

GENSCAN predicted genes in sequence contig3

0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 kb



10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 kb



20.0 21.0 22.0 23.0 24.0 25.0 26.0 27.0 28.0 29.0 30.0 kb



30.0 31.0 32.0 33.0 34.0 35.0 36.0 37.0 38.0 39.0 40.0 kb



Key:



Initial
exon



Internal
exon



Terminal
exon



Single-exon
gene



Optimal exon



Suboptimal exon