**Supplementary information**

**Legends for the supplementary figures and tables**

**Supplementary Figure 1**: QQ plots of dog herding, predation, temperament and trainability GWASs without **(A)**/with **(B)** including body size as covariates.

**Supplementary Figure 2**: Evolutionary conservation analysis results of *MSRB3* missense mutation in 10 species using Clustal W (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The amino acid sequence accession numbers of the 10 species are as follows: House mouse XP\_006513829.1, Chimpanzee XP\_016778576.1, Pig XP\_020947614.1, Cattle XP\_024848255.1, Sheep XP\_027823281.1, Chicken XP\_015137097.1, Dog XP\_013972688.1, Horse XP\_023499721.1, Human XP\_024304686.1 and Rhesus monkey NP\_001244780.1.

**Supplementary Figure 3**: Single-cell gene expression of 10 candidate genes through the neural development processes (oocyte, zygote, 2-cell, 4-cell, 8-cell,16-cell, blastocyst, human embryonic stem cells (hESC), H1\_24\_wells, H1\_96\_wells, neural\_D12 neural\_D26, neural\_D54, neural\_D80). Dn: cell line fused with endogenous SOX2 (a marker of progenitors) Dp: cell line fused with DCX (a marker of immature neurons).

**Supplementary Table 1.** Phenotypic information of 268 dogs. Case/control/missing are indicated by 2/1/NA.

**Supplementary Table 2.** Linkage disequilibrium sites of herding GWAS significant association sites (r2 > 0.8).

**Supplementary Table 3**. 2287 potentially functional private genes and priority candidate variants of herding dogs.