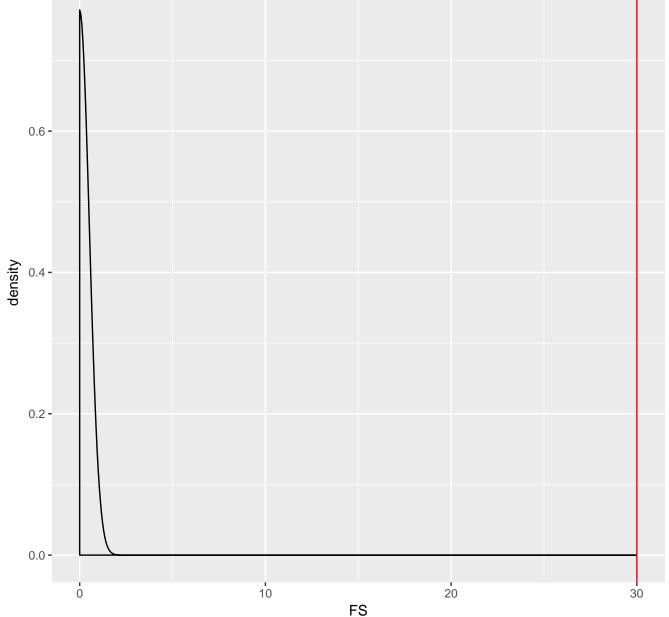
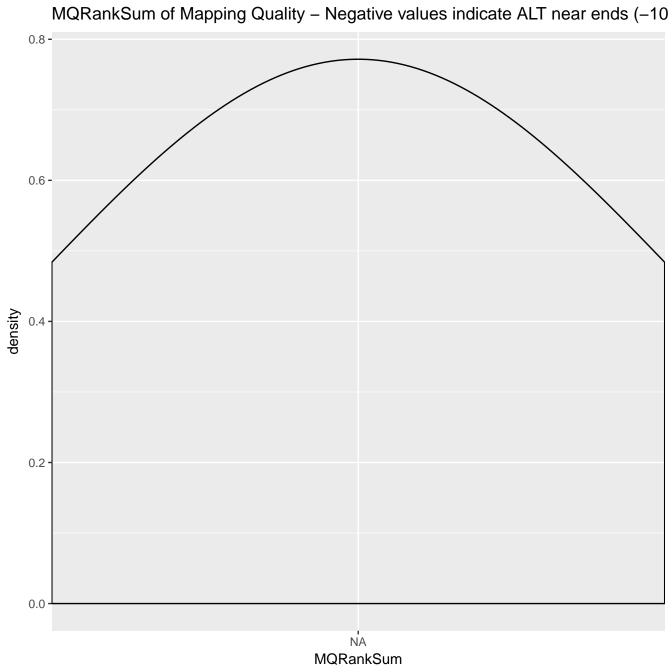
Fisher Strand (FS- Strand Bias Variant on F or R) - Greater than 30 removed



QD -variant qual/unfiltered depth - Below 2 removed 0.20 -0.15 density 0.10 -0.05 -0.00 -10 20 30 QD

ReadPosRankSum - Negative values indicate ALT near ends (cutoff -5.5) 0.8 -0.6 density 0.2 0.0 ΝA ReadPosRankSum



StrandOddsRatio (SOR) - Greater than 6 shows strand bias 3 density 1 -0 -2 SOR

Root Mean Square Error Mapping Quality (MQ) - Less than 50 removed 0.010 density 0.005 -0.000 -57.5 52.5 55.0 60.0 50.0 MQ

GQ- Genotype Quality (Phred score) - No current cutoff 0.008 -0.006 density 0.002 -0.000 -60 80 40 100 GQ

DP- Depth - Red line drawn at Mean + 5*STDEV 0.020 -0.015 density 0.010 -0.005 -0.000 -100 200 DP

epth Statistic

 mean
 SD
 mean_plus_5xSD

 1 108.875
 24.3389262978738
 230.569631489369