Supplementary materials: Reproducibility of SNV-calling in multiple sequencing runs from single tumors

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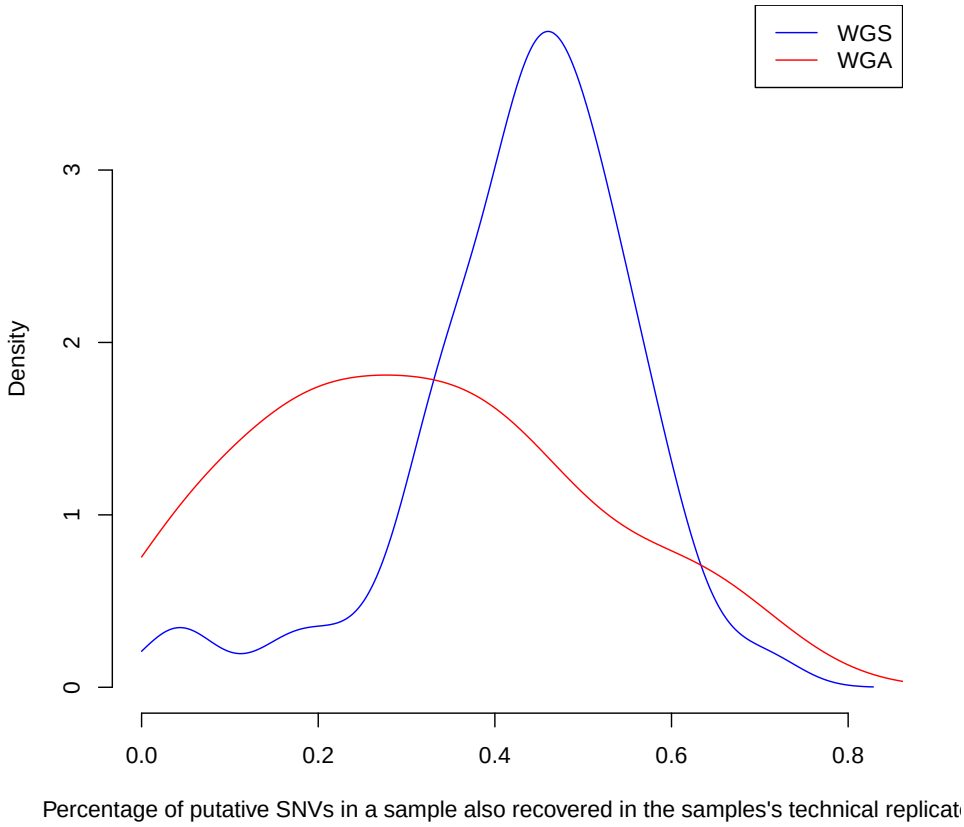

Figure 1: **Number of putative SNVs in WGS versus WGA, as called by SomaticSniper before filtering.** Each point represents data for a single patient. The line is $y = x$, so points falling below the line agree with the hypothesis that an additional amplification step produces more sequencing errors in a sample. The number of mutations found in one replicate correlates with the number of mutations found in the other replicate (Spearman $\rho = 0.42$, $S = 16142$, $P = 0.002$).