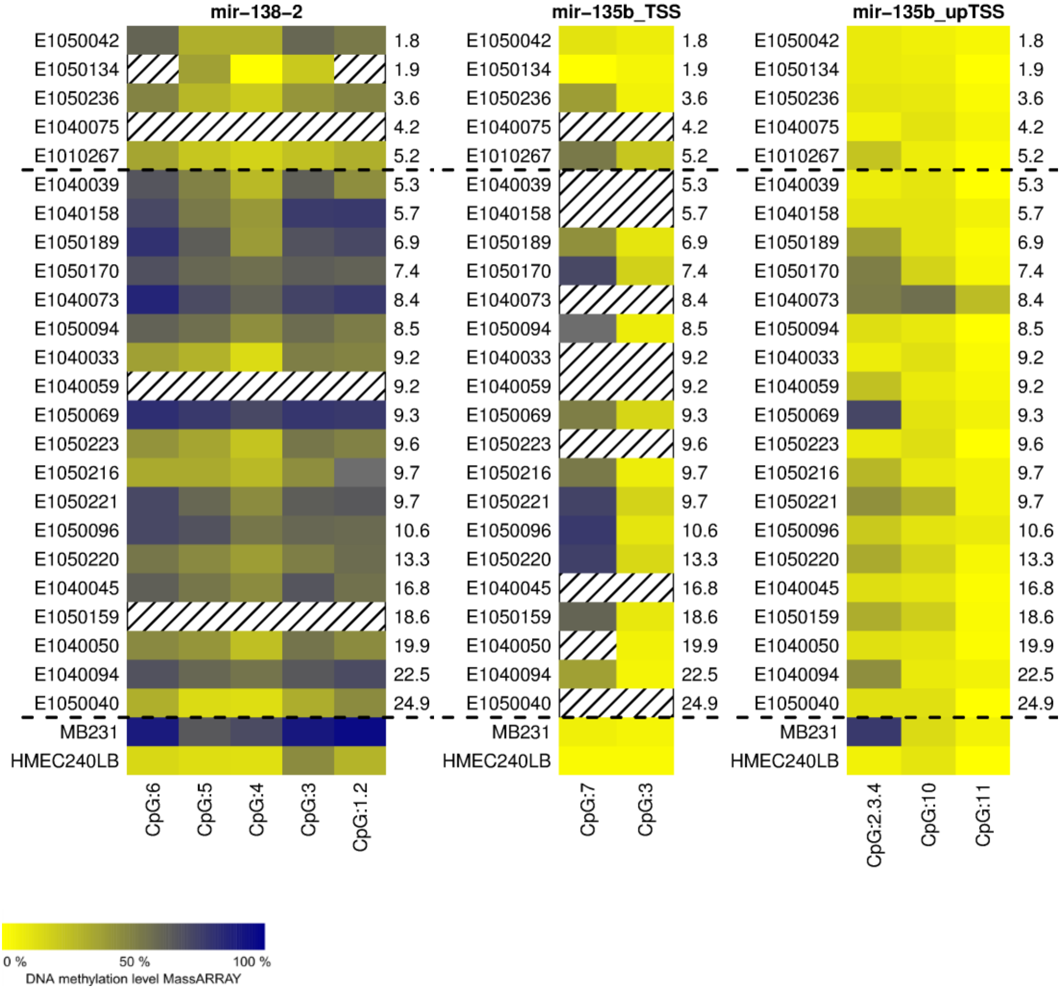
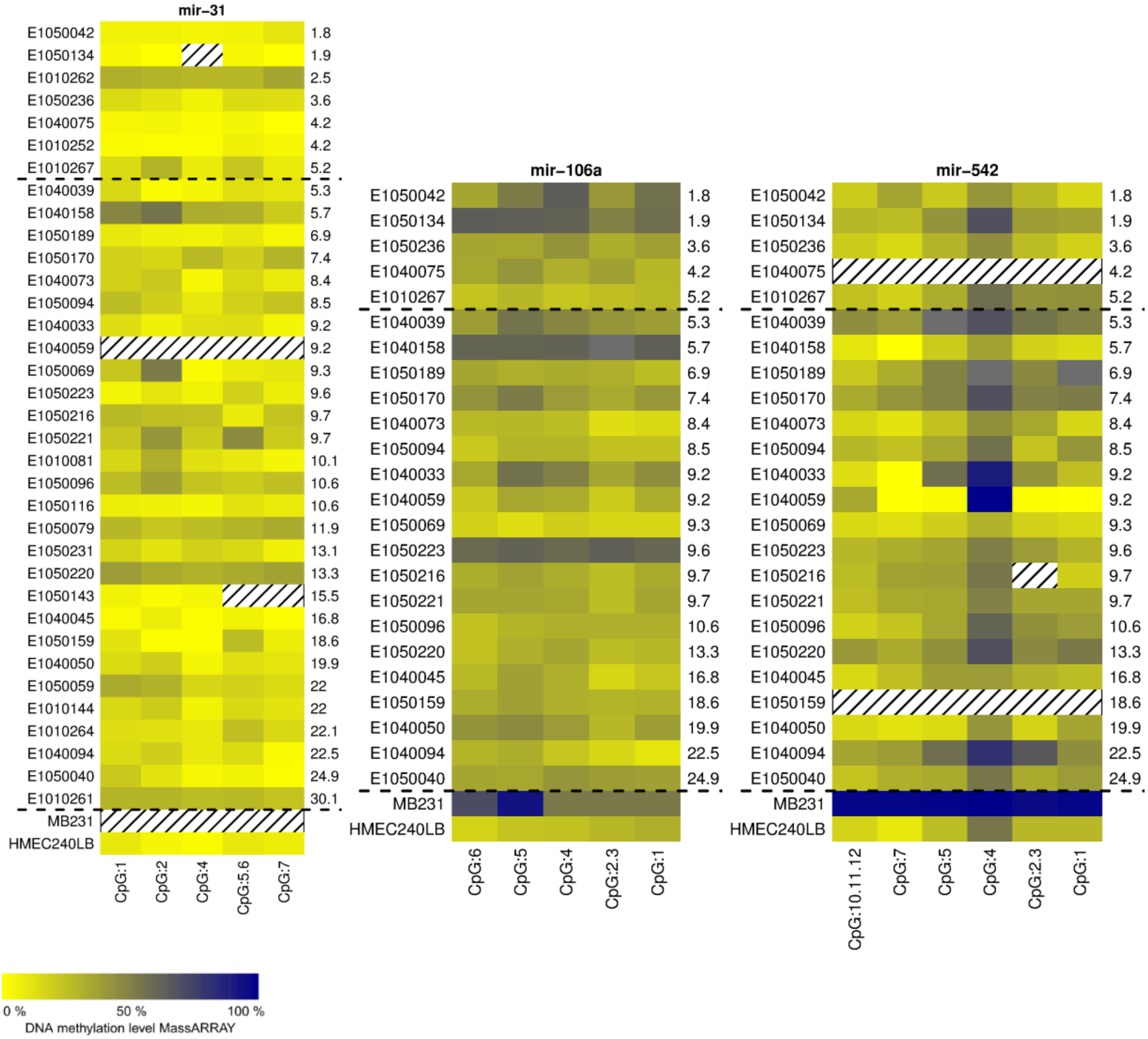
Figure A:



mir-138-2
mir-135b_TSS
mir-135b_upTSS
E1050042
E1050134
E1050236
E1040075
E1010267
E1040039
E1040158
E1050189
E1050170
E1040073
E1050094
E1040033
E1040059
E1050069
E1050223
E1050216
E1050221
E1050096
E1050220
E1040045
E1050159
E1040050
E1040094
E1050040
MB231
HMEC240LB
1.8
1.9
3.6
4.2
5.2
5.3
5.7
6.9
7.4
8.4
8.5
9.2
9.2
9.3
9.6
9.7
9.7
10.6
13.3
16.8
18.6
19.9
22.5
24.9
CpG:6
CpG:5
CpG:4
CpG:3
CpG:1.2
CpG:7
CpG:3
CpG:2.3.4
CpG:10
CpG:11
0 %
50 %
100 %
DNA methylation level MassARRAY

Figure B:



S1 Figure. Sequenom MassARRAY analysis. DNA methylation status across miRNA genes. MiRNAs investigated across 24 *Ella* FFPE breast tumor tissue samples, with the exception of mir-31, which was investigated across 35 samples. Rows represent individual samples (identified with the letter "E"), ordered based on time since last full-term pregnancy, from early to late (numerical values in years on the right-hand side of heatmaps). Columns represent CpG units (labeled at the bottom). Yellow indicates zero to low methylation. Blue indicates high to complete methylation. Dashed boxes indicate no data for that CpG unit, for that specific sample. Filtering of raw methylation data took into account a standard error more than 0.15, and if less than half of the CpG units were left, then that CpG unit was discarded. Dashed horizontal lines divide the early from the late postpartum group. MB231 represents a breast cancer cell line, while, HMEC240LB represents a human mammary epithelial cell line. Both were used as controls for the Sequenom MassARRAY. MB231 data for mir-31 (Figure B) is missing (dashed boxes) due to a homozygous deletion present in this cell line within the location of the mir-31 gene.