

Supplementary Figure Information

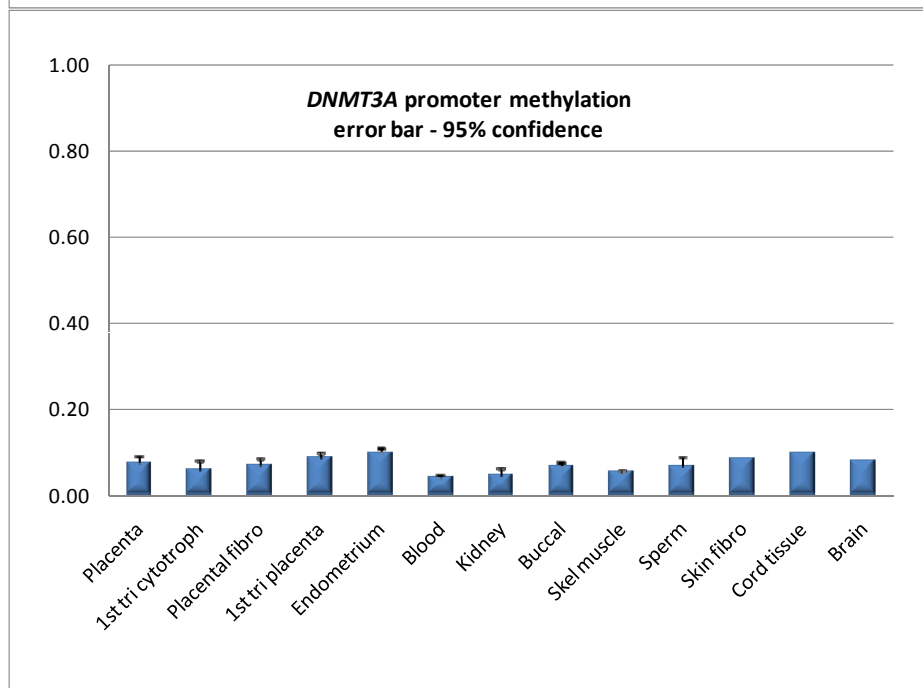
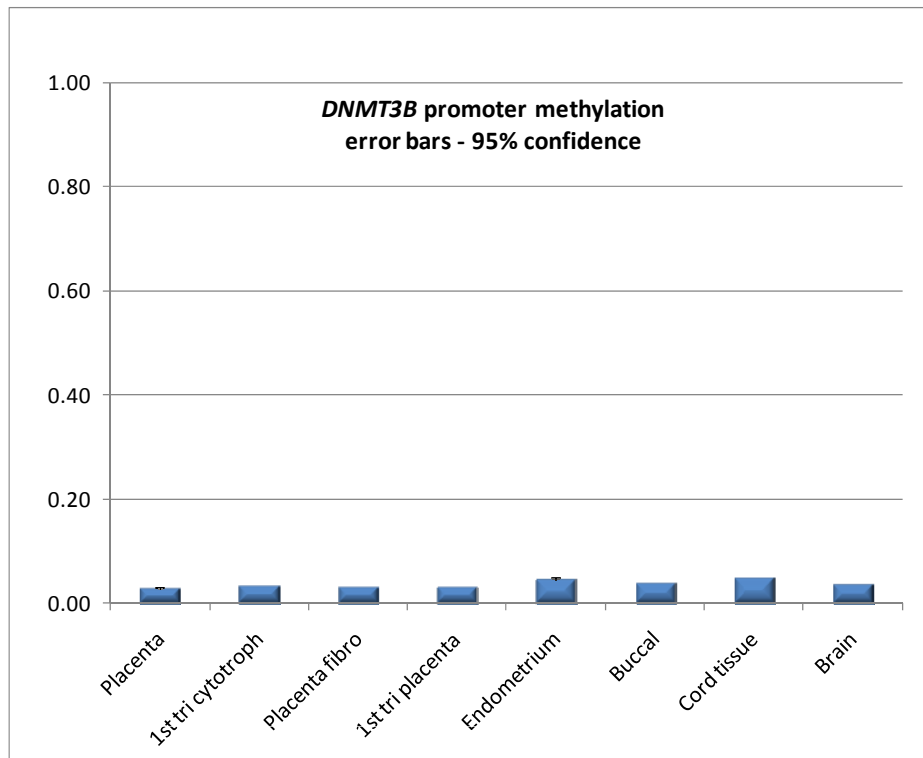
Supplementary Figure 1. Promoter methylation of the *DNMT3A* and *DNMT3B* genes in all human tissues including placenta.

Supplementary Figure 2. Bisulfite Sequencing analysis of *DNMT3L* in human placenta and somatic tissues. Low methylation levels with a highly variable distribution within specific alleles are seen in placental tissue and purified cytotrophoblasts (A). Variable distribution of methylated CpGs are also seen in other human tissues (B) and the JEG-3 cell line (C), with an overall increasing level of methylation relative to the placental tissue.

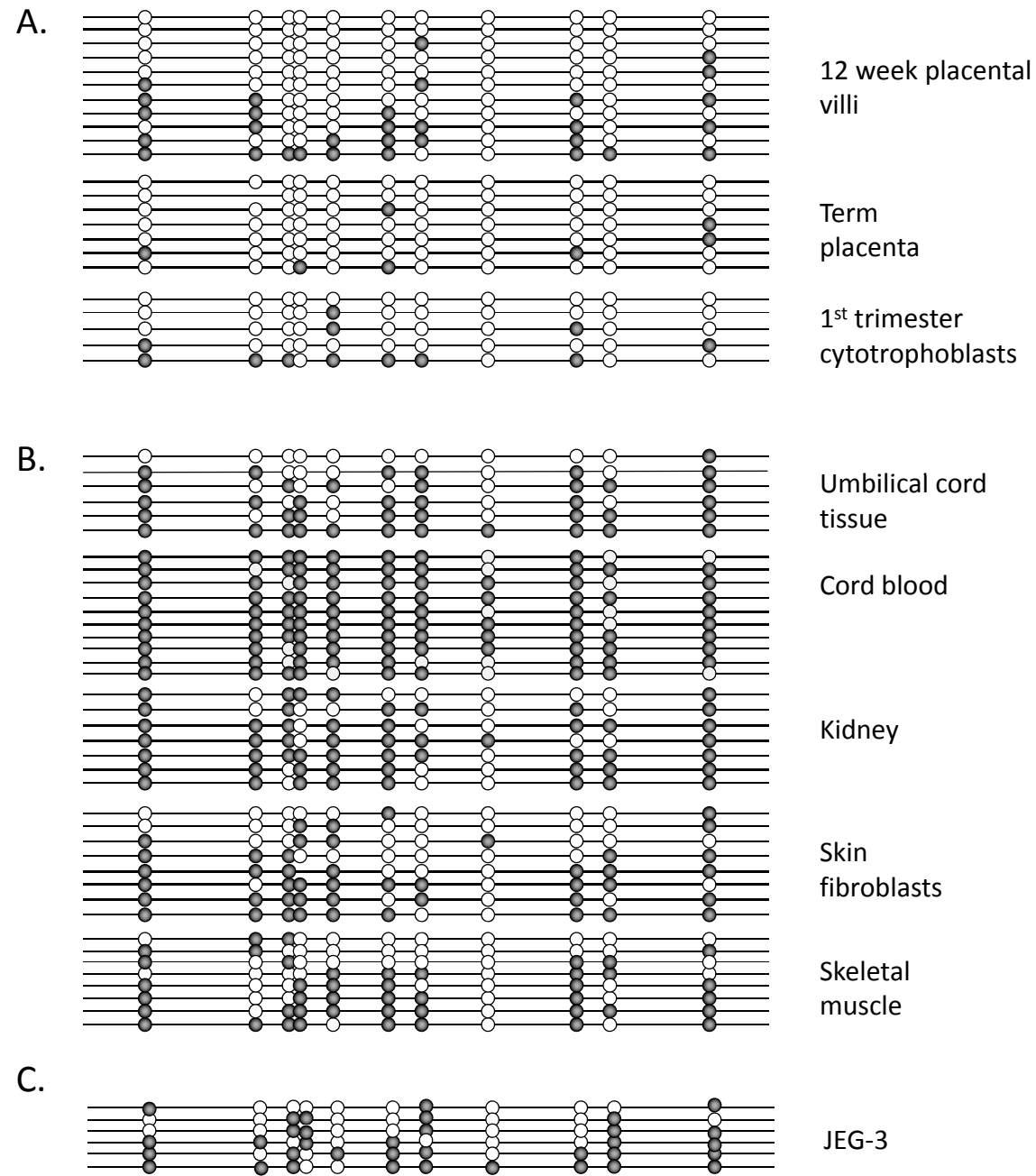
Supplementary Figure 3. Methylation of *DNMT1* and *DNMT3L* throughout pregnancy. Consistent individual CpG site methylation within the promoter regions of both genes is seen throughout the majority of pregnancy in human placental tissue.

Supplementary Figure 4. *DNMT1* hypomethylation in choriocarcinoma cell lines. Bisulfite sequencing data obtained using DNMT1_1 assay in A. BeWo, B. JAR, C. JEG-3 and D. mean methylation levels for three CCA cell lines. The *DNMT1* gene shows hypomethylation in all CCA cell lines relative to full term or first trimester human placental tissue or purified cytotrophoblasts.

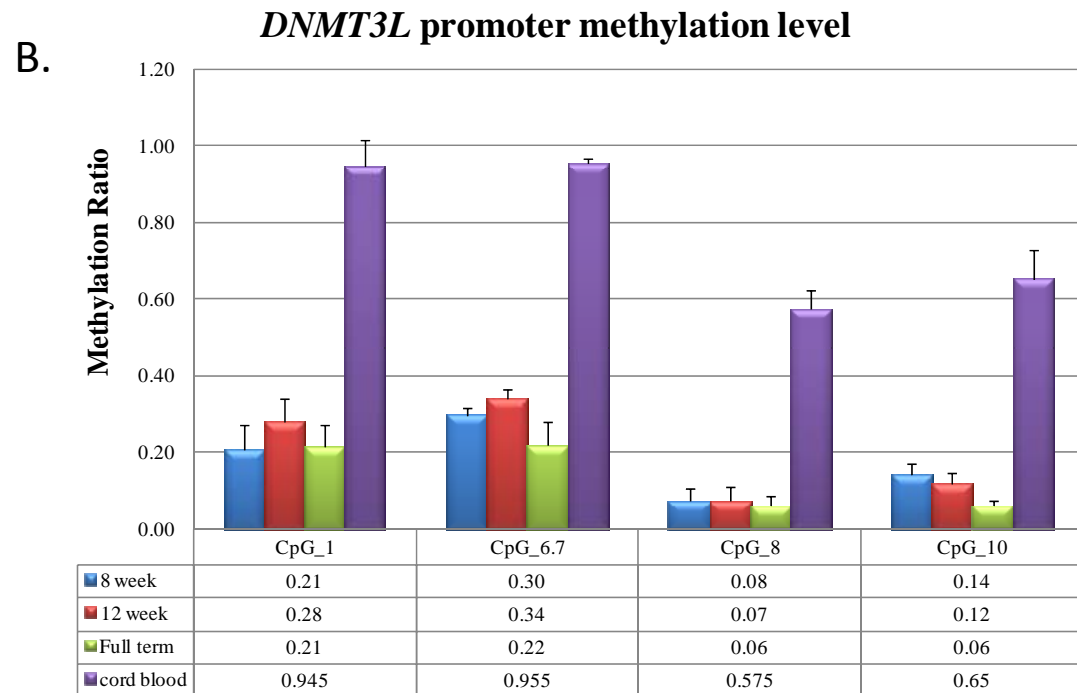
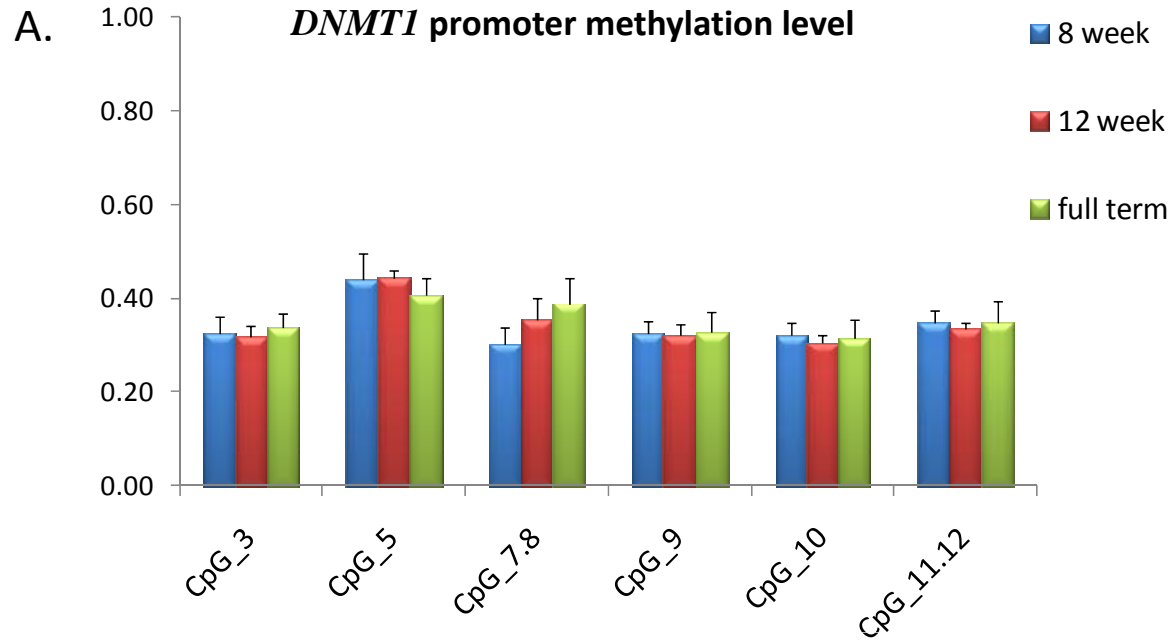
Supplementary Figure 5. Variable *DNMT3L* promoter methylation in JAR and JEG-3 CCA cell lines. Whereas JAR shows *DNMT3L* promoter hypomethylation relative to full term placenta or purified first trimester purified cytotrophoblasts, JEG-3 cells show an increasing level of methylation.



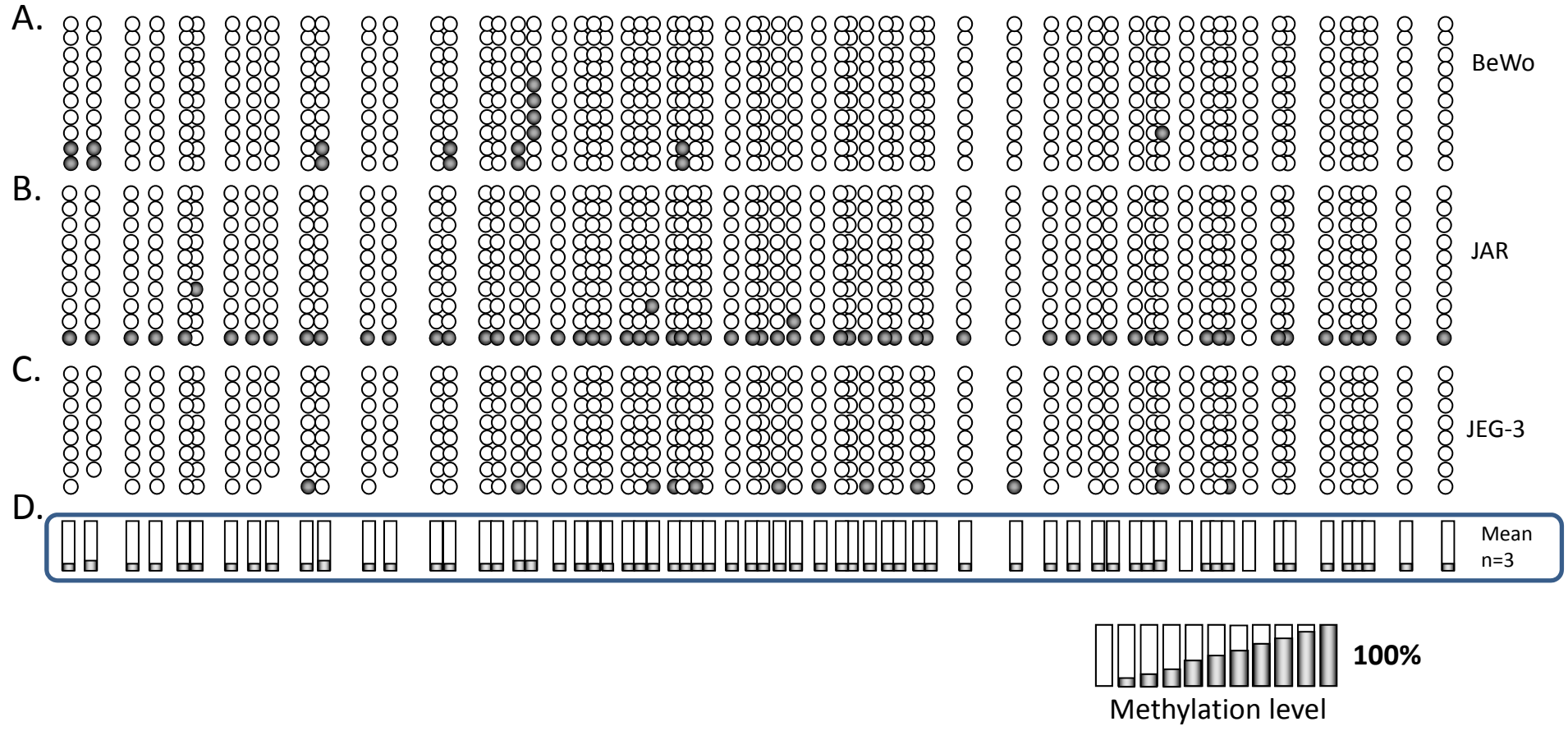
Supp Figure 1



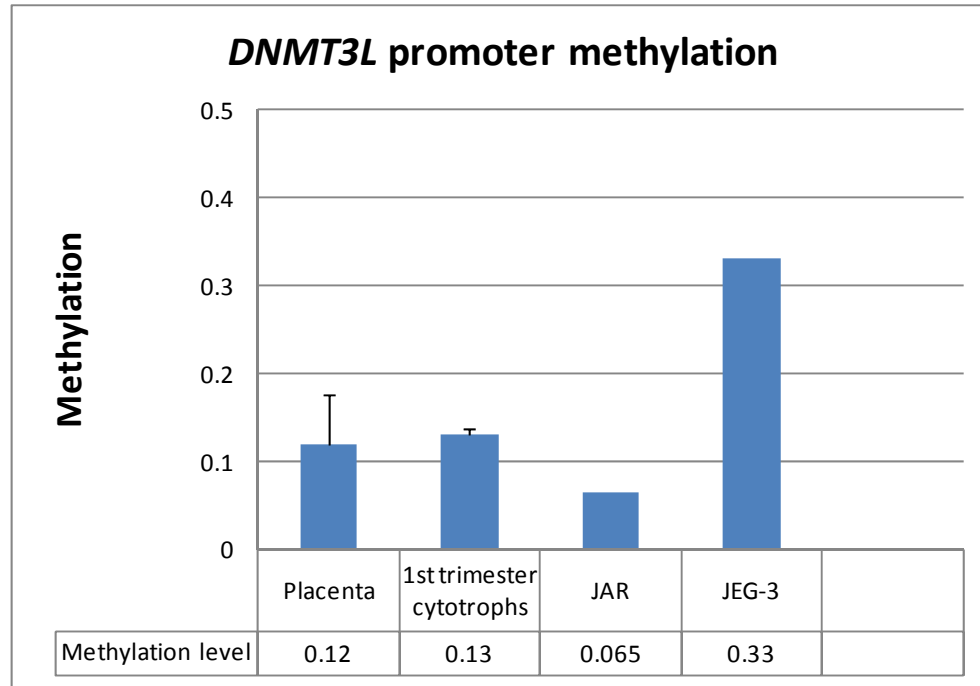
Supp Figure 2



Supp Figure 3



Supp figure 4



Supp Figure 5