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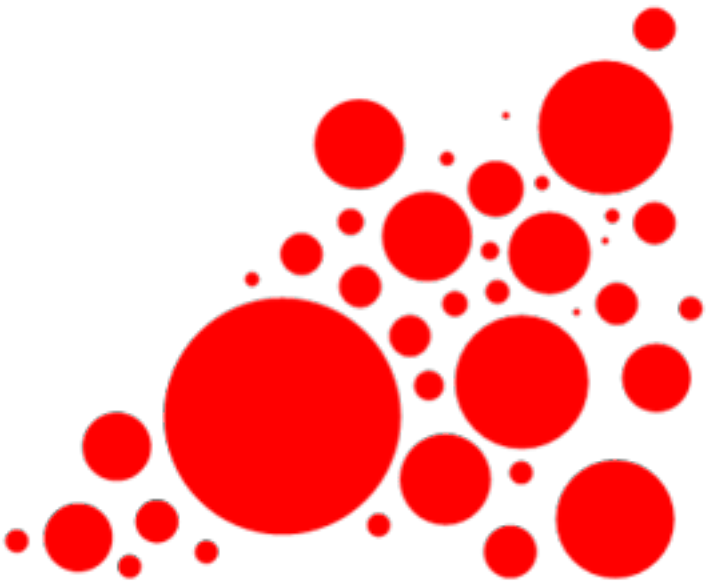
RESULT: MUTATED - observed in 990 samples based on 28355 analyses

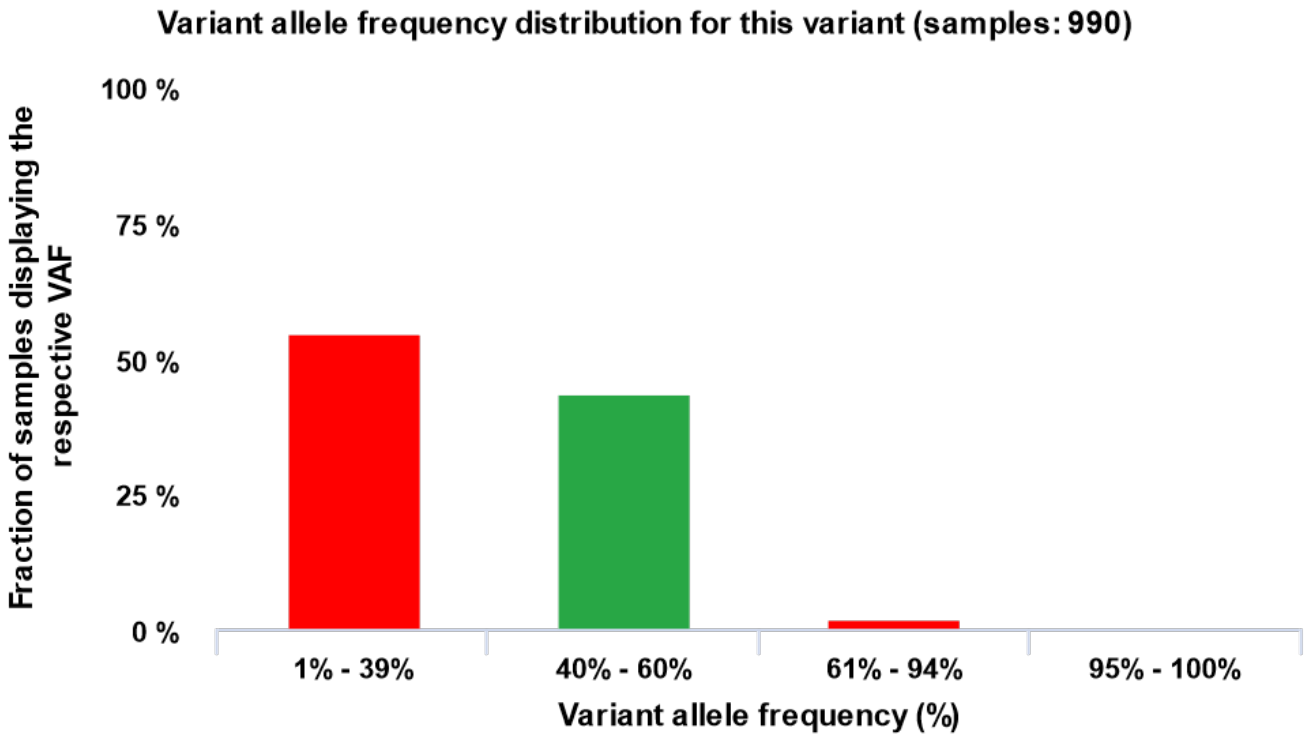
Gene	DNA change	Protein change	Transcript ID	Coordinate	# samples
SRSF2	c.284C>T	p.Pro95Leu	ENST00000392485	chr17:74732959	990

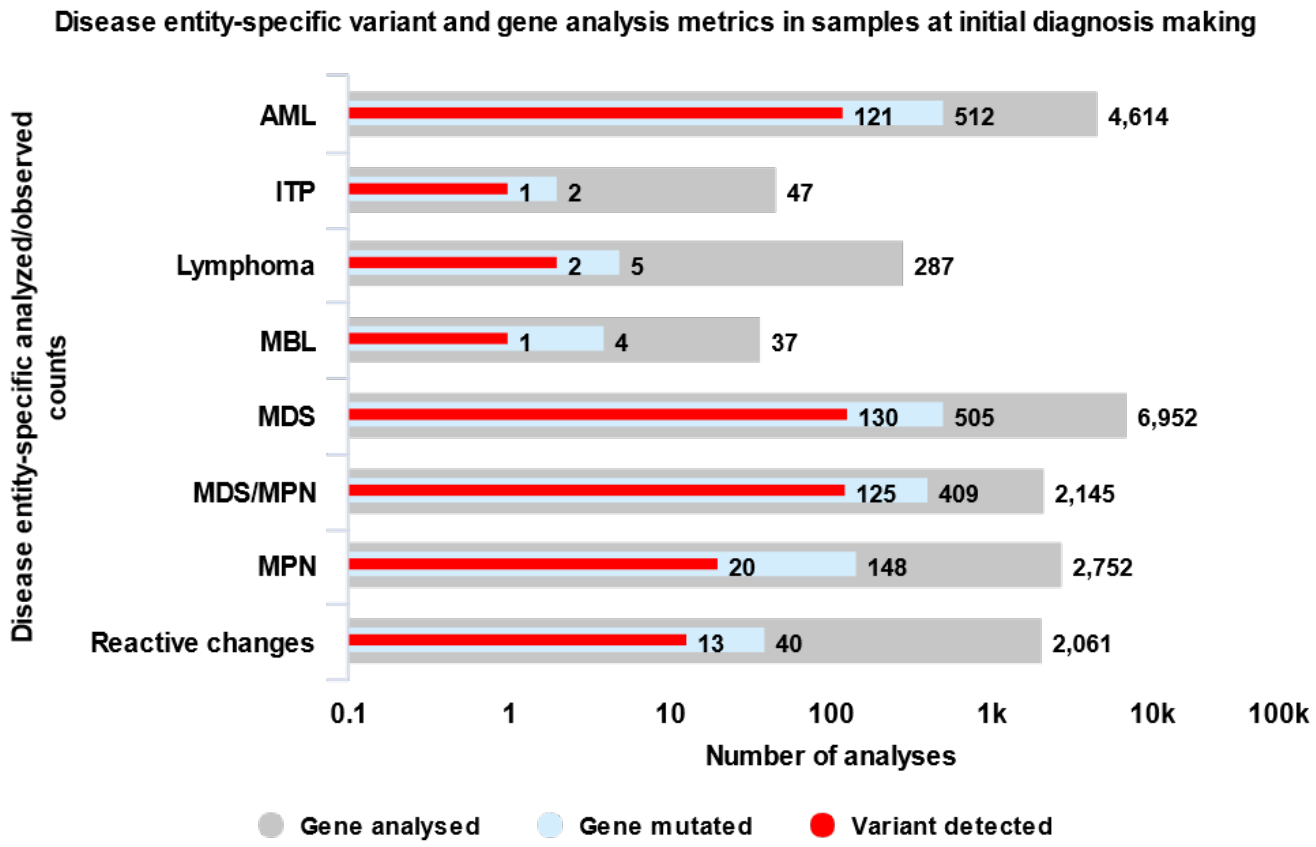


Variant allele frequency and entity-specific distribution pattern

The column chart is an aggregated plot of all samples harboring this particular variant in the database. Samples are binned into four intervals (1%-39%, 40% - 60%, 61% - 94%, >95%) based on the allele frequency of this variant (VAF) in each sample. In the absence of karyotypic abnormalities polymorphisms display variant allele frequencies (VAFs) of approximately 50% or 100%. Hence, the observation that a variant exceptionally occurs at VAFs of 40-60% or 95-100% in the majority of samples serves as indicator for the variant potentially being a polymorphism (termed wild type in MLLi:db). In contrast to that, variants most frequently occurring at VAFs of 1-39% or 61-94% are more likely to be somatic alterations (termed mutated in MLLi:db).

The bar chart provides a disease entity-specific overview of the analysis metrics exclusively based on samples investigated in the context of initial diagnosis making. The grey bar resembles the number of times the respective genomic region was analyzed. Whereas the red bar displays how often the respective variant was detected, the light blue bar indicates the number of times any variant classified as mutated was detected in the respective gene.





Cosmic Annotation

COSMIC (Catalogue Of Somatic Mutations In Cancer) is a data resource that is designed to store and display somatic mutation information and related details and contains information relating to human cancers. Data in COSMIC is curated from known Cancer Genes Literature and Systematic Screens.

ID	DNA	Protein	SNP	Somatic status	FATHMM-MKL	Count
COSM146288	c.284C>T	p.P95L	No	Reported in another cancer sample as somatic Confirmed somatic variant	PATHOGENIC	118

ID: Cosmic database accession ID
DNA: nucleotide change at DNA Level
Protein: amino acid change at protein level
FATHMM-MKL: Functional Consequences of variant

gnomAD Annotation

The Genome Aggregation Database (gnomAD) is a resource developed by an international coalition of investigators, with the goal of aggregating and harmonizing both exome and genome sequencing data from a wide variety of large-scale sequencing projects, and making summary data available for the wider scientific community.

Coordinate	Ref	Alt	Total	European (Non-Finnish)	European (Finnish)	African	South Asian	East Asian	Latino
chr17:74732959	G	A	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%	0.00%

Ref: Nucleotide alleles are on reference genome
Alt: Alternative alleles

dbSNP Annotation

The Single Nucleotide Polymorphism database (dbSNP) is a public-domain archive for a broad collection of simple genetic polymorphisms. This collection of polymorphisms includes single-base nucleotide substitutions (also known as single nucleotide polymorphisms or SNPs), small-scale multi-base deletions or insertions. The dbSNP has been designed to support submissions and research into a broad range of biological problems. These include physical mapping, functional analysis, pharmacogenomics, association studies, and evolutionary studies.

rsID	Coordinate	refNCBI	Obs.	Class	Submitter	Valid
rs751713049	chr17:74732958-74732959	G	A/C/G...	SNV	2	

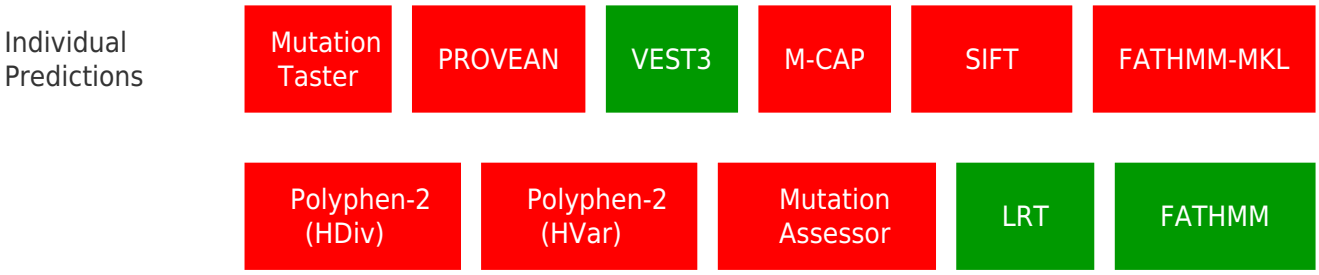
 Validated by frequency or genotype data: minor alleles observed in at least two chromosomes

dbNSFP Annotation

dbNSFP is a database developed for functional prediction and annotation of all potential non-synonymous single-nucleotide variants (nsSNVs) in the human genome. Its current version is based on the Gencode release 22 / Ensembl version 79 and includes a total of 83,422,341 nsSNVs and ssSNVs (splicing-site SNVs). It compiles prediction scores from 20 prediction algorithms (SIFT, Polyphen2-HDIV, Polyphen2-HVAR, LRT, MutationTaster2, MutationAssessor, FATHMM, MetaSVM, MetaLR, CADD, VEST3, PROVEAN, FATHMM-MKL coding, fitCons, DANN, GenoCanyon, Eigen coding, Eigen-PC, M-CAP, REVEL, MutPred), 6 conservation scores (PhyloP x 2, phastCons x 2, GERP++ and SiPhy) and other related information including allele frequencies observed in the 1000 Genomes Project phase 3 data, UK10K cohorts data, ExAC consortium data, gnomAD data and the NHLBI Exome Sequencing Project ESP6500 data, various gene IDs from different databases, functional descriptions of genes, gene expression and gene interaction information, etc..

Coordinate	Ref	Alt	AAref	AAalt	MLL Predictor
chr17:74732959	G	A	P	L	**Pathogenic**

Ensemble Predictions	REVEL	CADD	DANN	Eigen	Eigen-PC	MetaSVM	MetaLR


Individual Predictions
Mutation Taster
PROVEAN
VEST3
M-CAP
SIFT
FATHMM-MKL
Polyphen-2 (HDiv)
Polyphen-2 (HVar)
Mutation Assessor
LRT
FATHMM