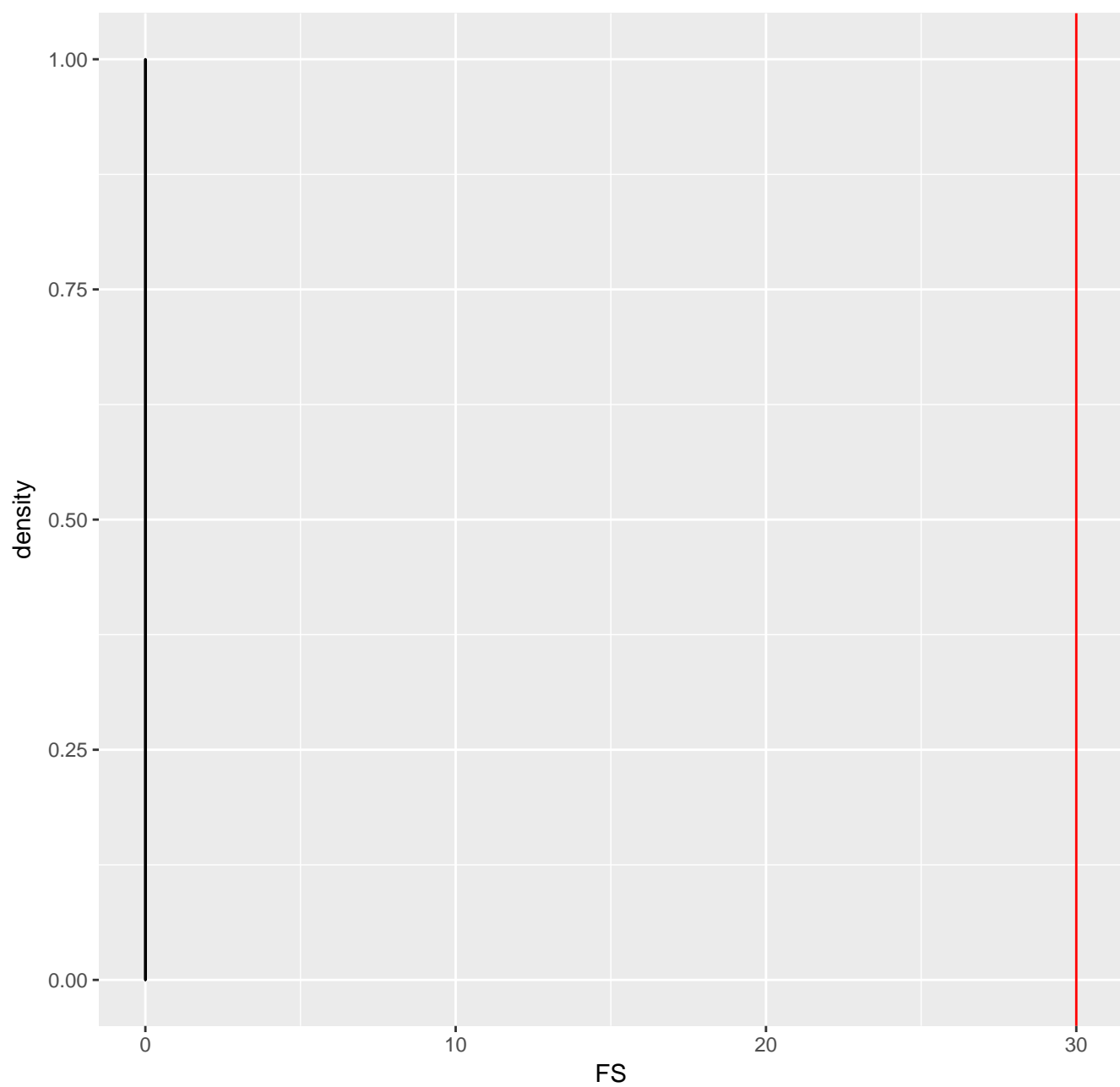
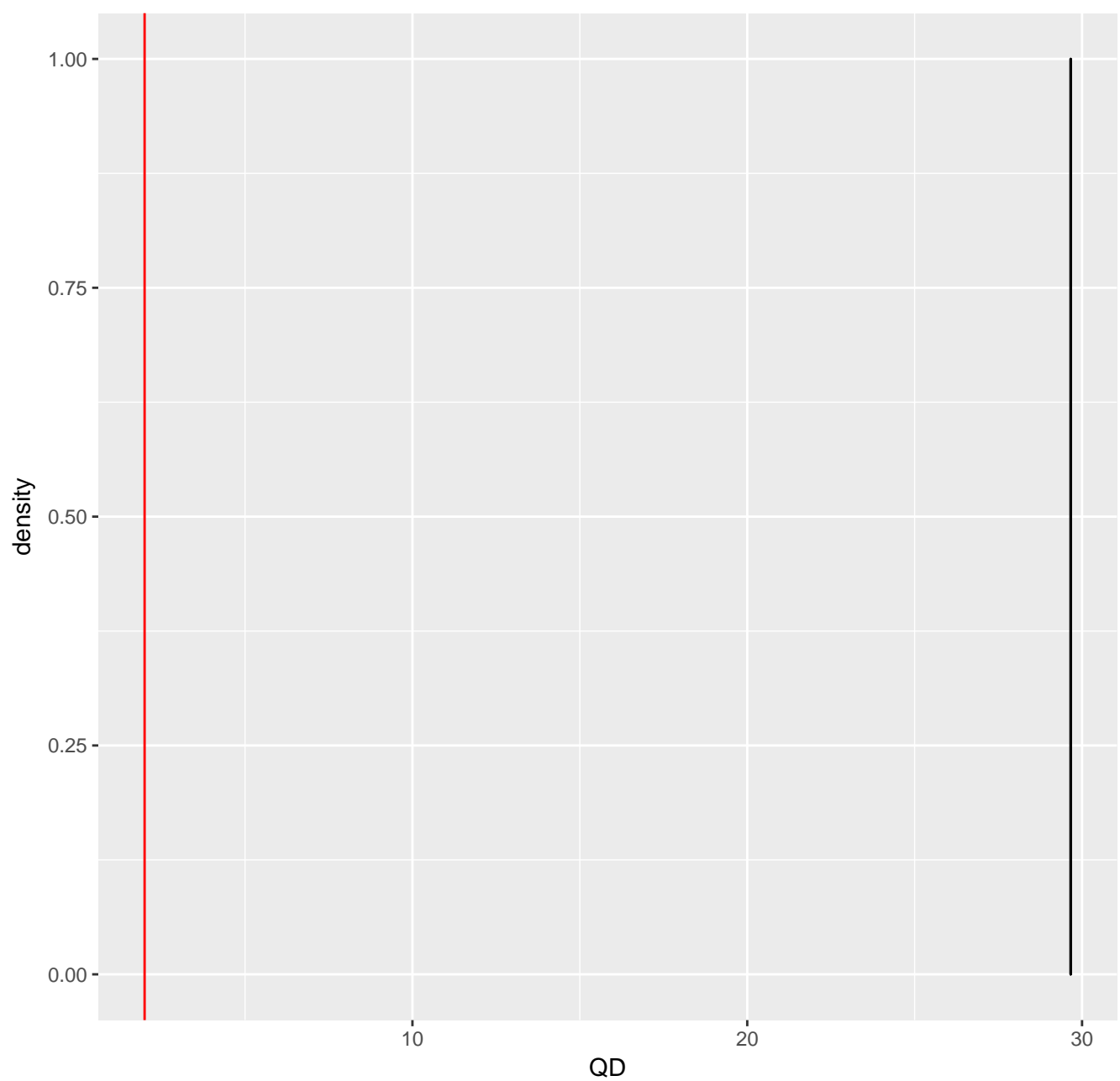


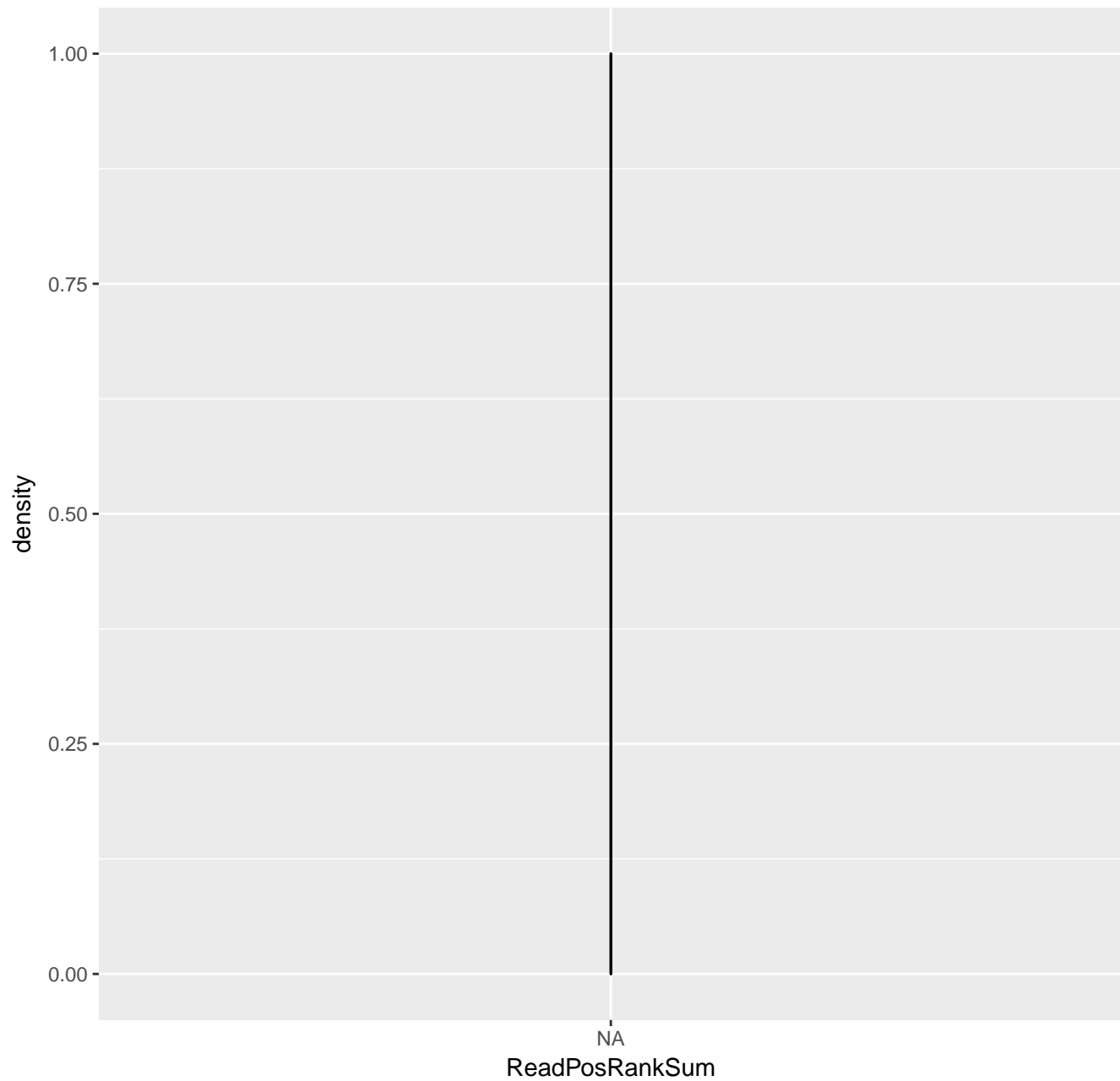
Fisher Strand (FS– Strand Bias Variant on F or R) – Greater than 30 removed



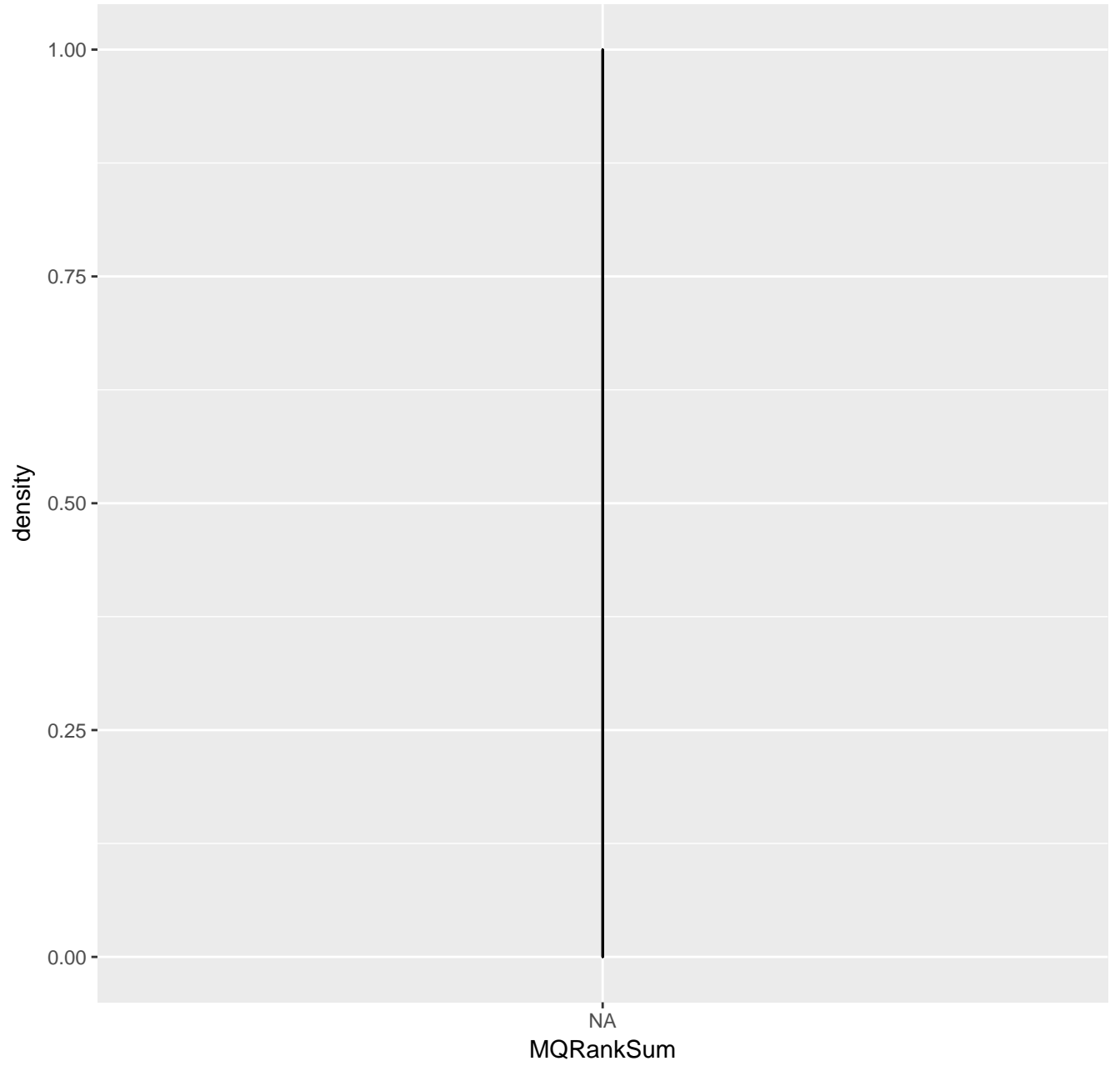
QD -variant qual/unfiltered depth – Below 2 removed



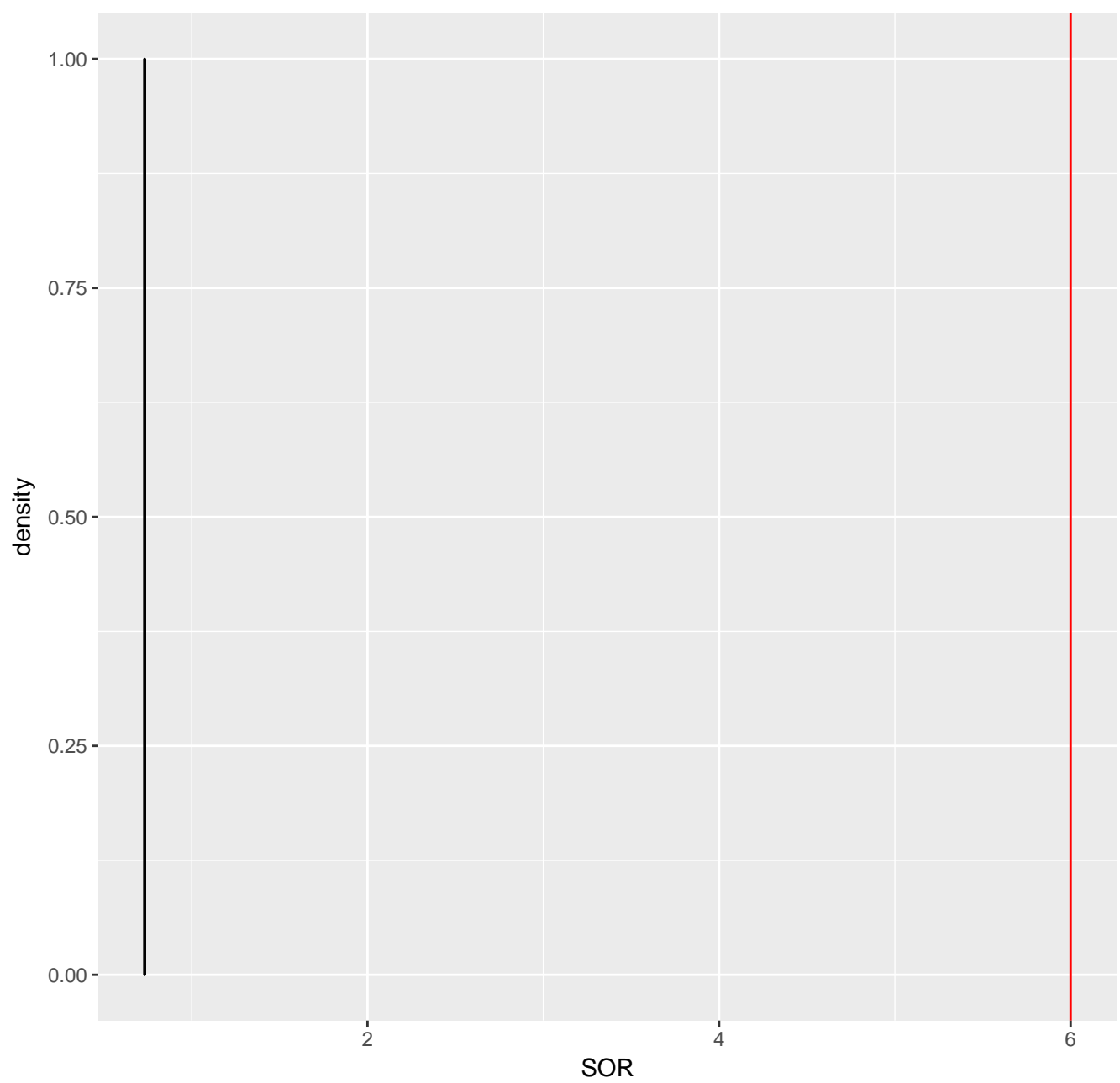
ReadPosRankSum – Negative values indicate ALT near ends (cutoff -5.5)



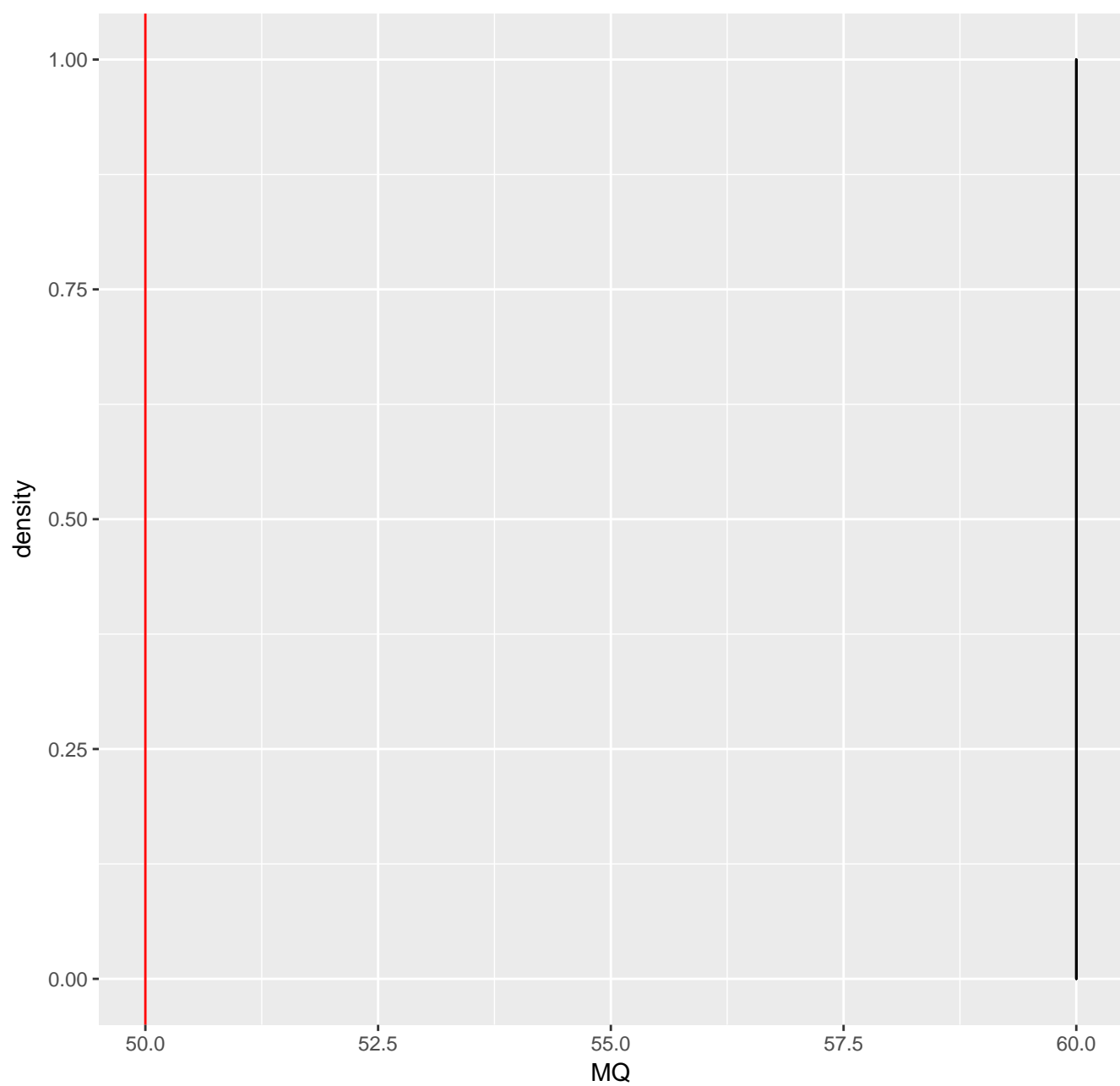
MQRankSum of Mapping Quality – Negative values indicate ALT near ends (–10



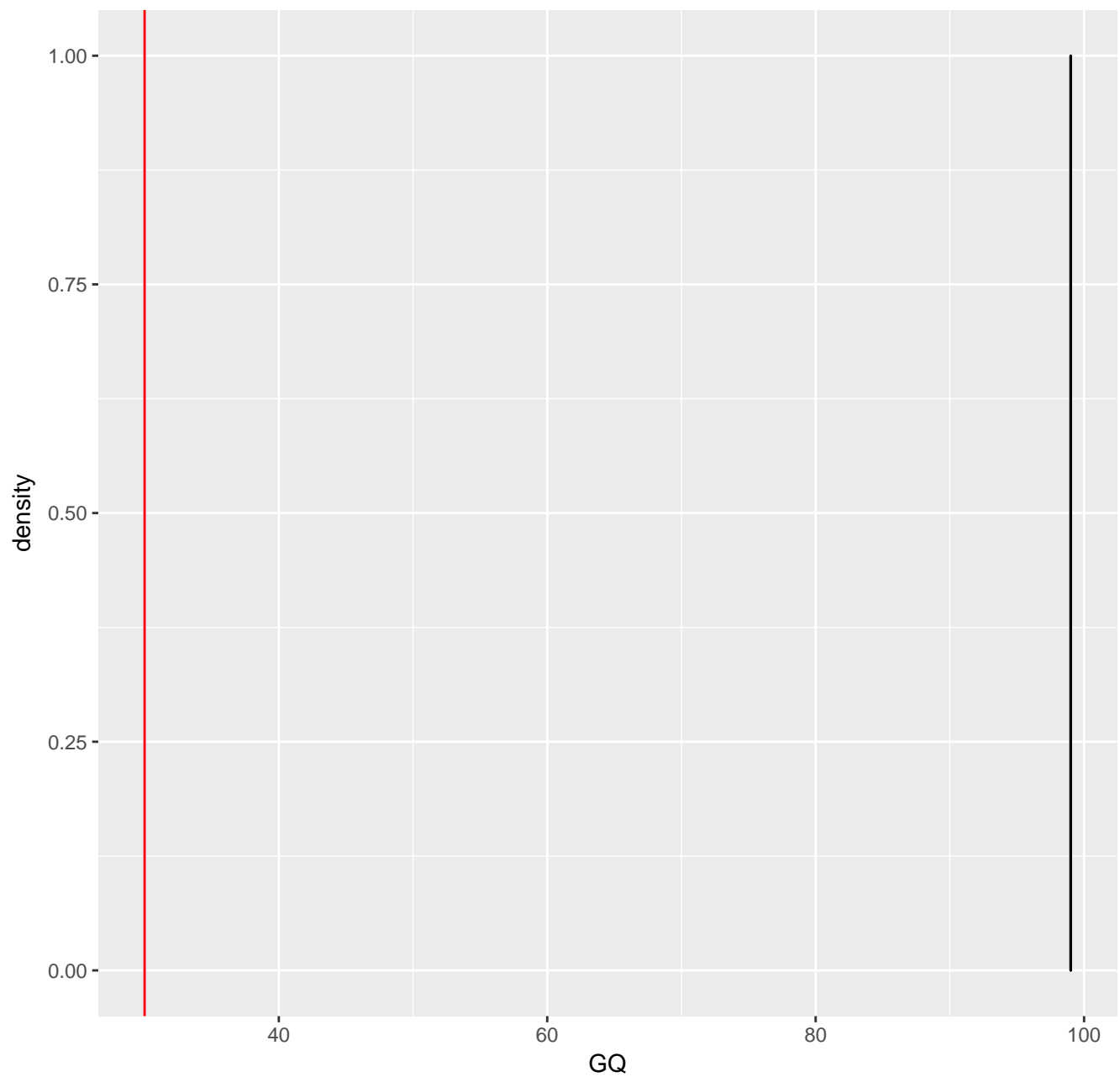
StrandOddsRatio (SOR) – Greater than 6 shows strand bias



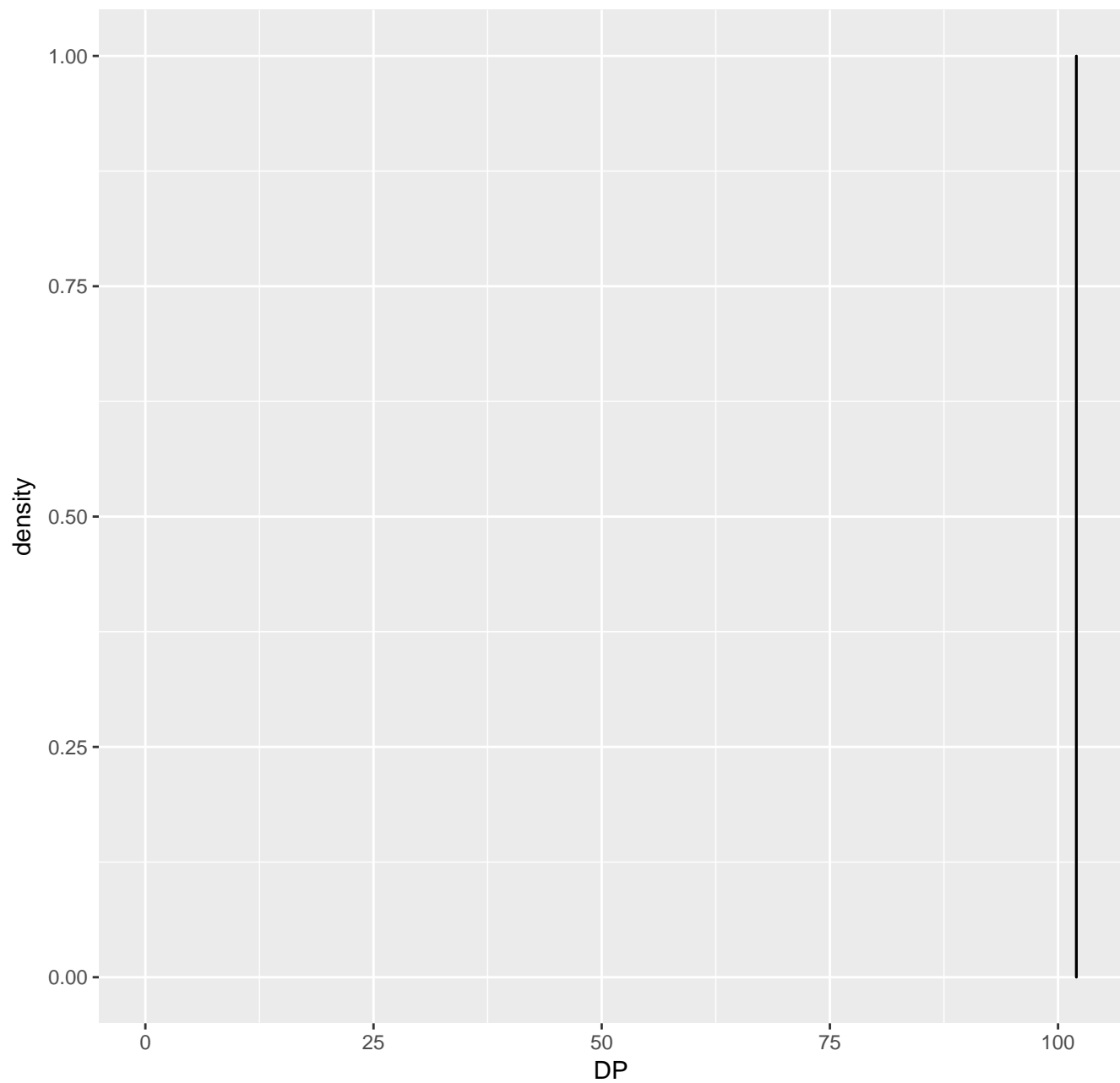
Root Mean Square Error Mapping Quality (MQ) – Less than 50 removed



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



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



both Statis

	mean	SD	mean_plus_5xSD
1	102	NA	NA