

List of Supplemental Files

File S1. *supplemental_file_list.pdf* – List of supplemental files

File S2. *supplemental_materials.pdf* – Figures S1-S11; Tables S1, S2; supplemental references

File S3. *at_risk_id_key.tsv* – Contains individual IDs and phenotypes for at-risk dogs.

File S4. *breed_id_key.tsv* – Contains individual IDs, breed, and sex information for breed dogs.

File S5. *at_risk.ped.gz** – Gzipped genotype data for at-risk dog analysis.

File S6. *at_risk.map* – Marker locations for at-risk dog analysis.

File S7. *breeds.ped.gz** – Gzipped genotype data for breed dog analysis.

File S8. *breeds.map* – Marker locations for breed dog analysis.

File S9. *postprocess_germline.py* – Python script for post-processing germline outputs as described in manuscript

* in the included genotype datasets, the pseudo-autosomal region of chromosome X has been combined with the X chromosome and re-labeled such that both are included as chr41.