

Table S1 Average genomic relationship between dogs in the reference and validation set for every scenario. For every dog in the validation set, the average and the maximum genomic relatedness (GRmean; GRmax) with the dogs in the reference set were calculated

Scenario	GRmean	GRmax
Ref10	0.04	0.13
Ref50	0.04	0.17
Ref90	0.04	0.18
REL	0.04	0.18
REL-C	0.04	0.17