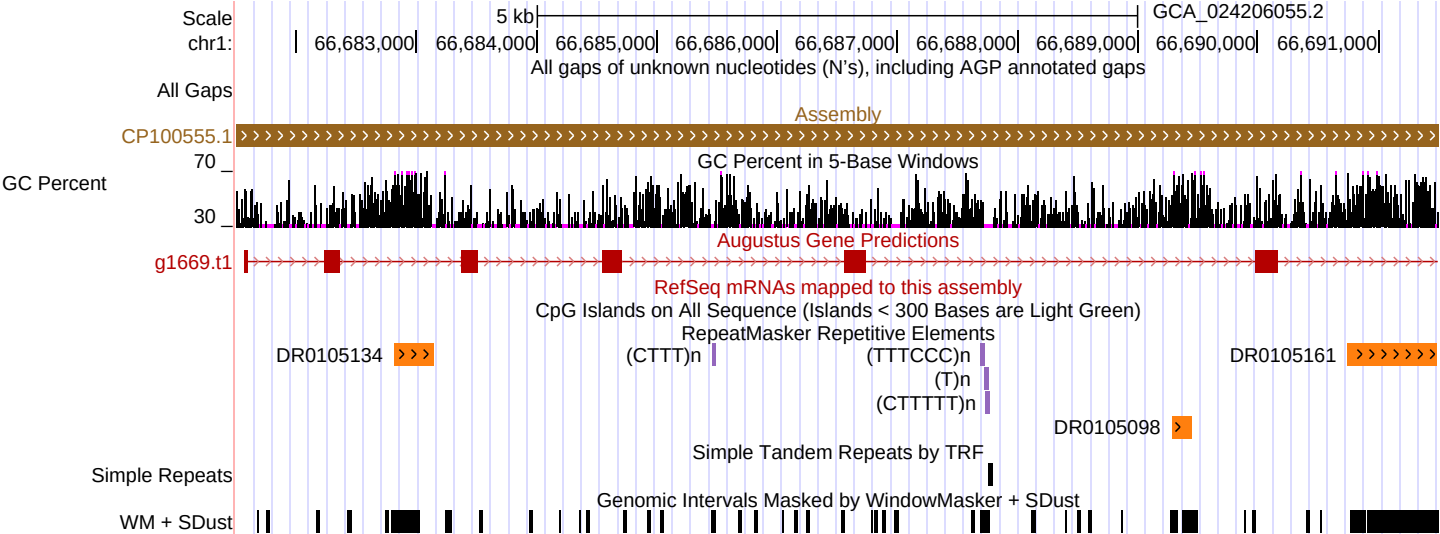
Scale
5 kb
GCA_024206055.2
chr1:
66,683,000
66,684,000
66,685,000
66,686,000
66,687,000
66,688,000
66,689,000
66,690,000
66,691,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
CP100555.1
70
GC Percent
30
GC Percent in 5-Base Windows
Augustus Gene Predictions
g1669.t1
RefSeq mRNAs mapped to this assembly
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0105134
(CTTT)n
(TTTCCC)n
(T)n
(CTTTTT)n
DR0105161
DR0105098
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust