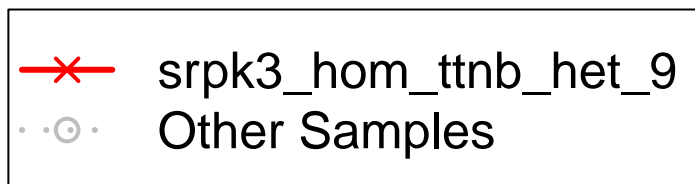
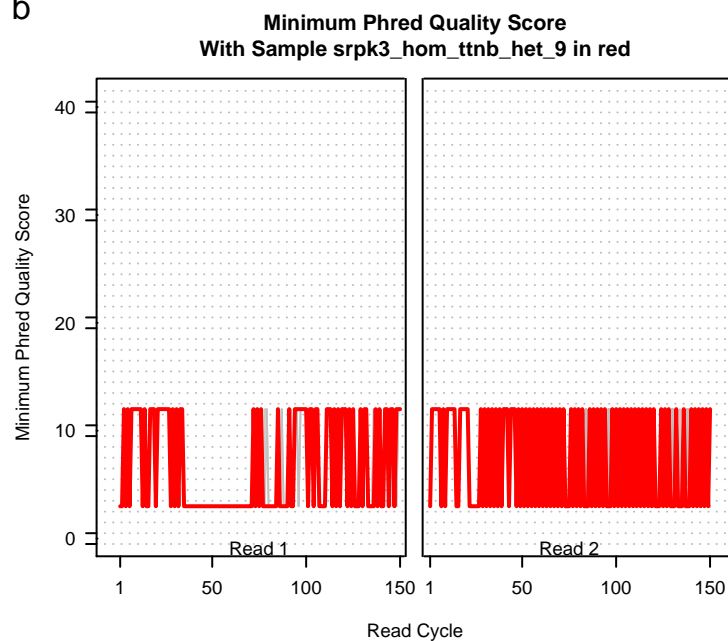


a

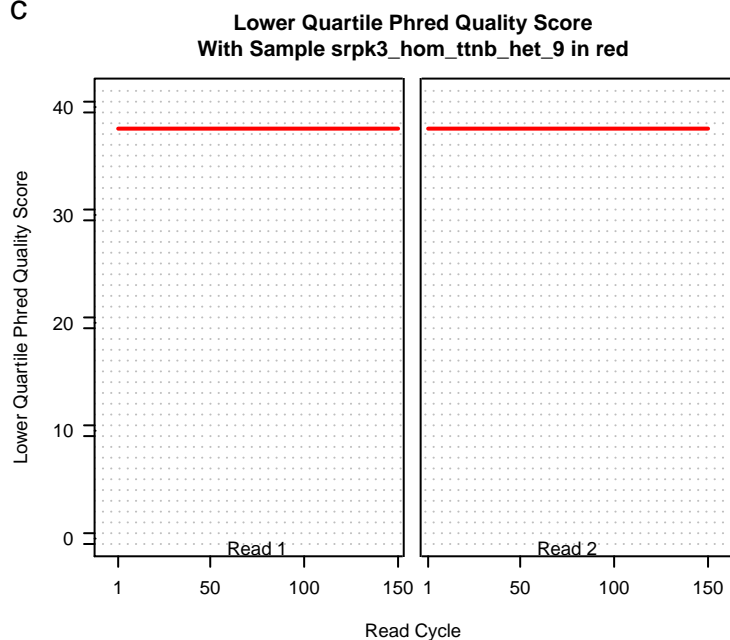
Sample Highlight:
srpk3_hom_ttnb_het_9



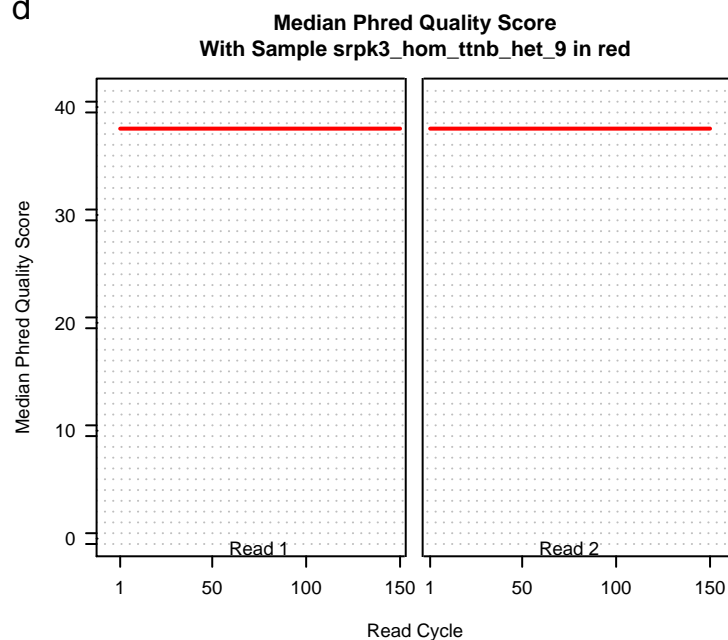
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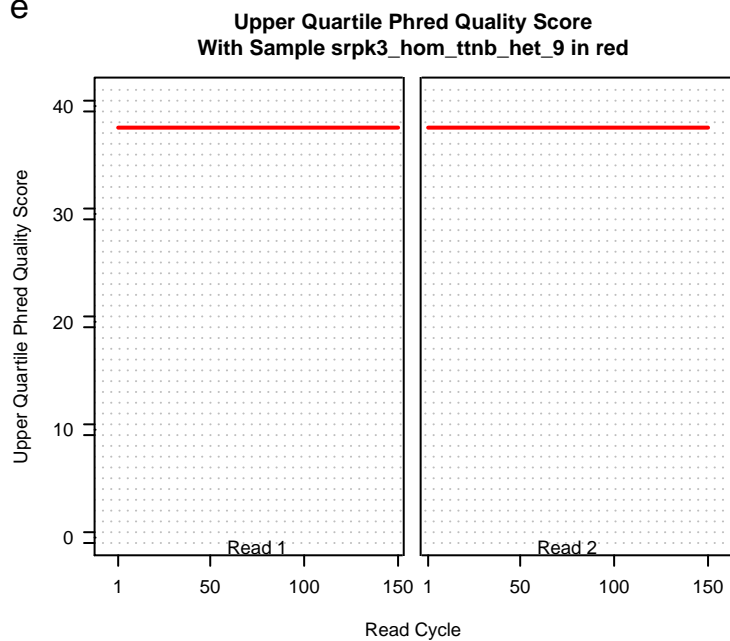
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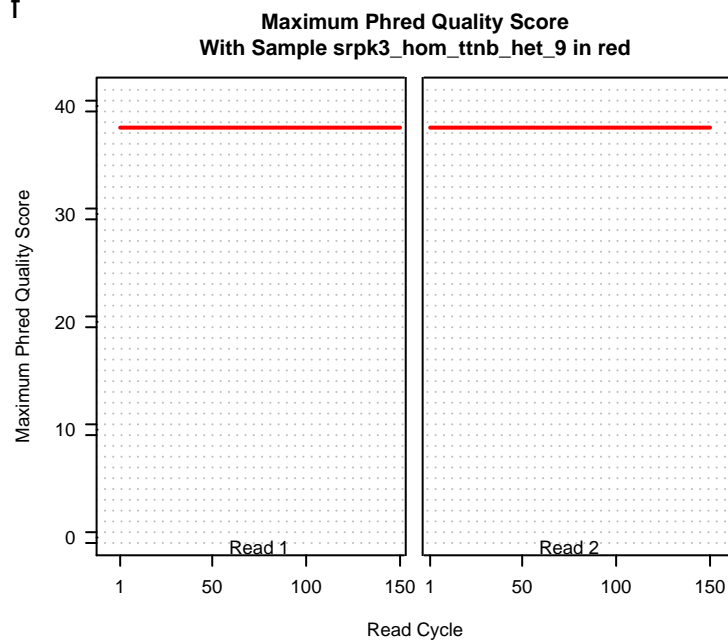
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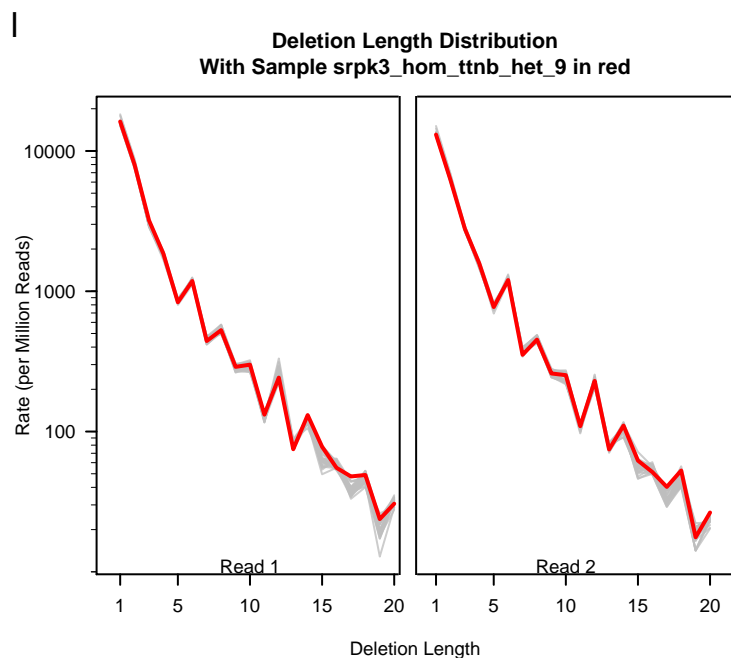
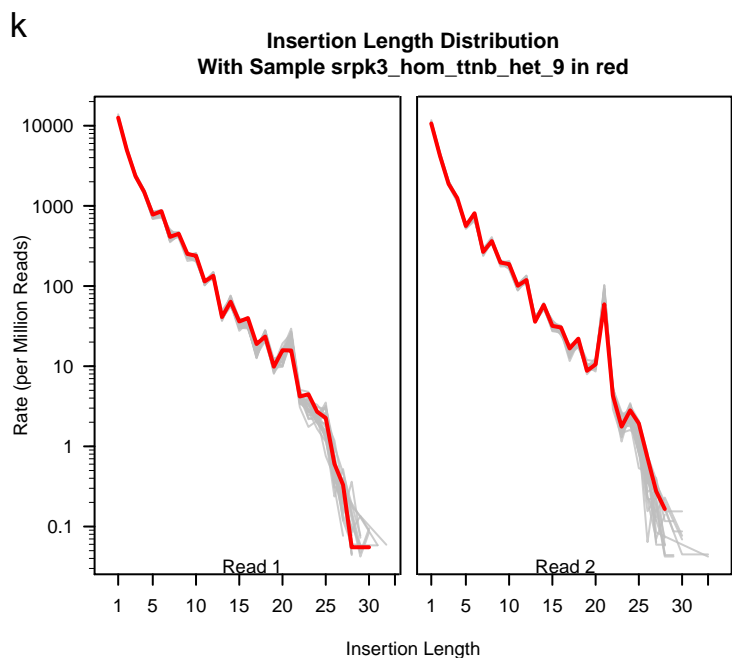
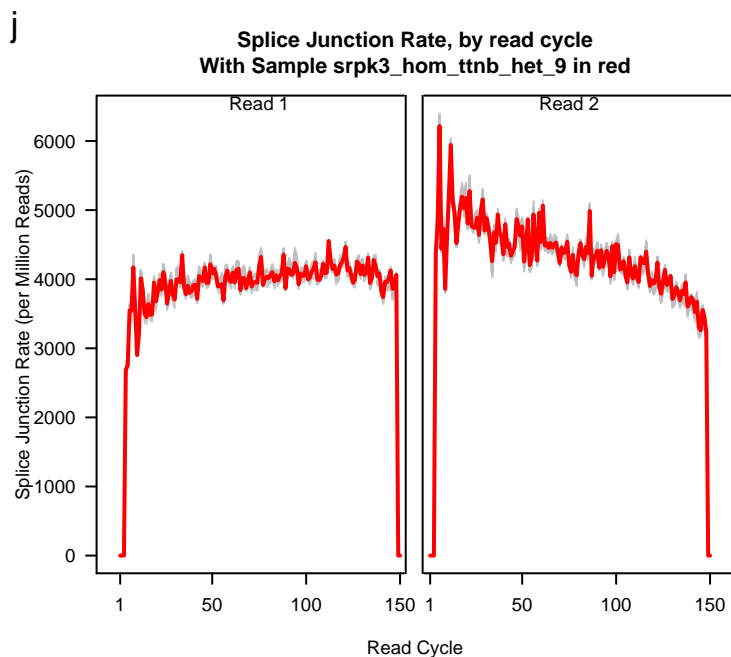
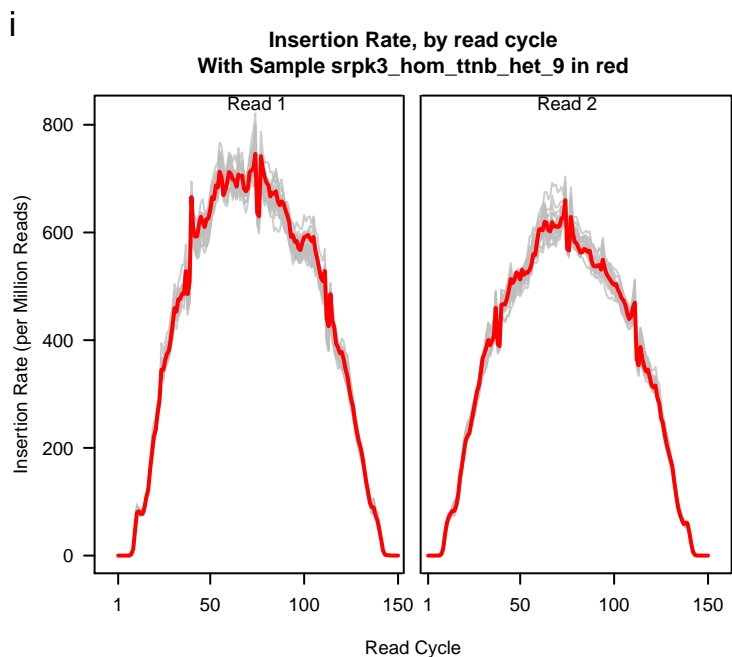
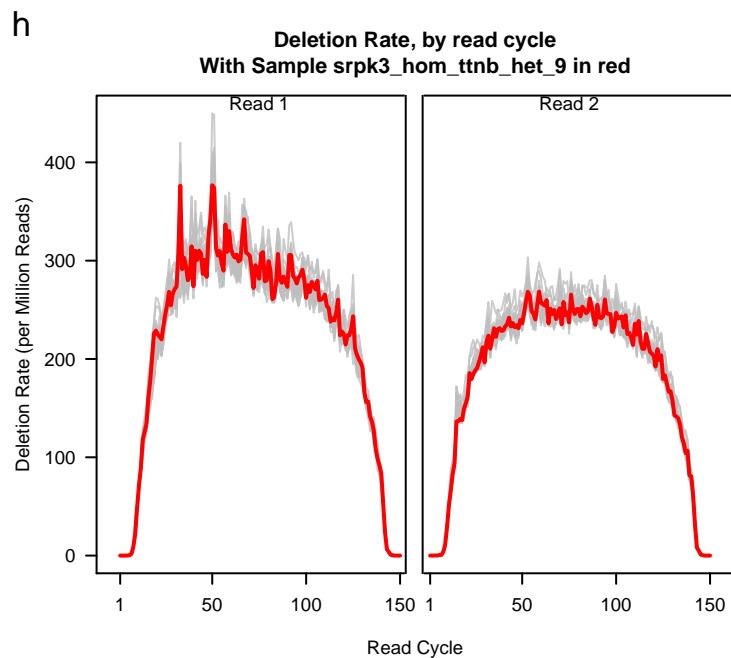
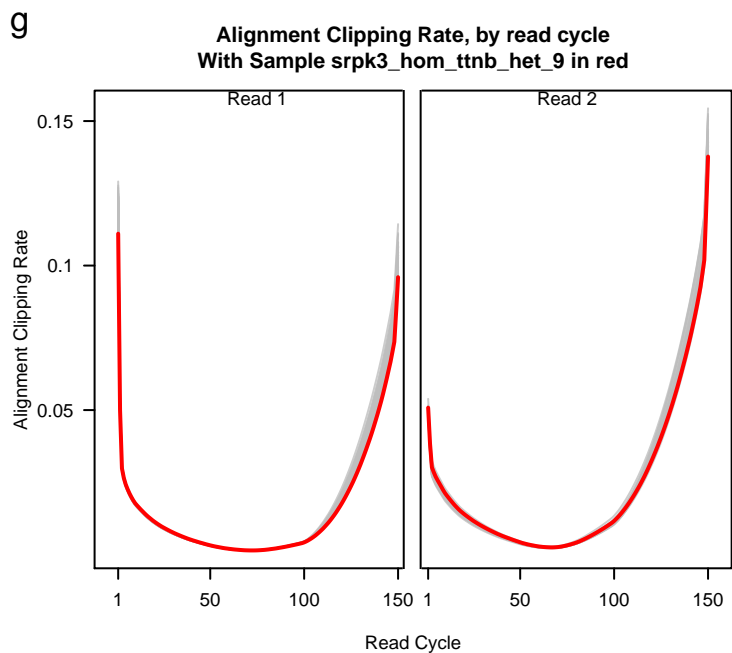


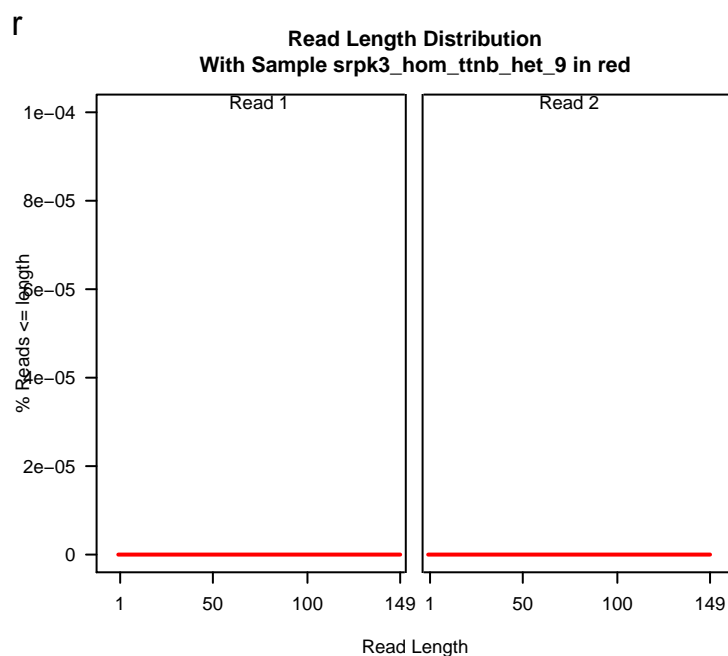
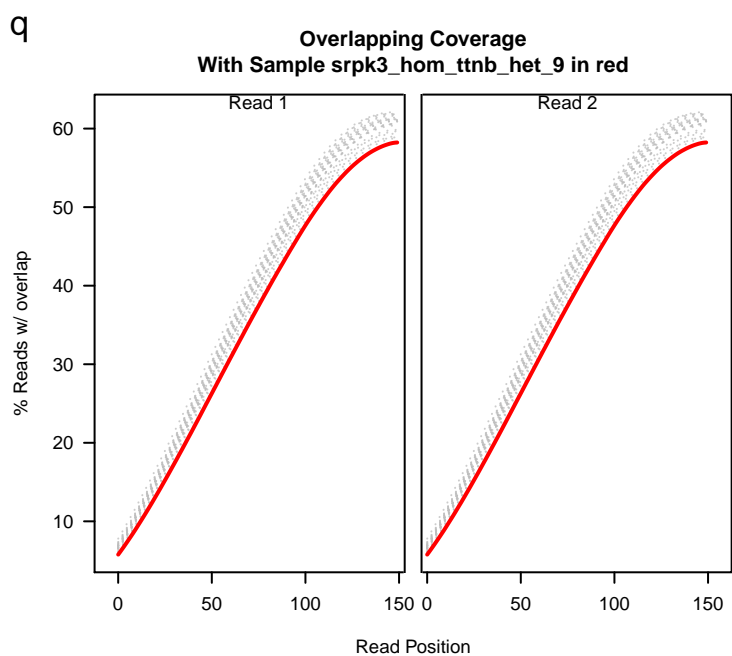
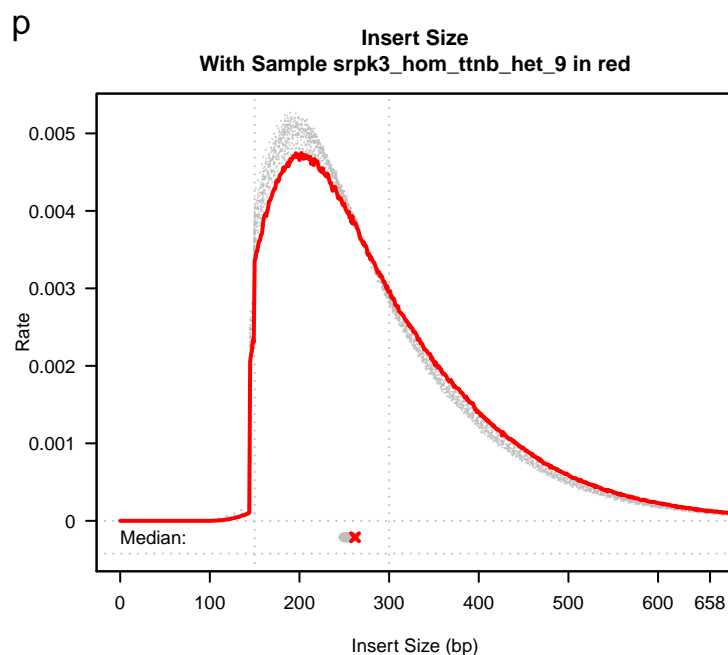
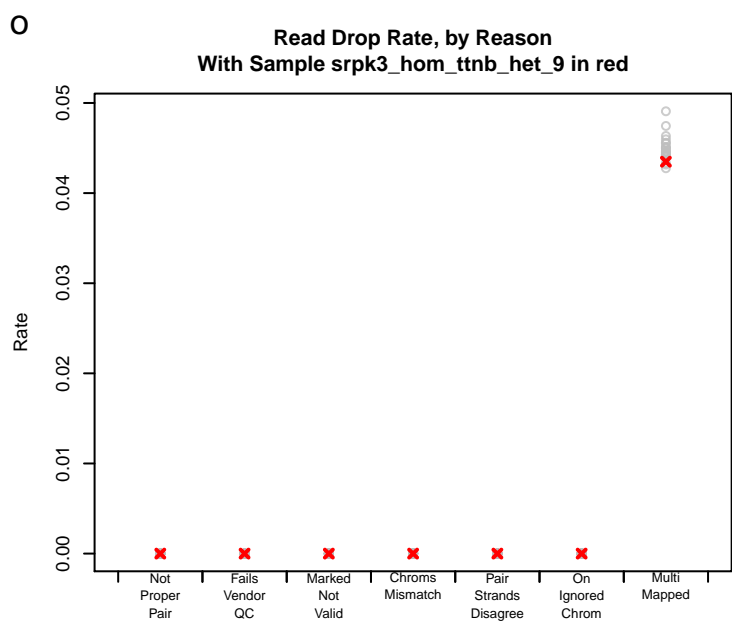
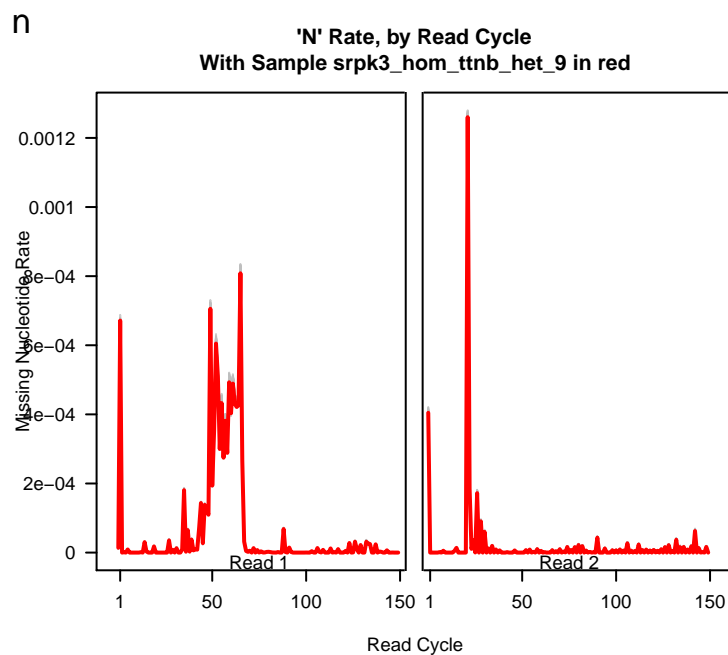
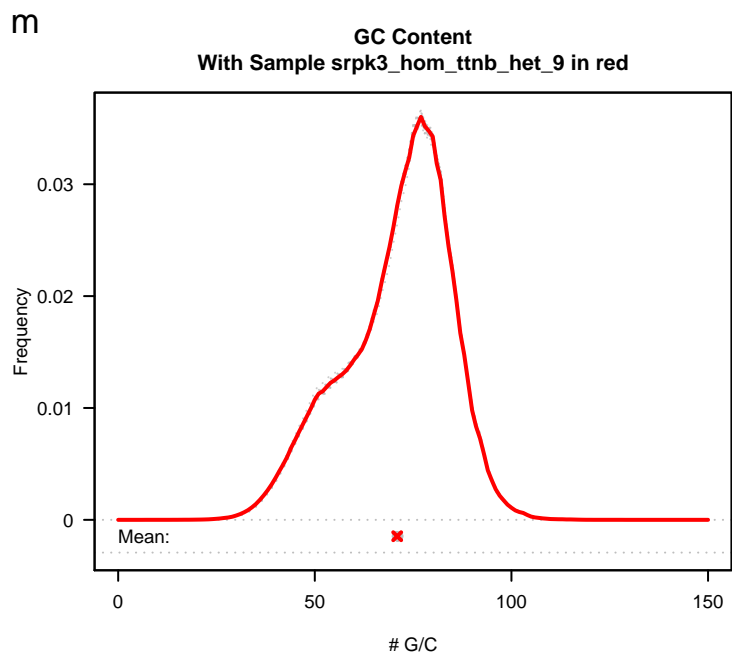
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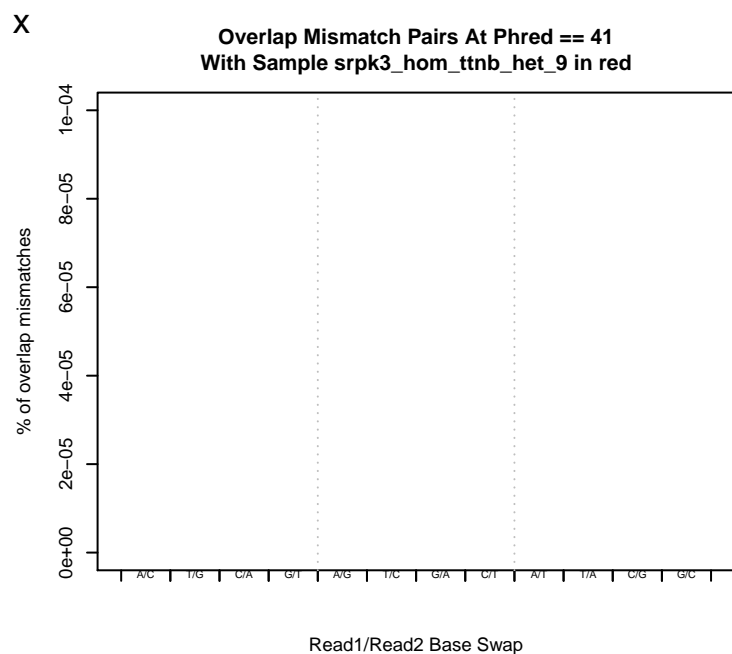
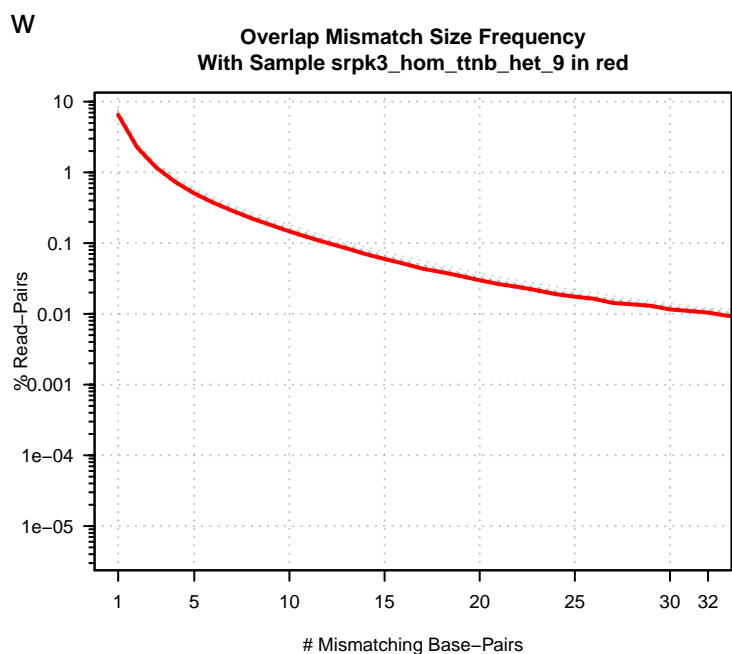
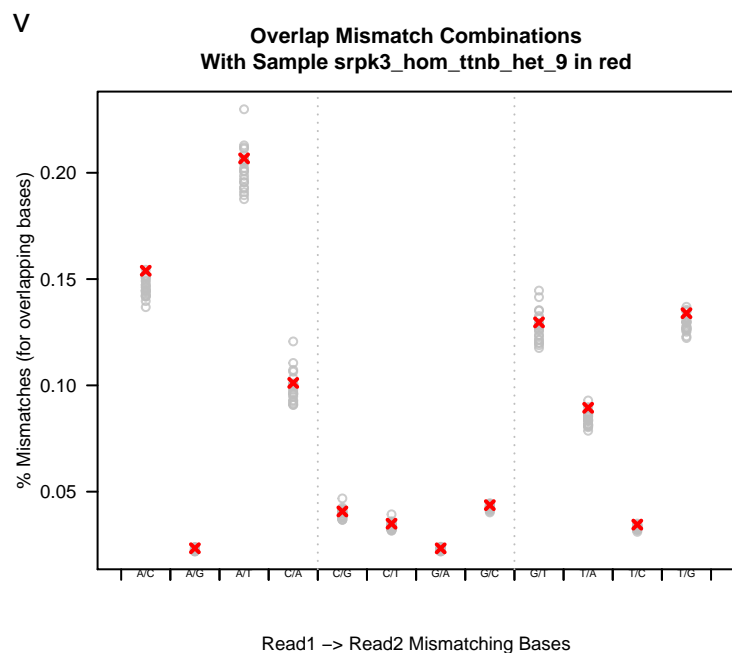
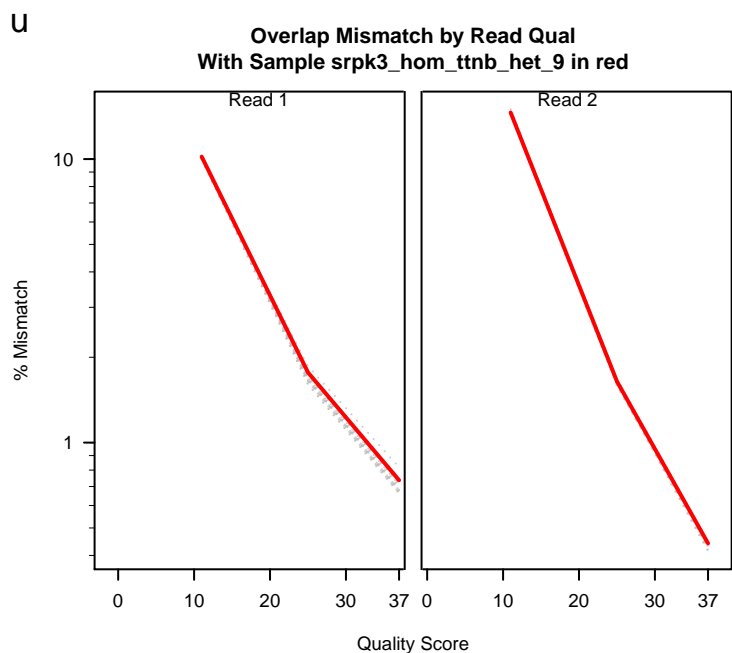
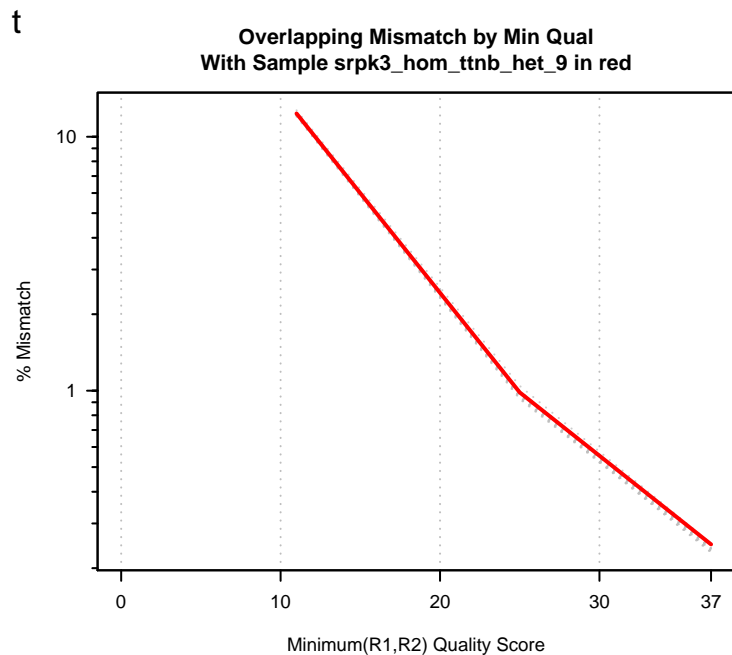
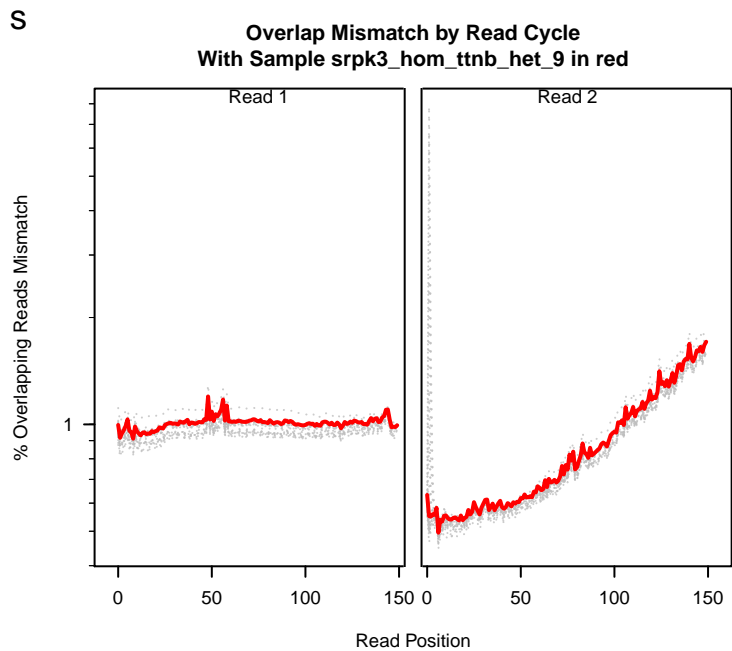


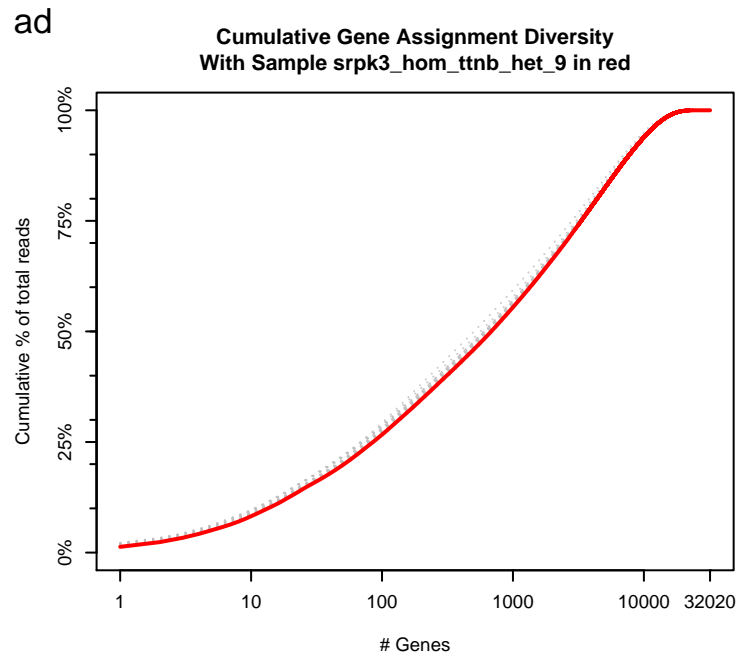
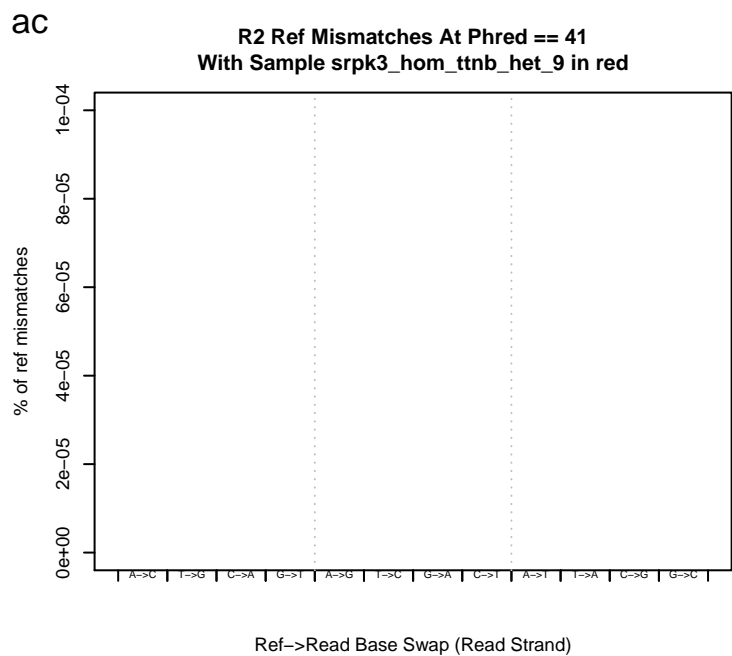
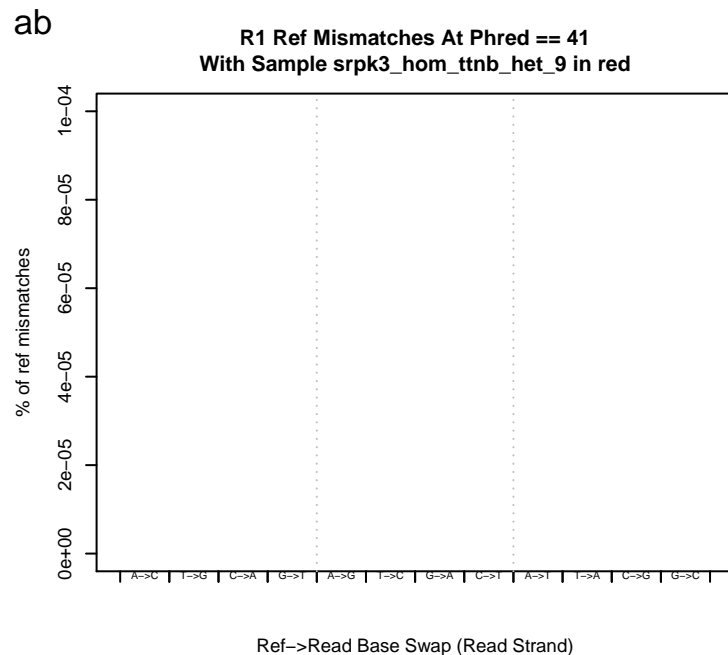
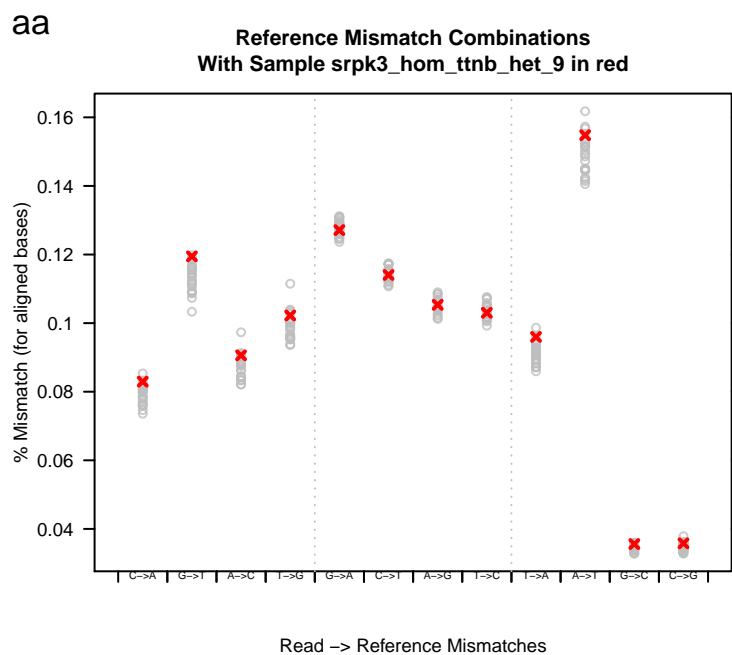
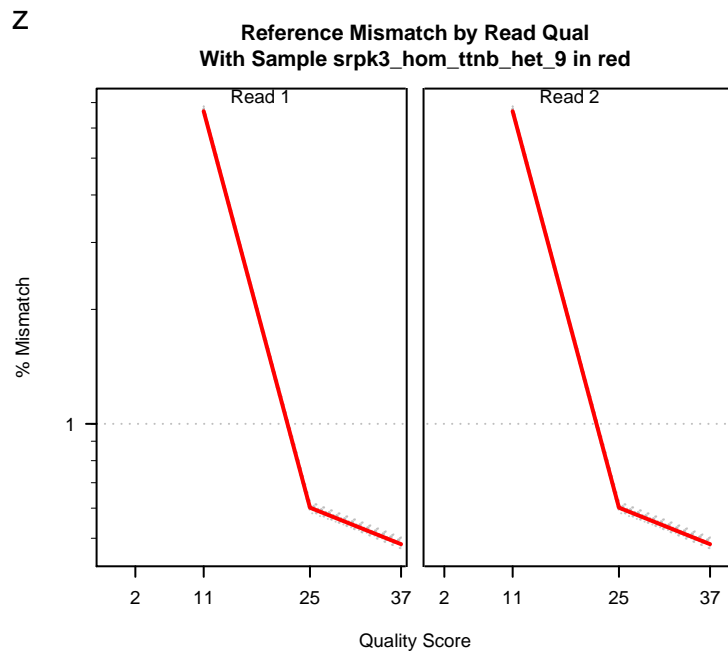
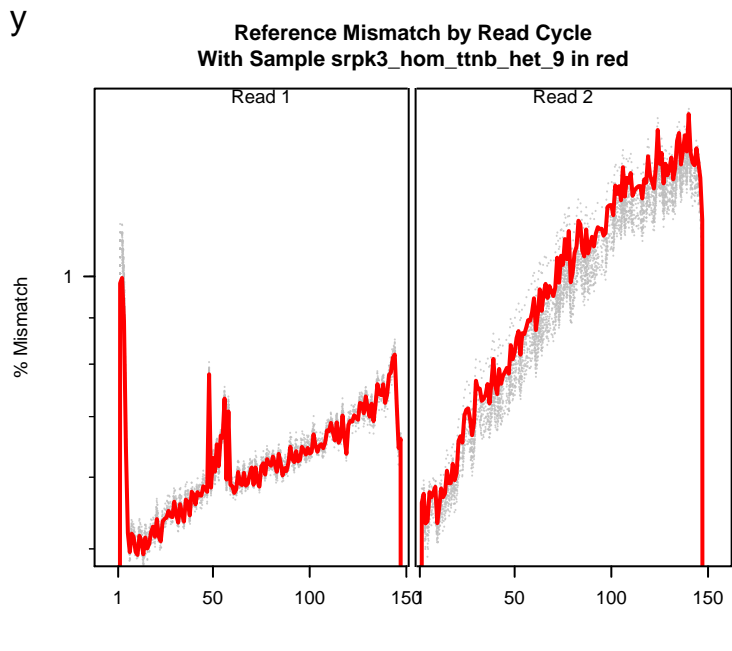
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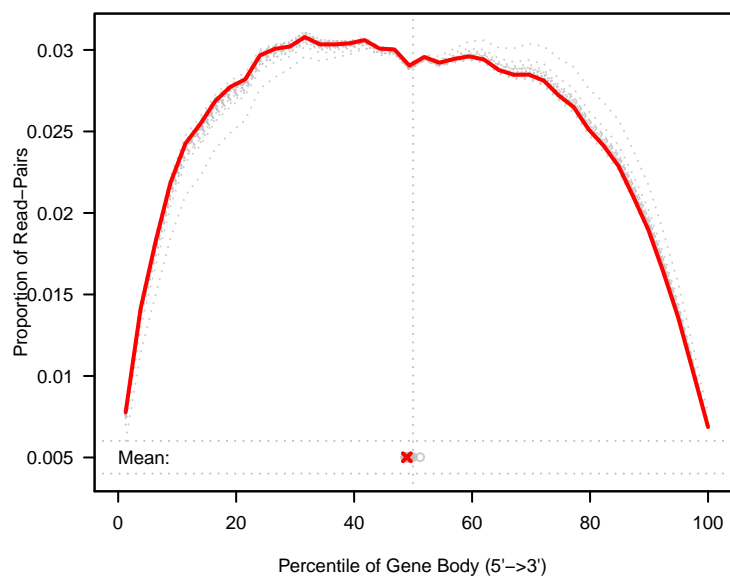






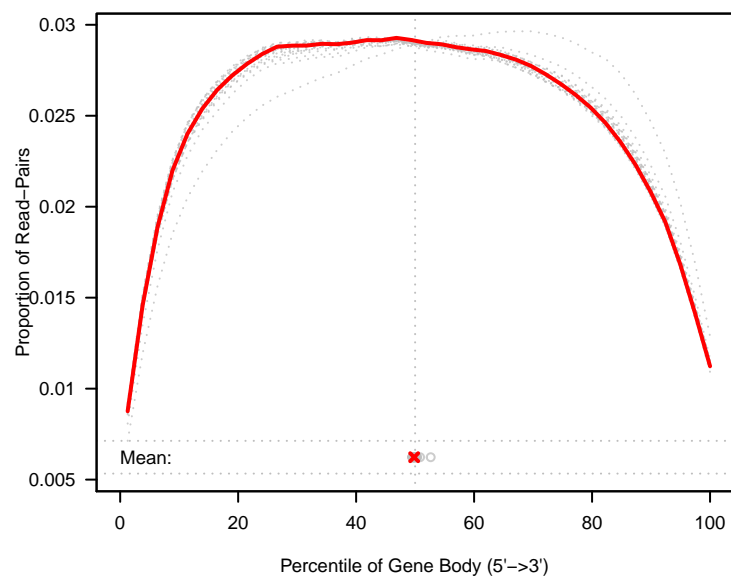
ae

Gene-Body Coverage
With Sample *srpk3_hom_ttnb_het_9* in red



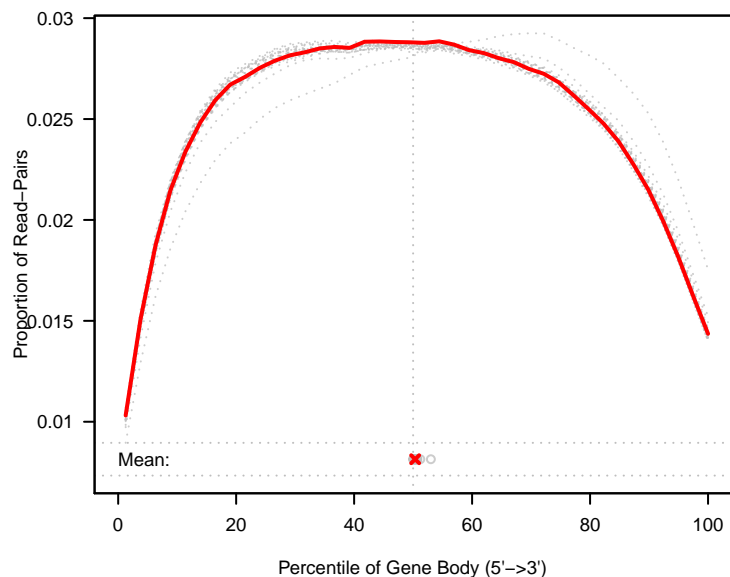
af

Gene-Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_hom_ttnb_het_9* in red



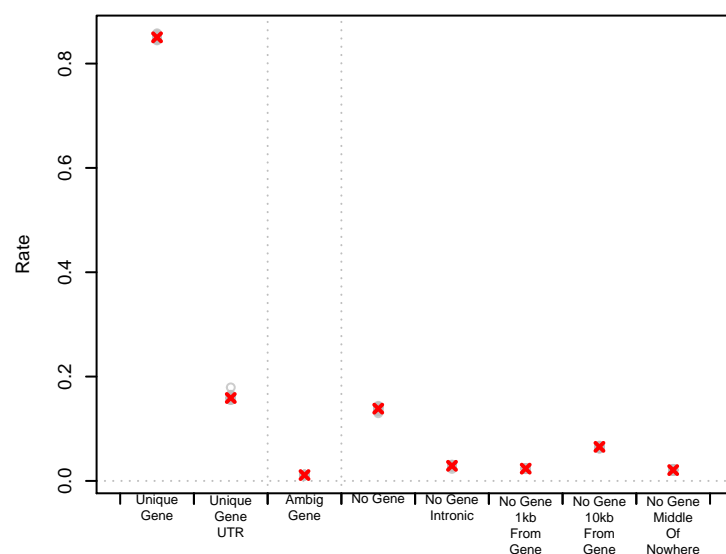
ag

Gene-Body Coverage, Low Expression Genes
With Sample *srpk3_hom_ttnb_het_9* in red



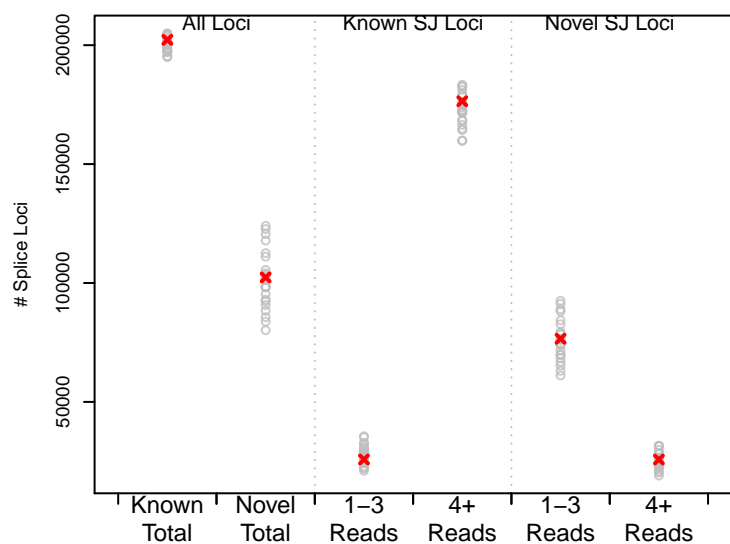
ah

Read Mapping Location Rates
With Sample *srpk3_hom_ttnb_het_9* in red



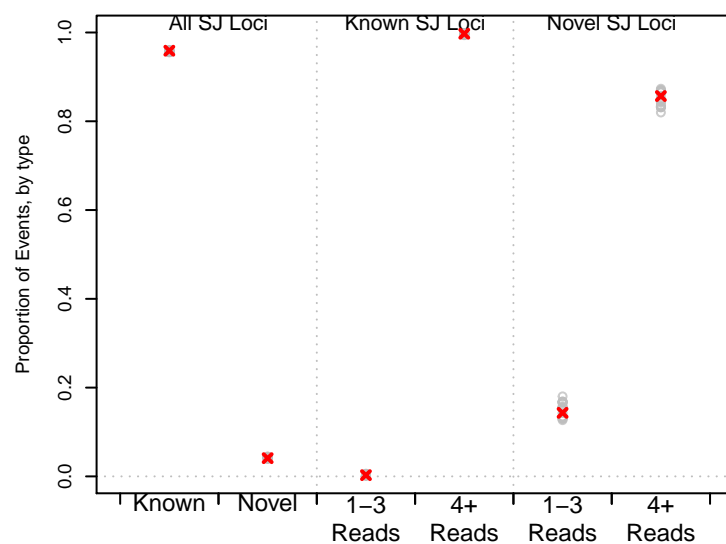
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_hom_ttnb_het_9* in red

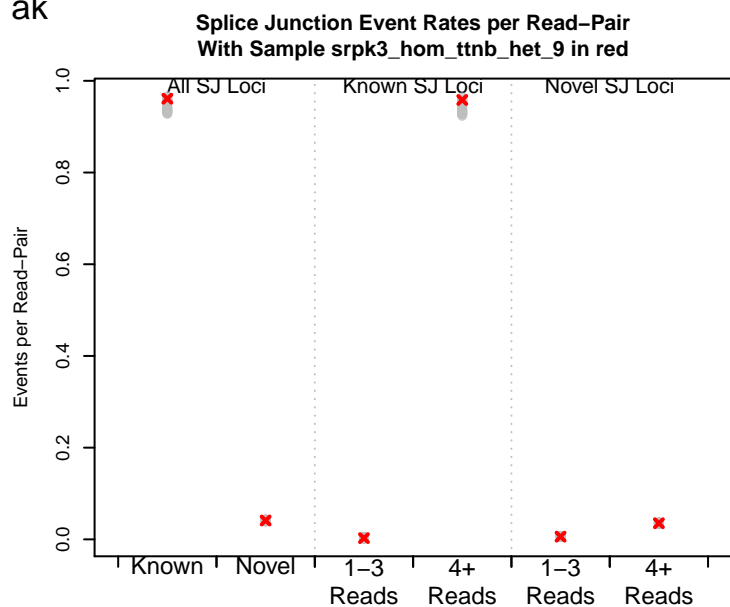


aj

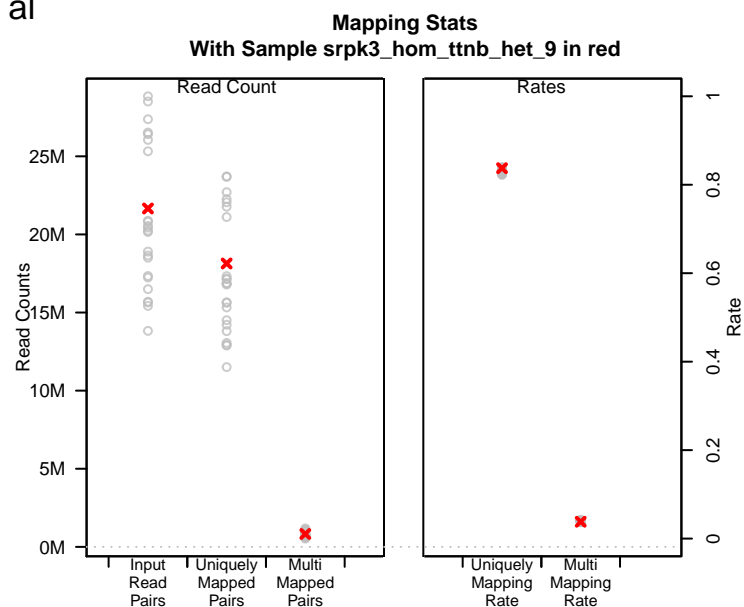
Breakdown of Splice Junction Events, by type
With Sample *srpk3_hom_ttnb_het_9* in red



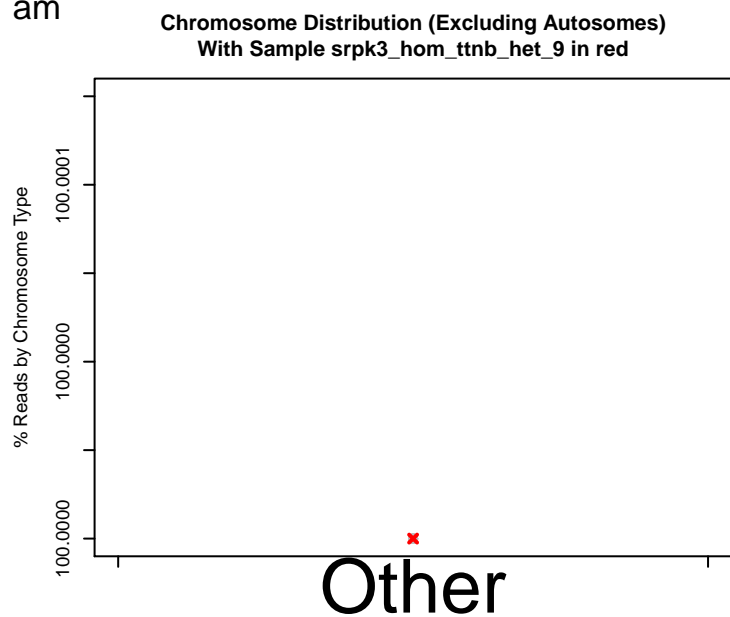
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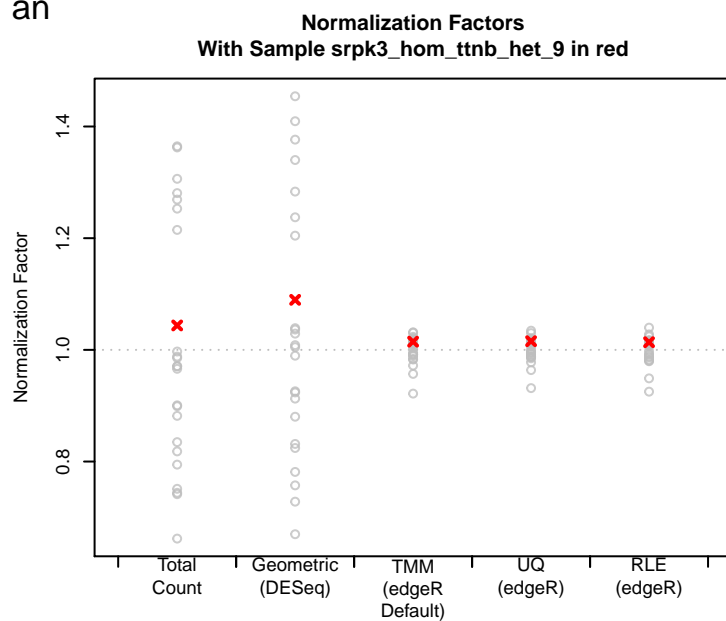
al



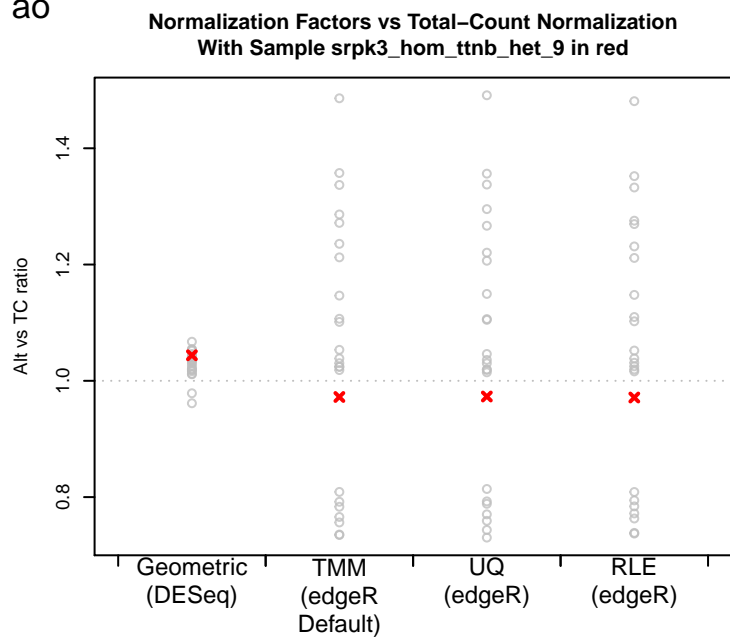
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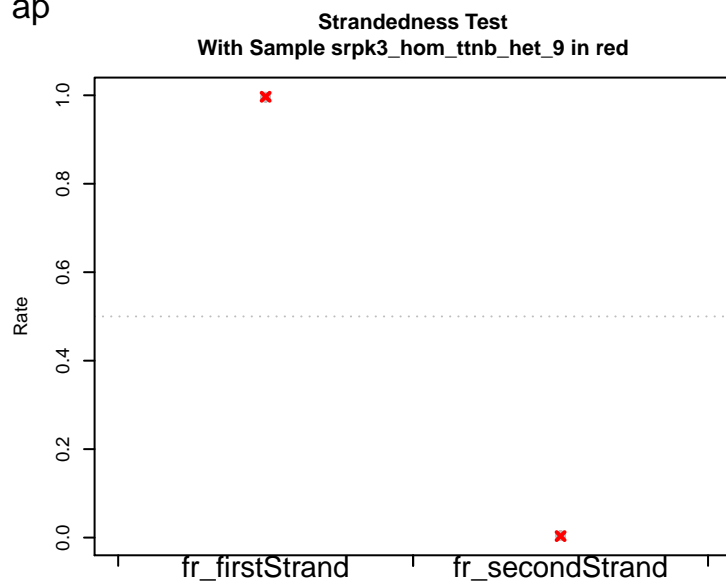
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ao

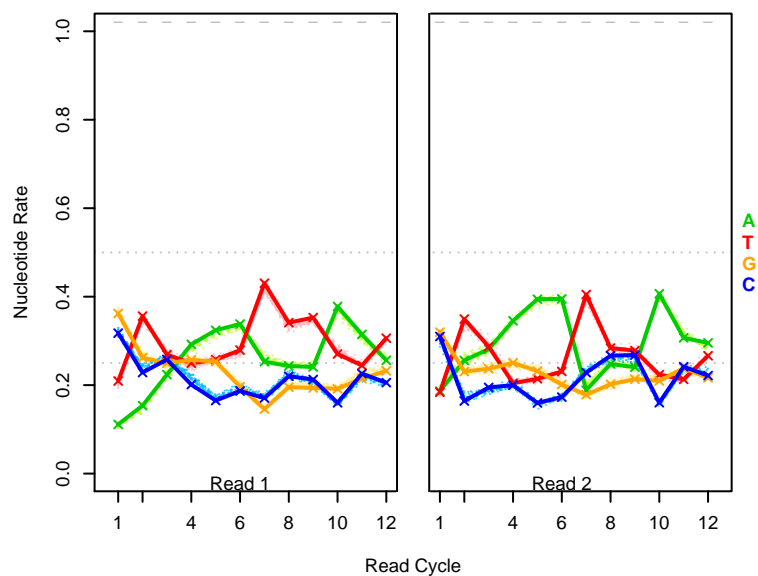


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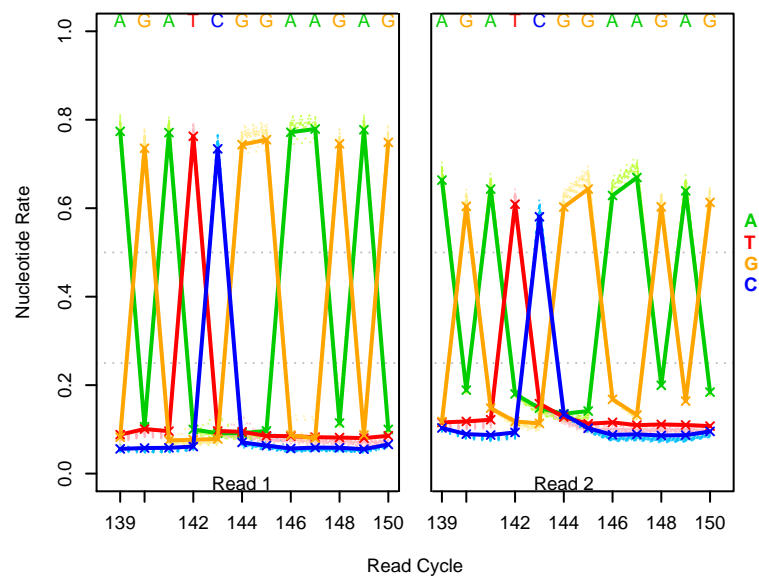
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srpk3_hom_ttnb_het_9 in red



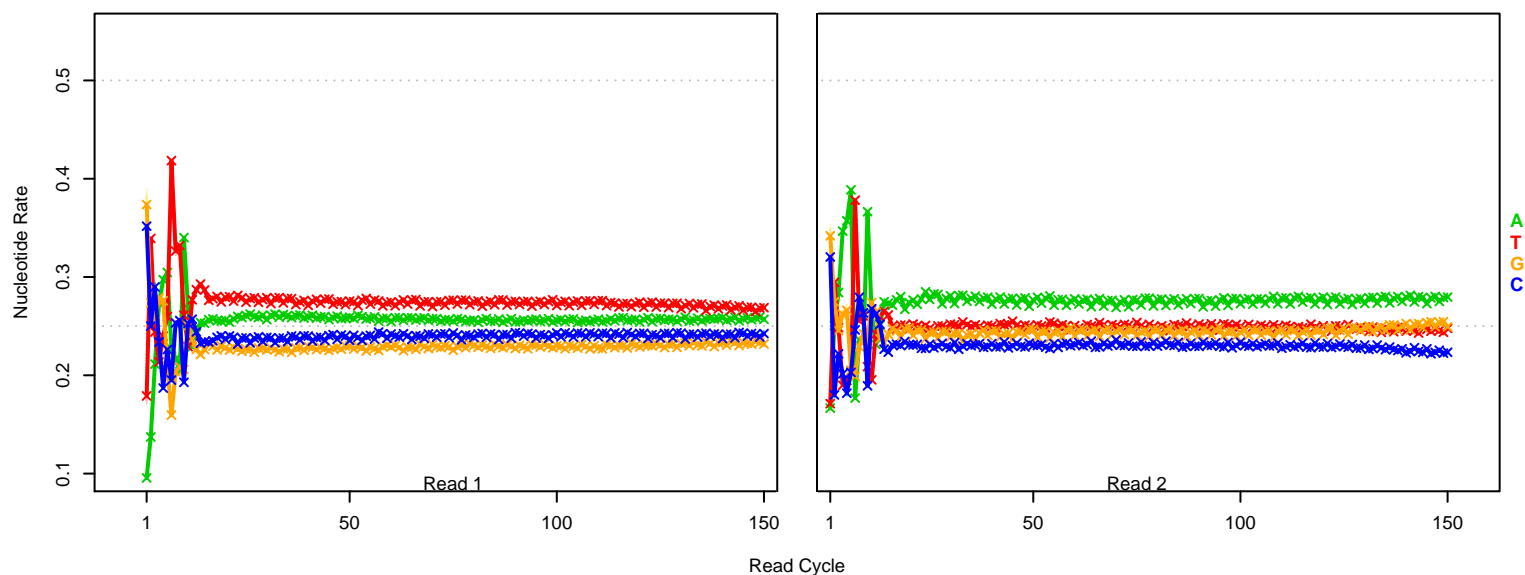
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srpk3_hom_ttnb_het_9 in red



as

Raw Nucleotide Rate by Cycle
With Sample srpk3_hom_ttnb_het_9 in red



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srpk3_hom_ttnb_het_9 in red

