## Supplemental Material to:

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## Detection of promoter methylation of tumor suppressor genes in serum DNA of breast cancer cases and benign breast disease controls

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Figure 1: Distribution of mean percent methylation levels of APC among the node positive, node negative and control subjects.



Figure 2: Distribution of mean percent methylation levels of BRAC1 among the node positive, node negative and control subjects.



Figure 3: Distribution of mean percent methylation levels of Cyclin D2 among the node positive, node negative and control subjects.



Figure 4: Distribution of mean percent methylation levels of ECAD among the node positive, node negative and control subjects.



Figure 5: Distribution of mean percent methylation levels of ER1 among the node positive, node negative and control subjects.



Figure 6: Distribution of mean percent methylation levels of GSTP1 among the node positive, node negative and control subjects.



Figure 7: Distribution of mean percent methylation levels of HIN1 among the node positive, node negative and control subjects.



Figure 8: Distribution of mean percent methylation levels of p16 among the node positive, node negative and control subjects.



Figure 9: Distribution of mean percent methylation levels of RAR- $\beta$  among the node positive, node negative and control subjects.



Figure 10: Distribution of mean percent methylation levels of RASSF1 among the node positive, node negative and control subjects.



Figure 11: Distribution of mean percent methylation levels of SRFP1 among the node positive, node negative and control subjects.



Figure 12: Distribution of mean percent methylation levels of TWIST among the node positive, node negative and control subjects.