

1 **Long-distance dispersal, ice sheet dynamics, and mountaintop isolation underlie the genetic**  
2 **structure of glacier ice worms**

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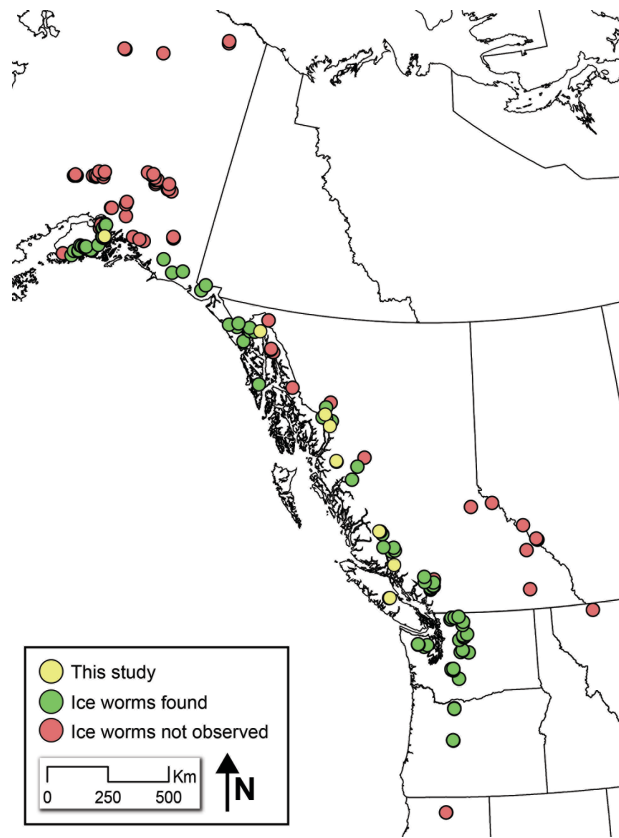
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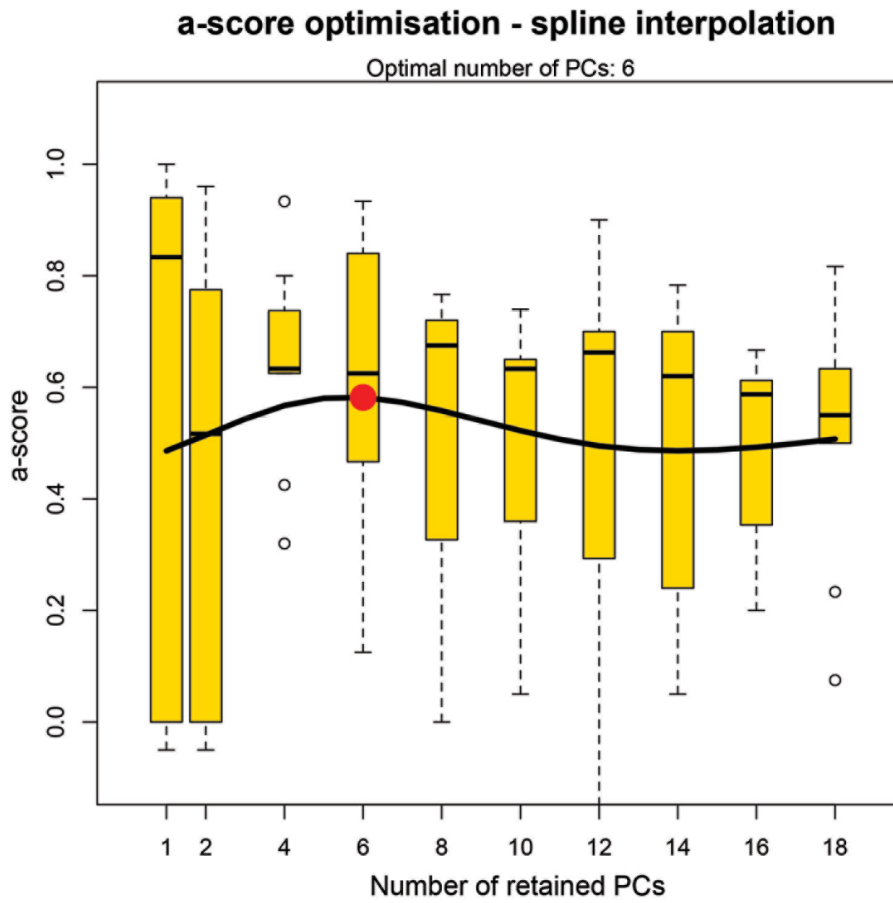
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18 **Supplementary Figures:**

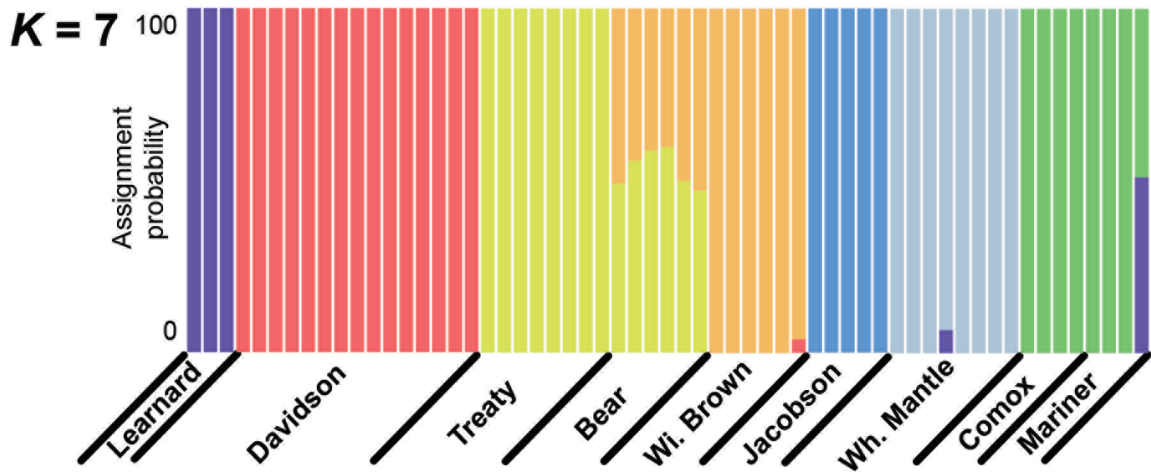


**Figure S1.** The known distribution of ice worms (*Mesenchytraeus solifugus*). Presence and absence information stems from a collection of personal communication with Roman Dial and previous published manuscripts [1-3].

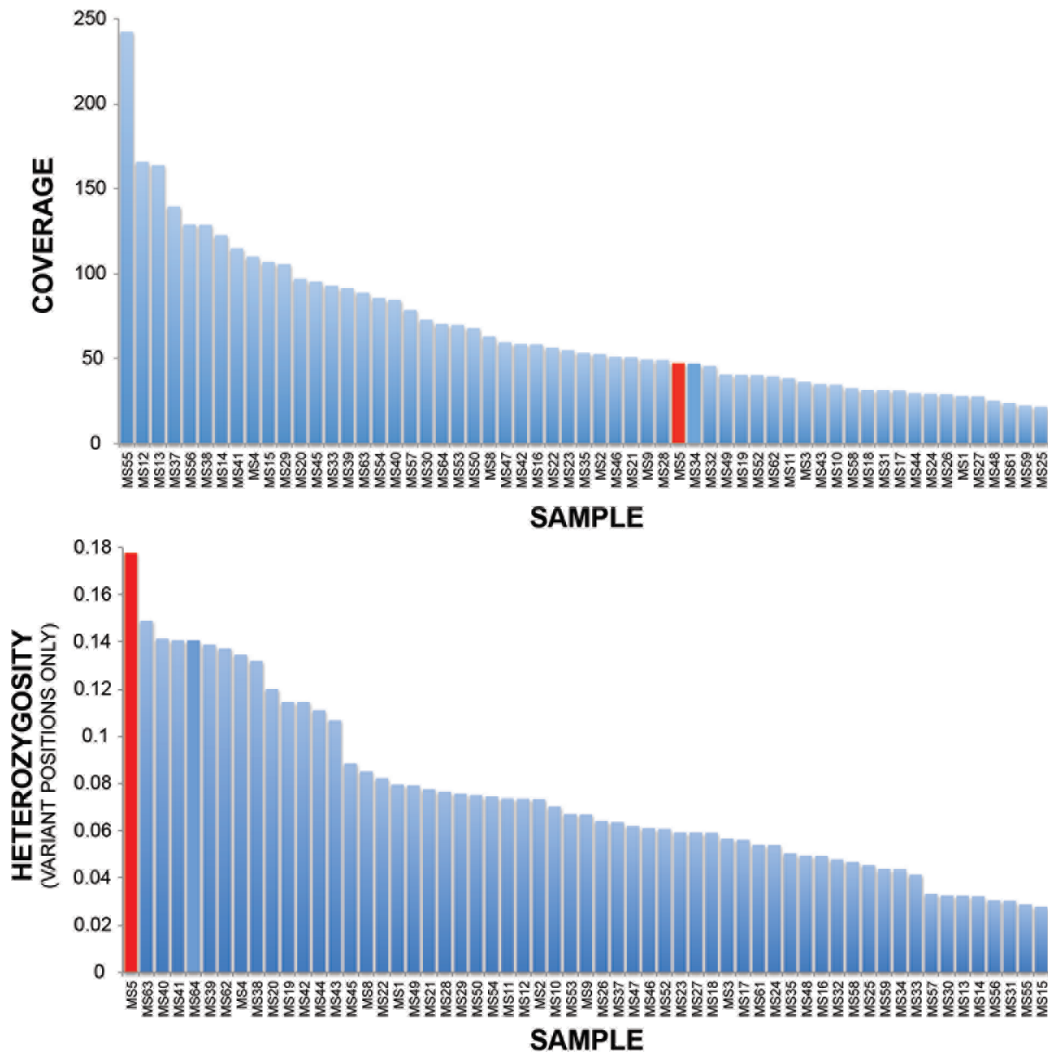


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**Figure S2.** An  $\alpha$ -score plot for identifying the optimal number of principal components (PCs) to retain in DAPC analyses. The optimal number of PCs to retain (6) is highlighted by a red circle.



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 30 **Figure S3.** A secondary ADMIXTURE solution for  $K = 7$  shared by several runs which were the  
 31 best-fit (minimized cross-validation error) for their individual replicates, but not the best-fit for  $K$   
 32  $= 7$  overall.



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**Figure S4.** Mean coverage and heterozygosity (variant positions only) for all ice worms included in this study. Red bars highlight a single individual (MS5) which bore a signature of substantial admixture between southern Alaska (Leonard Glacier population) and Vancouver Island (Mariner Glacier population).

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