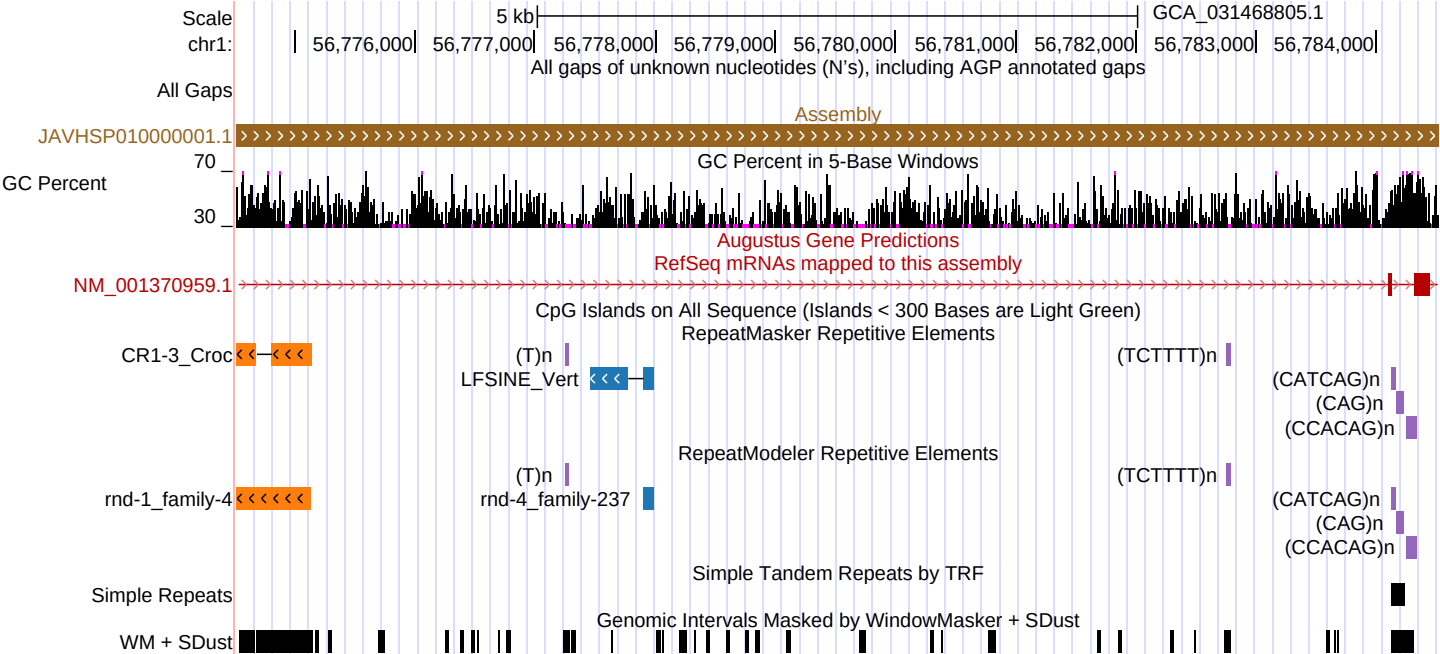
Scale
5 kb
GCA_031468805.1
chr1:
56,776,000
56,777,000
56,778,000
56,779,000
56,780,000
56,781,000
56,782,000
56,783,000
56,784,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAVHSP010000001.1
GC Percent in 5-Base Windows
70
GC Percent
30
Augustus Gene Predictions
RefSeq mRNAs mapped to this assembly
NM_001370959.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
CR1-3_Croc
(T)n
(TCTTTT)n
LFSINE_Vert
(CATCAG)n
(CAG)n
(CCACAG)n
RepeatModeler Repetitive Elements
(T)n
(TCTTTT)n
rnd-1_family-4
rnd-4_family-237
(CATCAG)n
(CAG)n
(CCACAG)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust