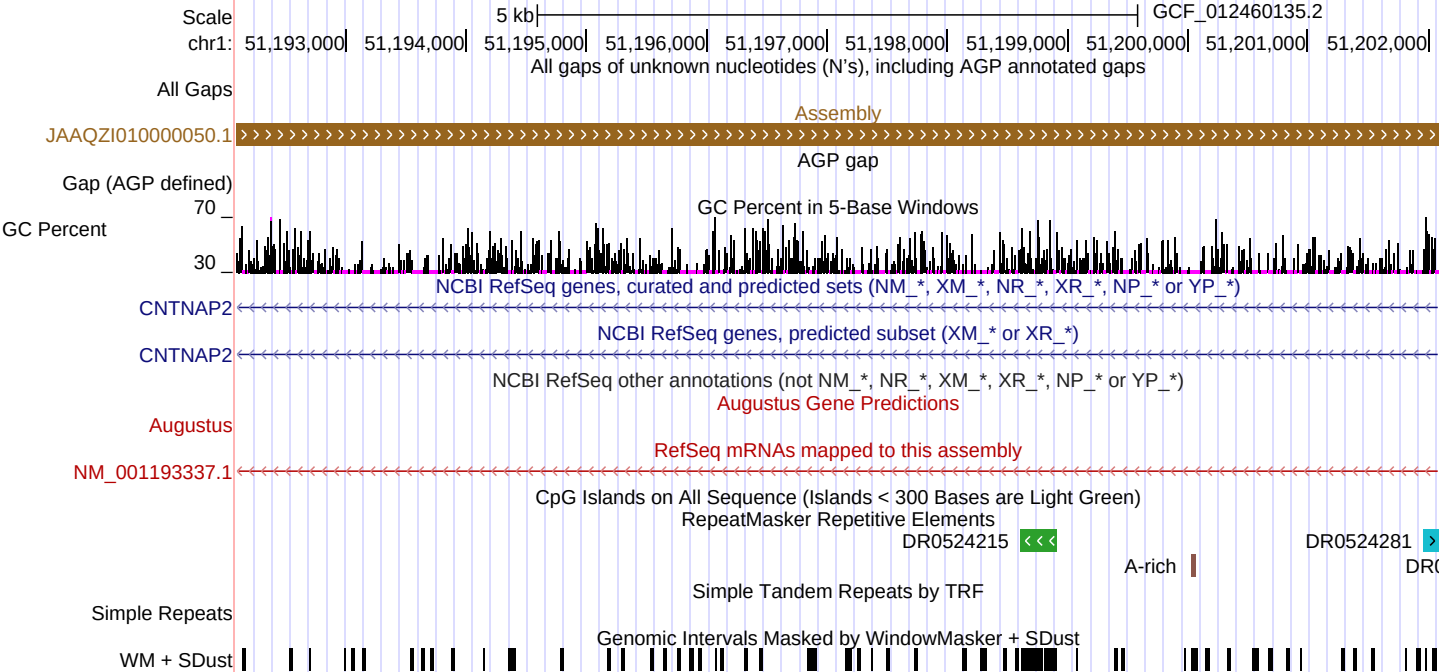
Scale
5 kb
GCF_012460135.2
chr1: 51,193,000 51,194,000 51,195,000 51,196,000 51,197,000 51,198,000 51,199,000 51,200,000 51,201,000 51,202,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JAAQZI010000050.1
AGP gap
Gap (AGP defined)
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
CNTNAP2
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
CNTNAP2
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Augustus Gene Predictions
Augustus
RefSeq mRNAs mapped to this assembly
NM_001193337.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0524215
DR0524281
A-rich
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust