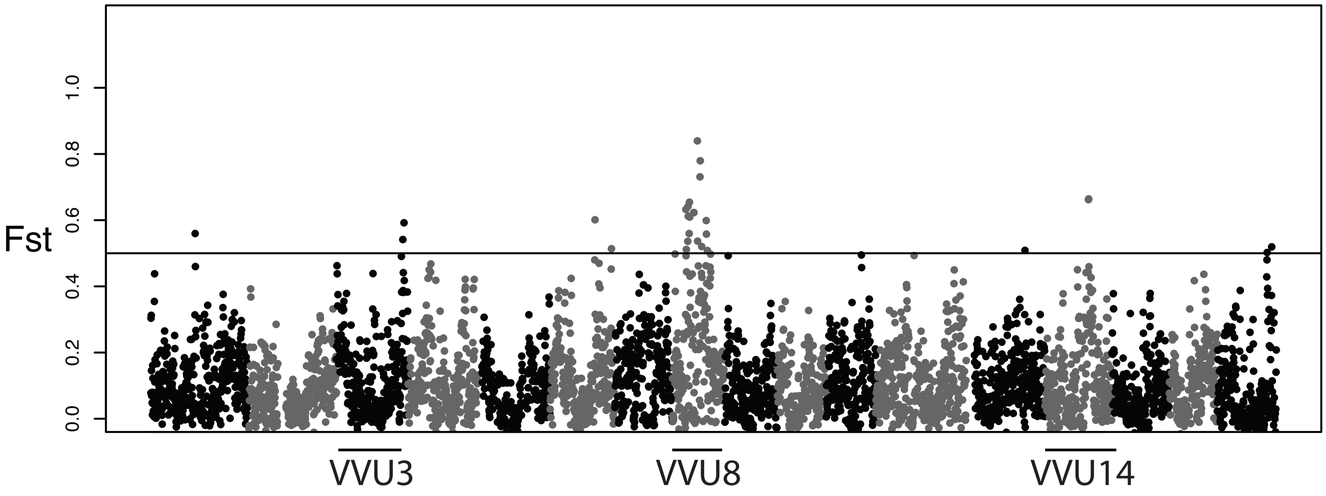
Figure S2. Fixation index (FST) analysis in fox populations.

Fixation index (FST) values were computed for 1 Mb windows for tame versus aggressive fox populations. The y-axis indicates “weighted_FST” 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 FST=0.5. The results of the FST analysis are consistent with the analysis of allele frequency differences.

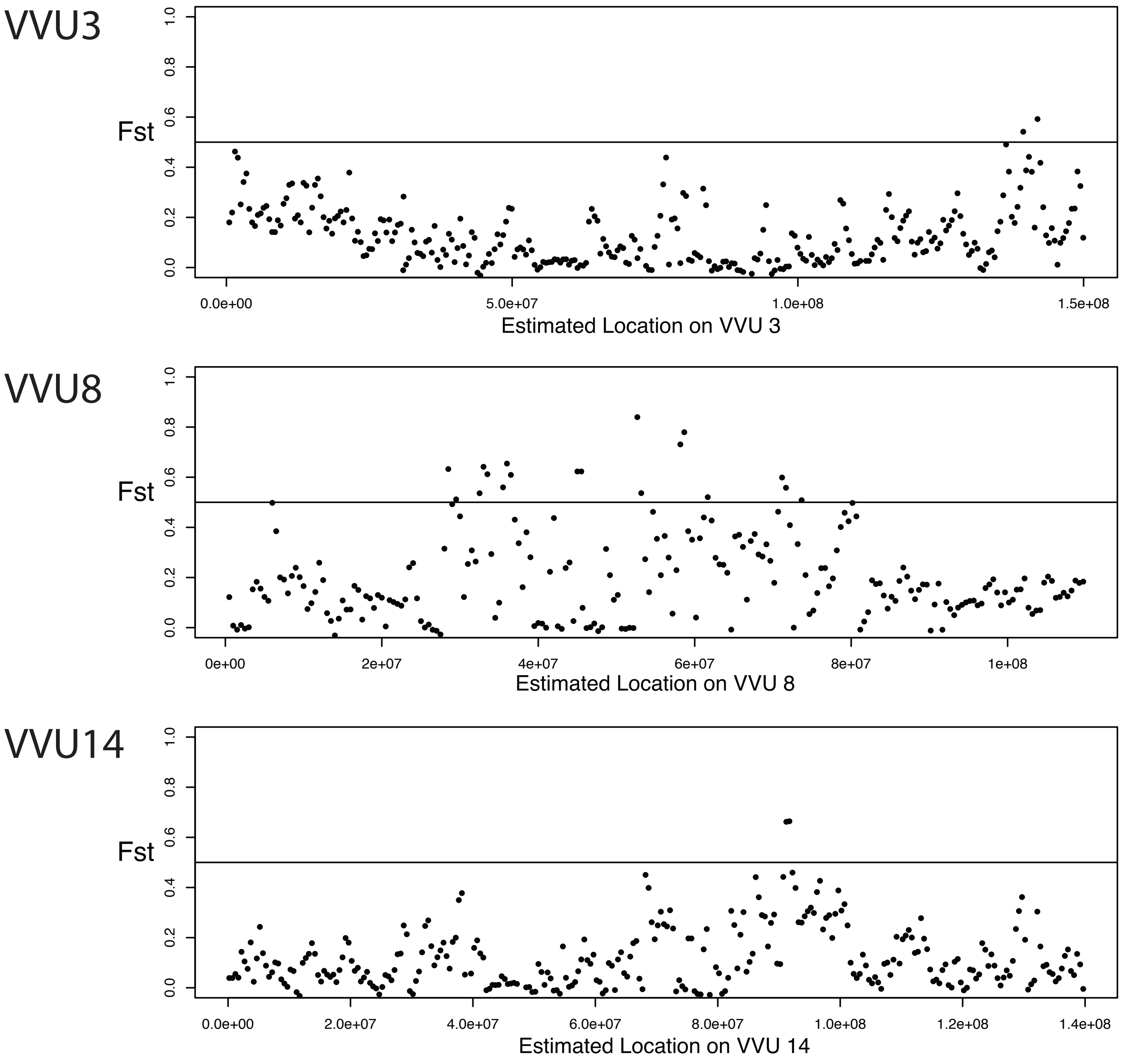
S2A. **Distribution of FST values in the fox genome.** The chromosomes are indicated by color change. The positions of VVU3, VVU8 and VVU14 are shown.

S2B. FST values on VVU3, VVU8, and VVU14. The regions with high FST values identified on these chromosomes overlap with the regions identified in the analysis of allele frequency differences (see also Table S6).

A.



B.


VVU3
Fst
0.0
0.2
0.4
0.6
0.8
1.0
0.0e+00
5.0e+07
1.0e+08
1.5e+08
Estimated Location on VVU 3
VVU8
Fst
0.0
0.2
0.4
0.6
0.8
1.0
0e+00
2e+07
4e+07
6e+07
8e+07
1e+08
Estimated Location on VVU 8
VVU14
Fst
0.0
0.2
0.4
0.6
0.8
1.0
0.0e+00
2.0e+07
4.0e+07
6.0e+07
8.0e+07
1.0e+08
1.2e+08
1.4e+08
Estimated Location on VVU 14