An SOP for the interpretation of pathogenicity of somatic variants in cancer (oncogenicity) {Draft 2.0}

(Note: If the somatic variant is in a gene known to cause predisposition to hereditary cancer, application of the ACMG/AMP ClinGen germline gene specific expert panel guidelines may be warranted in order to take gene specific nuances into account.)

Evidence of oncogenicity

Category Very strong

OVS1_somatic: Null variant (nonsense, frameshift, canonical ±1 or 2 splice sites, initiation codon, single or multi-exon deletion) in a bona fide tumor suppressor gene.

Caveats:

Use caution interpreting LOF variants at the extreme 3' end of a gene.

Use caution with splice variants that are predicted to lead to exon skipping but leave the remainder of the protein intact (in frame events). Also use caution if splice variant leads to expression of well-known alternative isoform which preserves tumor suppressor functionality.

Use caution in the presence of multiple transcripts.

Category Strong

OS1_somatic: Same amino acid change as a previously established oncogenic variant (by appropriate expert group) regardless of nucleotide change. Example: Val→Leu caused by either G>C or G>T in the same codon Caveat: Beware of changes that impact splicing rather than at the amino acid/protein level.

OS2_somatic: Well-established *in vitro* or *in vivo* functional studies supportive of an oncogenic effect of the variant. Note: Functional studies that have been validated and shown to be reproducible and robust in a clinical diagnostic laboratory setting are considered the most well established. If OS1_somatic is applicable, this rule can be used only if functional studies are based on the particular nucleotide change of the variant.

OS3_somatic: Located in one of the hotspots in cancerhotspots.org with at least 50 samples with a somatic variant at the same amino acid position and the same amino acid change count in cancerhotspots.org in at least 10 samples. (Use caution with hotspots driven by truncating somatic variants.) If the somatic variant is in a tumor type not well covered by cancerhotspots.org, resources such as COSMIC or a tumor type specific study could be used. This rule cannot be used if OS1_somatic is applicable, unless it is possible to observe hotspots based on the particular nucleotide change.

Category Moderate

OM1_somatic: Located in a critical and well-established functional domain (e.g., active site of an enzyme). This rule cannot be used if OS1_somatic or OS3_somatic is applicable.

Caveat: Population data for insertions/deletions may be poorly called by next-generation sequencing. Population data may contain somatic variants associated with clonal hematopoiesis.

OM2_somatic: Protein length changes as a result of in-frame deletions/insertions in known oncogene or tumor suppressor gene or stop-loss variants in known tumor suppressor gene.

OM3_somatic: Missense variant at an amino acid residue where a different missense variant determined to be oncogenic (by appropriate expert group) has been documented. Amino acid distance from reference amino acid should be greater or at least approximately the same as for missense change determined to be oncogenic. Example: Arg156His is oncogenic; now you observe Arg156Cys. This rule cannot be used if OS1_somatic or OS3_somatic or OM1_somatic is applicable. Caveat: Beware of changes that impact splicing rather than at the amino acid/protein level.

OM4_somatic: Located in one of the hotspots in cancerhotspots.org with less than 50 samples with a somatic variant at the same amino acid position and the same amino acid change count in cancerhotspots.org is at least 10 (Use caution with hotspots driven by truncating somatic variants). If the somatic variant is in a tumor type which is not covered well by cancerhotspots.org, resources such as COSMIC or a tumor type specific study could be used. This rule cannot be used if OM1_somatic or OM3_somatic is applicable.

Category Supporting

OP1_somatic: Multiple lines of computational evidence support an oncogenic effect of a variant (conservation/evolutionary, splicing impact, etc.).

Caveat: Because many *in silico* algorithms use the same or very similar input for their predictions, each algorithm should not be counted as an independent criterion. Can be used only once in any evaluation of a variant.

OP2_somatic: Somatic variant in a gene in malignancy with a single genetic etiology. Example: retinoblastoma is caused by bi-allelic RB1 inactivation.

Caveat: A small fraction of cases may be caused by an alternative mechanism; histological similarities may cause misdiagnosis.

OP3_somatic: Located in one of the hotspots in cancerhotspots.org and the particular amino acid change count in cancerhotspots.org is below 10 (use caution with hotspots driven by truncating somatic variants). If somatic variant is in a tumor type which is not covered well by cancerhotspots.org, resources such as COSMIC or a tumor type specific study could be used.

OP4_somatic: Absent from controls (or at extremely low frequency) in Genome Aggregation Database (gnomAD).

Evidence of benign impact

Category Very strong

BVS1_somatic: Minor allele frequency is >5% in Genome Aggregation Database (gnomAD) in any of 5 general continental populations: African, East Asian, European (Non-Finnish), Latino, and South Asian. If the somatic variant is in a gene known to cause predisposition to hereditary cancer, ACMG/AMP ClinGen germline expert panel gene specific guidelines (if they exist) must be consulted to establish a cutoff that takes disease prevalence into account.

Category Strong

BS1_somatic: Well-established in vitro or in vivo functional studies show no oncogenic effects.

BS2_somatic: Minor allele frequency is >1% in Genome Aggregation Database (gnomAD) in any of 5 general continental populations: African, East Asian, European (Non-Finnish), Latino, and South Asian. If the somatic variant is in a gene known to cause predisposition to hereditary cancer, ACMG/AMP ClinGen germline expert panel gene specific guidelines (if they exist) must be consulted to establish a cutoff that takes disease prevalence into account.

Category Supporting

BP1_somatic: Multiple lines of computational evidence suggest no impact of a variant (conservation/ evolutionary, splicing impact, etc.).

Caveat: Because many in silico algorithms use the same or very similar input for their predictions, each algorithm cannot be counted as an independent criterion. Can be used only once in any evaluation of a variant.

BP2_somatic: A synonymous (silent) variant for which splicing prediction algorithms predict no impact to the splice consensus sequence nor the creation of a new splice site AND the nucleotide is not highly conserved.

Point values for strength of evidence:

Evidence Strength	Oncogenic points	Benign points
Supporting	1	-1
Moderate	2	-2
Strong	4	-4
Very strong	8	-8

Point ranges for classification of somatic variants:

Category	Point ranges
Oncogenic	>= 10
Likely Oncogenic	6 to 9
VUS	0 to 5
Likely Benign	-1 to -6
Benign	<= -7

Intended scope of this SOP

This SOP is focused on interpretation of oncogenicity of small somatic genetic variants specifically in tumor cells.

This SOP should not be used for interpretation of pathogenicity of germline cancer predisposition variants.

Interpretation of oncogenicity of variants using this SOP should be done in context of relevant tumor type(s).

This SOP is not intended for interpretation of oncogenicity of fusions and other chromosomal rearrangements.

This SOP is not intended for determining the diagnostic, prognostic or therapeutic value of variants.

This SOP is primarily intended to be used in conjunction with AMP/ASCO/CAP style somatic guidelines.