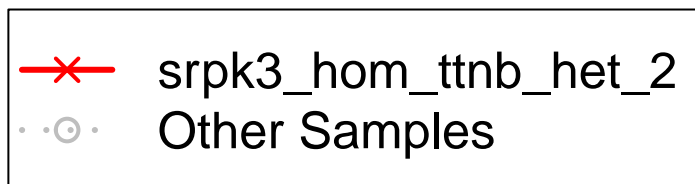


a

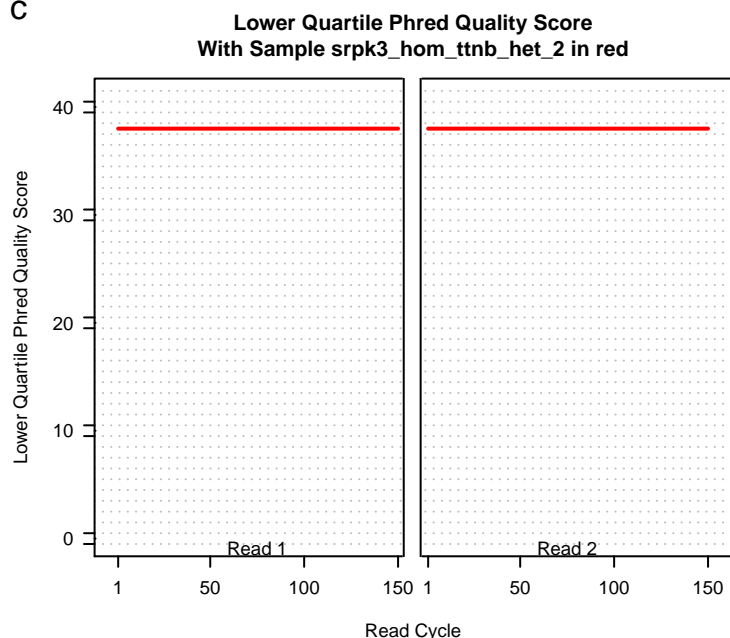
Sample Highlight:
srpk3_hom_ttnb_het_2



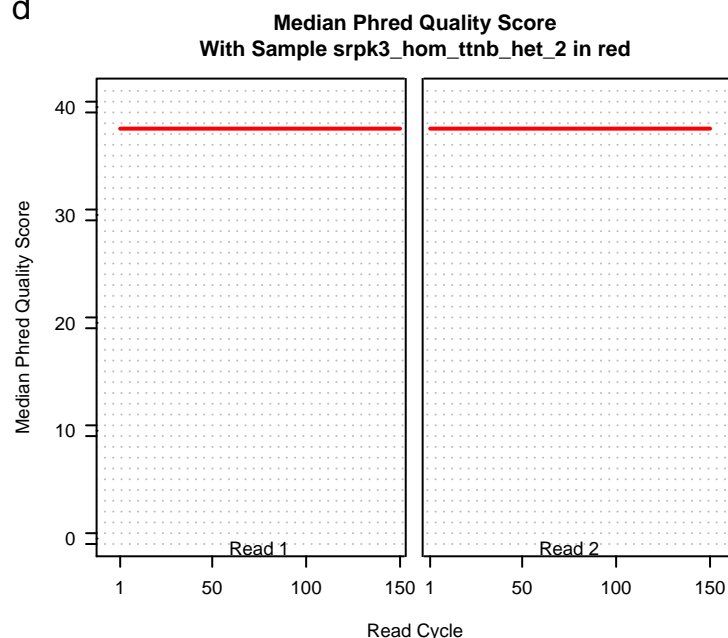
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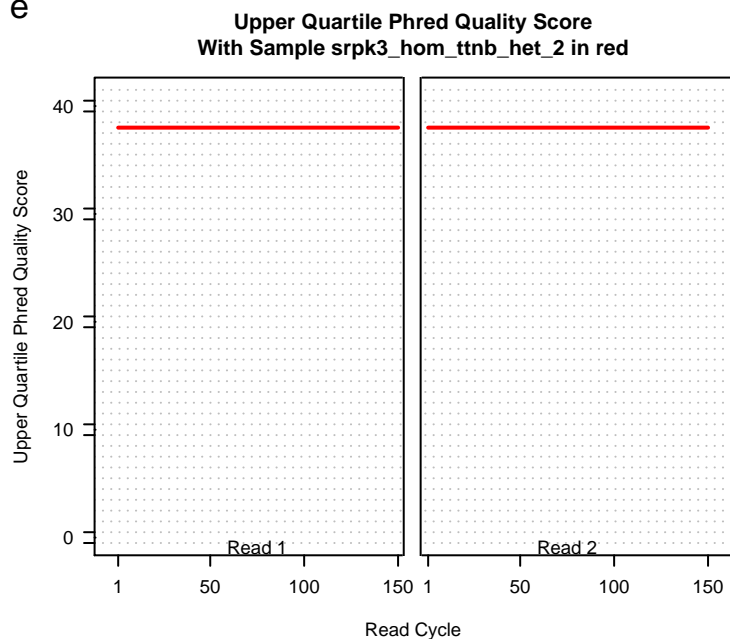
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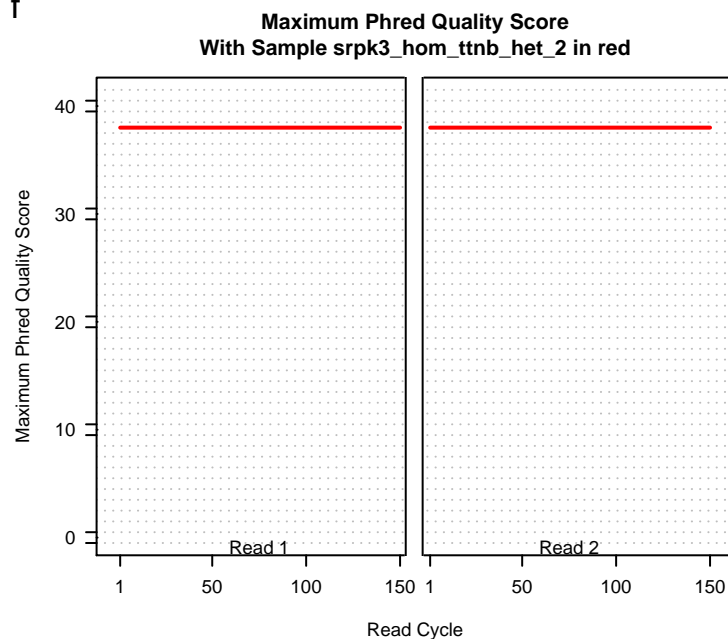
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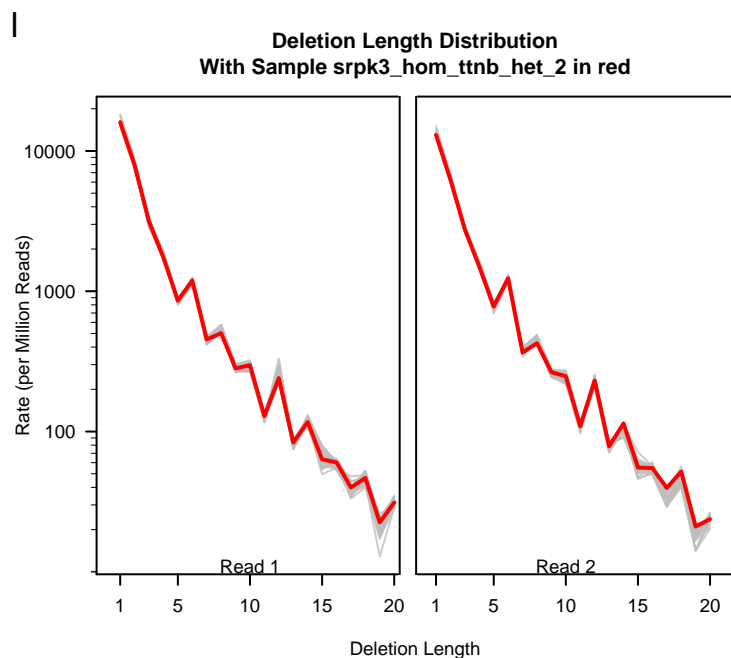
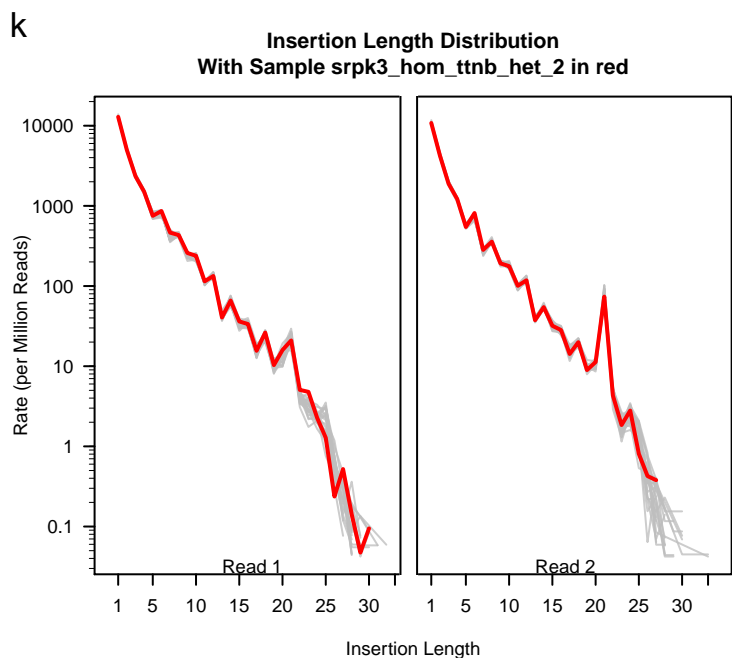
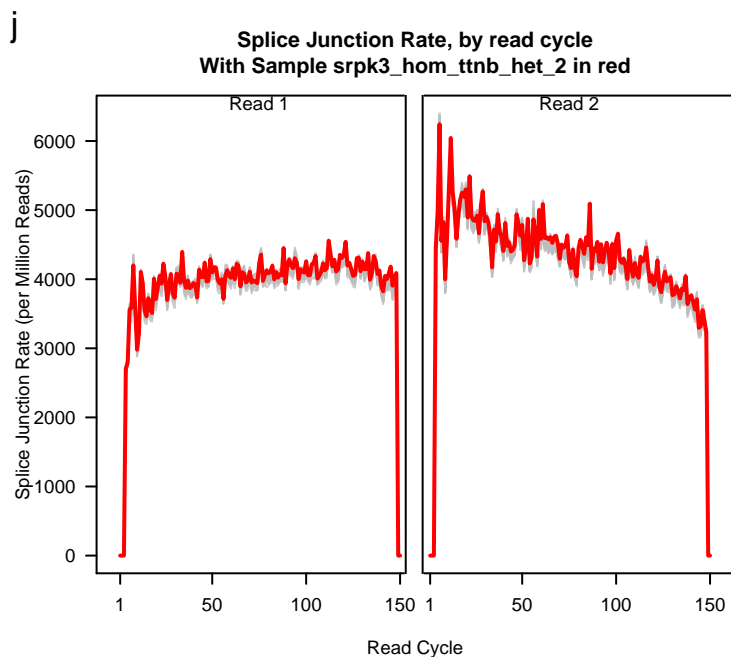
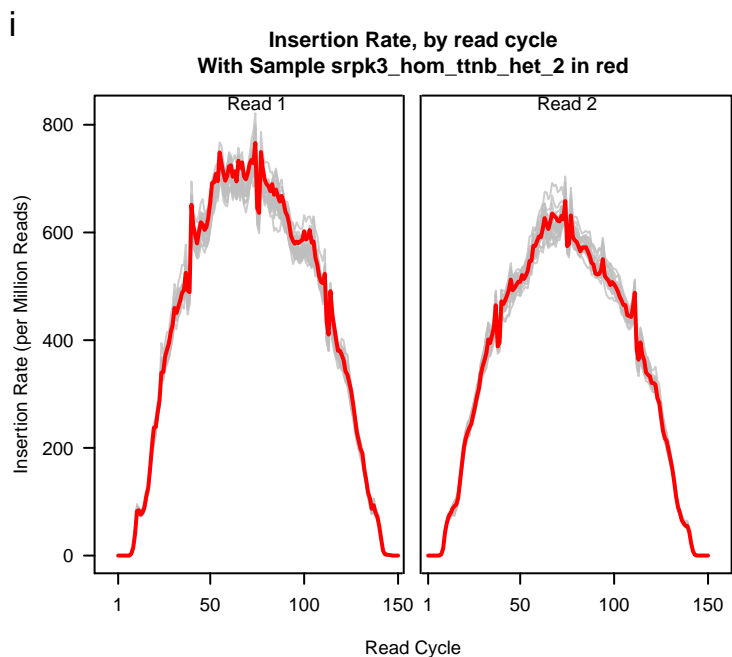
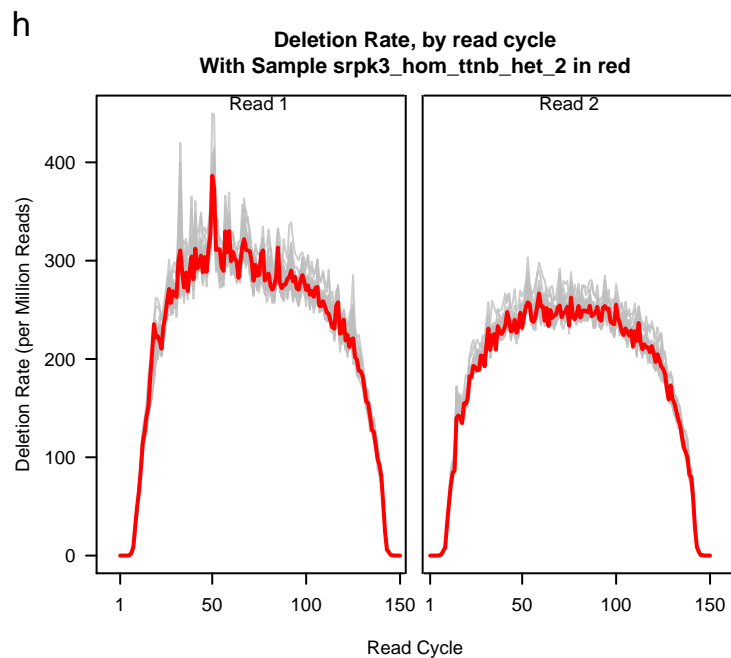
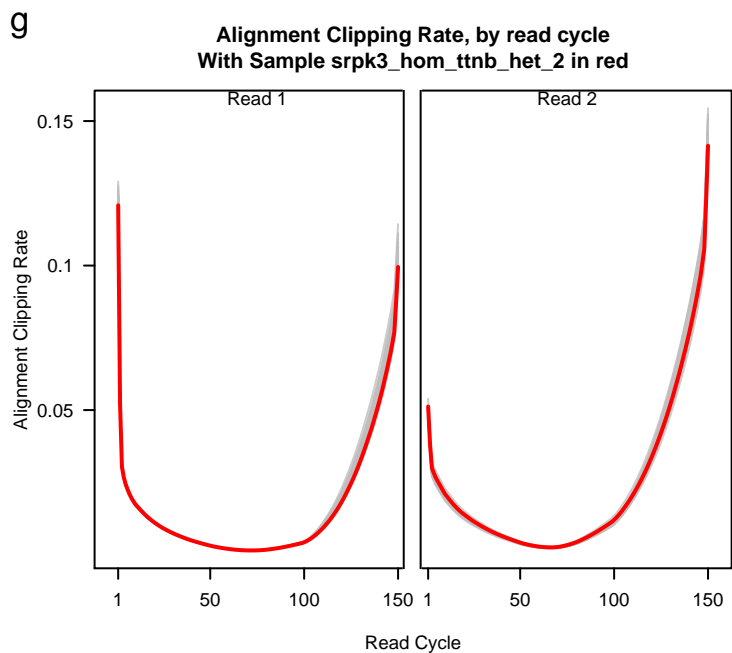


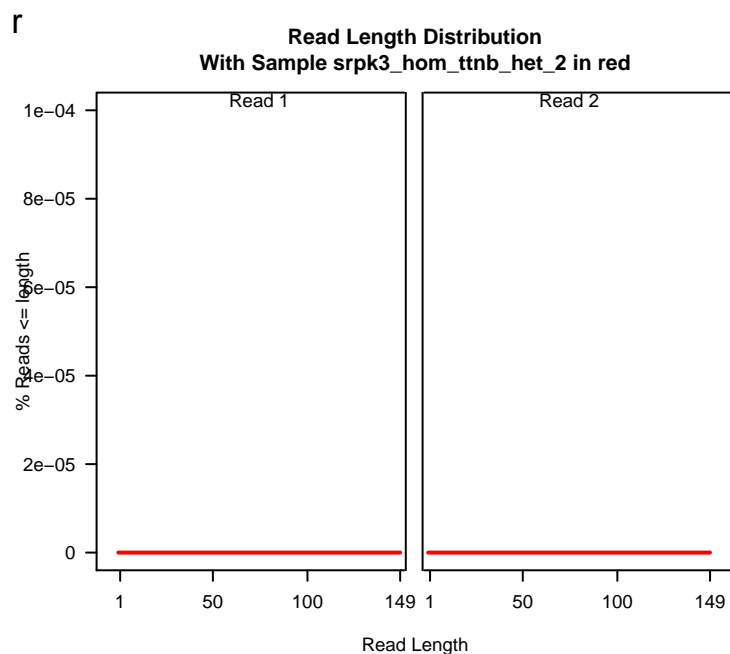
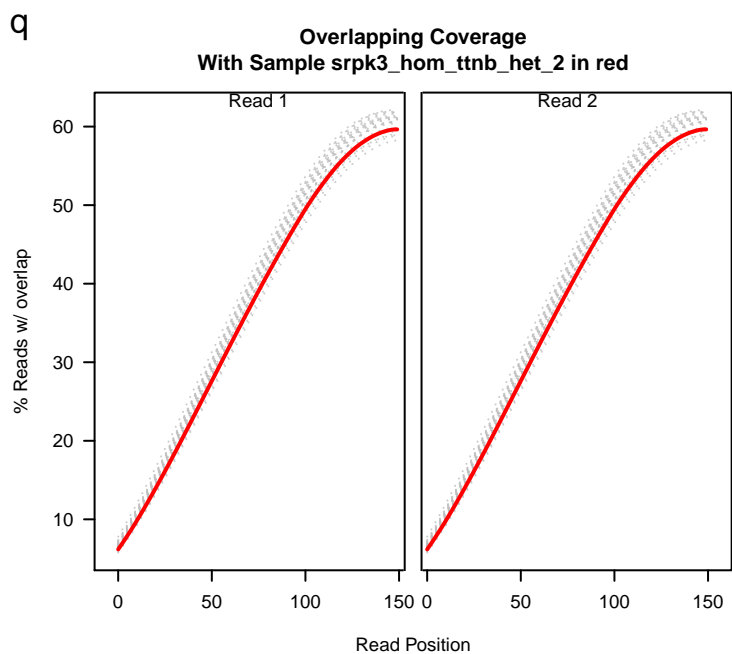
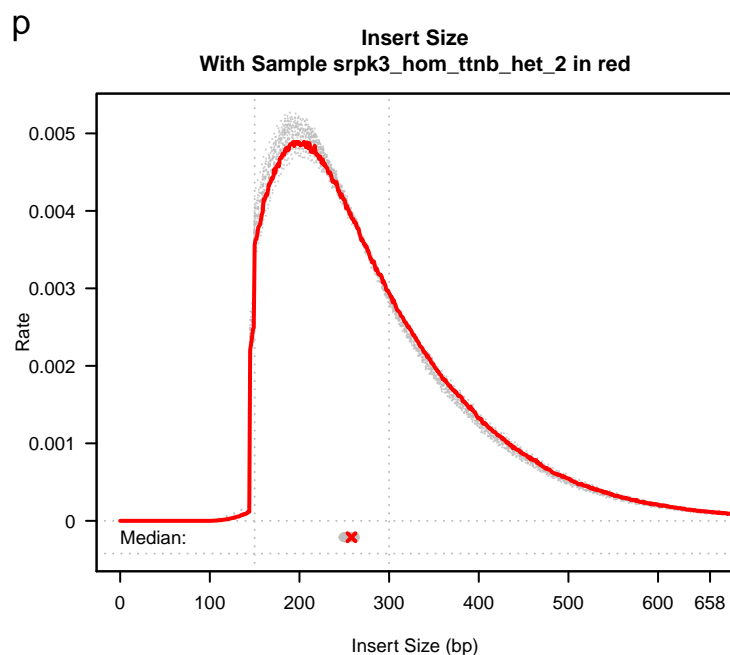
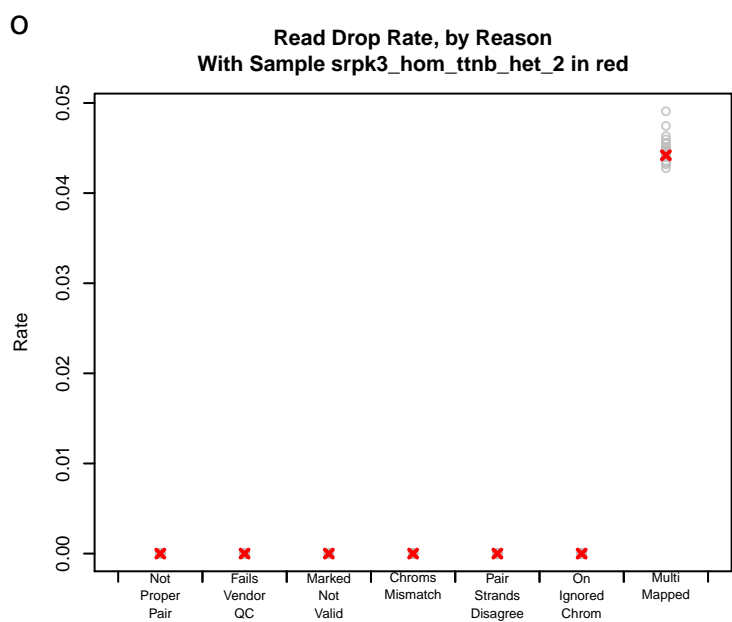
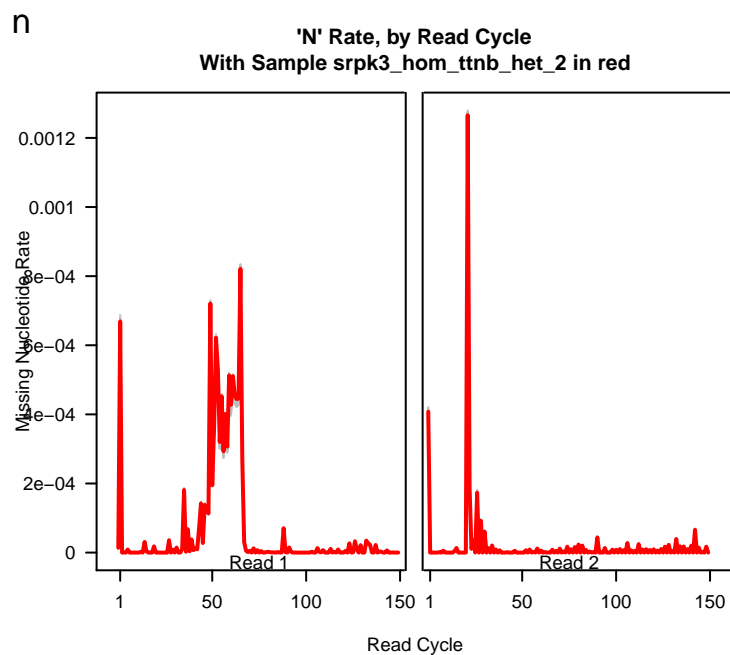
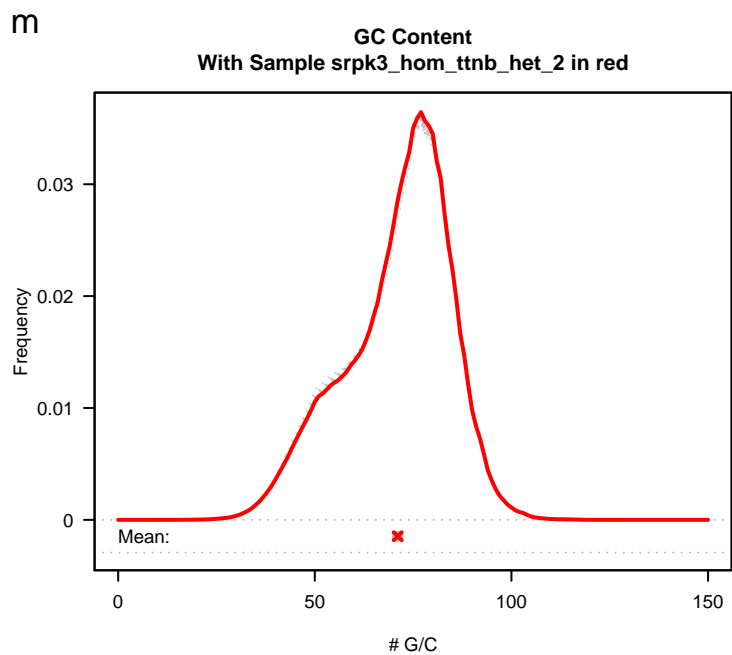
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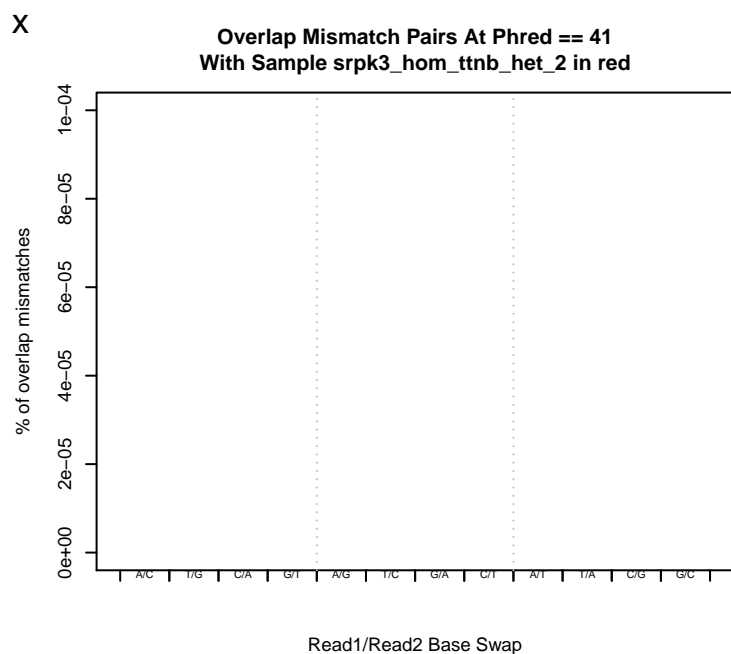
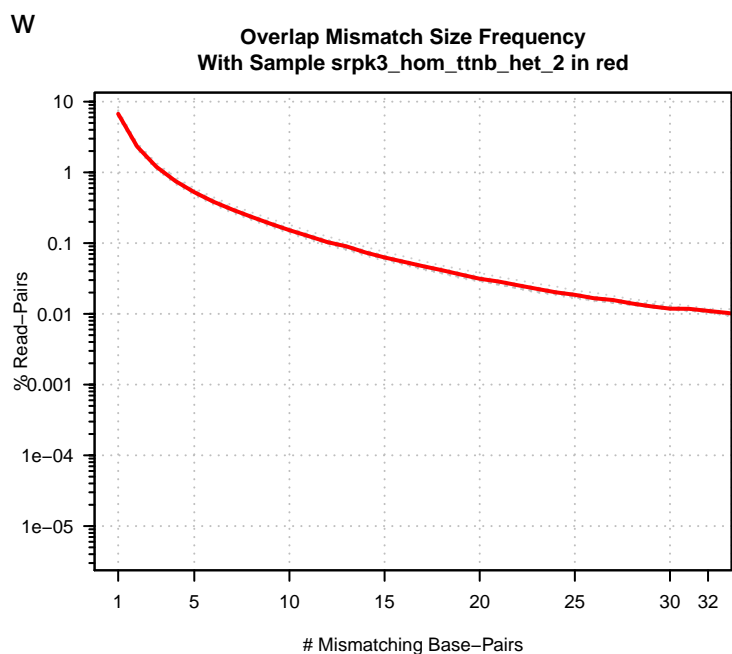
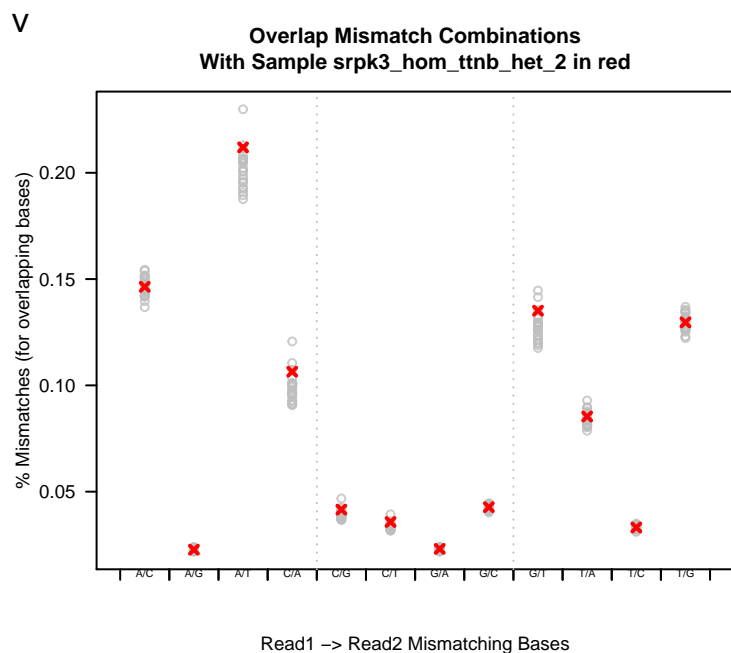
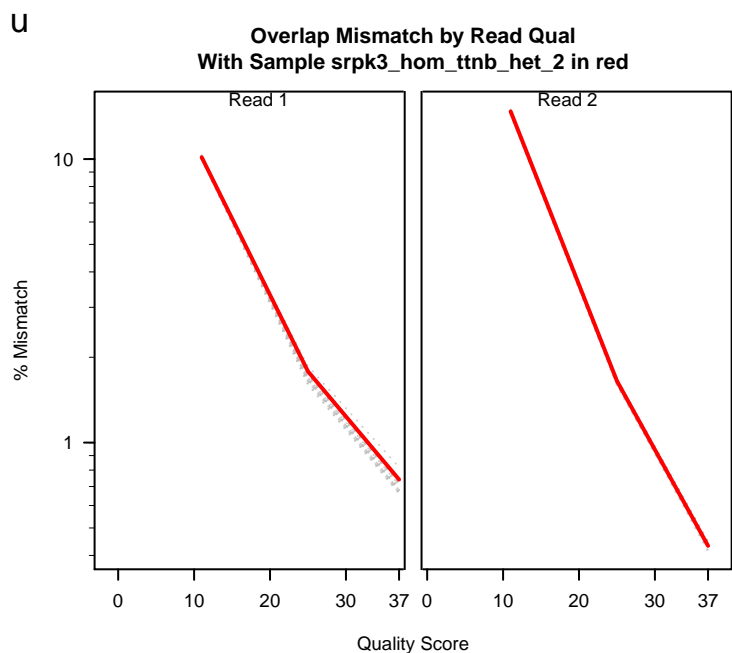
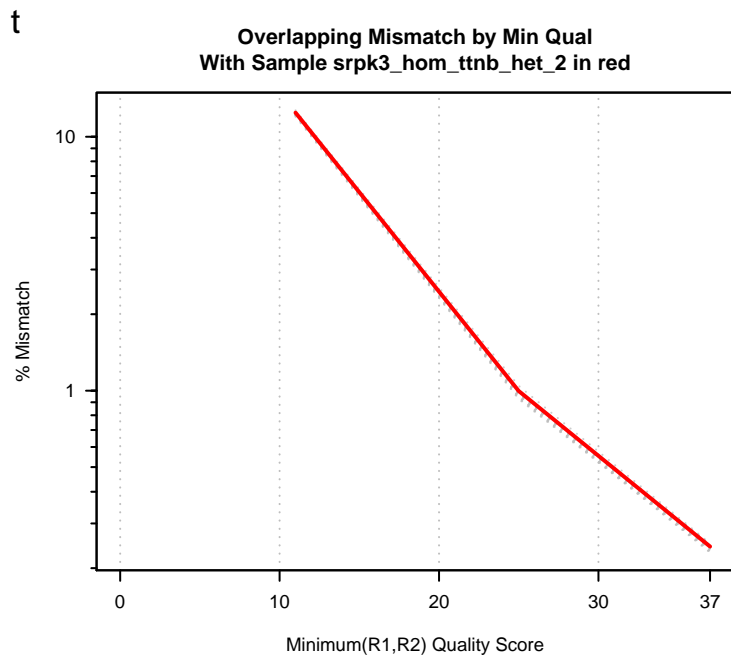
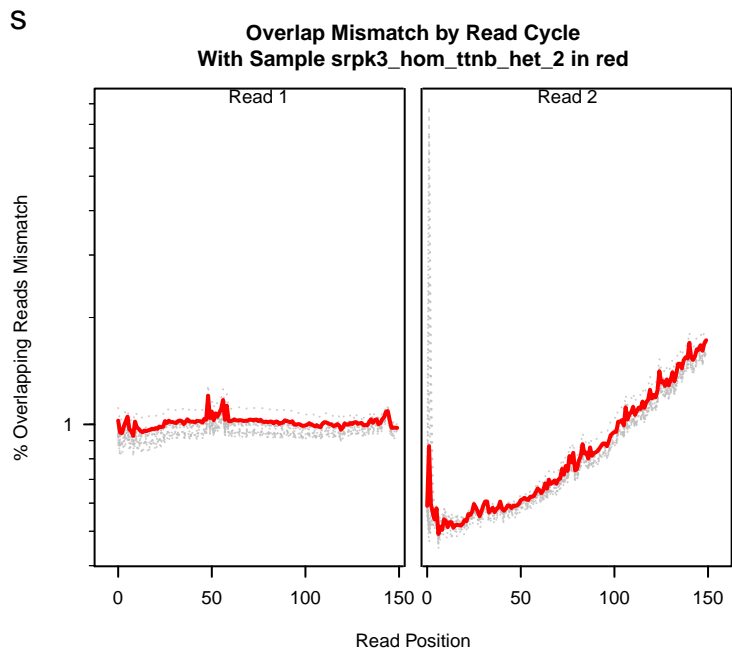


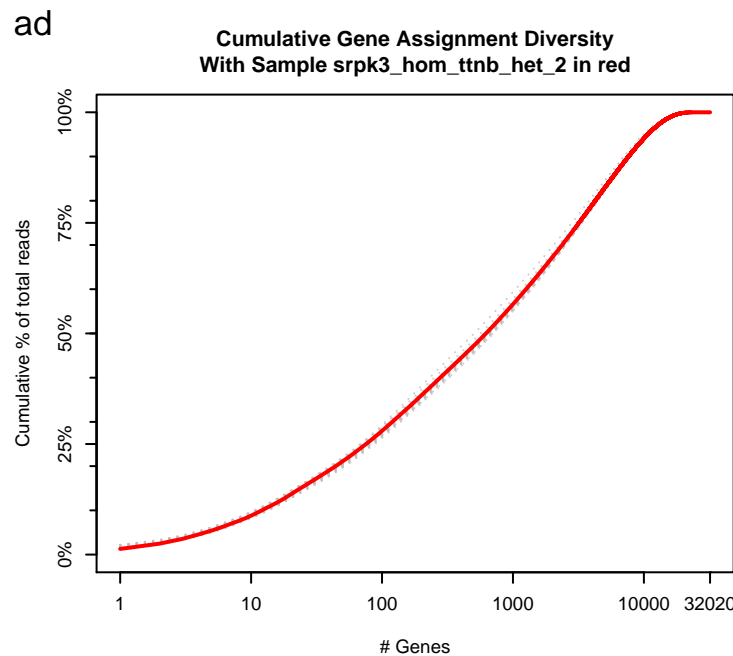
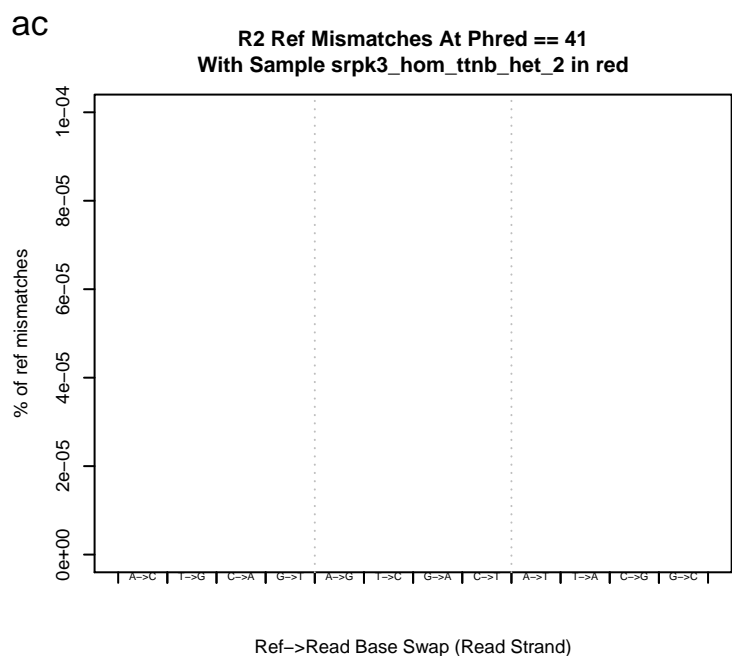
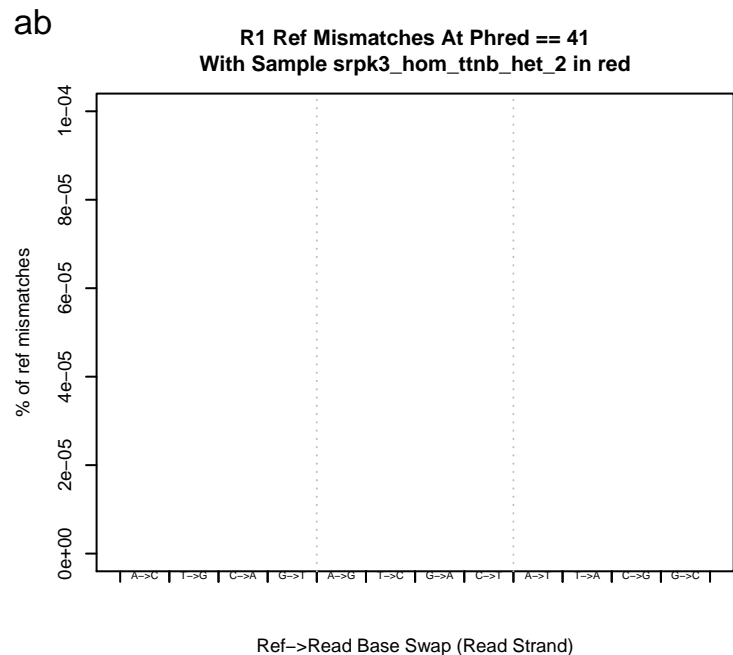
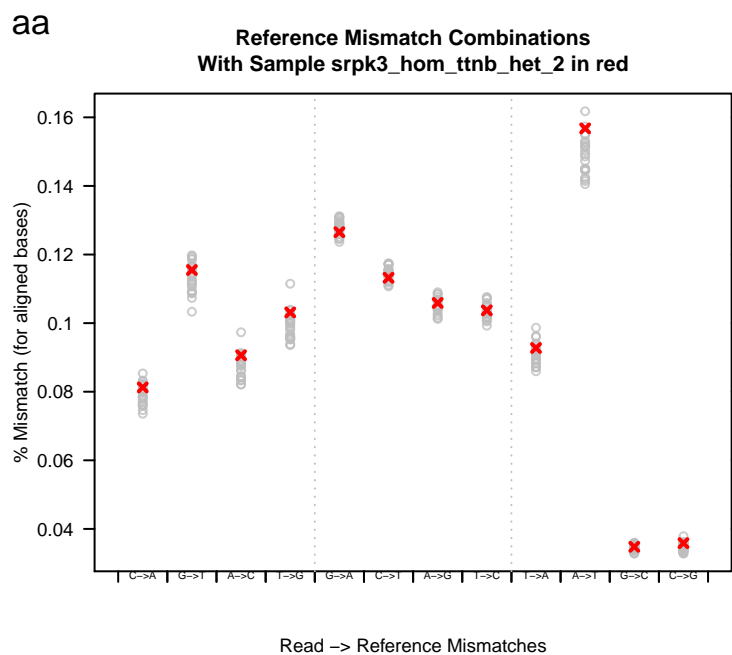
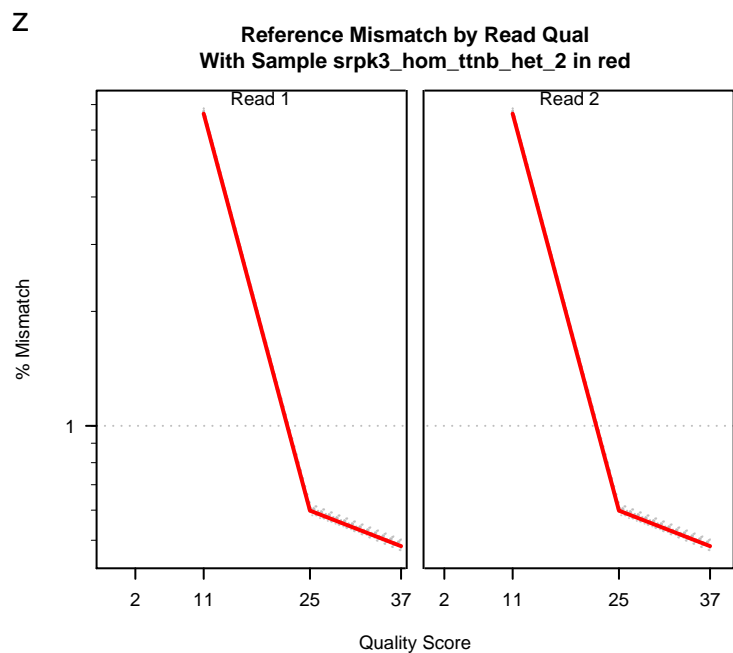
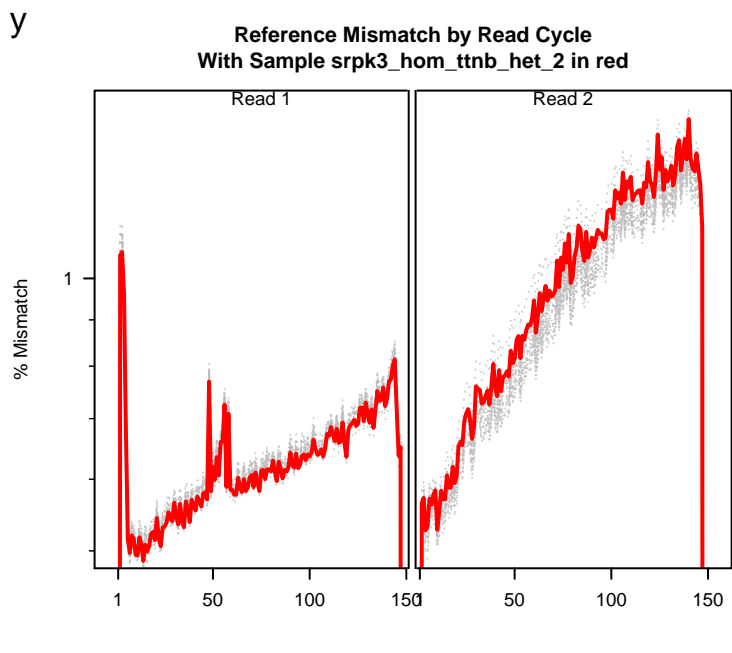
f





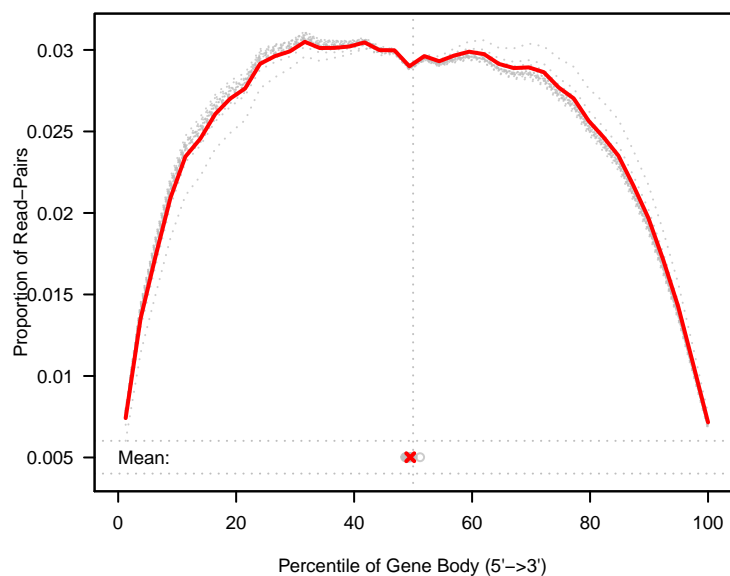






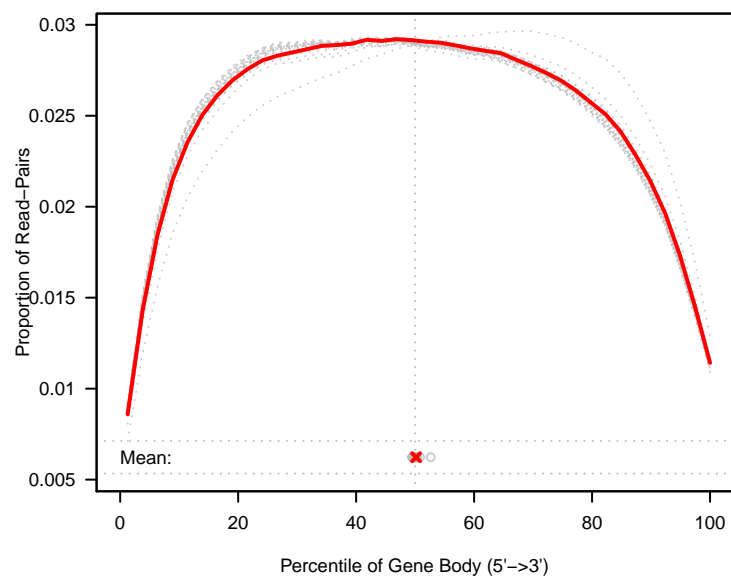
ae

Gene-Body Coverage
With Sample *srpk3_hom_ttnb_het_2* in red



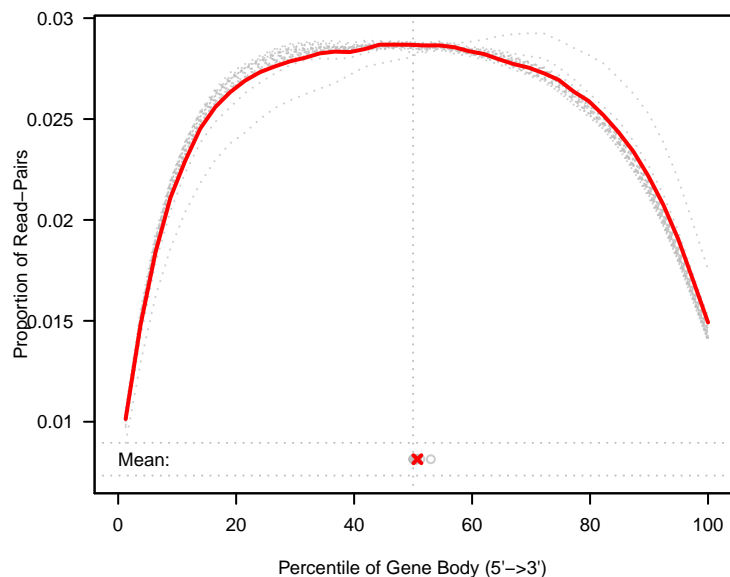
af

Gene-Body Coverage, Upper Middle Quartile Genes
With Sample *srpk3_hom_ttnb_het_2* in red



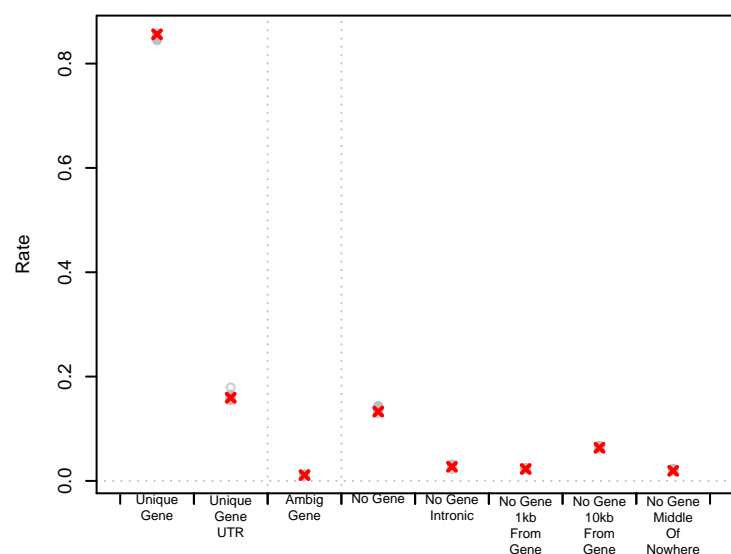
ag

Gene-Body Coverage, Low Expression Genes
With Sample *srpk3_hom_ttnb_het_2* in red



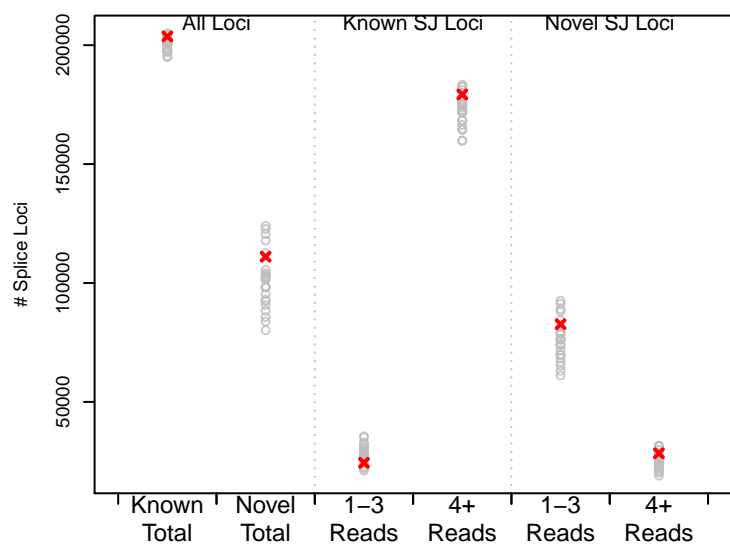
ah

Read Mapping Location Rates
With Sample *srpk3_hom_ttnb_het_2* in red



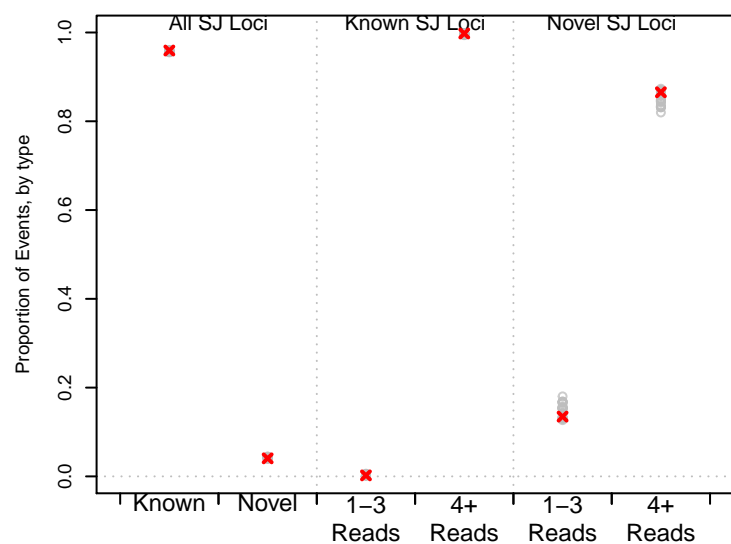
ai

Observed Splice Junction Loci, by type
With Sample *srpk3_hom_ttnb_het_2* in red

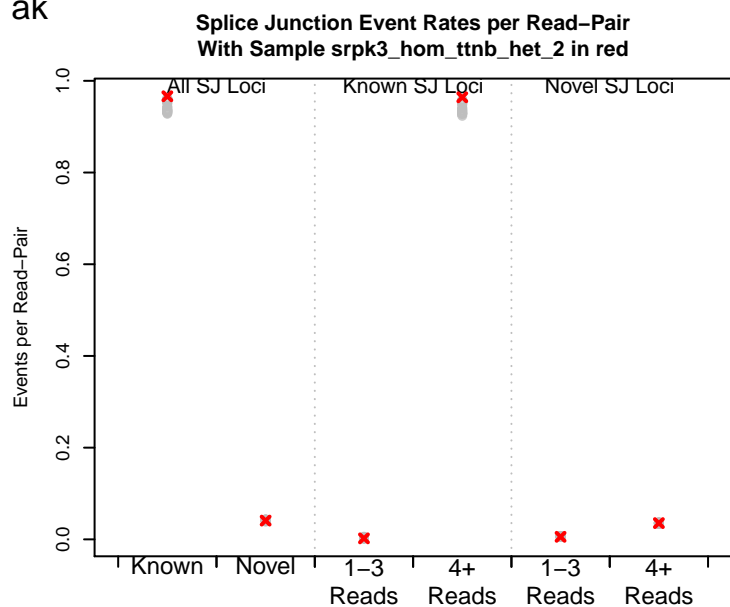


aj

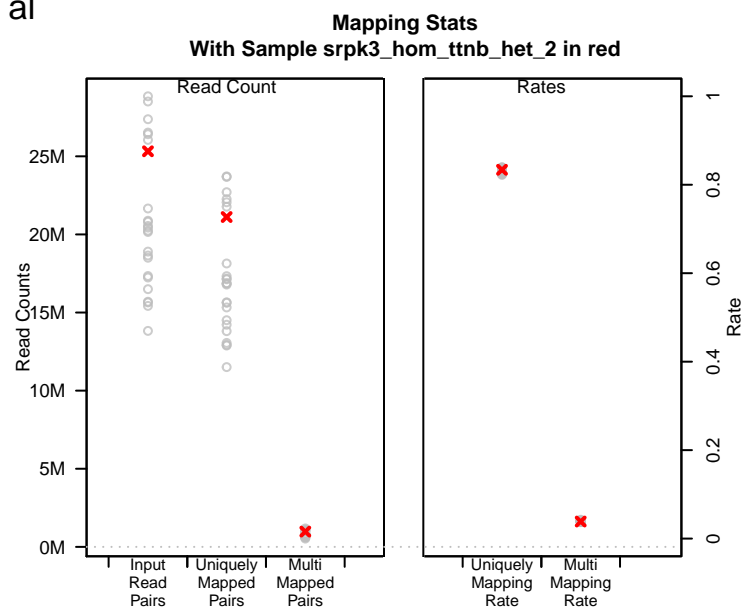
Breakdown of Splice Junction Events, by type
With Sample *srpk3_hom_ttnb_het_2* in red



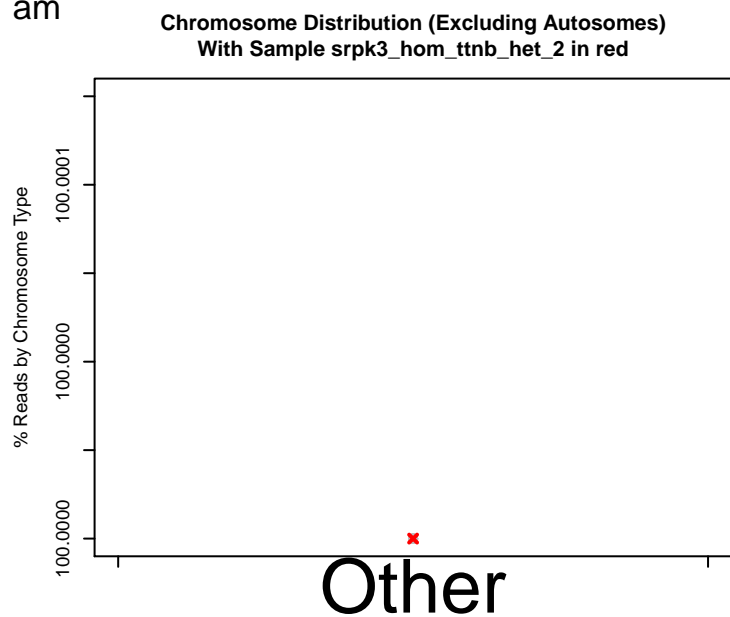
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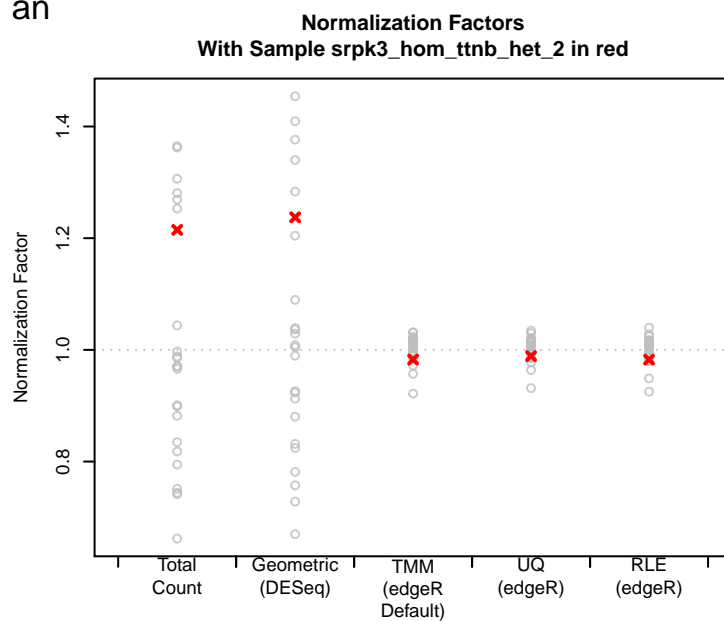
al



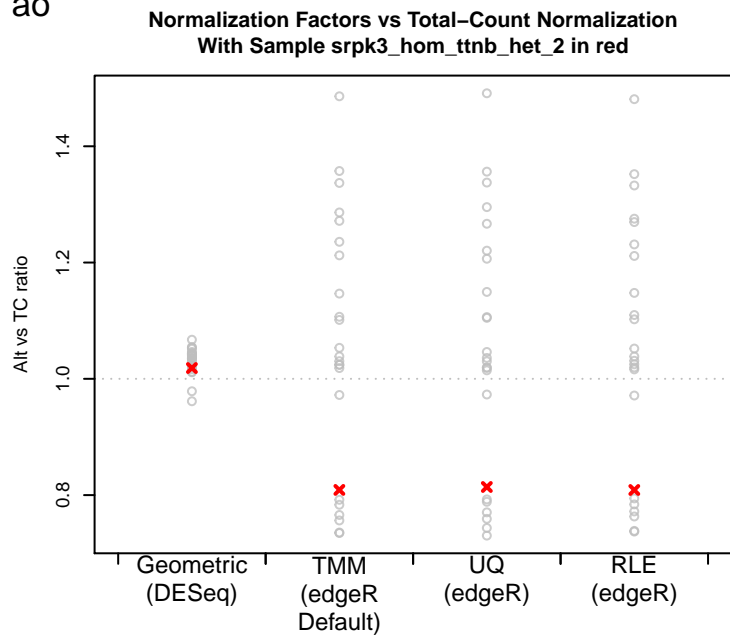
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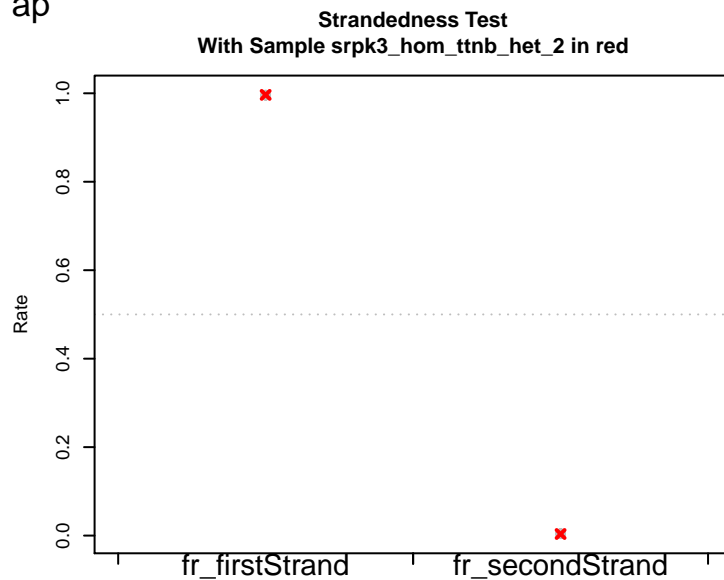
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ao

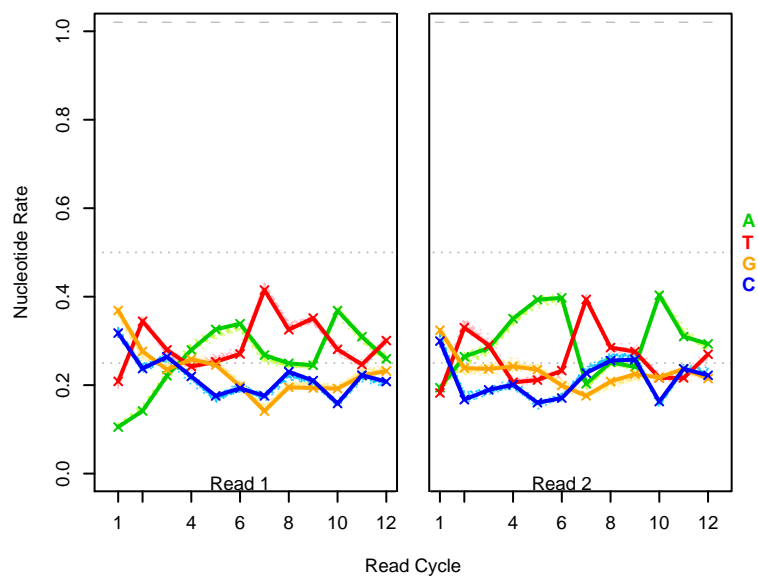


ap



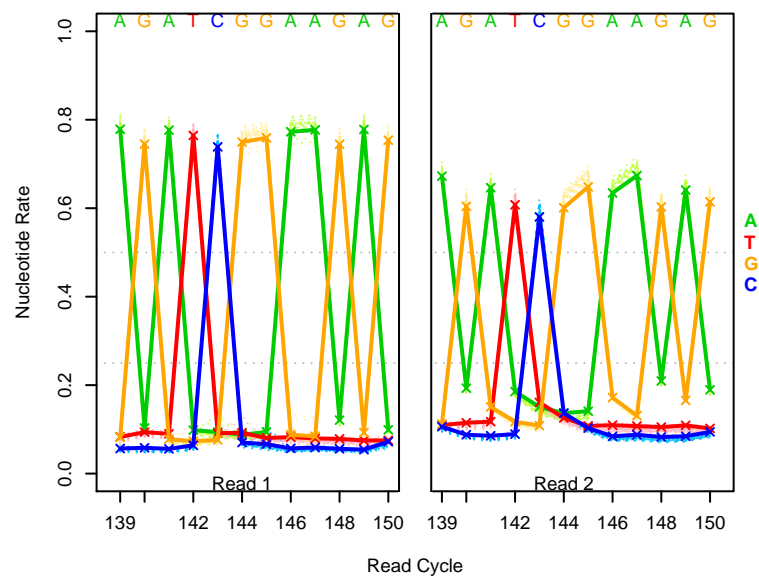
aq

Nucleotide Rate by Cycle, Leading Clipped bases (12)
With Sample srp33_hom_ttnb_het_2 in red



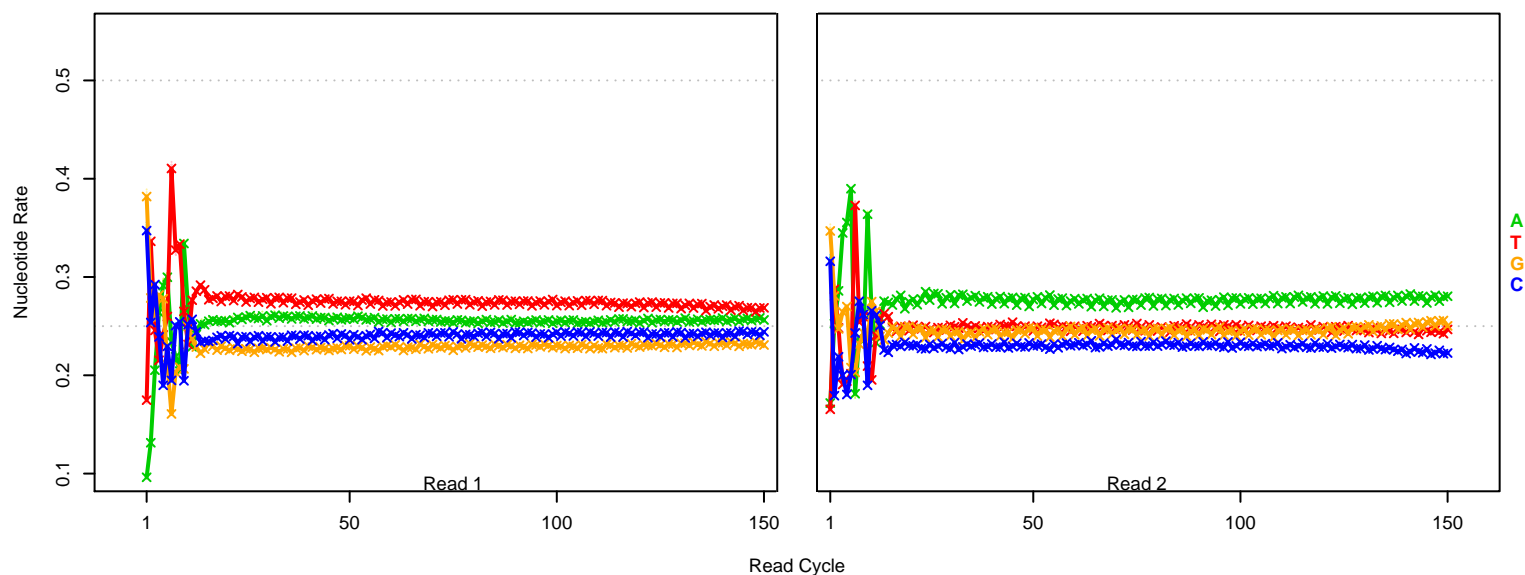
ar

Nucleotide Rate by Cycle, Trailing Clipped bases (12)
With Sample srp33_hom_ttnb_het_2 in red



as

Raw Nucleotide Rate by Cycle
With Sample srp33_hom_ttnb_het_2 in red



at

Nucleotide Rate by Cycle, Aligned bases only
With Sample srp33_hom_ttnb_het_2 in red

