Figure S2. Fixation index (F\textsubscript{ST}) analysis in fox populations.

Fixation index (F\textsubscript{ST}) values were computed for 1 Mb windows for tame versus aggressive fox populations. The y-axis indicates “weighted_F\textsubscript{ST}” values calculated with VCFtools. The x-axis indicates genomic positions on fox chromosomes, as extrapolated from syntenic regions in the dog genome. Each dot represents a 1 Mb window, the windows overlap by 500 kb. The horizontal black line indicates F\textsubscript{ST}=0.5. The results of the F\textsubscript{ST} analysis are consistent with the analysis of allele frequency differences.

S2A. Distribution of F\textsubscript{ST} values in the fox genome. The chromosomes are indicated by color change. The positions of VVU3, VVU8 and VVU14 are shown.

S2B. F\textsubscript{ST} values on VVU3, VVU8, and VVU14. The regions with high F\textsubscript{ST} values identified on these chromosomes overlap with the regions identified in the analysis of allele frequency differences (see also Table S6).
B.

**VVU3**

![Graph of Fst vs. Estimated Location on VVU 3](image)

**VVU8**

![Graph of Fst vs. Estimated Location on VVU 8](image)

**VVU14**

![Graph of Fst vs. Estimated Location on VVU 14](image)