

Supporting Information

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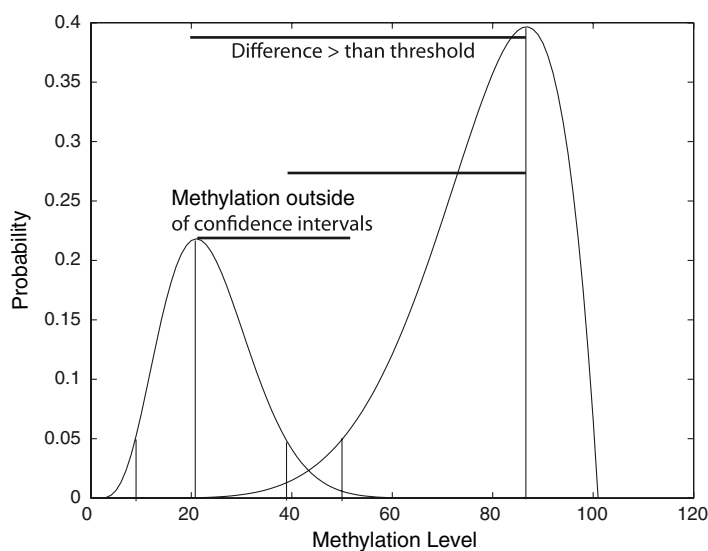


Fig. S1. Epimutation identification. The identification of epimutations (differentially methylated sites) requires that the implied methylation level of each sample be outside of the 5% confidence intervals based on a binomial distribution. It also requires that the methylation difference be greater than a threshold determined to be the overall mean of that context-specific methylation.

Other Supporting Information Files

- [Dataset S1 \(XLSX\)](#)
- [Dataset S2 \(XLSX\)](#)
- [Dataset S3 \(XLSX\)](#)
- [Dataset S4 \(XLSX\)](#)
- [Dataset S5 \(XLSX\)](#)
- [Dataset S6 \(XLSX\)](#)
- [Dataset S7 \(XLSX\)](#)
- [Dataset S8 \(XLSX\)](#)