Whole-genome resequencing reveals domestication and signatures of selection in Ujimqin, Sunit, and Wu Ranke Mongolian sheep breeds

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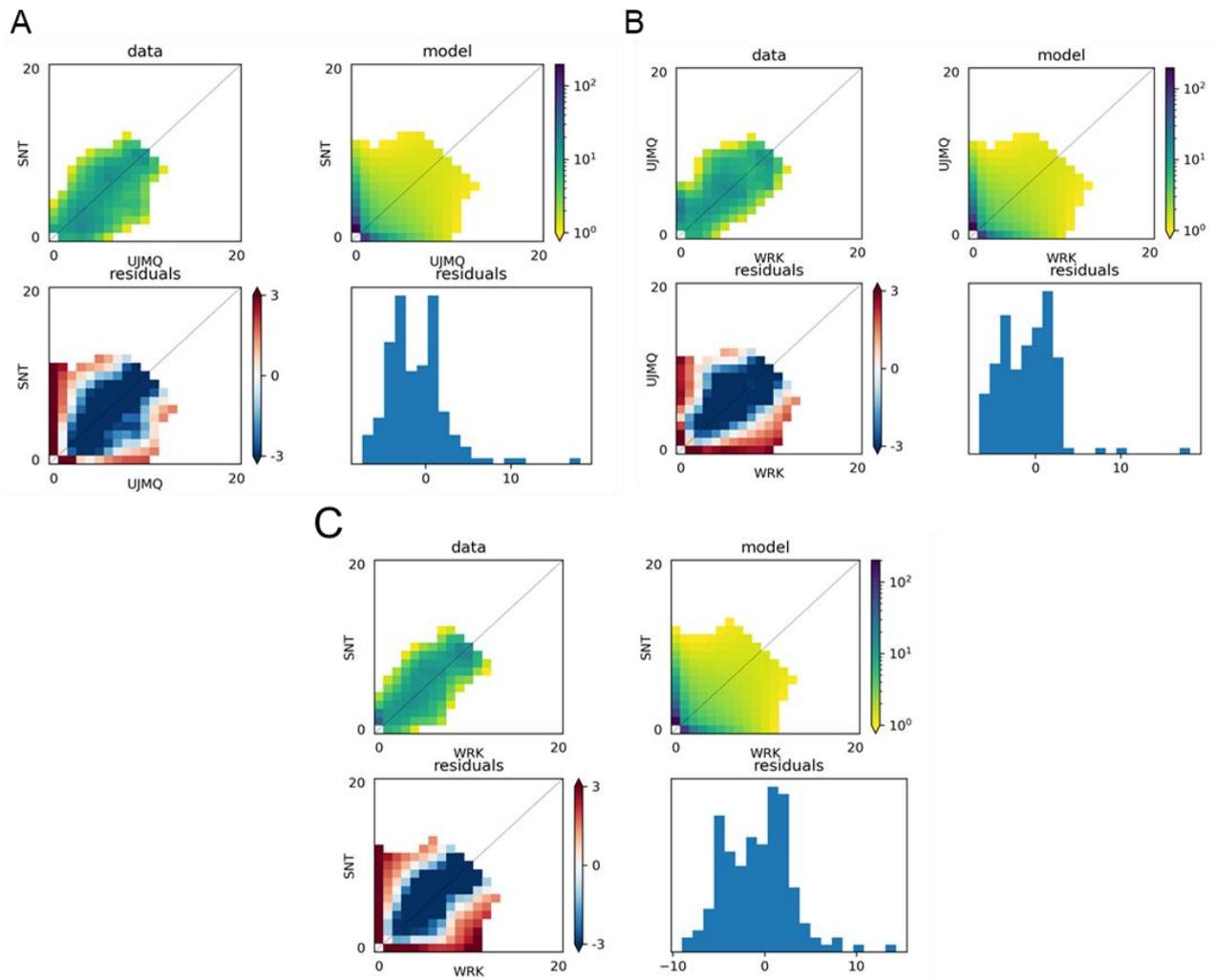[a] These authors contributed equally to this work.

Figure S1. Two-dimensional comparison for joint estimation between SNT and UJMQ (**a**), WRK and UJMQ (**b**), SNT and WRK (**c**) sheep breeds populations. The two panels upside are marginal spectra for data and the maximum-likelihood model, respectively. The two panels downside show the residuals.
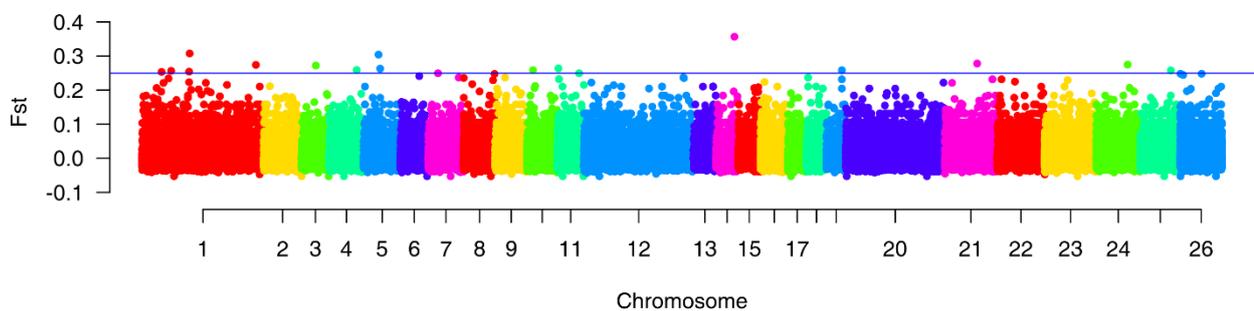

Figure S2. Genome-wide analysis of global *Fst* between WRK and SNT populations.