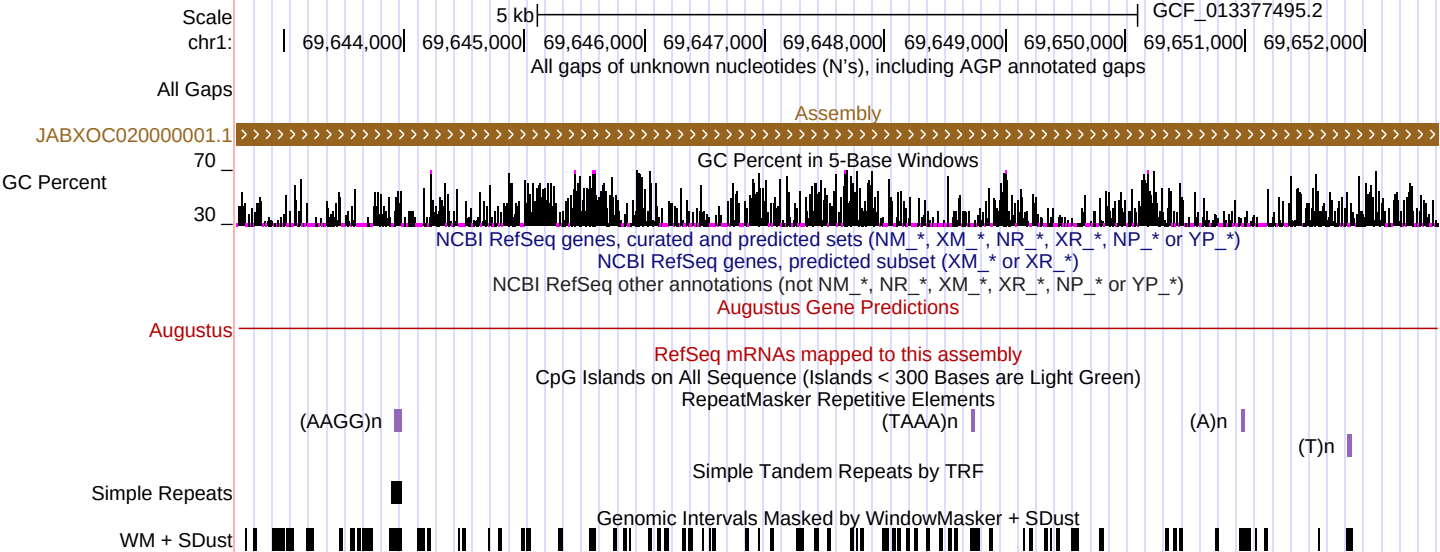
Scale
5 kb
GCF_013377495.2
chr1:
69,644,000
69,645,000
69,646,000
69,647,000
69,648,000
69,649,000
69,650,000
69,651,000
69,652,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JABXOC020000001.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Augustus Gene Predictions
Augustus
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
(AAGG)n
(TAAA)n
(A)n
(T)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust