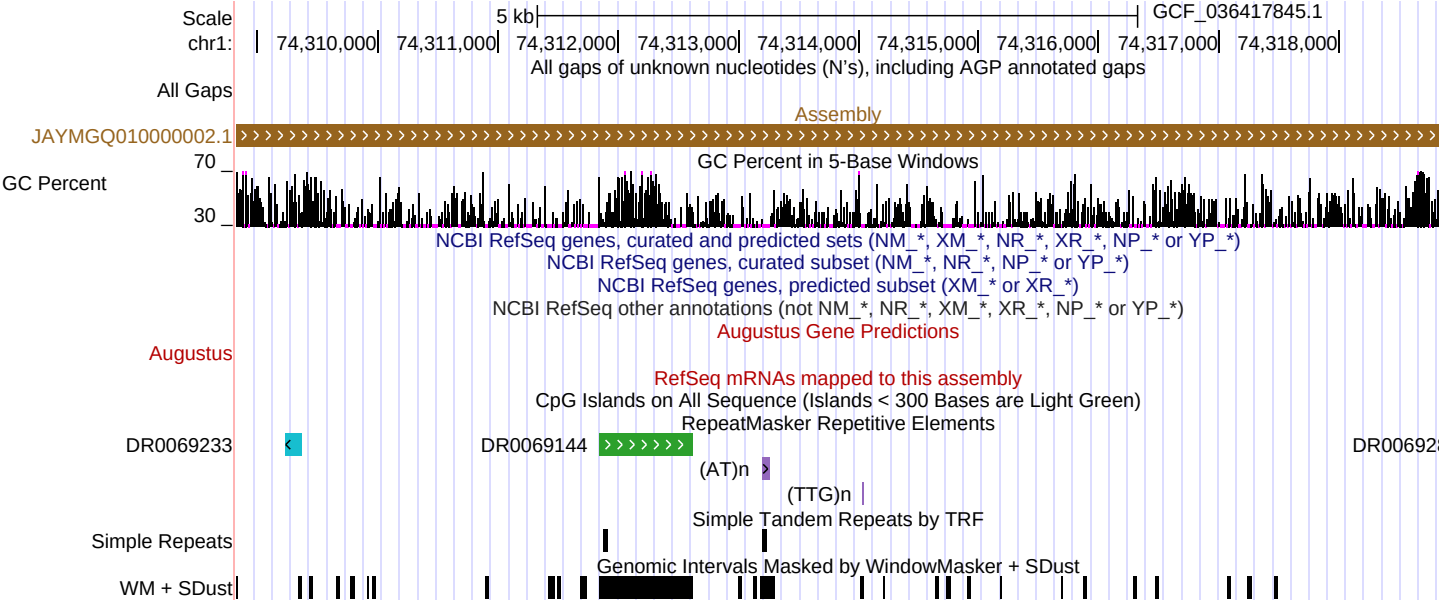
Scale
5 kb
GCF_036417845.1
chr1:
74,310,000
74,311,000
74,312,000
74,313,000
74,314,000
74,315,000
74,316,000
74,317,000
74,318,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAYMGQ010000002.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, 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
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0069233
DR0069144
(AT)n
(TTG)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust