Supporting information for:

High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal

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**Fig. S1.** Phylogenomic trees for the analyzed seal lice. (A) Maximum-likelihood tree based on a concatenated sequence matrix, (B) coalescent tree calculated from 1043 gene-specific trees. Numbers above branches are bootstrap proportions (%) in (A) and quartet-based local posterior probability values in (B). Specimen codes next to branch tips indicate the louse individual (starting with “Echor”) and the seal host individual from which the louse was collected (starting with “Phs”). Specimen labels and circles next to the labels are colored according to the seal individual that each louse was collected from, while circle shading indicates sampling locations across the three main areas of Lake Saimaa (see legend).

**Fig. S2.** Cross-validation error in relation to the number of ancestral populations ($K$).

**Table S1.** Collection information for the sequenced seal lice and their seal host individuals, with information on individual-level heterozygosity, inbreeding, and data (numbers of sites and reads, and accession numbers). (.xlsx file)

**Table S2.** Pairwise kinship coefficients between the analyzed seal lice. Matrix cells are color coded by values, so that higher values are darker. Framed values along the diagonal are self-kinship coefficients, values in bold font indicate the second-highest kinship coefficient for each louse (by column). (.xlsx file)
(A) ML tree, concatenated data

(B) Astral tree

Fig. S1
