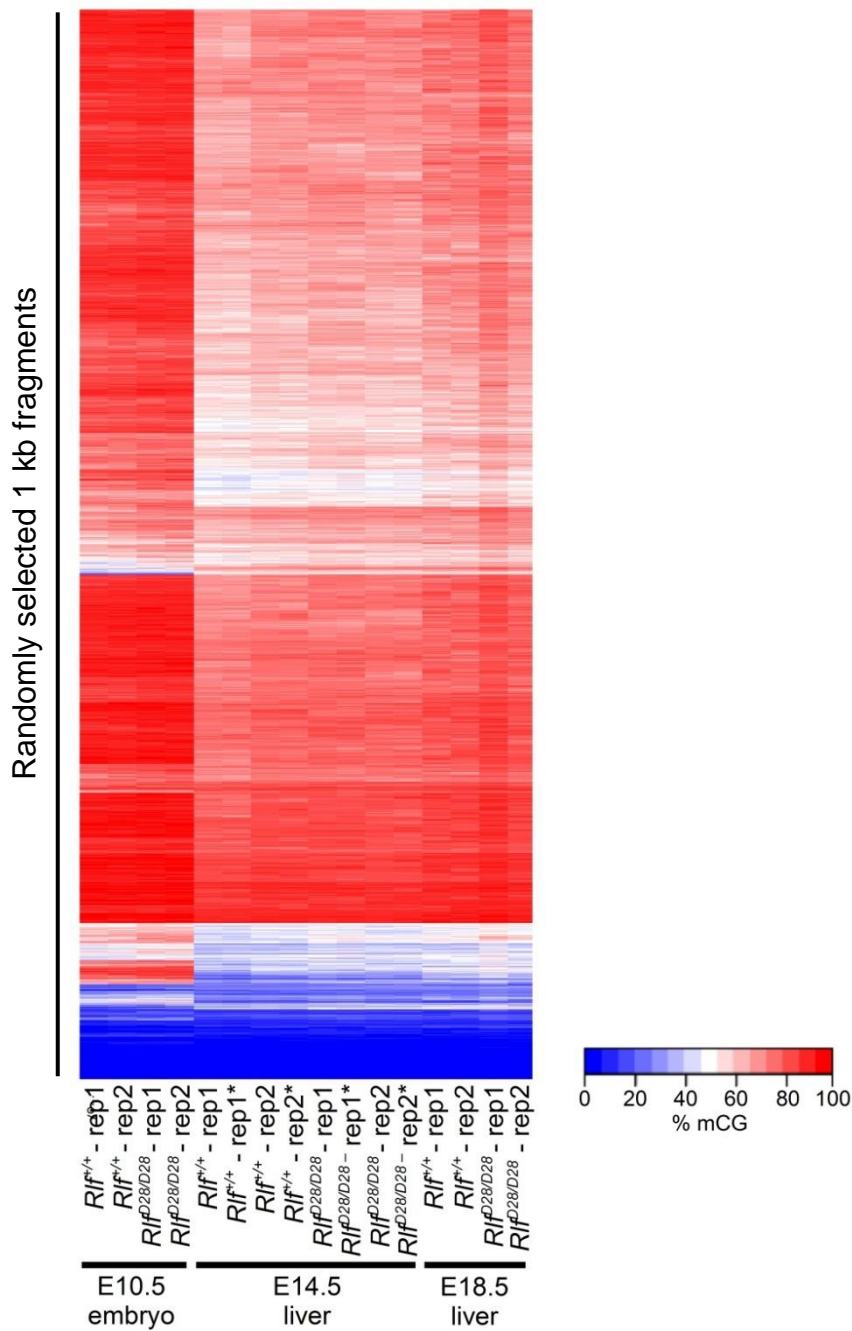


Supplemental Figure 3



### Hierarchical clustering of %mCG for random 1kb regions from the bisulphite converted genomes prepared for this study

Weighted CpG methylation averages for 9000 randomly selected 1kb regions from the mouse genome, each with >7 CpGs and a per-CpG read coverage > 5 across all datasets, were plotted. Two wild-type and two *Rlf*<sup>MommeD28/MommeD28</sup> mice were used for each tissue. The E14.5 livers, initially sequenced to ~30-fold coverage, were sub-sampled (indicated by \*) to ~15-fold coverage to allow for direct comparisons with the E10.5 embryo and E18.5 liver datasets (both sequenced to ~15-fold coverage).