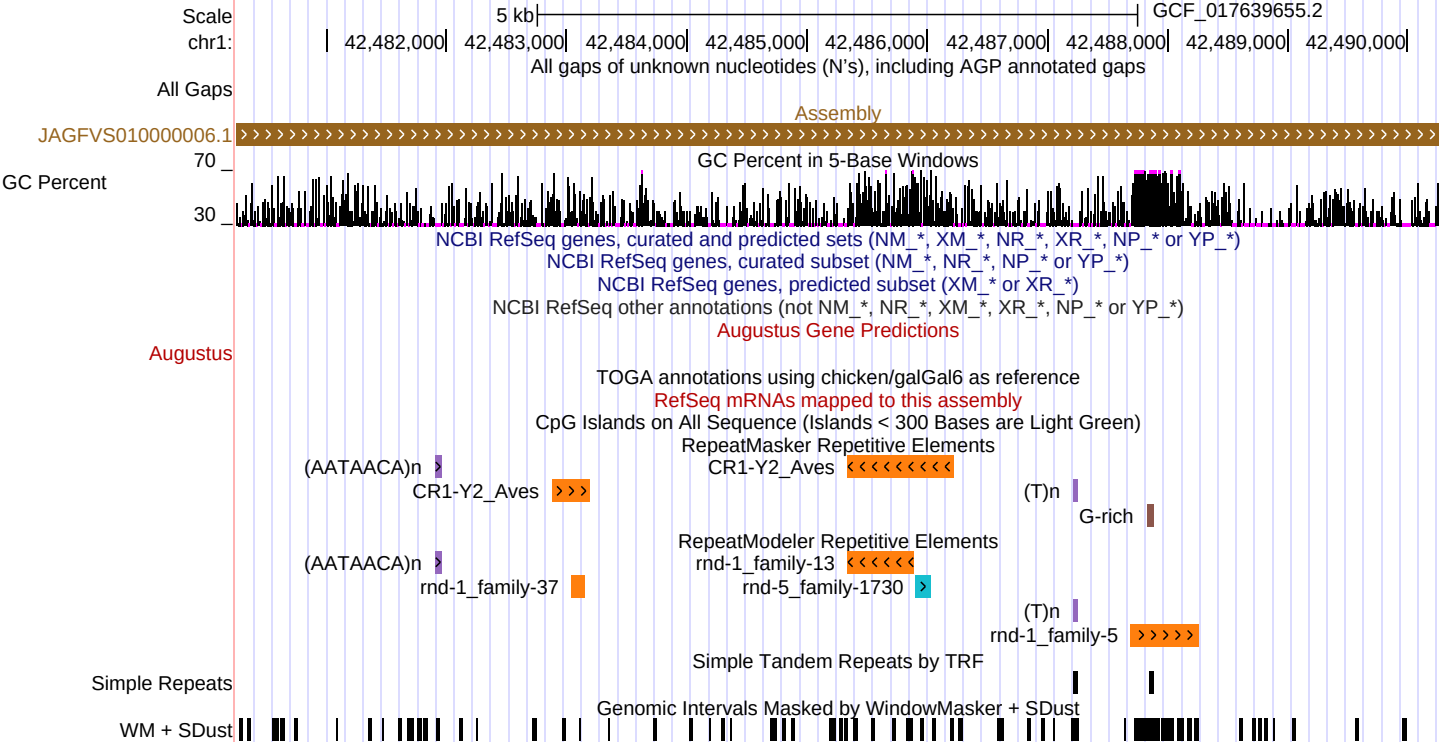
Scale
5 kb
GCF_017639655.2
chr1:
42,482,000
42,483,000
42,484,000
42,485,000
42,486,000
42,487,000
42,488,000
42,489,000
42,490,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAGFVS010000006.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*)
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Augustus Gene Predictions
Augustus
TOGA annotations using chicken/galGal6 as reference
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
(AATAACA)n
CR1-Y2_Aves
CR1-Y2_Aves
(T)n
G-rich
RepeatModeler Repetitive Elements
(AATAACA)n
rnd-1_family-13
rnd-1_family-37
rnd-5_family-1730
(T)n
rnd-1_family-5
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust