

Scale chr1: | 64,971,000 | 64,972,000 | 64,973,000 | 64,974,000 | 64,975,000 | 64,976,000 | 64,977,000 | 64,978,000 | 64,979,000 | GCF_023343835.1
All gaps of unknown nucleotides (N's), including AGP annotated gaps

All Gaps

Assembly

JAMCCT010000006.1

70

GC Percent in 5-Base Windows

30

GC Percent

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

SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5

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

SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5
SOX5

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

Augustus

Augustus Gene Predictions

RefSeq mRNAs mapped to this assembly

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

RepeatMasker Repetitive Elements

(A)n

(A)n

RepeatModeler Repetitive Elements

(A)n

rnd-5_family-10136 >>

rnd-1_family-4 >>>

rnd-1_family-49 <<<

rnd-1_family-60 >>

rnd-3_family-347 <

rnd-1_family-58 >

rnd-1_family-42 >>>>

rnd-1_family-4 |

Simple Tandem Repeats by TRF

Simple Repeats

Genomic Intervals Masked by WindowMasker + SDust

WM + SDust