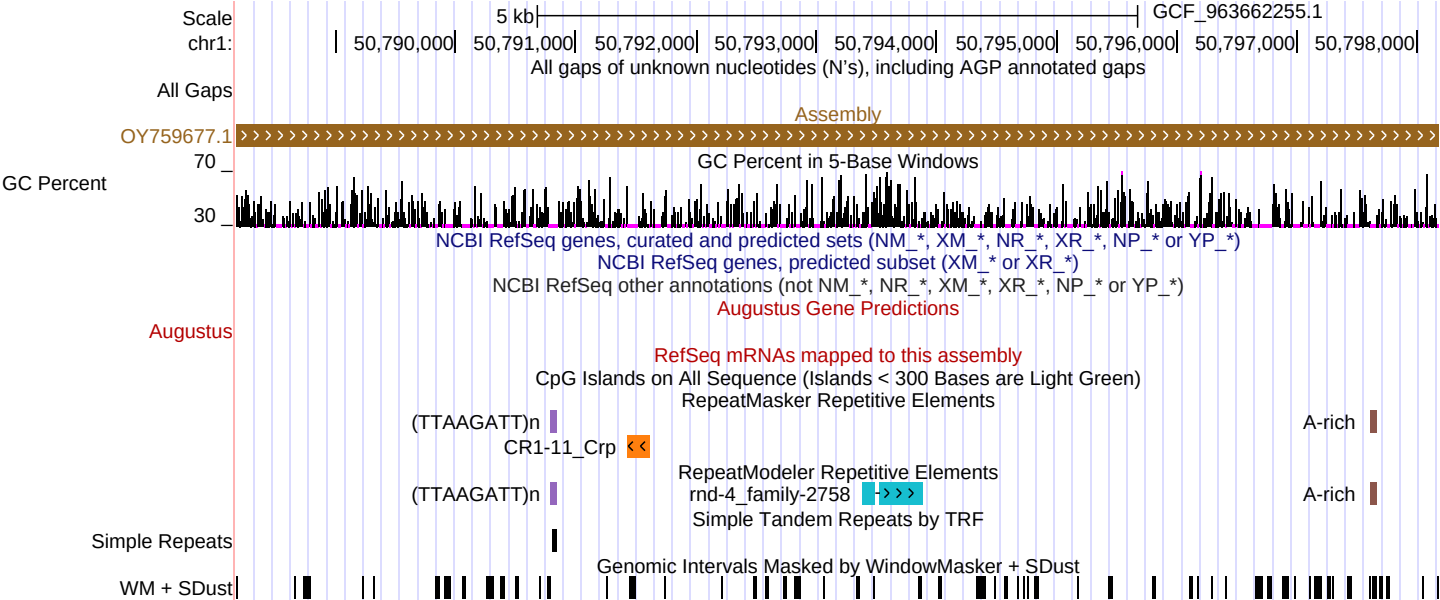
Scale
5 kb
GCF_963662255.1
chr1:
50,790,000
50,791,000
50,792,000
50,793,000
50,794,000
50,795,000
50,796,000
50,797,000
50,798,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
OY759677.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, curated 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
(TTAAGATT)n
A-rich
CR1-11_Crp
RepeatModeler Repetitive Elements
(TTAAGATT)n
rnd-4_family-2758
A-rich
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust