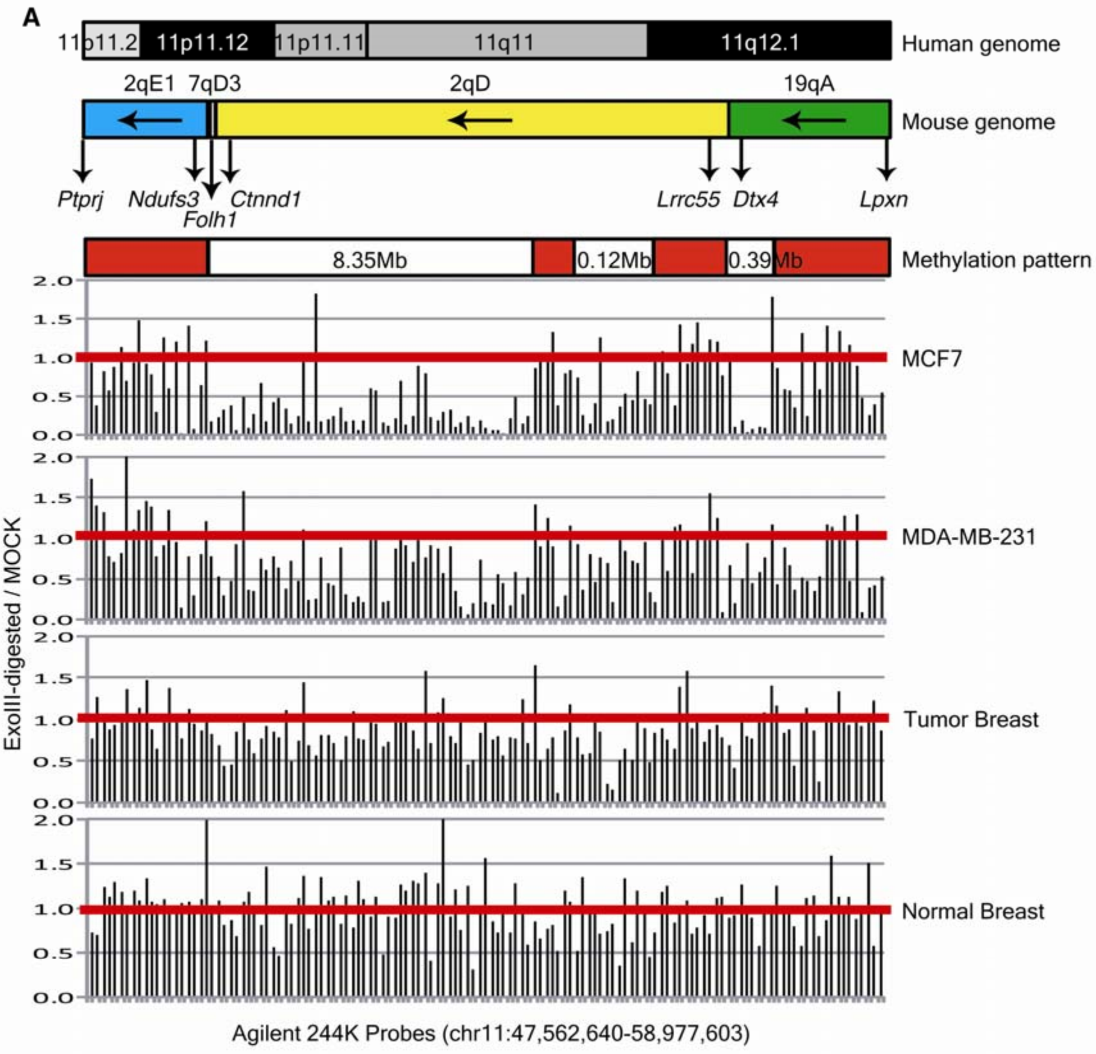
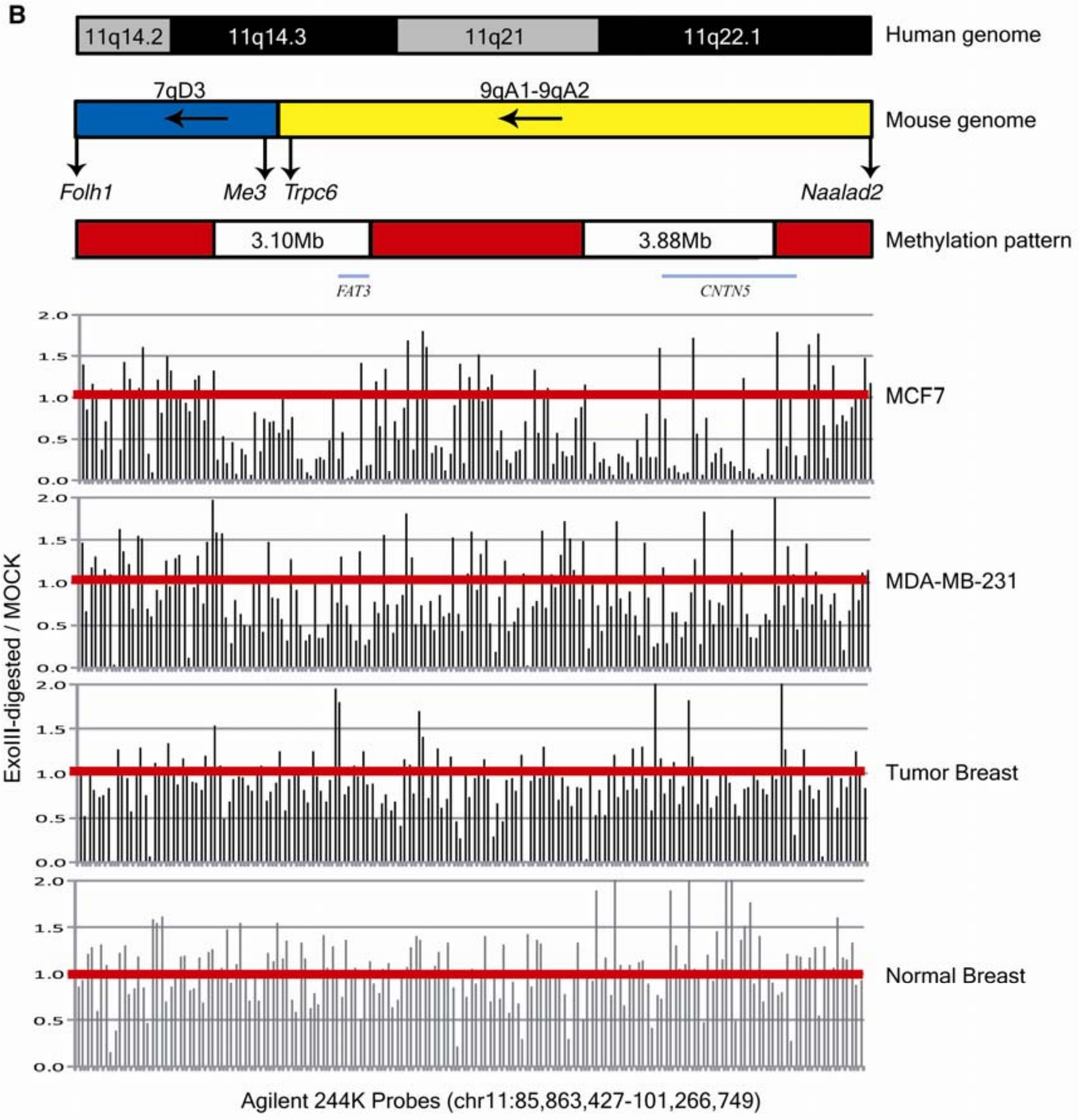
Supplemental Figure 5.



B
11q14.2
11q14.3
11q21
11q22.1
Human genome
7qD3
9qA1-9qA2
Mouse genome
Folh1
Me3
Trpc6
Naalad2
3.10Mb
3.88Mb
Methylation pattern
FAT3
CNTN5
ExoIII-digested / MOCK
2.0
1.5
1.0
0.5
0.0
MCF7
MDA-MB-231
Tumor Breast
Normal Breast
Agilent 244K Probes (chr11:85,863,427-101,266,749)

Supplemental Figure 5. Megabase-size hypomethylation zones which contain clusters of tissue-specific genes in tumor cells. (A) The hypomethylated regions in 11p11-q11 are found in the genomes of MCF-7($P < 0.01$, Fisher's exact test), MDA-MB-231 ($P < 0.01$, Fisher's exact test) and less prominently in primary breast tumor as compared with normal breast genome. (B) The hypomethylated regions in 11q14.2-22.1 are found in the genomes of MCF-7 ($P < 0.01$, Fisher's exact test), and less prominently in MDA-MB-231 and primary breast tumor as compared with normal breast genome. The red horizontal line represents ratio of 1 between signals of exoIII digested and mock digested DNA.