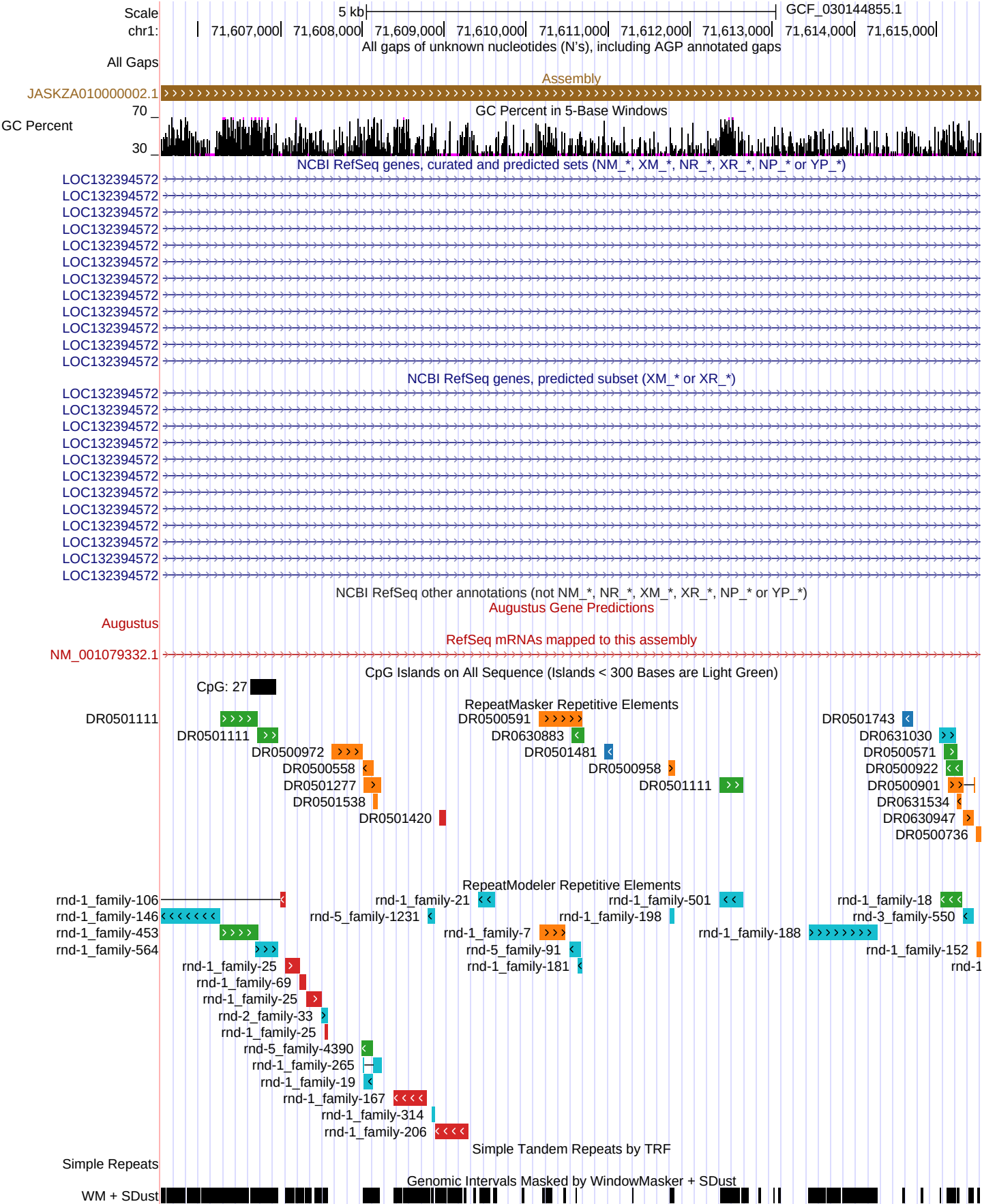
Scale
5 kb
GCF_030144855.1
chr1:
71,607,000
71,608,000
71,609,000
71,610,000
71,611,000
71,612,000
71,613,000
71,614,000
71,615,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JASKZA010000002.1
GC Percent in 5-Base Windows
70
GC Percent
30
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
LOC132394572
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
NM_001079332.1
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
CpG: 27
RepeatMasker Repetitive Elements
DR0501111
DR0500591
DR0501743
DR0630883
DR0631030
DR0500972
DR0501481
DR0500571
DR0500558
DR0500958
DR0500922
DR0501277
DR0501111
DR0500901
DR0501538
DR0631534
DR0501420
DR0630947
DR0500736
RepeatModeler Repetitive Elements
rnd-1_family-106
rnd-1_family-21
rnd-1_family-501
rnd-1_family-18
rnd-1_family-146
rnd-5_family-1231
rnd-1_family-198
rnd-3_family-550
rnd-1_family-453
rnd-1_family-7
rnd-1_family-188
rnd-1_family-564
rnd-5_family-91
rnd-1_family-152
rnd-1_family-25
rnd-1_family-181
rnd-1_family-69
rnd-1_family-25
rnd-2_family-33
rnd-1_family-25
rnd-5_family-4390
rnd-1_family-265
rnd-1_family-19
rnd-1_family-167
rnd-1_family-314
rnd-1_family-206
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust