

GENSCAN predicted genes in sequence contig21

0.0 2.0 4.0 6.0 8.0 10.0 12.0 14.0 16.0 18.0 20.0 kb



20.0 22.0 24.0 26.0 28.0 30.0 32.0 34.0 36.0 38.0 40.0 kb



40.0 42.0 44.0 46.0 48.0 50 kb



Key:

Initial
exon

Internal
exon

Terminal
exon

Single-exon
gene

Optimal exon
Suboptimal exon