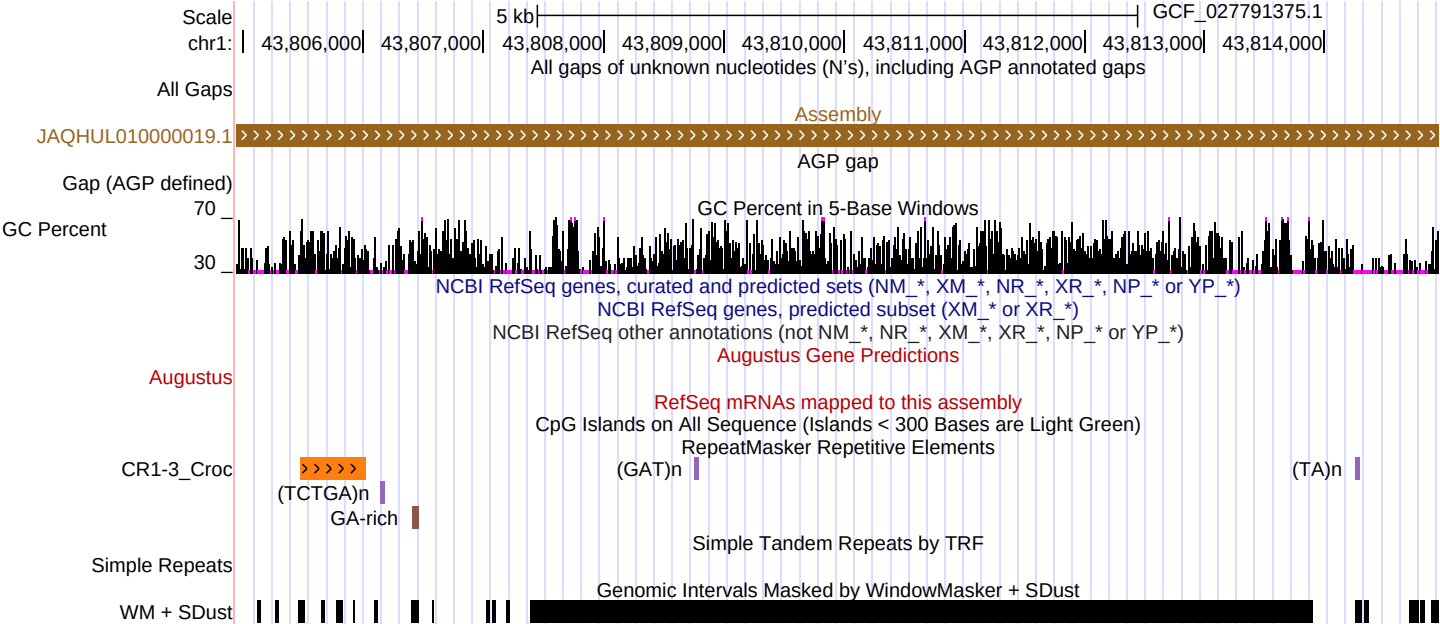
Scale
5 kb
GCF_027791375.1
chr1:
43,806,000
43,807,000
43,808,000
43,809,000
43,810,000
43,811,000
43,812,000
43,813,000
43,814,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAQHUL010000019.1
AGP gap
Gap (AGP defined)
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
NCBI RefSeq genes, 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
CR1-3_Croc
(GAT)n
(TA)n
(TCTGA)n
GA-rich
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust