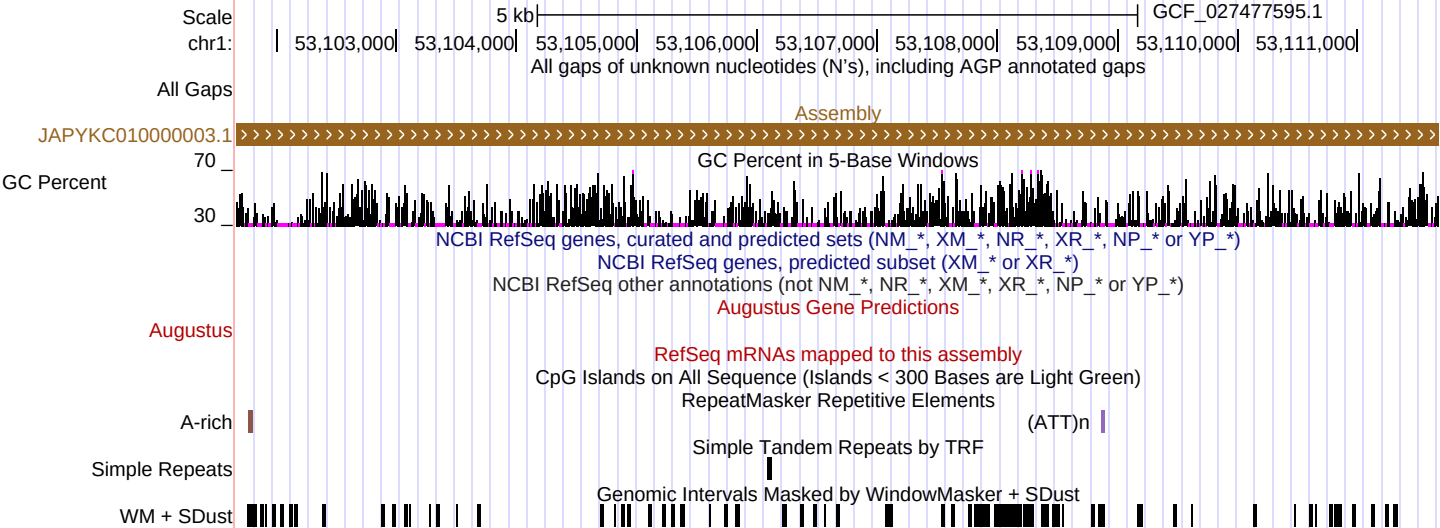
Scale
5 kb
GCF_027477595.1
chr1:
53,103,000
53,104,000
53,105,000
53,106,000
53,107,000
53,108,000
53,109,000
53,110,000
53,111,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAPYKC010000003.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, 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
(ATT)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust