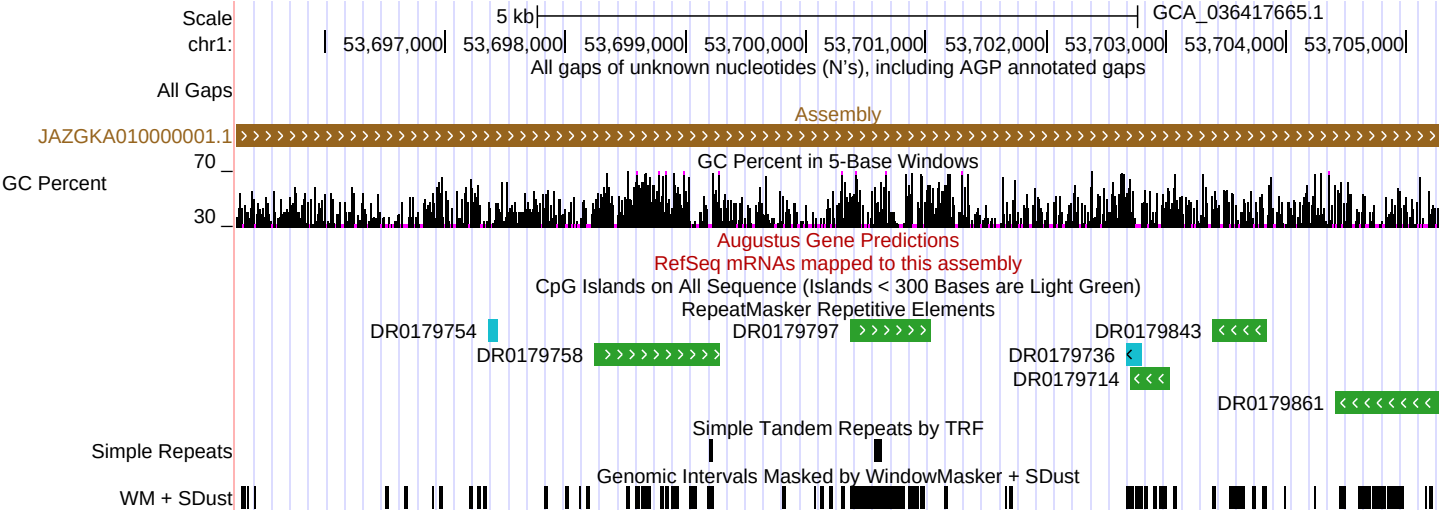
Scale
5 kb
GCA_036417665.1
chr1:
53,697,000
53,698,000
53,699,000
53,700,000
53,701,000
53,702,000
53,703,000
53,704,000
53,705,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAZGKA010000001.1
70
GC Percent in 5-Base Windows
GC Percent
30
Augustus Gene Predictions
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0179754
DR0179797
DR0179843
DR0179758
DR0179736
DR0179714
DR0179861
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust