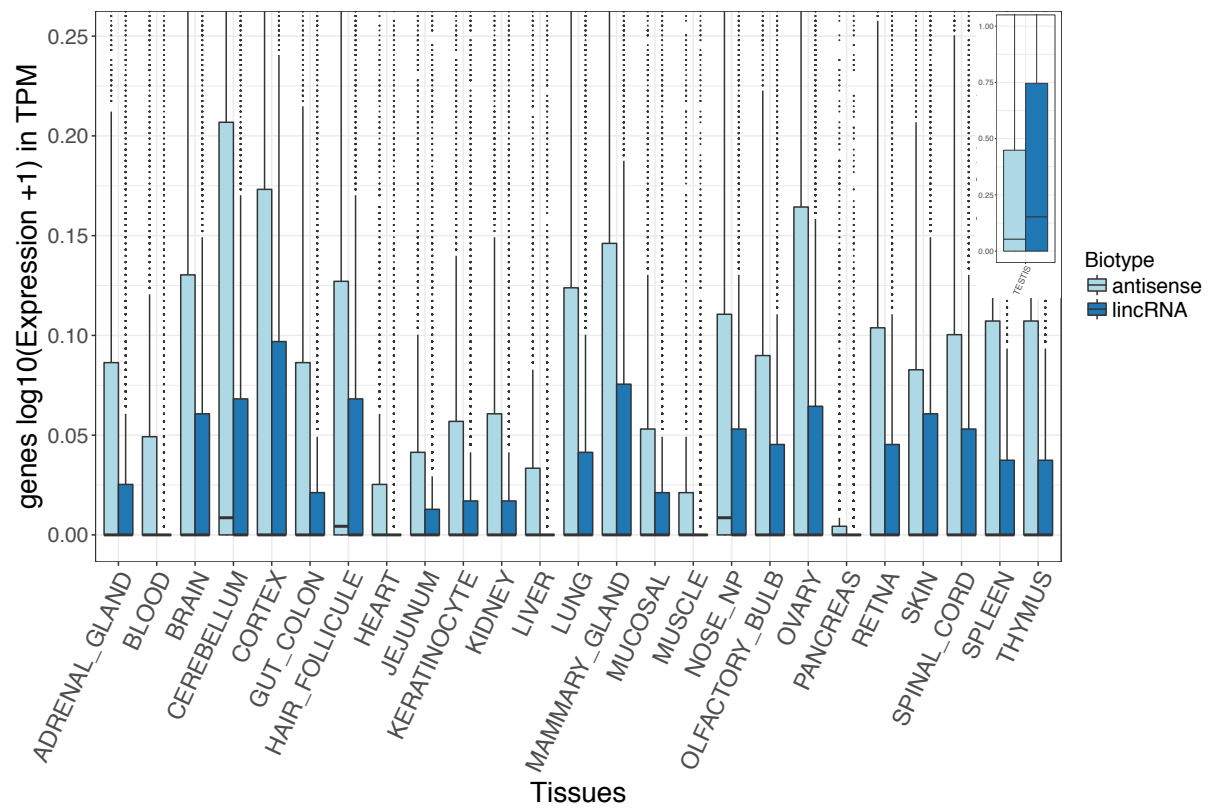


Organ	Dog breed	Total reads	Data origine
Adrenal_gland	Bernese Mountain Dog	54,776,586	(Wucher et al. 2017)
Blood	Beagle	25,294,750	(Hoeppner et al. 2014)
Brain	Beagle	39,268,738	(Hoeppner et al. 2014)
Cerebellum	Great Swiss Mountain Dog	44,902,865	(Wucher et al. 2017)
Cortex	Belgian Shepherd	41,319,413	(Wucher et al. 2017)
Gut_colon	Bernese Mountain Dog	52,310,396	(Wucher et al. 2017)
Hair_follicule	Labrador	45,694,722	(Wucher et al. 2017)
Heart	Beagle	24,930,702	(Hoeppner et al. 2014)
Jejunum	Labrador	50,569,866	(Wucher et al. 2017)
Keratinocyte	Beagle	54,482,221	(Hoeppner et al. 2014)
Kidney	Beagle	27,691,951	(Hoeppner et al. 2014)
Liver	Beagle	25,010,943	(Hoeppner et al. 2014)
Lung	Beagle	22,278,693	(Hoeppner et al. 2014)
Mammary_gland	Great Swiss Mountain Dog	44,349,725	(Wucher et al. 2017)
Mucosal	Labrador	44,195,944	(Le Béguec et al. 2018)
Muscle	Beagle	24,808,375	(Hoeppner et al. 2014)
Nasal_planum	Labrador	69,193,538	(Wucher et al. 2017)
Olfactory_bulb	Great Swiss Mountain Dog	45,799,491	(Wucher et al. 2017)
Ovary	Beagle	69,193,538	(Hoeppner et al. 2014)
Pancreas	Belgian Shepherd	47,171,936	(Wucher et al. 2017)
Retina	Border Collie	50,480,134	(Wucher et al. 2017)
Skin	Beagle	52,275,710	(Wucher et al. 2017)
Spinal_cord	Great Swiss Mountain Dog	46,844,306	(Wucher et al. 2017)
Spleen	Belgian Shepherd	49,604,583	(Wucher et al. 2017)
Testis	Beagle	26,743,805	(Hoeppner et al. 2014)
Thymus	Saluki	51,079,197	(Wucher et al. 2017)

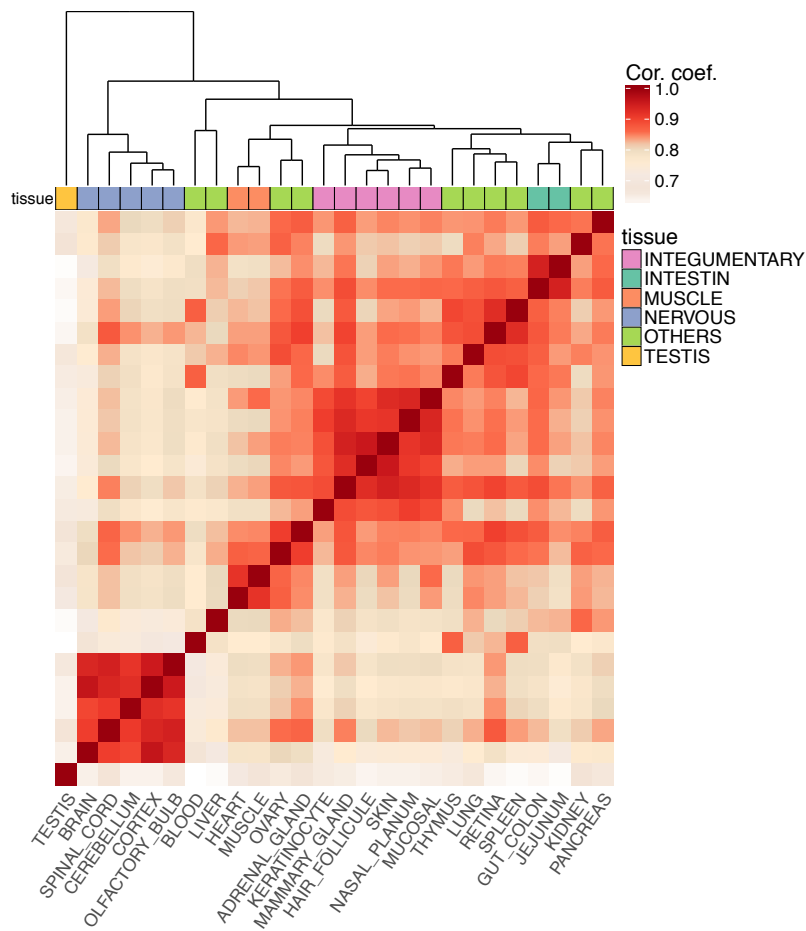
Supplementary Table S1. Description for each tissue of the breed, the number of total reads and the publication come from.



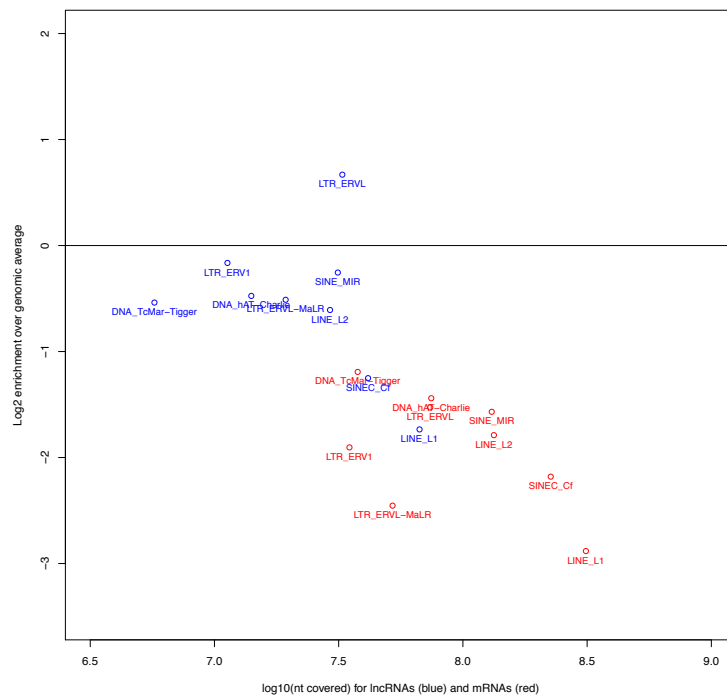
Supplementary Fig. S1. Comparative analysis of expression levels (in $\log(\text{TPM} + 1)$) between overlapping antisense of mRNAs (*antisense*) in light blue and long intergenic ncRNAs (lincRNAs) in dark blue genes in 26 canine tissues. Given the high proportion of genes specifically expressed in the testis tissue, it is represented in the box at the top-right of the figure.

Number of gene	%	Tissues	Number of gene	%	Tissues
3001	65.3	Testis	156	3.4	Cerebellum
138	3.0	Thymus	132	2.9	Kidney
118	2.6	Hair_follicule	104	2.3	Liver
97	2.1	Ovary	90	2.0	Adrenal_gland
74	1.6	Nasal_planum	60	1.3	Cortex
59	1.3	Heart	58	1.3	Lung
53	1.2	Gut_colon	47	1.0	Keratinocyte
45	1.0	Blood	44	1.0	Olfactory_bulb
43	0.9	Spleen	40	0.9	Jejunum
37	0.8	Retina	34	0.7	Muscle
34	0.7	Brain	32	0.7	Skin
31	0.7	Spinal_cord	30	0.7	Mammary_gland
24	0.5	Pancreas	18	0.4	Mucosal

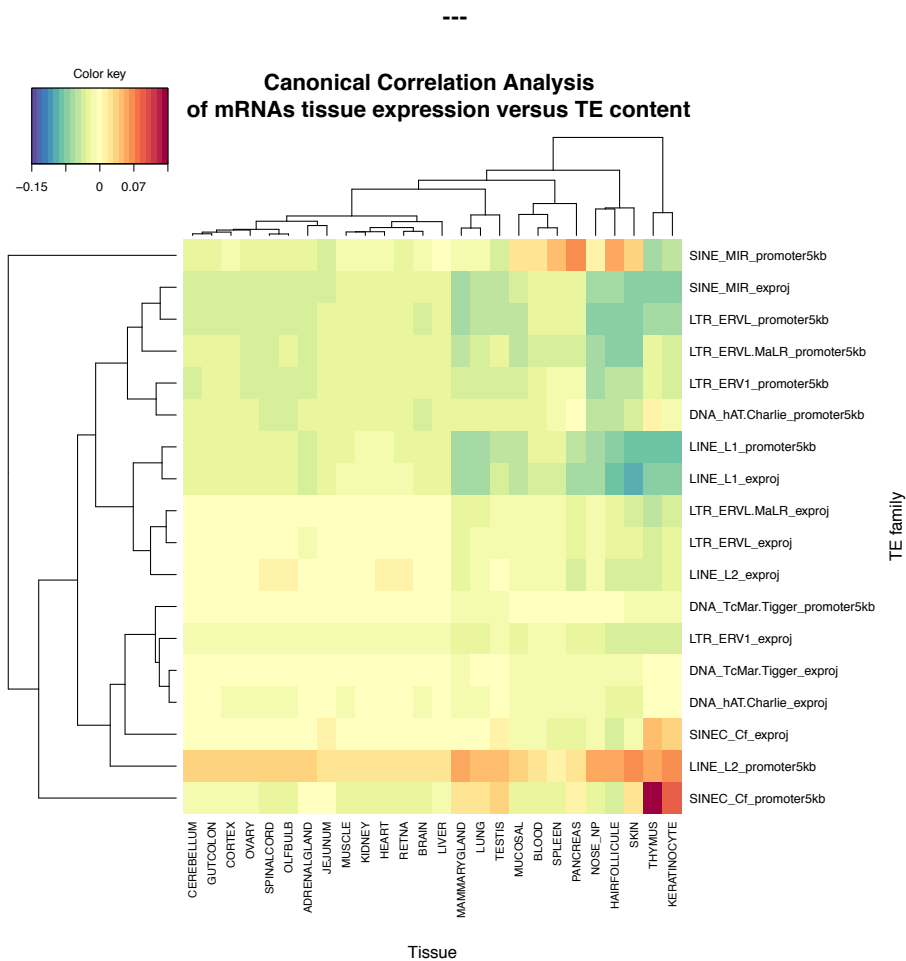
Supplementary Table S2. Number of lincRNAs tissue specific per tissue and the percentage compared to the 4,599 lincRNAs tissue specific.



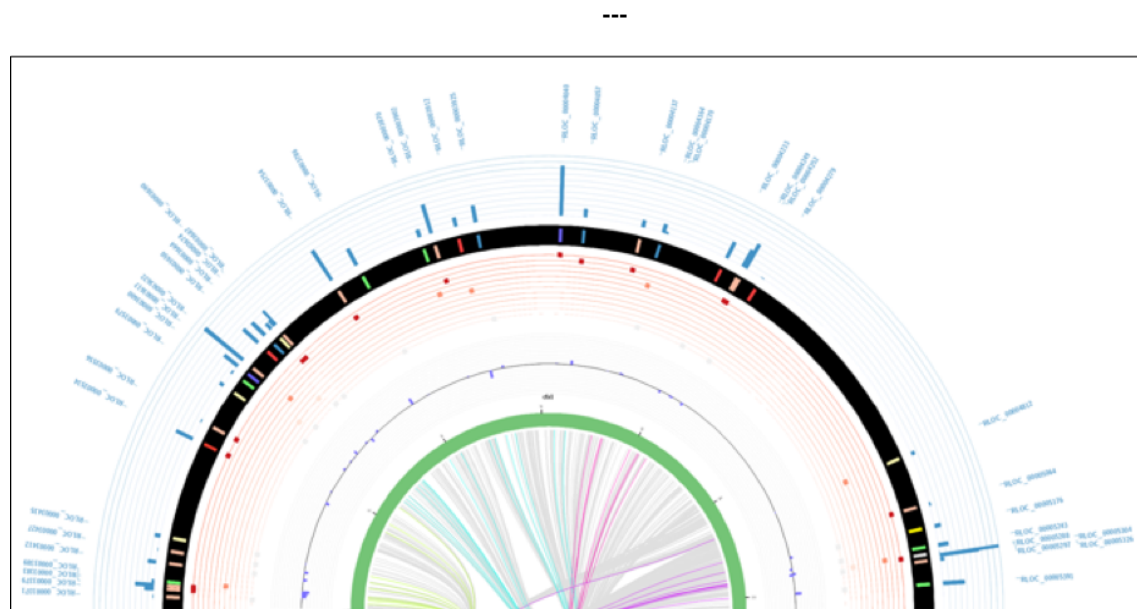
Supplementary Fig. S2. Hierarchical clustering of the 26 canine tissues based on Spearman correlations (Correlation coefficient) measured from protein-coding genes expression data (normalized in TPM).



Supplementary Fig. S3. TE family frequencies for lincRNAs (blue) versus mRNAs (red) compared to the genomic average. Larger families are on the right. Enrichments are above zero on the y-axis whereas depletions are below zero.



Supplementary Fig. S4. Canonical correlations between mRNAs expression in the 26 tissues (column) and TE families in rows in exons and promoters.

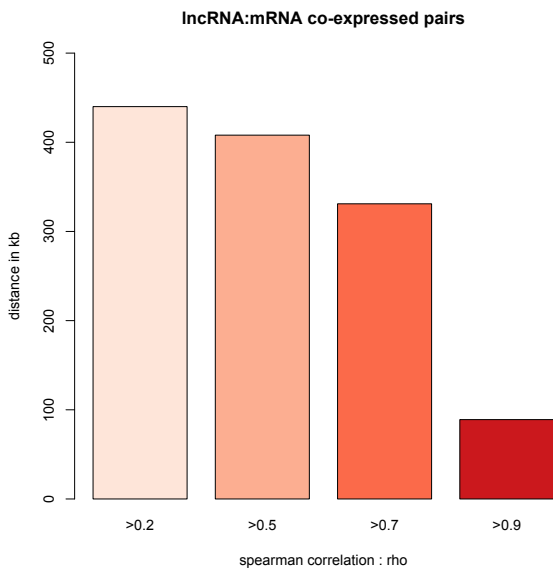


Supplementary Fig. S5. Circos one example and link for others...

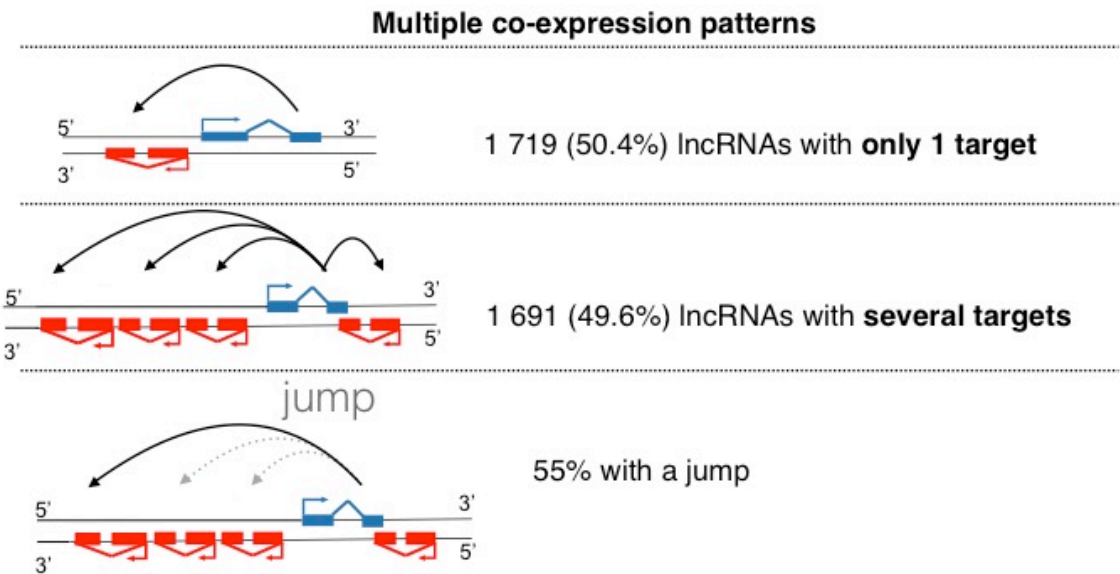
		All genes	mRNA	lncRNA	mRNA (othologous)	lncRNA (orthologous)
Dog	Number of gene	32,254	21,810	10,444	8,832	939
	Number of exon per gene in mean	7.5	9.8	2.5	12.2	3.1
Human	Number of gene	35,635	22,810	12,825	8,832	939
	Number of exon per gene in mean	7.7	10.4	2.8	12.7	3.6

Supplementary Table S3. Effective and number of exon per gene in mean for dog and human data.

Supplementary Fig. S6. [Link html with all barplots of comparative transcriptomics](#)



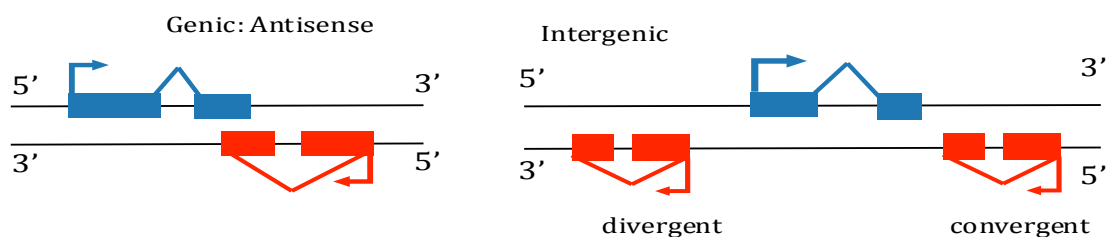
Supplementary Fig. S7. lncRNA:mRNA co-expression Spearman rho values from >0.2 to >0.9 in function of the distance between lncRNA and mRNA



Supplementary Fig S8. Schema representing multiple co-expression patterns, with the proportion

GO terms	Description	FDR	Nb of genes
GO:0007423	Sensory organ development	0.6×10^{-3}	147
GO:0007389	Pattern specification process	0.7×10^{-3}	127
GO:0048736	Appendage development	4.1×10^{-3}	58
GO:0048089	Positive regulation of cellular component biogenesis	4.1×10^{-3}	129
GO:0061564	Axon development	5.1×10^{-3}	129
GO:0018205	Peptidyl lysine modification	5.1×10^{-3}	115
GO:0051961	Negative regulation of nervous system development	6.7×10^{-3}	81
GO:0030902	Hinbrain development	6.7×10^{-3}	49
GO:0010975	Regulation of neuron projection development	7.5×10^{-3}	116
GO:0048568	Embryonic organ development	8.9×10^{-3}	118
GO:0050804	modulation_of_synaptic_transmission	8.9×10^{-3}	84
GO:0016049	Cell growth	1.1×10^{-2}	135
GO:0007033	Vacuole organization	1.1×10^{-2}	54
GO:0016570	Histone modification	1.1×10^{-2}	120
GO:0060021	Palate development	1.2×10^{-2}	32
GO:0060560	Developmental growth involved in morphogenesis	1.7×10^{-2}	65
GO:0051962	Positive regulation of nervous system development	1.9×10^{-2}	121
GO:0001701	In utero embryonic development	2.0×10^{-2}	92
GO:0022604	Regulation of cell morphogenesis	2.2×10^{-2}	118
GO:0016358	Dendrite development	2.4×10^{-2}	58
GO:0007224	Smoothened signaling pathway	3.5×10^{-2}	40
GO:0010720	Positive regulation of cell development	4.0×10^{-2}	118

Supplementary Table S4. Enrichment analysis of mRNA GO terms significantly co-expressed in 8139 lncRNA:mRNA pairs using the WebGestalt website (www.webgestalt.org/). GO terms are ranked according to their FDR together with the number of genes presenting the specific GO term.



Supplementary Fig. S9. Schema representing *antisense* and lincRNA (divergent and convergent)