Figure S3. Allele frequency differences and significant Fst windows on VVU8.

The black dots within the gray bar on the top indicate regions with Fst ≥ 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 -log10 (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 (-log10 = 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.