### Table A1  Description of German Shepherd dog populations. Summary statistics for behaviour traits and other dog attributes within the UK and the Swedish GSD populations.

|                        | UK         | Sweden     |
|------------------------|------------|------------|
| **Number**             | 182        | 68         |
| **Behaviour traits†**  |            |            |
| Stranger-directed aggression | 0.29±0.88 | -0.04±0.9  |
| Dog-directed aggression  | -0.13±0.97 | 0.21±1.14  |
| Stranger-directed fear  | -0.02±1.11 | -0.13±1.1  |
| Human-directed playfulness | -0.2±1.08 | 0.23±0.77  |
| Excitability           | 0.06±0.95  | 0.17±0.99  |
| Separation anxiety     | 0.03±0.89  | 0.02±0.96  |
| Lack of obedience      | -0.09±0.95 | -0.02±0.85 |
| Stranger-directed interest | 0.24±0.96 | -0.08±0.79 |
| Attachment/ Attention seeking | -0.12±1  | 0.06±0.94  |
| Chasing                | 0.24±0.93  | -0.3±0.97  |
| Non-social fear        | 0.11±1     | 0.17±1.15  |
| Dog-directed fear      | -0.01±0.92 | 0.11±0.97  |
| Touch-sensitivity      | -0.02±0.87 | -0.04±1    |
| **Sex‡**               |            |            |
| Male                   | 97 (53%)   | 38 (56%)   |
| Female                 | 85 (47%)   | 30 (44%)   |
| **Role‡**              |            |            |
| Pet dog                | 152 (84%)  | 37 (51%)   |
| Show dog               | 22 (12%)   | 1 (1%)     |
| Show and working dog   | 2 (1%)     | 0          |
| Working dog            | 6 (3%)     | 19 (28%)   |
| **Coat length**        |            |            |
| Short                  | 106 (58%)  | 31 (46%)   |
| Long                   | 70 (38%)   | 35 (51%)   |
| **Coat colour‡**       |            |            |
| Saddle tan/ Black tan   | 125 (69%)  | 13 (19%)   |
| Sable                  | 41 (23%)   | 32 (47%)   |
| Black                  | 12 (7%)    | 16 (24%)   |
| Other                  | 4 (2%)     | 7 (10%)    |

†Mean and SD
‡Count and percentage
Table A4  Significance of associations between population attributes and genetic ancestries. The proportion of ancestries estimated by ADMIXTURE (cluster 1, cluster 2, cluster 3) based on markers located within selection signature regions were fitted as fixed effects in separate linear models to test their association with different response variables (population attributes: behaviour traits, role of the dog, coat colour and coat length). The P-values for the respective models are shown in the table.

| Behaviour traits† | Cluster 1 | Cluster 2 | Cluster 3 |
|-------------------|-----------|-----------|-----------|
| Stranger-directed aggression | 0.214 | 0.497 | 0.111 |
| Dog-directed aggression | 0.324 | 0.750 | 0.395 |
| Stranger-directed fear | 0.527 | 0.527 | 0.282 |
| Human-directed playfulness | 0.242 | 0.797 | 0.280 |
| Excitability | 0.670 | 0.795 | 0.573 |
| Separation anxiety | 0.210 | 0.641 | 0.291 |
| Lack of obedience | 0.694 | 0.733 | 0.570 |
| Stranger-directed interest | 0.056 | 0.891 | 0.045* |
| Attachment/ Attention seeking | 0.213 | 0.262 | 0.475 |
| Chasing | 0.535 | 0.082 | 0.120 |
| Non-social fear | 0.992 | 0.081 | 0.406 |
| Dog-directed fear | 0.027* | 0.158 | 0.118 |
| Touch-sensitivity | 0.746 | 0.503 | 0.998 |
| Show dog | 0.037* | 0.851 | 0.027* |
| Working dog | 4.61e-06*** | 0.580 | 1e-05*** |
| Coat length | 4.96e-05*** | 0.0914 | 0.001** |
| Coat colour | <2e-16*** | 0.979 | <2e-16*** |

† Behaviour traits were adjusted based on other fixed effects as defined in a previous study¹. However, the population was not fitted as fixed effect for all behaviour traits and coat colour not for Chasing because the ancestry might be confounded with these attributes.

*P < 0.05
**P < 0.01
***P < 0.0001
Table A6  Overlaps between genes located in selection signature regions and candidate genes for morphological traits and behaviour reported in other studies. A list of candidate genes in canids was compiled using the following references and was compared to genes located in regions detected as selection signatures in this study.

| Putative trait       | Candidate gene†                                                                 | Study                                      |
|----------------------|--------------------------------------------------------------------------------|--------------------------------------------|
| Athletic success     | ARFGGEF3, ASIP, CACHD1, CPQ, GRK4, HTT, RGS12                                   | Kim et al. 201812                         |
| Barking              | CLINT1                                                                       | Ilska et al. 201710                       |
| Behaviour            | ANKRD27, CAB39L, CEP126, EBPL, EPB41L1, FNDCA3, FYN, GRAMD1C, HTT, KPNA3, LDLRAD4, LRP1B, NUDCD1, PREX2, RASGEF1B, RCBTB1, RFX1, SETDB2, SHISA6, SLC17A8, SORCS2, SPATA5, STIM2, TBC1D14, TOP3A, USF3, ZRANB3 | MacLean et al. 20195, Zapata et al. 201619, Friedrich et al. 20191 |
| Brain development    | CACNA1A, RAII                                                                  | Pendleton et al. 201814                   |
| Coat colour          | ASIP, RALY                                                                    | Vaysse et al. 201217, Dreger et al. 20137, Freedman et al. 20168, Boyko et al. 20104 |
| Domestication        | RAB3GAP1                                                                     | Axelsson et al. 2013³                      |
| Fur length, shedding | MC5R                                                                         | Hayward et al. 20169, Schlamp et al. 201516 |
| Tameness             | CCSER1, DEK, EPAS1, FOXN2, GRAMD1C, GRK7, ITCH, KDM1B, NAA50, NCAM1, NCOA6, PIGU, RNF7, SIDT1, SPICE1, TP53INP2, ZDHHC23 | Kukekova et al. 201813                     |
| Weight               | R3HDM1                                                                       | Plassais et al. 201915                    |

†Candidate genes for multiple traits are highlighted in bold
Figure A1  Ancestry proportions of GSDs based on genotypes of SNPs from putatively selected regions assuming three underlying ancestries (K = 3 clusters) as revealed by ADMIXTURE. Each cluster is represented by a colour and the length of the specific coloured segment indicates the dog’s proportion of membership in that cluster. The labels indicate the origin of the dog (Sweden or UK) and the coat colour (1 = saddle tan, 0 = sable, black or others).
Figure A2  Fine-mapping of target regions under divergent selection between German Shepherd dog populations. Particularly compelling regions that showed evidence of divergent selection in all three selection signature test statistics (SNP window-based $F_{ST}$, $\Delta ROH_{prop}$, and XP-EHH) are located on Chr 1, 24 and 32. The plots illustrate the FDR-adjusted P-values from association analyses for phenotypic traits (behaviour, coat colour, coat length) (above, “Regional association”) and the selection signature test statistics (below, “Selection signatures”) for all SNPs in these regions. The plots were created using a modified R code from that of Saxena et al. 2007\textsuperscript{90}.

Chromosome 1 (24.0 to 25.5Mb)
Chromosome 24 (22.0 to 26.0 Mb)

Regional association

Selection signatures
Chromosome 32 (53.5 to 56.7Mb)

Regional association

Selection signatures