



Figure 16. Organization of Centromere 7 Region of *N. crassa*

Contigs 249, 255, and 21 of genomic sequence release 7.0 (http://www.broad.mit.edu/annotation/fungi/neurospora_crassa_7/index.html), and all except the first 400 kb of sequence contig 10, were assembled, and the combined sequence file was analyzed in 200-bp increments for the "RIP indices" (TpA/ApT [blue] and CpA+TpG/ApC+GpT [red]) (Galagan et al. 2003; Selker et al. 2003; Galagan and Selker 2004). An ~360-kb region with a high density of transposable elements (TE) inactivated by RIP (retrotransposon relics in blue; DNA transposon relic in violet) was found between markers flanking the centromere, which was mapped genetically. The ~1.5-Mb segment shown includes 383 annotated genes (above and below line to indicate genes in opposite orientations), of which only 20 short predicted genes are within the predicted centromere region. The sizes of sequence gaps between the contigs (positions 0.5466, 0.6956, and 0.9058 Mb in the figure) are unknown.