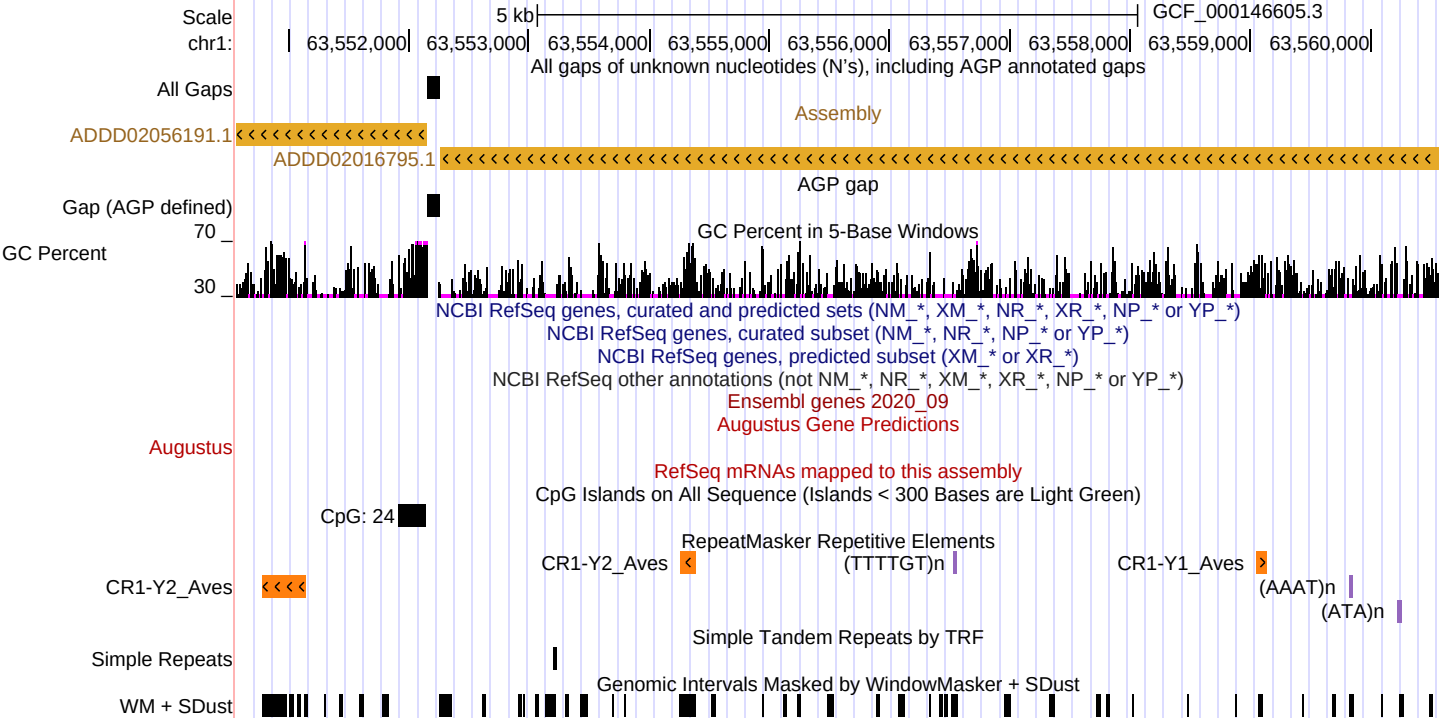
Scale
5 kb
GCF_000146605.3
chr1:
63,552,000
63,553,000
63,554,000
63,555,000
63,556,000
63,557,000
63,558,000
63,559,000
63,560,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
ADDD02056191.1
ADDD02016795.1
AGP gap
Gap (AGP defined)
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*)
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Ensembl genes 2020_09
Augustus Gene Predictions
Augustus
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
CpG: 24
RepeatMasker Repetitive Elements
CR1-Y2_Aves
(TTTTGT)n
CR1-Y1_Aves
CR1-Y2_Aves
(AAAT)n
(ATA)n
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust