



Indels just pass the frequency filter.

The compound heterozygous filter looks for two or more heterozygous variants in one gene. Note that both variants have to pass the other filters (except the annotation filter). Custom regions specified in the gene sets count as one additional gene (i.e., if  $\geq 2$  heterozygous variations are found in the custom regions of a gene set, they are reported as compound heterozygous recessive).