

Supplemental Methods

Determination Gene Ontology categories affected in dog CNV. Genes affected by dog CNVs were tested for overrepresentation of Gene Ontology (GO) categories using the DAVID software package (Dennis et al. 2003. Genome Biol 4: P3.). In brief, genes spanning all the CNV regions (ENSEMBL ID gene list, Table S1) were used to generate a “Functional Annotation Chart” (**Supplemental Table S3**). The following genes were absent from all overrepresented categories: ENSG00000006757, ENSG00000165349, ENSG00000159266, ENSG00000140307, ENSG00000173947, ENSG00000176349, ENSG00000198173, ENSG00000144218, ENSG00000196693, ENSG00000196693, ENSG00000196693, ENSG00000182472, ENSG00000048707, ENSG00000196693, ENSG00000196693, ENSG00000196693, ENSG00000135486, ENSG00000135486, ENSG00000189321, ENSG00000196693, ENSG00000196693, ENSG00000196693, ENSG00000180358.

PCR conditions

For the Fig. 4 Southern probe generation, we amplified 50 ng genomic DNA in 25 ul reactions according to the manufacturer's instructions (JumpStart REDTaq, Sigma). Thermal conditions were 94C/1m., followed by 32 cycles of 94C/30s., 58C/30s., 72C/40s, ending with 72C/5m. (Eppendorf Mastercycler ep gradient S). Similar conditions were used to screen the Rottweiler *CSMD1* CNV (Fig. 5), except 20 ng of DNA and 40 thermal cycles were used.

Primers used in the validation of structural variants.

Fig. 4 Southern Blotting probe generated by PCR

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CanVEGF_F    CCA GGC CAG ACC TCT CTG C
CanVEGF_R    CAG GCA ACA CAA AGT TTG GAA CCT C
CanEWSR1_F   GTC TTC CAC AGC CAG CAG TGC
CanEWSR1_R   TCT TGC CAG CCA GGA CCT CC
CanCYP3A38_F CCT AGA ACT GAA GAC AAT TTC CTA ACC ATG
CanCYP3A38_R GGC TTA ATT CAG AGT TGA GTG TAG TCA C
CanATBF1_F   TCG CCA TGG TGG CTT GTG C
CanATBF1_R   GTG GAG CTT TGA TGA AGG ACA TTG G
CanCTNNA3_F  CCA GAG CTT CAA GGC TTG TAC TAG
CanCTNNA3_R  CCT GGC TCA AAT AAT GCA AGT TCA TTA TTA C
CanNotch2_F  CTG CAC CTG CGA GTG TTC TCC
CanNotch2_R  TCC AGT AGC TGC TAG ATG TAT CTG
CanCBD103_F  GCA ACC AAC TGT GCT TCT ATA GGC
CanCBD103_R  CTG TTC TTG ATG CCT GTT CCA GG
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Fig. 5 Rottweiler SV PCR

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Can16_59M_F2 CTG TCA ACA CAG AGC AGA ACT CAG
Can16_59M_R2 AGG TGT GTT TAG AGC GTC TGT TCT C
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Fig. 5 control PCR

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Can16_59M_F2 CTG TCA ACA CAG AGC AGA ACT CAG
Can16_59M_R1 CTA TGT GGT ATC CAG CAA GTC ACG
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Two copy loss of *SLITRK1* in OSW cell line (data not shown)

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Can22_39M_F  CCT TAC AGA ACC TGG TCT GGT G
Can22_39M_R  TGT ATC AGA GAG GCA AGG TCA GTC
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