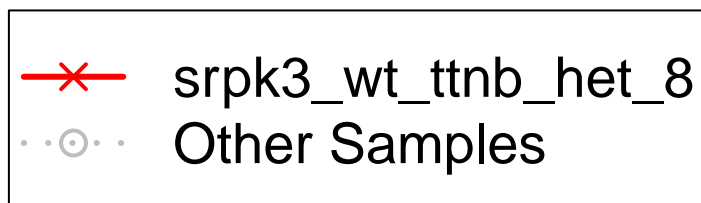


a

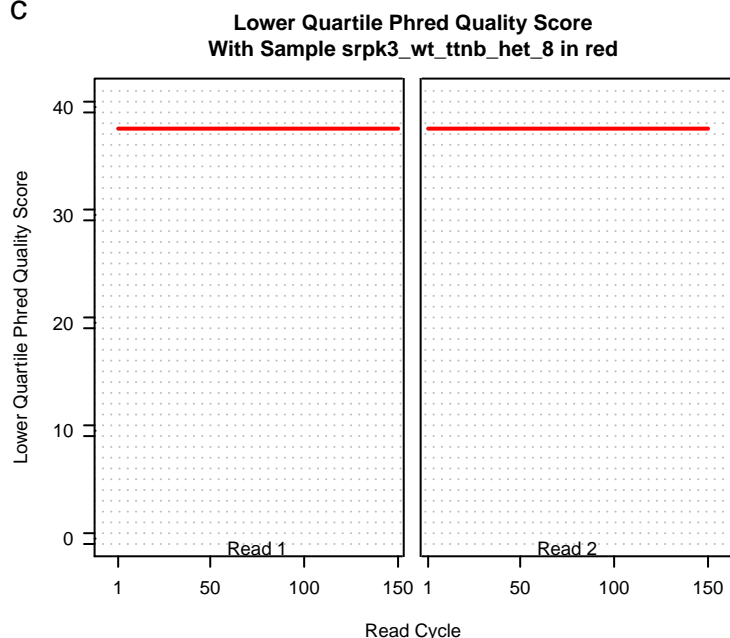
Sample Highlight:
srpk3_wt_ttnb_het_8



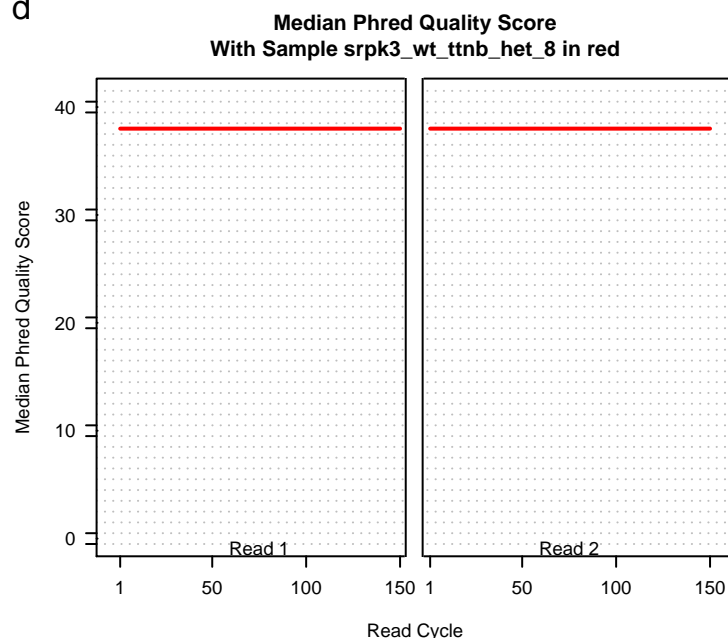
b



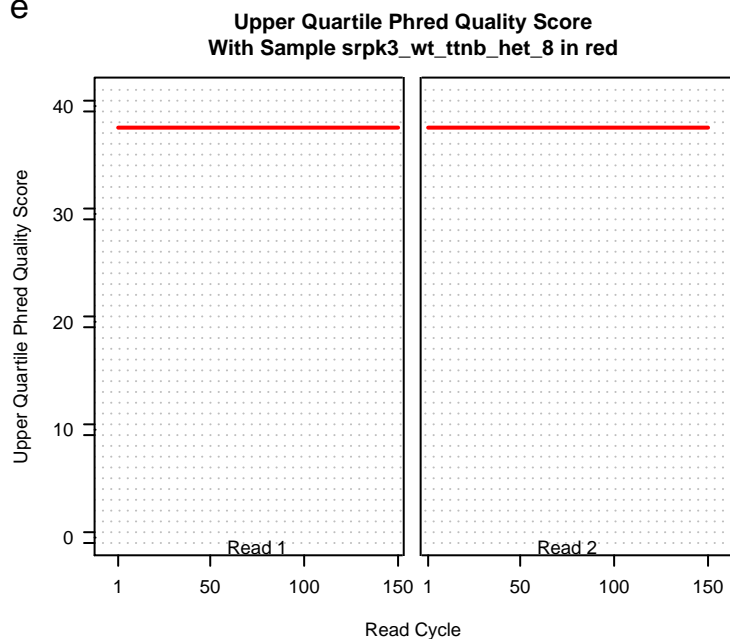
c



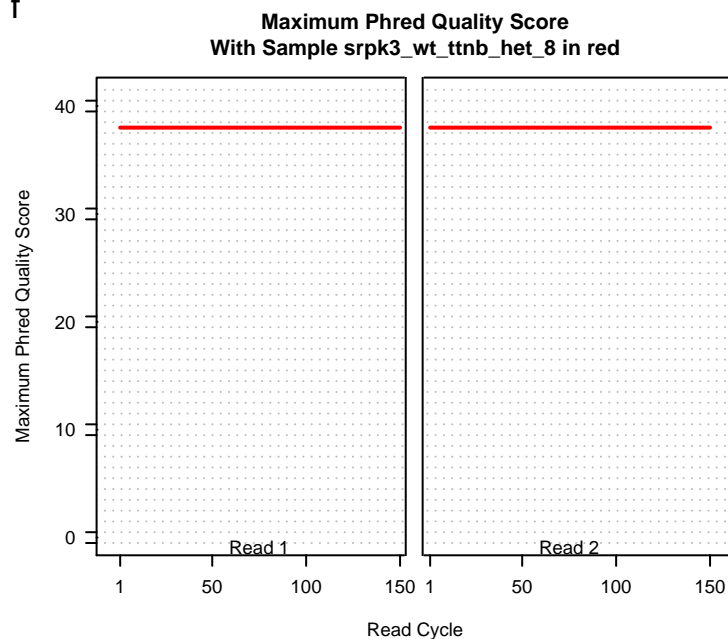
d

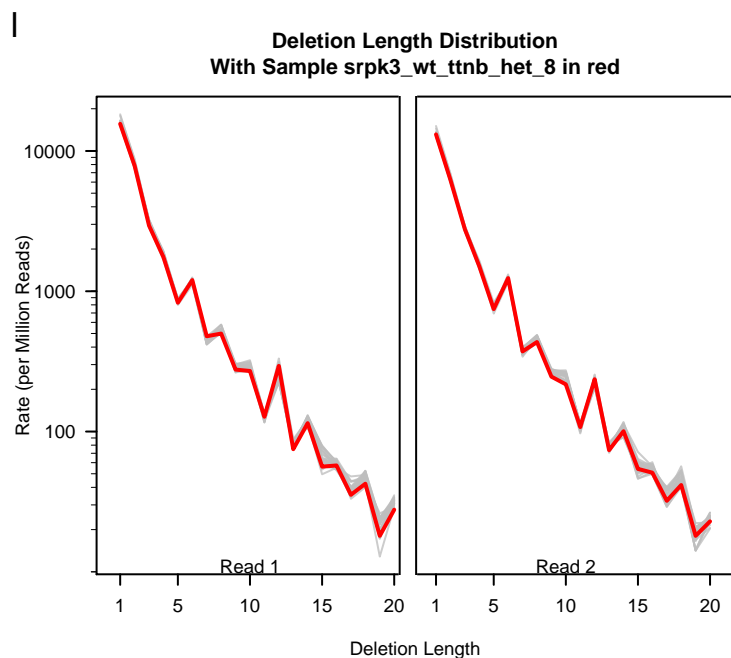
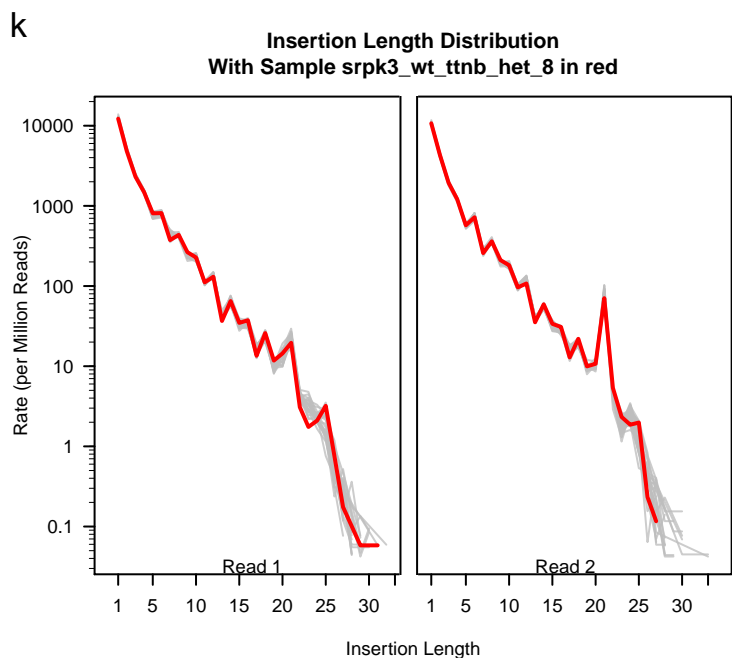
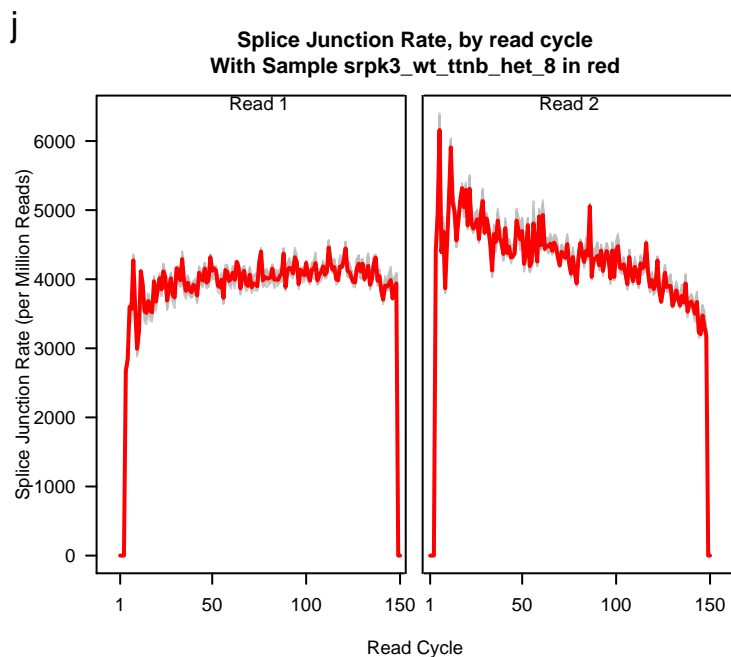
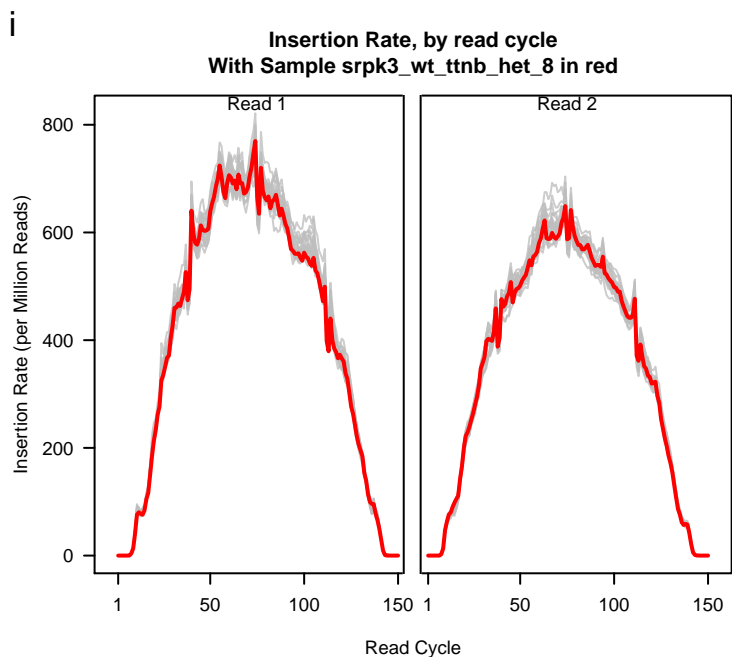
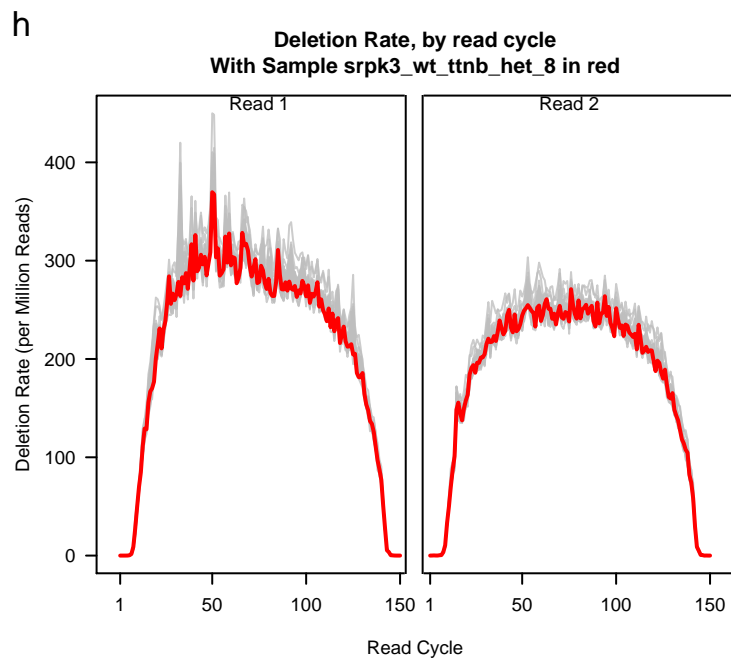
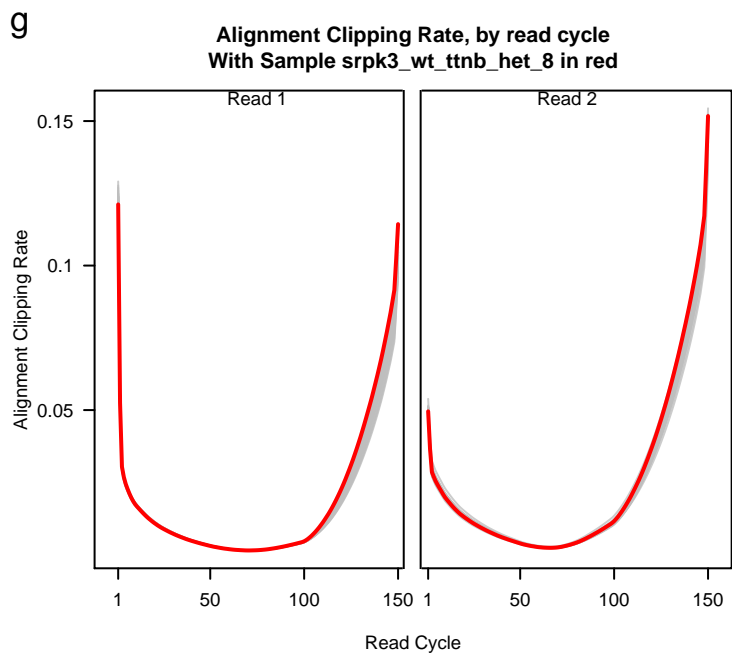


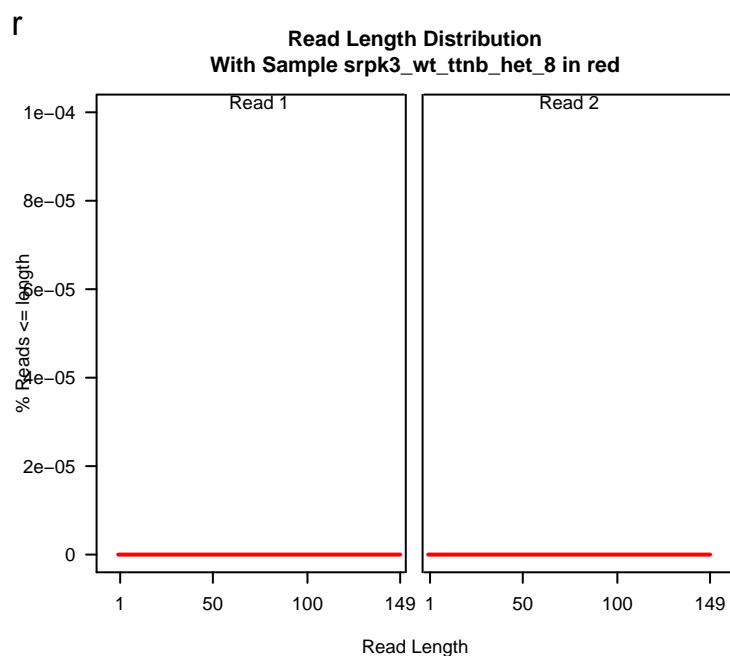
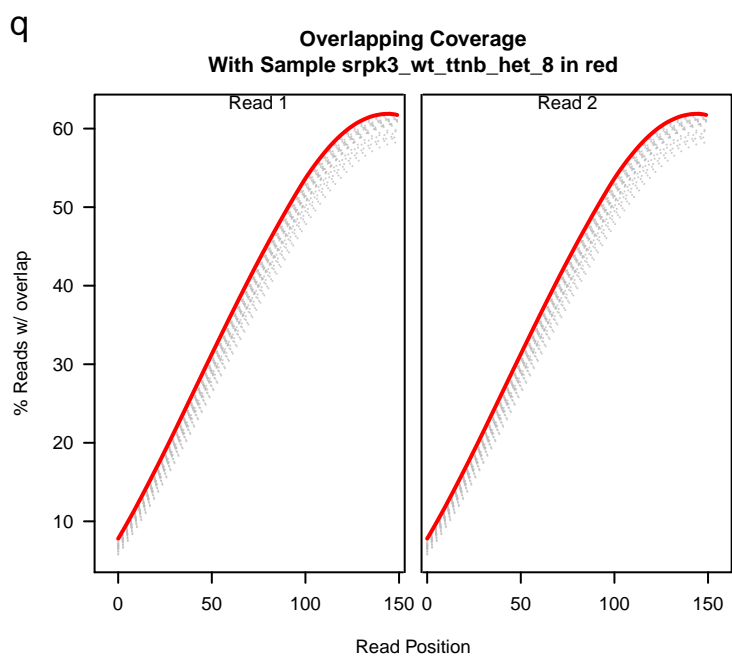
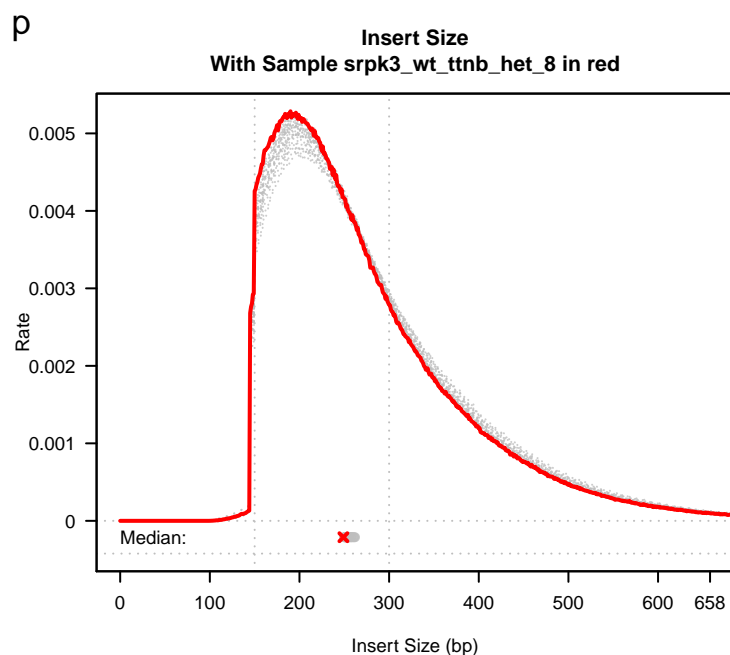
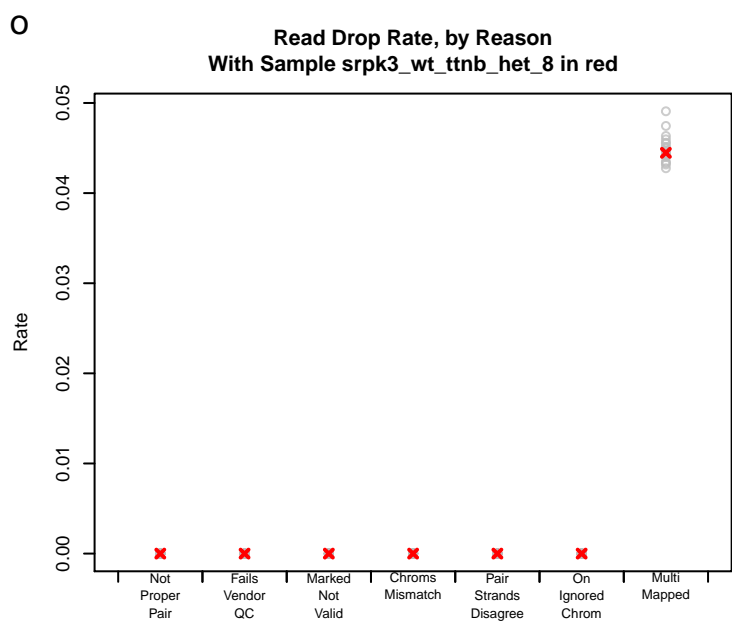
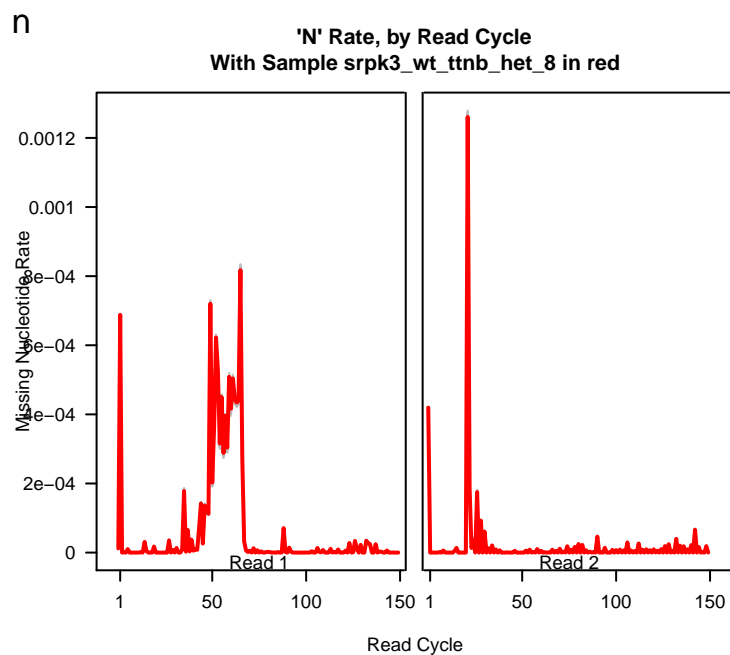
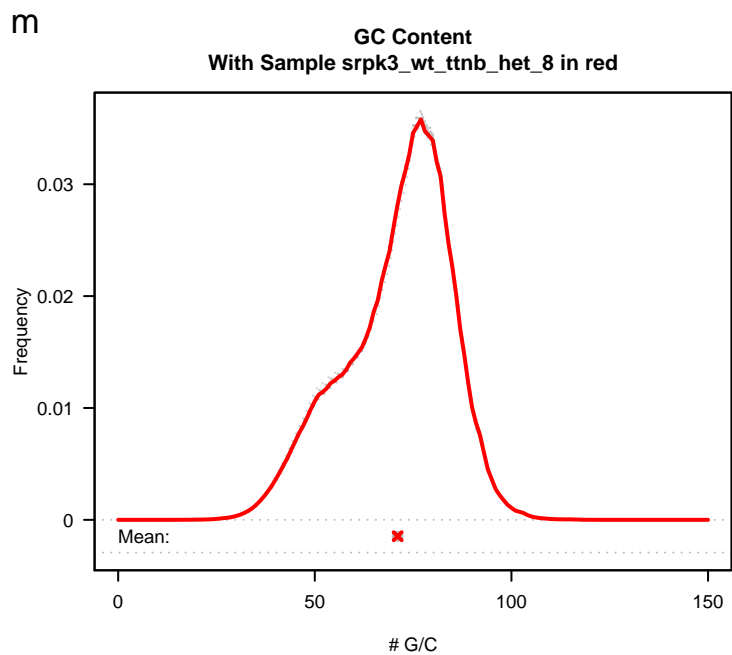
e

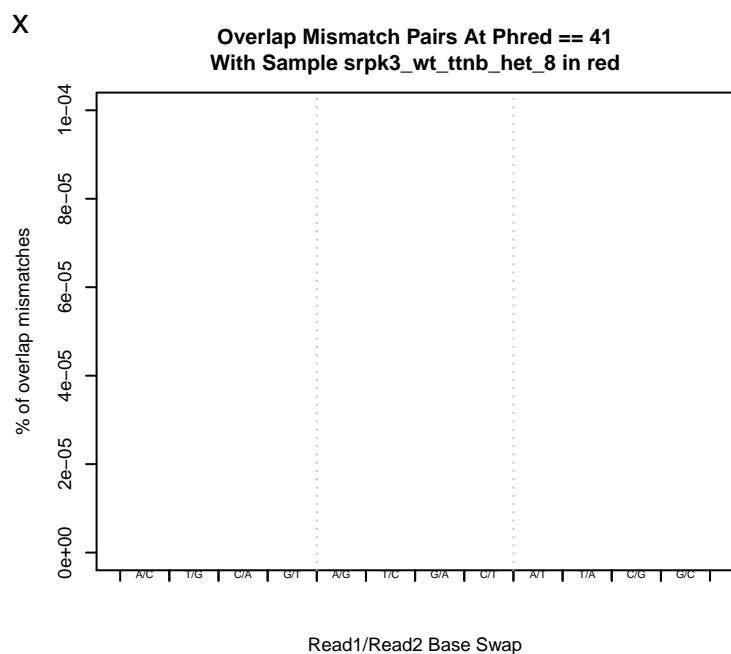
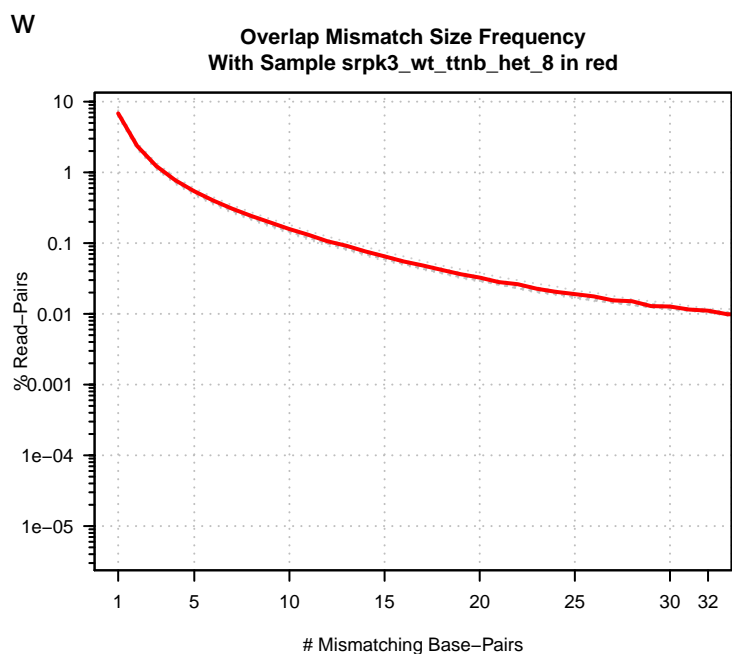
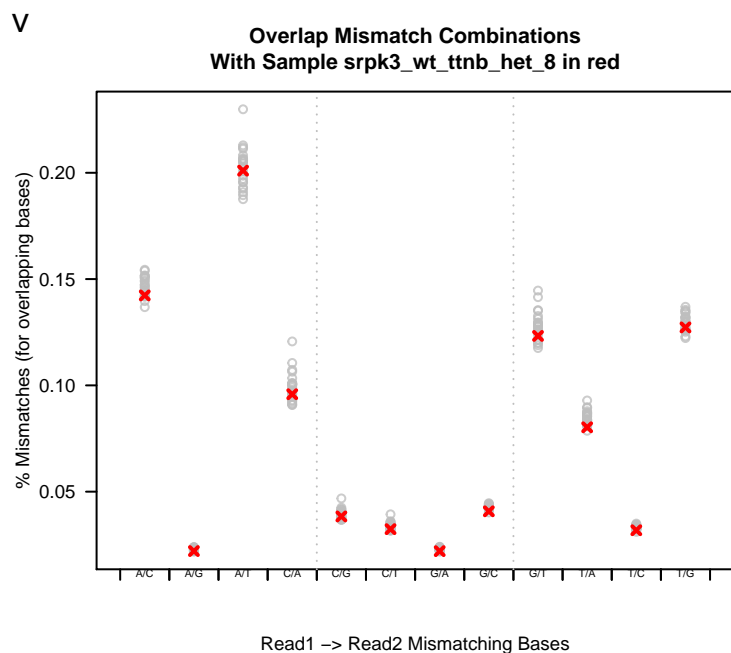
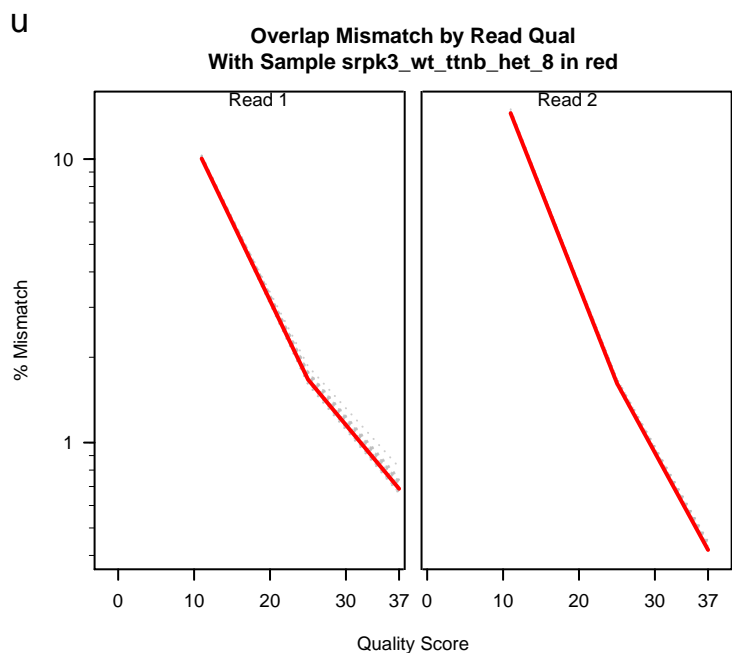
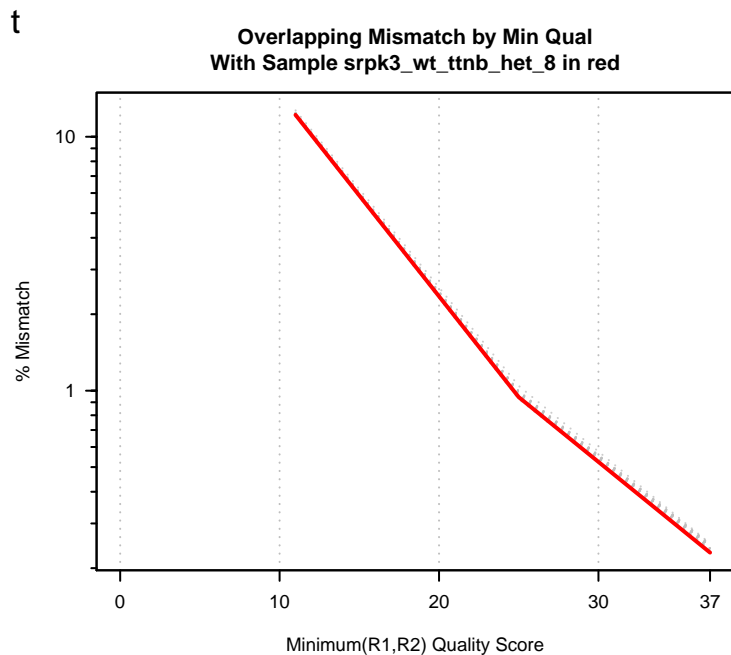
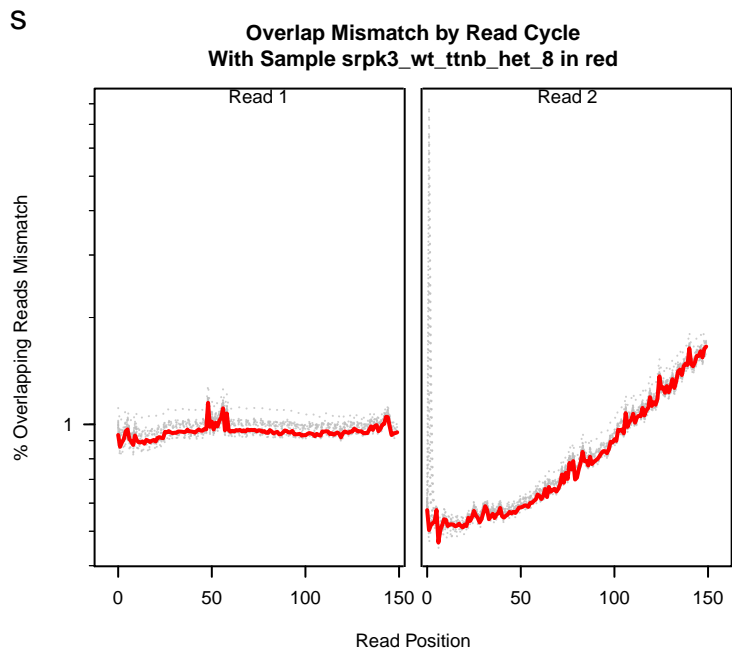


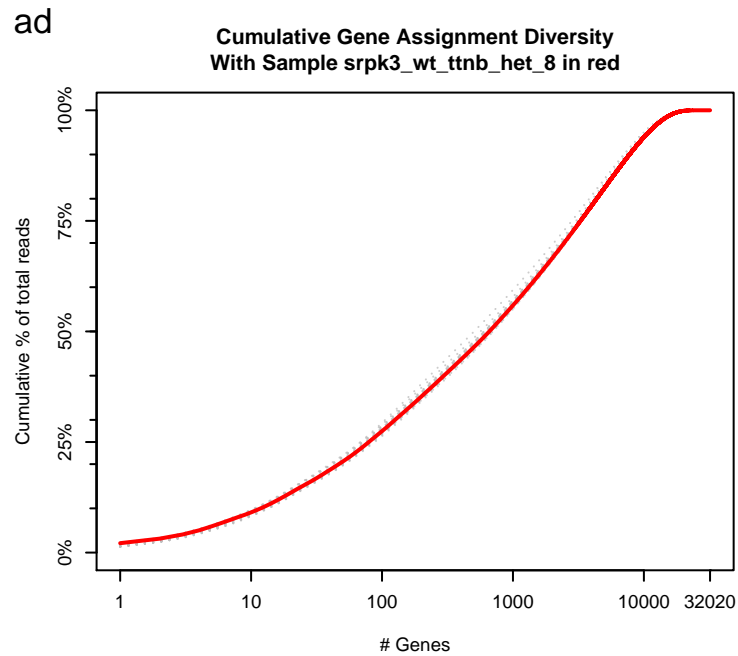
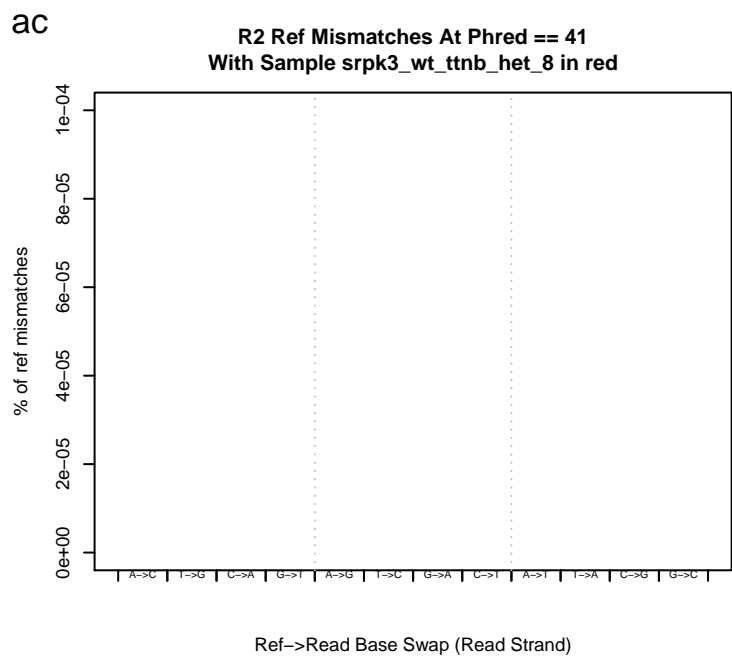
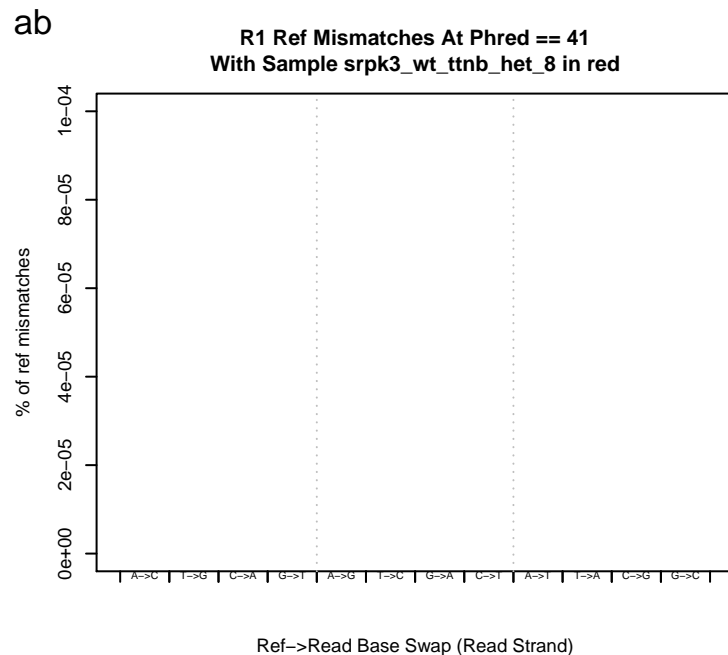
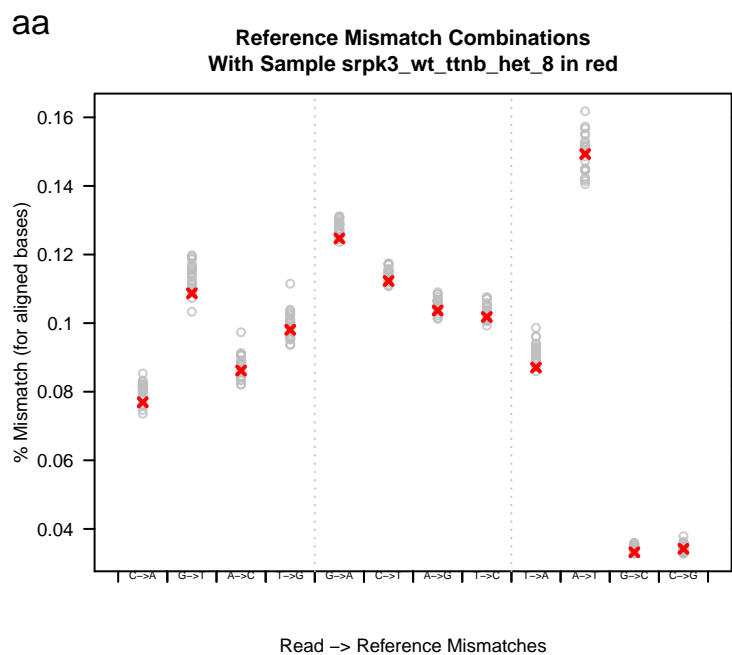
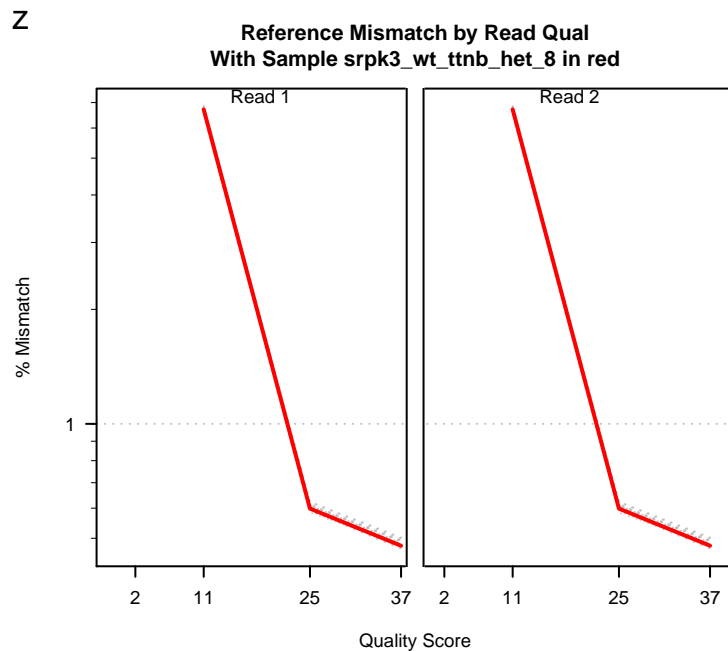
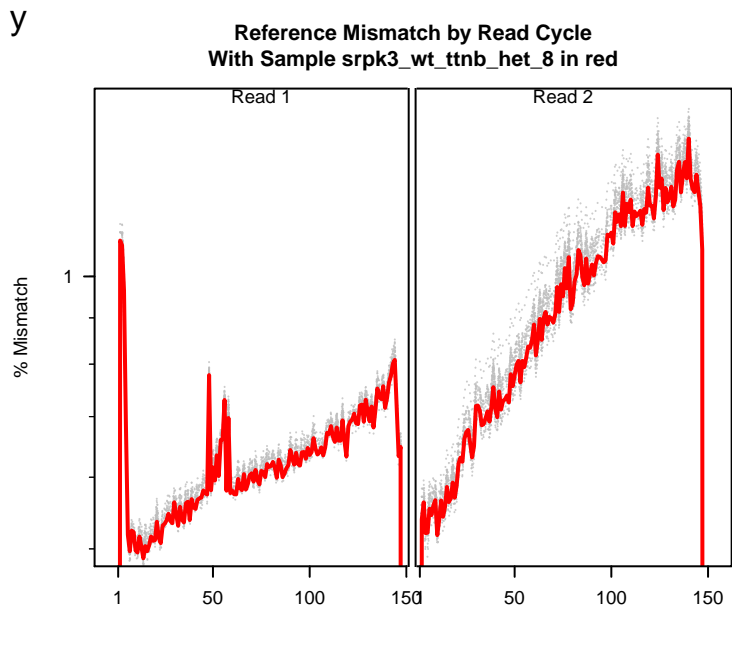
f





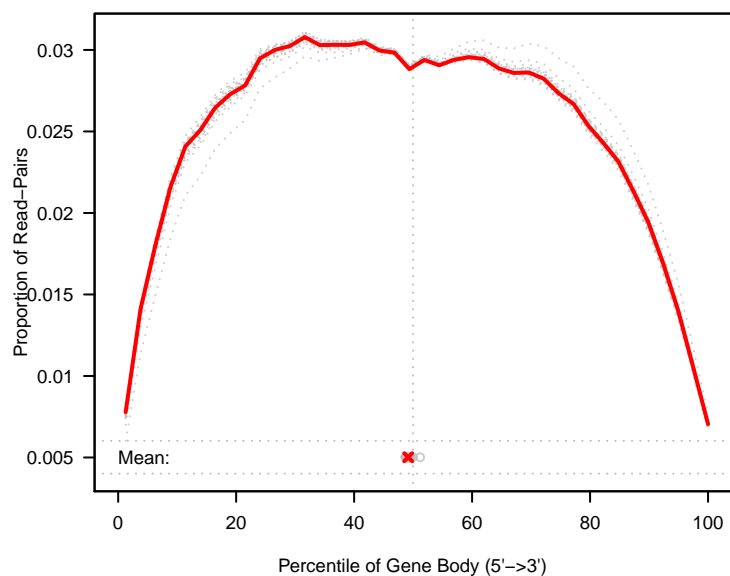






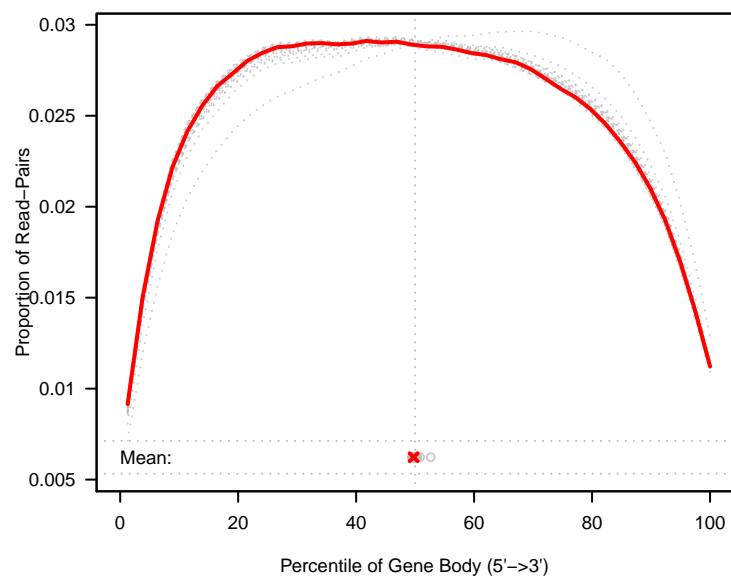
ae

Gene–Body Coverage
With Sample *srpk3_wt_ttnb_het_8* in red



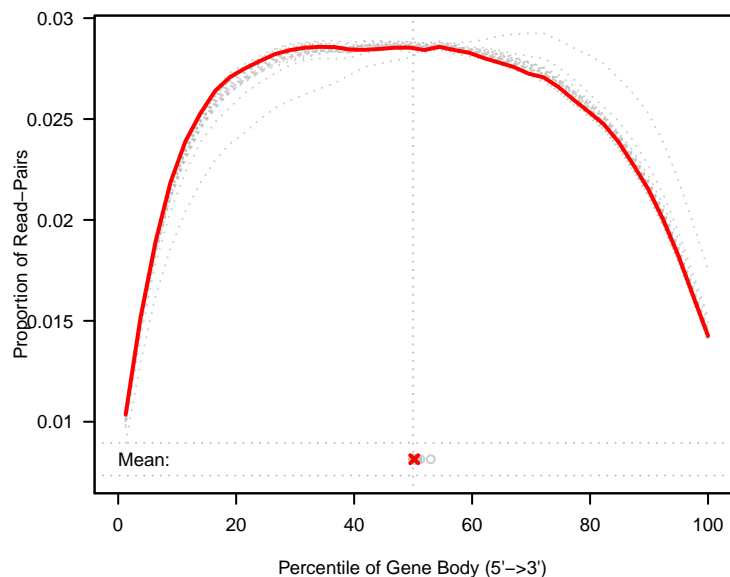
af

Gene–Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_wt_ttnb_het_8* in red



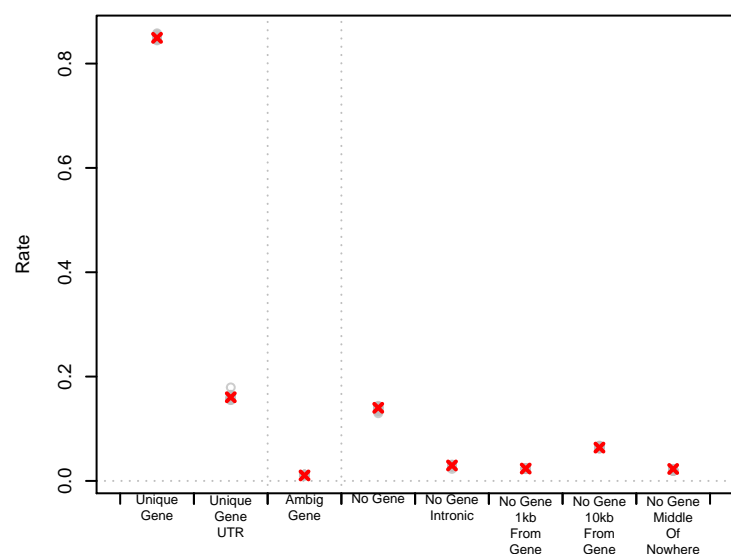
ag

Gene–Body Coverage, Low Expression Genes
With Sample *srpk3_wt_ttnb_het_8* in red



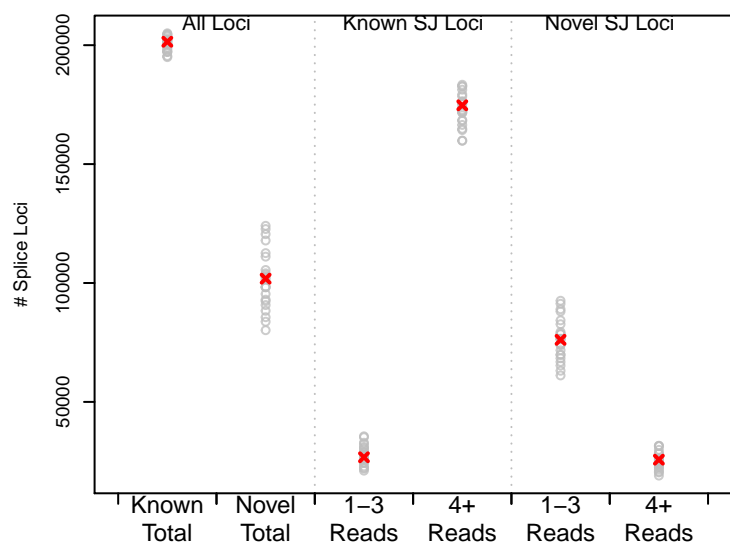
ah

Read Mapping Location Rates
With Sample *srpk3_wt_ttnb_het_8* in red



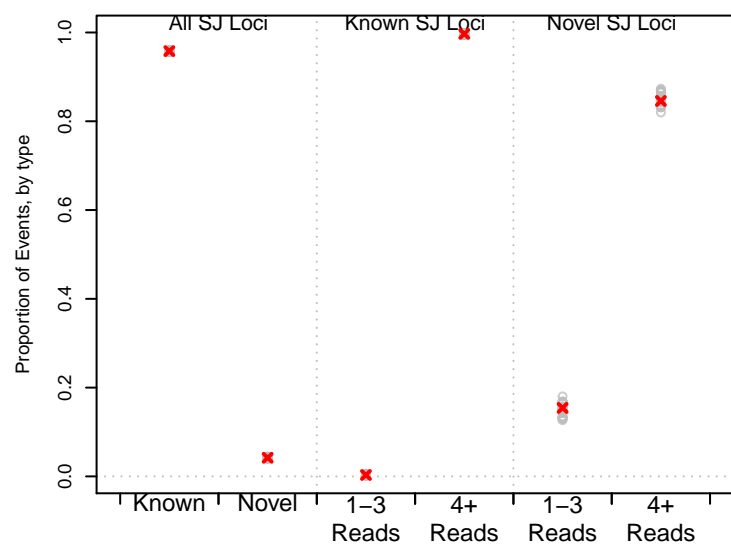
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_wt_ttnb_het_8* in red

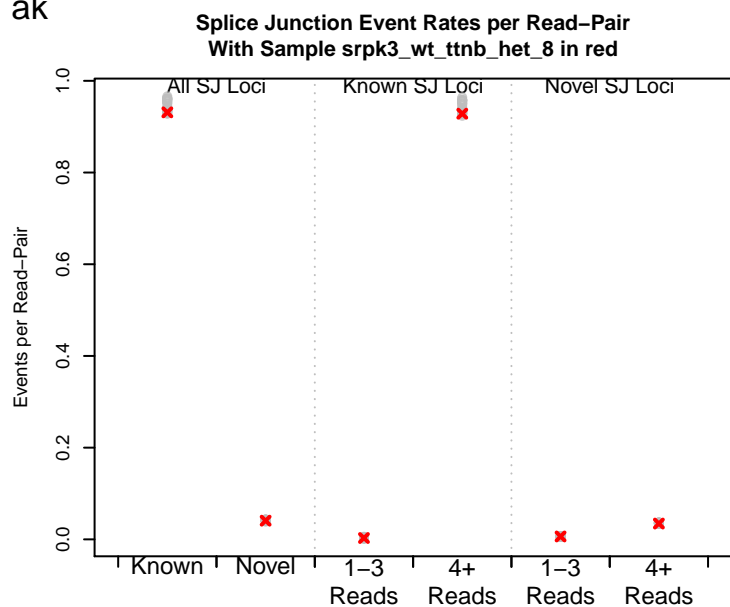


aj

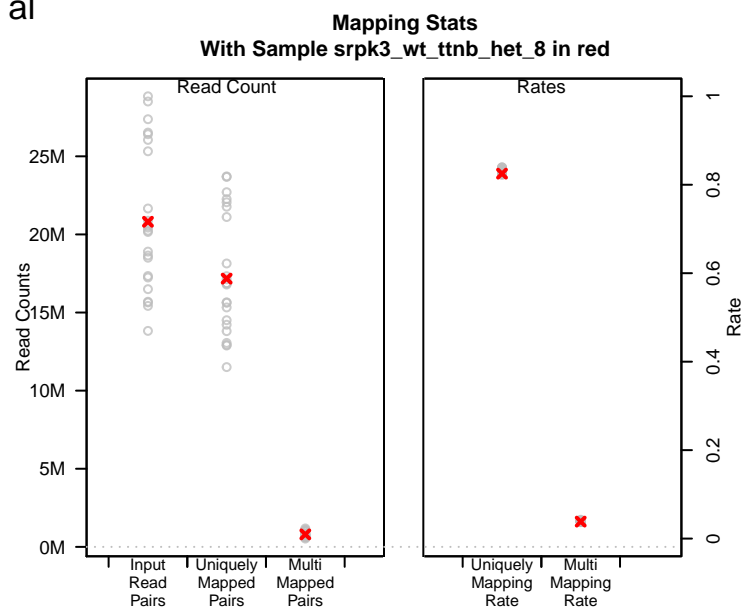
Breakdown of Splice Junction Events, by type
With Sample *srpk3_wt_ttnb_het_8* in red



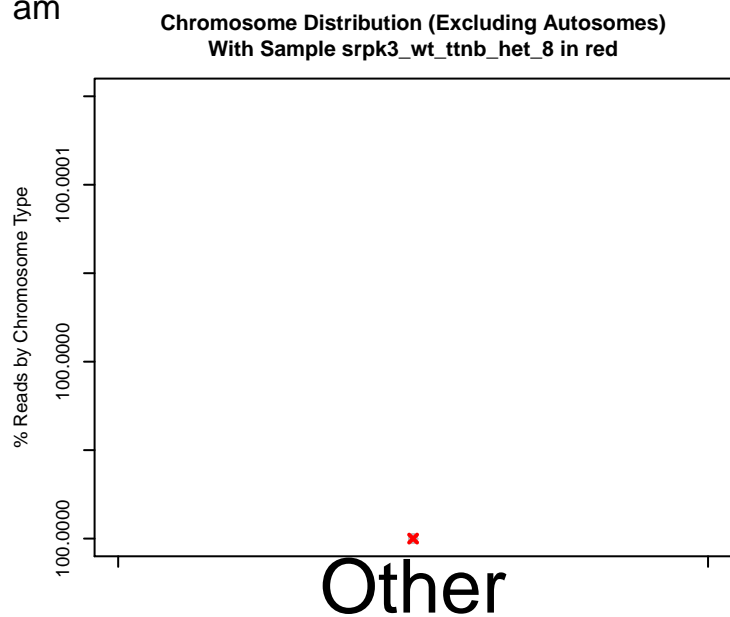
ak



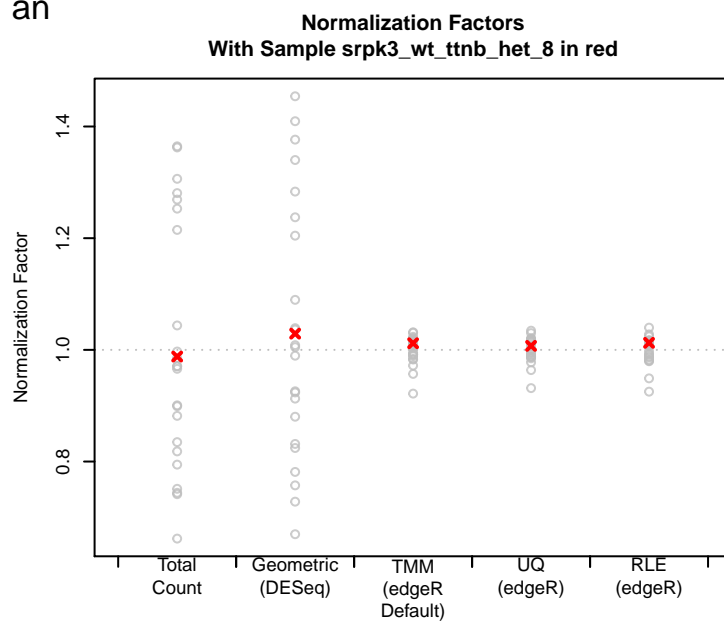
al



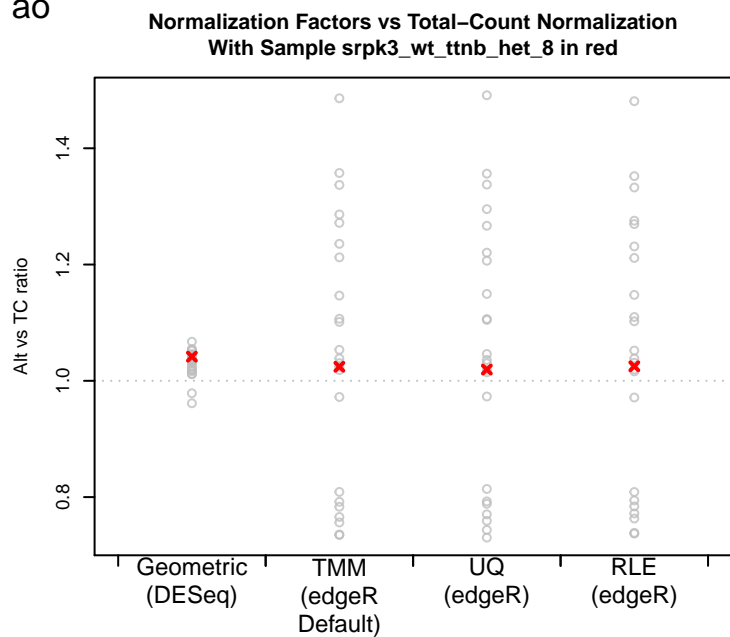
am



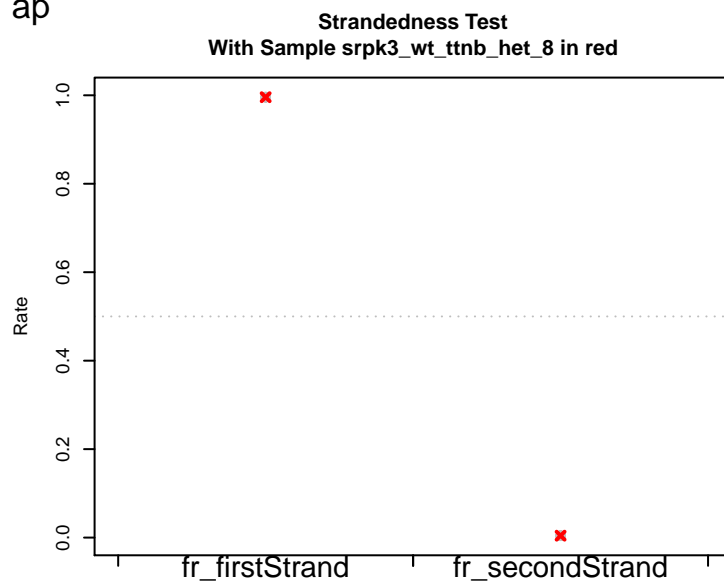
an



ao

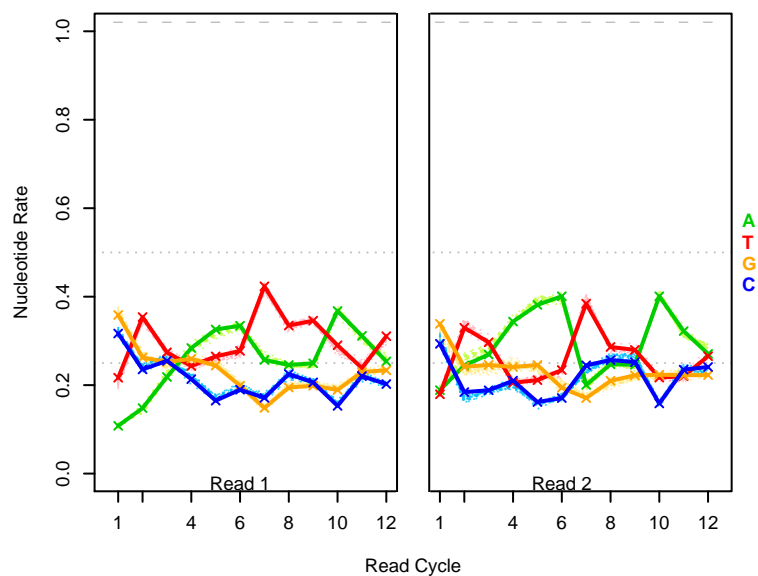


ap



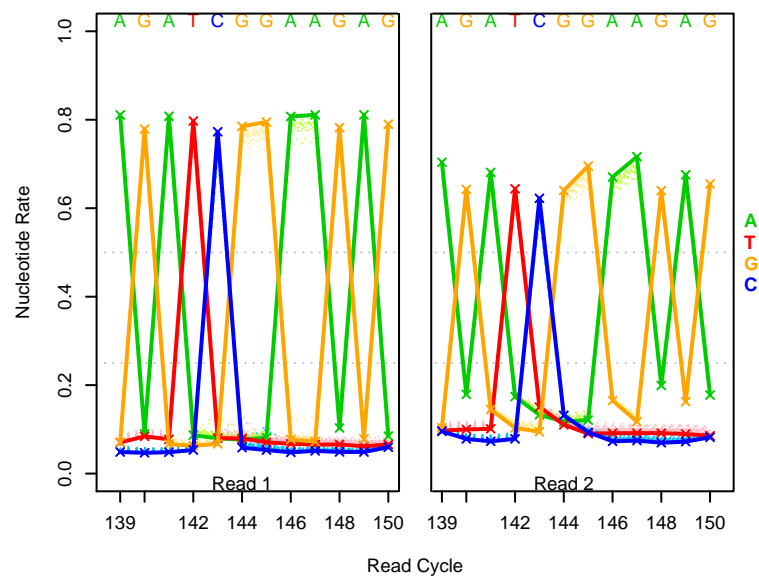
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srpk3_wt_ttnb_het_8 in red



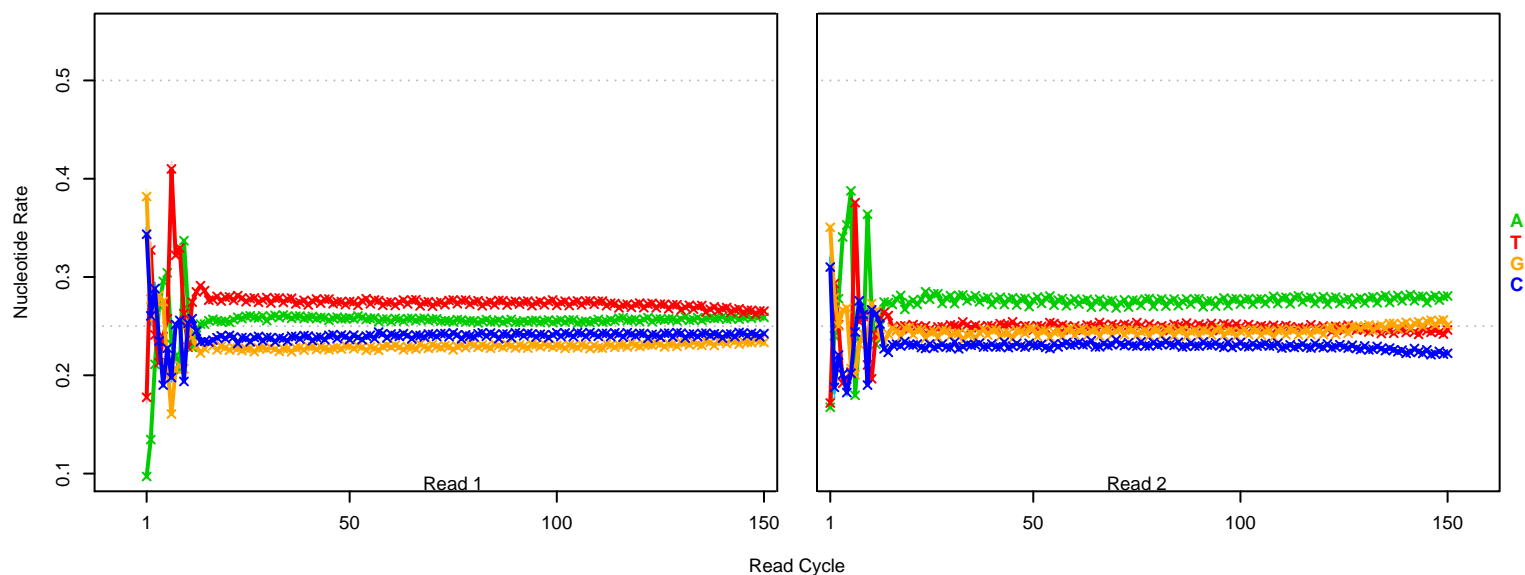
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_wt_ttnb_het_8 in red



as

Raw Nucleotide Rate by Cycle
With Sample srpk3_wt_ttnb_het_8 in red



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_wt_ttnb_het_8 in red

