



FIGURE S5.—Transcription Start Site Analyses using data from CAGE experiments. For tag clusters with number of tags > 100, Carninci et al. (2006) found that the distribution of the number of tags in a cluster falls into 4 broad categories (Broad [BR], Single dominant peak [SP], Bi- or Multi-modal [MU], and Broad Dominant Peak [PB]). We overlapped these different classes of TSSs on to the three different classes of promoters (LSCGI, NCGI, and SCGI). Within each promoter class (LCGI, SCGI, NCGI), we found the proportion of TSSs that belonged to each TSS class (BR, SP, MU, PB) in the human (Figure S5A) and the mouse (Figure S5B) genomes, respectively.