S16 Figure. Distribution of GATK annotation scores. The vertical lines indicate the used cut-offs. DP - combined depth per SNP across samples. QD - variant confidence standardized by depth. MQ - Mapping quality of a SNP. FS - strand bias in support for REF vs ALT allele calls. SOR - sequencing bias in which one DNA strand is favored over the other. MQRankSum - rank sum test for mapping qualities of REF vs. ALT reads. ReadPosRankSum – indicates if all the reads supporting a SNP call tend to be near the end of a read. Indels were not used in this study.