

**Table : Benchmarking of Cancer-Specific Somatic Mutations:** 'Yes' signifies that the method predicted the mutation, while 'No' indicates the mutation was not predicted. A **Yes** in bold indicates that the in-house pipeline detected a common mutation using either Mutect2 or Varscan2. In the 'Gene' column, a gene name in bold letters indicates that the gene matches the provided pan-cancer reference file.

Chromosome	Position	Ref>Alt	Mutect2	Varscan2	Inhouse	Gene
NC_000006.12	43507679	C>T	Yes	No	No	LRRC73
NC_000016.10	4694276	G>A	Yes	No	No	NUDT16L1
NC_000017.11	7675088	C>T	Yes	No	<b>Yes</b>	<b>TP53</b>
NC_000018.10	51054859	C>G	<b>Yes</b>	<b>Yes</b>	<b>Yes</b>	<b>SMAD4</b>
NC_000018.10	51054923	T>C	Yes	No	No	<b>SMAD4</b>
NC_000018.10	51058112	C>G	Yes	No	No	<b>SMAD4</b>
NC_000023.11	71141250	G>A	No	Yes	No	<b>MED12</b>
NC_000023.11	71141262	G>A	No	Yes	No	<b>MED12</b>
NC_000023.11	71141301	A>ACAGCAACACCAG	No	Yes	No	<b>MED12</b>
NC_000023.11	71141322	G>C	No	Yes	No	<b>MED12</b>
NC_000005.10	56882045	ACAG>A	No	No	Yes	LOC100130849
NC_000007.14	55181298	C>A	No	No	Yes	<b>EGFR</b>
NC_000007.14	55181370	G>A	No	No	Yes	<b>EGFR</b>
NC_000009.12	21974833	T>C	No	No	Yes	<b>CDKN2A</b>
NC_000012.12	107933512	C>A	No	No	Yes	-

NC_000012.12	107933690	G>A	No	No	Yes	-
NC_000017.11	7675254	A>G	No	No	Yes	<b>TP53</b>
NC_000017.11	81071966	G>T	No	No	Yes	BAIAP2
NC_000019.10	15614347	T>G	No	No	Yes	-
NC_000019.10	15614398	C>G	No	No	Yes	-
NC_000019.10	15614417	C>T	No	No	Yes	-
NC_000023.11	71141302	CAGCAACACCAG>CAGCAACACCAGTAGCAACACCAG	No	No	Yes	<b>MED12</b>