**Supplementary Information 1**

Phenotypic records of sea lice counts (SLC) were collected for all offspring. SLC had a positively skewed distribution with a mean of 25.5 and median 23.5. SLC was logarithmically transformed and loge(SLC) had a mean of 3.11 and median of 3.16.

**Figure S1.** **Distributions of SLC and loge(SLC)**

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Data structure exploration was conducted using classical multi-dimensional scaling (CMDS) (function “cmdscale” in R/3.1.2) to visualize the genetic distances between individuals for three dimensions, using the genomic relationships matrix. The analysis did not reveal any sub-clustering in the data (Figure S1), and no family-specific clustering was observed (Figure S2).

**Figure S2.** **CMDS plots for three principal coordinates (left panel), and CMDS plot where different colours represent the different families in the data (right panel)**

