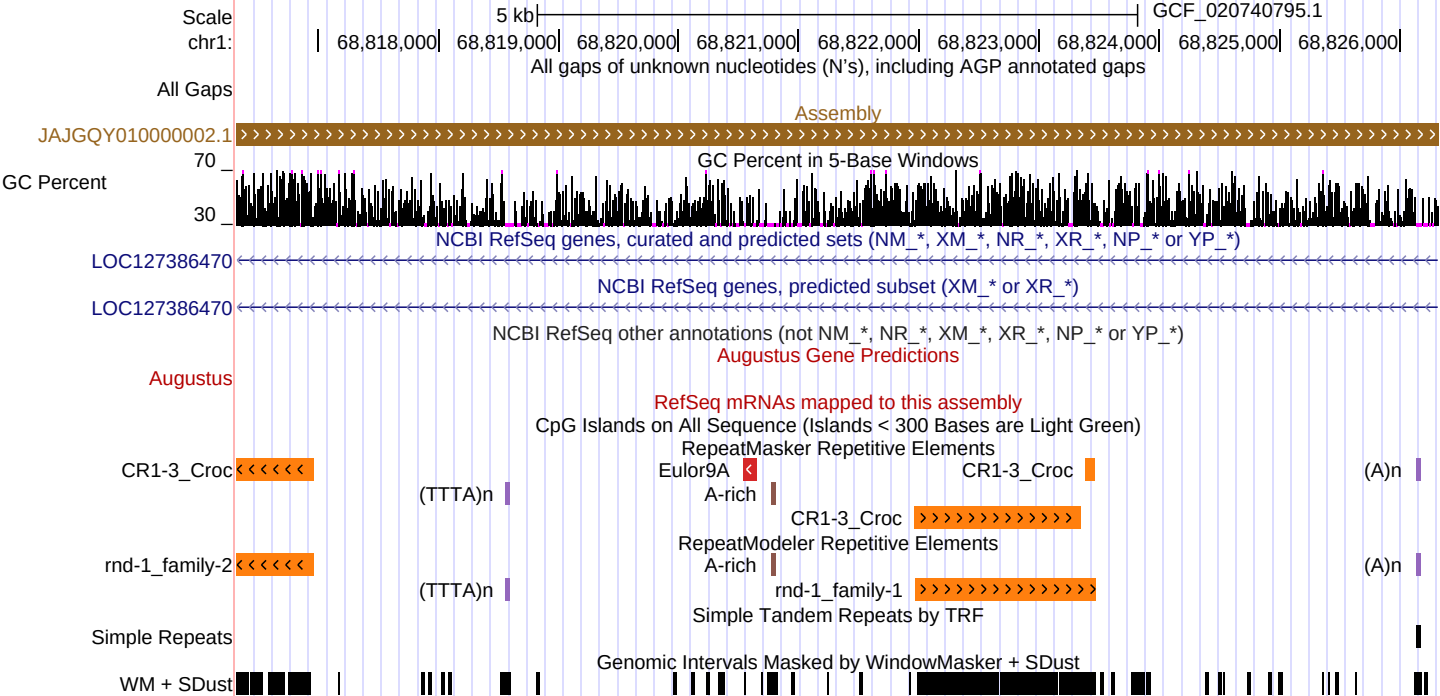
Scale
5 kb
GCF_020740795.1
chr1:
68,818,000
68,819,000
68,820,000
68,821,000
68,822,000
68,823,000
68,824,000
68,825,000
68,826,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAJGQY010000002.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
LOC127386470
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
LOC127386470
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
Eulor9A
CR1-3_Croc
(A)n
(TTTA)n
A-rich
CR1-3_Croc
RepeatModeler Repetitive Elements
rnd-1_family-2
A-rich
(A)n
(TTTA)n
rnd-1_family-1
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust