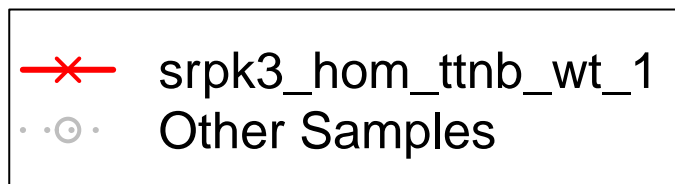


a

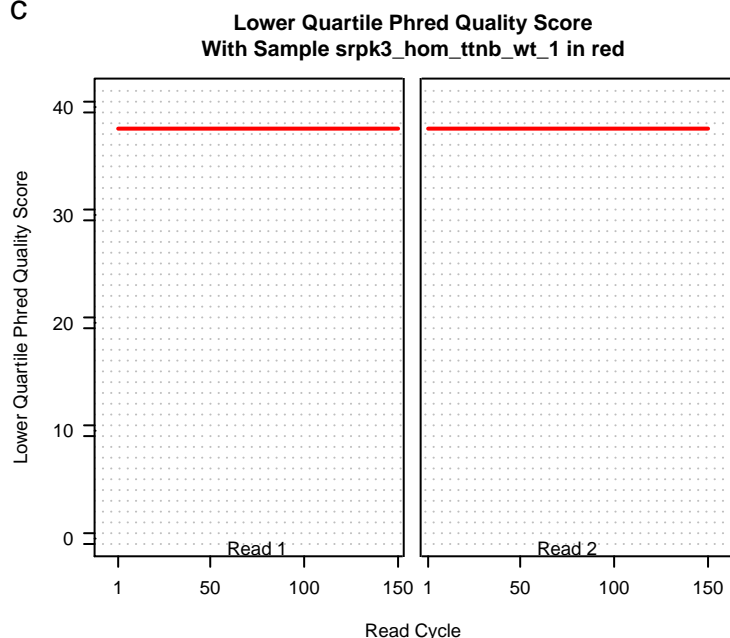
Sample Highlight:
srpk3_hom_ttnb_wt_1



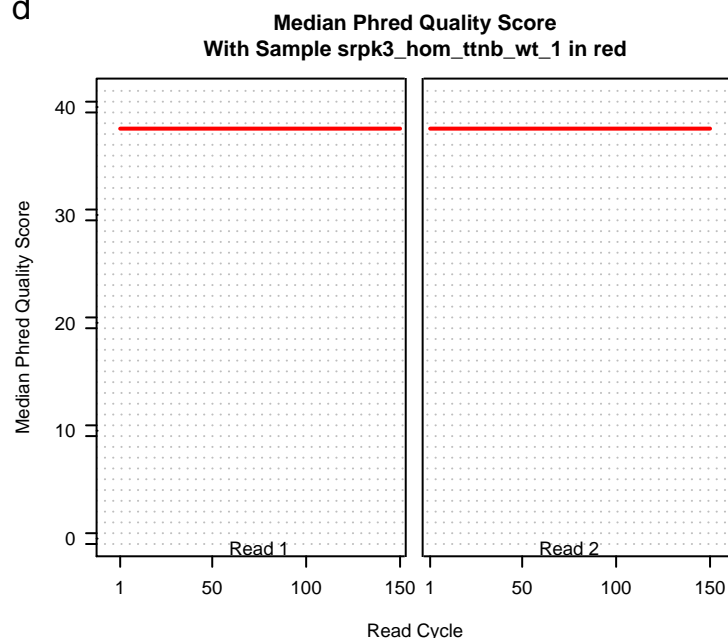
b



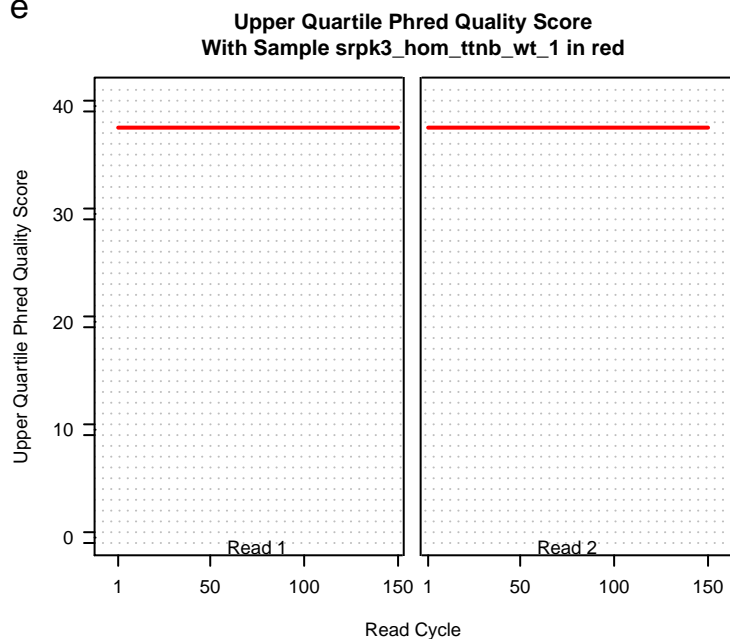
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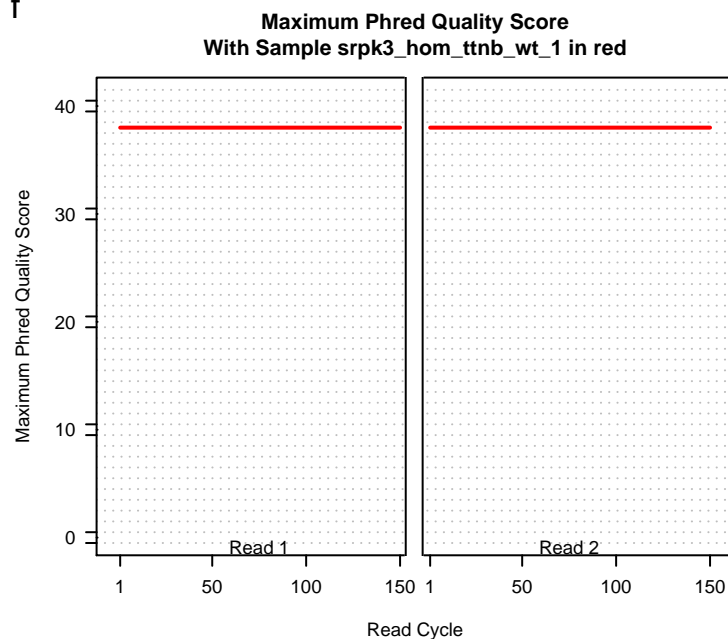
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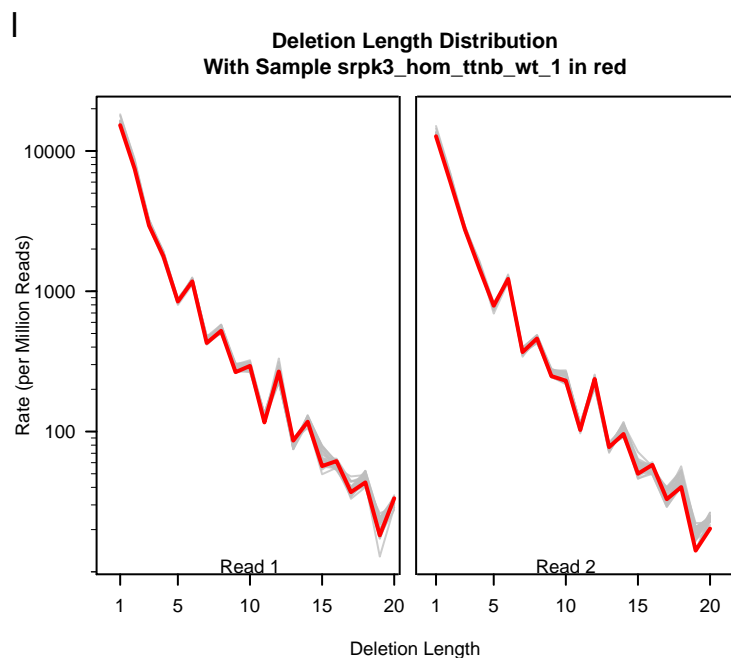
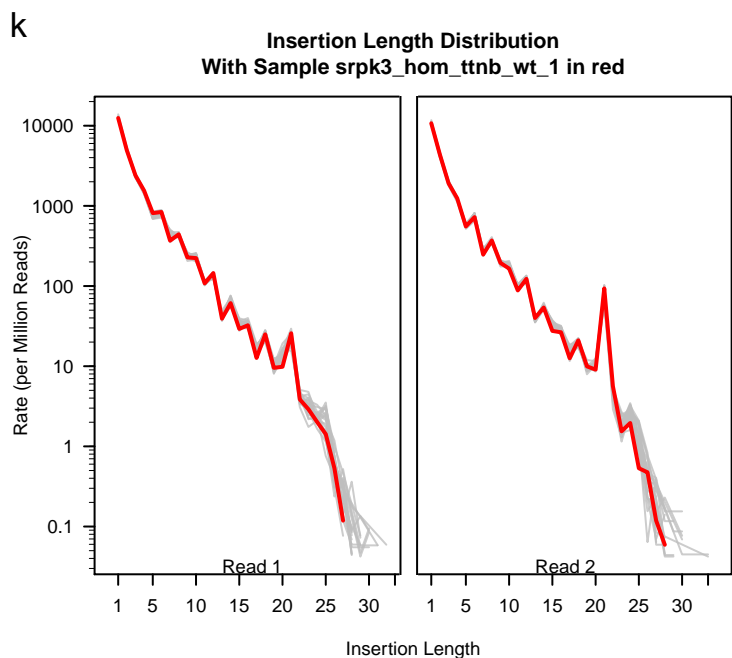
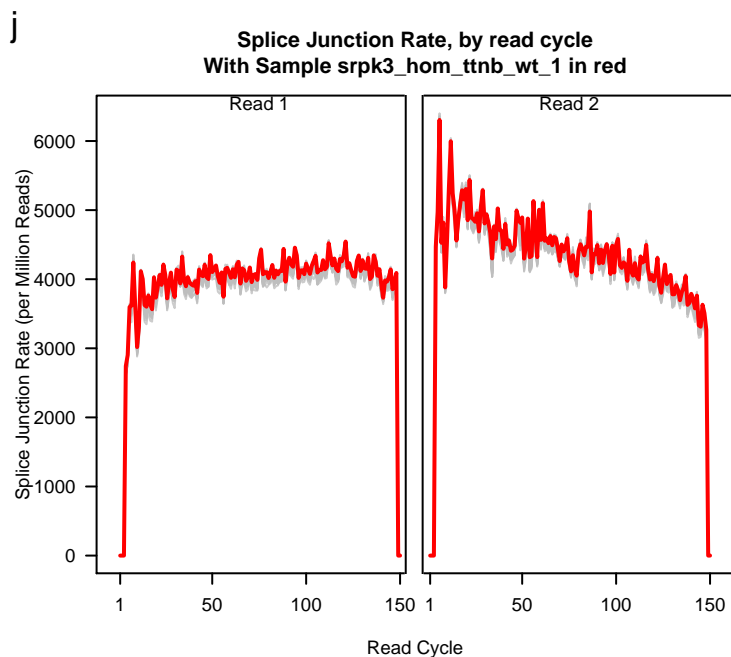
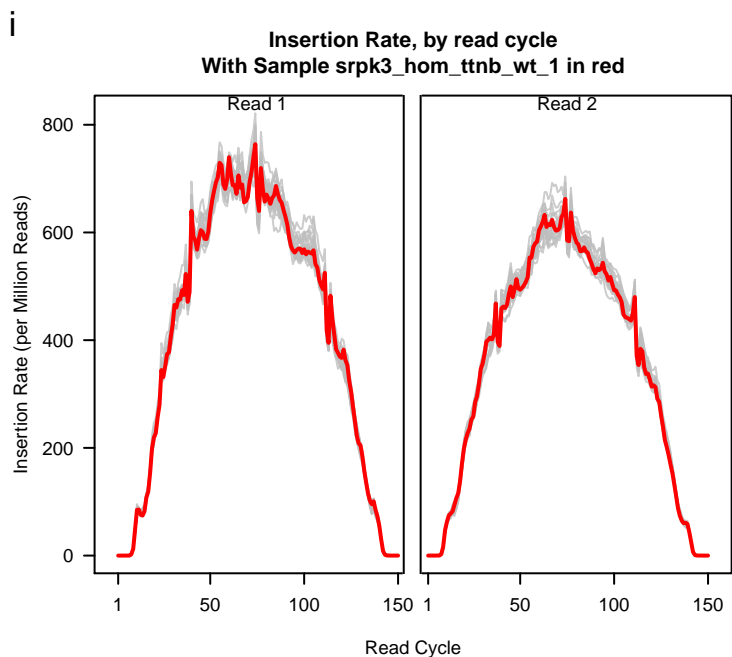
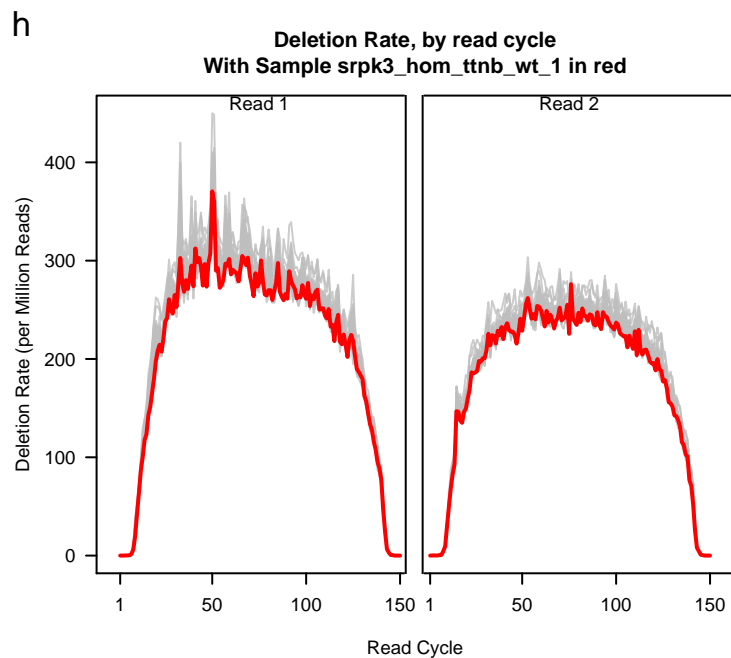
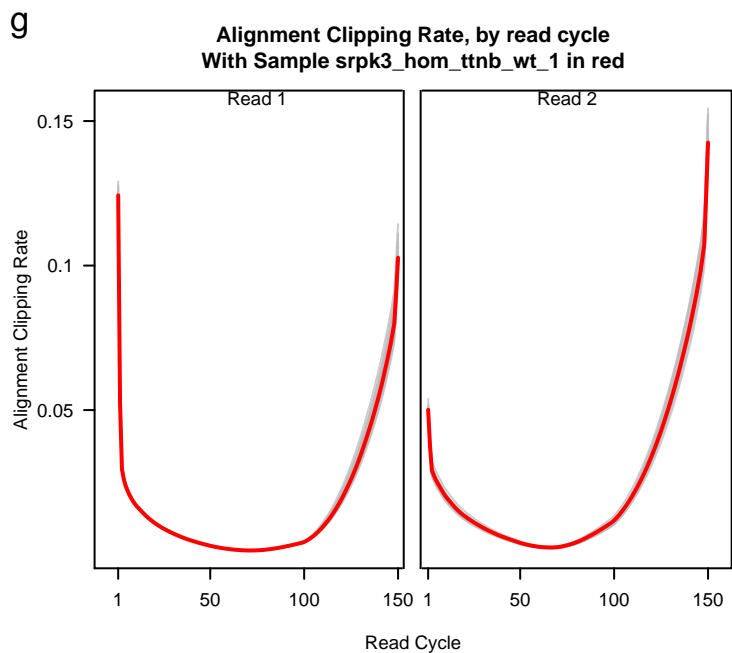


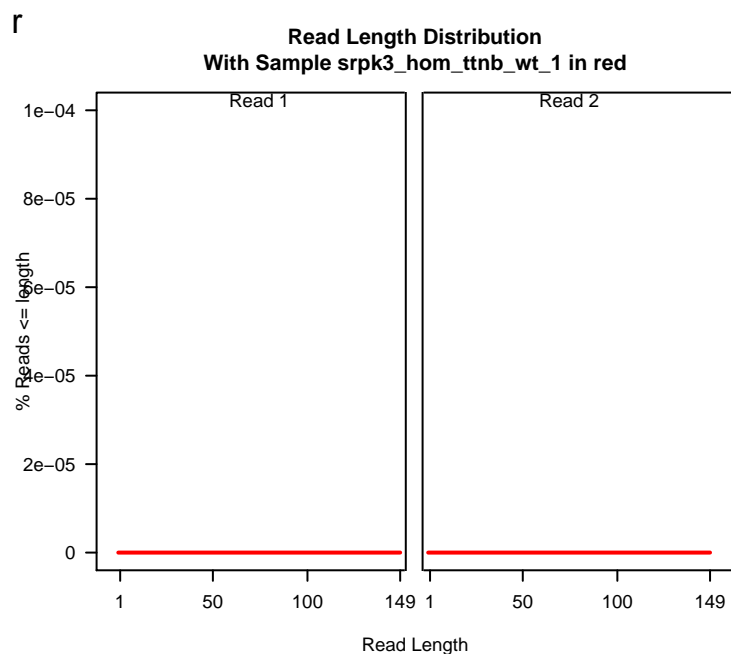
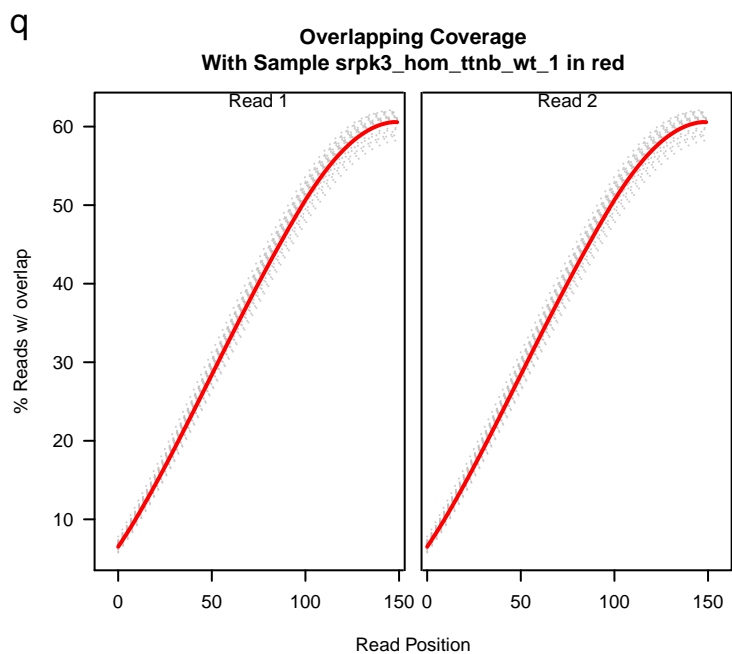
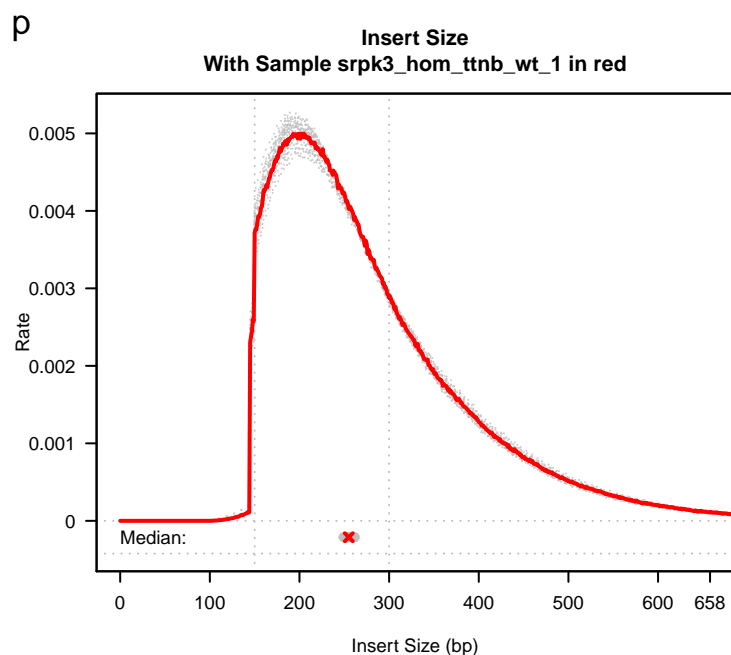
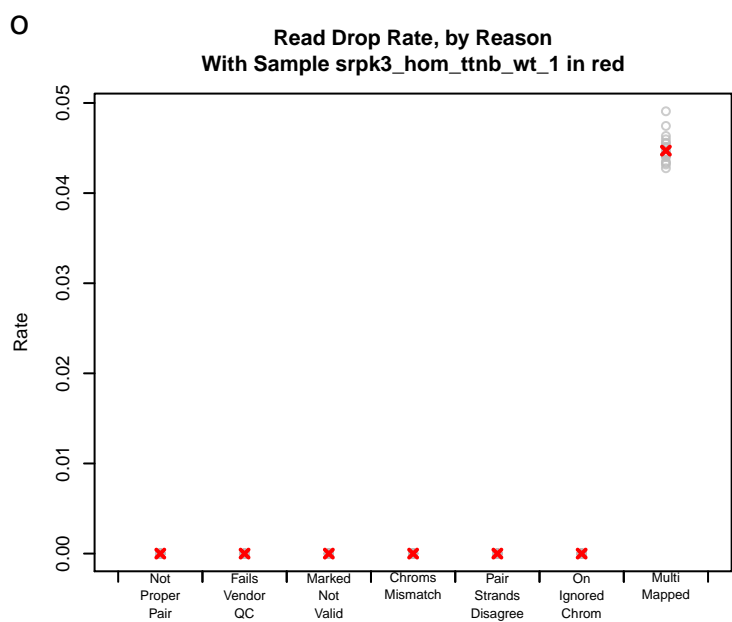
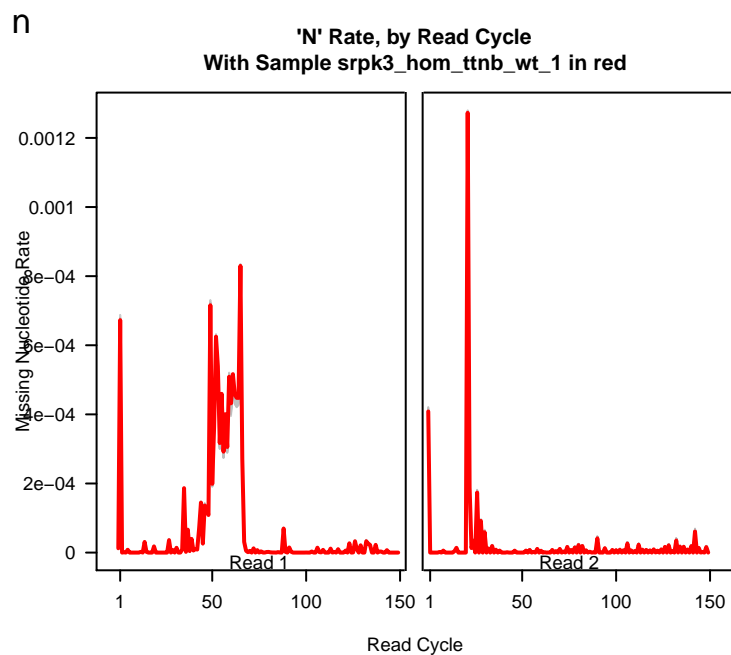
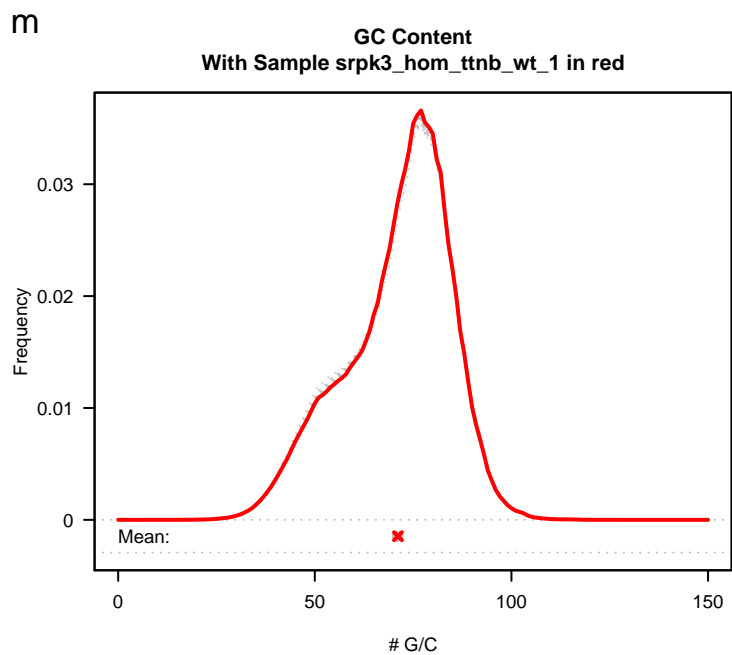
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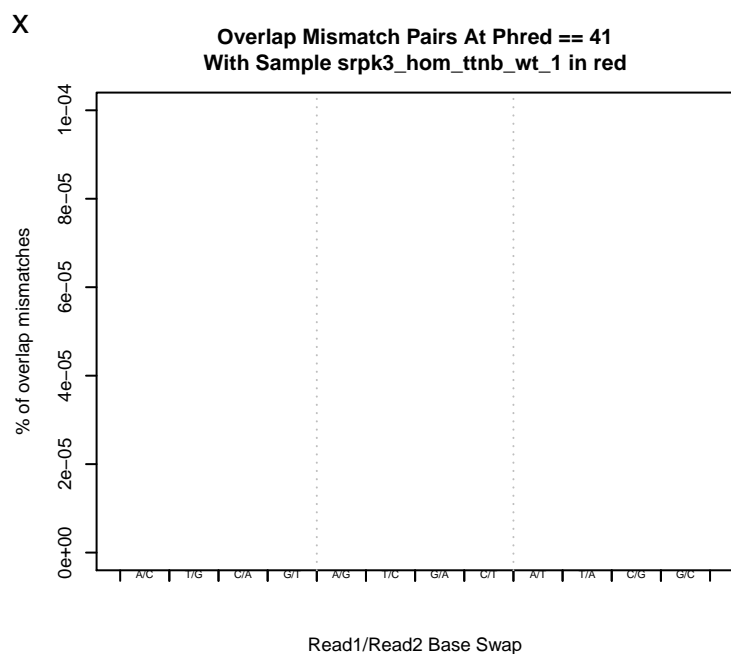
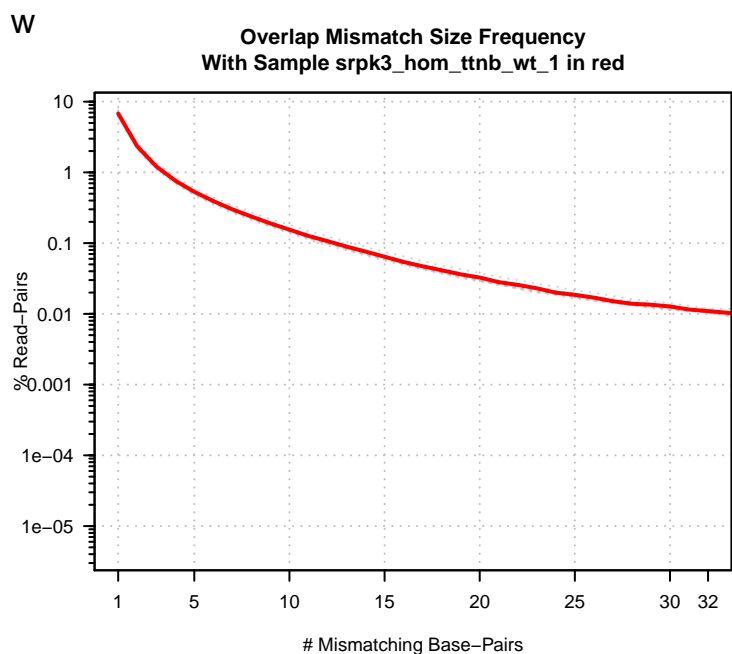
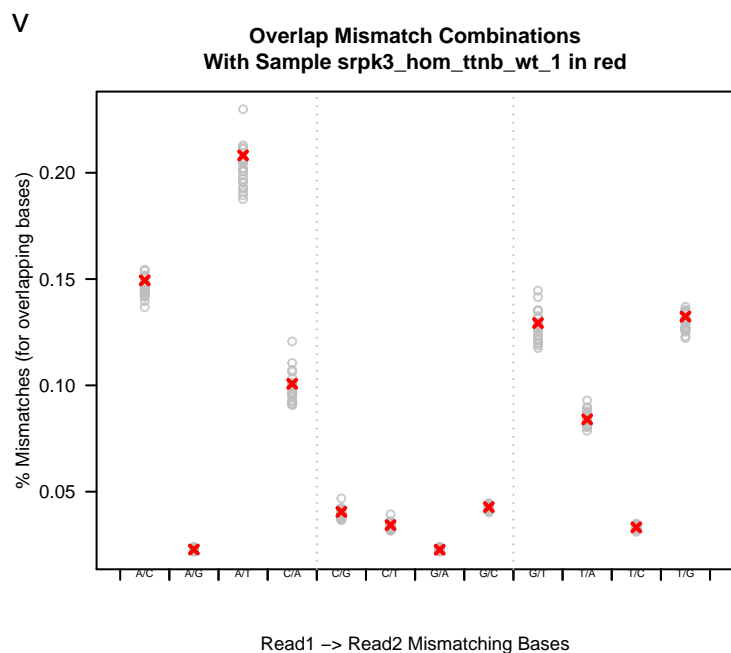
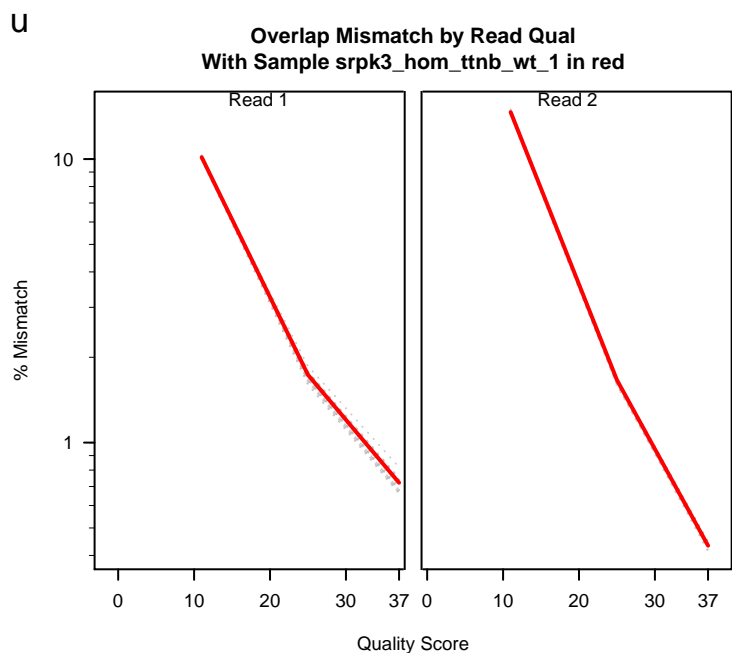
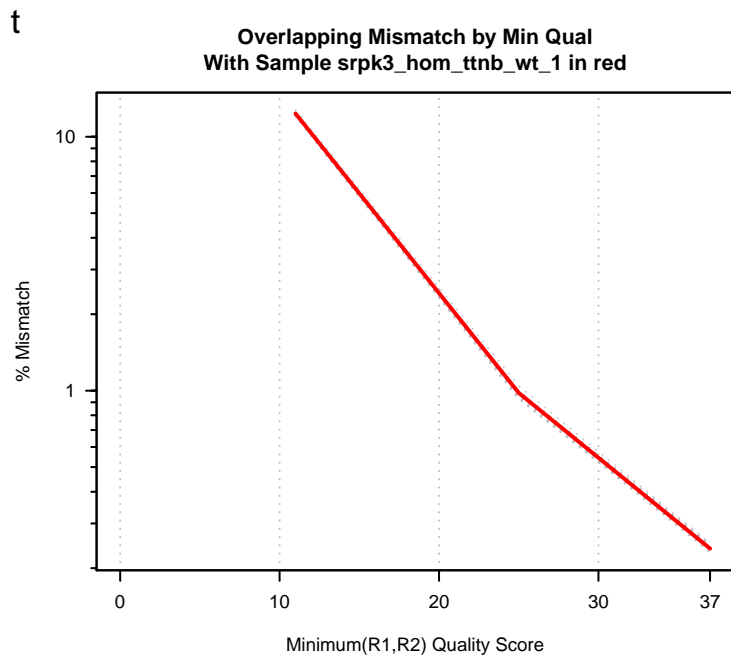
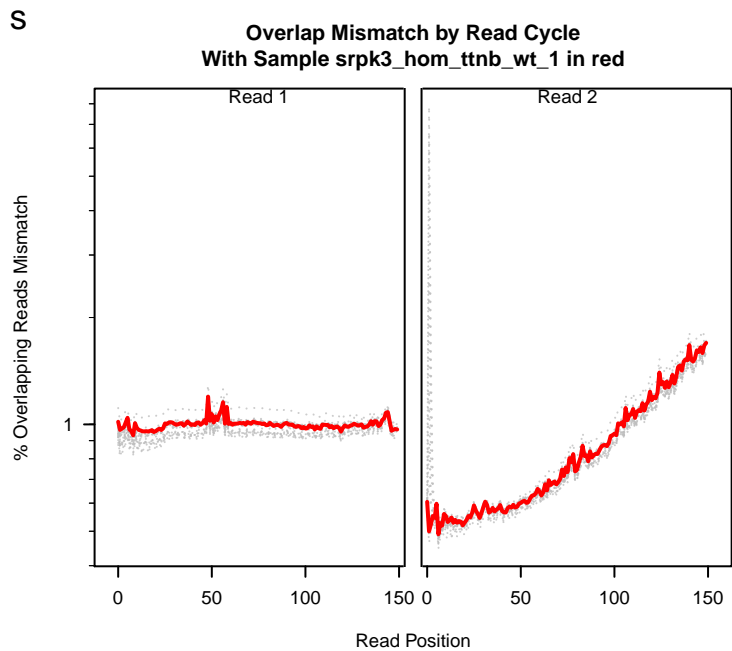


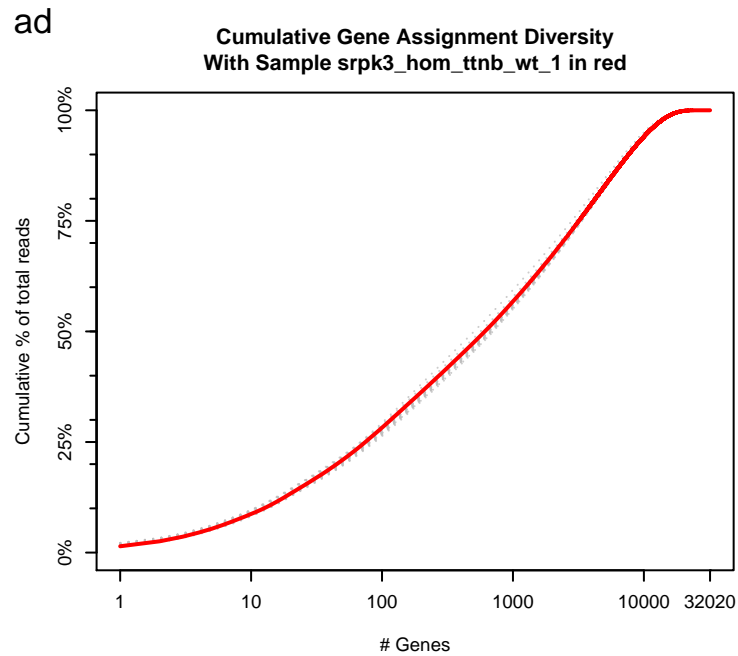
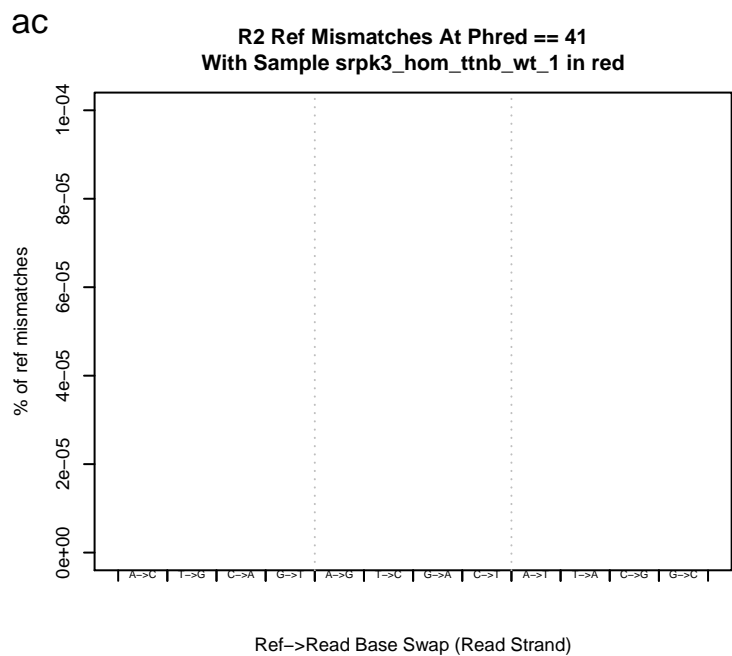
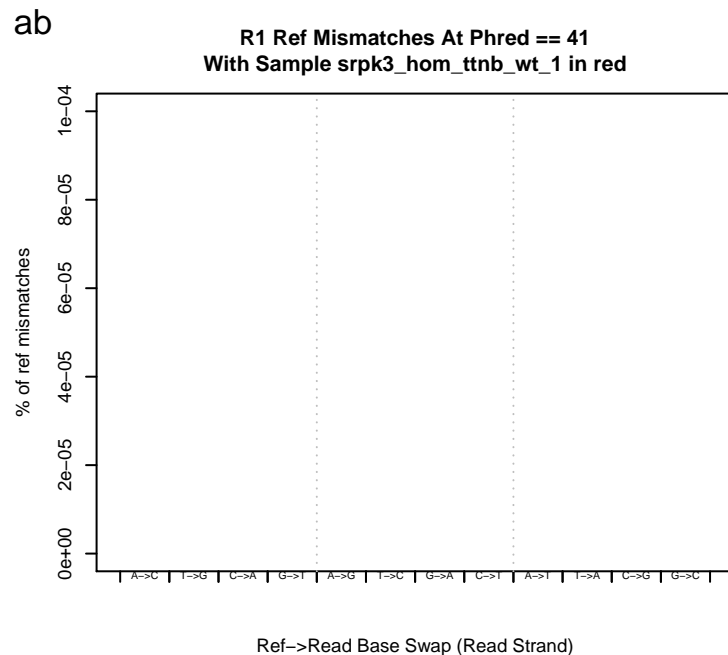
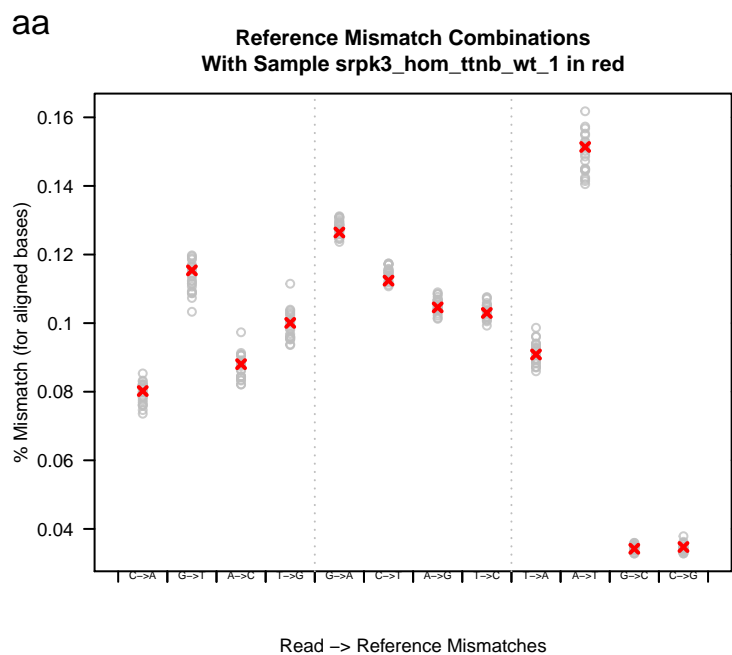
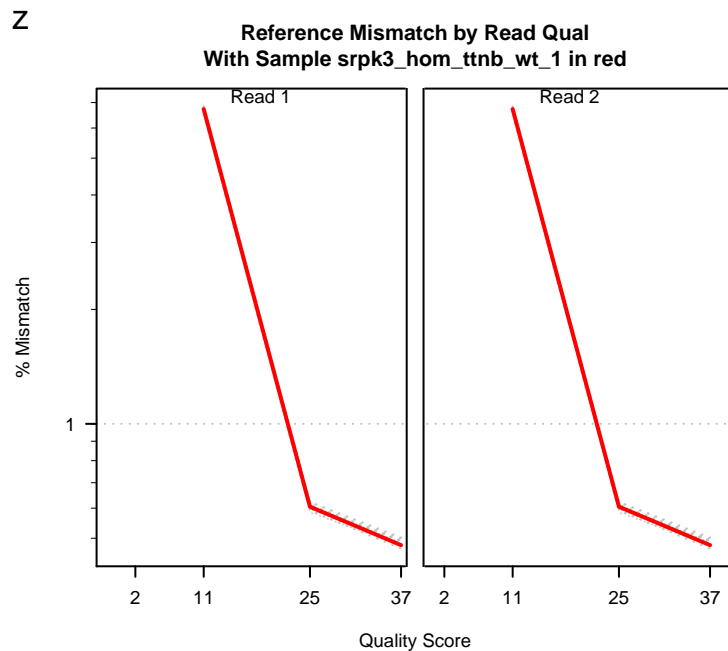
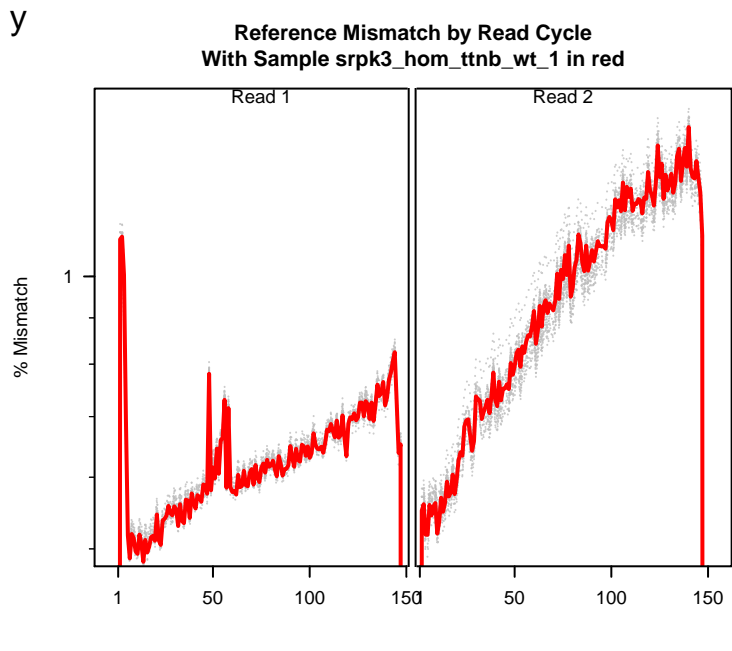
f





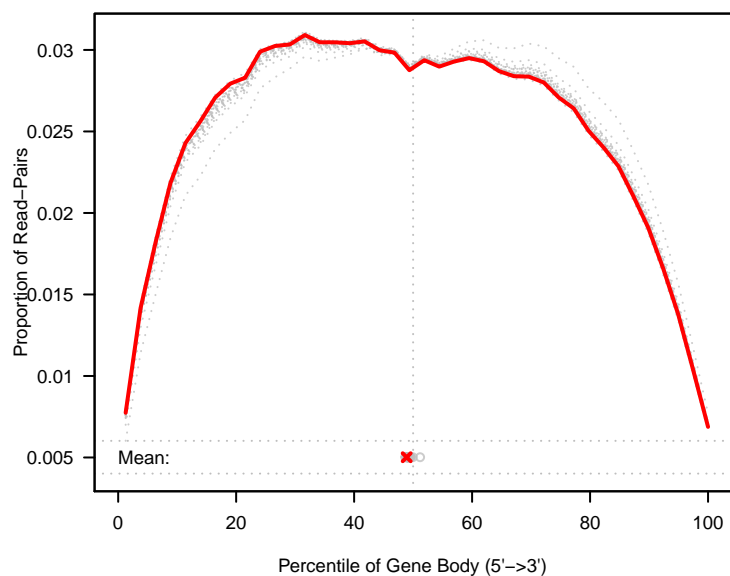






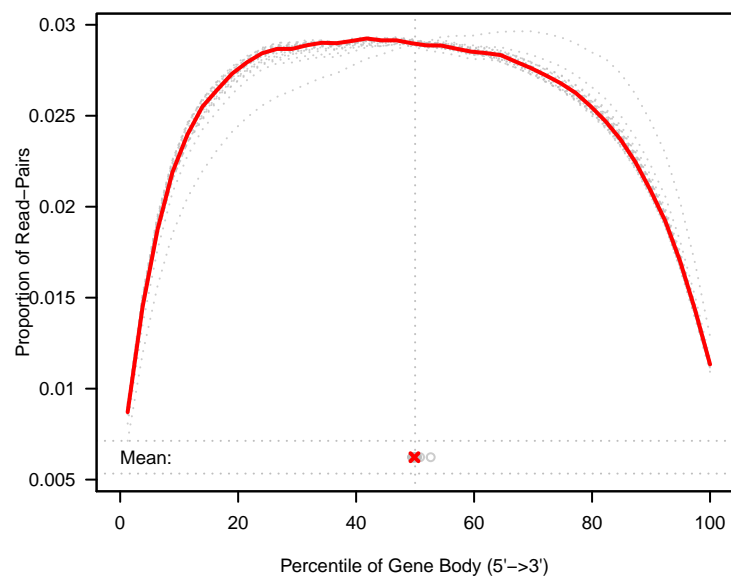
ae

Gene–Body Coverage
With Sample *srpk3_hom_ttnb_wt_1* in red



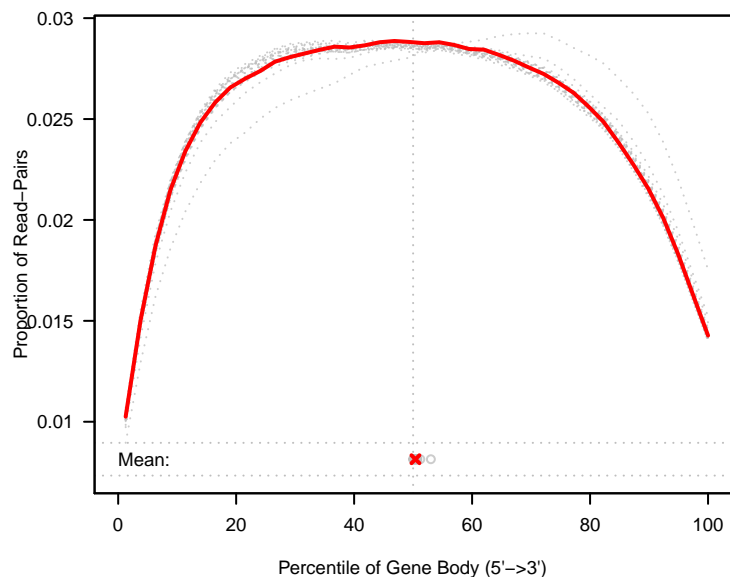
af

Gene–Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_hom_ttnb_wt_1* in red



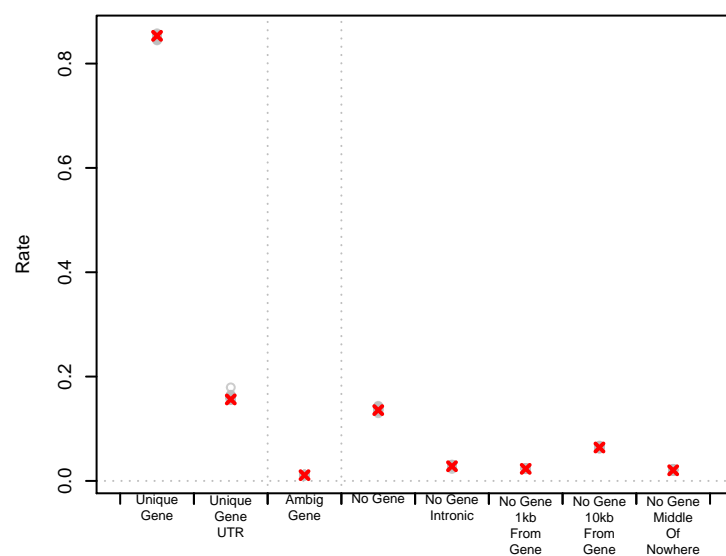
ag

Gene–Body Coverage, Low Expression Genes
With Sample *srpk3_hom_ttnb_wt_1* in red



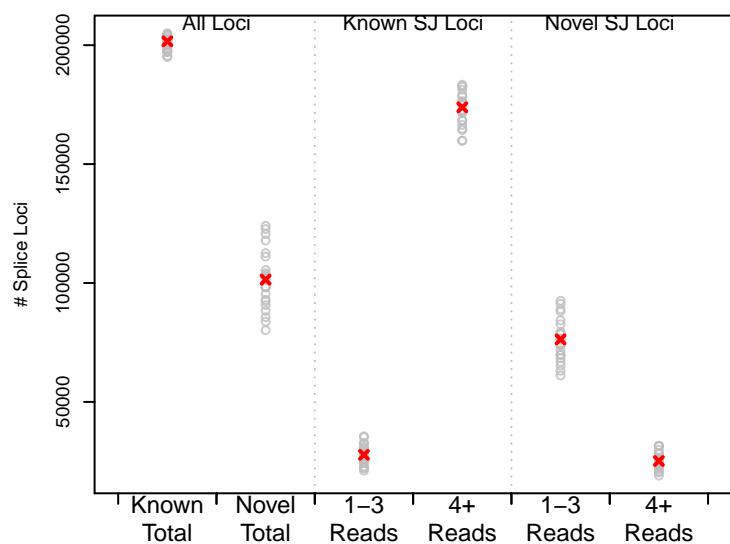
ah

Read Mapping Location Rates
With Sample *srpk3_hom_ttnb_wt_1* in red



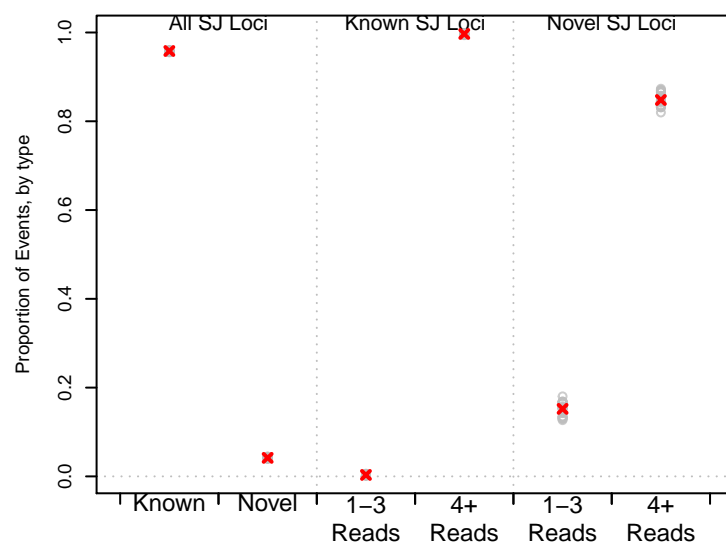
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_hom_ttnb_wt_1* in red

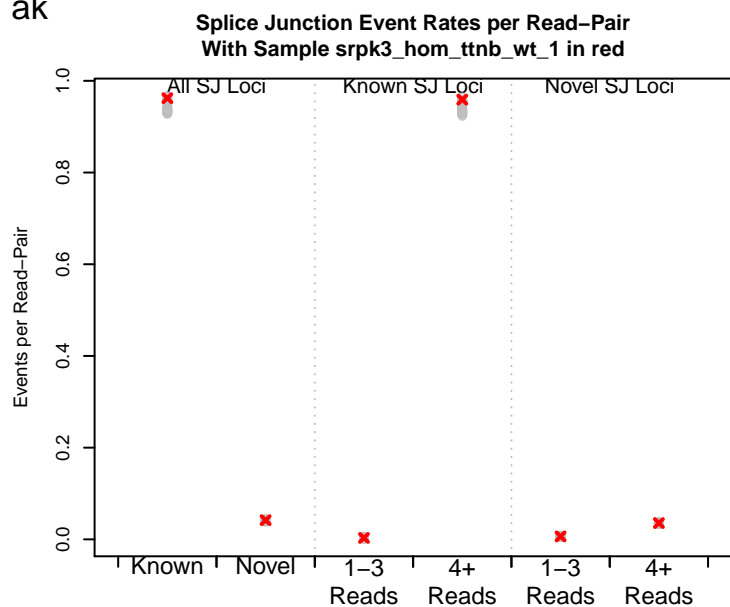


aj

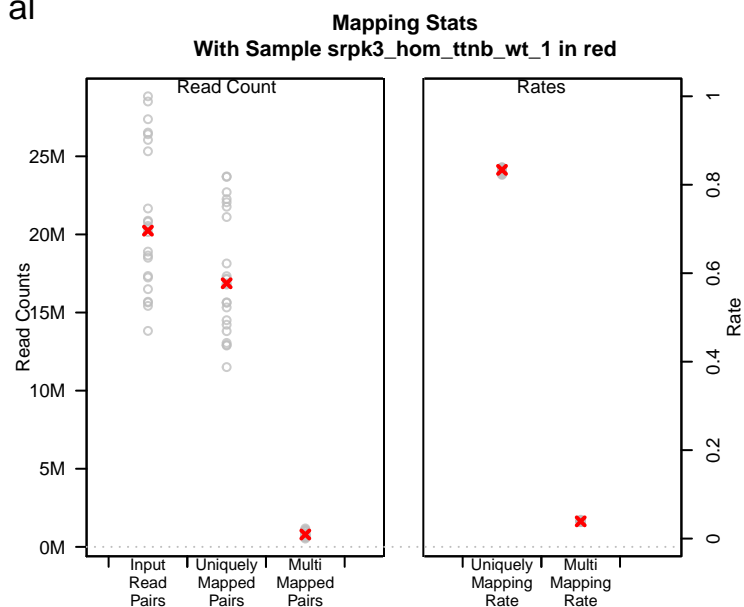
Breakdown of Splice Junction Events, by type
With Sample *srpk3_hom_ttnb_wt_1* in red



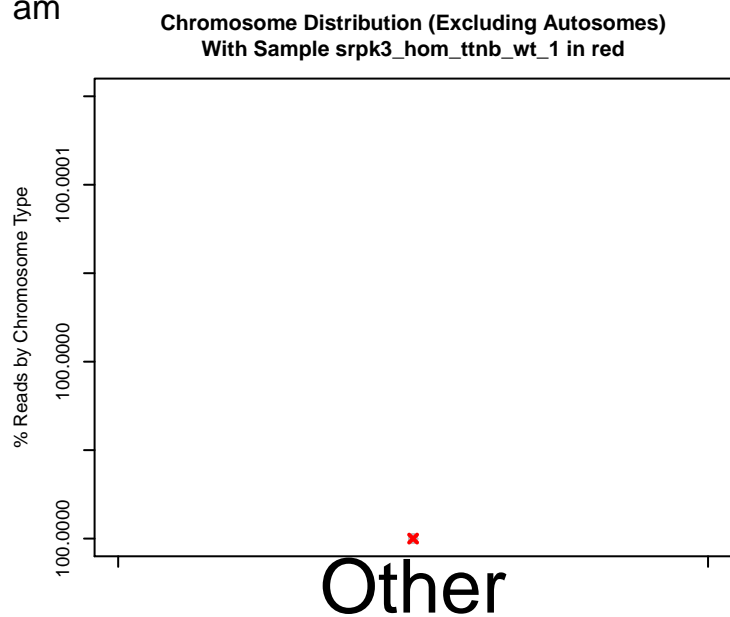
ak



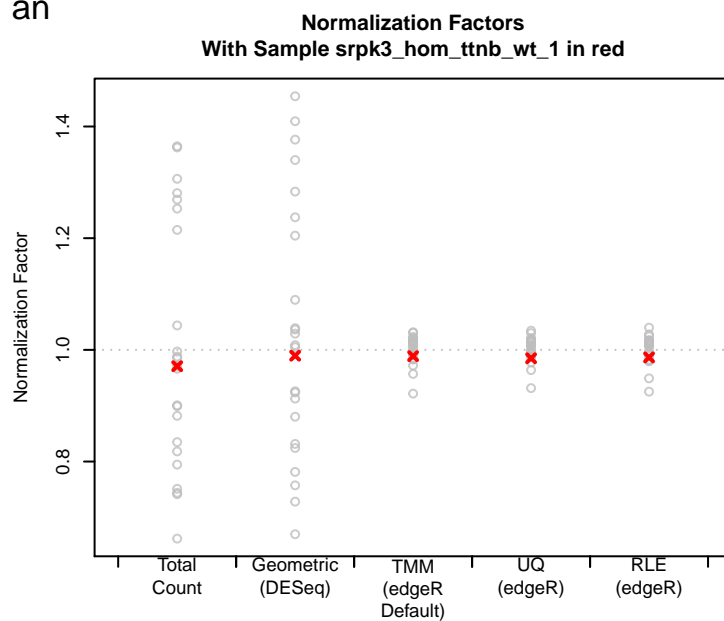
al



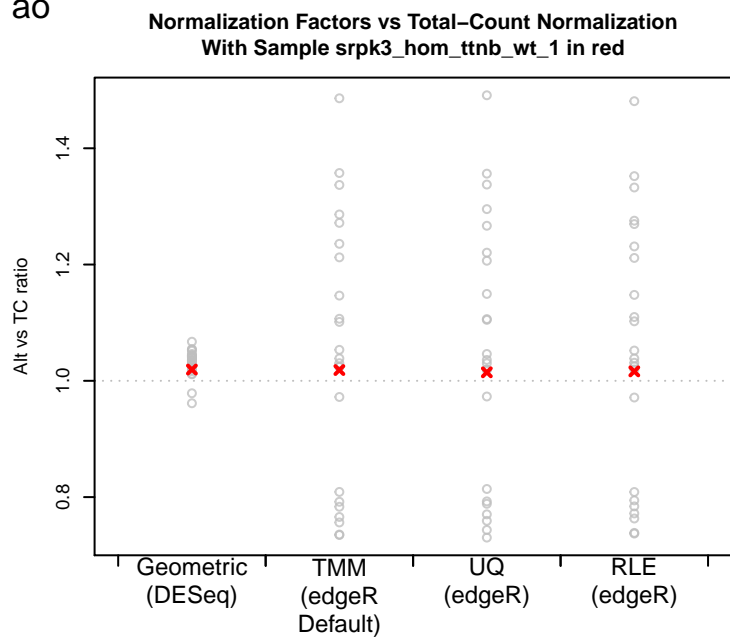
am



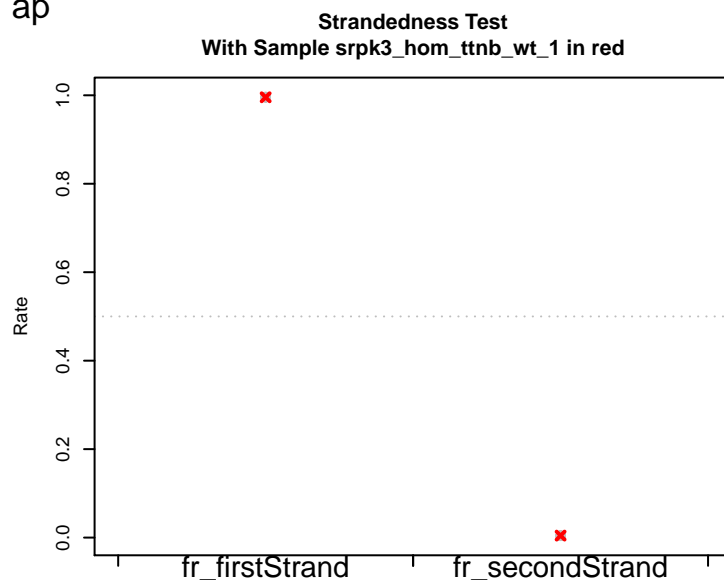
an



ao

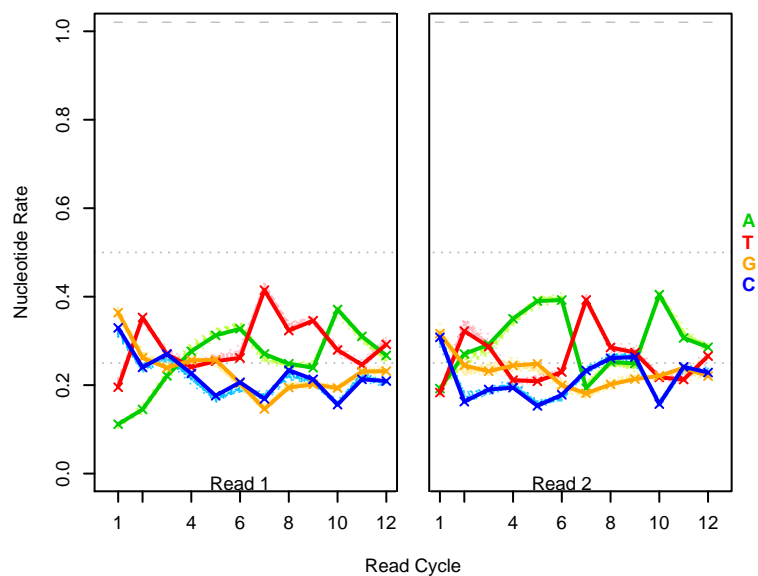


ap



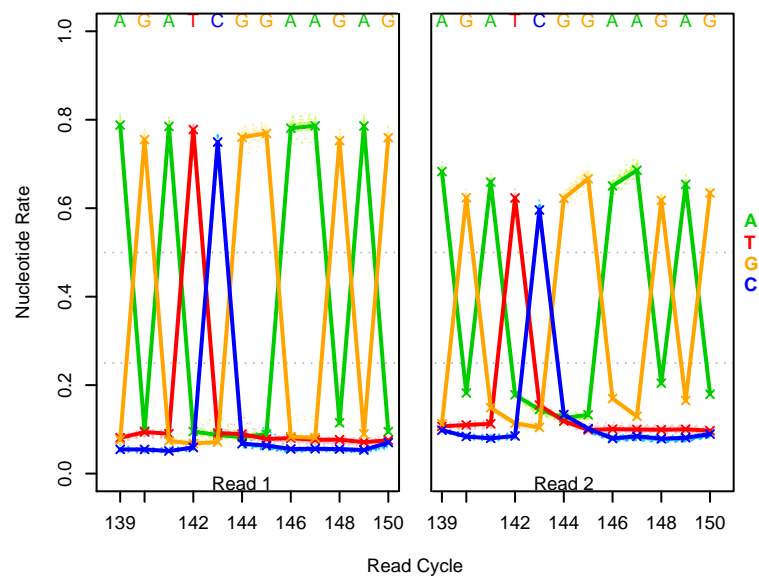
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srp3k3_hom_ttnb_wt_1 in red



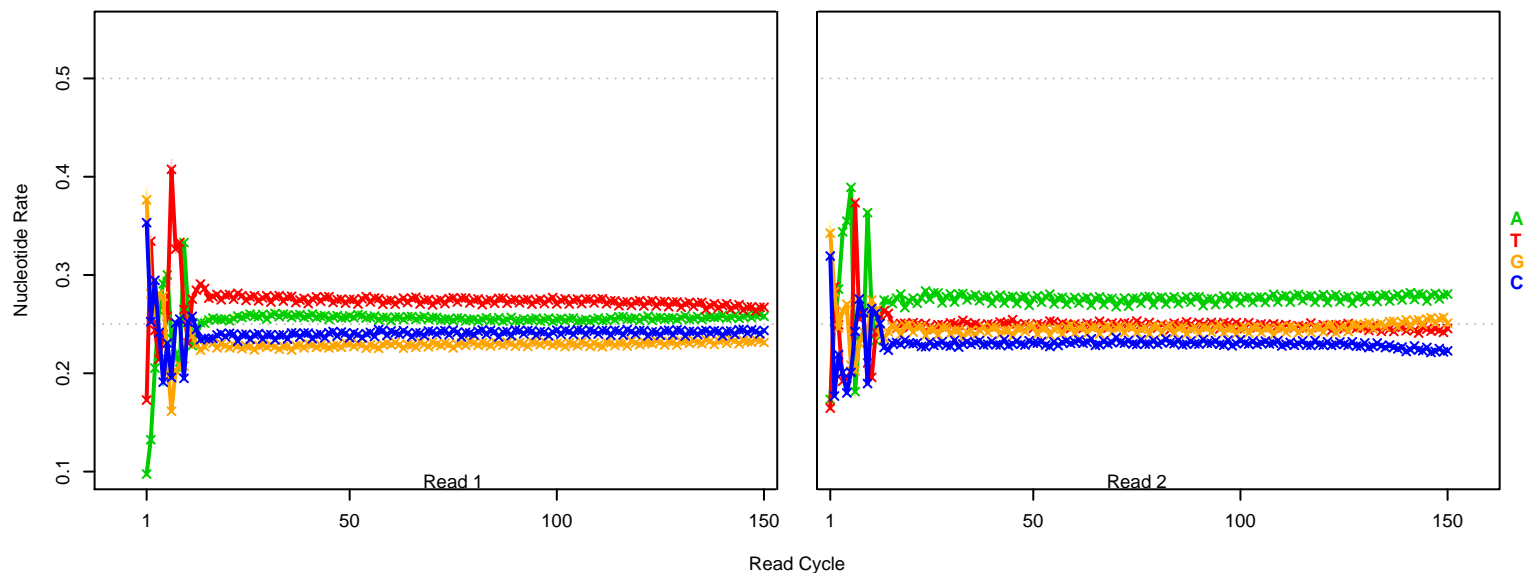
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srp3k3_hom_ttnb_wt_1 in red



as

Raw Nucleotide Rate by Cycle
With Sample srp3k3_hom_ttnb_wt_1 in red



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srp3k3_hom_ttnb_wt_1 in red

