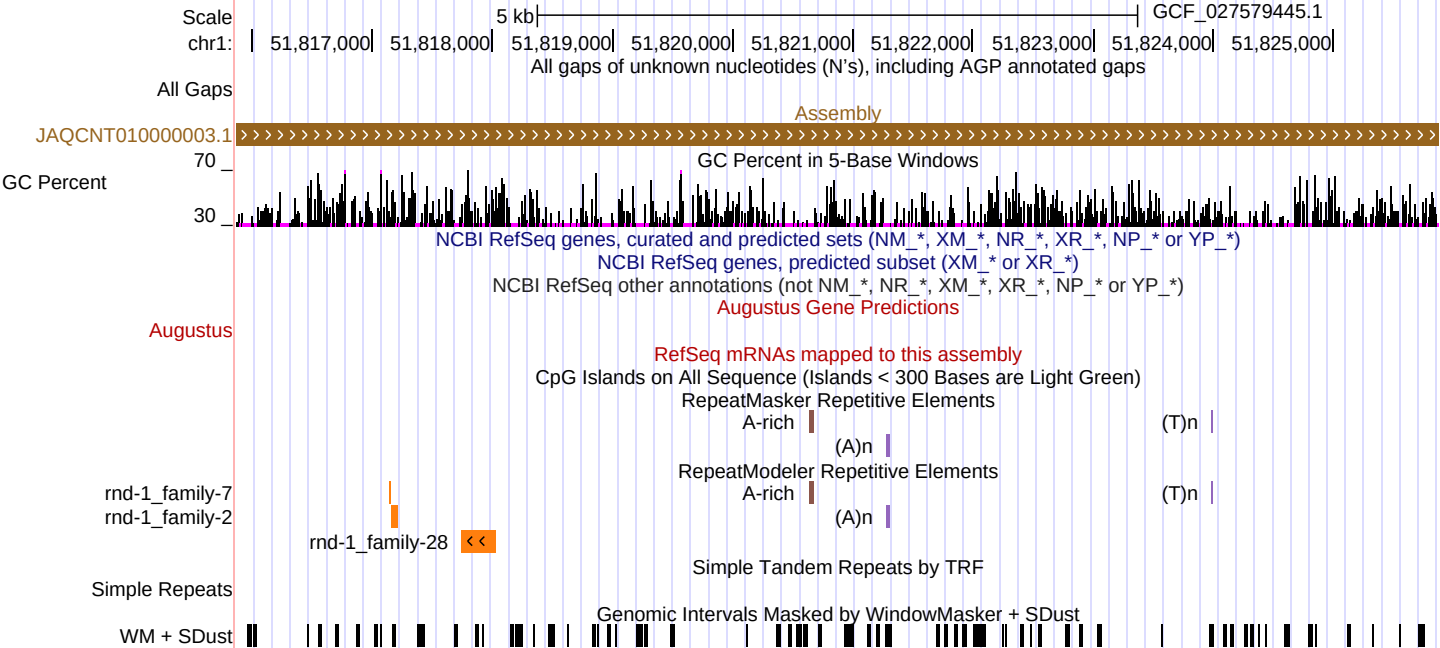
Scale
5 kb
GCF_027579445.1
chr1:
51,817,000
51,818,000
51,819,000
51,820,000
51,821,000
51,822,000
51,823,000
51,824,000
51,825,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAQCNT010000003.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, 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
A-rich
(T)n
(A)n
RepeatModeler Repetitive Elements
rnd-1_family-7
A-rich
(T)n
rnd-1_family-2
(A)n
rnd-1_family-28
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust