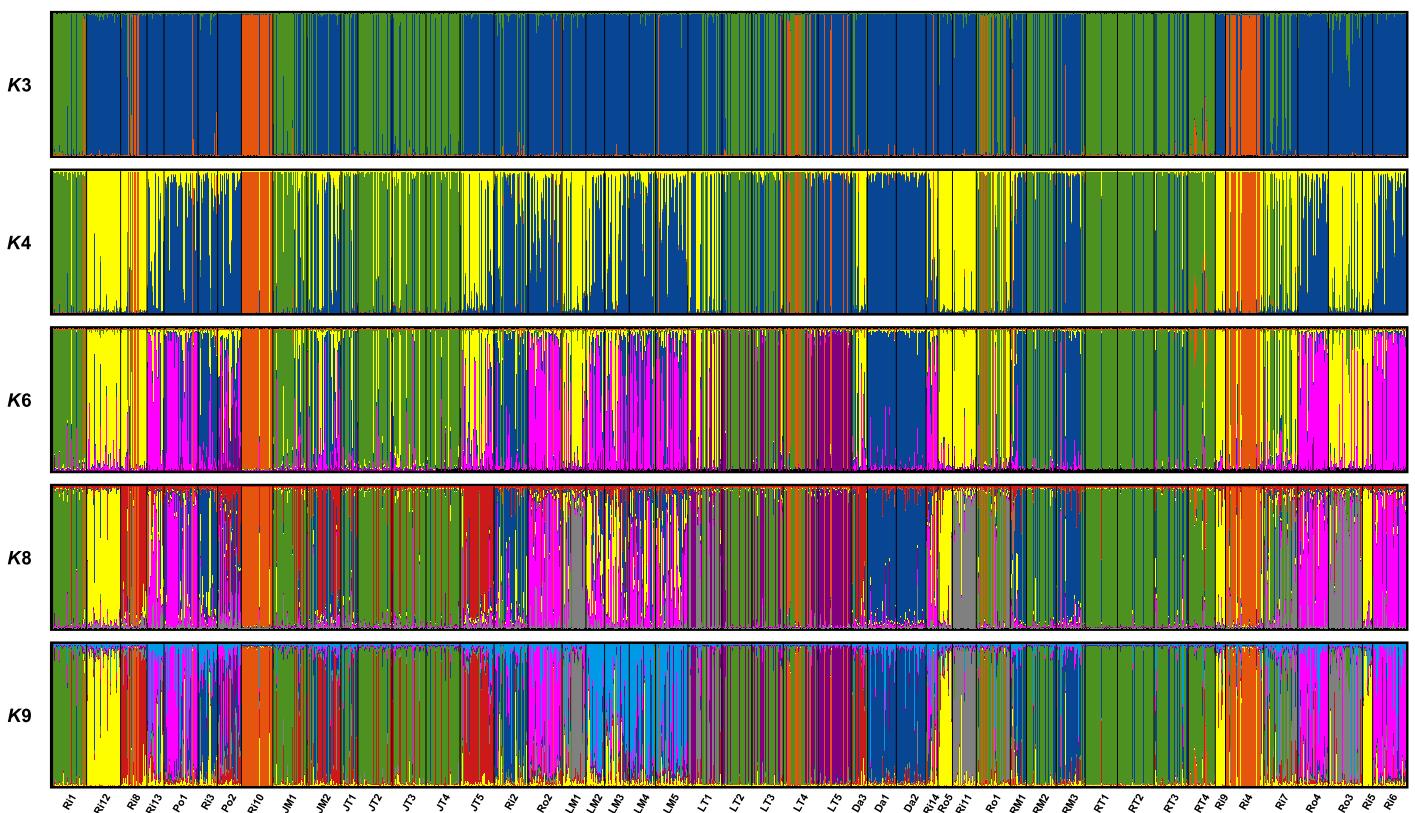


#### Additional file 4. Results from Bayesian clustering (STRUCTURE).

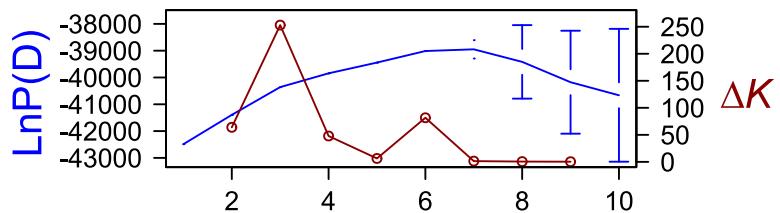
Individual assignment results from Bayesian clustering following Pritchard *et al.* (2000) performed on **(a)** 1591 individuals of the *B. alpinus* group (*s.l.*), including *B. alpinus* and *B. melanonyx* (corrected for multimodality) and, **(b)** *B. alpinus* cryptic lineages and *B. melanonyx* datasets separately. **(c)** STRUCTURE results for separate *B. alpinus* cryptic lineages and *B. melanonyx* datasets: mean ( $\pm$ SD) probabilities of the data  $\text{Ln Pr}(X|K)$  over 30 replicated runs plotted as a function of the putative number of clusters  $K$  (blue dots) and the standardized second-order rate of change of  $\text{Ln Pr}(X|K)$ ,  $\Delta K$ , as a function of  $K$  (red dots).

**a**

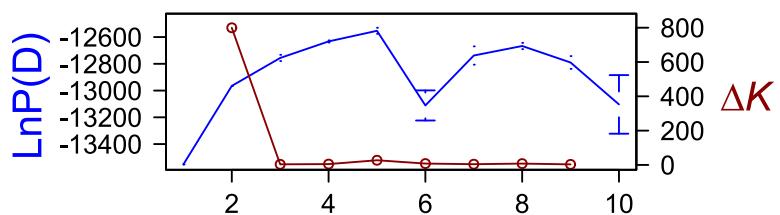


**C**

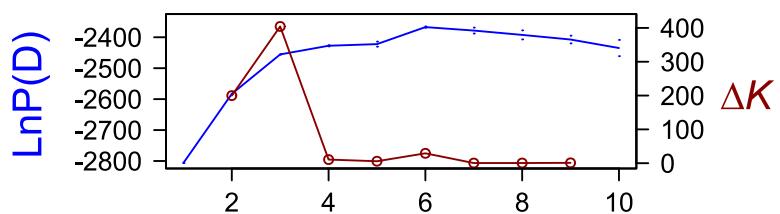
***B. alpinus* lineage A**



***B. alpinus* lineage B**



***B. melanonyx***



Reference:

Pritchard JK, Stephens M, Donnelly P: **Inference of population structure using multilocus genotype data.** *Genetics* 2000, **155**(2):945-959.