT predicts the pathogenicity (as either benign, recessive or dominant disease-causing) of premature stop [and](#) [frameshift](#) mutations based on a model trained on known data. ALoFT can also take as input a 5-column tab-delimited file containing chromosome, position, variant ID, reference allele and alternate allele as its columns.

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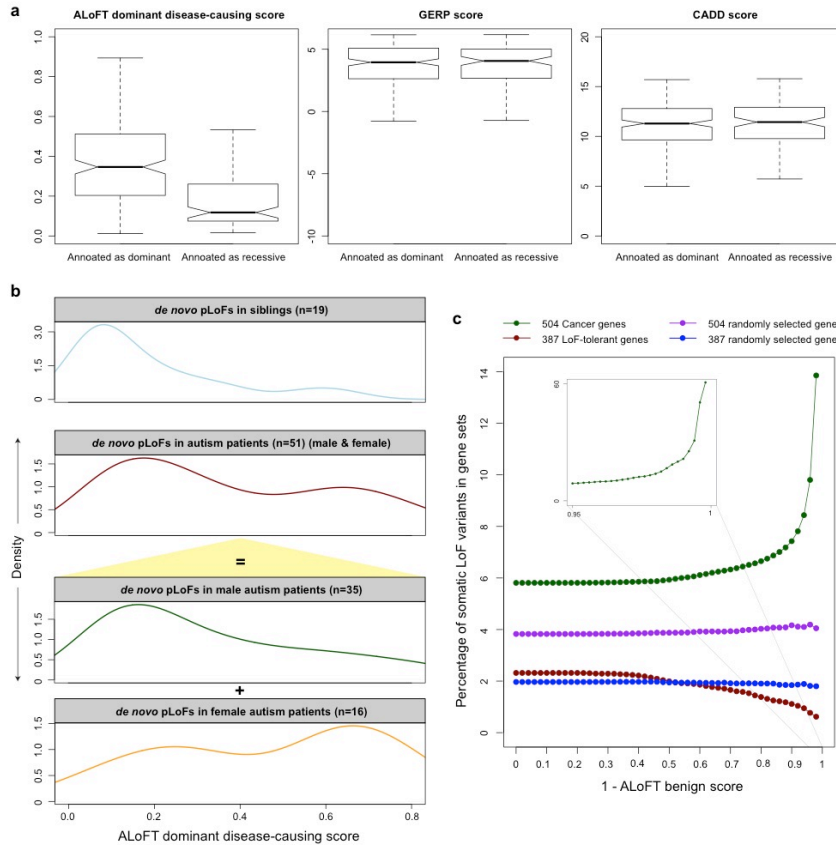


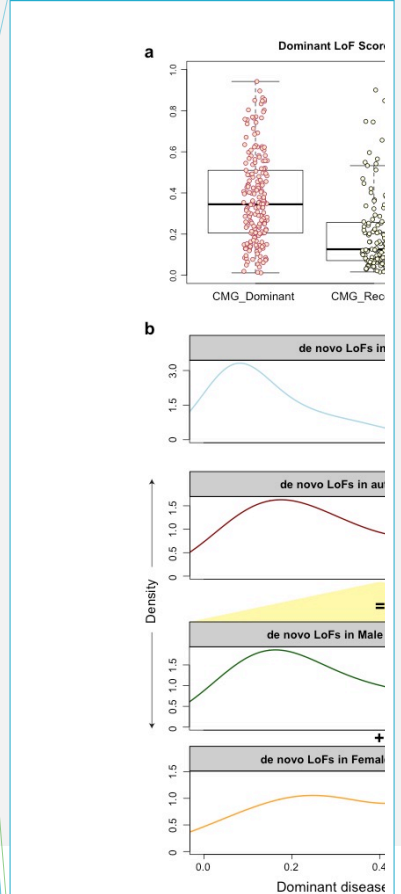
Figure 2 – ALoFT classification of premature stop variants from Mendelian disease, autism and cancer studies

a) ALoFT dominant [disease-causing](#) score, GERP and CADD score for ClinVar variants. All training variants are excluded. Average tolerance scores are 0.097 and 0.115 respectively for dominant and recessive datasets.

b) The top two panels show the dominant [disease-causing](#) scores of *de novo* premature stop mutations in autism patients and siblings; mutations in patients are further separated by gender, as shown in the bottom two panels.

c) The fraction of mutations occurring in various gene categories (Y-axis) as a function of predicted disease-causing score for cancer somatic premature stop variants (X-axis). Disease-causing score is calculated as $(1 - \text{predicted benign score})$. We calculated the fraction of somatic premature stop mutations in 504 known cancer driver genes and 504 randomly selected genes. To ensure that the cancer driver genes and the selected random genes have similar length distributions, the 504 random genes were selected from genes with matched length. Similarly, we compared the fraction of somatic premature stop mutations in 397 LoF-tolerant genes and 397 randomly selected genes with similar length distribution. LoF-tolerant genes are genes that have at least one homozygous LoF variant in at least one individual in the [1KG](#) cohort.

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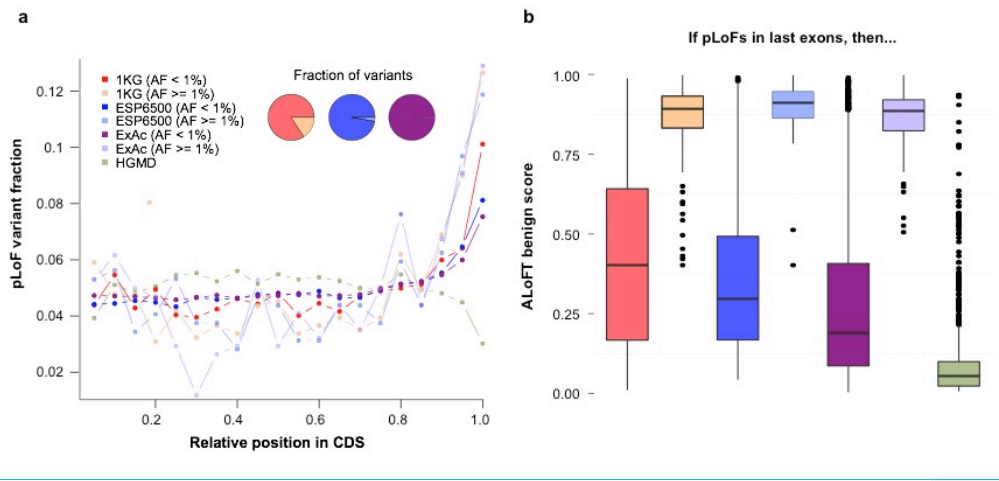


Figure 3 – pLoFs in last exons

a) Position of premature stop variants in coding transcripts. Compared to HGMD variants, both common and rare 1KG, 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.

b) Predicted benign scores for premature stop variants in the last coding exons. Training variants are excluded in this plot.

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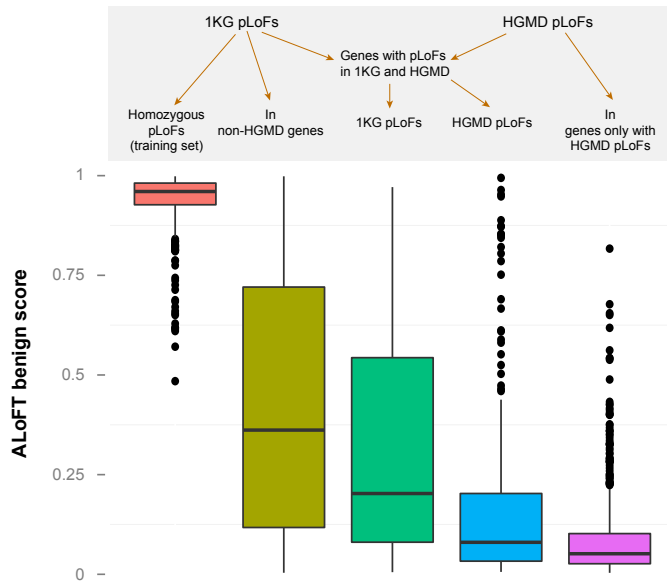


Figure 4 - ALoFT classification of 1000 Genomes and HGMD variants

Benign score for premature stop variants in 1KG and HGMD. For this plot, we randomly selected one variant per gene. "Benign pLoFs" set includes homozygous premature stop variants discovered in 1KG. The third (dark green) box plot pertains to premature stop variants in healthy 1KG individuals occurring in disease-causing genes obtained from HGMD. The fourth (blue) box plot pertains to pLoF variants in the subset of HGMD genes where 1KG pLoFs are also seen. "1KG pLoFs in non-HGMD genes" include 1KG variants not in HGMD genes, i.e. non-disease genes. "In genes only with HGMD pLoFs" include HGMD variants in only those disease genes where 1KG pLoFs are not seen.

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