Table S2. Forty-three Regions from *Cen8* that Matched Active Genes[a] Elsewhere in the Genome

Category	**Total Regions**	**Deterioration**[b]
Intergenic	15[c]	13[c]
Active gene[a], exon	17	1
Best match	12	0
Not best match	5	1
Active gene[a], intron	2	2
Inactive gene, exon	6	6
Non-coding	3	3
Total	43[c]	25[c]

[a] Active genes are either supported by ESTs/cDNAs or were verified by RT-PCR.

[b] Deterioration: the presence of premature stop codon, frame shift, or truncation of CDS.

[c] Three of these regions were in the CENH3 subdomains.