## A. CpG methylation clustering of offspring Distance method: correlation; Clustering method: ward.D 8.0 9.0 Height 0.4 0.2 0.0 G1 family Paternal treatment Offspring treatment-B. NMDS of offspring DNA methylation variation Variation in distances between samples (PERMANOVA): 7.6% explained by interaction of paternal treatment and G1 family Paternal treatment: Control father Infected father 1.5% explained by paternal treatment 1% explained by offspring treatment 0.03-0.03 -0.01 0.02 0.02 MDS2 MDS3 MDS3 0.00 0.01 0.01 -0.01 0.00 0.00 -0.01 -0.01-0.020.00 0.02 -0.02 0.02 -0.02 -0.01 -0.02 0.00 0.00 0.01 MDS1 MDS1 MDS2 Infected Offspring treatment: O Control 0.03-0.03 -0.01 0.02 0.02 MDS2 MDS3 MDS3 0.00 0.01 0.01 -0.010.00 0.00 -0.01-0.01 -0.02-0.020.00 0.02 -0.020.02 0.01 0.00 -0.02 -0.010.00 MDS1 MDS1 MDS2