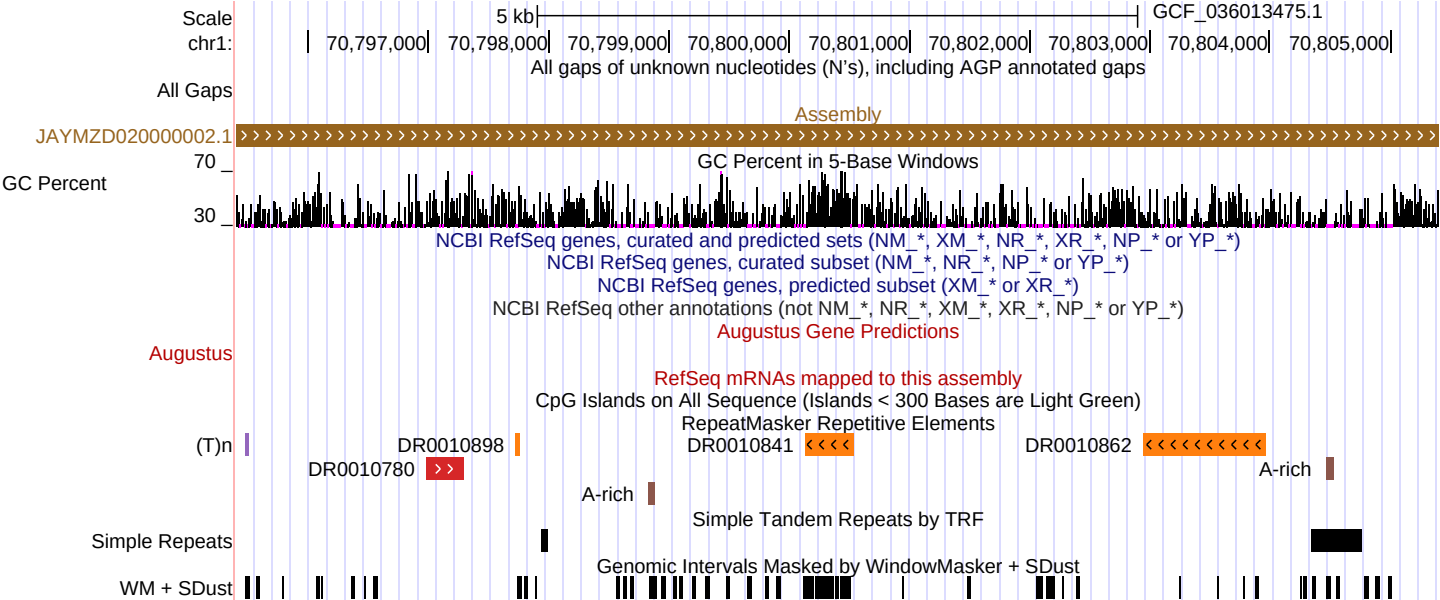
Scale
5 kb
GCF_036013475.1
chr1:
70,797,000
70,798,000
70,799,000
70,800,000
70,801,000
70,802,000
70,803,000
70,804,000
70,805,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAYMZD020000002.1
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, 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
(T)n
DR0010898
DR0010841
DR0010862
DR0010780
A-rich
A-rich
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust