COSMIC for Clinical

With over 71 million somatic mutations across 1,400 cancer types, COSMIC is the world's largest source of expert manually curated somatic mutation information relating to human cancers. Trusted by over 20,000 users and cited in the AMP/ASCO/CAP Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer, it is integral to any clinical assessment of somatic variants.

Integrating the COSMIC database into your NGS pipeline accelerates cancer sample analysis by rapidly prioritizing cancer driver mutations, distinguishing VUSes, and determining if an alteration is common or rare in the cancer type of interest when compared to similar cancer subtypes.

Value	Benefits	Features
Reproducible NGS workflow	Take over control of the data content	Users can precisely map genomic coordinates within their pipeline without error-prone and time consuming manual look-up of mutations in COSMIC
	Integrate the raw dataset into your NGS pipelines.	Users can schedule the integration of newly released datasets to suit their individual workflows
	Derive consistent results	
Automatable variant annotations	Scale up your NGS workflow without deploying added resources	High quality, standardized dataset manually curated by Ph.D. scientists, with transparency to underlying high-quality cancer publications
		Genomic annotations mapped to reference genome GRCh37 and GRCh38
Trustworthy and reliable variant selection	Identify variants that are likely somatic	Dataset covers more than 37 million coding mutations, > 15 million non-coding variants, gene expression data, CNVs, fusions
	Prioritize cancer drivers during clinical assessment with precision	Variants can be prioritized in context of over 1,400 cancer types
		Variants can be annotated with additional datasets include the mutational significance of 37 million coding mutations, resistance and druggable mutations COSMIC IDs can be added for further action

COSMIC, one of the most relevant databases during clinical assessment of somatic variants, listed in the AMP/ASCO/CAP guidelines as Evidence Source*

Table 4 Tier I: Variants with Strong Clinical Significance

Evidence source/type	Available evidence
FDA-approved therapies, PG, investigational therapies	Therapeutic: FDA approved or investigational with strong evidence*
	Diagnostic: In PG or reported evidence with consensus
	Prognostic: In PG or reported evidence with consensus
Mutation type	Activating, LOF (missense, nonsense, indel, splicing), CNVs, fusions
Variant frequencies	Mostly mosaic
Potential germline†	Mostly nonmosaic (VAF approximately 50% or 100%)
Population database: *ESP, dbSNP, 1000Genome, ExAC*	Absent or extremely low MAF
Germline database: *HGMD, ClinVar*	May or may not be present
Somatic database: *COSMIC*	Most likely present

*Adapted from Li MM et al., The Journal of Molecular Diagnostics, Volume 19, Issue 1, 2017, Pages 4-23, ISSN 1525-1578, https://doi.org/10.1016/j.jmoldx.2016.10.002