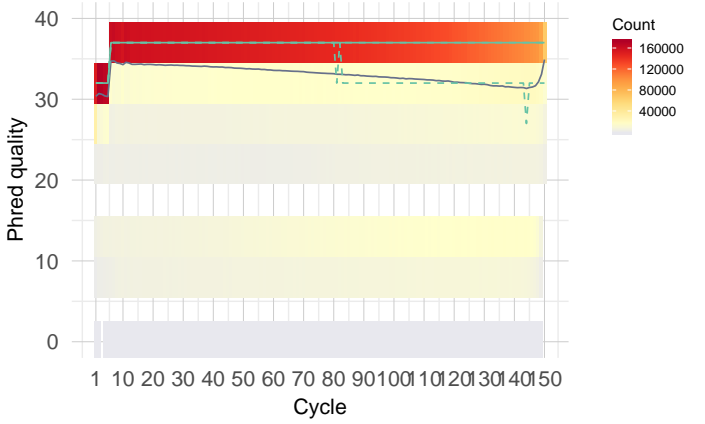
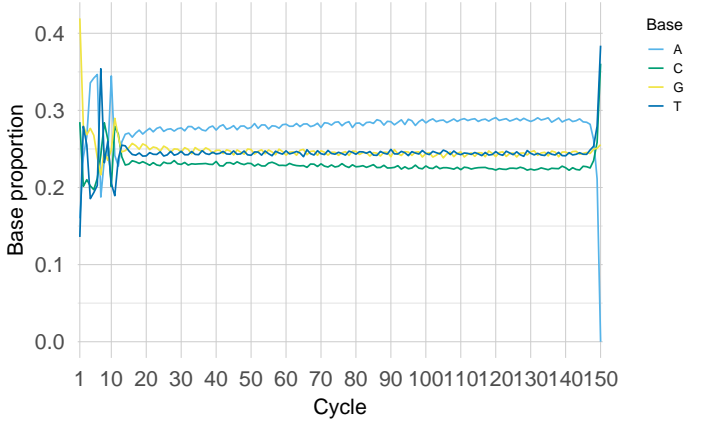


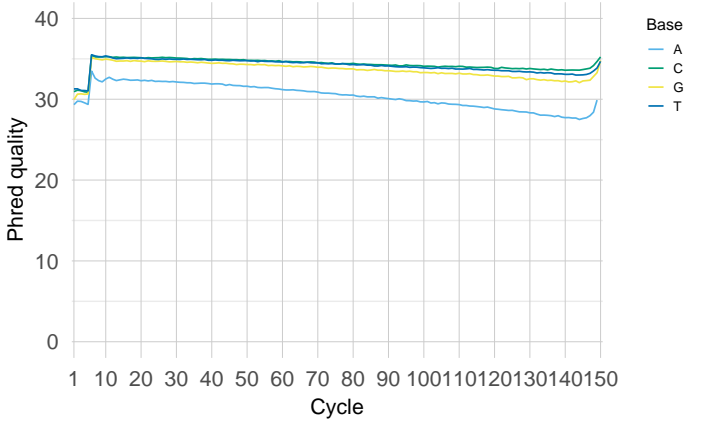
SRR1804235: Per cycle base quality



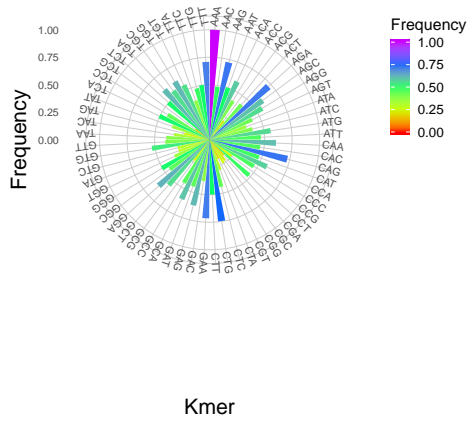
SRR1804235: Per cycle base frequency



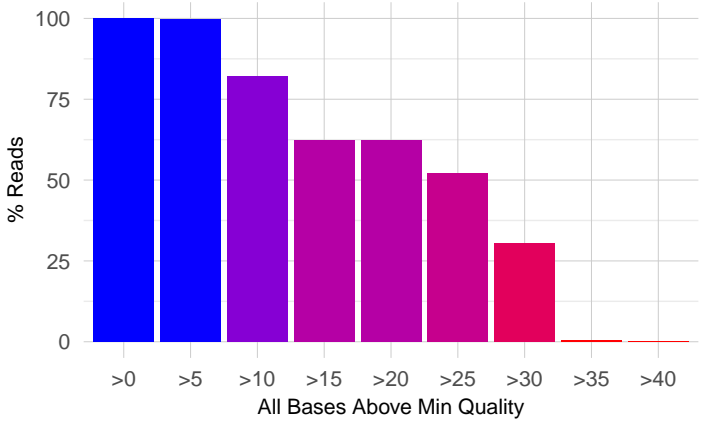
SRR1804235: Per cycle average base quality



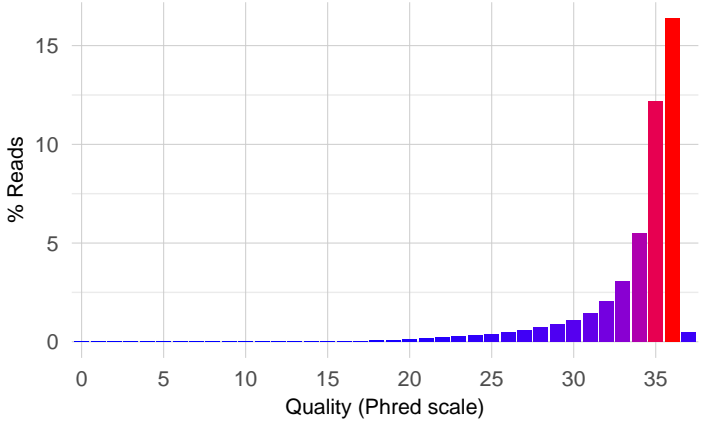
SRR1804235: Trinucleotide frequency



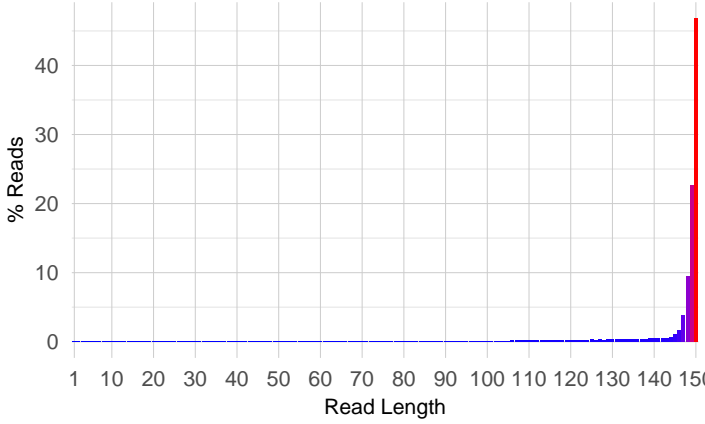
SRR1804235: Phred score quality cutoffs



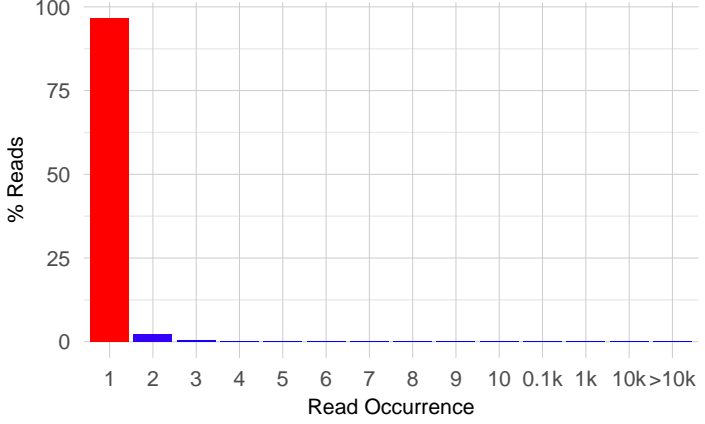
SRR1804235 : read quality for 191,680 of 3,833,604 reads



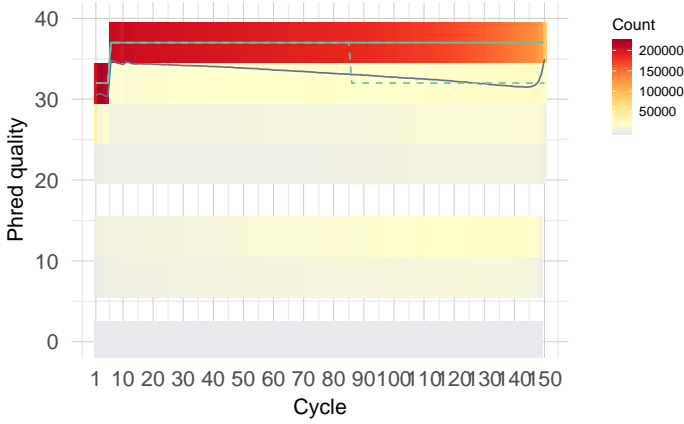
SRR1804235: Read length distribution



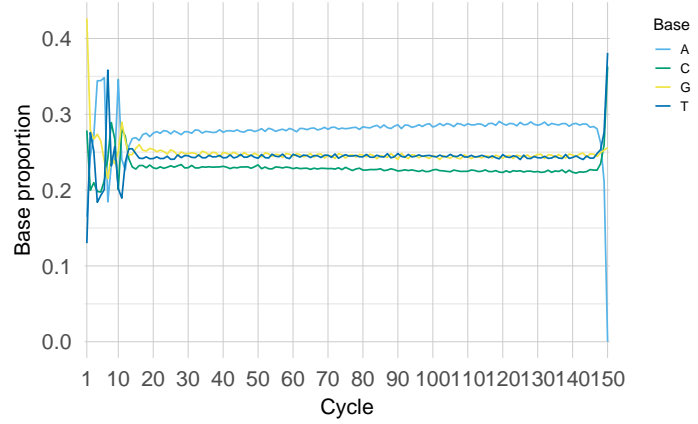
SRR1804235: Read occurrence distribution



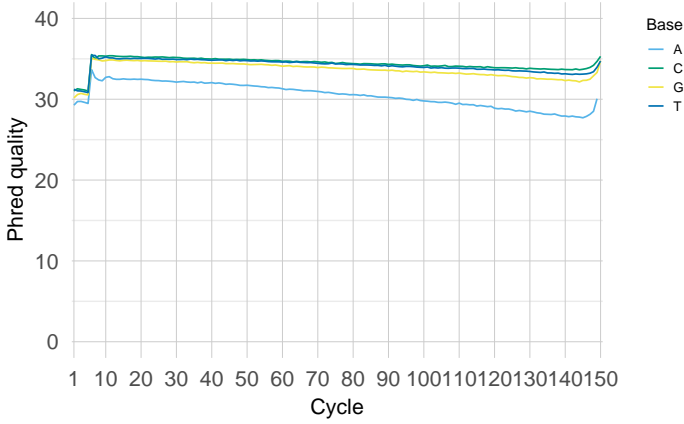
SRR1804236: Per cycle base quality



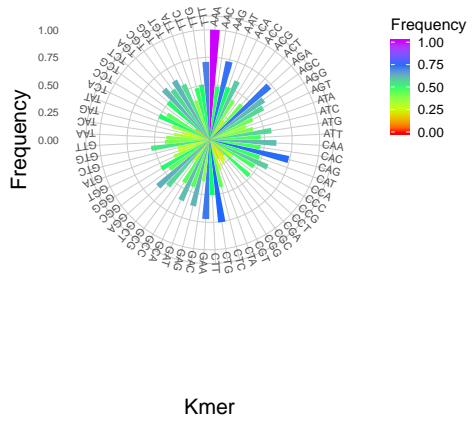
SRR1804236: Per cycle base frequency



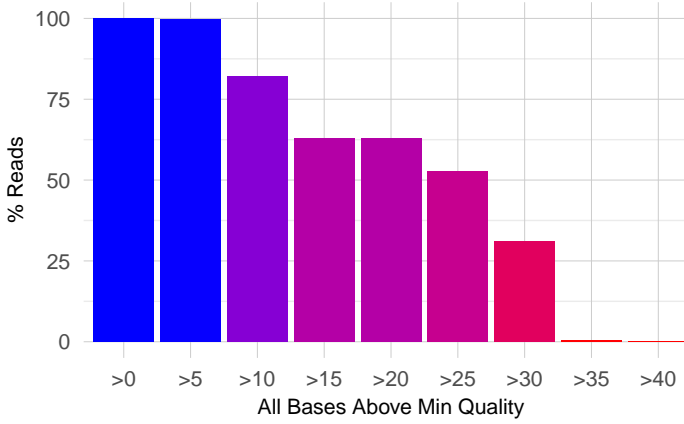
SRR1804236: Per cycle average base quality



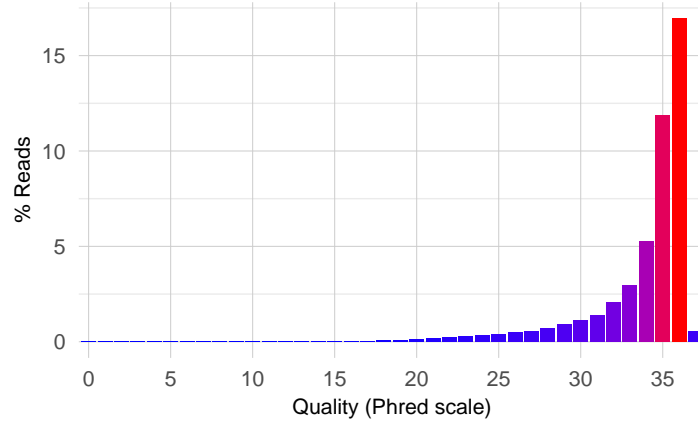
SRR1804236: Trinucleotide frequency



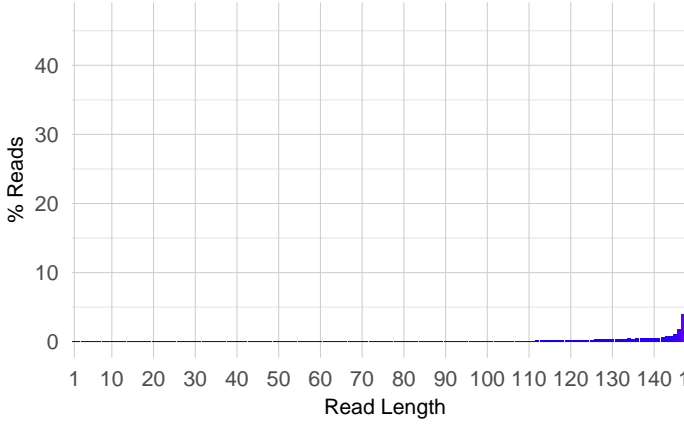
SRR1804236: Phred score quality cutoffs



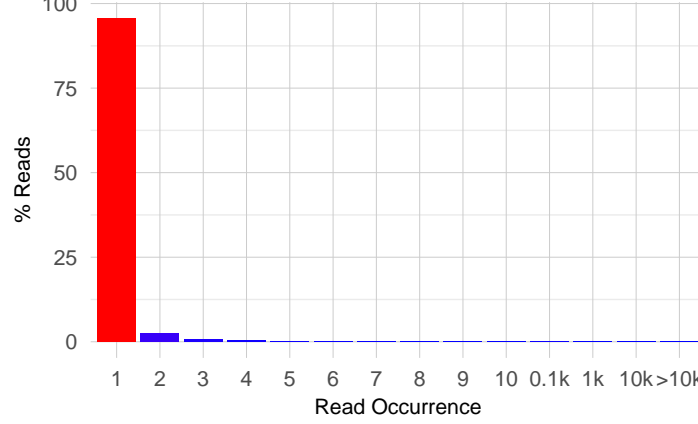
SRR1804236 : read quality for 247,937 of 4,958,739 reads



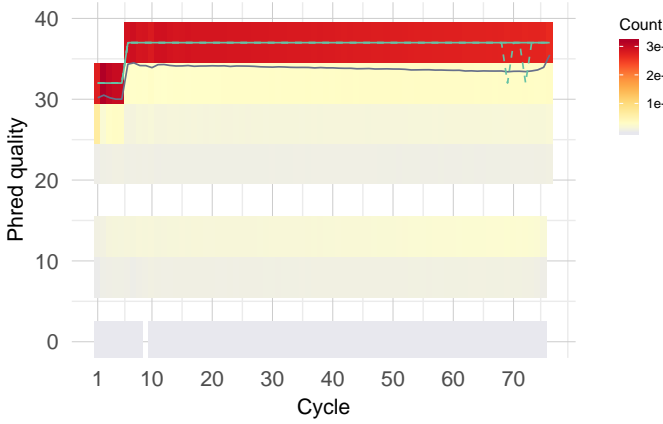
SRR1804236: Read length distribution



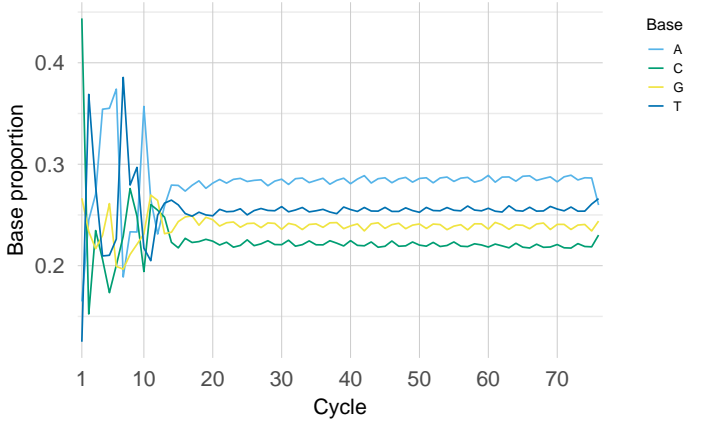
SRR1804236: Read occurrence distribution



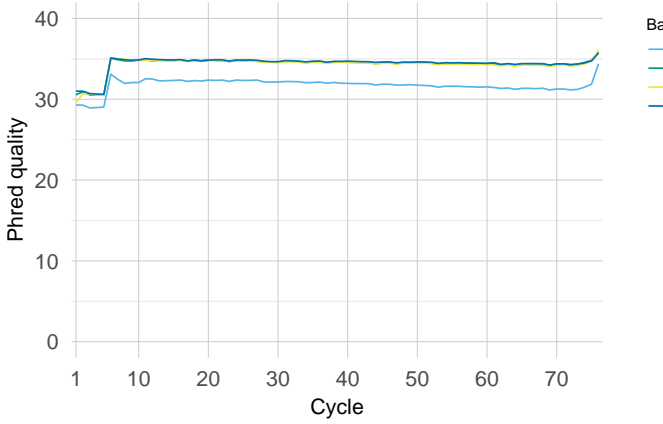
SRR1804237: Per cycle base quality



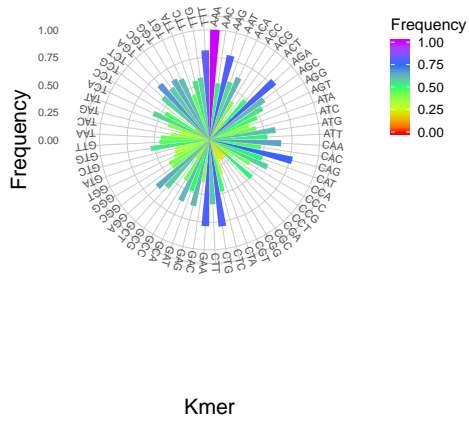
SRR1804237: Per cycle base frequency



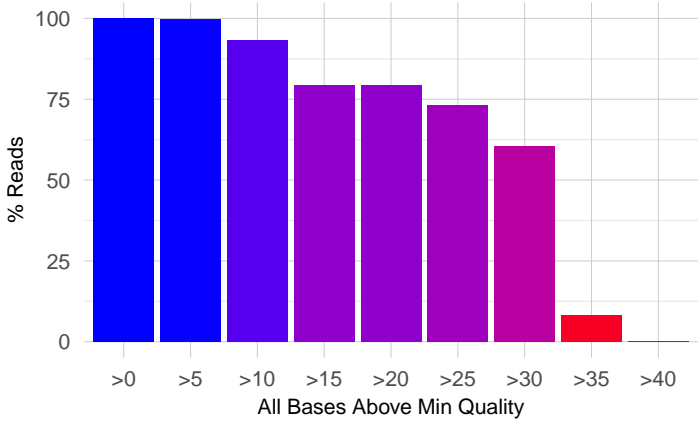
SRR1804237: Per cycle average base quality



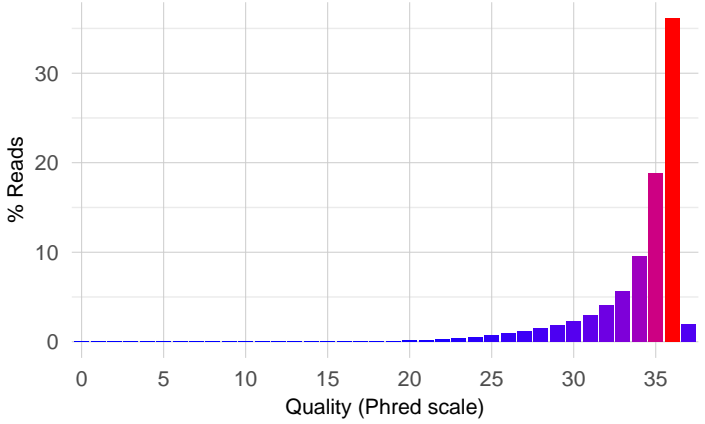
SRR1804237: Trinucleotide frequency



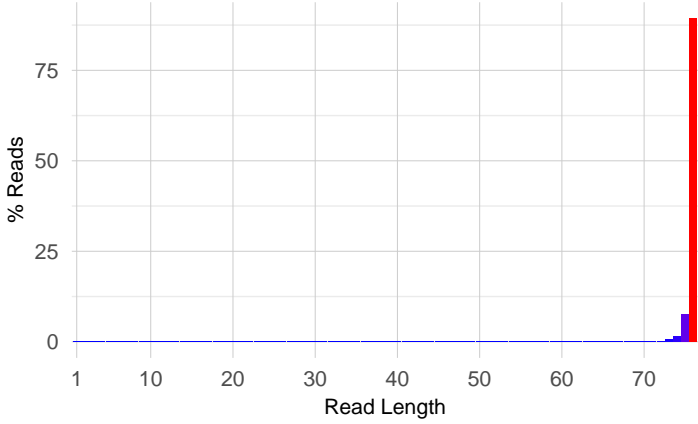
SRR1804237: Phred score quality cutoffs



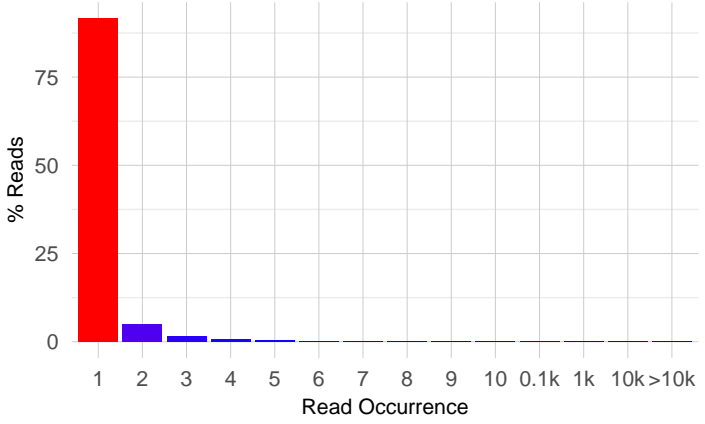
SRR1804237 : read quality for 360,118 of 7,202,354 reads

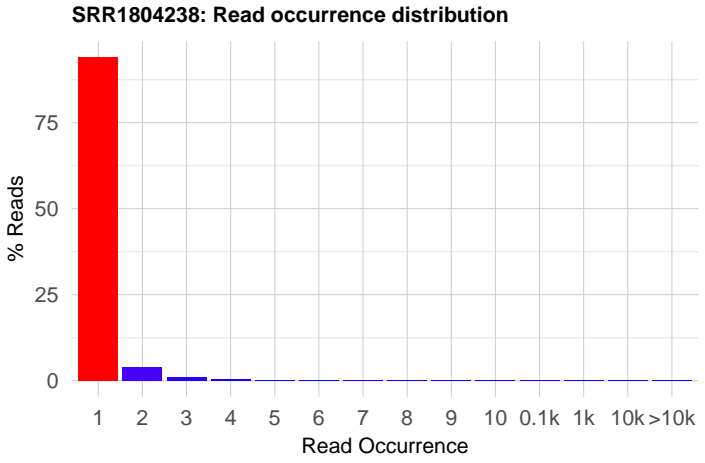
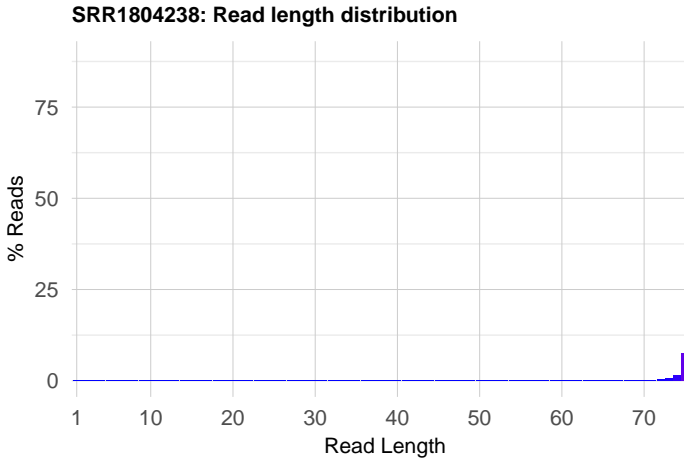
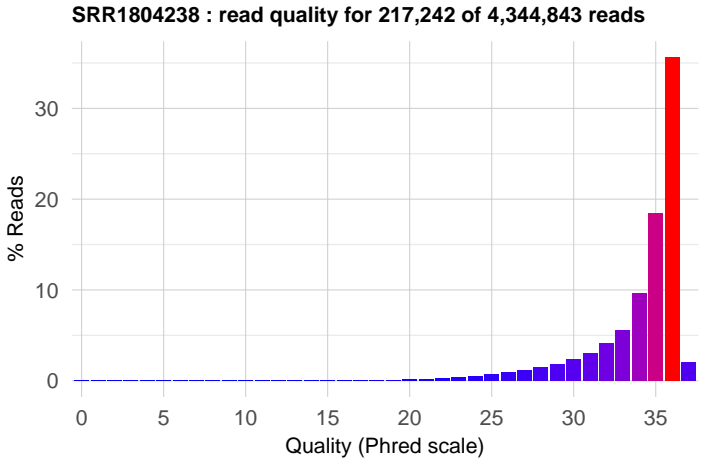
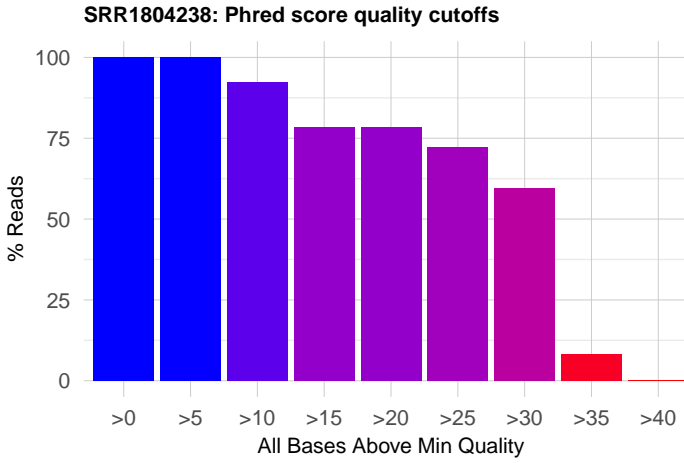
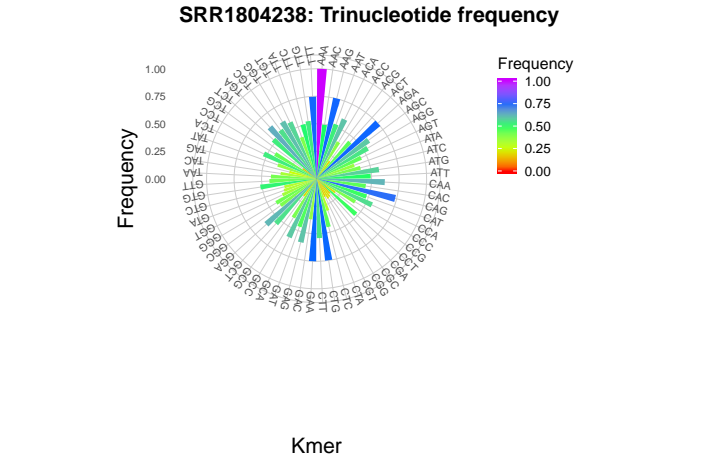
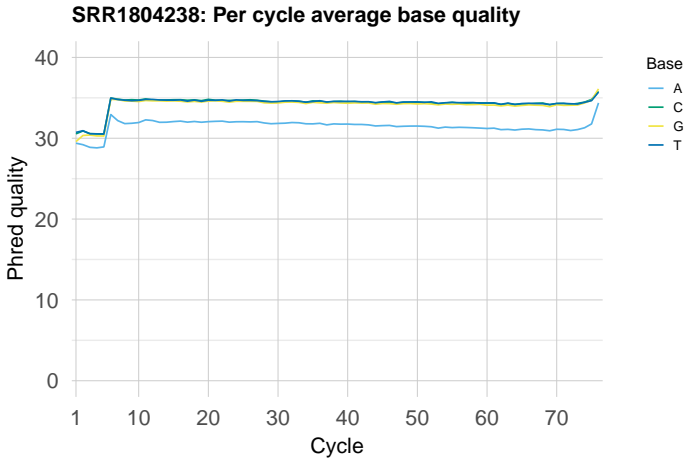
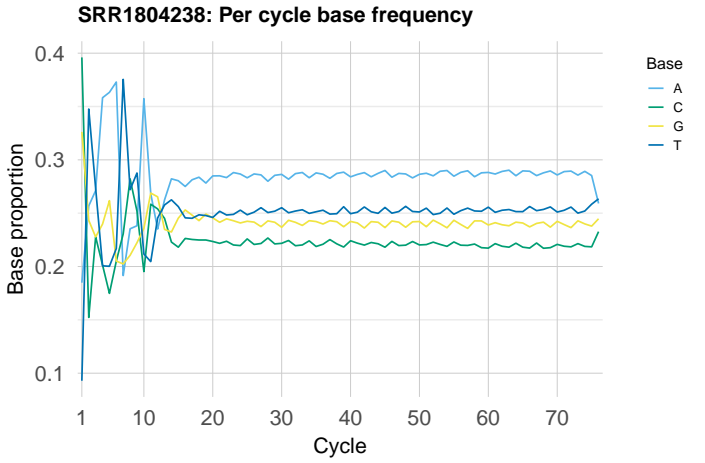
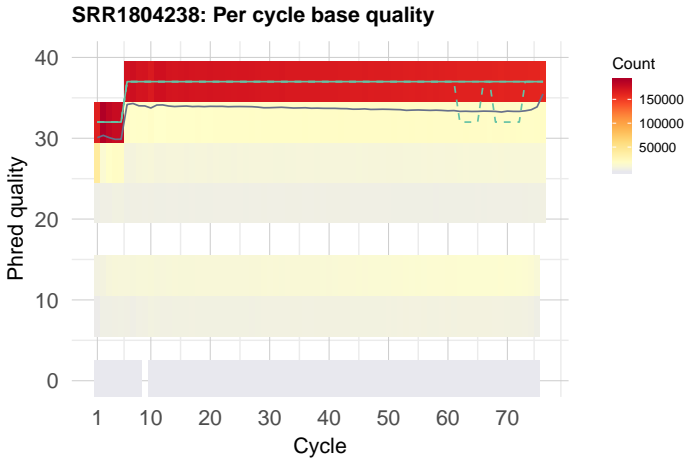


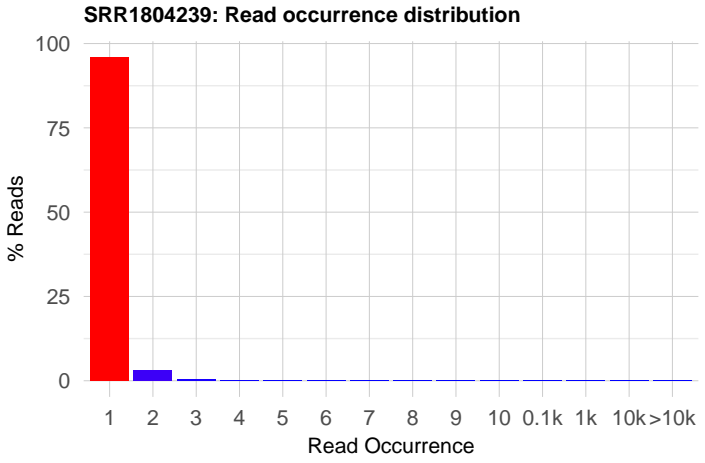
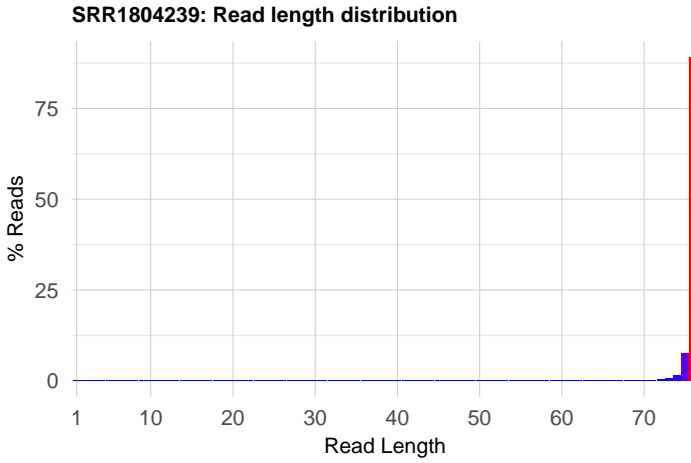
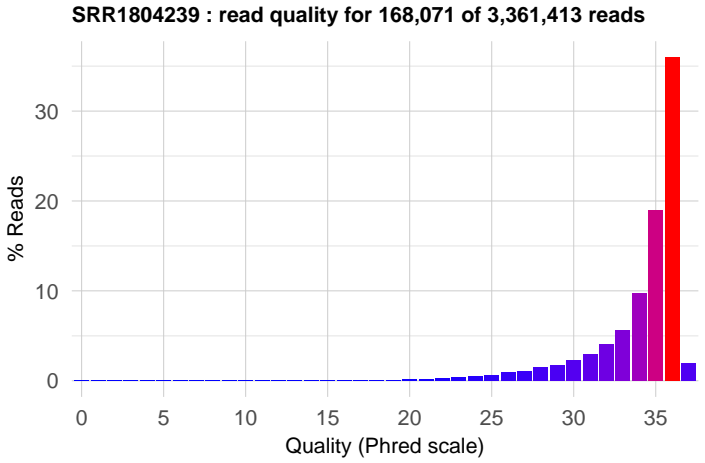
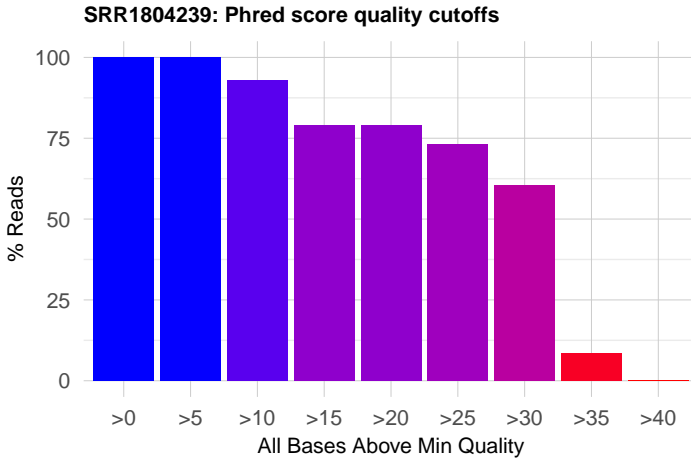
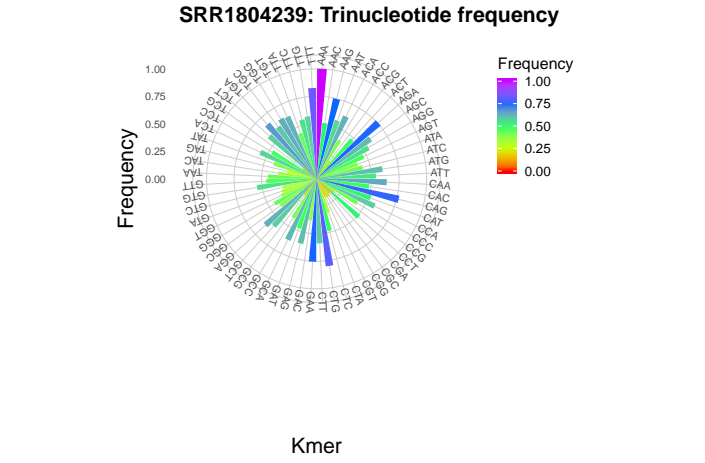
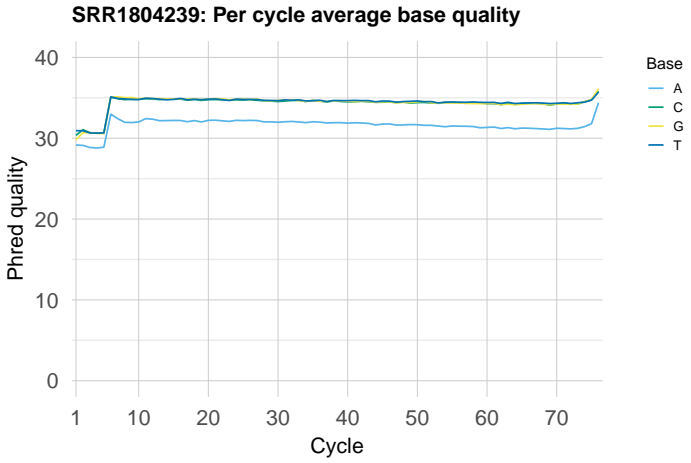
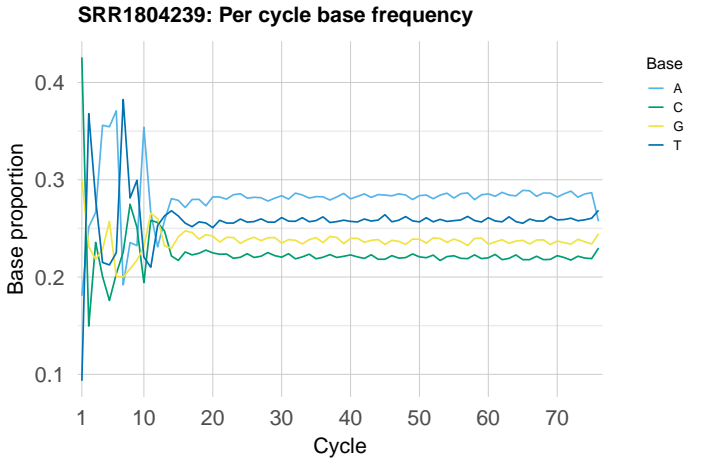
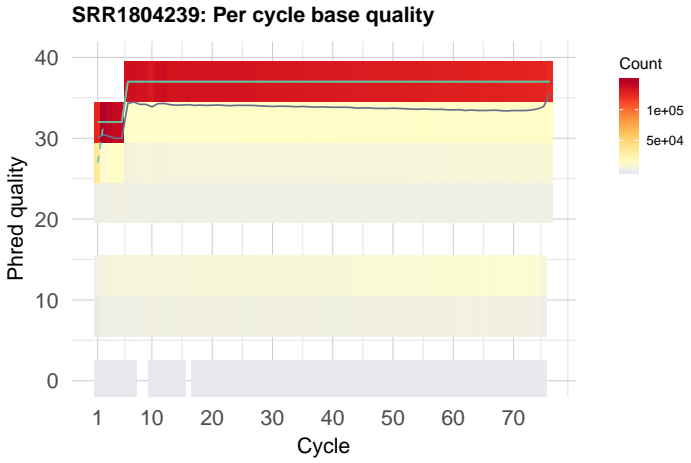
SRR1804237: Read length distribution

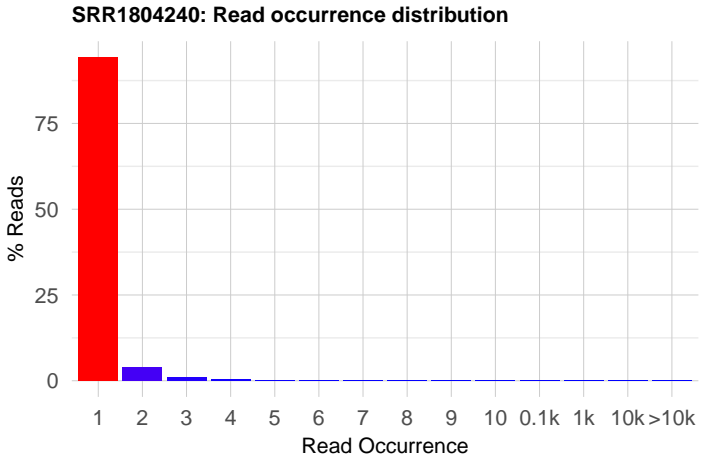
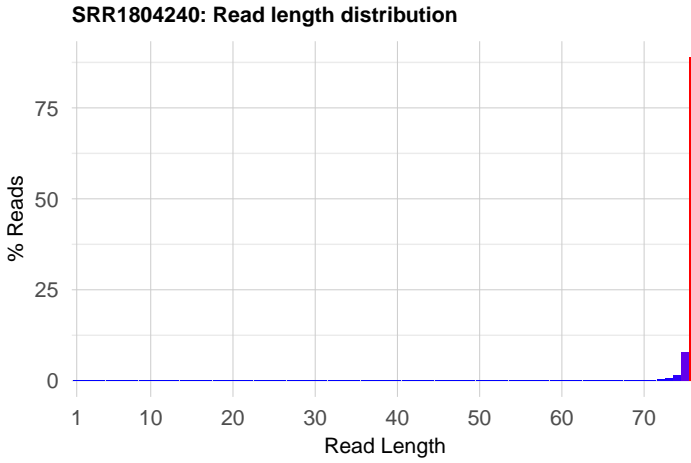
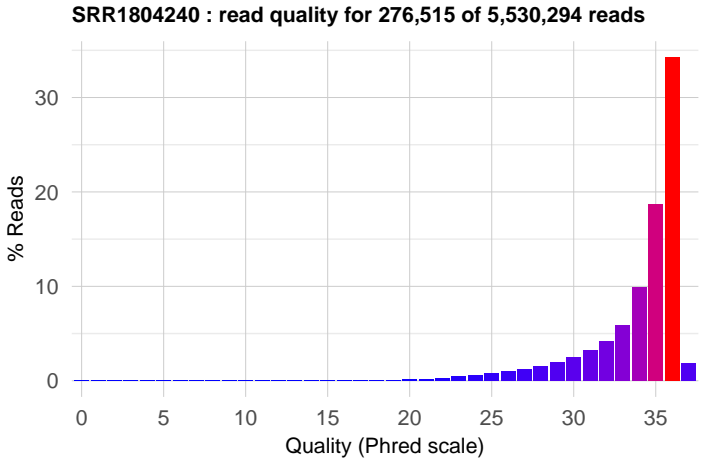
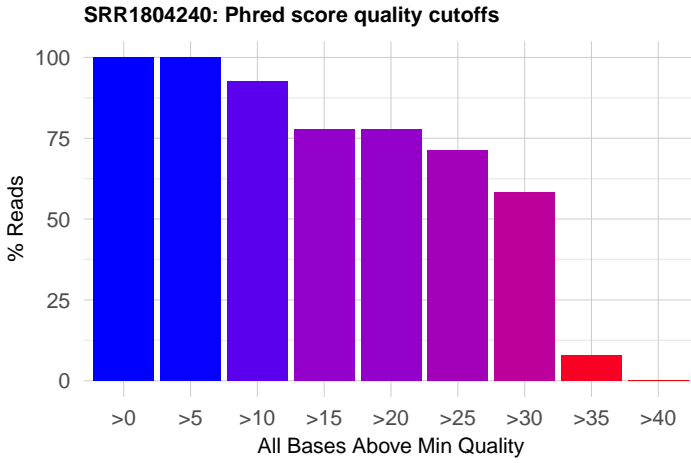
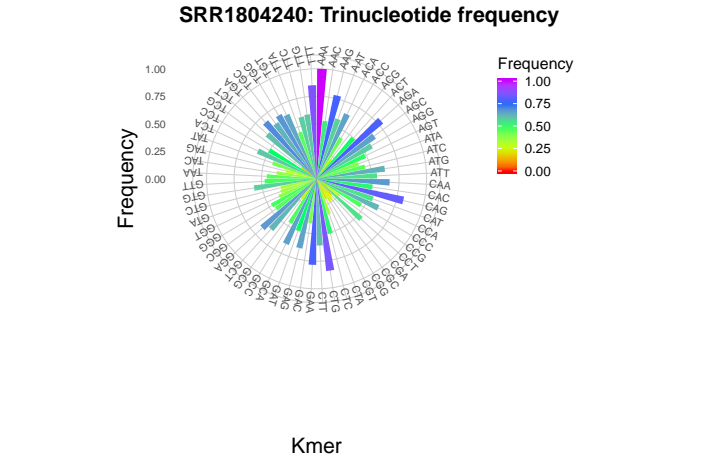
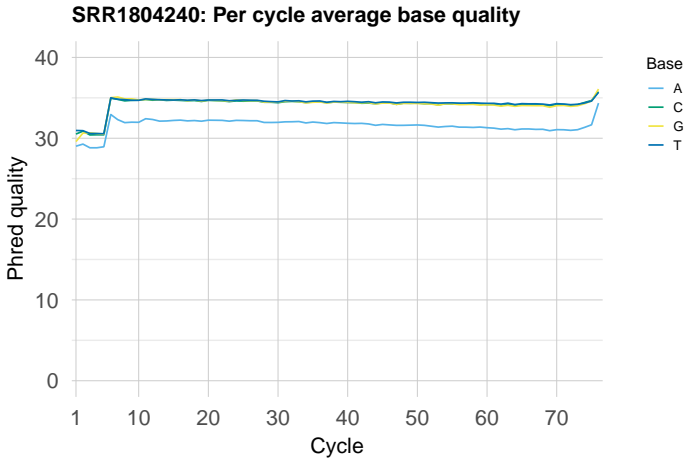
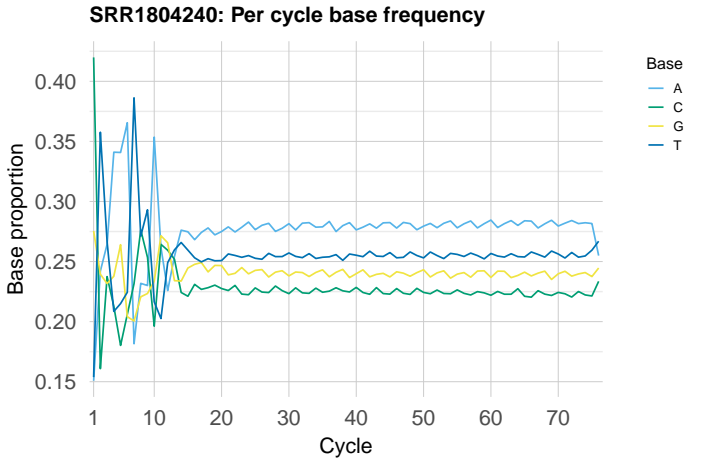
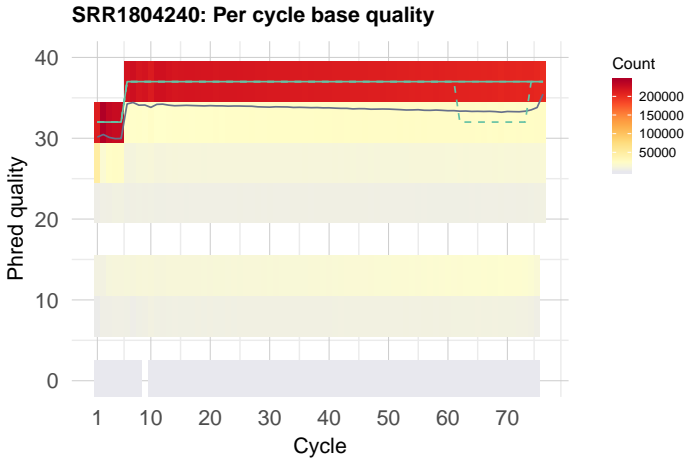


SRR1804237: Read occurrence distribution

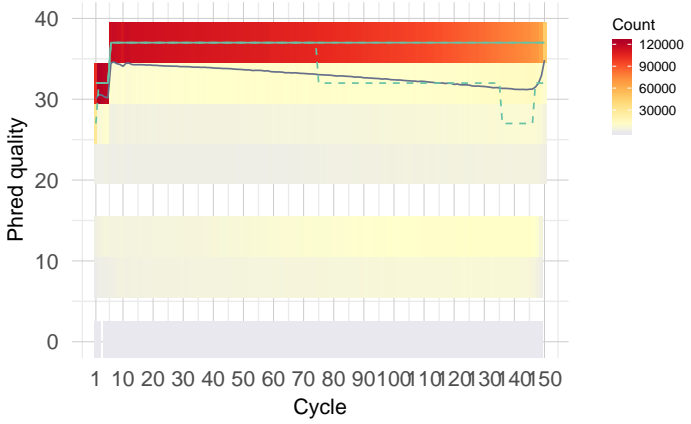




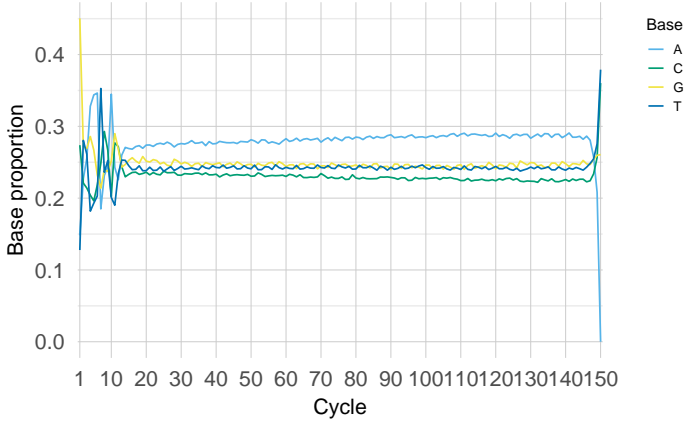




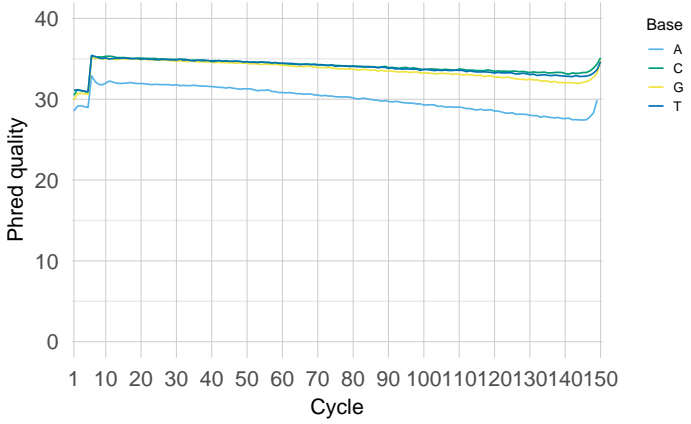
SRR1804241: Per cycle base quality



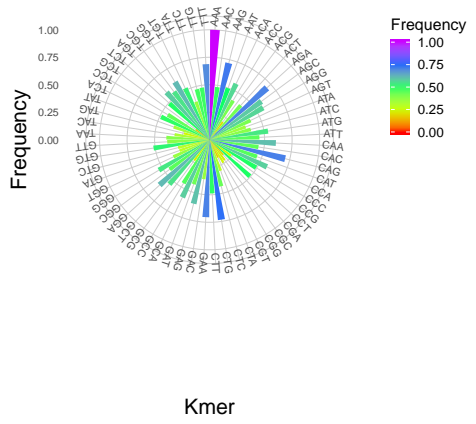
SRR1804241: Per cycle base frequency



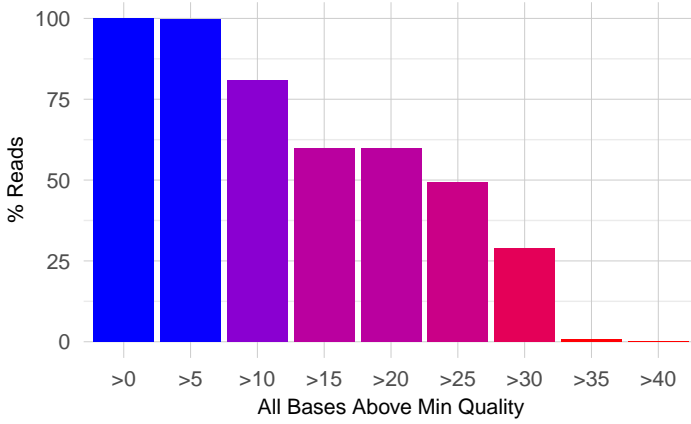
SRR1804241: Per cycle average base quality



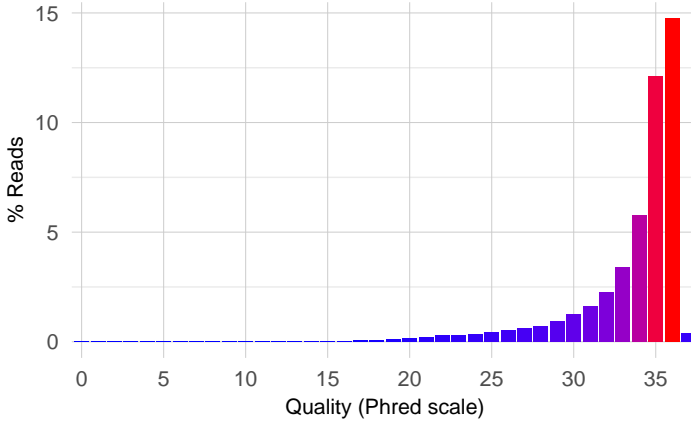
SRR1804241: Trinucleotide frequency



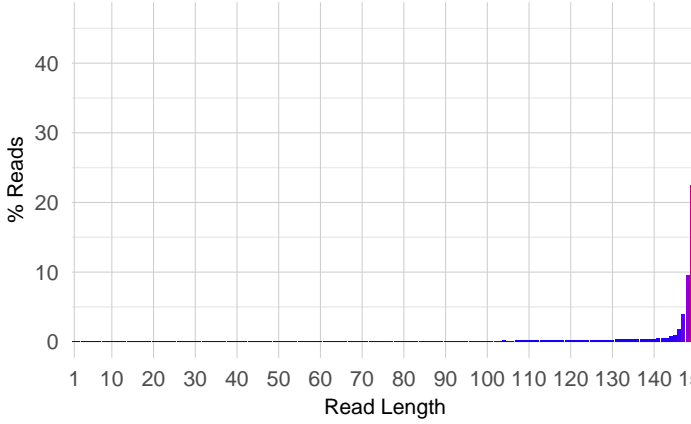
SRR1804241: Phred score quality cutoffs



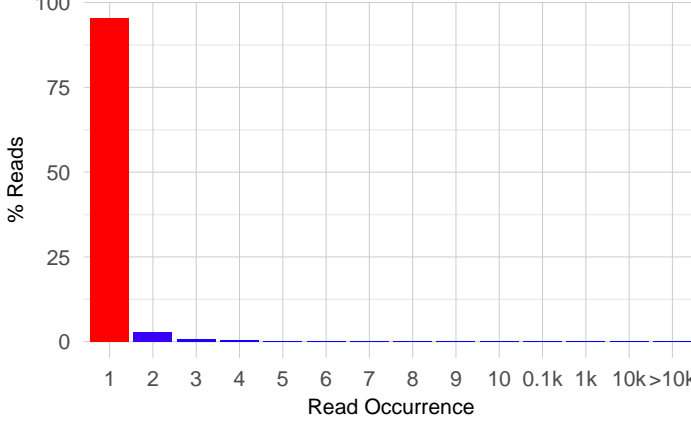
SRR1804241 : read quality for 138,869 of 2,777,383 reads



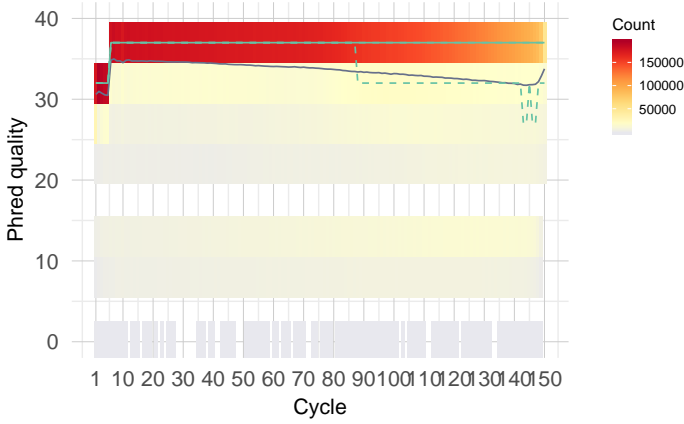
SRR1804241: Read length distribution



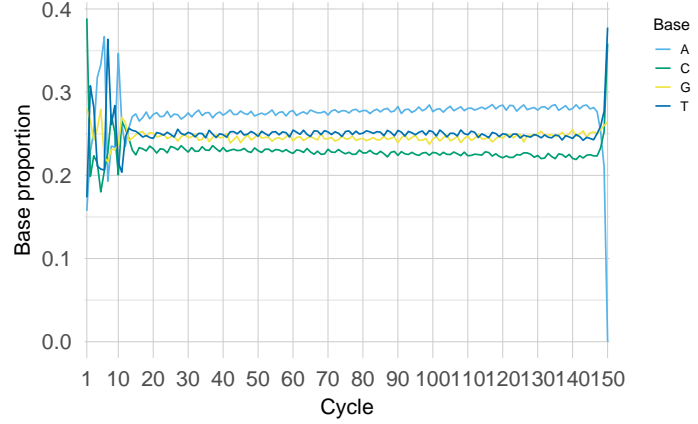
SRR1804241: Read occurrence distribution



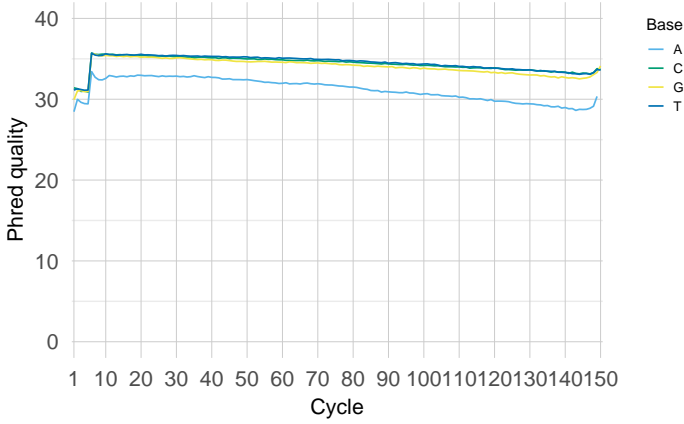
SRR1804242: Per cycle base quality



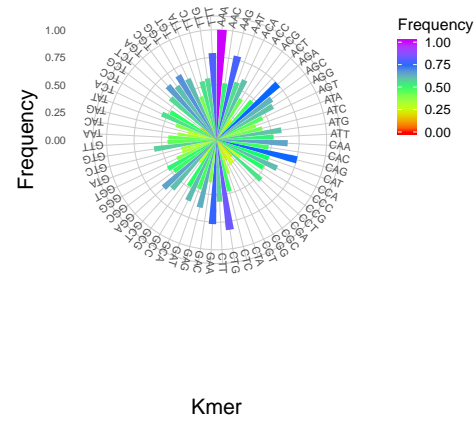
SRR1804242: Per cycle base frequency



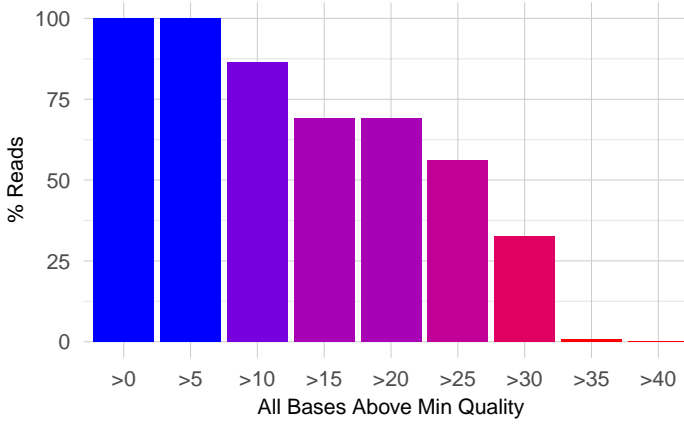
SRR1804242: Per cycle average base quality



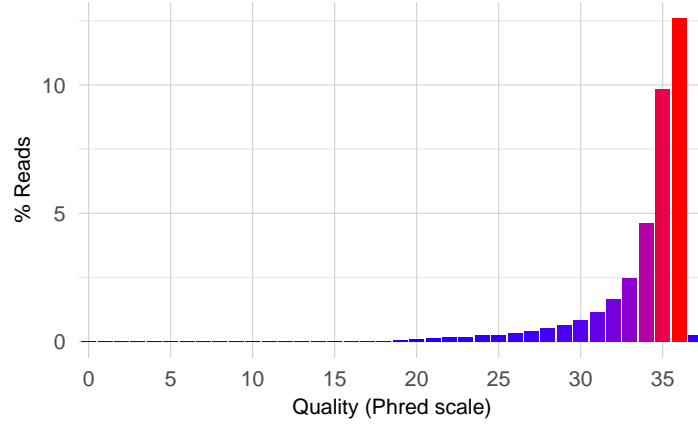
SRR1804242: Trinucleotide frequency



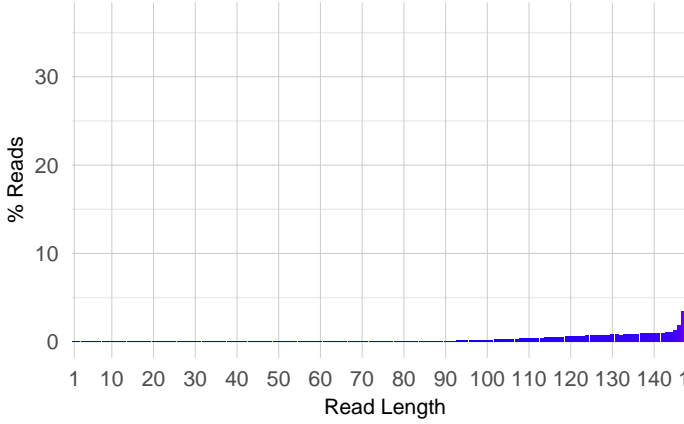
SRR1804242: Phred score quality cutoffs



SRR1804242 : read quality for 212,385 of 4,247,705 reads



SRR1804242: Read length distribution



SRR1804242: Read occurrence distribution

