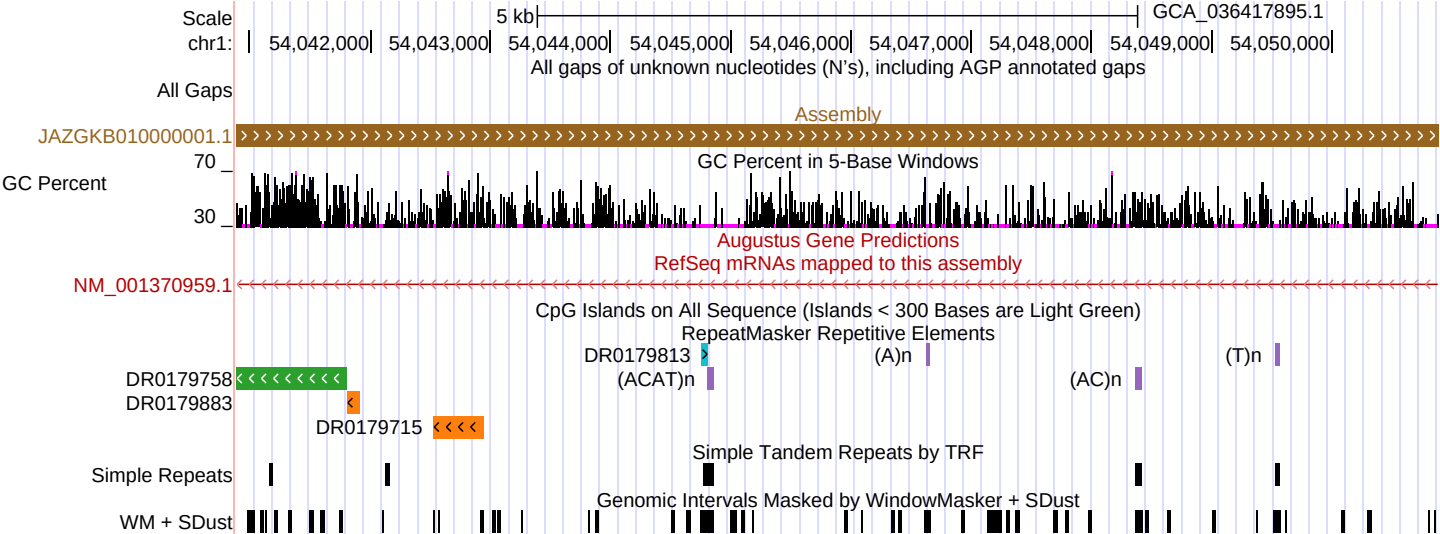
Scale
5 kb
GCA_036417895.1
chr1:
54,042,000
54,043,000
54,044,000
54,045,000
54,046,000
54,047,000
54,048,000
54,049,000
54,050,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAZGKB010000001.1
GC Percent in 5-Base Windows
70
GC Percent
30
Augustus Gene Predictions
RefSeq mRNAs mapped to this assembly
NM_001370959.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0179813
(A)n
(T)n
DR0179758
(ACAT)n
(AC)n
DR0179883
DR0179715
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust