

**TRANSCRIPTOME ANALYSIS OF CANINE CUTANEOUS MELANOMA AND
MELANOCYTOMA REVEALS A MODULATION OF GENES REGULATING
EXTRACELLULAR MATRIX METABOLISM AND CELL CYCLE**

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Supplementary Table 1. Summary statistics on the sequenced samples in read pairs of samples submitted to RNA-seq.

Case No.	Raw Reads	QC Passed	Discarded Seqs (%)	Uniquely Mapped	Uniquely Mapped %
1	33.934.336	33.701.111	0,69	27.971.790	83,00%
4	39.249.148	38.781.813	1,19	6.515.145	16,80%
5	70.144.356	69.180.820	1,37	10.829.792	15,65%
6	31.183.354	30.938.657	0,78	17.684.984	57,16%
13	23.794.350	23.611.093	0,77	17.364.063	73,54%
16	27.417.386	27.308.707	0,40	25.489.959	93,34%
17	33.658.370	33.528.972	0,38	29.011.664	86,53%
18	28.632.604	28.544.089	0,31	26.615.786	93,24%

Supplementary Table 2. Differentially expressed genes ranked by fold change. Annotation was added with Biomart.

Ensembl Gene ID	logFC	PValue	FDR (qValue)	Gene Name	Description
ENSCAFG00000029553	4.852	1.60E-06	1.27E-03		
ENSCAFG00000019985	4.580	2.15E-05	7.90E-03	COL11A1	collagen, type XI, alpha 1
ENSCAFG00000000903	4.365	1.23E-05	5.56E-03	COL11A2	collagen, type XI, alpha 2
ENSCAFG00000010530	4.306	2.14E-10	1.85E-06	CCDC80	coiled-coil domain containing 80
ENSCAFG00000005603	3.990	8.44E-09	1.99E-05	ISM1	isthmin 1 homolog
ENSCAFG00000017618	3.907	3.33E-07	3.27E-04	DRP2	dystrophin related protein 2
ENSCAFG00000007036	3.790	2.34E-05	8.36E-03	CD22	CD22 molecule
ENSCAFG000000031675	3.687	2.13E-05	7.90E-03	COL8A1	collagen, type VIII, alpha 1
ENSCAFG000000017018	3.621	7.80E-10	3.06E-06	COL1A1	collagen, type I, alpha 1
ENSCAFG000000018642	3.442	5.03E-005	0.014784381	NOS2	nitric oxide synthase
ENSCAFG000000000874	3.230	3.20E-08	5.38E-05	THBS2	thrombospondin-2
ENSCAFG000000023774	3.197	9.67E-005	0.023694412	RAMP1	receptor (G protein-coupled) activity modifying protein 1
ENSCAFG000000012718	3.179	2.49E-07	2.70E-04	CPXM2	carboxypeptidase X, member 2
ENSCAFG000000018761	3.178	9.69E-07	8.77E-04	PIEZO2	piezo-type mechanosensitive ion channel component 2
ENSCAFG000000005527	3.106	5.74E-06	3.24E-03	P4HA3	prolyl 4-hydroxylase, alpha polypeptide III
ENSCAFG000000002069	3.093	3.14E-10	1.85E-06	COL1A2	collagen, type I, alpha 2
ENSCAFG000000000868	3.075	2.52E-07	2.70E-04	SMOC2	SPARC related modular calcium binding 2
ENSCAFG000000006865	2.943	3.62E-05	1.15E-02	PAMR1	peptidase domain containing associated with muscle regeneration 1
ENSCAFG000000002307	2.933	2.15E-06	1.49E-03	ASPN	asporin
ENSCAFG000000014812	2.898	4.20E-08	6.18E-05	COL3A1	collagen, type III, alpha 1
ENSCAFG000000002947	2.896	0.000230822	0.046828998	PRSS35	protease, serine, 35

ENSCAFG0000005843	2.892	0.000210632	0.043482483	LTBP1	latent transforming growth factor binding protein 1
ENSCAFG0000000667	2.890	4.17E-06	2.58E-03	FNDC1	fibronectin type III domain containing 1
ENSCAFG00000010930	2.851	1.97E-09	5.78E-06	COL16A1	collagen, type XVI, alpha 1
ENSCAFG00000009282	2.751	8.78E-06	4.49E-03	CREB3L1	cAMP responsive element binding protein 3-like 1
ENSCAFG00000005880	2.742	7.33E-005	0.019612931		
ENSCAFG00000006608	2.699	1.94E-06	1.42E-03	CPXM1	carboxypeptidase X, member 1
ENSCAFG00000014837	2.635	7.01E-08	9.16E-05	COL5A2	collagen, type V, alpha 2
ENSCAFG00000019238	2.605	5.79E-06	3.24E-03	MMP23B	matrix metalloproteinase 23B
ENSCAFG00000020166	2.517	2.67E-08	5.23E-05	ANGPTL2	angiopoietin-like 2
ENSCAFG00000032273	2.498	0.000182255	0.04046415		
ENSCAFG00000012762	2.482	0.00012663	0.029521978	COCH	coagulation factor C homolog, cochlin
ENSCAFG00000011908	2.462	7.06E-06	3.77E-03	SHTN1	shootin 1
ENSCAFG00000013079	2.445	4.06E-06	2.58E-03	OLFML2B	olfactomedin-like 2B
ENSCAFG00000019848	2.443	1.09E-05	5.14E-03	COL5A1	collagen, type V, alpha 1
ENSCAFG00000020367	2.428	0.00019811	0.042384719	PLEKHG4	pleckstrin homology domain containing, family G member 4
ENSCAFG00000028461	2.397	9.82E-06	4.82E-03	LOX	lysyl oxidase
ENSCAFG00000006424	2.389	4.27E-05	1.32E-02	GXYLT2	glucoside xylosyltransferase 2
ENSCAFG00000008056	2.370	6.47E-005	0.018125915	RYR3	ryanodine receptor 3
ENSCAFG00000010061	2.344	7.70E-005	0.020142478	ABCC11	ATP-binding cassette, sub-family C, member 11
ENSCAFG00000000686	2.315	0.000127953	0.029521978		
ENSCAFG00000014670	2.247	4.61E-05	1.39E-02	NID2	nidogen 2 (osteonidogen)
ENSCAFG00000016828	2.142	2.84E-05	9.43E-03	COPZ2	coatamer protein complex, subunit zeta 2
ENSCAFG00000017262	2.136	2.88E-05	9.43E-03	MYH10	myosin, heavy chain 10

ENSCAFG00000006234	2.081	6.81E-005	0.018646387	ADAM33	ADAM metallopeptidase domain 33
ENSCAFG00000010387	2.055	1.62E-06	1.27E-03	FAP	fibroblast activation protein, alpha
ENSCAFG00000019943	2.051	2.59E-05	8.95E-03	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2
ENSCAFG00000001792	2.033	0.000100326	0.024092502	LIMCH1	LIM and calponin homology domains 1
ENSCAFG00000003044	2.013	0.000208688	0.043482483	FKBP14	FK506 binding protein 14
ENSCAFG00000008341	2.001	0.000243386	0.048256918	SPON1	Uncharacterized protein
ENSCAFG00000006073	1.971	0.000246062	0.048256918	POSTN	periostin
ENSCAFG00000013256	1.957	1.46E-05	5.94E-03	MRC2	mannose receptor, C type 2
ENSCAFG00000012226	1.931	9.66E-005	0.023694412	COL6A3	collagen, type VI, alpha 3
ENSCAFG00000001875	1.876	8.97E-005	0.022950061	CKAP4	cytoskeleton-associated protein 4
ENSCAFG00000000334	1.849	1.84E-05	7.22E-03	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2
ENSCAFG00000014322	1.661	6.44E-005	0.018125915	PCOLCE	procollagen C-endopeptidase enhancer
ENSCAFG00000018570	-2.306	0.00018037	0.04046415	SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1
ENSCAFG00000023349	-4.142	1.44E-05	5.94E-03		
ENSCAFG00000011838	-5.263	1.40E-05	5.94E-03	ST8SIA1	ST8 alpha-N-acetylneuraminide alpha-2,8-sialyltransferase 1
ENSCAFG00000012848	-6.947	0.000185903	0.040509549	COL20A1	collagen, type XX, alpha 1

Supplementary Table 4. Primer were designed based on available sequences using the Primer-BLAST software.

Gene	Accession	Forward	Reverse	Efficiency	Amp. Size
<i>GUSβ</i>	NM_001003191	GTGCTGGATCAGAAACGCAA	CTTTGGGTTGTCTCTGGCGA	96%	136
<i>HMBS</i>	XM_546491.5	GGTGGGCGTGTTCATGA	AGGTACAGTTGCCATCCTTCATAG	105%	132
<i>THBS2</i>	NM_001197156	ATTCGCCATCAAGGCAAGGA	CCACGGACCCAAACTCATCA	110%	85
<i>COL1A1</i>	NM_001003090	AGAGCATGACCGACGGATTC	ACGCTGTTCTTGCAAGTGGTA	90	139
<i>COL11A1</i>	XM_005621852	AAGCTCAAGCTCAGGCGATT	TCACCACTCTCACCTTTGGC	87%	133
<i>NOS2</i>	NM_001313848	CCTACCAGTACGACTTGACCG	TGGGGTCATCCTGTGTCCT	99%	96
<i>ADAMTS2</i>	XM_843844	GTGGAGTGGGAGTACAGGGA	GTATGTCAGCGAGATCCGGG	113%	120