Supplemental information for manuscript:

**Environment-driven reprogramming of gamete DNA methylation occurs during maturation and is transmitted intergenerationally in Atlantic Salmon**

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**Supplemental Figure 1:** Distribution of methylation proportion (# methylated bases / read coverage) for 16.4 million CpG sites from adult sperm samples.



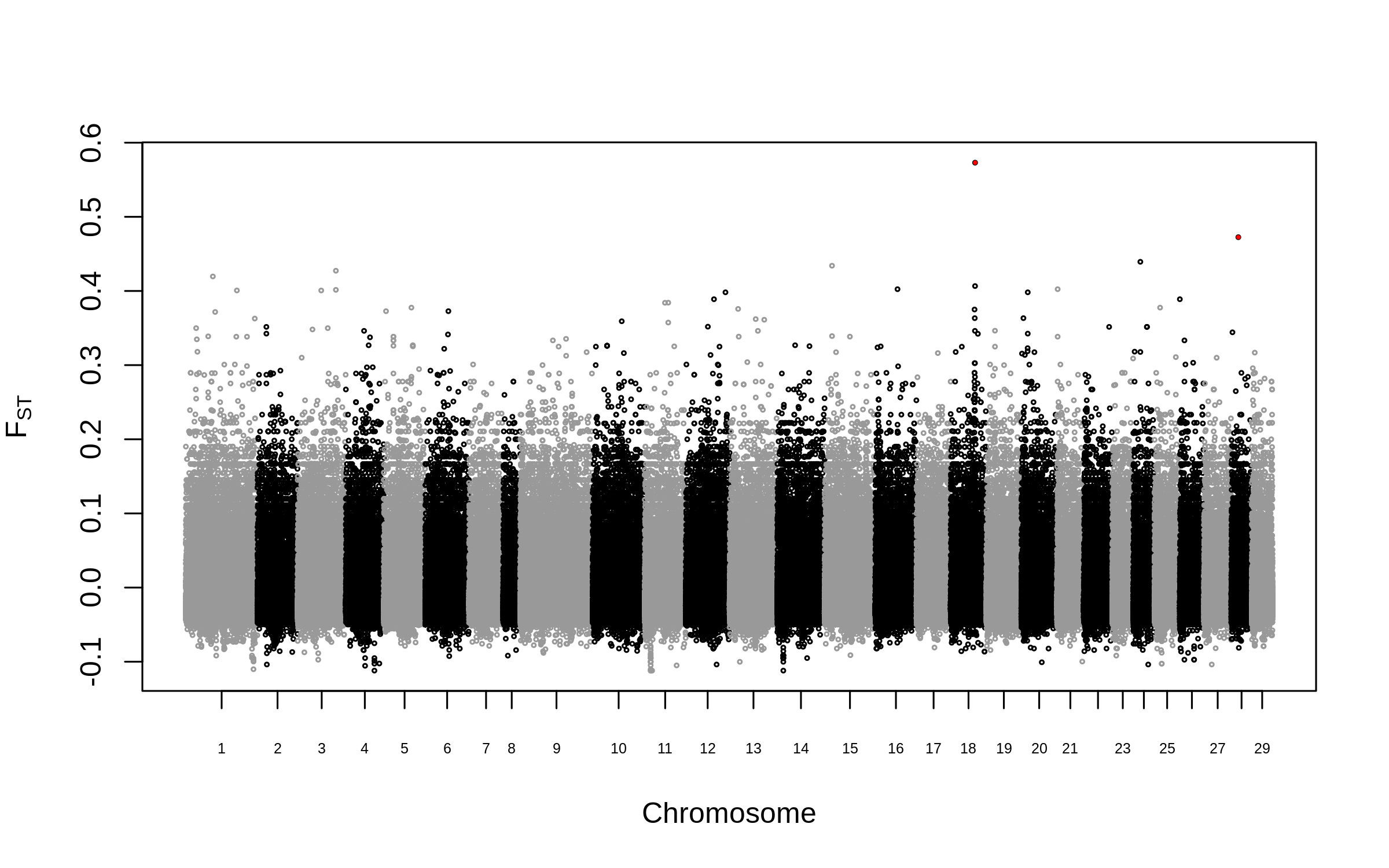
**Supplemental Figure 2:** Distribution of methylation proportion (# methylated bases / read coverage) for 23.1 million CpG sites from juvenile liver samples.



**Supplemental Figure 3:** Differential methylated regions (DMR) between SAS (yellow) and wild (blue) salmon that overlapped (A-B) or targeted the same gene (C) between sperm (solid lines) and juvenile liver tissues (dashed lines). Grey boxes highlight the extent of DMRs and the lower tracks indicate annotated genes.



**Supplemental Figure 4:** Heatmap of methylation – phenotype correlations for all modules (represented by color names on the y-axis) with at least one significant correlation. Colors and values in the cells represent the magnitude and direction of the correlation coefficient (blue = negative correlation, red = positive correlation) with the statistical significance of the correlation coefficient in parentheses (p-value). Phenotypes on the x-axis: WT = weight in g, FL and TL = fork length and total length in mm, and CF = condition factor (105 \* WT / FL^3).



**Supplemental Figure 5:** Distribution of genetic divergence (FST) between SAS and wild salmon for 974,219 single nucleotide polymorphisms. The genome-wide average divergence (FST) did not differ from zero (AMOVA; 1000 permutations: p = 0.77). Outliers (FDR < 0.01) identified by OutFLANK are highlighted in red. Neither BayeScan, nor a polygenic framework (RDA, R2 = 0, p = 0.71) identified any outliers.