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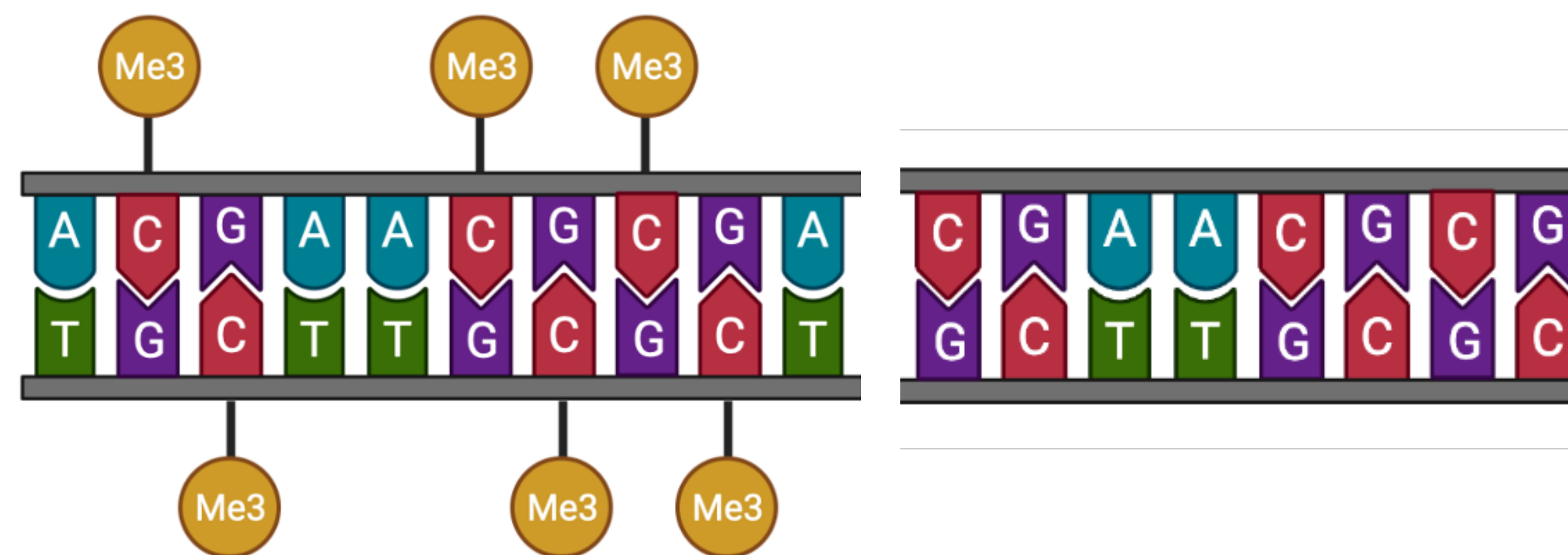
Background

- **Alzheimer's disease (AD):** a chronic neurodegenerative disease that is the most common cause of dementia.
- Dietary factors can influence AD risk and prevalence, but the mechanism is unknown.

Typical American Diet (TAD) ↑ AD Risk and Prevalence

Mediterranean Diet (MD) ↓ AD Risk and Mortality

- **Epigenetic modifications:** changes to the genome *other* than changes in the DNA sequence which can influence gene expression, including DNA methylation of cytosines at CpG dinucleotides.

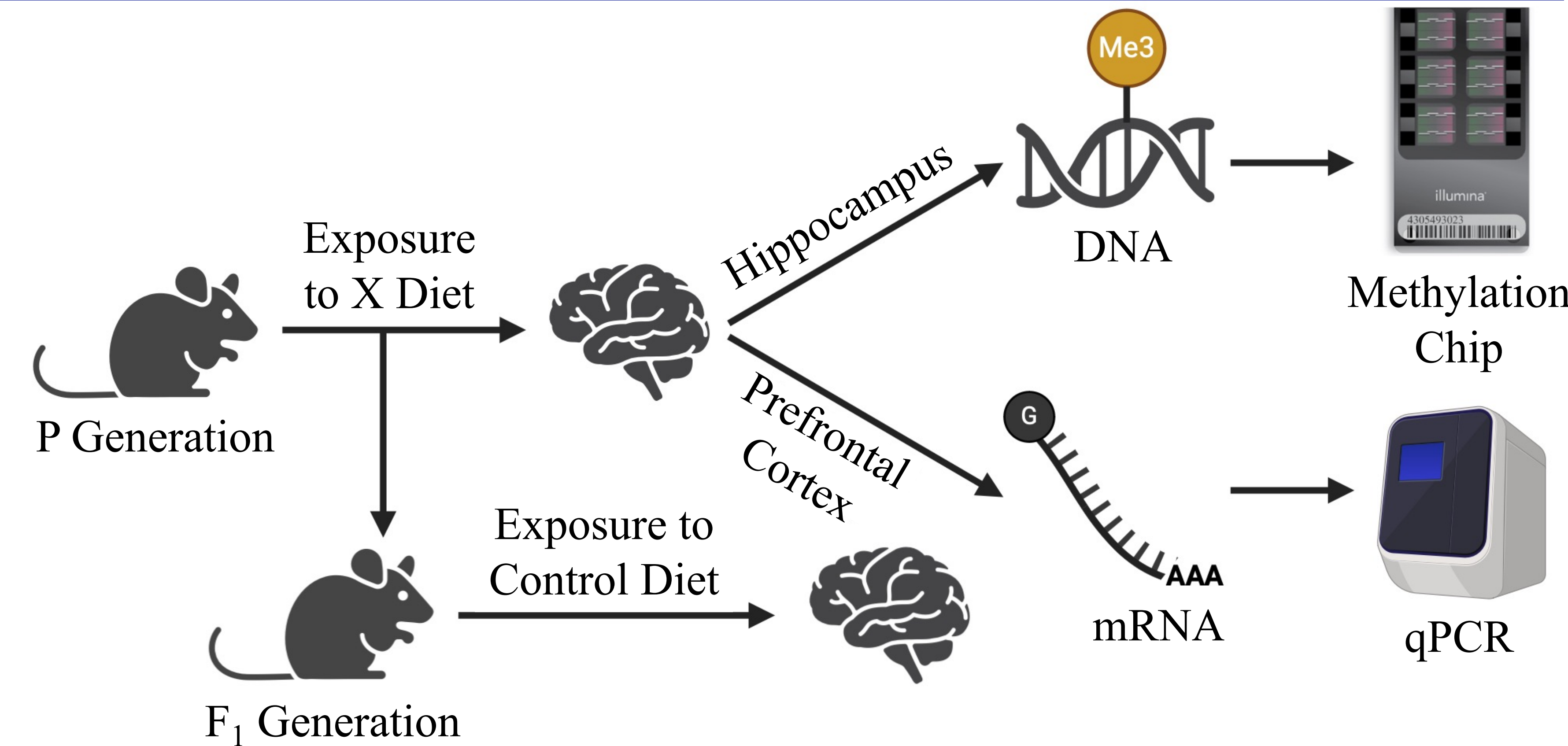


Hypermethylation \approx \downarrow Gene Expression
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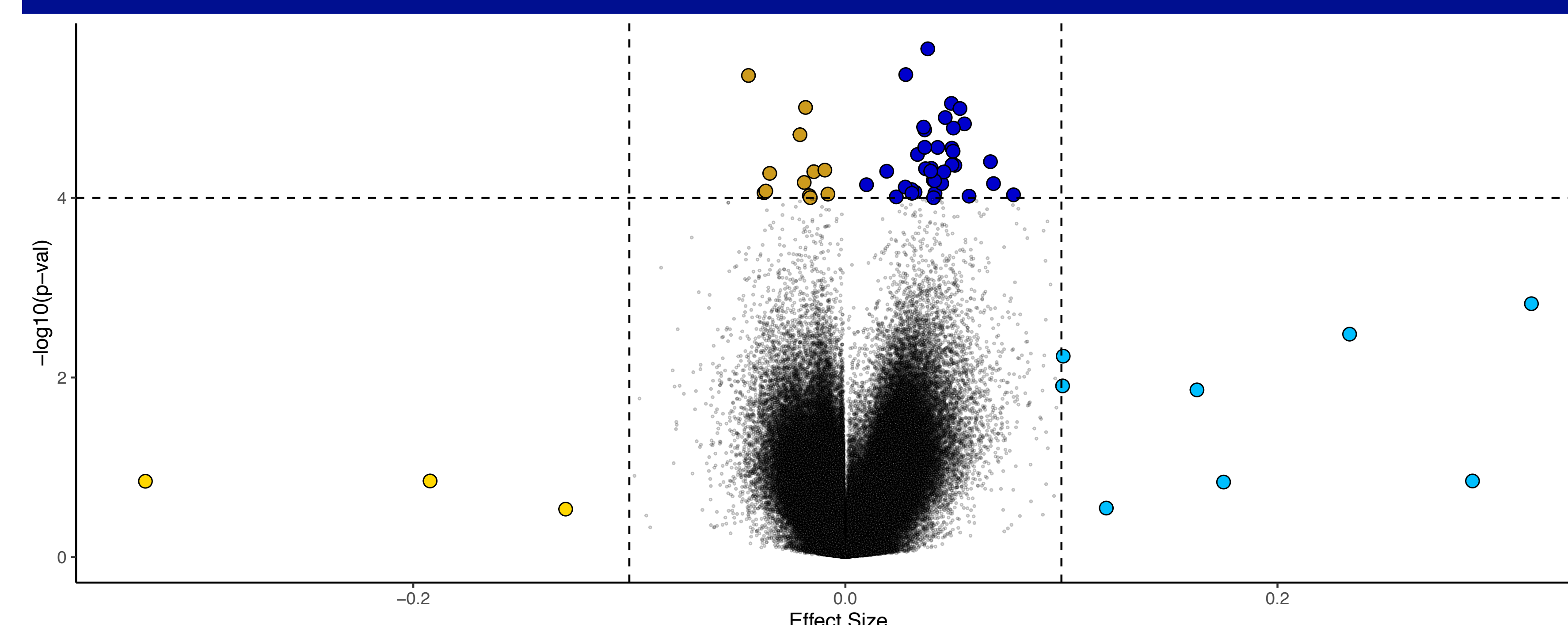
Objective

Determine whether **diet** can induce **epigenetic modifications** that contribute to **AD** development and/or prevention, and if such modifications are **heritable**.

Methods



Methylation Results



DML Type: ● MD Eff ● MD Sig ● TAD Eff ● TAD Sig

Figure 1. Volcano plot of DMLs based off of diet according to effect size ($\geq 10\%$) and statistical significance ($p\text{-val} \leq 0.0001$).

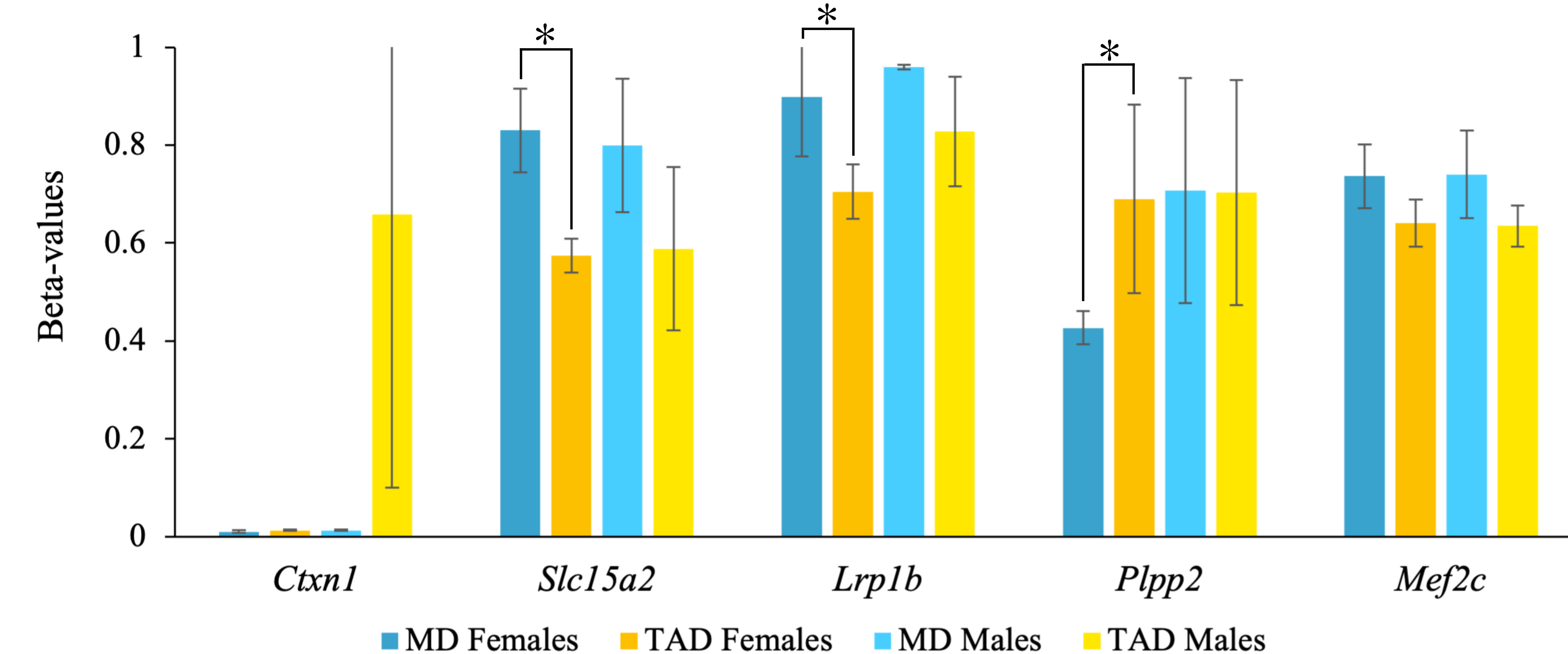


Figure 2. Avg. P beta-values of effect size DMLs based off of diet and sex. Error bars depict standard deviation. Independent t-test with $\alpha=0.05$. $p\text{-val} < 0.05$ indicated by *.

Gene Expression Results

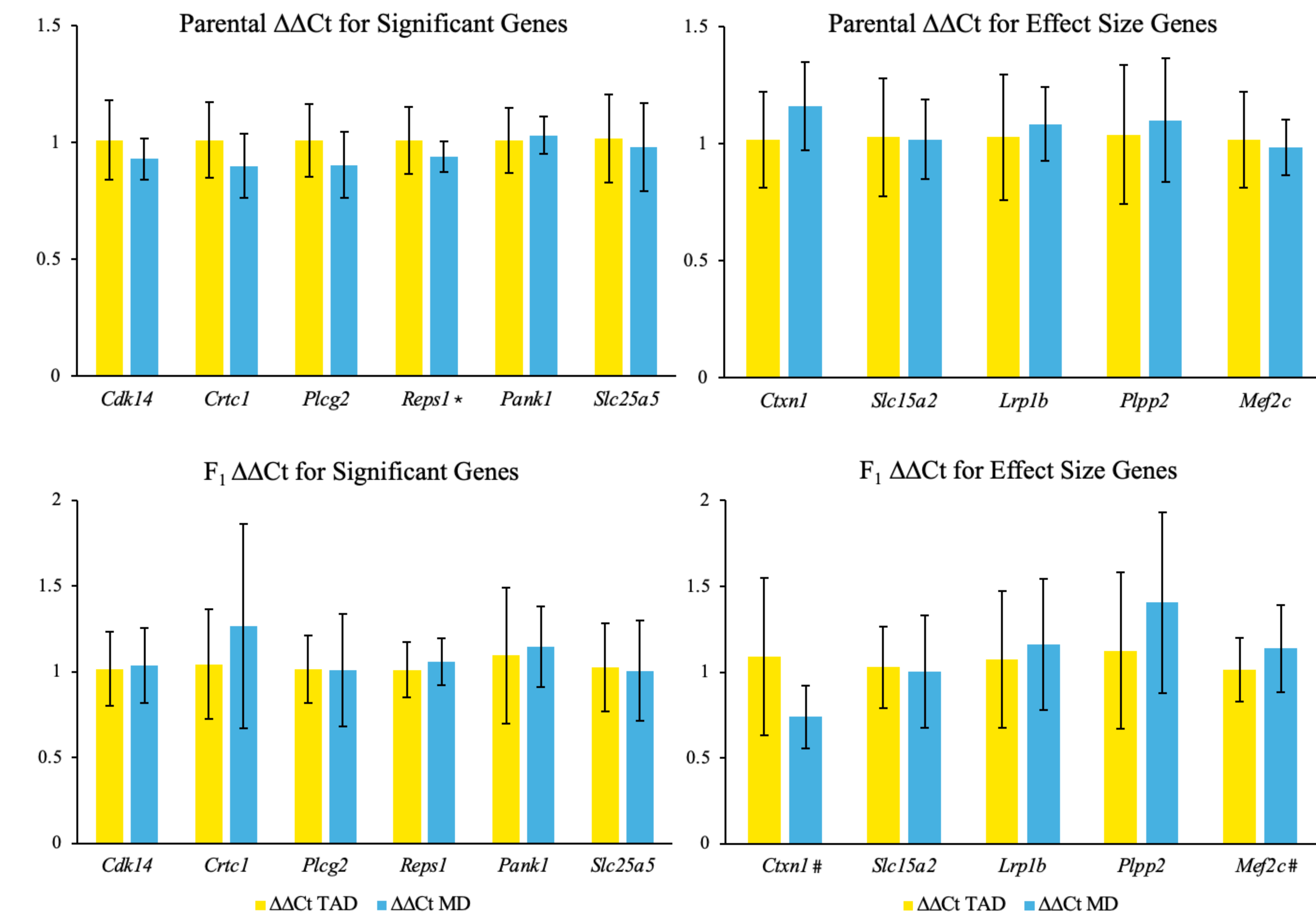


Figure 3. $\Delta\Delta Ct$ scores for selected loci for both generations (collapsing by sex) with TAD set as the reference group. Significant differential expression in females only indicated by #; differential expression in males only indicated by *.

Conclusions

- No genes with at least 10% differential methylation were found to be statistically significant.
- Small sample size led to high variance within groups.
- Significant differences in beta-values and gene expression based on sex indicate sex difference according to diet.

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