

5 kb

GCF_003254395.2

Scale

chrLG1:

9,252,000|9,252,500|9,253,000|9,253,500|9,254,000|9,254,500|9,255,000|9,255,500|9,256,000|9,256,500|9,257,000|9,257,500|9,258,000|9,258,500|9,259,000|9,259,500|9,260,000|9,260,500|9,261,000

GC Percent in 5-Base Windows

GC Percent

LOC409927

LOC409927

LOC409927

LOC409927

Augustus

Unmasked CpG

Simple Repeats

WM + SDust

NCBI RefSeq genes, curated and predicted sets (NM_*, XM_*, NR_*, XR_*, NP_* or YP_*)

LOC409926

LOC551728

LOC551728

NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*)

NCBI RefSeq genes, predicted subset (XM_* or XR_*)

LOC409926

LOC551728

LOC551728

NCBI RefSeq other annotations (not NM_*, NR_*, XM_*, XR_*, NP_* or YP_*)

Augustus Gene Predictions

RefSeq mRNAs mapped to this assembly

CpG Islands (Islands < 300 Bases are Light Green)

RepeatMasker Repetitive Elements

(ATTTA)n

(ATTATAA)n

(TA)n

(AT)n

A-rich

(GAAT)n

(AT)n

A-rich

Simple Tandem Repeats by TRF

Genomic Intervals Masked by WindowMasker + SDust