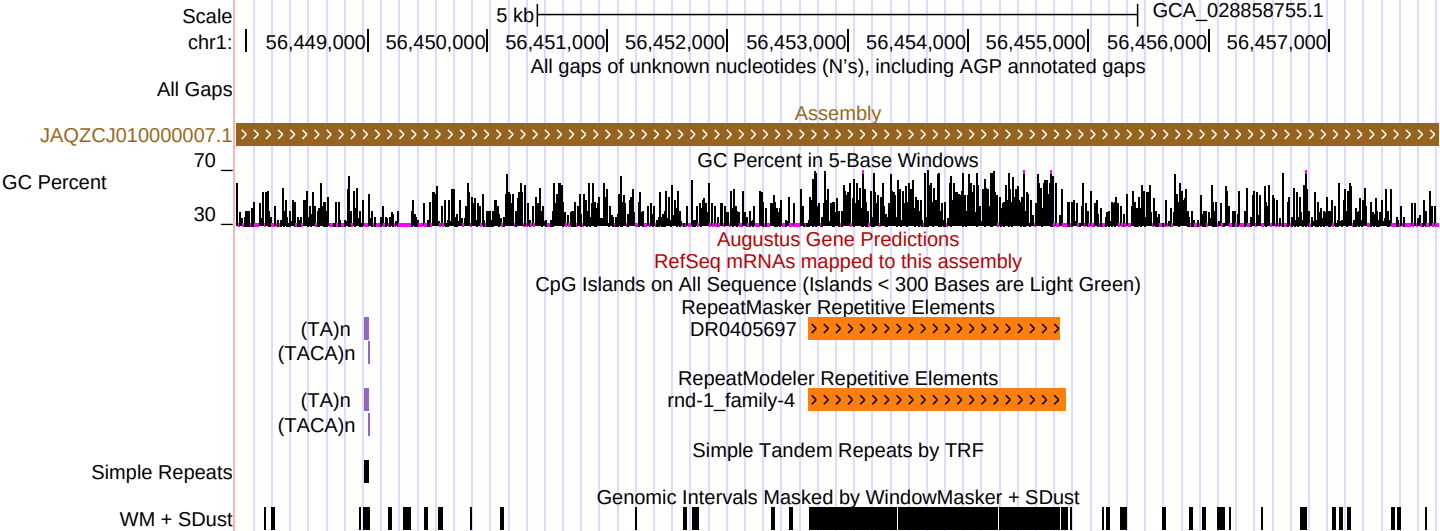
Scale
5 kb
GCA_028858755.1
chr1:
56,449,000
56,450,000
56,451,000
56,452,000
56,453,000
56,454,000
56,455,000
56,456,000
56,457,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAQZCJ010000007.1
70
GC Percent in 5-Base Windows
GC Percent
30
Augustus Gene Predictions
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
(TA)n
DR0405697
(TACA)n
RepeatModeler Repetitive Elements
(TA)n
rnd-1_family-4
(TACA)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust