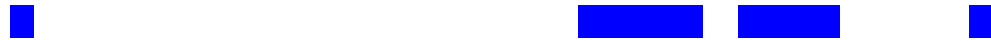


GENSCAN predicted genes in sequence contig33

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 kb

Key:



Initial
exon



Internal
exon



Terminal
exon



Single-exon
gene



Optimal exon
Suboptimal exon