

Figure S1. Cross tissue differences are largely consistent between individuals. Individual patterns of cord blood (red) and placental (blue) methylation levels in twenty tissue-specific probes (CpG sites where the difference in methylation proportion between the two tissues is >0.1 for all 174 samples).

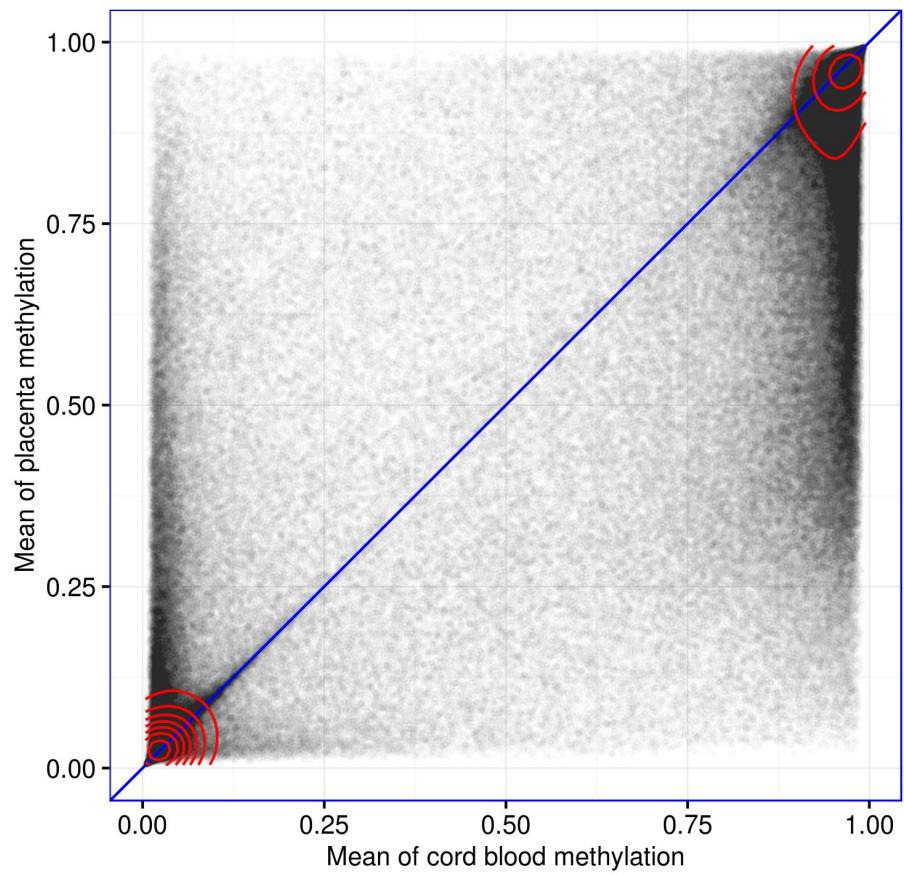


Figure S2. Scatter plot between the mean of cord blood and placental methylation values across all subjects. The overlaid red contour lines show the density of the set of analyzed sites.

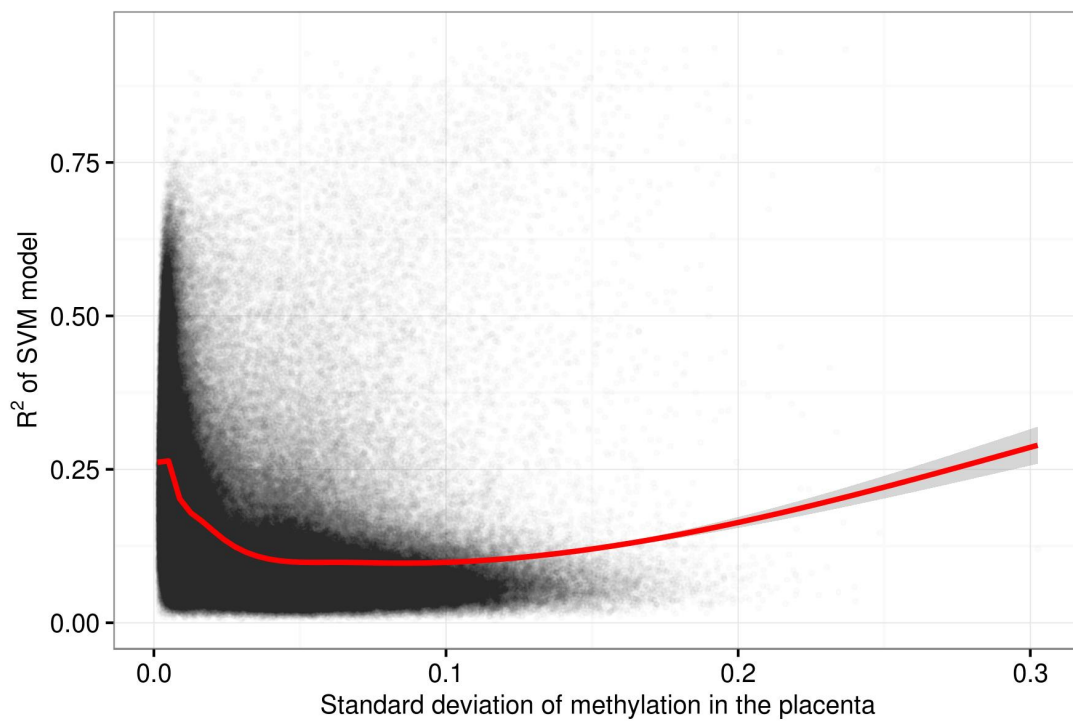


Figure S3. Scatter plot between the standard deviation of the placental methylation values across all subjects and the R² between measured and SVM-predicted placental methylation values obtained by 10-fold cross-validation. Each point is a single methylation site. The red line shows a gam smoother.