Supplementary Figures for

Genome-wide relaxation of selection and the evolution of the island syndrome in Orkney voles

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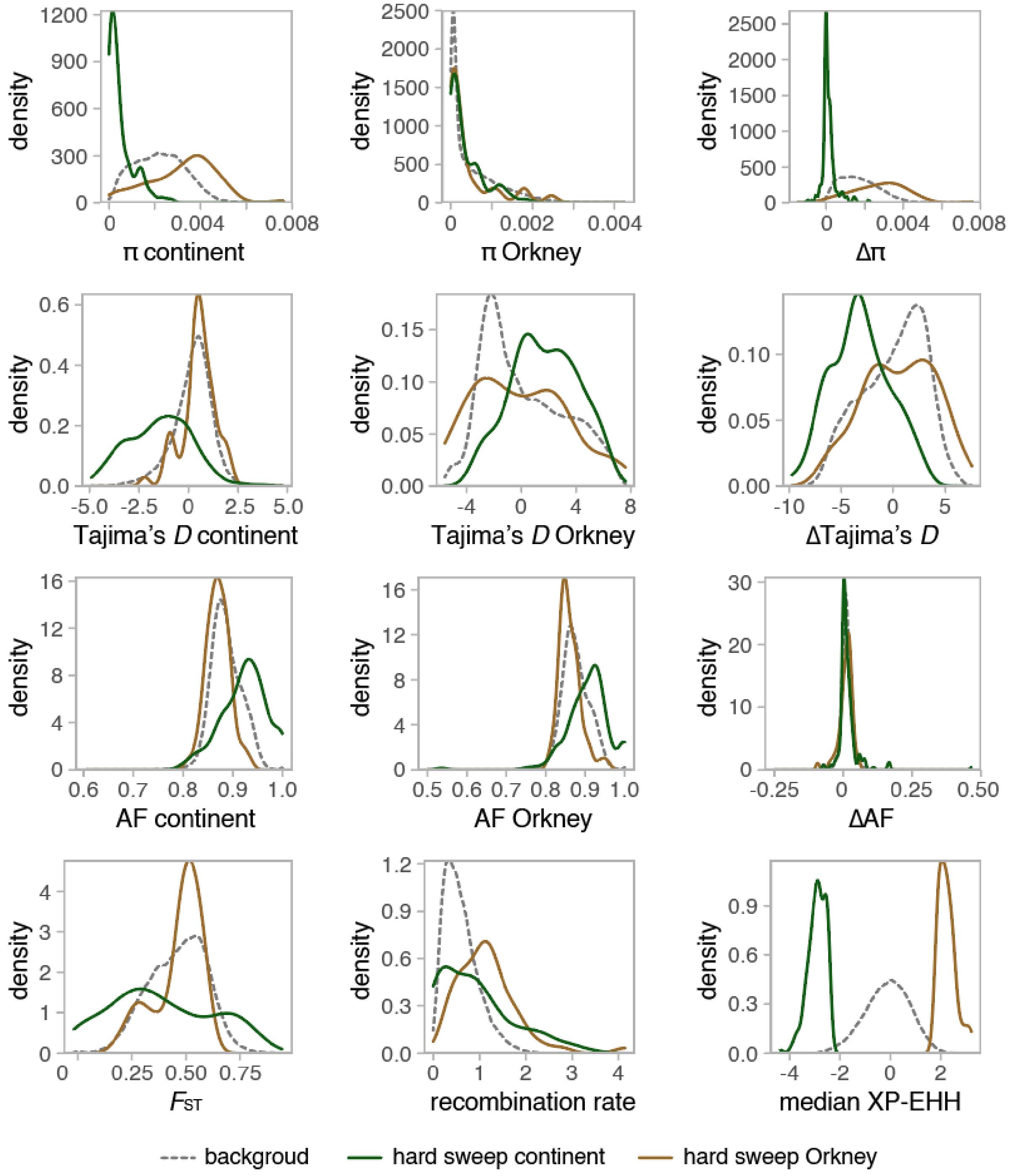

Figure S1. The density distributions of genomic parameters used for test for selective sweeps in both groups, including π, Tajima's D and allele frequency (AF) in both groups; between groups: Δπ ($\pi_{\text{continent}} - \pi_{\text{Orkney}}$), ΔTajima's D (Tajima's $D_{\text{continent}}$ – Tajima's D_{Orkney}), ΔAF ($AF_{\text{continent}} - AF_{\text{Orkney}}$), F_{ST} and median XP-EHH value; and recombination rate. The distribution of background windows (the majority cluster from DBSCAN, N=38,859) are shown as dashed line in grey. The distribution of windows of hard sweeps in continental voles (N=178) are shown as solid line in green and in Orkney voles (N=57) in brown.

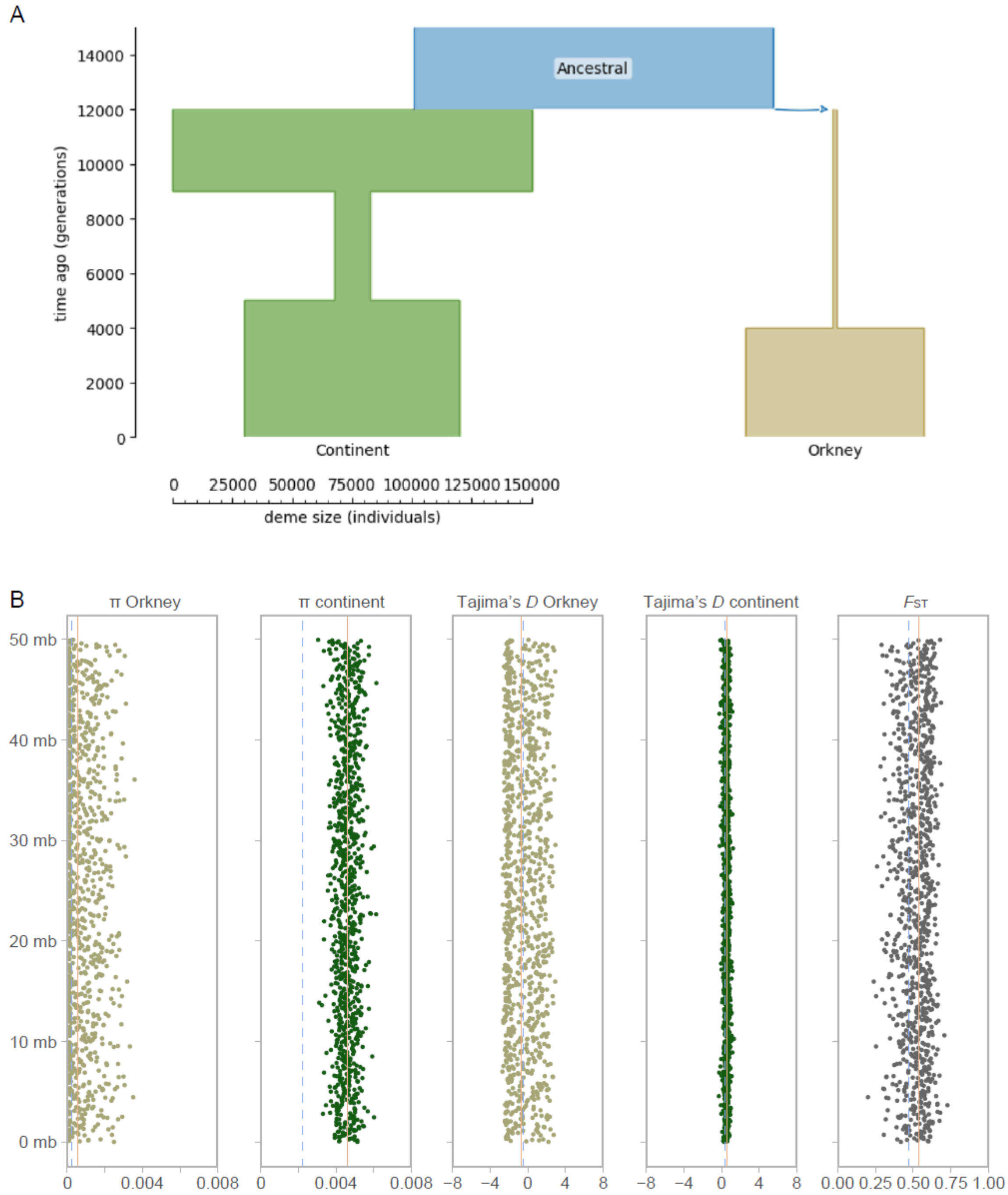

Figure S2. Demographic model and genomic landscapes for the simulations of selectively neutral genomic data with msprime. **A**. The simulated ancestral vole population was 150,000 individuals for 2,000 generations. The Orkney population experienced after the colonization a bottleneck for 8,000 generations with N=2,000 after the split, then N recovered to 75,000. The continental population experienced 3,000 generations after the split a bottleneck for 4,000 generations with N=15,000 and recovered then to N=90,000. For details on the empirical demographic history see Wang et al. (2023). **B**. Genomic landscapes along the simulated 50 mb genome. Solid orange lines show the median values of estimations from simulated data and dashed blue lines show the median values from empirical data.

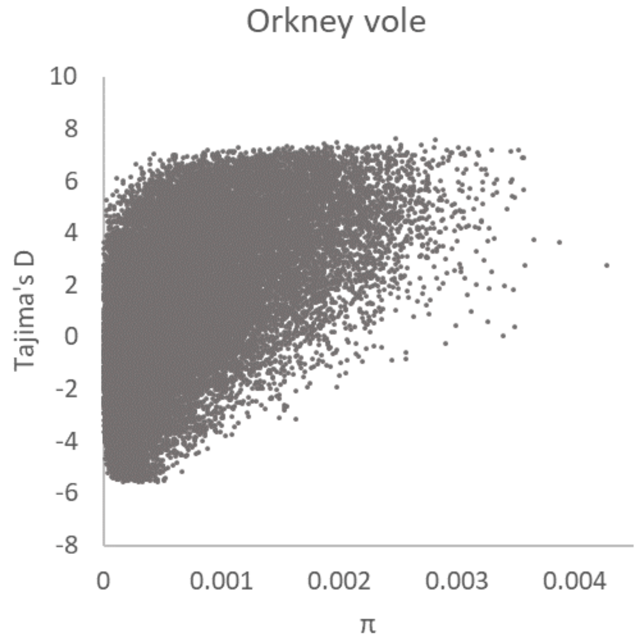

Figure S3. Positive correlation between π and Tajima’s D (Peason coefficient *r* = 0.673) in Orkney voles fits the expectation of genomic features after an ancient bottleneck.

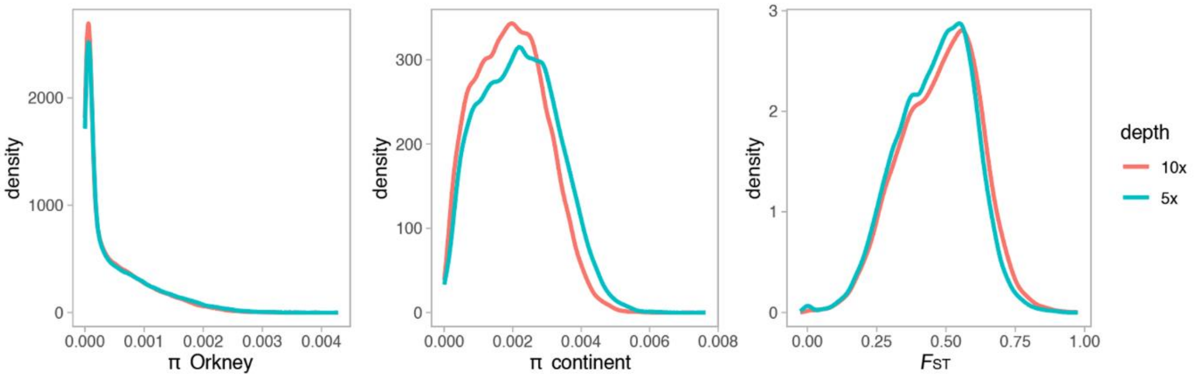

Figure S4. Density distributions of π of Orkney voles and F_{ST} in 50 kb windows over the whole genome with lowest depth filter of SNPs at 5x and 10x. Average π in Orkney voles with the threshold at 5x: 0.00052; with a threshold of 10x: 0.00049. Average π in continental voles with the threshold at 5x: 0.0022; with the threshold at 10x: 0.0020. The average F_{ST} at 5x: 0.46 and at 10x: 0.48.

Reference

Wang X, Peischl S, Heckel G. 2023. Demographic history and genomic consequences of 10,000 generations of isolation in a wild mammal. *Current Biology* doi:10.1016/j.cub.2023.04.042.