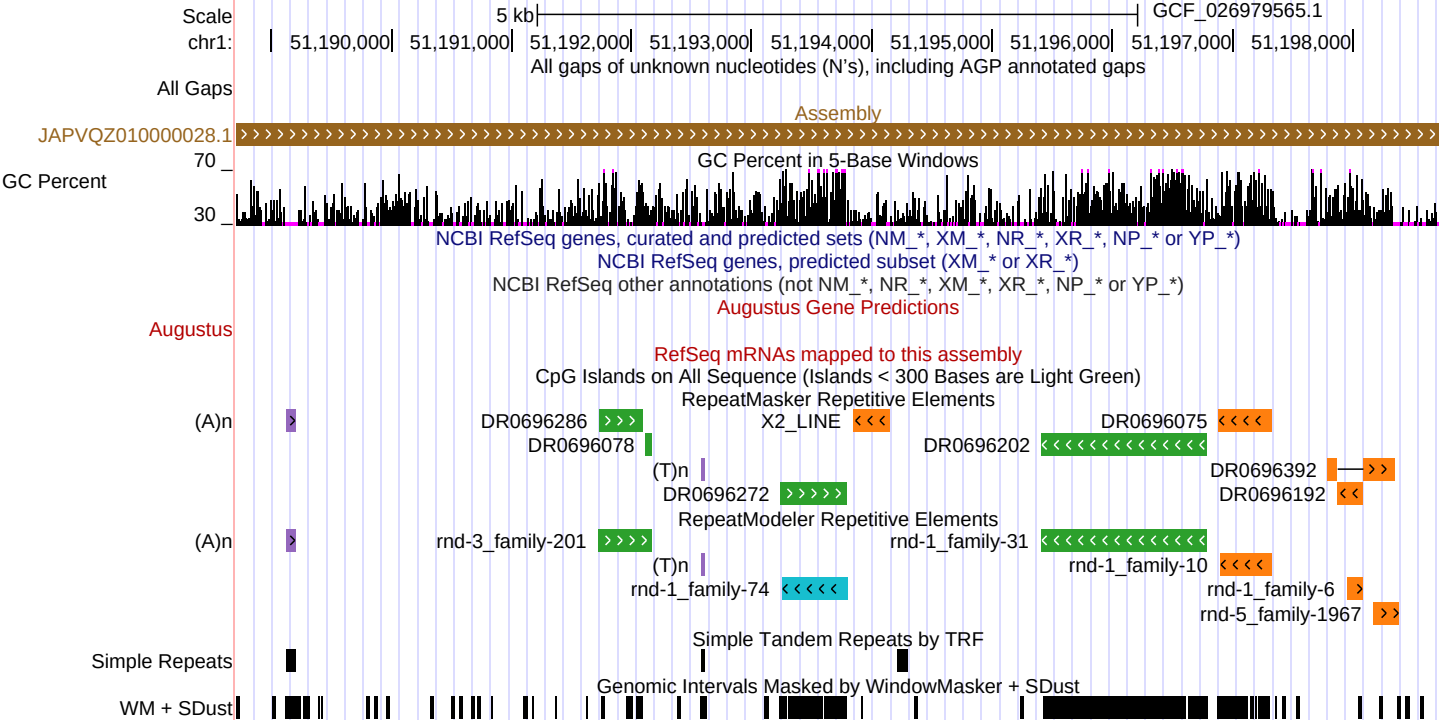
Scale
5 kb
GCF_026979565.1
chr1:
51,190,000
51,191,000
51,192,000
51,193,000
51,194,000
51,195,000
51,196,000
51,197,000
51,198,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAPVQZ010000028.1
70
GC Percent in 5-Base Windows
GC Percent
30
NCBI RefSeq genes, 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
(A)n
DR0696286
X2_LINE
DR0696075
DR0696078
DR0696202
(T)n
DR0696392
DR0696272
DR0696192
RepeatModeler Repetitive Elements
(A)n
rnd-3_family-201
rnd-1_family-31
(T)n
rnd-1_family-10
rnd-1_family-74
rnd-1_family-6
rnd-5_family-1967
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust