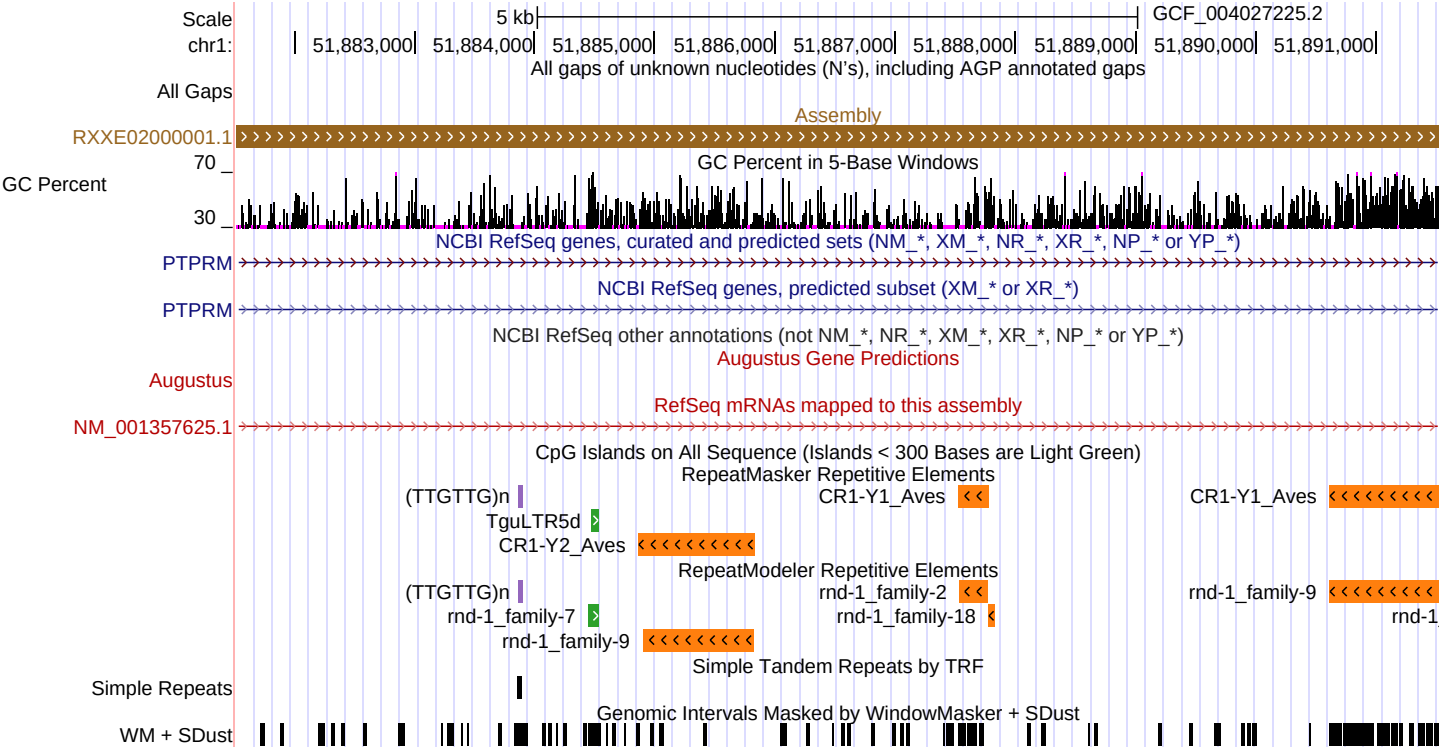
Scale
5 kb
GCF_004027225.2
chr1:
51,883,000
51,884,000
51,885,000
51,886,000
51,887,000
51,888,000
51,889,000
51,890,000
51,891,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
RXXE02000001.1
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
PTPRM
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
PTPRM
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Augustus Gene Predictions
Augustus
RefSeq mRNAs mapped to this assembly
NM_001357625.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
(TTGTTG)n
CR1-Y1_Aves
CR1-Y1_Aves
TguLTR5d
CR1-Y2_Aves
RepeatModeler Repetitive Elements
(TTGTTG)n
rnd-1_family-2
rnd-1_family-9
rnd-1_family-7
rnd-1_family-18
rnd-1
rnd-1_family-9
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust