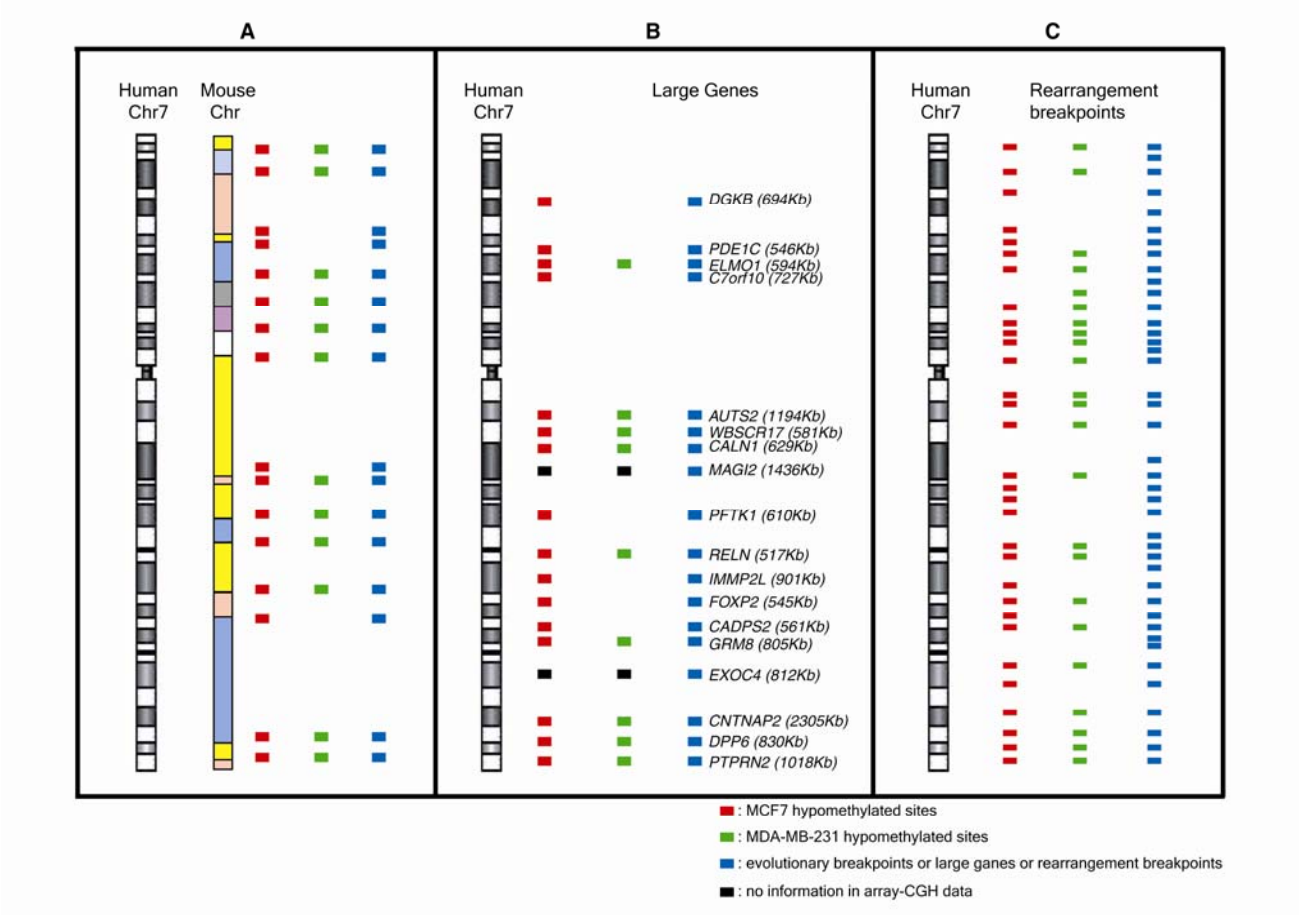
Supplemental Figure 3.



Supplemental Figure 3. Megabase-size hypomethylated zones in tumor cell lines associate with large genes, evolutionary breakpoints and chromosomal rearrangement breakpoints in chromosome 7. (A) 100% and 75% evolutionary breakpoints in chromosome 7 were hypomethylation in MCF-7 and MDA-MB-231 respectively. (B) hypomethylated zones were association with large genes. (C) 78% and 65% rearrangement breakpoints were in hypomethylated zone in MCF7 and MDA-MB-231 respectively. Red and green short lines represent hypomethylated zones in MCF-7 and MDA-MB-231. Blue short lines represent all evolutionary and rearrangement breakpoints in chromosome 7 and black short lines mean that there's no information in the 53,728 *Tsp*RI fragments containing *Hpa*II sites in array-CGH. The information of evolutionary, rearrangement breakpoints and large genes are according to the literature, Scherer, 2003, Science 300: 767-772.