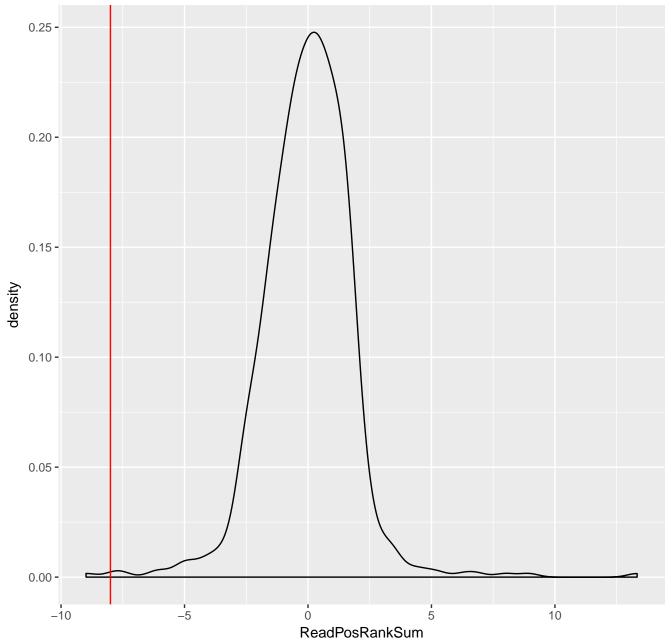
Fisher Strand (FS- Strand Bias Variant on F or R) 0.20 -0.15 density 0.10 -0.05 -0.00 -0 25 50 75 100 FS

QD -variant qual/unfiltered depth 0.09 density 0.03 -0.00 -10 20 QD 30 40 ReadPosRankSum – Negative values indicate ALT near ends

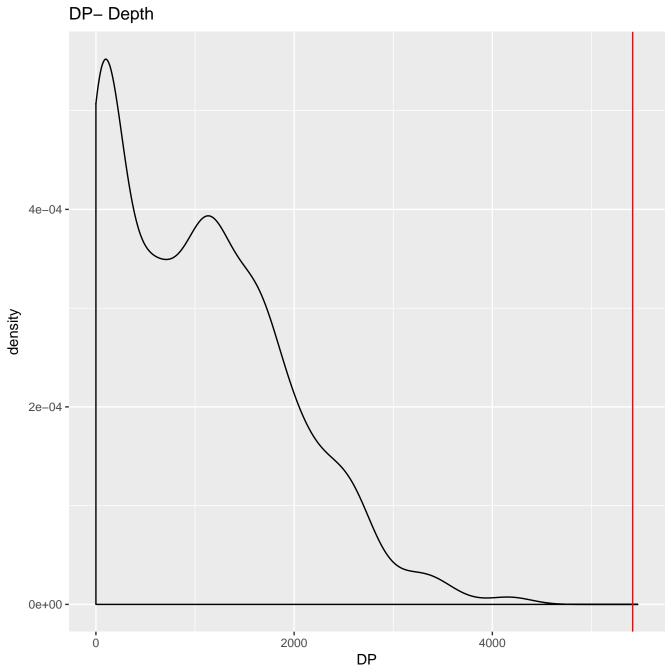


MQRankSum of Mapping Quality - Negative values indicate ALT near ends 0.2 density 0.1 -0.0 -10 **-**5 -10 5 ${\sf MQRankSum}$

StrandOddsRatio (SOR) - Greater than 3 shows strand bias 0.4 -0.3 density 0.2 -0.1 -0.0 -9 Ö SOR

Root Mean Square Error Mapping Quality (MQ) - Less than 40 removed 0.06 -0.04 density 0.02 -0.00 -30 50 60 40 MQ

GQ- Genotype Quality 0.075 -0.050 density 0.025 -0.000 -25 50 **GQ** 75 100



Depth Statistics

	mean	SD	mean_plus_5xSD
1	1049.349609375	873.308548542732	5415.89235208866