Short-tail (Bob-tail)

Applicable breeds: Australian Shepherd, Bourbonnais Pointer, Brittany, Jack Russell Terrier, Pembroke Welsh Corgi, Polish Lowland Sheepdog, Schipperke, Spanish Water Dog, Swedish Vallhund

This test will identify those dogs which have a naturally occurring short-tail ("bob-tail"), which is a desired trait in some breeds. It may be valuable for breeders to be able to prove that their dog has a naturally occurring short tail, rather than a docked tail, in situations where docking is banned.

Please note this test is only relevant in those breeds listed; in other breeds where natural short-tails occur other as yet undiscovered genes are responsible.

Short-tail is inherited in a dominant manner. This means that dogs which have only one copy of the mutation will have a short tail. No dogs with two copies of the mutation have been found - it is thought that this is lethal to the embryo, which dies early during development. Short-tail dogs will pass the short-tail gene on to an average of 50% of their offspring.

This test is particularly useful for breeders:

- to prove that their dog is naturally short-tailed and has not been docked

This test will be reported as:

Long-tail : no evidence of the short-tail gene
Short-tail : naturally short-tailed - this will be passed on to 50% of offspring

The genetic status of dogs can be used to predict breeding outcomes when different combinations are mated:

Long-tail X Long-tail = 100% Long-tail
Long-tail X Short-tail = 50% Long-tail, 50% Short-tail
Short-tail X Short-tail = 67% Short-tail, 33% Long-tail

References

Haworth K, Putt W, Cattanach B, Breen M, Binns M, Lingaas F, Edwards YH (2001) Canine homolog of the T-box transcription factor T; failure of the protein to bind to its target leads to a short-tail phenotype. Mammalian Genome 12: 212-218

Hytonen MK, Grall A, Hedan B, Dreano S, Seguin SJ, Delattre D, Thomas A, Galibert F, Paulin L, Lohi H, Sainio K, Andre C (2009) Ancestral T-box mutation is present in many, but not all, short-tailed dog breeds. Journal of Heredity 100(2): 236-240