

Supplementary Figure 1

For each Forward/Reverse probe pair the mean of the log (Forward/Reverse) was calculated across all 62 chips from the FMR1 design. Probes are binned by base composition with each bin corresponding to the excess of A over T nucleotides plus the excess of C over G nucleotides on the Forward strand. The numbers on the figure correspond to the number of distinct features that are observed in the bin. Observed (o) and expected means (*) are plotted for each bin.

