

Figure S3 (part 1 of 2)



Figure S3 (part 2 of 2)

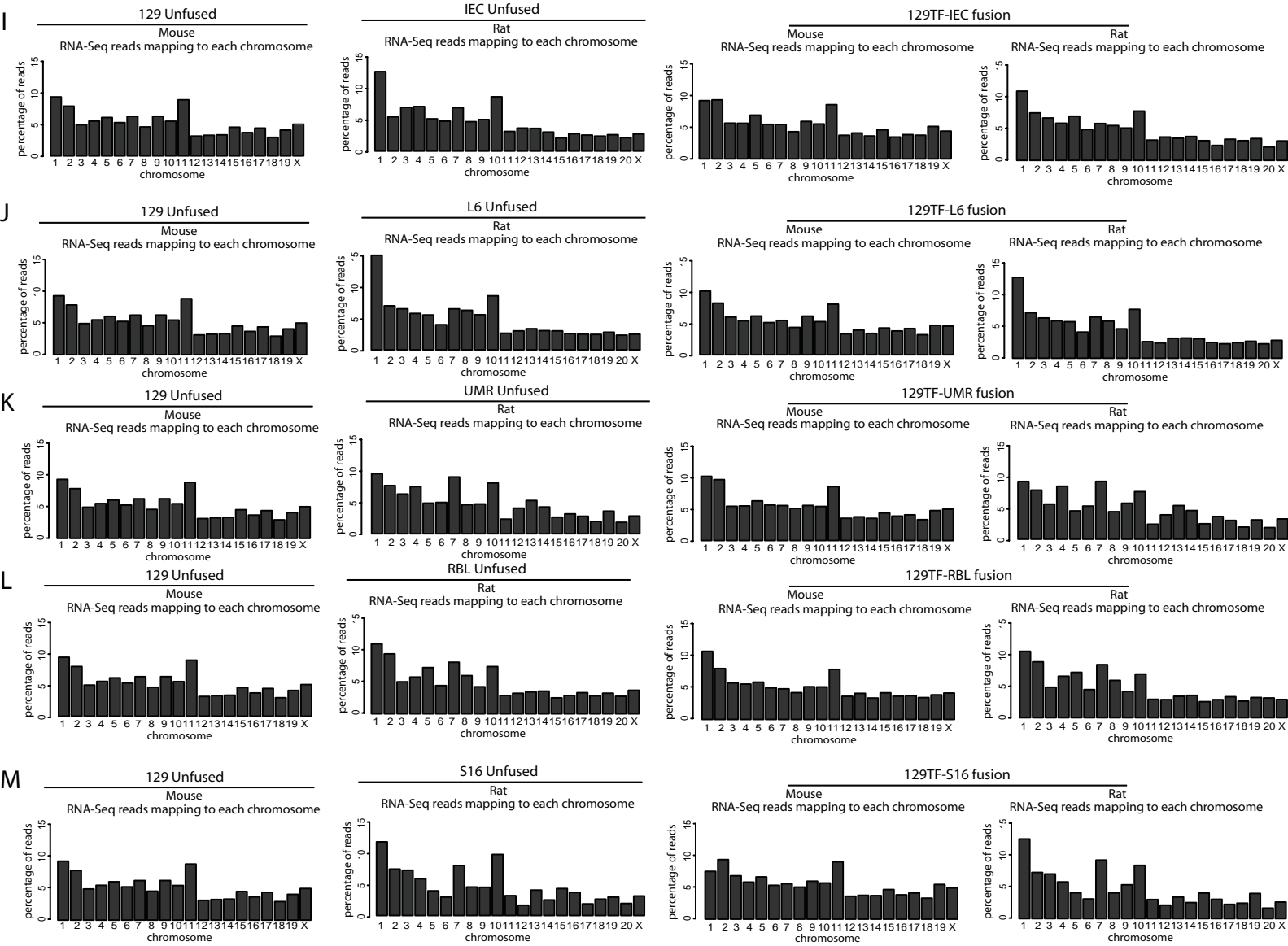


Figure S3. Bioinformatic chromosome loss analysis showing that the identification of occluded genes is not an artifact of chromosome loss in fused cells. Graphs were generated by mapping RNA-seq reads to a reference library consisting of the combined mouse-rat genomes. The proportion of these reads mapping to each chromosome was then tallied and displayed as a bar plot. Data from unfused parental cells are presented as a control. All fusion cells contain the full complement of chromosomes from each genome, and the proportion of reads mapping to each chromosome is generally comparable to that of the unfused parental cells. These data indicate that there is no complete loss of a chromosome in any of the fusion samples.