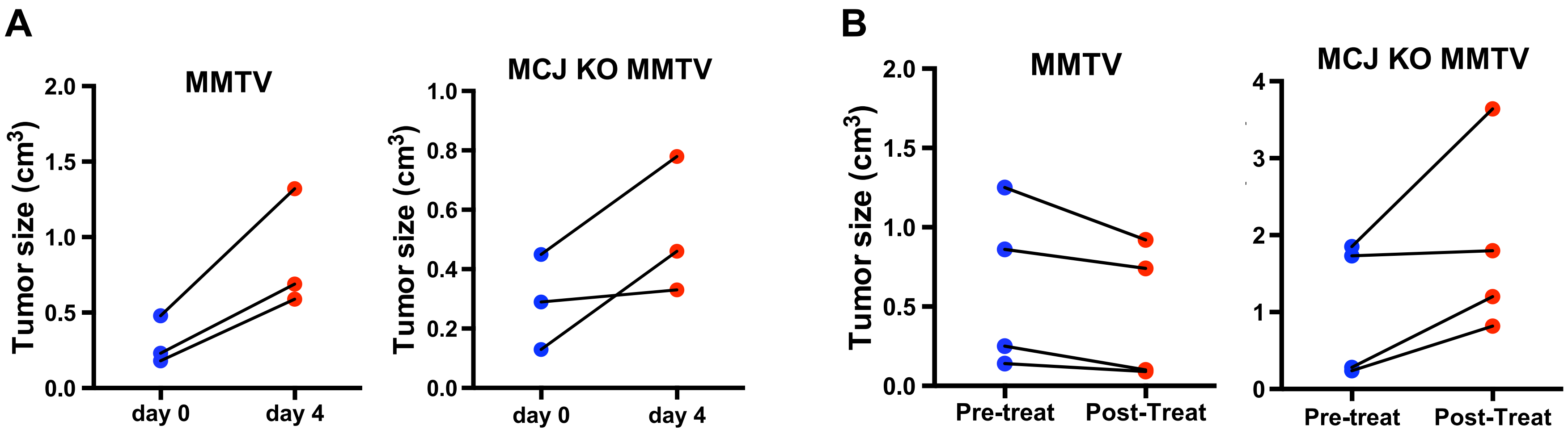
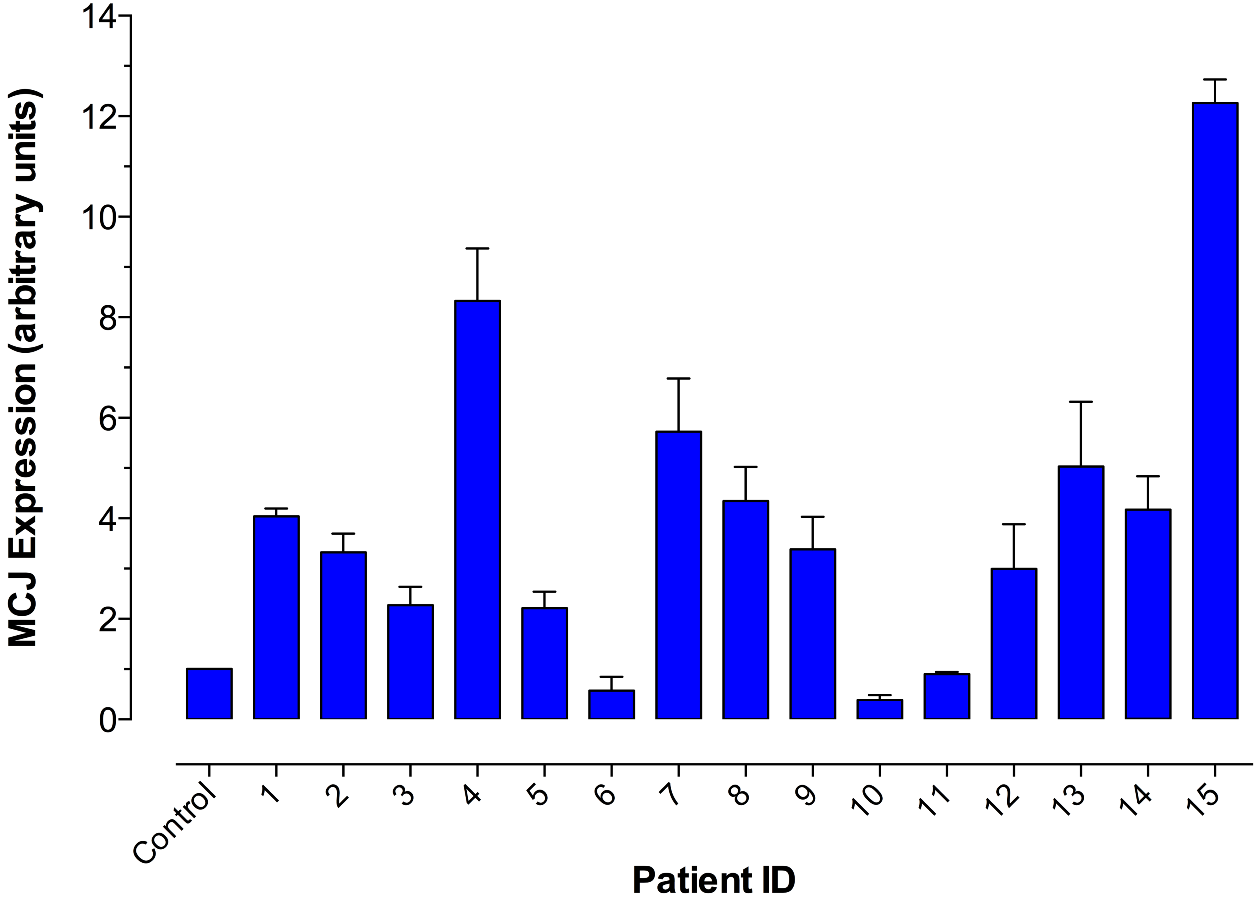
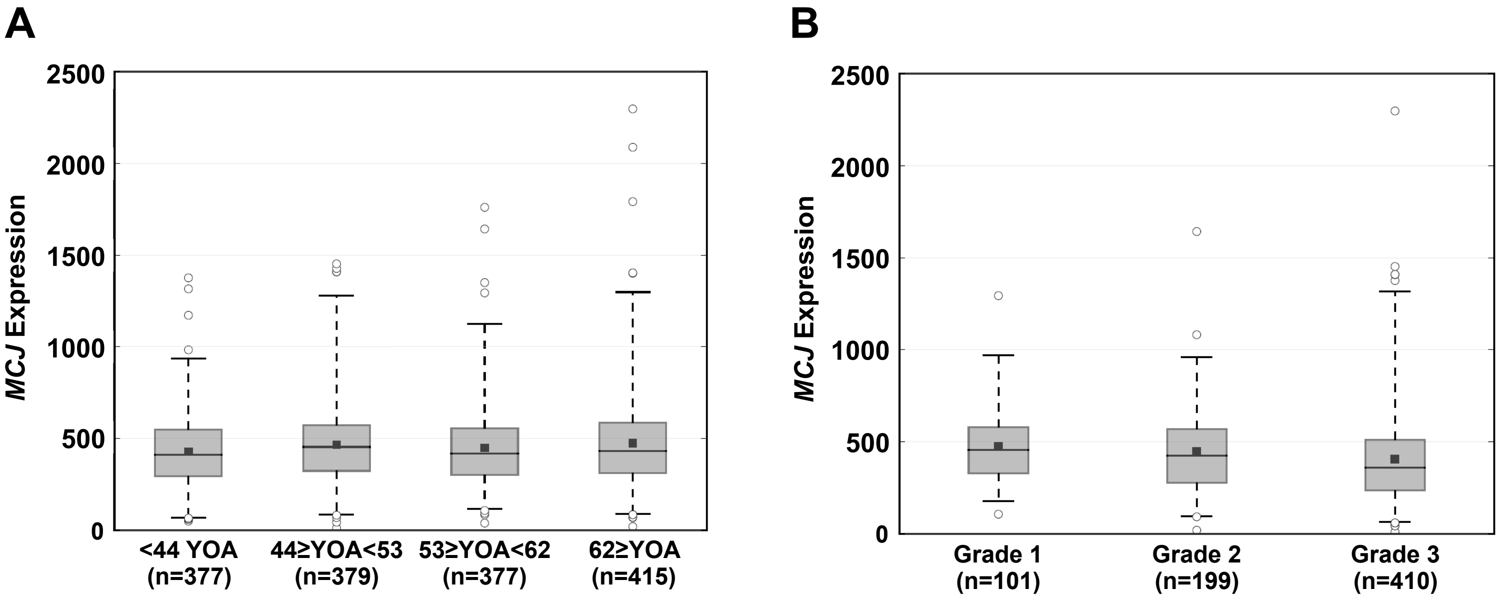
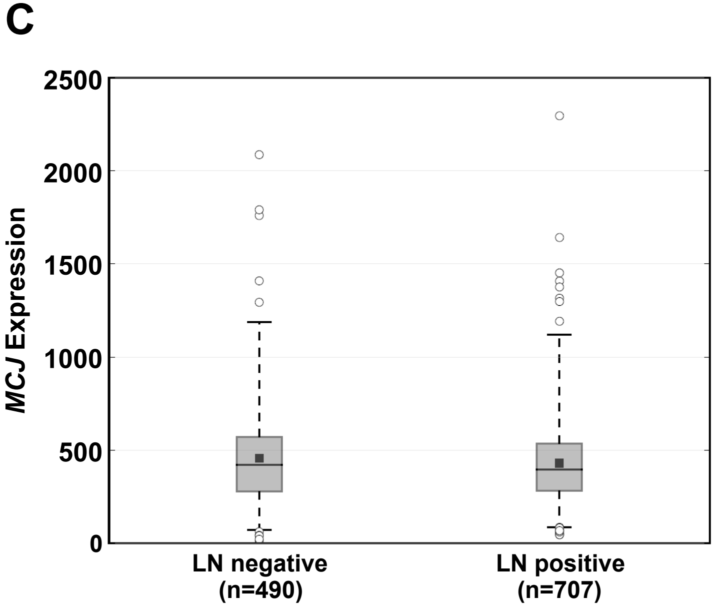


Supplementary Figure S1. Mammary tumor growth in MMTV and MCJ KO MMTV mice. (**A**) Mammary tumor size in individual MMTV mice and MCJ KO MMTV mice that were untreated and followed for four days. There was no significant difference between the two genotypes in the rate of tumor growth calculated as a percentage of size increase (d4 relative to d0, n=3, p=0.3 by unpaired *t* test). (**B**) Individual mammary tumor size in MMTV and MCJ KO MMTV mice shown in Fig. 1E, pre-treatment (pre-treat) and after treatment with doxorubicin (post-treat) for two weeks (n=4).

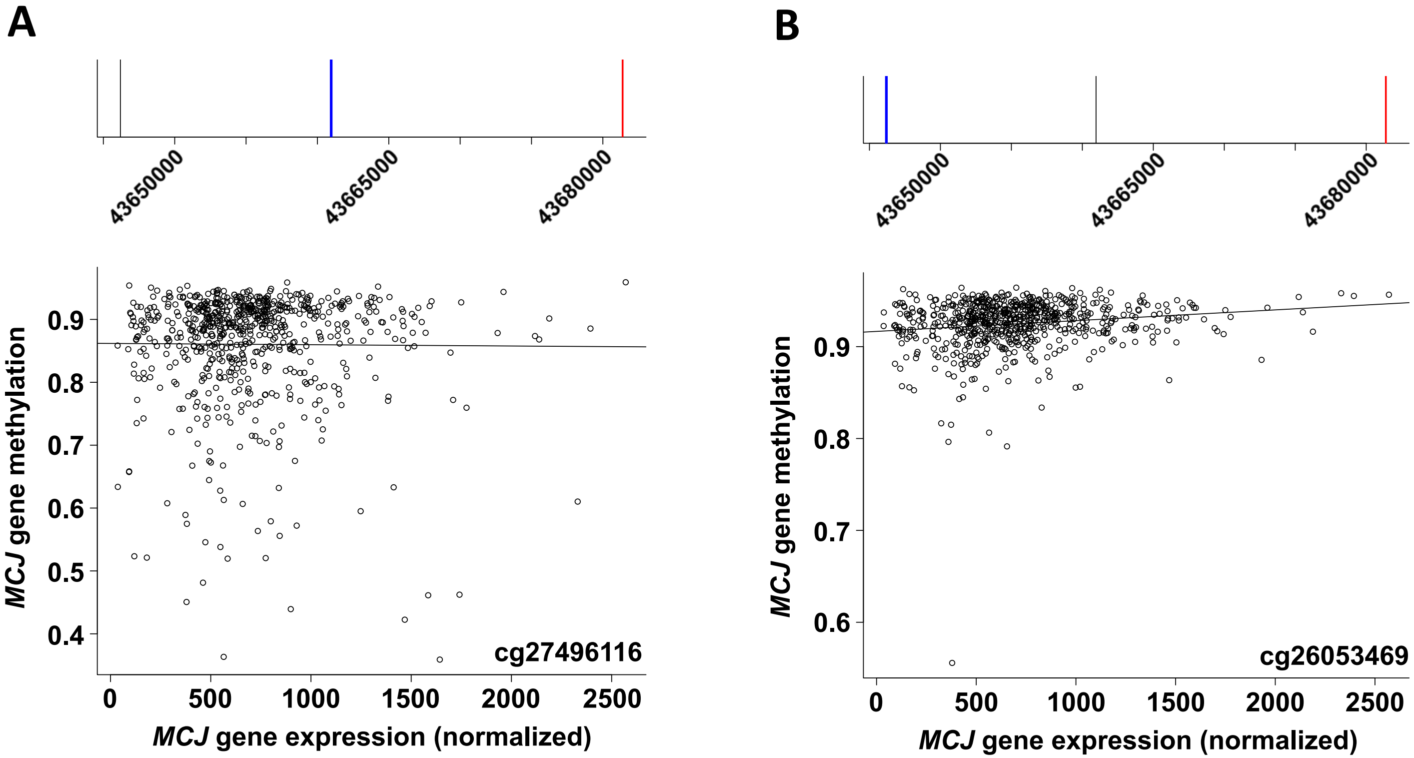


Supplementary Figure S2. Characterization of *MCJ* mRNA expression. Relative expression levels of *MCJ* (*DNAJC15*) mRNA in primary tumor tissue isolated from core needle biopsies at diagnosis were determined by qRT-PCR. The data depict the mean ± SEM of relative expression levels for each patient sample, which was run at least in triplicate. MCJ expression among all patients ranged from 0.4 to 12.3 arbitrary units with respect to the reference standard.

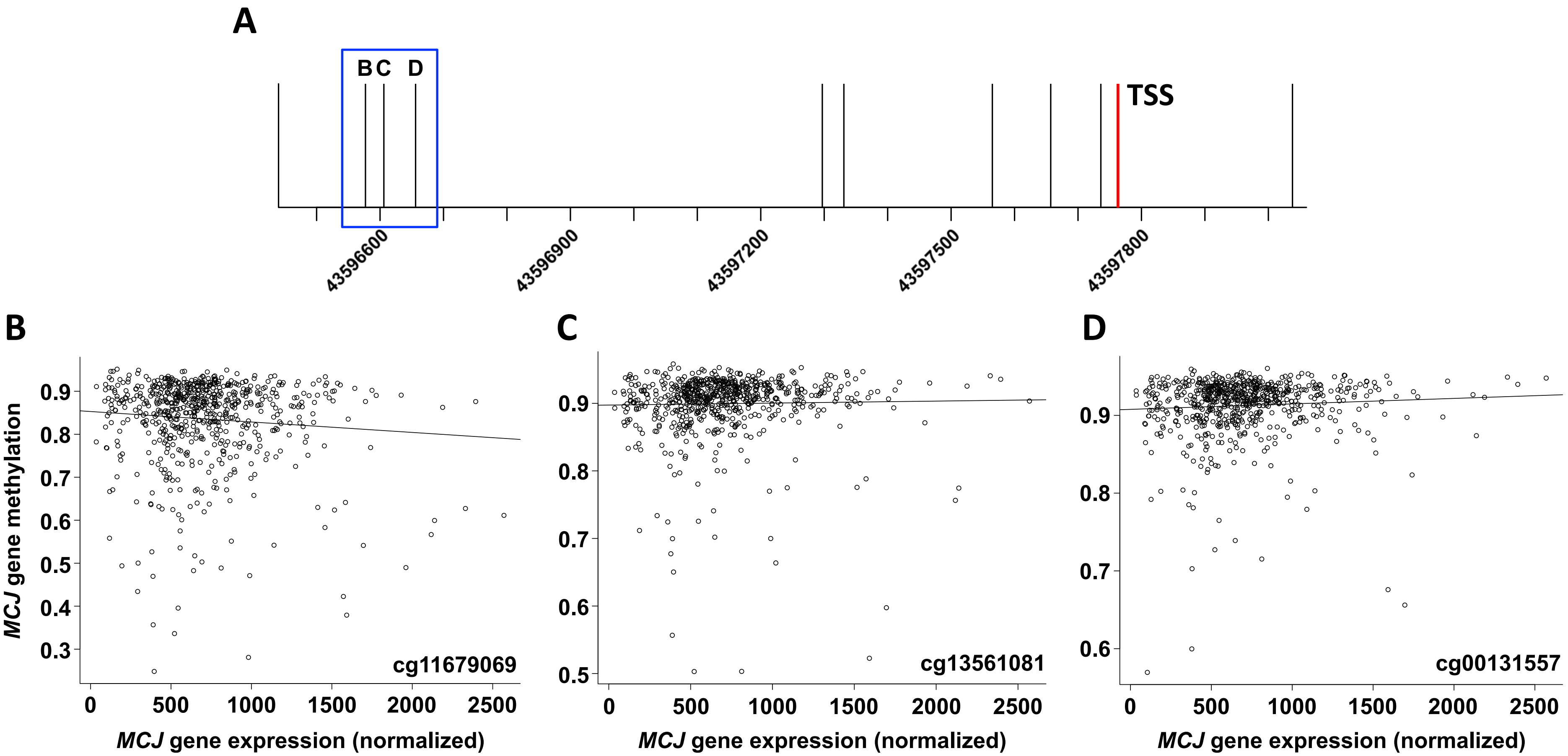




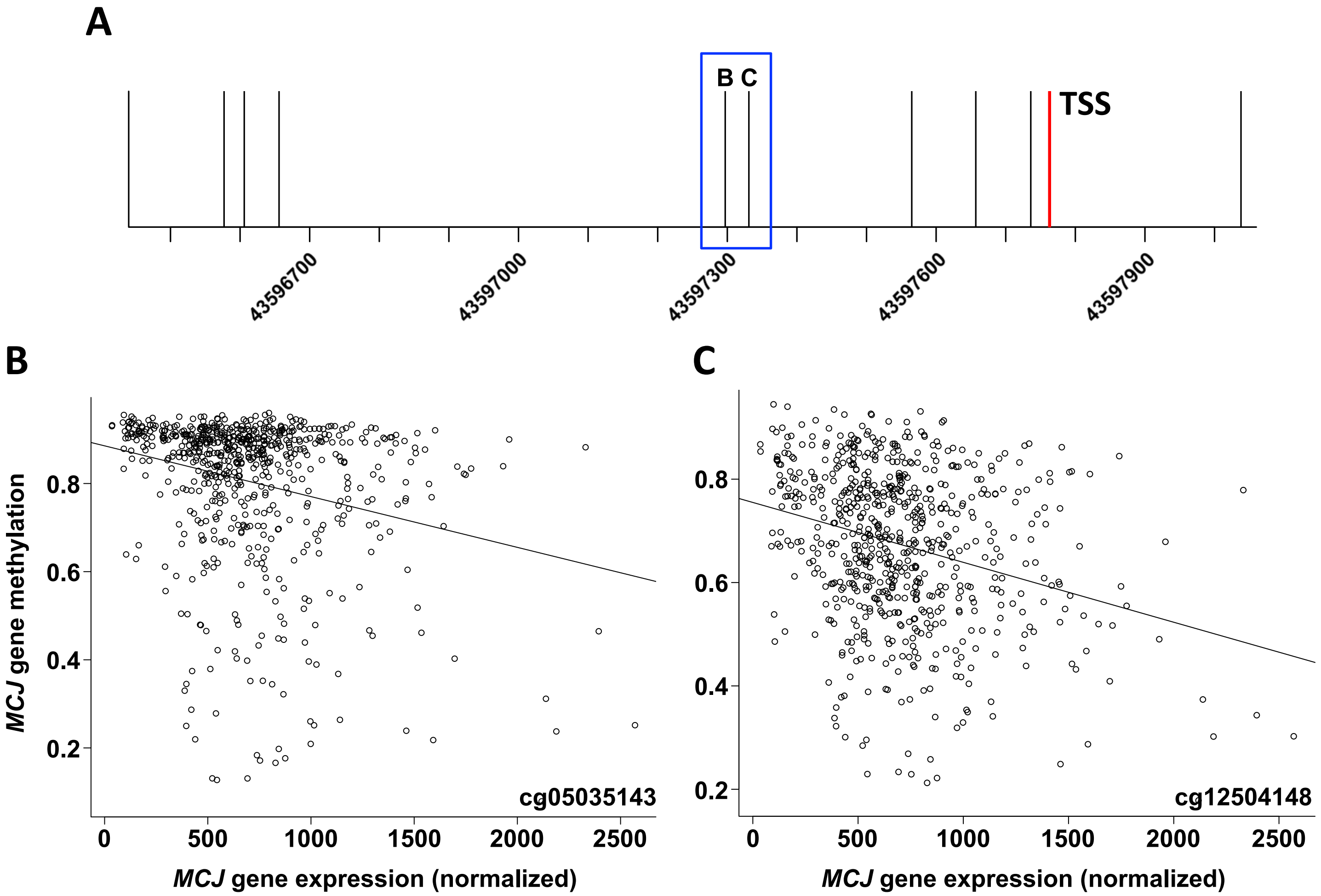
Supplementary Figure S3. Characterization of MCJ/DNAJC15 mRNA expression as a function of age, grade and lymph node (LN) involvement. Relative expression levels of *MCJ* mRNA and associated clinical variables were available from the KM plot project. Age was not significantly correlated with expression except patients that had breast cancer younger tend toward tumors that have lowered expression versus those that were older (p=0.038). Similarly grade 3 cancers have a tendency for lowered expression versus lesser grades (p<0.005), while lymph node status had no significant affect (p=0.372).



Supplemental Figure S4. ***MCJ/DNAJC15*** **gene body DNA methylation and gene expression in TCGA breast tumors.** (**A,B**) Top: line drawing of the *MCJ/DNAJC15* gene body region with genomic position and transcription end site in red, vertical lines indicate CpG sites, the blue line indicates the CpGs plotted in bottom panels. Bottom: Gene body methylation is not related with *MCJ/ DNAJC15* gene expression in TCGA breast tumors (n=684).



Supplemental Figure S5. *MCJ/DNAJC15* upstream promoter DNA methylation and gene expression in TCGA breast tumors. (***A***) Line drawing of the *MCJ/DNAJC15* gene promoter region with genomic position and transcription start site (TSS) in red. Vertical lines indicate CpG sites and are labeled to indicate CpGs plotted in panels B-D. (**B-D**) *MCJ/DNAJC15* gene expression versus DNA methylation in TCGA breast tumors (n=684) at upstream promoter CpGs cg11679069 (**B**), cg13561081 (**C**), and cg00131557 (**D**) indicates no relation of gene expression with DNA methylation at these CpG sites.



Supplemental Figure S6. *MCJ/DNAJC15* promoter DNA methylation and gene expression in TCGA breast tumors. (**A**) Line drawing of the *MCJ/DNAJC15* gene promoter region with genomic position and transcription start site (TSS) in red. Vertical lines indicate CpG sites and are labeled to indicate CpGs plotted in panels B-C. (**B-C**) *MCJ/DNAJC15* gene expression versus DNA methylation in TCGA breast tumors (n=684) at promoter CpGs cg05035143 (**B**) and cg12504148 (***C***) indicate a relation of increase gene expression with decreased DNA methylation at these CpG sites (cg05035143, p=4.7x10^{-11} and cg12504148, p=5.2x10^{-14} by linear regression).