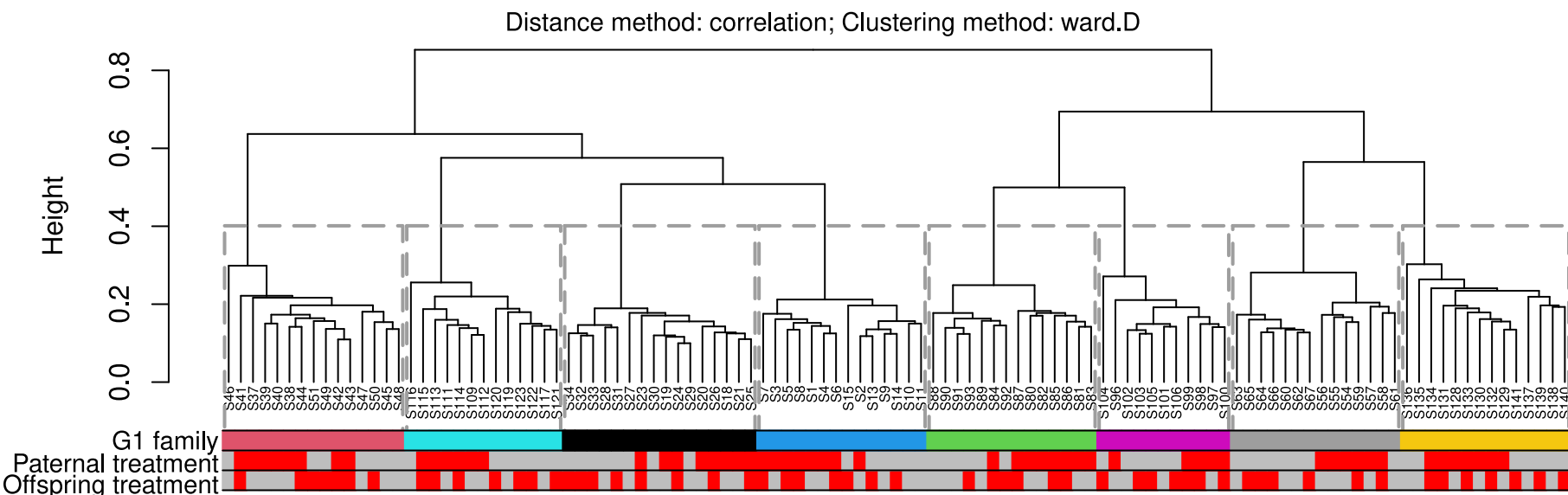


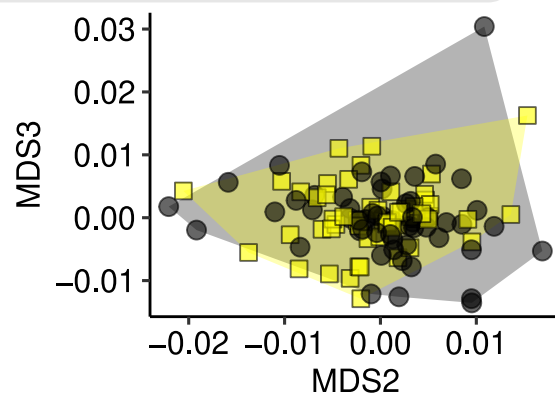
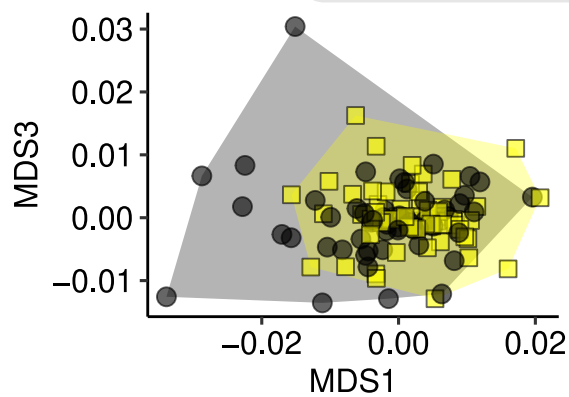
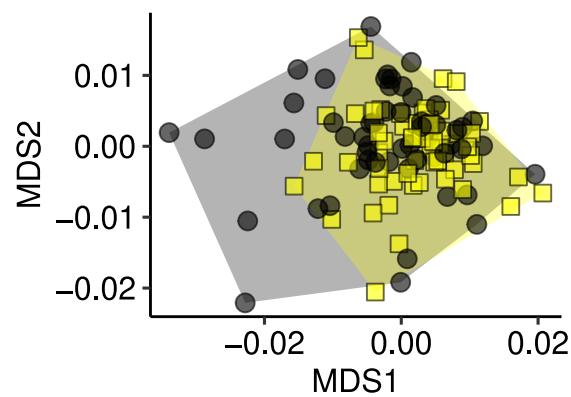
A. CpG methylation clustering of offspring



B. NMDS of offspring DNA methylation variation

Variation in distances between samples (PERMANOVA):
7.6% explained by interaction of paternal treatment and G1 family
1.5% explained by paternal treatment
1% explained by offspring treatment

Paternal treatment: ● Control father □ Infected father



Offspring treatment: ○ Control ■ Infected

