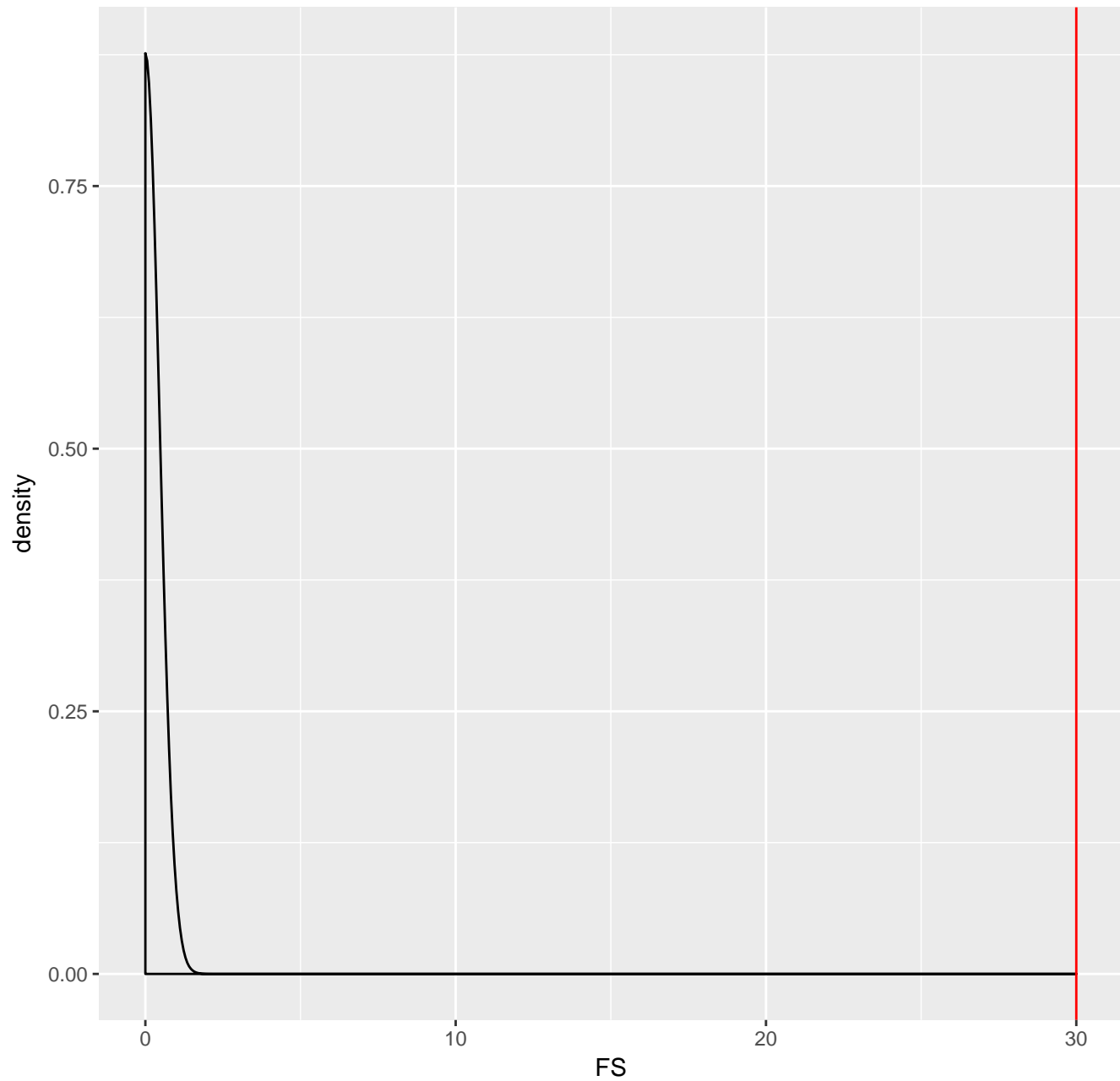
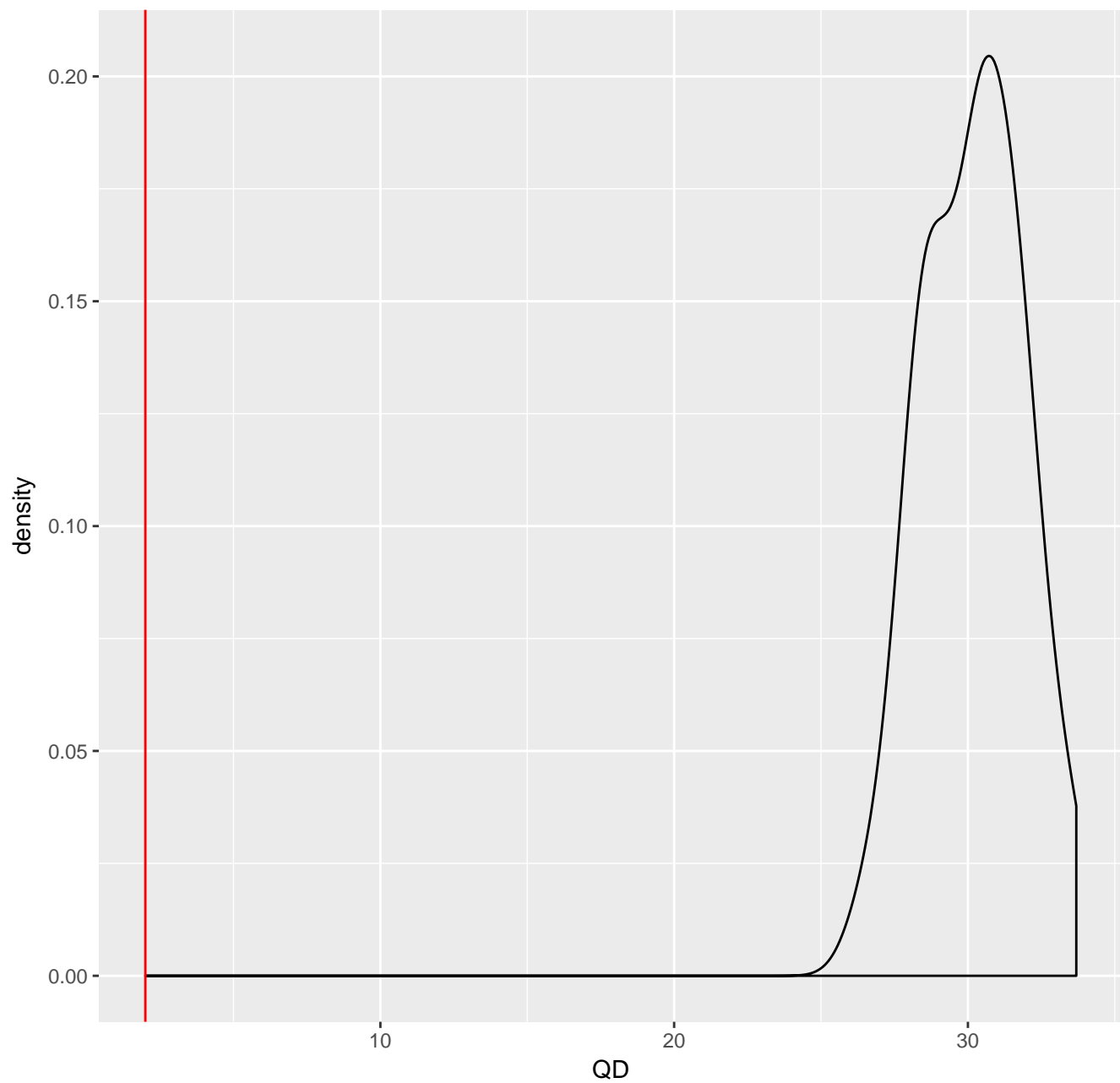


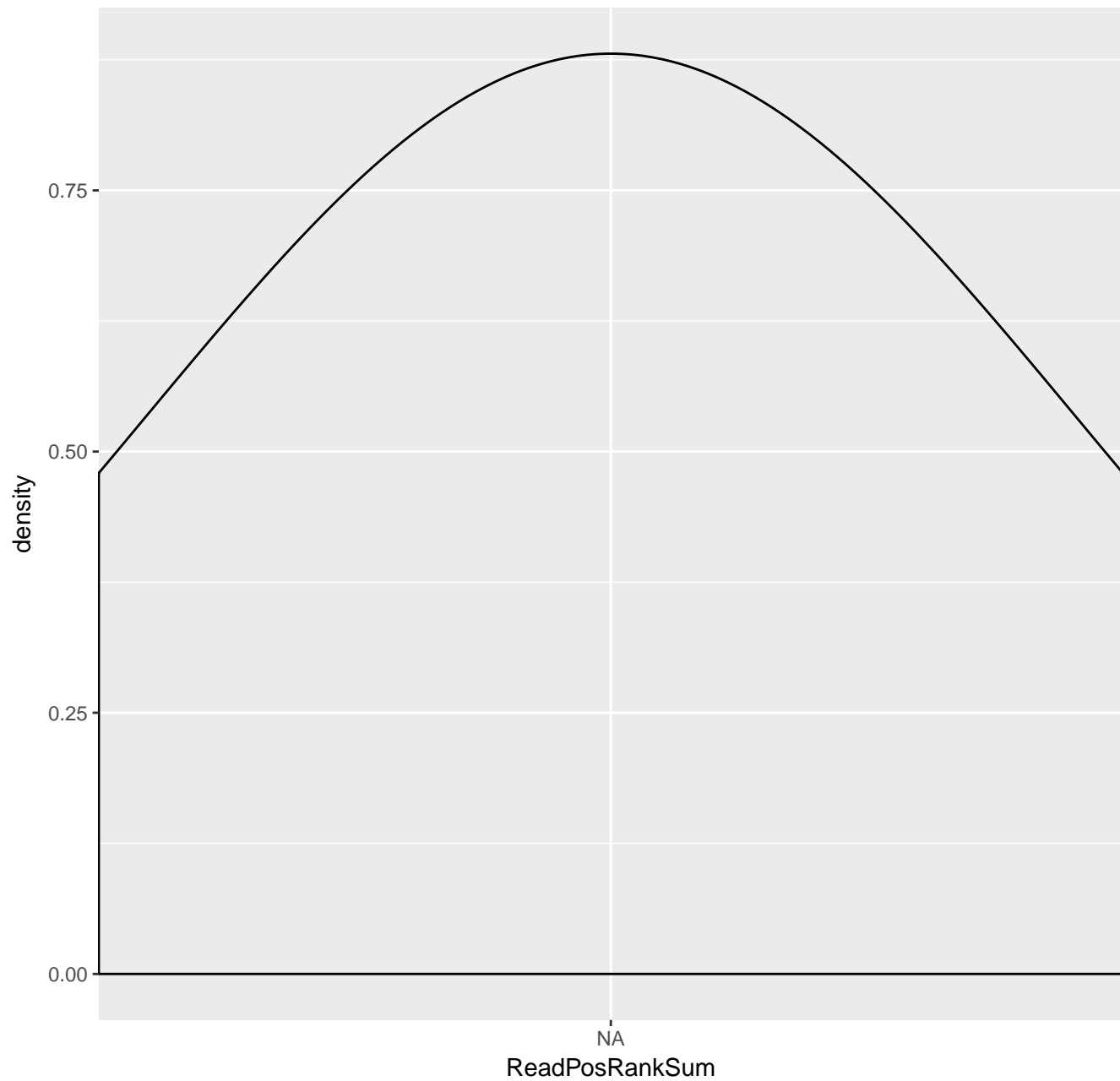
Fisher Strand (FS– Strand Bias Variant on F or R) – Greater than 30 removed



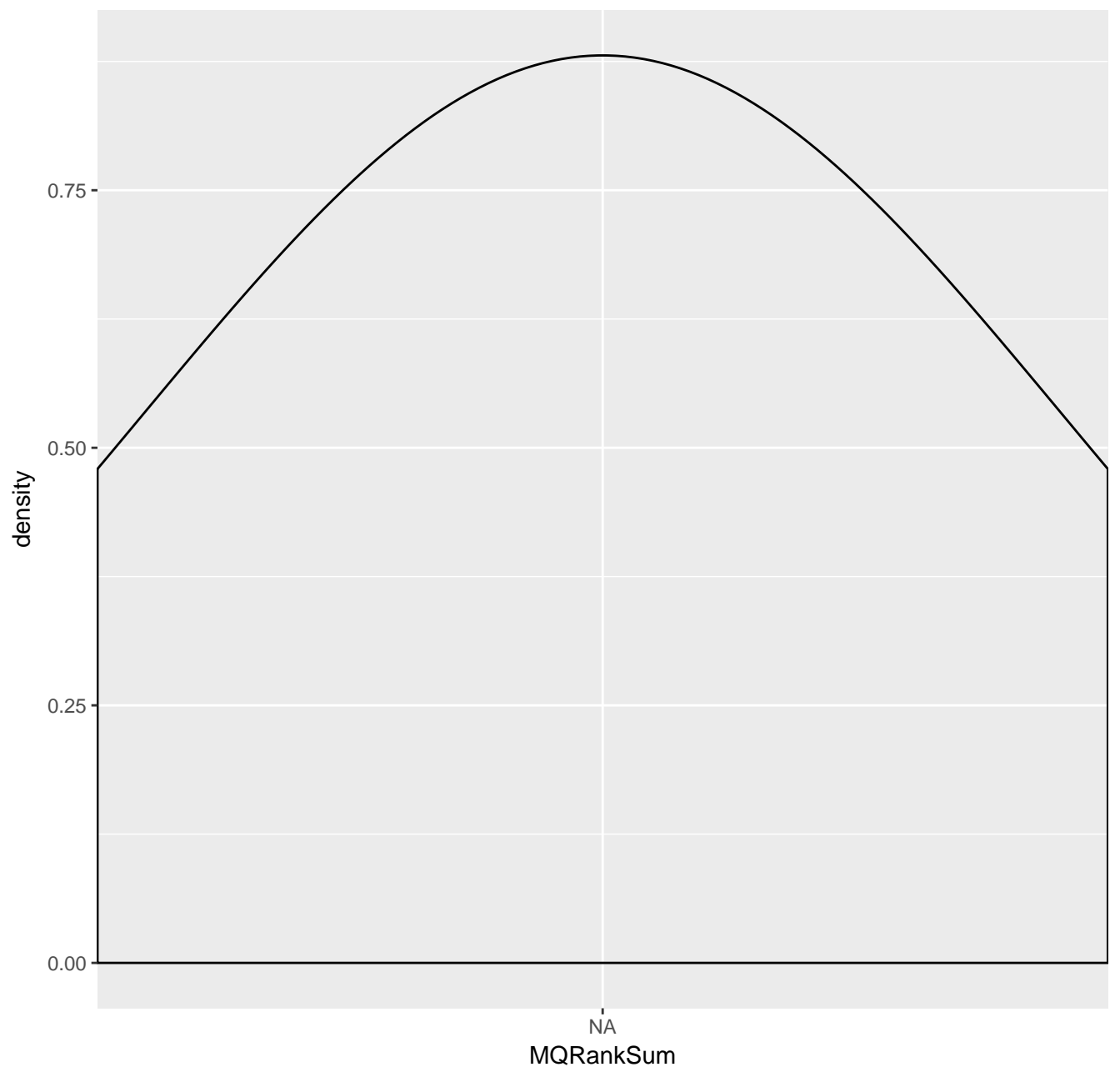
QD -variant qual/unfiltered depth – Below 2 removed



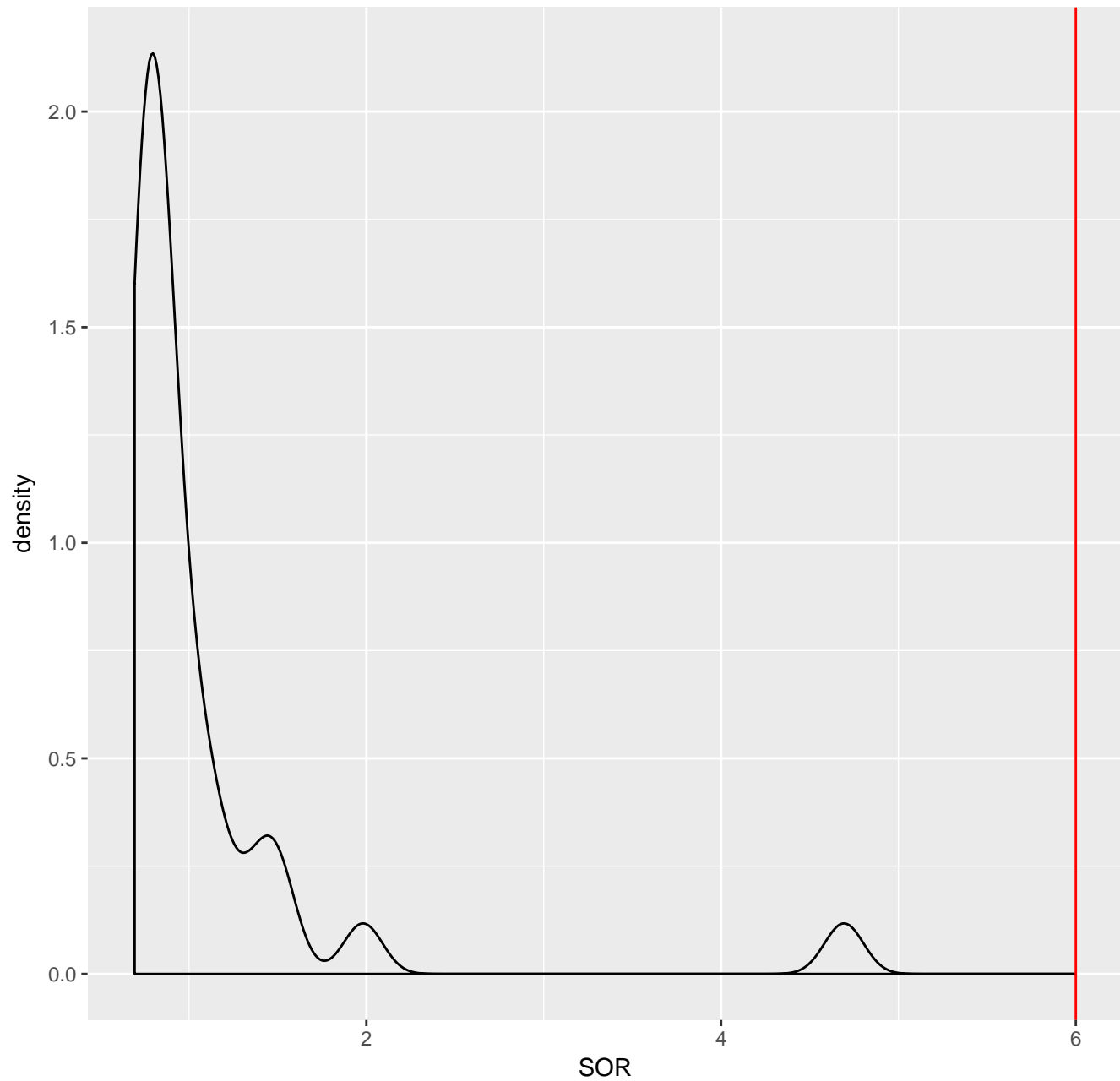
ReadPosRankSum – Negative values indicate ALT near ends (cutoff  $-5.5$ )



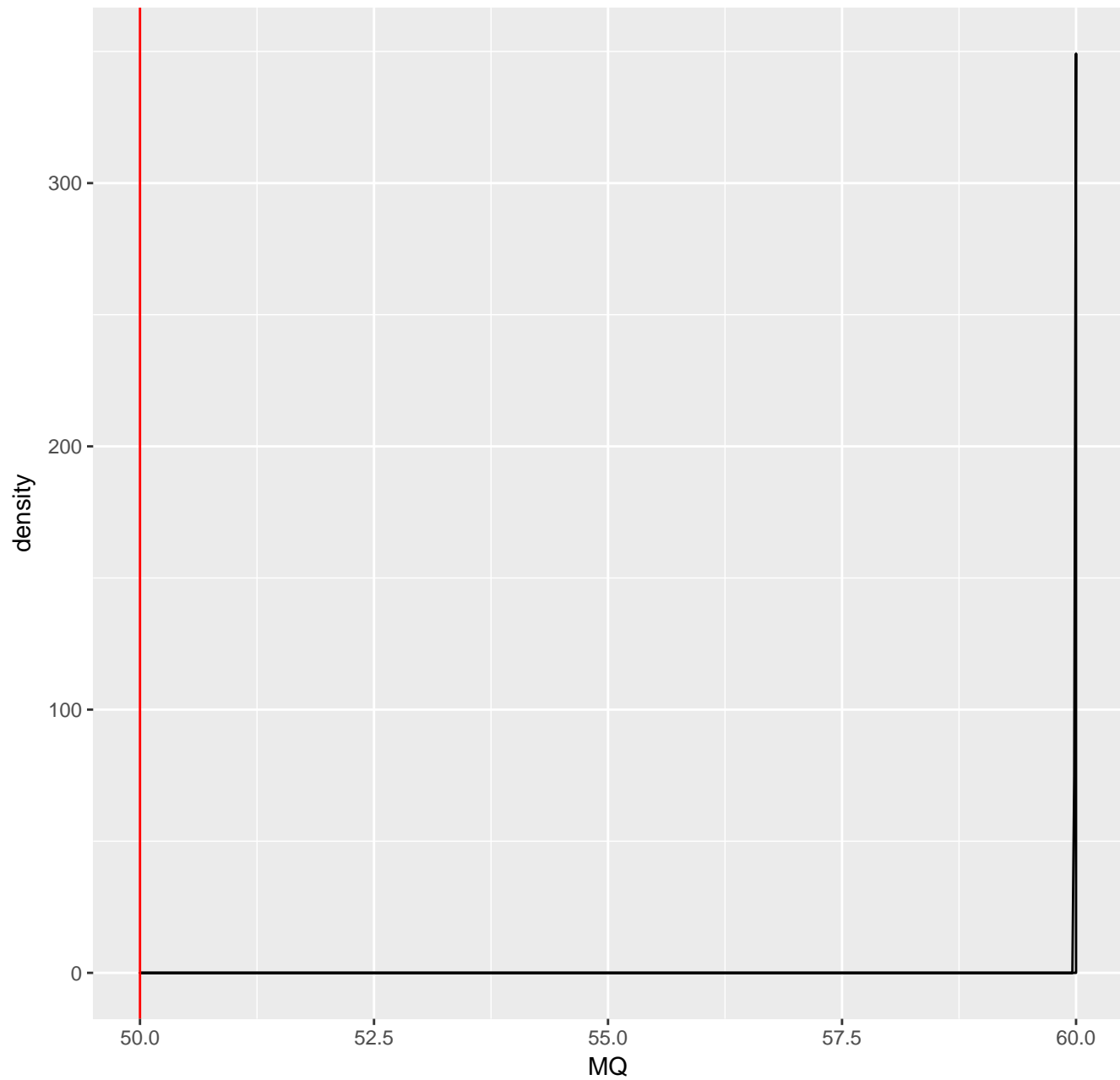
MQRankSum of Mapping Quality – Negative values indicate ALT near ends (–100)



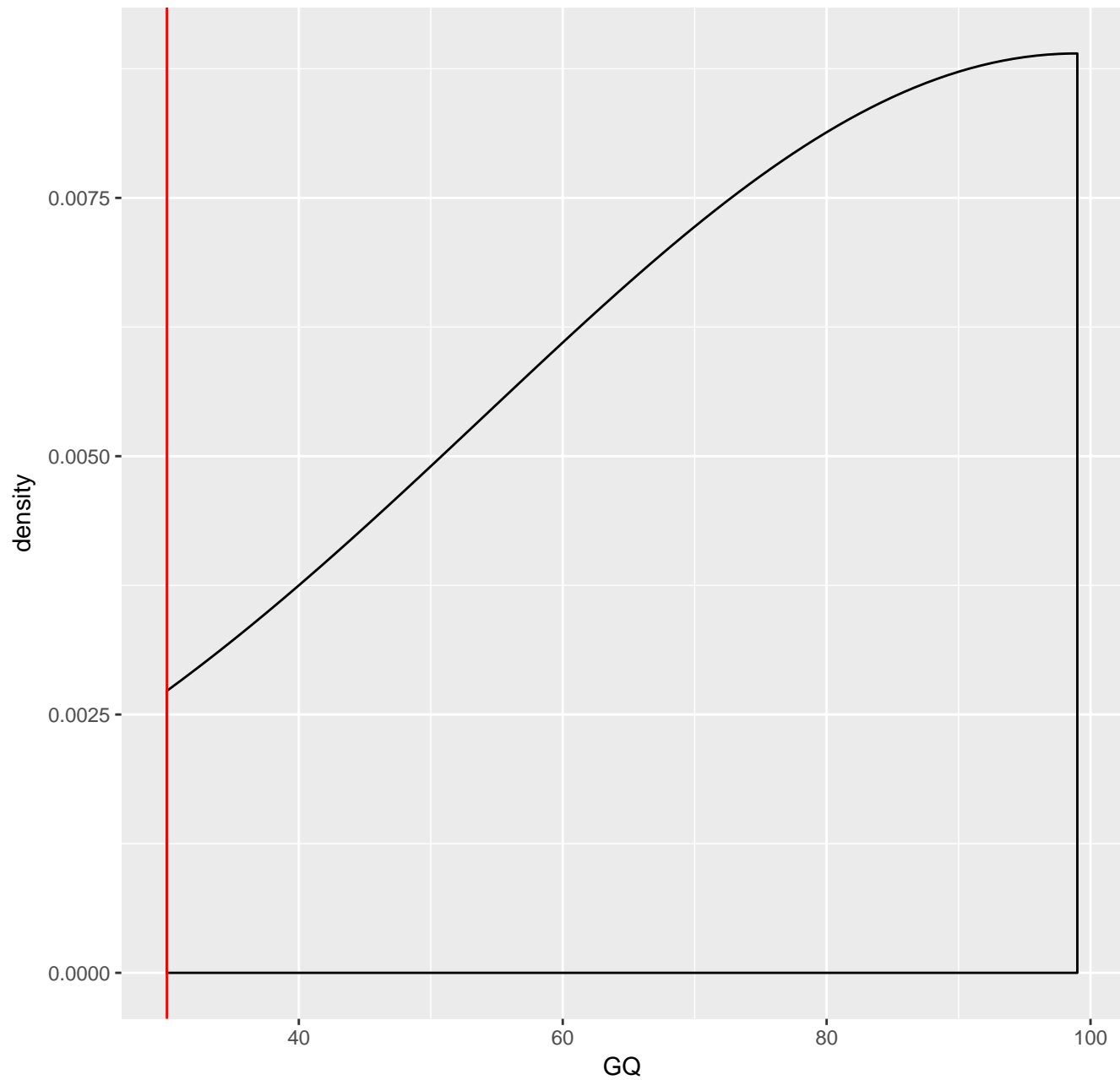
StrandOddsRatio (SOR) – Greater than 6 shows strand bias



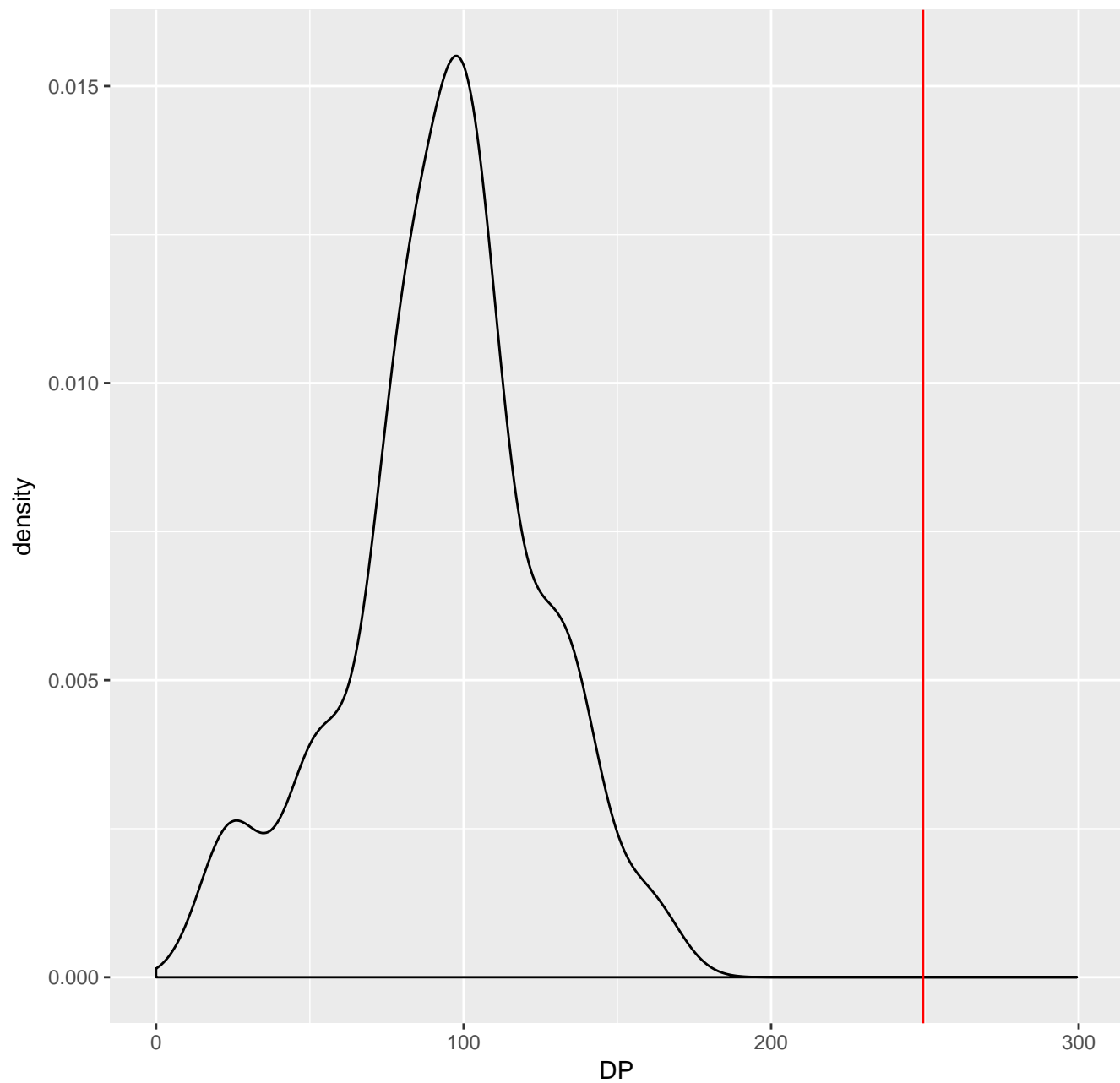
Root Mean Square Error Mapping Quality (MQ) – Less than 50 removed



GQ – Genotype Quality (Phred score) – No current cutoff



DP– Depth – Red line drawn at Mean + 5\*STDEV





# Depth Statistics

	mean	SD	mean_plus_5xSD
1	93.2258064516129	31.2374878177054	249.41324554014