**Table S2. Summary of variant effects that segregated across the 33 dog genomes**

|  |  |
| --- | --- |
| Variant Effect | Number of Variants |
| Intron | 71 |
| Intergenic | 58 |
| Upstream | 10 |
| Downstream | 1 |
| SynonymousPUS7L:c.278A>G *p.(=)* | 1 |
| Frameshift*ADAMTS20*: c.1360\_1361delAA p.Lys453Ilefs\*3 | 1 |
| Total | 142 |

All variant effects were predicted by SnpEff software [[1]](#_ENREF_2).

1. Cingolani P, Platts A, Wang le L, Coon M, Nguyen T, et al. (2012) A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. Fly (Austin) 6: 80-92.