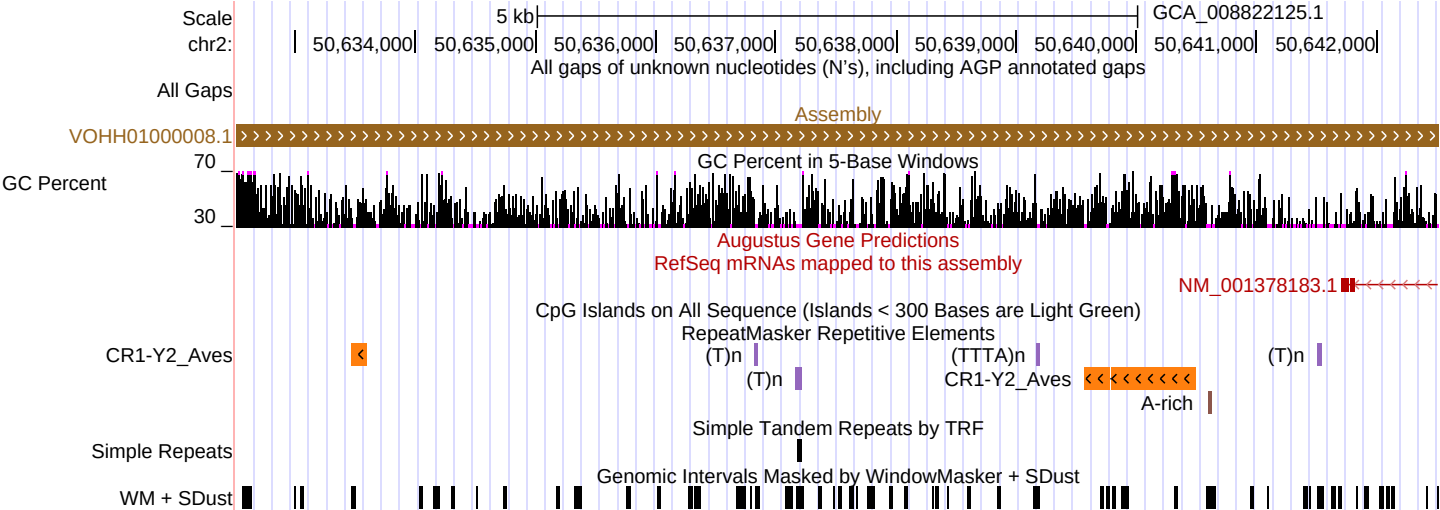
Scale
5 kb
GCA_008822125.1
chr2:
50,634,000
50,635,000
50,636,000
50,637,000
50,638,000
50,639,000
50,640,000
50,641,000
50,642,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
VOHH01000008.1
70
GC Percent in 5-Base Windows
GC Percent
30
Augustus Gene Predictions
RefSeq mRNAs mapped to this assembly
NM_001378183.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
CR1-Y2_Aves
(T)n
(TTTA)n
(T)n
(T)n
CR1-Y2_Aves
A-rich
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust