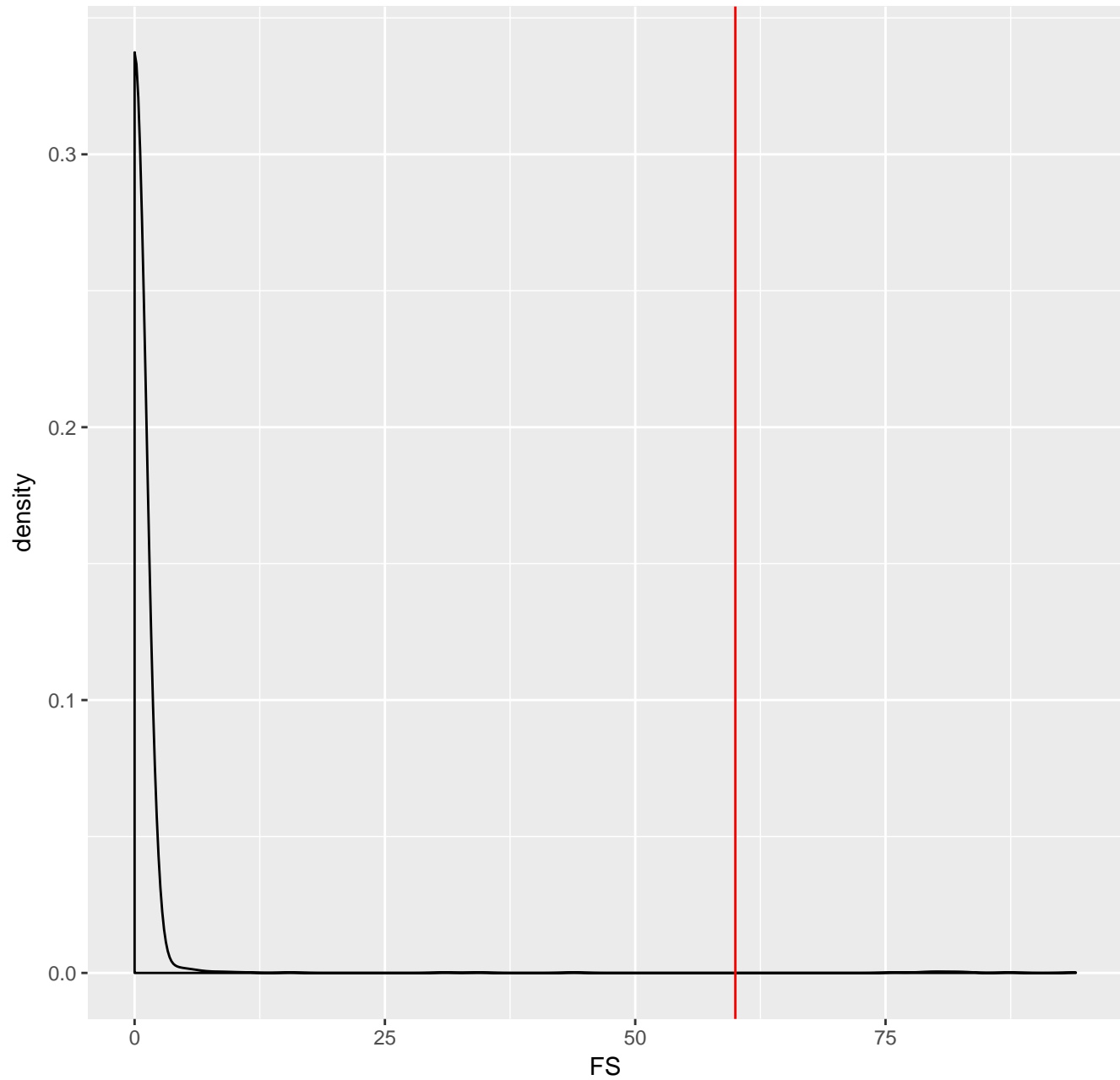
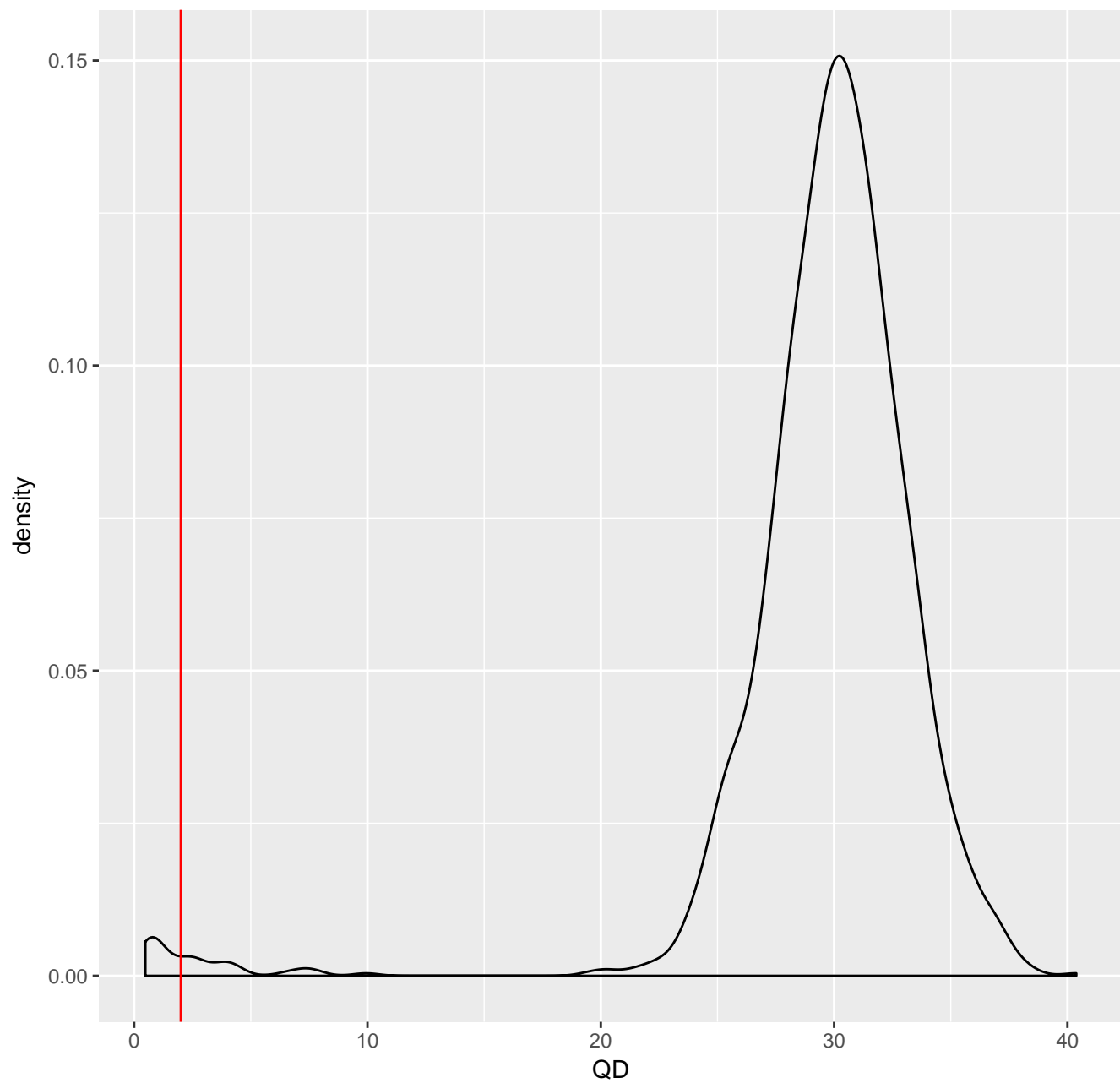


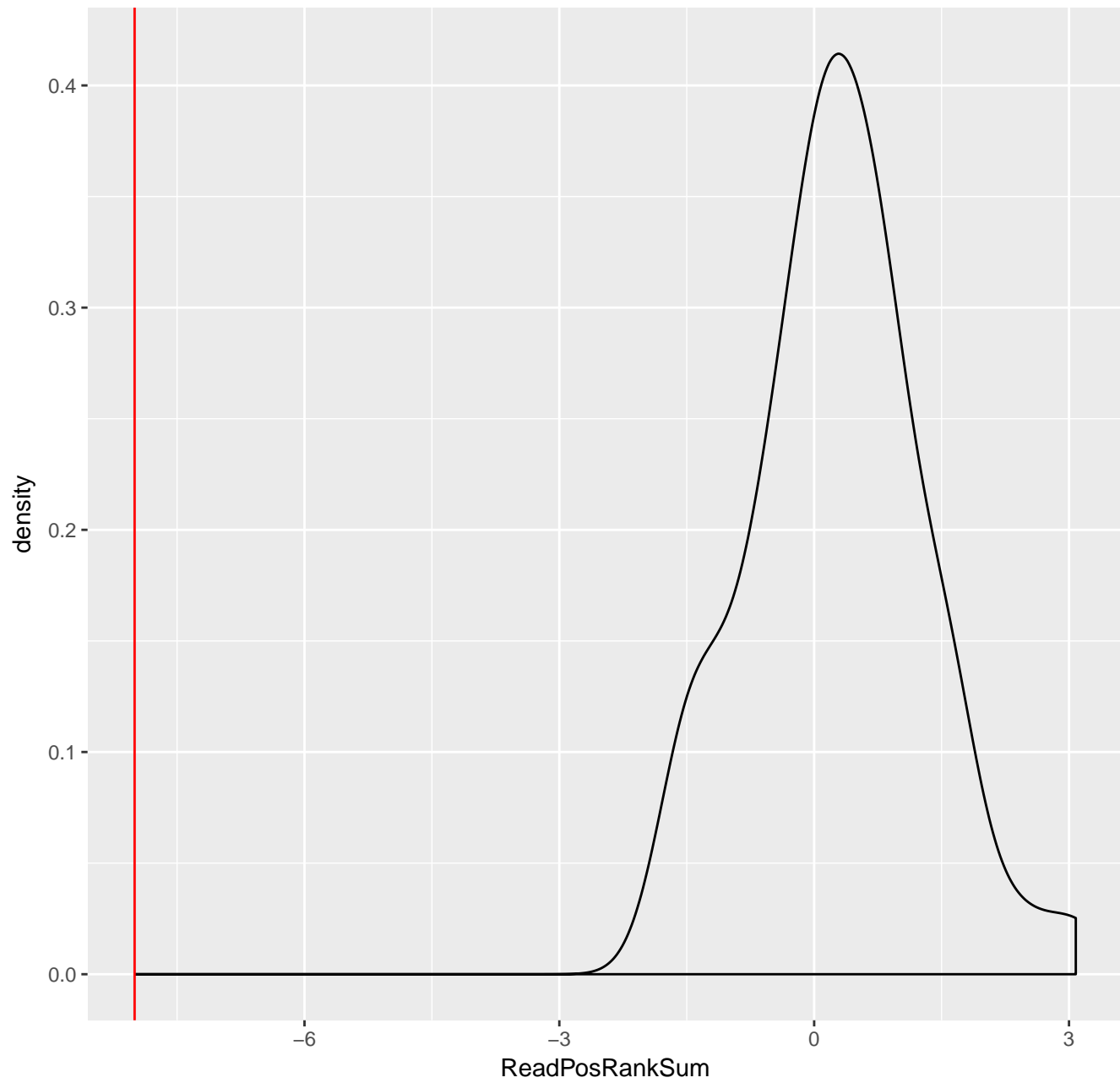
Fisher Strand (FS– Strand Bias Variant on F or R) – Greater than 60 removed



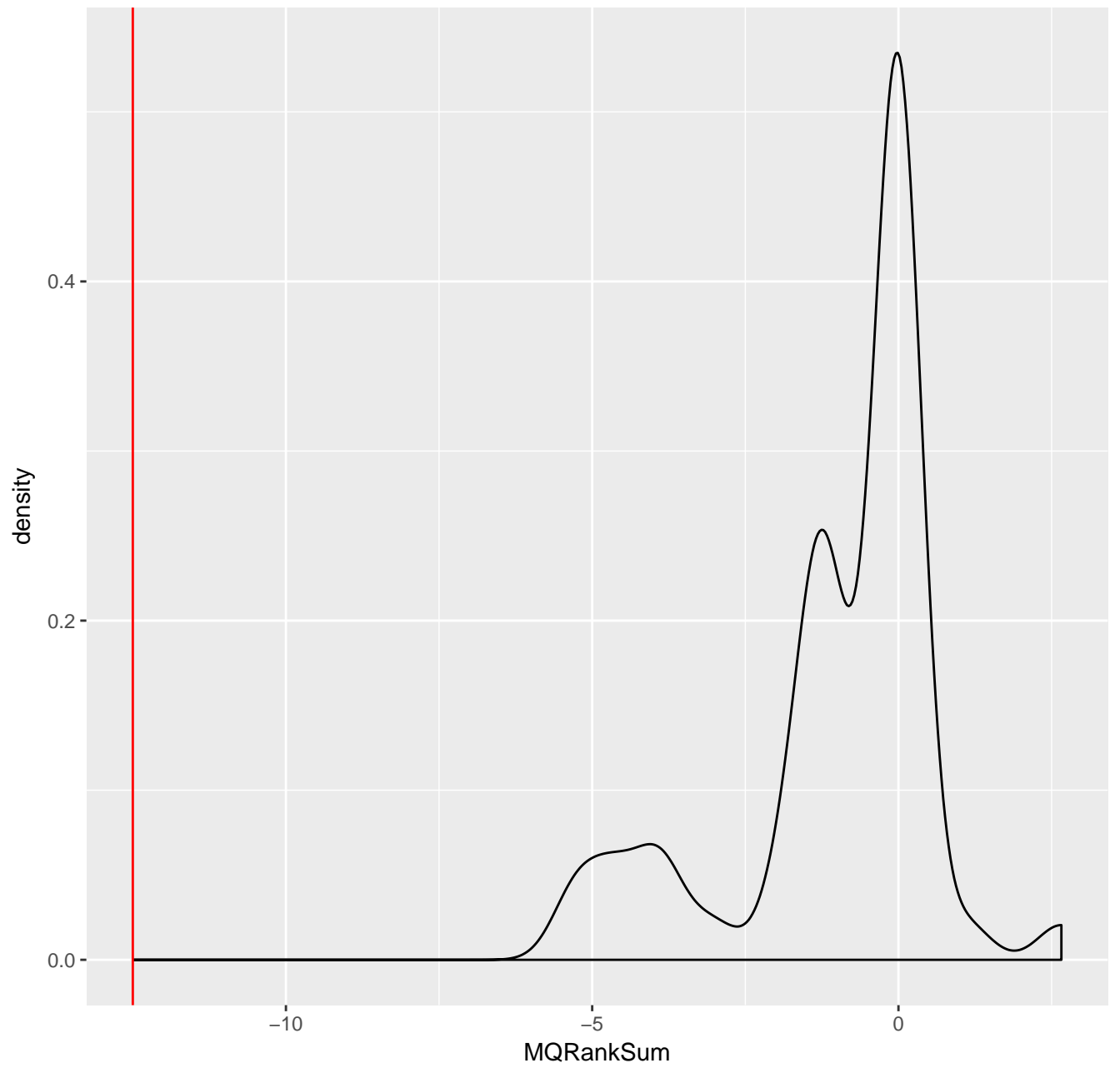
QD -variant qual/unfiltered depth – Below 2 removed



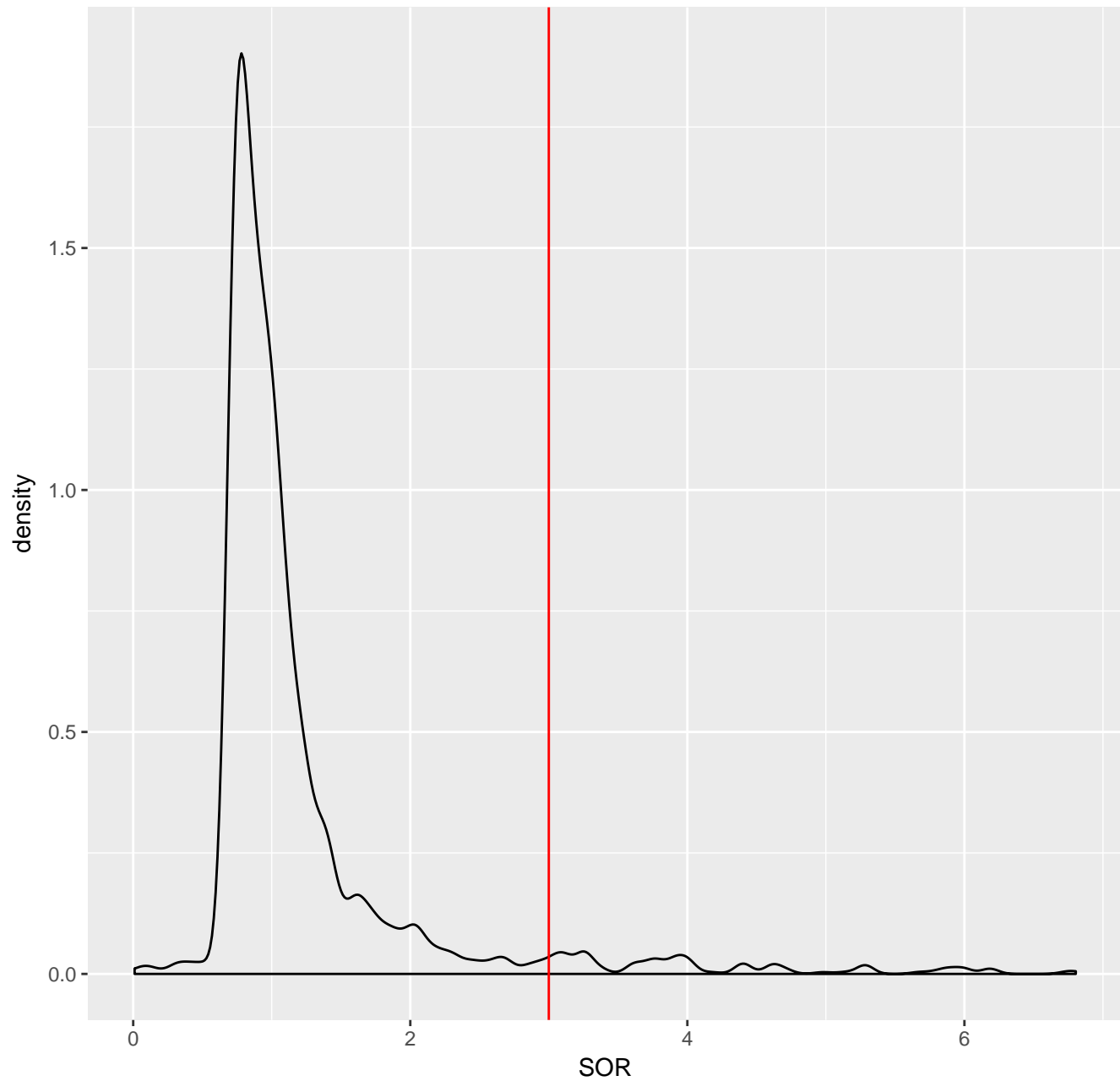
ReadPosRankSum – Negative values indicate ALT near ends (cutoff -8)



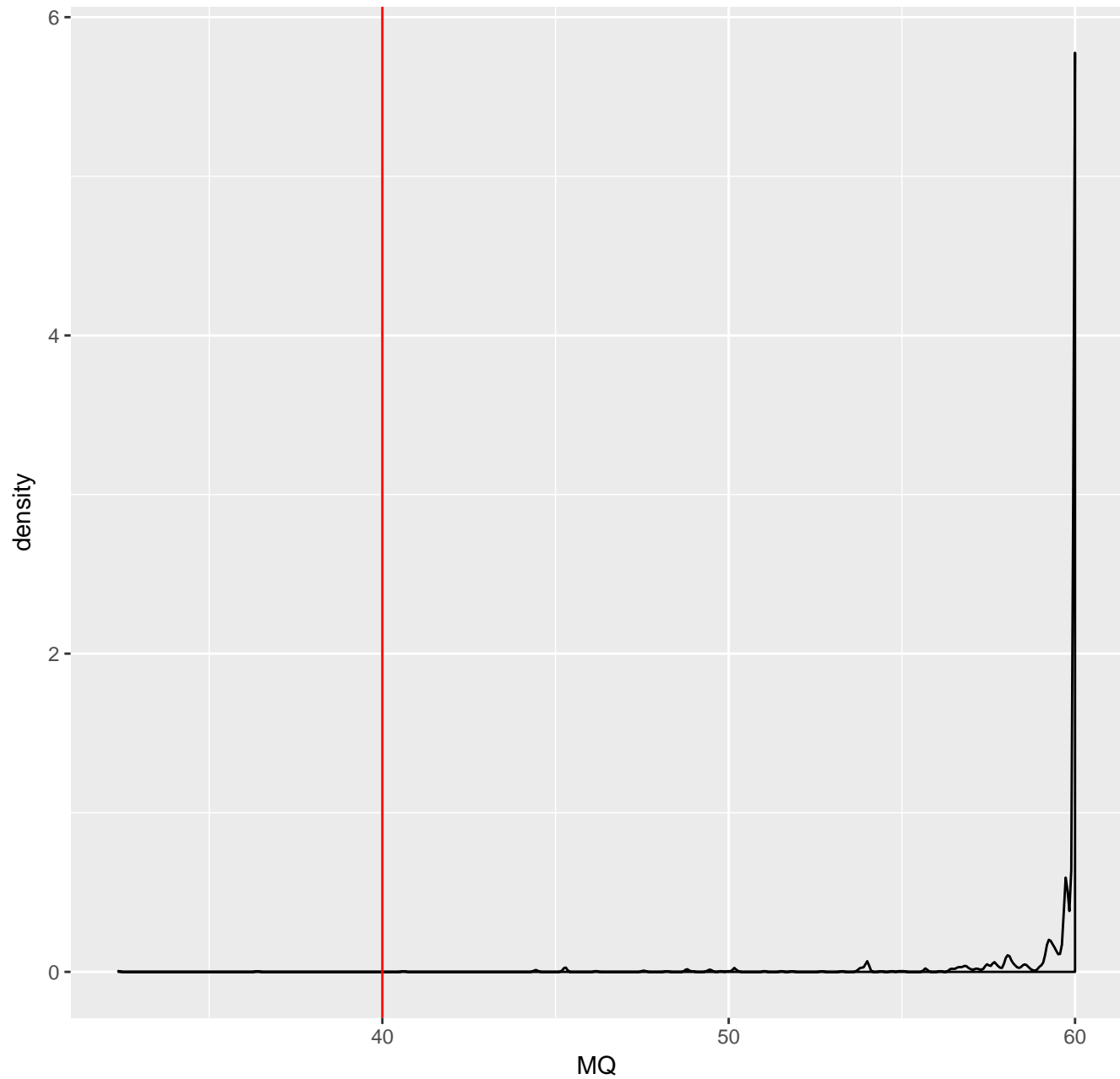
MQRankSum of Mapping Quality – Negative values indicate ALT near ends (–12.



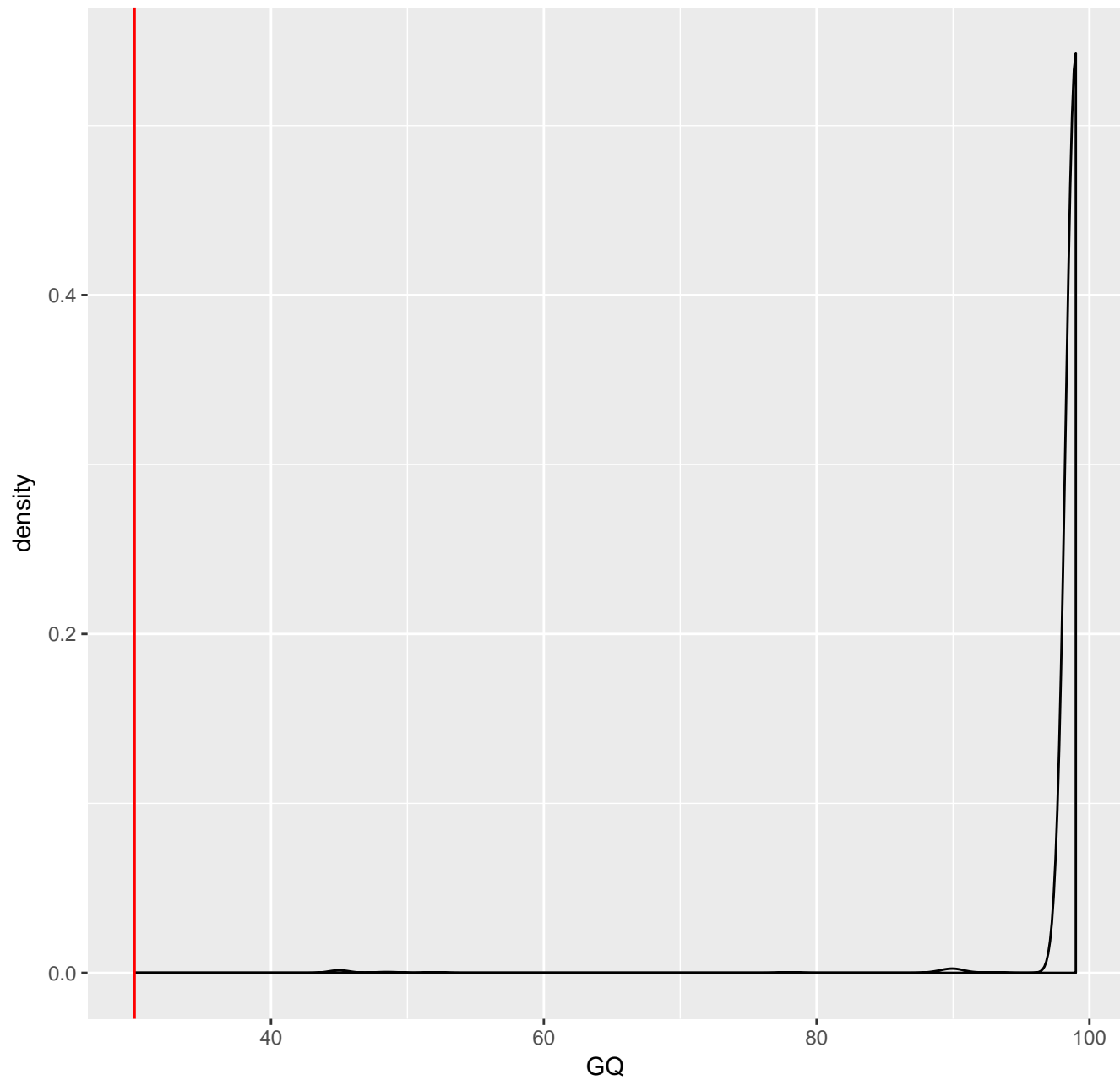
StrandOddsRatio (SOR) – Greater than 3 shows strand bias



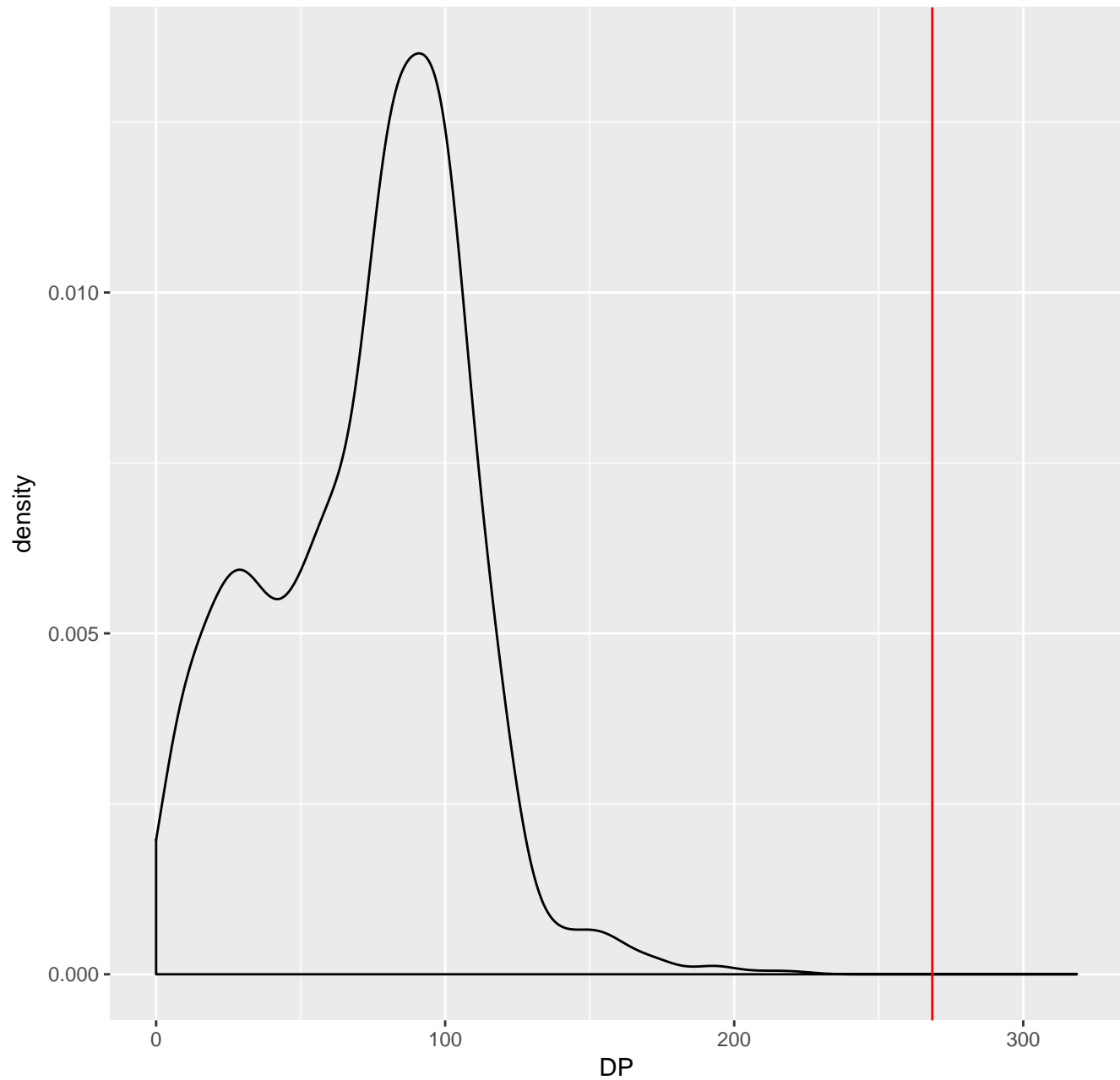
Root Mean Square Error Mapping Quality (MQ) – Less than 40 removed



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	74.3651059085842	38.8348273125831	268.539242471499