

Scale

5 kb

GCF_028858705.1

chr1: | 73,291,000| 73,292,000| 73,293,000| 73,294,000| 73,295,000| 73,296,000| 73,297,000| 73,298,000| 73,299,000|

All gaps of unknown nucleotides (N's), including AGP annotated gaps

All Gaps

Assembly

JARBUS010000001.1

70

GC Percent in 5-Base Windows

GC Percent

30

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

LOC129206131
LOC129206131
LOC129206131

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

LOC129206131
LOC129206131
LOC129206131

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

Augustus Gene Predictions

Augustus

RefSeq mRNAs mapped to this assembly

CpG Islands on All Sequence (Islands < 300 Bases are Light Green)

RepeatMasker Repetitive Elements

Chompy-6_Croc <<

DR0462169 <<<<<<

RepeatModeler Repetitive Elements

rnd-1_family-2 <<<<<<

Simple Tandem Repeats by TRF

Simple Repeats

Genomic Intervals Masked by WindowMasker + SDust

WM + SDust

