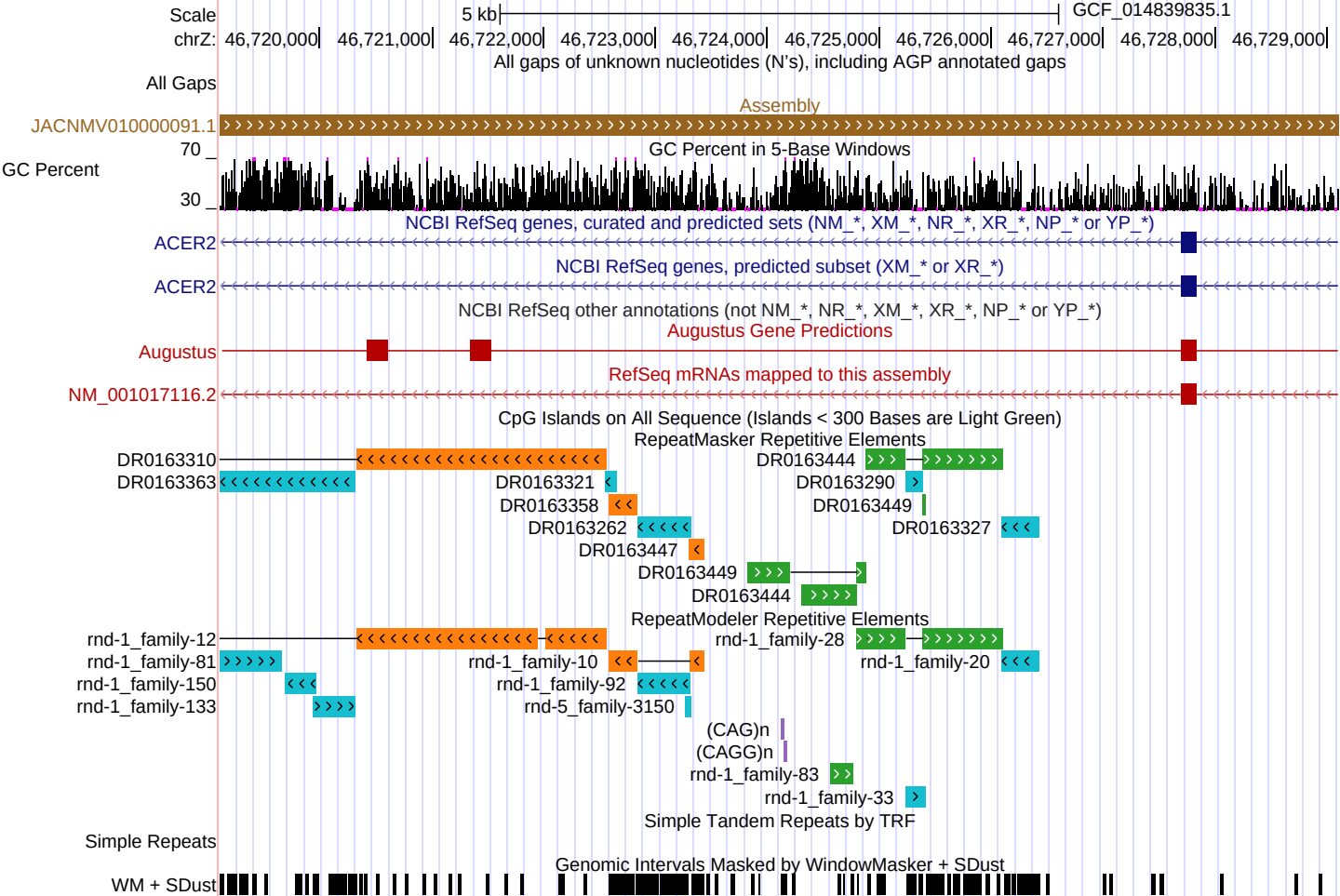
Scale
5 kb
GCF_014839835.1
chrZ: 46,720,000 46,721,000 46,722,000 46,723,000 46,724,000 46,725,000 46,726,000 46,727,000 46,728,000 46,729,000
All gaps of unknown nucleotides (N's), including AGP annotated gaps
All Gaps
Assembly
JACNMV010000091.1
70
GC Percent
30
GC Percent in 5-Base Windows
NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)
ACER2
NCBI RefSeq genes, predicted subset (XM_* or XR_*)
ACER2
NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)
Augustus Gene Predictions
Augustus
RefSeq mRNAs mapped to this assembly
NM_001017116.2
CpG Islands on All Sequence (Islands < 300 Bases are Light Green)
RepeatMasker Repetitive Elements
DR0163310
DR0163363
DR0163444
DR0163321
DR0163290
DR0163358
DR0163449
DR0163262
DR0163327
DR0163447
DR0163449
DR0163444
RepeatModeler Repetitive Elements
rnd-1_family-12
rnd-1_family-28
rnd-1_family-81
rnd-1_family-10
rnd-1_family-20
rnd-1_family-150
rnd-1_family-92
rnd-1_family-133
rnd-5_family-3150
(CAG)n
(CAGG)n
rnd-1_family-83
rnd-1_family-33
Simple Tandem Repeats by TRF
Simple Repeats
Genomic Intervals Masked by WindowMasker + SDust
WM + SDust