**SUPPLEMENTAL FIGURE LEGENDS**

**Supplemental Figure S1**. Boxplots for tail *Avy* methylation percent across coat colors (n=299). Boxes represent the interquartile range (IQR), lines represent the median, whiskers represent maximum or minimum observation if within 1.5\*IQR (interquartile range), circles represent values outside 1.5\*IQR.

**Supplemental Figure S2.** Tail DNA methylation at the *Avy* locus across exposure groups in *Avy/a* offspring. Methylation was averaged across four CpG sites at the *Avy* locus for each mouse. Because *Avy* methylation was bimodally distributed in several exposure groups, the variation appears to be very large in box plot form. This box plot is most informative when comparing between *Avy* methylation and global IAP methylation. Lines within boxes represent medians and whiskers represent 1.5\*IQR. Gray dots are values outside of 1.5\*IQR.

**Supplemental Figure S3**. Histograms of mean tail DNA methylation at the *Avy* locus in each exposure group. A) Controls (n=49), B) DEHP (n=49), C) DBP (n=49), D) DINP (n=44), E) DEHP+DINP (n=52), F) DEHP+DINP+DBP (n=56).

**Supplemental Figure S4**. Tail global IAP DNA methylation across exposure groups in *a/a* mice. Mean global IAP methylation across four CpG sites in female (n=81) and male (n=68) *a/a* mice. Linear mixed models were used to compare each exposure group to controls. Lines within boxes represent medians and whiskers represent 1.5\*IQR. Gray dots are values outside of 1.5\*IQR. ^p < 0.10, \*p < 0.05.