**Table S2.** Variants of interest and corresponding Provean [42, 43] predictions. Location and affected genes are based on the CanFam3.1 reference genome available on Ensembl [24].

| CFA | POS | Provean Prediction | Variant Type | Gene Symbol or Ensembl ID |
|---|---|---|---|---|
| 12 | 663014 | Neutral | missense variant | DDR1 |
| 12 | 682971 | Neutral | missense variant | VARS2 |
| 12 | 815793 | Deleterious | missense variant | C12H6orf15 |
| 12 | 815806 | Neutral | missense variant | C12H6orf15 |
| 12 | 840504 | NA | splice acceptor variant & intron variant | ENSCAFG00000041540 |
| 12 | 854936 | NA | frameshift variant | TCF19 |
| 12 | 855098 | NA | frameshift variant | TCF19 |
| 12 | 857756 | Neutral | missense variant | TCF19 |
| 12 | 857757 | Neutral | missense variant | TCF19 |
| 12 | 858526 | Neutral | missense variant | TCF19 |
| 12 | 894038 | Neutral | missense variant | DLA88 |
| 12 | 983519 | Neutral | missense variant | DLA-64 |
| 12 | 1080999 | Neutral for 201; Deleterious for transcript 202 | missense variant | LTB |
| 12 | 1105607 | Neutral | missense variant | AIF1 |
| 12 | 1193544 | Neutral | missense variant | LY6G6D |
| 12 | 1201059 | Neutral | missense variant | LY6G6C |
| 12 | 1268748 | Neutral | missense variant | VARS1 |
| 12 | 1279238 | Neutral | missense variant | ENSCAFG00000035349 |
| 12 | 1279343 | Neutral | disruptive inframe deletion | ENSCAFG00000035349 |
| 12 | 1300624 | Neutral | missense variant | ENSCAFG00000000641 |
| 12 | 1417675 | Neutral | missense variant | SKIV2L |
| 12 | 1437707 | Neutral | missense variant | ENSCAFG00000000701 |
| 12 | 1438500 | Neutral | missense variant | ENSCAFG00000000701 |
| 12 | 1438623 | Neutral | missense variant | ENSCAFG00000000701 |
| 12 | 1440096 | Neutral | missense variant | ENSCAFG00000000701 |
| 12 | 1459925 | Deleterious | missense variant | TNXB |
| 12 | 1461286 | Neutral | missense variant | TNXB |
| 12 | 1469050 | Neutral | missense variant | TNXB |
| 12 | 1469337 | Deleterious | missense variant | TNXB |
| 12 | 1470758 | Neutral | missense variant | TNXB |
| 12 | 1470833 | Neutral | missense variant | TNXB |
| 12 | 1476360 | Deleterious | missense variant | TNXB |
| 12 | 1476467 | Neutral | missense variant | TNXB |
| 12 | 1476809 | Neutral | missense variant | TNXB |
| 12 | 1489066 | Neutral | missense variant | TNXB |
| 12 | 1500451 | Neutral | missense variant | TNXB |
| 12 | 1526455 | Neutral | missense variant | FKBPL |
| 12 | 1547611 | Neutral | disruptive inframe deletion | PRRT1 |
| 12 | 1574485 | Neutral | conservative inframe deletion | AGER |
| 12 | 1585012 | NA | frameshift variant | GPSM3 |
| 12 | 2225122 | Neutral | missense variant | DLA-DQA1 |
| 12 | 2248914 | Deleterious | missense variant | HLA-DQB2 |
| 12 | 6077432 | Deleterious | missense variant | FGD2 |

CFA – canine chromosome; NA – not applicable – Provean is not able to assess variant type; POS – position of variant based on the CanFam3.1 reference genome

[42]Choi, Y.; Sims, G.E.; Murphy, S.; Miller, J.R.; Chan, A.P. Predicting the Functional Effect of Amino Acid Substitutions and Indels. *PLOS ONE* **2012**, *7*, e46688, doi:10.1371/journal.pone.0046688.

[43]Choi, Y.; Chan, A.P. PROVEAN web server: a tool to predict the functional effect of amino acid substitutions and indels. *Bioinformatics* **2015**, *31*, 2745-2747, doi:10.1093/bioinformatics/btv195

[24]Howe, K.L.; Achuthan, P.; Allen, J.; Allen, J.; Alvarez-Jarreta, J.; Amode, M.R.; Armean, I.M.; Azov, A.G.; Bennett, R.; Bhai, J.; et al. Ensembl 2021. Nucleic Acids Research 2020, 49, D884-D891, doi:10.1093/nar/gkaa942