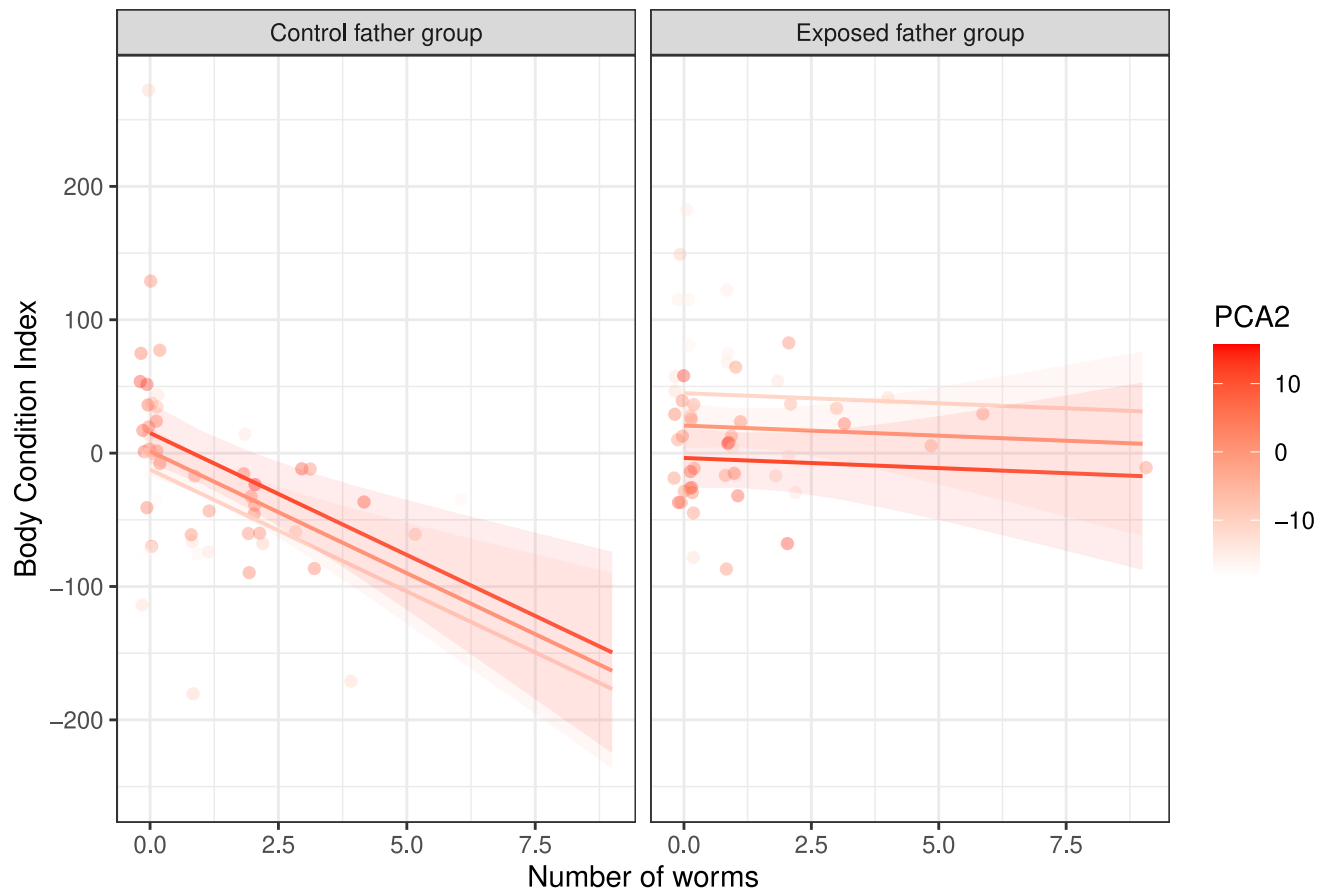


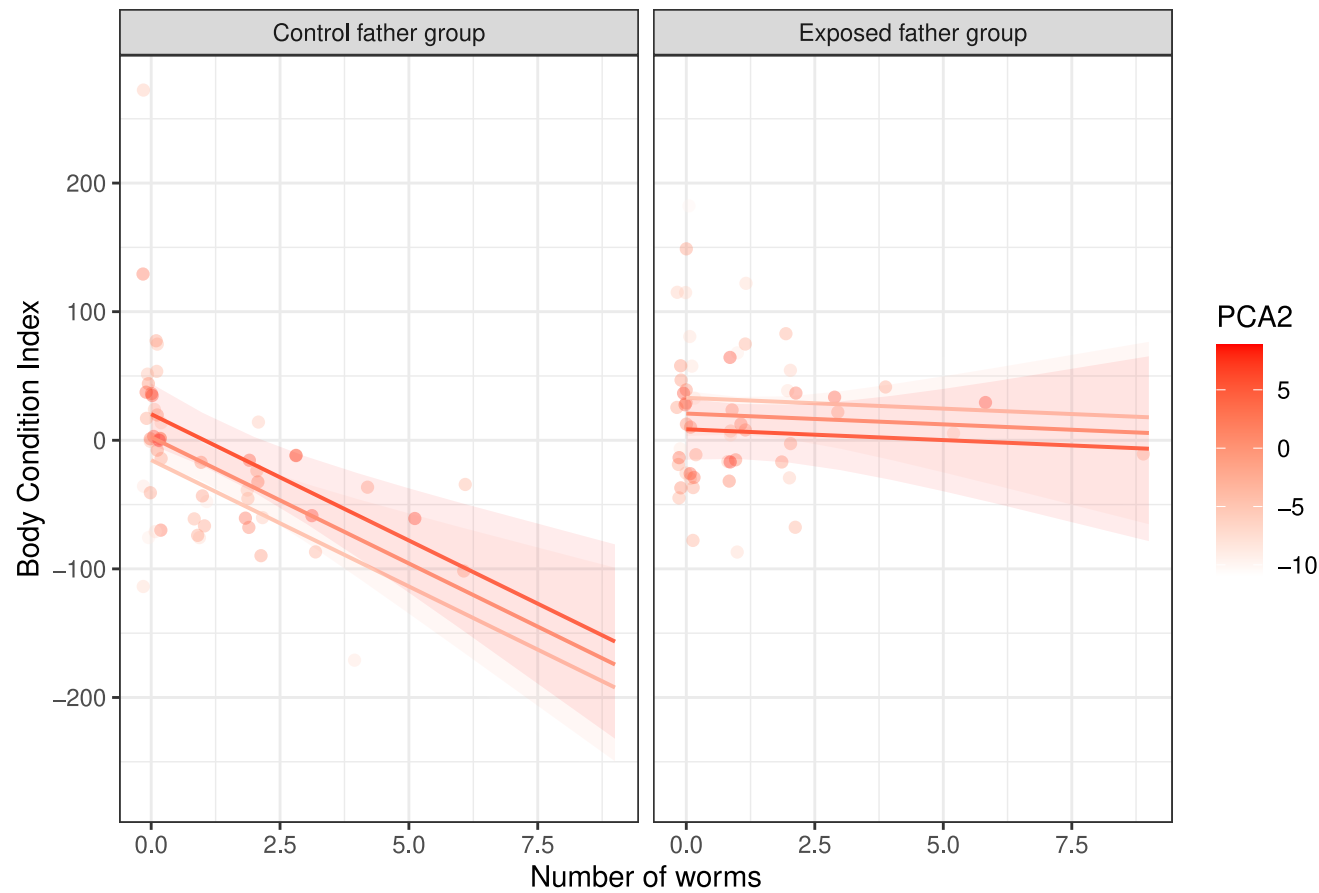
1640 DMS linked with intergenerational origin
 862 CpG sites most correlated ($p < 0.05$) with PCA1
 826 CpG sites most correlated ($p < 0.05$) with PCA2
 The chosen model is:
 $BCI \sim PCA2 + No.Worms + paternal\ treatment + PCA2:paternal\ treatment + No.Worms:paternal\ treatment + (1 | father's\ family) + (1 | Sex)$
 Backward reduced elimination with Satterthwaite method
 $PCA2:paternal\ treatment\ F=12.48, p-value<0.001$
 $No.Worms:paternal\ treatment\ F=6.47, p-value=0.012$
 Variance in BCI associated with:
 $No.Worms=10.4\%$ $paternal\ treatment=22\%$ $PCA2=9.6\%$

Predicted values of Body Condition Index in offspring: intergenerational

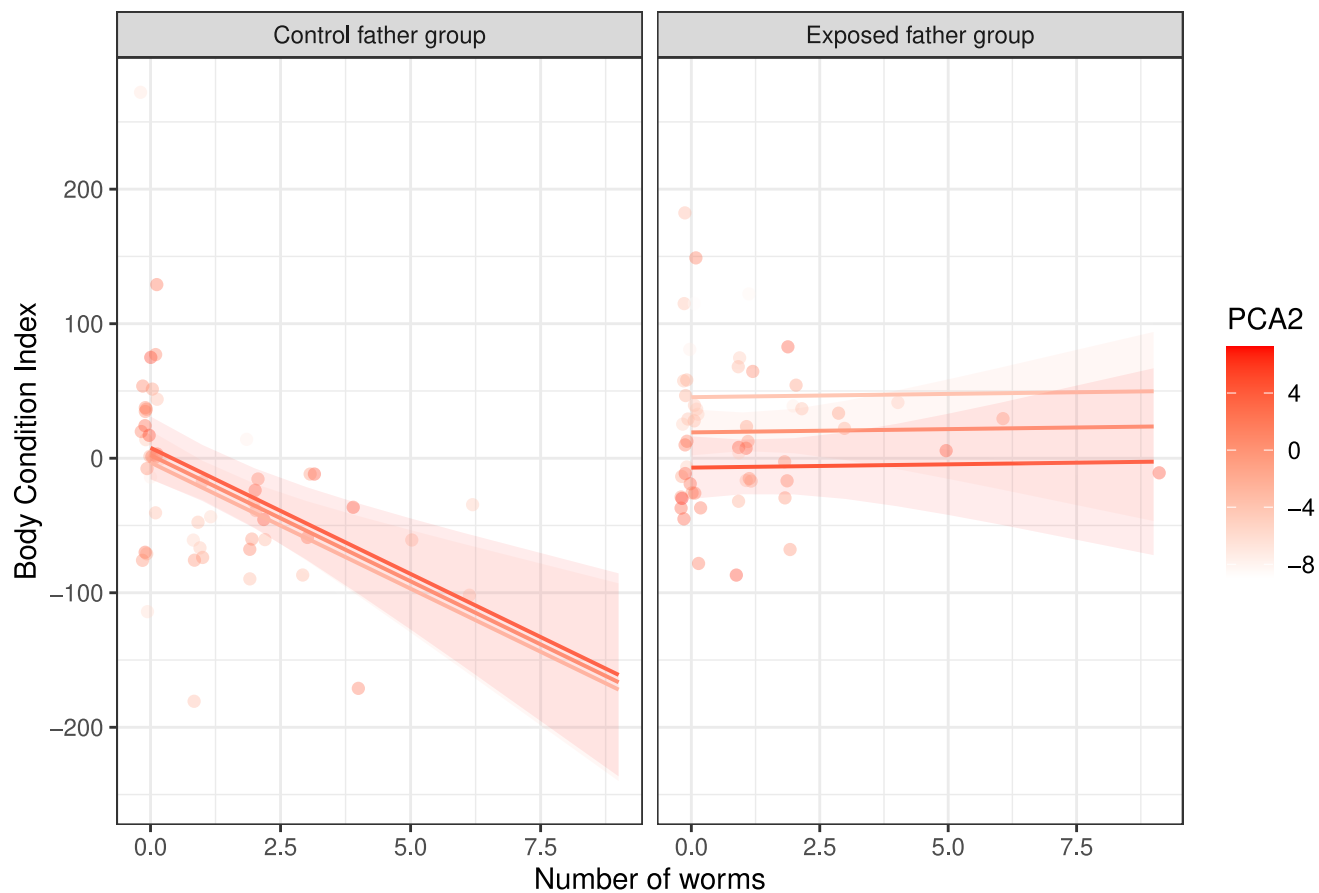


309 DMS linked with infection-induced origin
 181 CpG sites most correlated ($p < 0.05$) with PCA1
 178 CpG sites most correlated ($p < 0.05$) with PCA2
 The chosen model is:
 $BCI \sim PCA2 + No.Worms + paternal\ treatment + PCA2:paternal\ treatment + No.Worms:paternal\ treatment + (1 | father's\ family) + (1 | Sex)$
 Backward reduced elimination with Satterthwaite method
 $PCA2:paternal\ treatment\ F=12.48, p-value<0.001$
 $No.Worms:paternal\ treatment\ F=6.47, p-value=0.012$
 Variance in BCI associated with:
 $No.Worms=11.8\%$ $paternal\ treatment=18.9\%$ $PCA2=6.1\%$

Predicted values of Body Condition Index in offspring: infection-induced

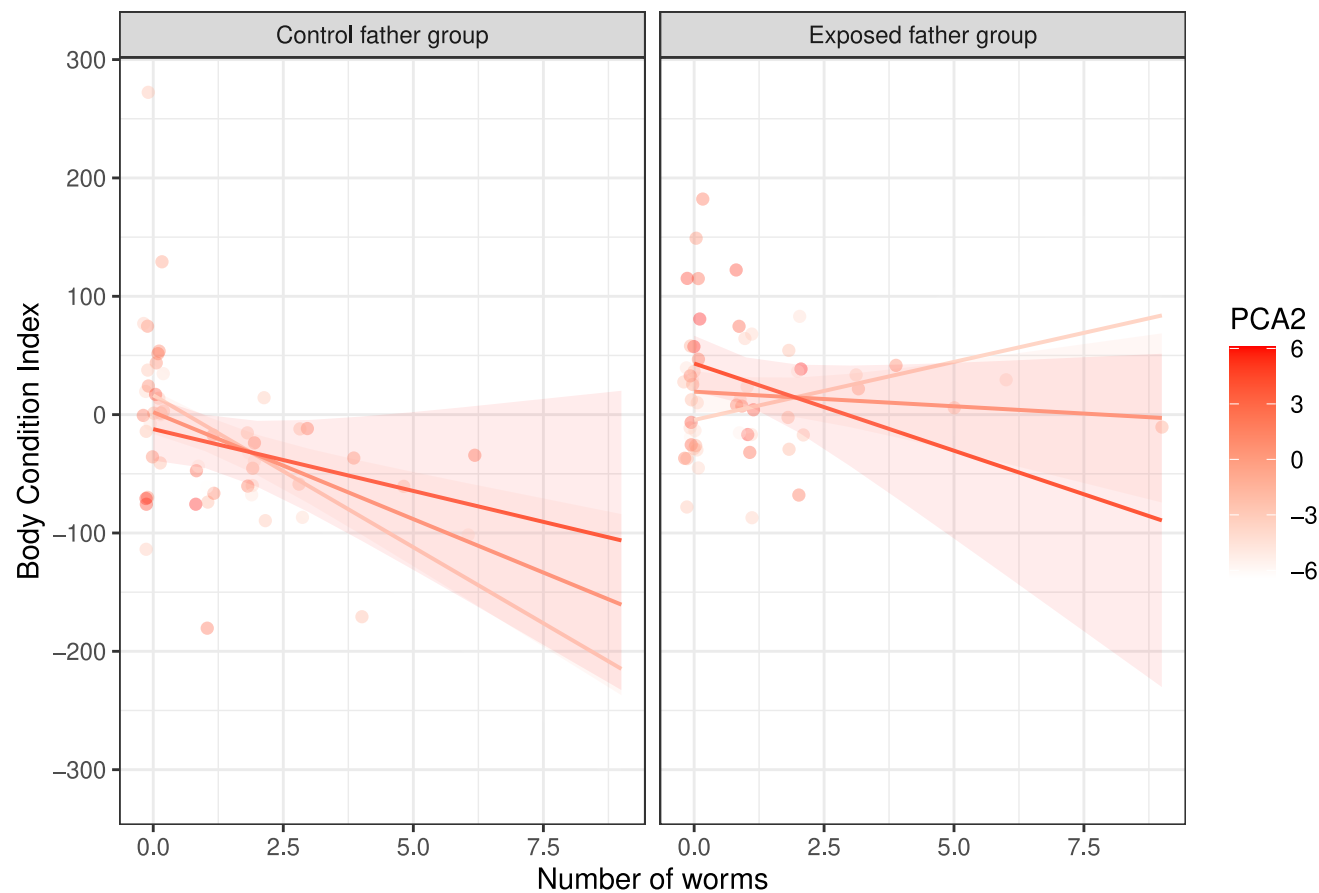


Predicted values of Body Condition Index in offspring: additive



173 DMS linked with additive origin
 95 CpG sites most correlated ($p < 0.05$) with PCA1
 81 CpG sites most correlated ($p < 0.05$) with PCA2
 The chosen model is:
 $BCI \sim PCA2 + No.Worms + paternal\ treatment + PCA2:paternal\ treatment + No.Worms:paternal\ treatment + (1 | father's\ family) + (1 | Sex)$
 Backward reduced elimination with Satterthwaite method
 $PCA2:paternal\ treatment\ F=12.48, p-value<0.001$
 $No.Worms:paternal\ treatment\ F=6.47, p-value=0.012$
 Variance in BCI associated with:
 $No.Worms=10.9\%$ $paternal\ treatment=20\%$ $PCA2=9.2\%$

Predicted values of Body Condition Index in offspring: interaction



151 DMS linked with interaction origin
 72 CpG sites most correlated ($p < 0.05$) with PCA1
 54 CpG sites most correlated ($p < 0.05$) with PCA2
 The chosen model is:
 $BCI \sim PCA2 + No.Worms + paternal\ treatment + PCA2:No.Worms + PCA2:paternal\ treatment + No.Worms:paternal\ treatment + (1 | father's\ family) + (1 | Sex)$
 Backward reduced elimination with Satterthwaite method
 $PCA2:paternal\ treatment\ F=12.48, p-value<0.001$
 $No.Worms:paternal\ treatment\ F=6.47, p-value=0.012$
 Variance in BCI associated with:
 $No.Worms=14.8\%$ $paternal\ treatment=19\%$ $PCA2=7.1\%$