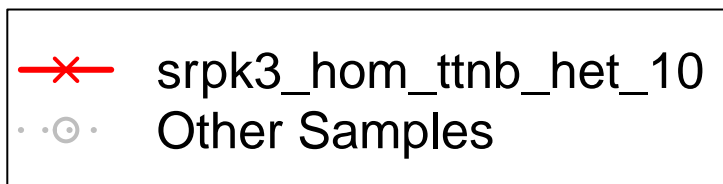
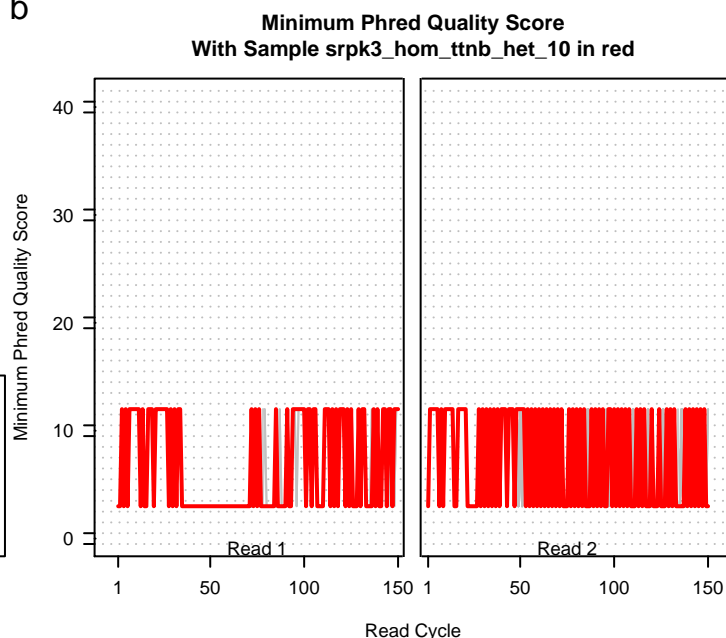


a

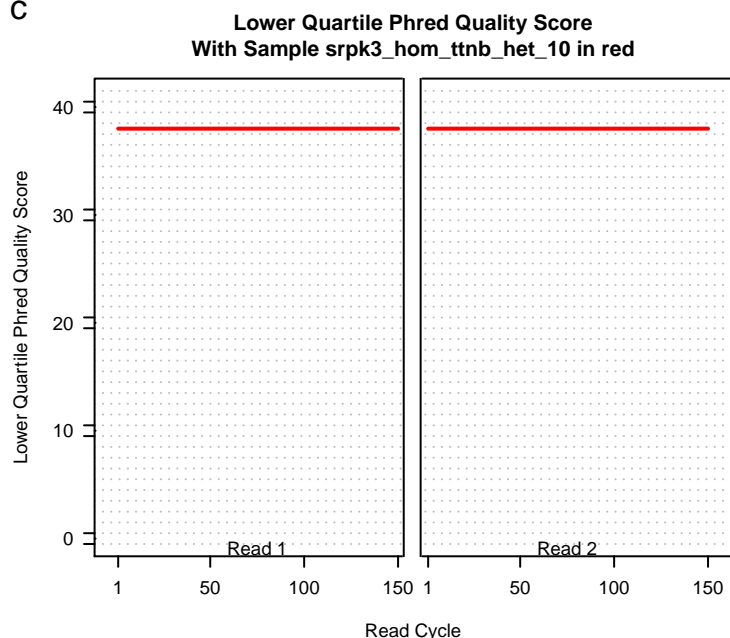
Sample Highlight:
srpk3_hom_ttnb_het_10



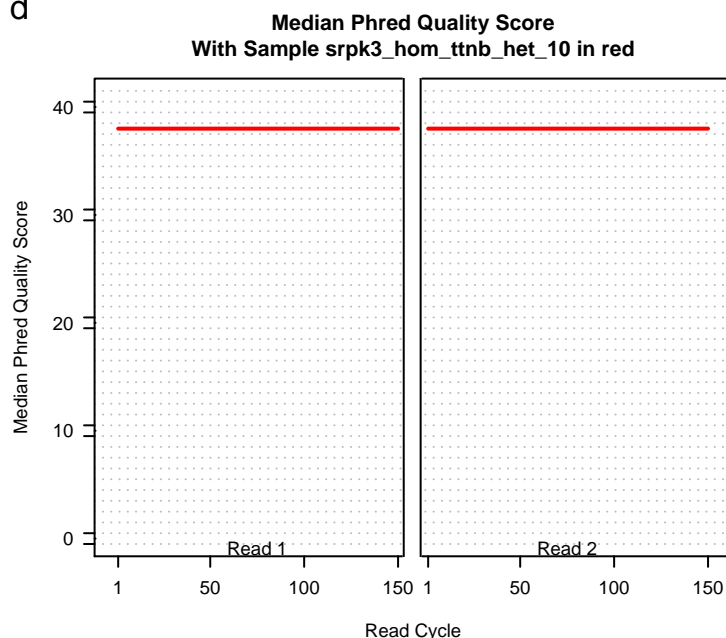
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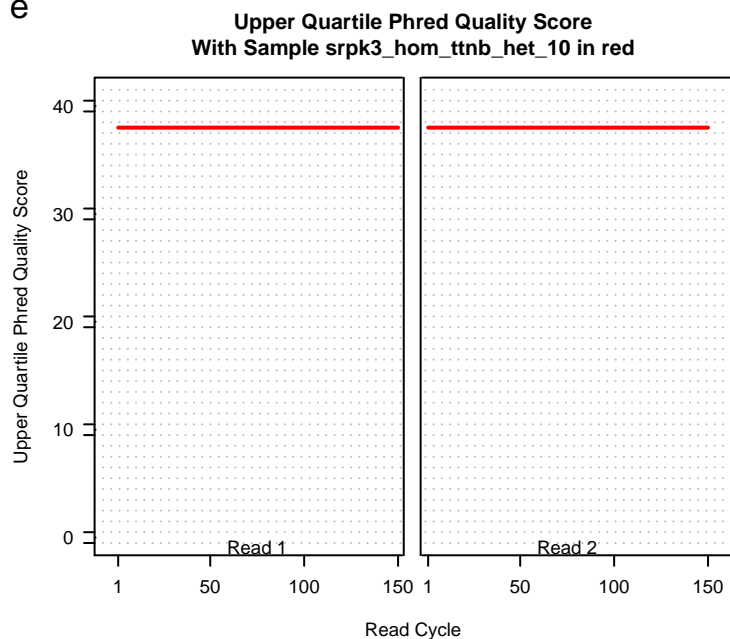
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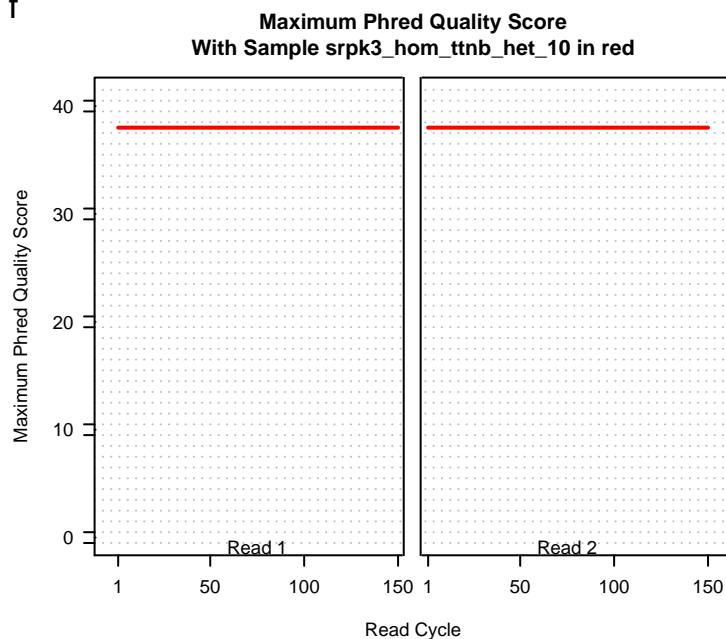
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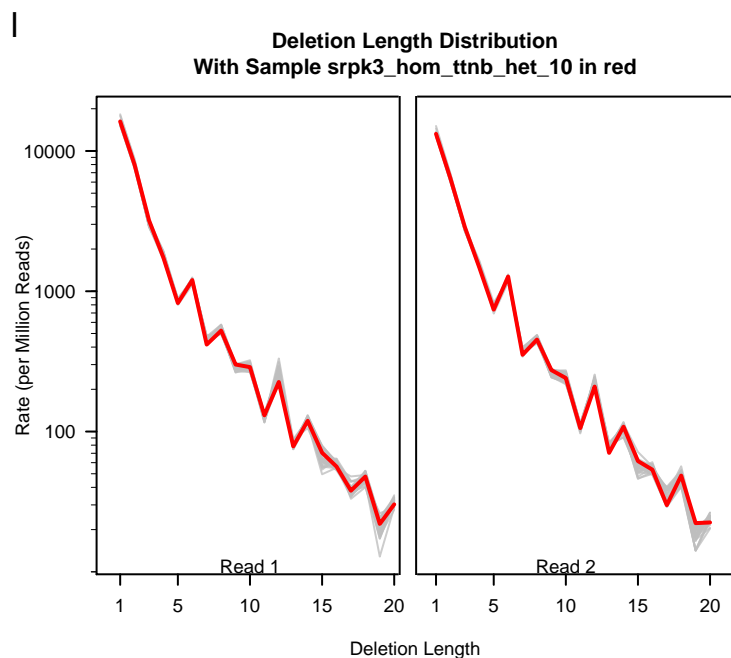
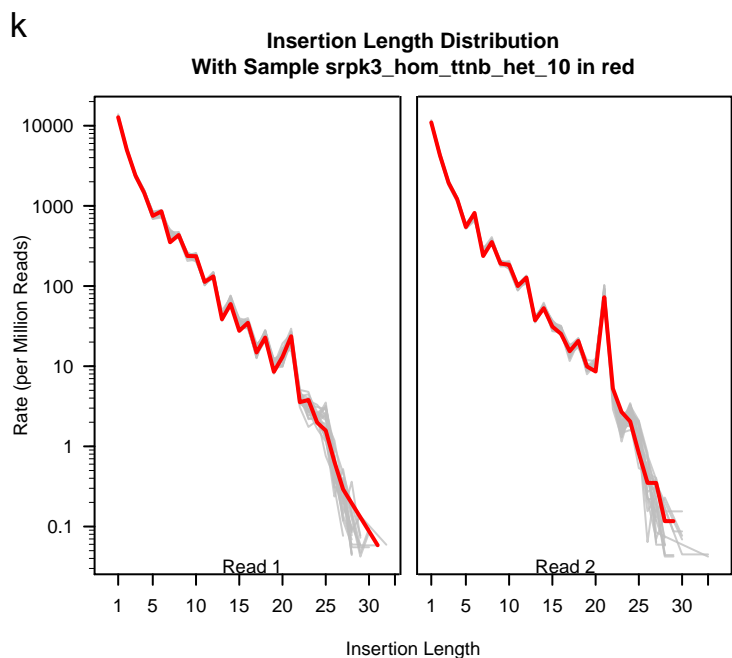
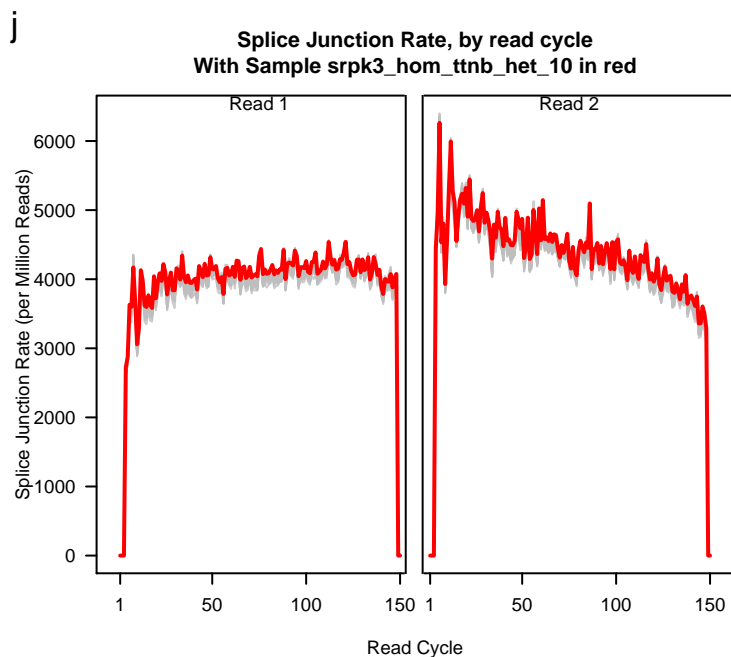
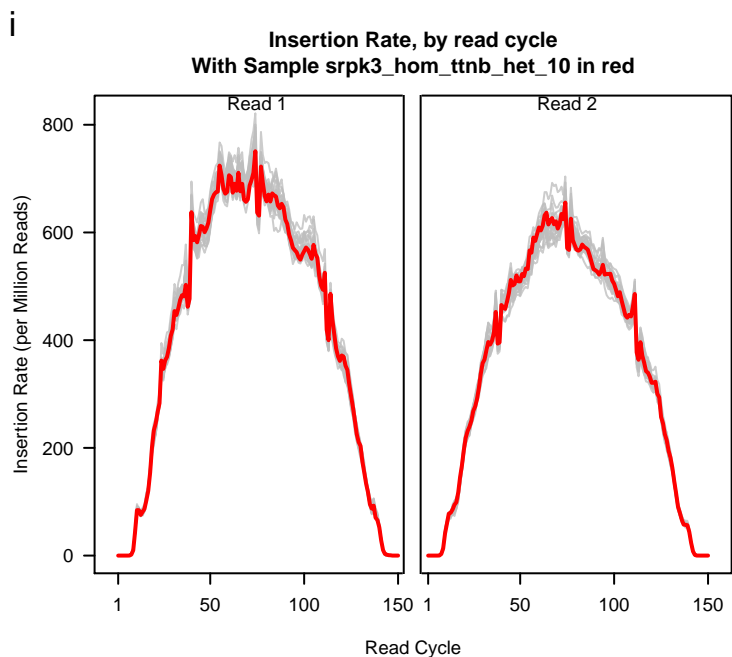
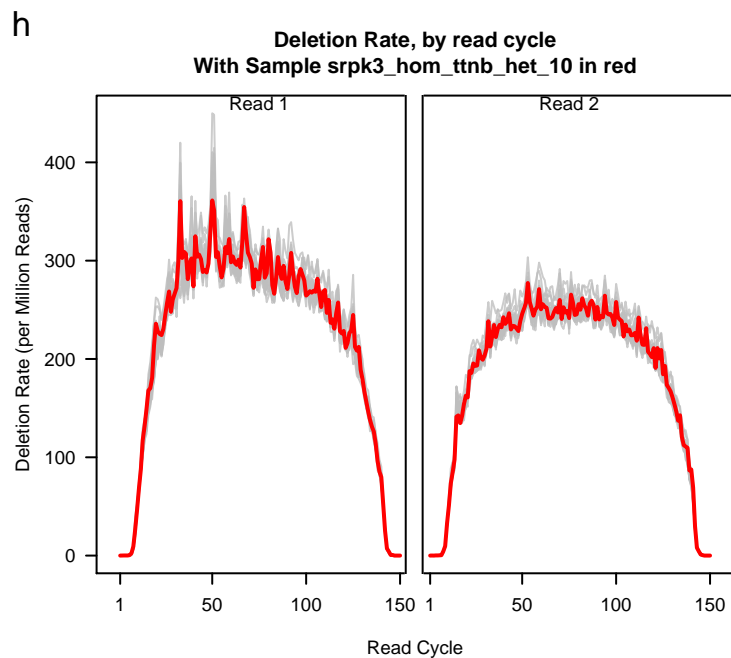
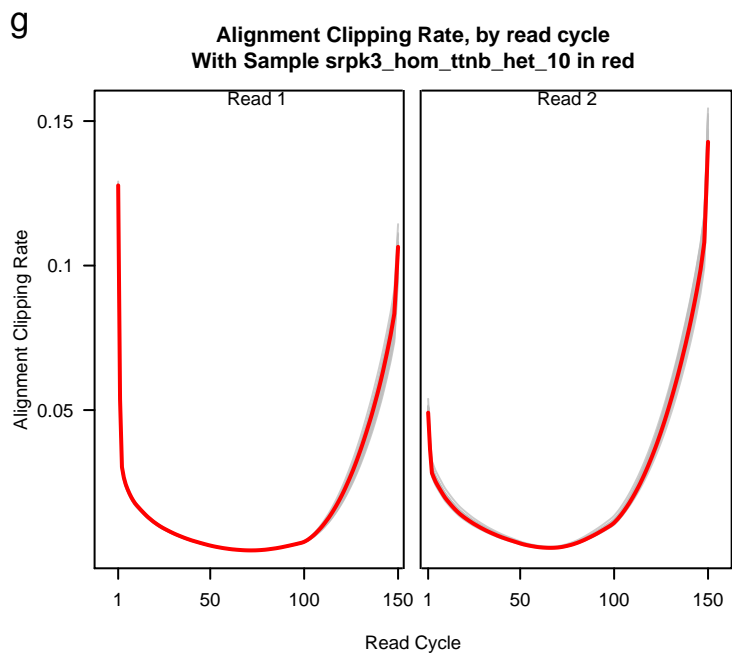


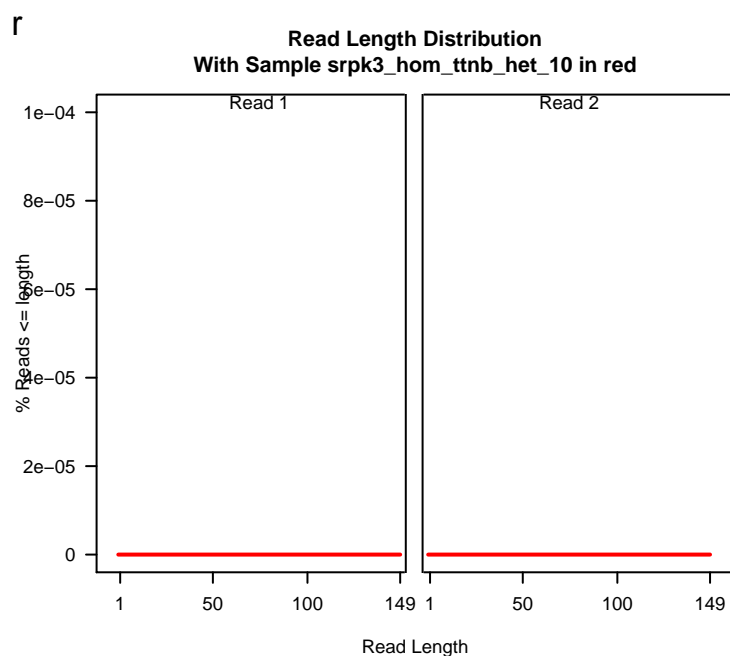
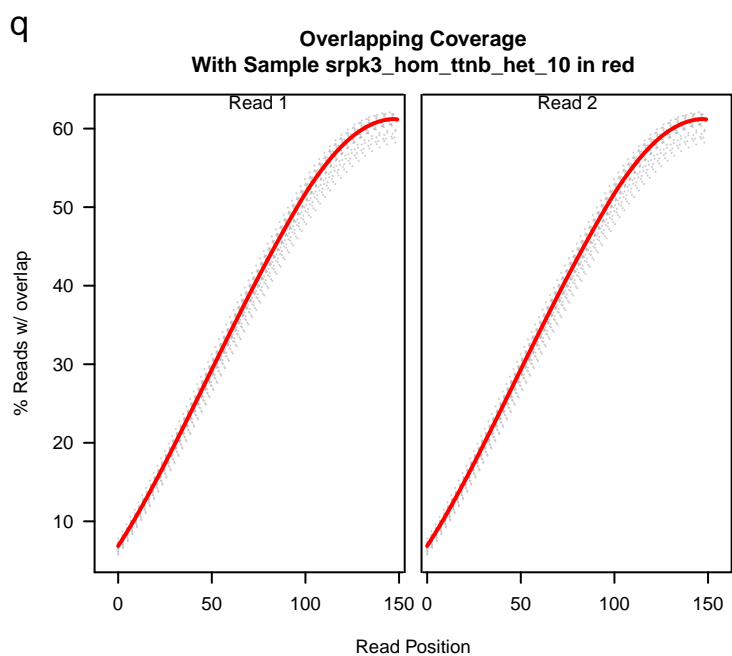
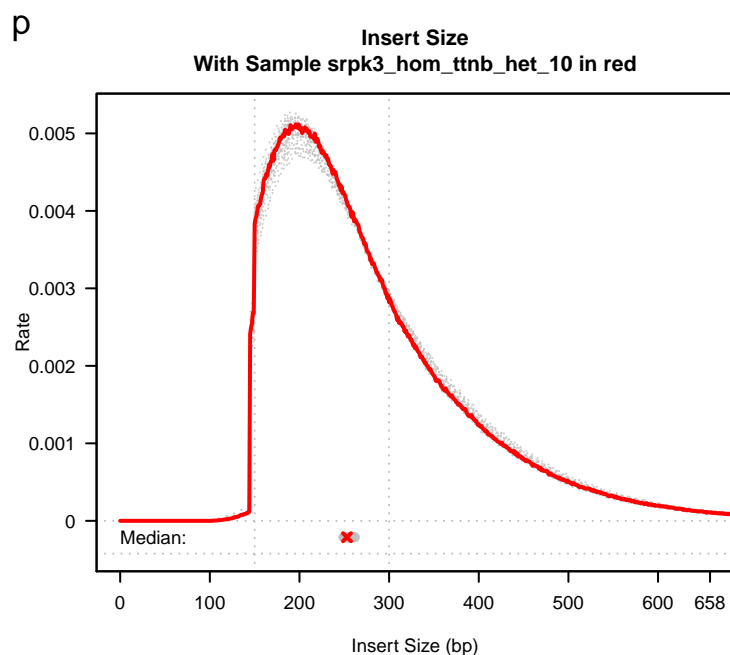
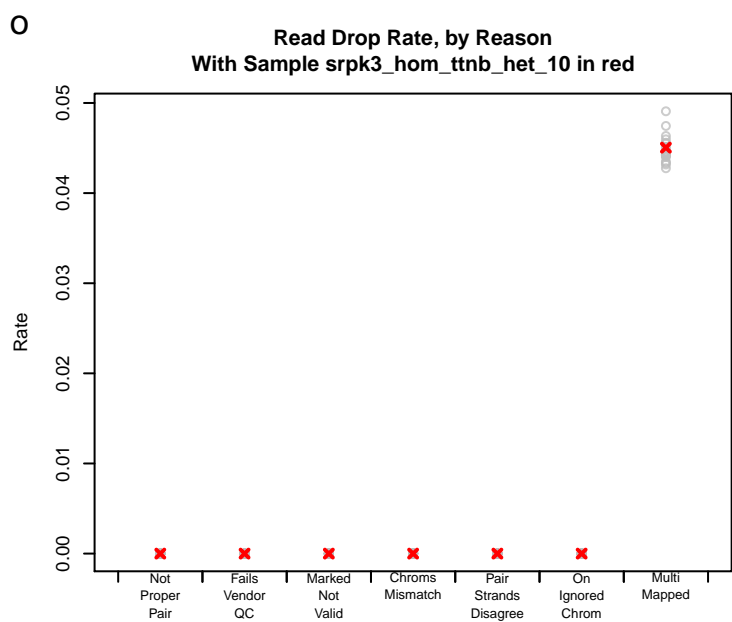
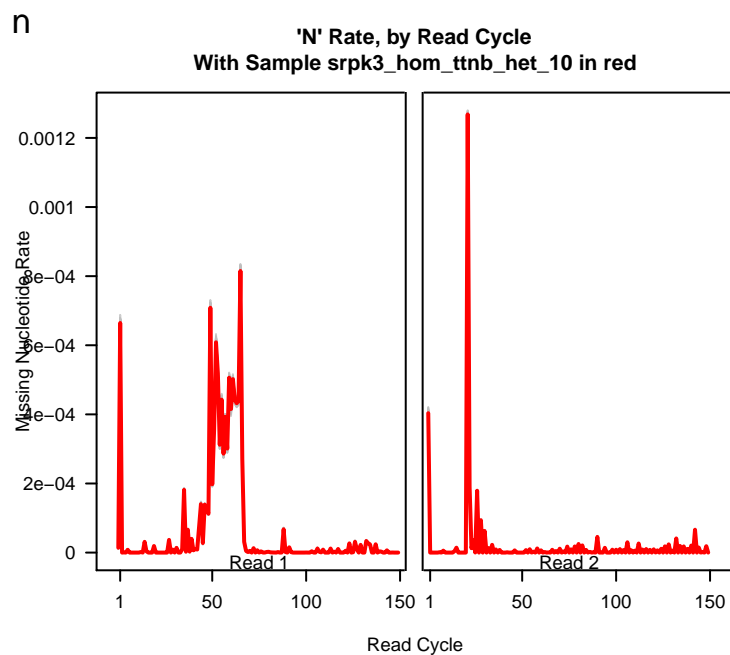
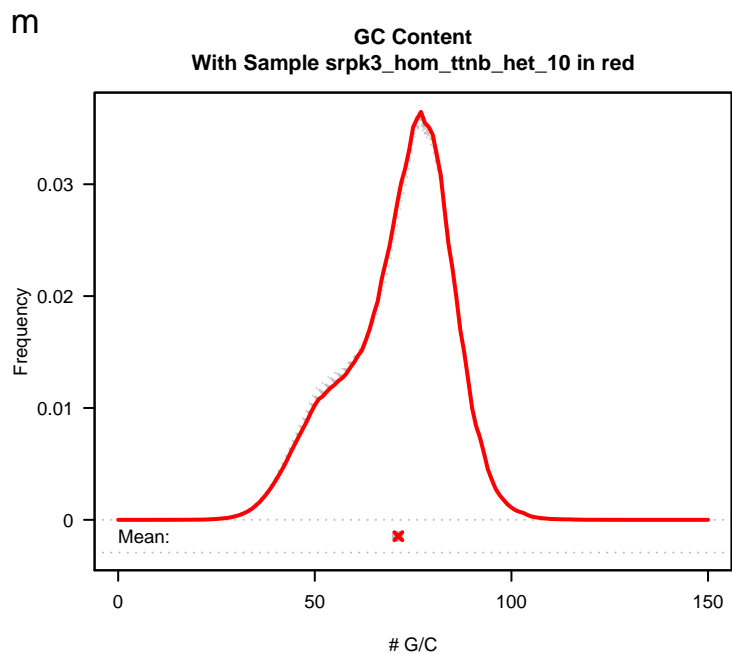
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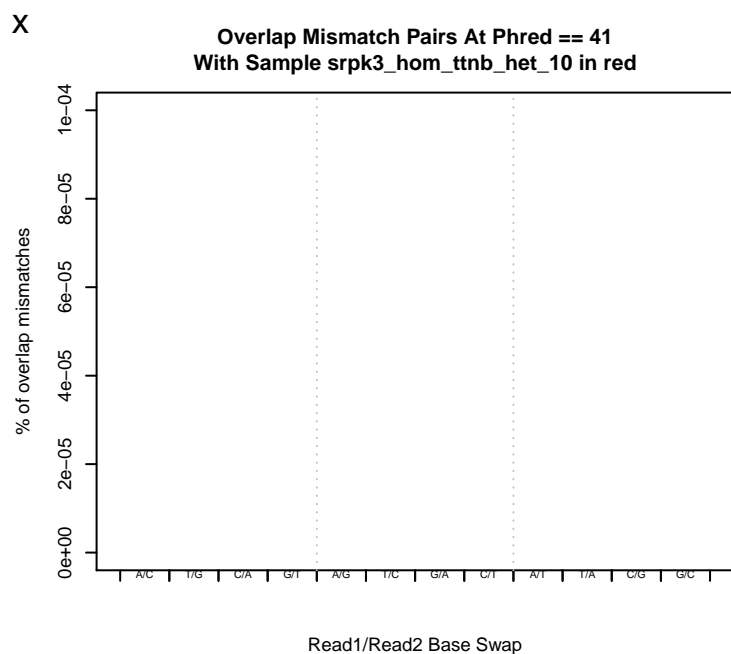
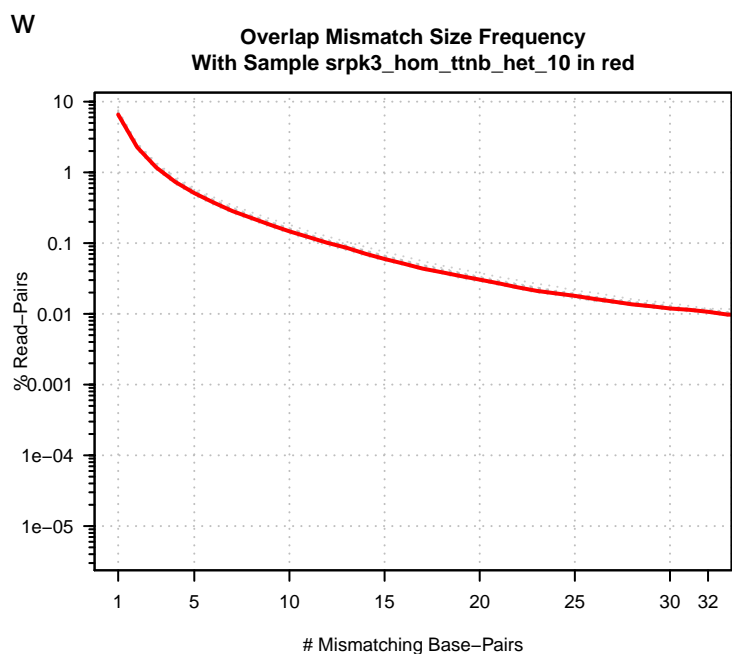
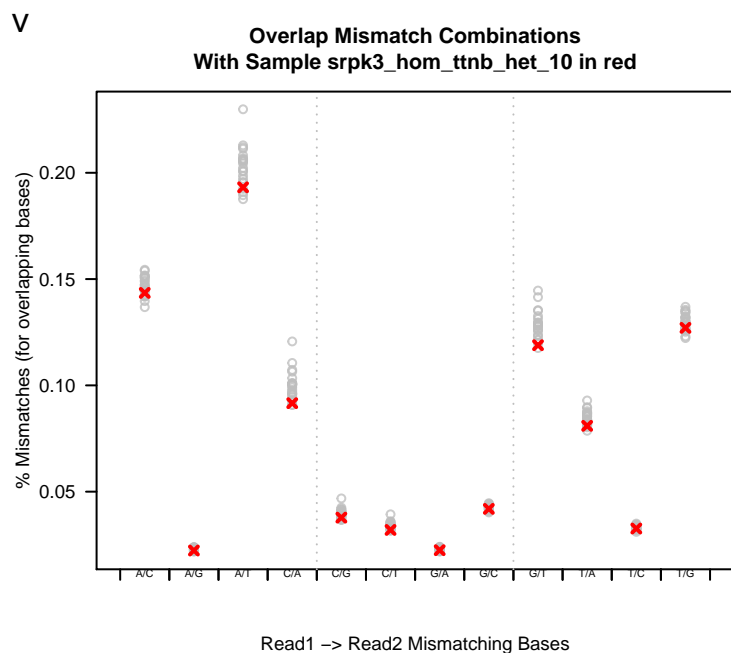
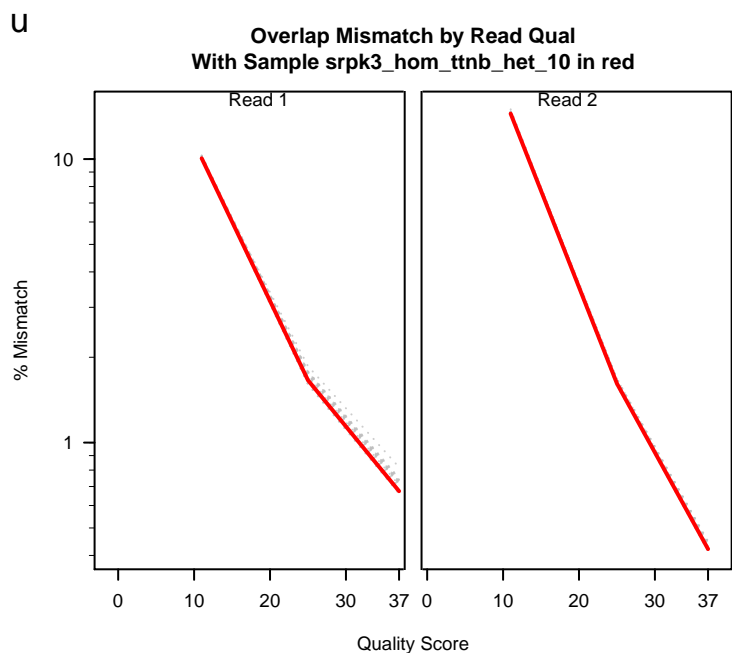
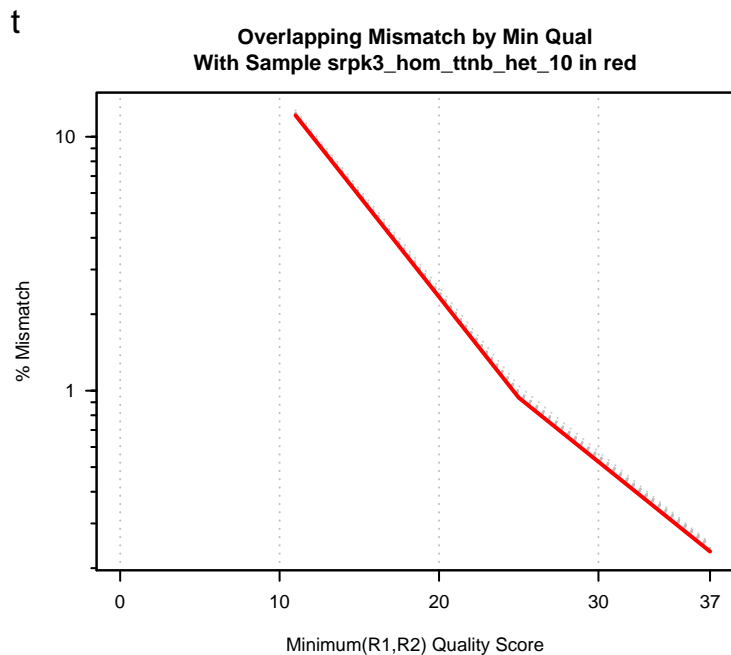
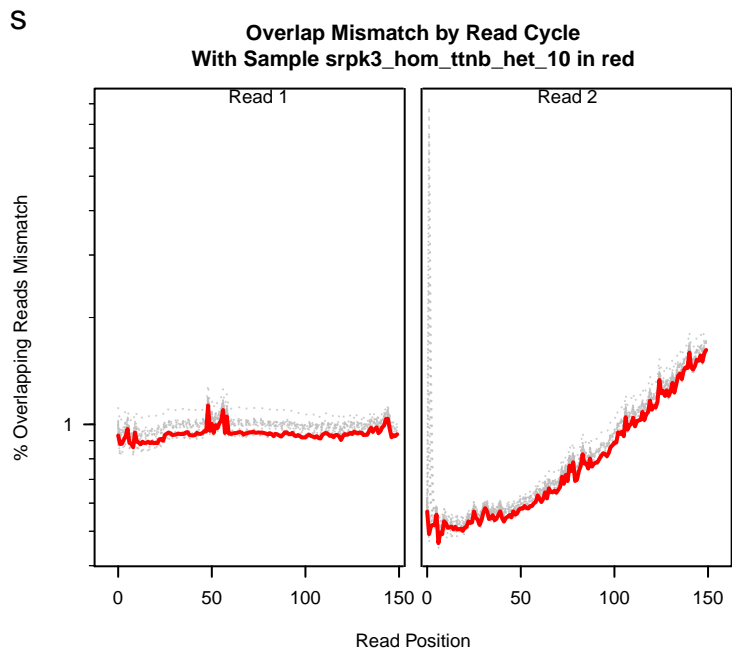


f



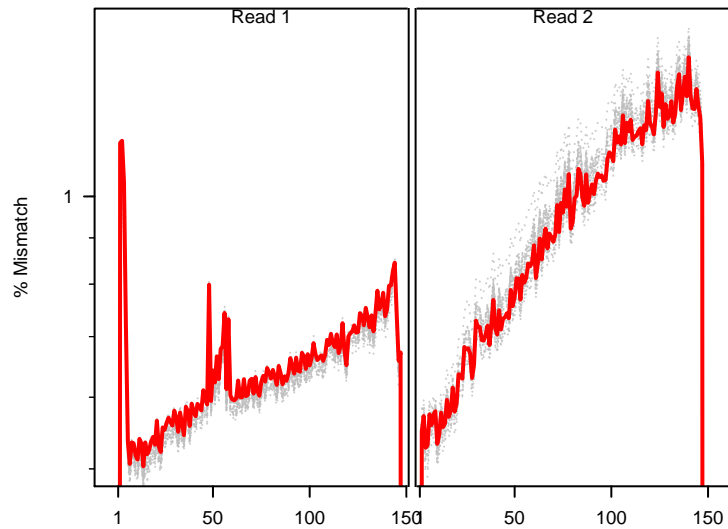






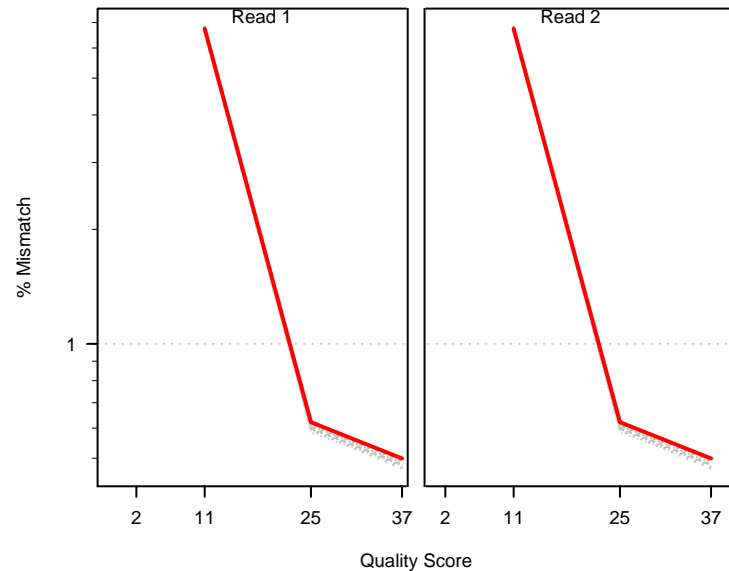
y

Reference Mismatch by Read Cycle
With Sample srpk3_hom_ttnb_het_10 in red



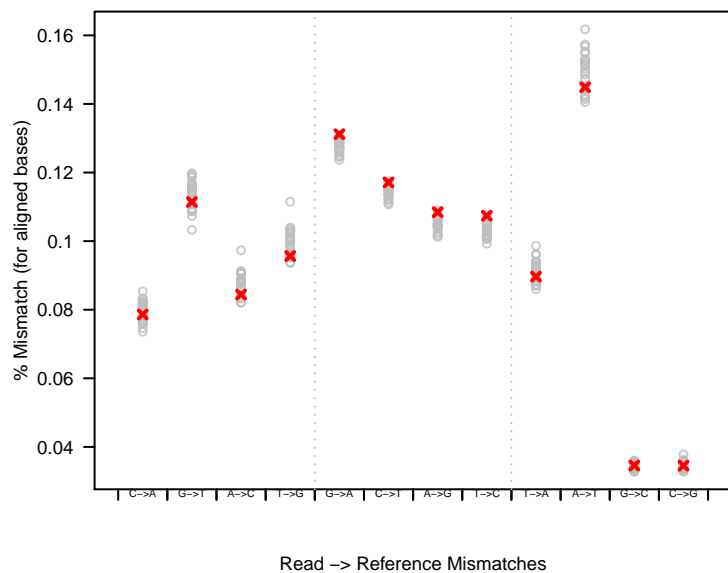
Z

Reference Mismatch by Read Qual
With Sample srpk3_hom_ttnb_het_10 in red



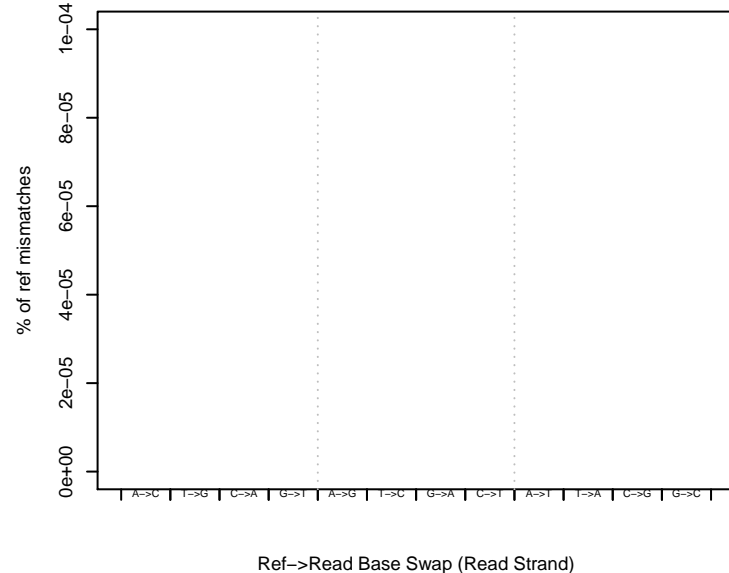
aa

Reference Mismatch Combinations
With Sample srpk3_hom_ttnb_het_10 in red



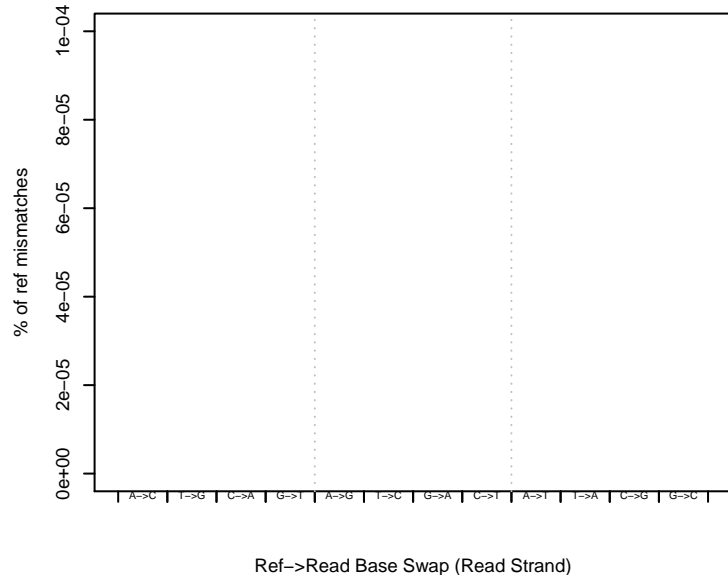
ab

R1 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_het_10 in red



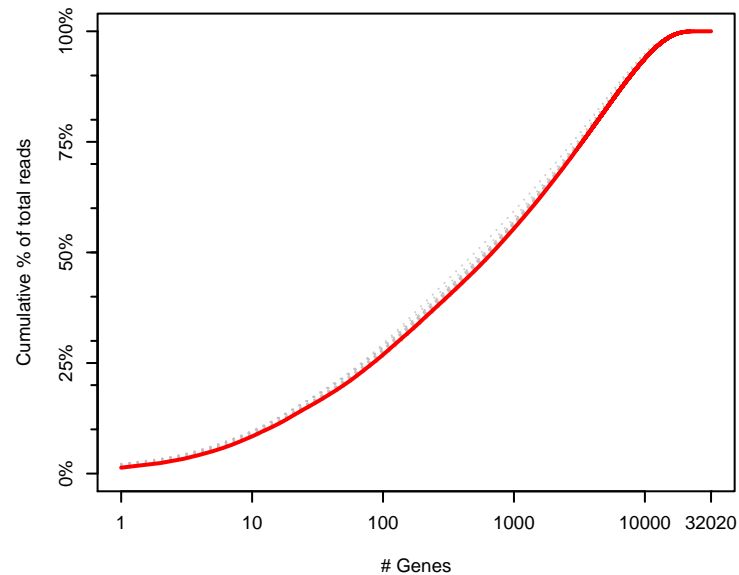
ac

R2 Ref Mismatches At Phred == 41
With Sample srpk3_hom_ttnb_het_10 in red



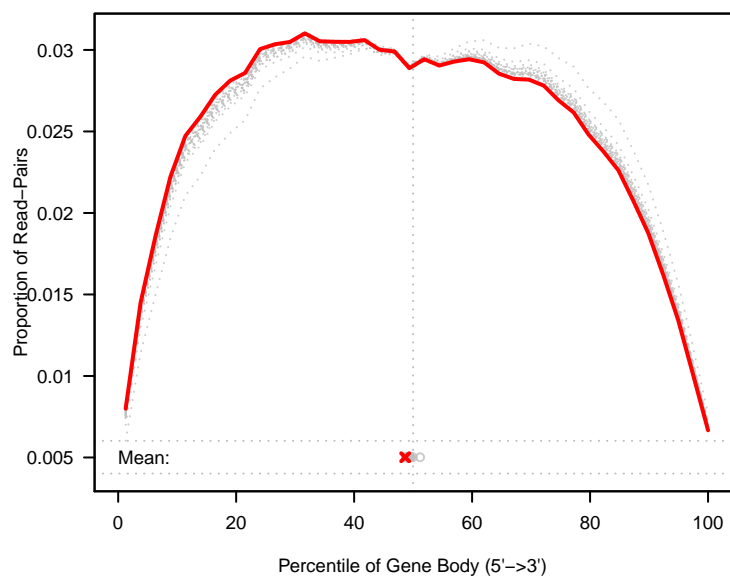
ad

Cumulative Gene Assignment Diversity
With Sample srpk3_hom_ttnb_het_10 in red



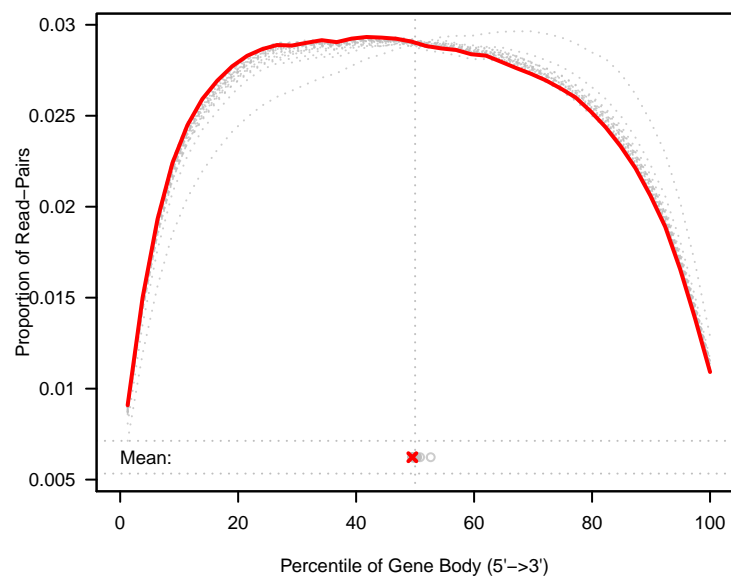
ae

Gene–Body Coverage
With Sample *srpk3_hom_ttnb_het_10* in red



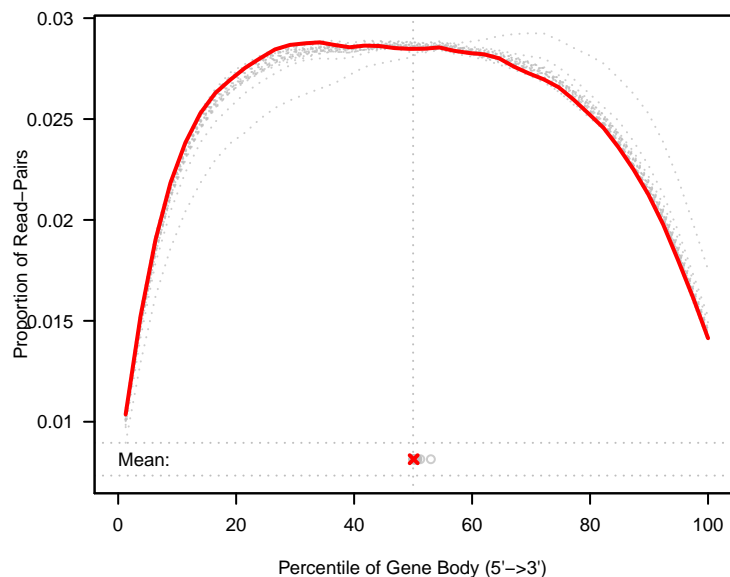
af

Gene–Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_hom_ttnb_het_10* in red



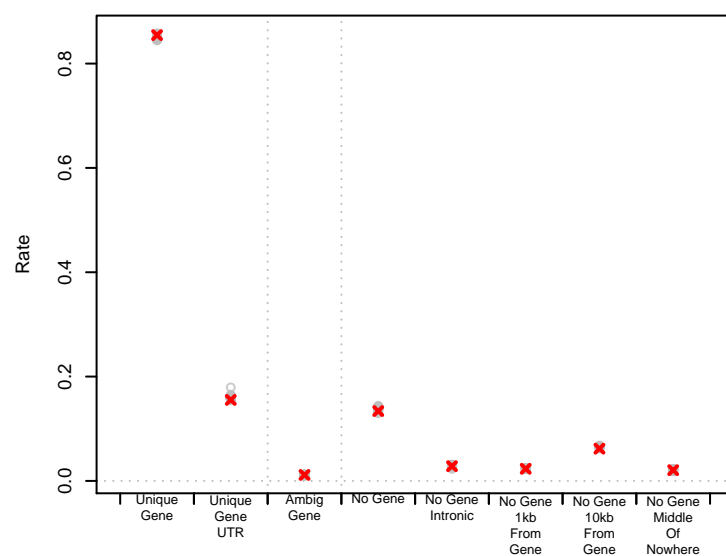
ag

Gene–Body Coverage, Low Expression Genes
With Sample *srpk3_hom_ttnb_het_10* in red



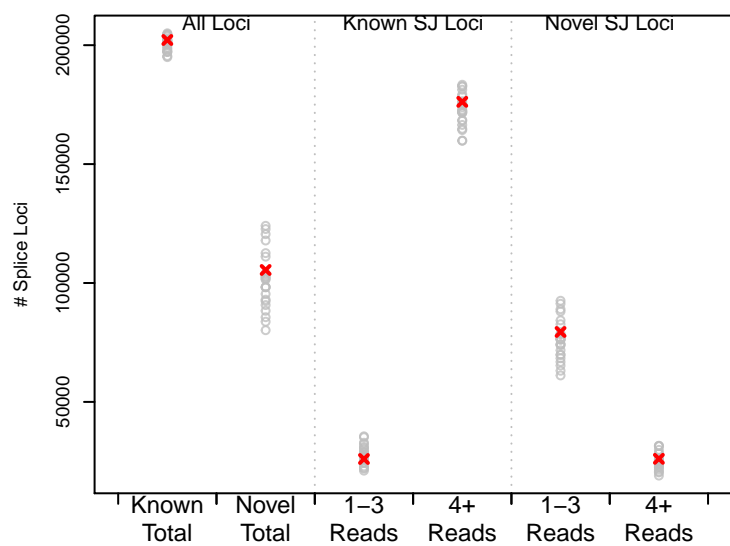
ah

Read Mapping Location Rates
With Sample *srpk3_hom_ttnb_het_10* in red



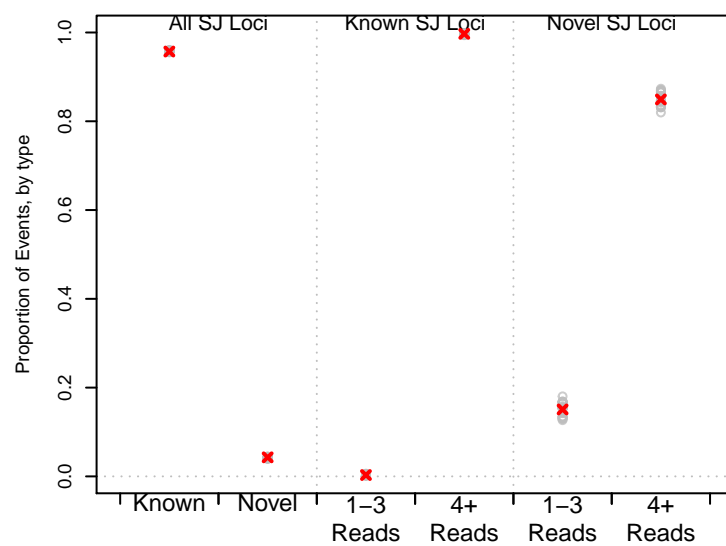
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_hom_ttnb_het_10* in red

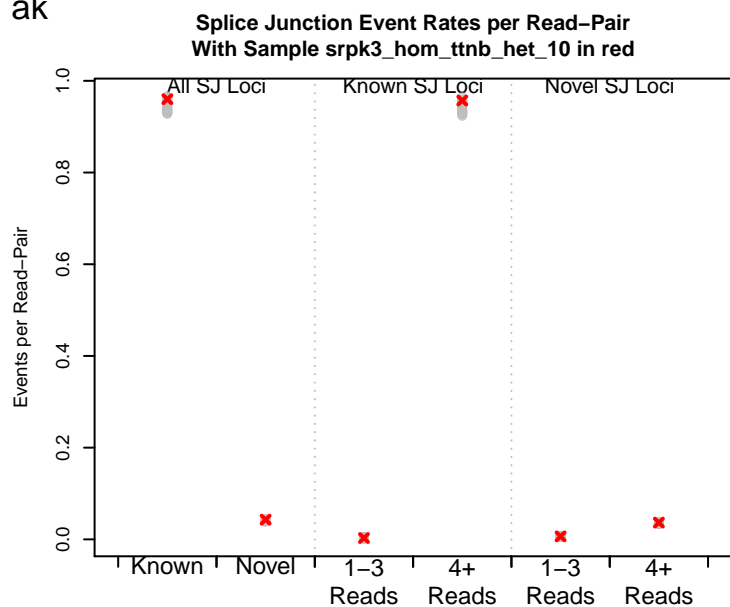


aj

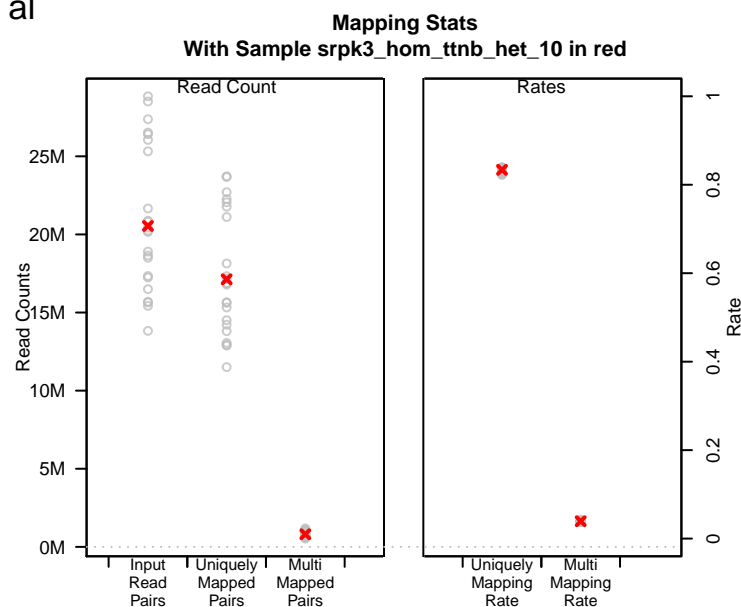
Breakdown of Splice Junction Events, by type
With Sample *srpk3_hom_ttnb_het_10* in red



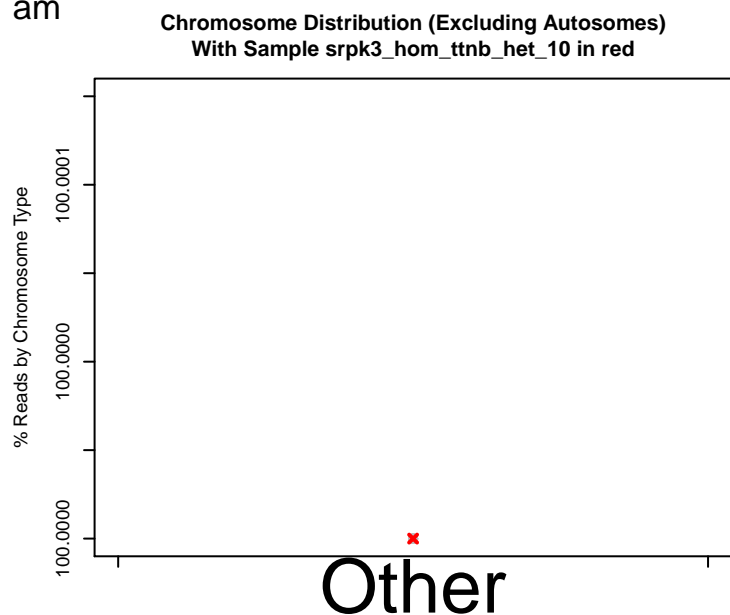
ak



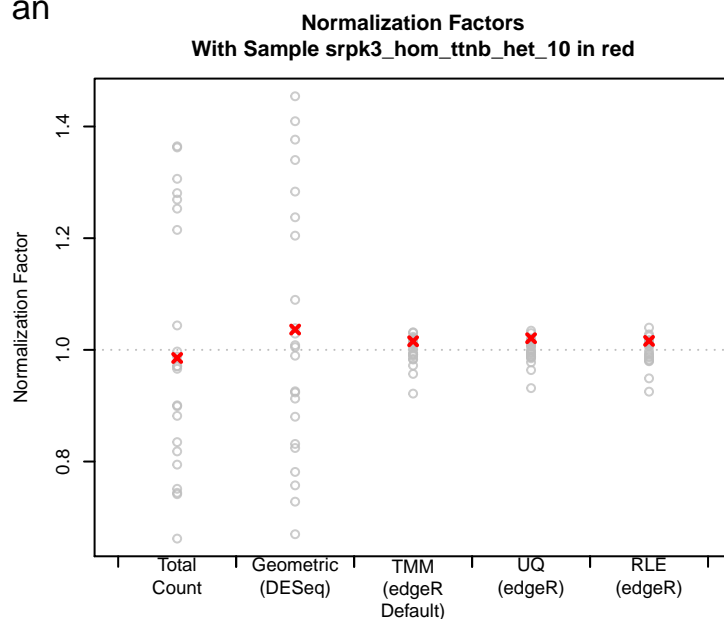
al



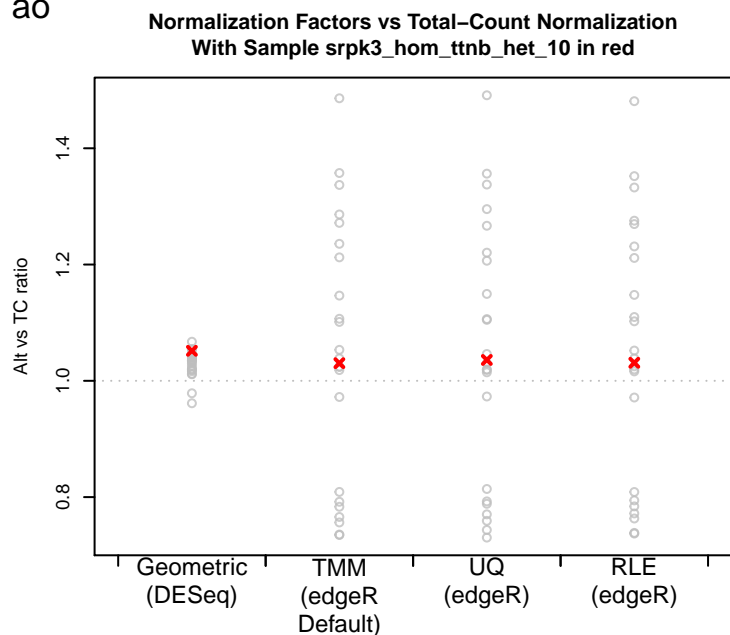
am



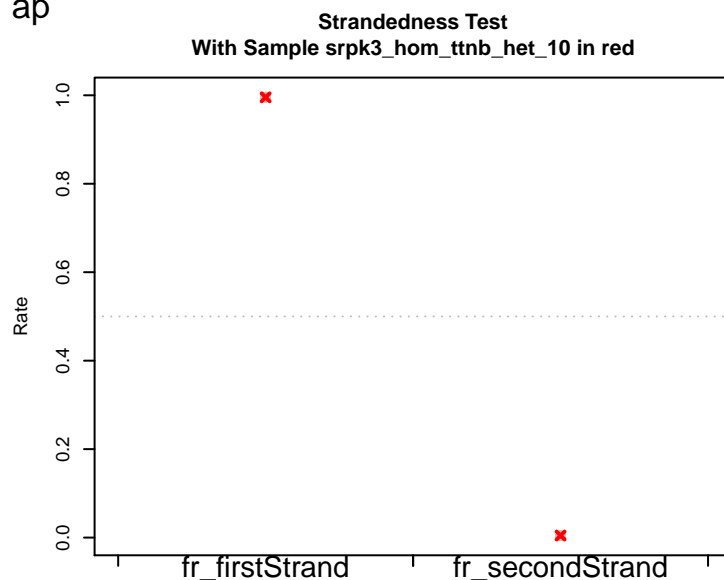
an



ao

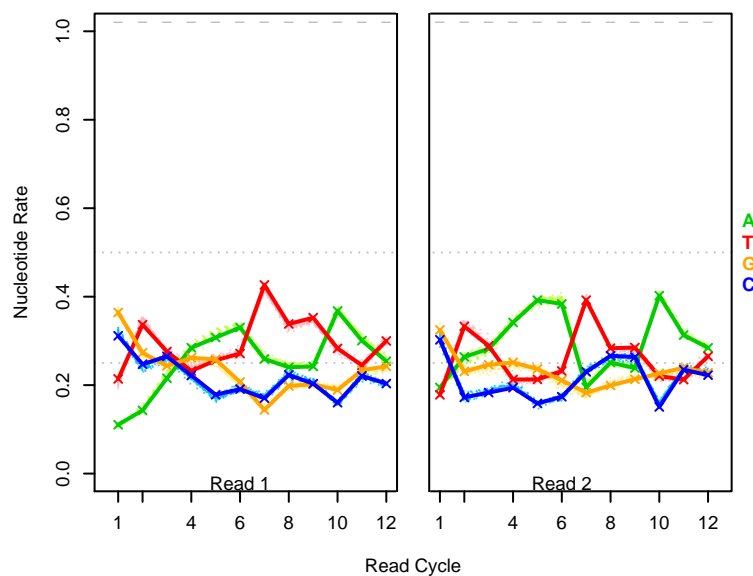


ap



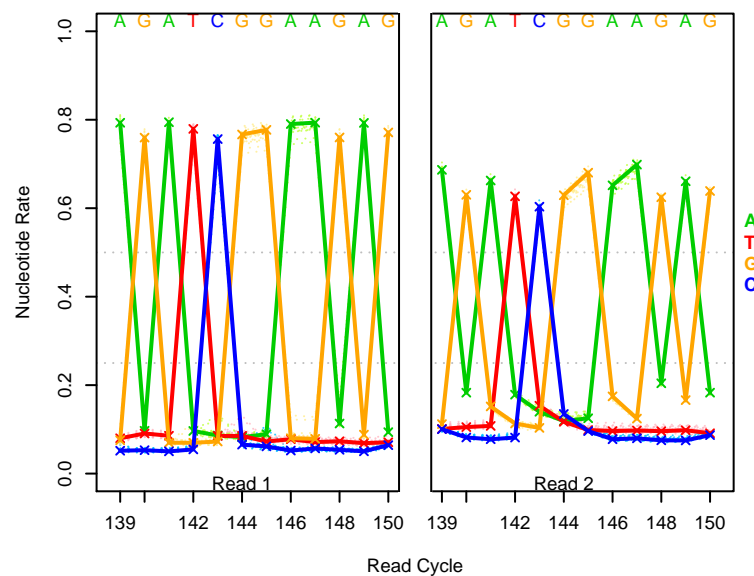
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srpk3_hom_ttnb_het_10 in red



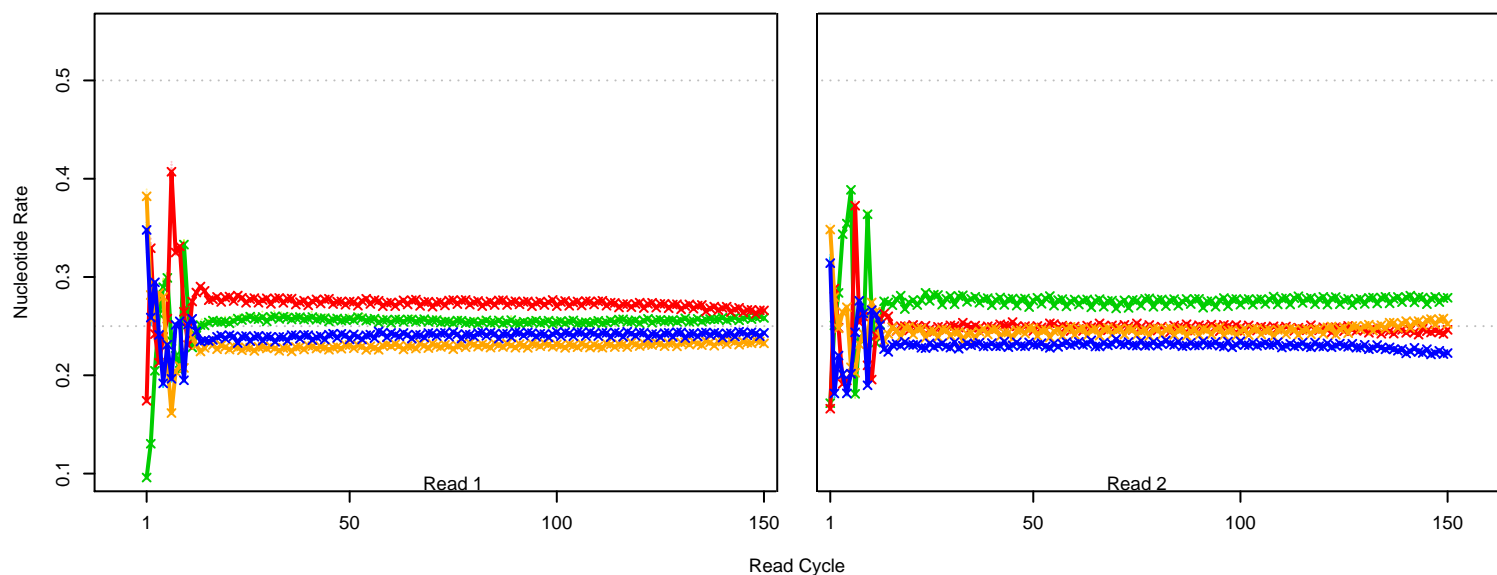
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_hom_ttnb_het_10 in red



as

Raw Nucleotide Rate by Cycle
With Sample srpk3_hom_ttnb_het_10 in red



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_hom_ttnb_het_10 in red

