

filter	software	purpose
GATK	GATK	Removes putative SNVs with GATK quality scores less than 40 (as part of the GATK processing, with indel realignment and base recalibration)
SS	SomaticSniper	Removes putative SNVs with a SomaticScore less than 40
VAQ	SomaticSniper	Removes putative SNVs with Somatic-Sniper Variant Allele Quality scores less than 20
LOH	SomaticSniper, python	Removes putative SNVs that are identified as loss of heterozygosity
10bp-SNV	python	Removes putative SNVs located within a 10 bp window of any other putative SNV
10bp-INDEL	python	Removes putative SNVs located within a 10 bp window of indels
dbSNP	python	Removes putative SNVs that overlap with dbSNP coverage
<10%	python	Removes putative SNVs if, in the tumor data, the percentage of reads covering the site with the alternate allele is less than 10%