

Figure S3. Allele frequency differences and significant F_{ST} windows on VVU8.

The black dots within the gray bar on the top indicate regions with $F_{ST} \geq 0.5$. Yellow dots are the Bonferroni corrected significance of the allele frequency differences between the tame and aggressive populations calculated by PLINK2. The y-axis indicates $-\log_{10}$ (Bonferroni corrected p-value) for SNP allele frequency differences. Genomic positions in fox, as extrapolated from syntenic regions in the dog genome, are plotted on the x-axis. The black horizontal line corresponds to a significance cutoff of $(-\log_{10} = 6)$ for the allele frequency differences. The horizontal colored bars on the x-axis correspond to syntenic dog chromosomes. Two genes, *GRIN2B* (*NMDA*) and *GABARAPL1* (*GEC1*), that represent interesting positional candidate genes are shown.

