

Pfaff *et al.*: Proteogenomics uncovers critical elements of host response in bovine soft palate epithelial cells following *in vitro* infection with foot-and-mouth disease virus

A

Inoculation with FMDV (or mock),
Incubation for up to 28 days

Soft palate tissue is collected after slaughter
Primary soft palate cells cultured at air-liquid interface
TRIzol extraction
RNA
proteins

RNAseq
RT-qPCR
quantitative proteomics

differentially expressed genes
confirmation of selected genes
corroborating evidence on protein level

B

	before inoculation	02 hpi	24 hpi	48 hpi	7 dpi	28 dpi
RNAseq	mock	■ ■ ■ ■		■ ■ ■ ■		■ ■ ■ ■
	FMDV		■ ■ ■ ■	■ ■ ■ ■		■ ■ ■ ■
RT-qPCR	mock	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
	FMDV	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
proteomics	mock	■ ■ ■ ■		■ ■ ■ ■		■ ■ ■ ■
	FMDV		■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■

Figure S1. Schematic visualization of the proteogenomic workflow. (A). Soft palate (SP) tissue was received from two cattle that were slaughtered for food production. A primary SP cell culture was established at an air-liquid interface und was subsequently inoculated with lysate from infected (FMDV) or uninfected (mock) cell cultures. The inoculated SP cell cultures were then incubated for up to 28 days. At each sample time point, two replicate cultures were harvested and total RNA and proteins were isolated using TRIzol. The RNA fraction was used for comparative RNA sequencing and identification of differentially expressed genes. Among these, six target genes and two reference genes were selected for confirmation by RT-qPCR. Furthermore, the corresponding protein fraction was used for quantitative proteomics in order to corroborate the transcription data on the protein level. (B) Replicate SP cell cultures from the two animals (1 and 2, black silhouettes) were harvested at different time points: immediately before inoculation, 2 hours post inoculation (hpi), 24 hpi, 48 hpi, 7 days post inoculation (dpi) and 28 dpi. The heatmap shows the number of replicates (squares) from mock (blue) and FMDV infected (orange) cell cultures that have been analyzed using RNA sequencing, RT-qPCR or proteomics at each time point.

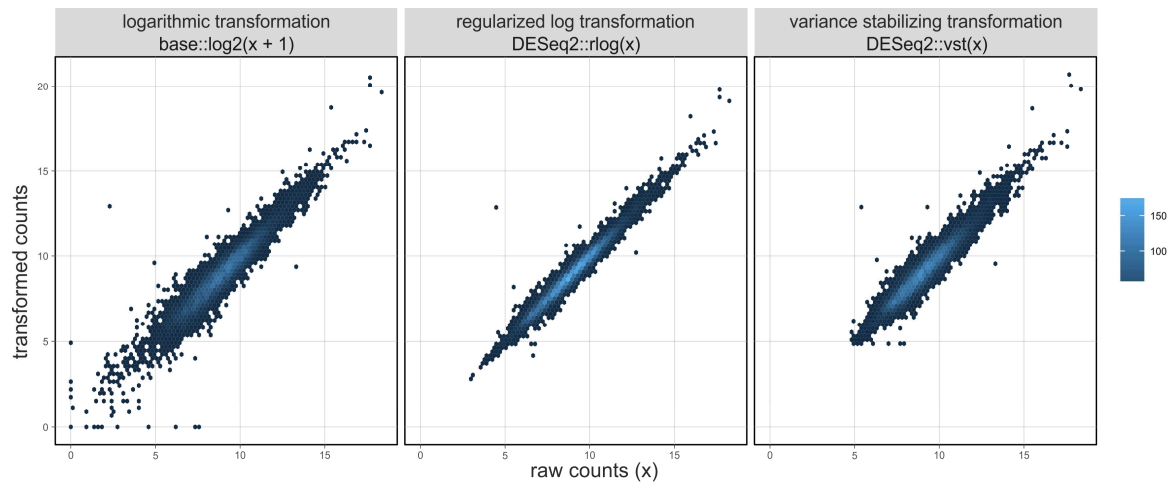


Figure S2. Comparison of different transformation methods for the raw reads counts per gene. The log2 transformation using sequence depth normalized counts (left) shows high deviation of transformed from raw counts that may artificially contribute to data variance. The regularized log (middle) and the variance stabilizing transformation as implemented in DESeq2 considers sequence depth and performs better than the logarithmic transformation. For variance-based approaches, the regularized log transformation was chosen as the best performing model. The color corresponds to the number of binned per gene counts and the function corresponds to the used R package and call.

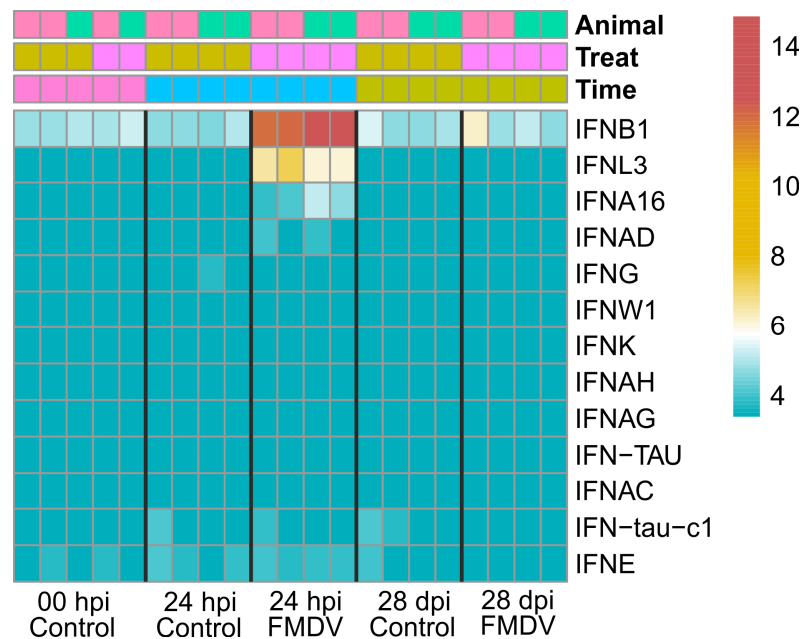


Figure S3. Comparison of interferon expression. The raw read counts for all available interferon typ I, II and III genes were extracted from an unfiltered dataset and transformed using the variance stabilizing transformation (vst) method, in order to avoid negative values for better visibility. The transformed data was visualized in a heatmap, were rows represent genes and columns represent samples from different time points (00 hpi, 24 hpi and 28 dpi), treatments (FMDV or controls) and animals.

Supplementary Tables

Table S1. Summary of primary soft palate cell culture samples used for RNA sequencing along with information on experimental treatment, such as inoculation agent and time as well as animal-specific properties and outcome of sequencing.

No	Sample ID	Treatment	Time	Animal	Total Reads
1	lib02459	control	0 hpi	1 (♀)	23,764,020
2	lib02460	control	0 hpi		23,830,051
3	lib02453	control	24 hpi		23,679,150
4	lib02454	control	24 hpi		25,959,245
5	lib02451	FMDV	24 hpi		24,194,883
6	lib02452	FMDV	24 hpi		26,512,041
7	lib02457	control	28 dpi		24,502,499
8	lib02458	control	28 dpi		24,923,161
9	lib02455	FMDV	28 dpi		22,879,371
10	lib02456	FMDV	28 dpi		25,383,683
11	lib02343	control	0 hpi	2 (♂)	23,766,199
12	lib02344	control	0 hpi		24,205,215
13	lib02360	control	0 hpi		25,499,001
14	lib02362	control	24 hpi		25,545,365
15	lib02346	control	24 hpi		24,372,618
16	lib02361	FMDV	24 hpi		25,894,882
17	lib02345	FMDV	24 hpi		24,405,453
18	lib02348	control	28 dpi		28,018,704
19	lib02350	control	28 dpi		24,381,295
20	lib02347	FMDV	28 dpi		21,855,393
21	lib02349	FMDV	28 dpi		24,818,395

Table S2. Summary of excluded and included RNA reference transcripts. A total of 57,846 RNA sequences of the *Bos taurus* reference genome (GCF000003055.6 Bos Taurus UMD 3.1.1) were filtered according to their RNA feature qualifiers and only a subset of reference sequences were further included in the analysis of differently expressed genes

	Qualifier	Entries	Description
Included			
	mRNA	48,655	messenger RNA
	partial mRNA	335	partial messenger RNA
	ncRNA	6169	non-coding RNA <200 nt
	non-coding RNA	25	non-coding RNA <200 nt
	long non-coding RNA	43	non-coding RNA >200 nt
	misc RNA	1808	any transcript or RNA product that cannot be defined by other RNA keys
	total	57,035	
Excluded			
	microRNA	806	micro RNA ~22 nt
	telomerase RNA	1	RNA component of telomerase
	ribosomal RNA	2	ribosomal ribonucleic acid
	RNase MRP RNA	1	RNA molecule essential for the catalytic activity of RNase MRP
	SRP RNA	1	signal recognition particle
	total	811	

S3 Table. Replaced gene aliases of the *Bos taurus* reference genome (GCF000003055.6 Bos Taurus UMD 3.1.1)

Original	Replacement	Description	Associated Accession
C28H10ORF10	DEPP1	Autophagy Regulator	NM_001046515.2
C10H15ORF48	NMES1	Normal mucosa of esophagus-specific gene 1 protein	NM_001206976.1
C7H19ORF66	C19ORF66	Repressor Of Yield Of Dengue Virus	NM_001038181.1
C1H21ORF91	C21ORF91	Cold Sore Susceptibility Gene 1	XM_005201150.3, XM_005201152.3, XM_010800942.2, NM_001037617.2
C1H3ORF38	C3ORF38	May be involved in apoptosis regulation	NM_001206451.2, XM_005201179.3
PVRL2	NECTIN2	Nectin Cell Adhesion Molecule 2	XM_005219196.1, XM_005219198.1
C3H1ORF109	C1ORF109	May promote cancer cell proliferation.	XM_010803595.2, NM_001101892.1
C8H9ORF91	TMEM268	Transmembrane Protein 268	XM_005210539.3, XM_005210540.3, XM_005210541.3, XM_015472690.1
C11H2ORF44	WDCP	WD Repeat And Coiled Coil Containing	XM_005213088.3, XM_015473568.1, XM_002691506.5
LOC784525, LOC525550, LOC100337470, IFNB3	IFNB1	Interferon beta 1	XM_002689540.4, XM_002689541.3, XM_002689537.4, NM_001114297.1

S4 Table. Sequences of primers used for the RT-qPCR analysis

Target	Forward Primer (3' → 5')	Reverse Primer (3' → 5')
ACTB	CTCTTCCAGCCTTCCTTCCT	GGCAGTGATCTCTTTCTGC
ANKRD1	GACGAAC TTCGGGTCAACAT	CTCTGCCTCTCGCTGTTTCT
CASP7	GAACAGATGGCAAGACAGCA	AACGGGGATTAGCATCAGTG
GAPDH	GGGTCATCATCTCTGCACCT	GGTCATAAGTCCCTCCACGA
IDO1	TGCTGTATGAAGGCATCTGG	TGAGCTGGTGGCATGTATGT
IFIH1	CGAAGTCAAAGAGCCACTCC	TGCCCATGTTGCTGTTATGT
NCAM1	CATCTACAACGCCAACATCG	CTTCTCCCTCCCTGAACTCC
OAS2	AACGAGTCACCTGGACCATC	GCTGGAGAAAGTCCTTGACG

S5 Table. Differentially expressed genes with an adjusted p-value (padj) <0.001 and a |log2 fold change| (LFC) >1

Gene	Entrez ID	Gene Description	24 hpi		28 dpi	
			LFC	padj	LFC	padj
ABCD4	5826	ATP binding cassette subfamily D member 4	3.06	1.83E-10		
ABHD1	84696	abhydrolase domain containing 1	5.72	6.33E-19		
ACSL5	51703	acyl-CoA synthetase long chain family member 5	2.05	1.36E-07		
ADAR	103	adenosine deaminase, RNA specific	2.76	2.24E-11		
ADPGK	83440	ADP dependent glucokinase	2.26	5.35E-05		
AIDA	64853	axin interactor, dorsalization associated	2.16	1.82E-08		
ALDH1A2	8854	aldehyde dehydrogenase 1 family member A2			-3.09	7.84E-05
ANKRD1	27063	ankyrin repeat domain 1			-4.19	6.58E-05
ANXA1	301	annexin A1	2.79	1.70E-13		
APOBEC3B	9582	apolipoprotein B mRNA editing enzyme catalytic subunit 3B	2.88	2.80E-06		
AREL1	9870	apoptosis resistant E3 ubiquitin protein ligase 1	1.79	2.74E-06		
ARF3	377	ADP ribosylation factor 3	2.17	1.77E-04		
ARNTL2	56938	aryl hydrocarbon receptor nuclear translocator like 2	3.30	3.11E-05		
ARSH	347527	arylsulfatase family member H	2.77	1.26E-07		
ATAD1	84896	ATPase family, AAA domain containing 1	2.59	5.03E-07		
ATP10A	57194	ATPase phospholipid transporting 10A (putative)	2.91	5.49E-07		
ATP8B4	79895	ATPase phospholipid transporting 8B4 (putative)	3.60	1.08E-25		
ATXN3	4287	ataxin 3	2.63	1.20E-05		
BAG3	9531	BCL2 associated athanogene 3	1.97	4.79E-05		
BATF2	116071	basic leucine zipper ATF-like transcription factor 2	4.83	9.27E-56		
BCL2L12	83596	BCL2 like 12	3.07	5.71E-13		
BHLHE41	79365	basic helix-loop-helix family member e41	3.48	1.36E-04		
BIN3	55909	bridging integrator 3	2.00	2.56E-06		
BOLA-DMB	282491	major histocompatibility complex, class II, DM beta	3.63	1.41E-17		
BPNT1	10380	3'(2'), 5'-bisphosphate nucleotidase 1	3.25	3.02E-13		
C19ORF66			3.14	7.30E-08		
C1ORF109			2.25	6.69E-08		
C21ORF91			3.01	2.38E-05		
C3ORF38			2.70	4.88E-11		
CA13	377677	carbonic anhydrase 13	-3.22	3.56E-04		
CALCOCO2	10241	calcium binding and coiled-coil domain 2	2.58	1.65E-08		
CASP4	837	caspase 4	2.98	1.07E-06		
CASP7	840	caspase 7	2.66	2.59E-13		
CCDC82	79780	coiled-coil domain containing 82	1.92	4.37E-05		
CCL2	6347	C-C motif chemokine ligand 2	3.17	3.24E-10		
CCL5	6352	C-C motif chemokine ligand 5	6.66	8.74E-19	4.70	3.02E-07
CCL8	6355	C-C motif chemokine ligand 8	11.79	1.00E-21		
CD200	4345	CD200 molecule	3.30	1.19E-05		
CD274	29126	CD274 molecule	4.67	2.71E-25		
CD40	958	CD40 molecule	4.29	2.84E-13		

CD83	9308	CD83 molecule	5.08	8.81E-05		
CDADC1	81602	cytidine and dCMP deaminase domain containing 1	3.40	1.25E-33		
CDKN2AIP	55602	CDKN2A interacting protein	3.19	1.10E-18		
CELA3B	23436	chymotrypsin like elastase family member 3B	2.78	1.54E-04		
CFLAR	8837	CASP8 and FADD like apoptosis regulator	2.88	2.79E-05		
CHST12	55501	carbohydrate sulfotransferase 12	1.88	1.19E-04		
CLEC2D	29121	C-type lectin domain family 2 member D	3.45	7.80E-08		
CMPK2	129607	cytidine/uridine monophosphate kinase 2	8.22	6.07E-39	4.37	8.48E-08
CMTR2	55783	cap methyltransferase 2	3.48	3.24E-20		
CNP	1267	2',3'-cyclic nucleotide 3' phosphodiesterase	2.25	2.32E-10		
COL1A1	1277	collagen type I alpha 1 chain			-3.50	4.15E-04
COL3A1	1281	collagen type III alpha 1 chain			-3.28	3.22E-04
CRYM	1428	crystallin mu	5.73	3.78E-08		
CSDC2	27254	cold shock domain containing C2	3.86	3.21E-28		
CSRN1	64651	cysteine and serine rich nuclear protein 1	2.64	2.49E-04		
CTC1	80169	CST telomere replication complex component 1	3.26	3.61E-16		
CTSS	1520	cathepsin S	2.84	8.90E-08		
CXCL10	3627	C-X-C motif chemokine ligand 10	11.01	1.33E-12		
CXCL2	2920	C-X-C motif chemokine ligand 2	6.08	4.82E-06		
CXCL8	3576	C-X-C motif chemokine ligand 8	6.68	3.76E-05		
CYP2J2	1573	cytochrome P450 family 2 subfamily J member 2	7.05	1.28E-07		
CYTH1	9267	cytohesin 1	1.98	2.52E-06		
DAXX	1616	death domain associated protein	2.82	1.21E-13		
DDX58	23586	DEXD/H-box helicase 58	5.18	4.24E-77	3.72	1.08E-31
DEPP1	11067	DEPP1, autophagy regulator	3.61	6.41E-05		
DHX58	79132	DEXH-box helicase 58	5.86	2.92E-75	3.99	2.90E-27
DNAJC1	64215	DnaJ heat shock protein family (Hsp40) member C1	2.42	4.92E-07		
DRAM1	55332	DNA damage regulated autophagy modulator 1	3.49	1.21E-24		
DTX3L	151636	deltex E3 ubiquitin ligase 3L	4.82	6.81E-94	3.61	2.86E-42
EGR2	1959	early growth response 2	3.67	2.65E-17		
EHD4	30844	EH domain containing 4	3.46	1.21E-09		
EIF2AK2	5610	eukaryotic translation initiation factor 2 alpha kinase 2	3.33	2.23E-08		
ELMO2	63916	engulfment and cell motility 2	2.36	2.84E-13		
EPSTI1	94240	epithelial stromal interaction 1	4.51	1.86E-15	3.32	4.47E-06
ERAP2	64167	endoplasmic reticulum aminopeptidase 2	2.29	8.35E-05		
ESPNL	339768	espin like	2.78	2.31E-05		
FAM111B	374393	family with sequence similarity 111 member B	3.08	2.21E-04		
FAM192A	80011	family with sequence similarity 192 member A	2.20	1.24E-05		
FAM3B	54097	family with sequence similarity 3 member B	9.41	8.65E-13	6.80	2.65E-05
FAM46A	55603	family with sequence similarity 46 member A	2.51	2.24E-07		
FBP1	2203	fructose-bisphosphatase 1			4.09	2.93E-05
FBXO16	157574	F-box protein 16	3.17	3.24E-09		
FBXO33	254170	F-box protein 33	3.61	6.56E-13		

FCHSD2	9873	FCH and double SH3 domains 2	2.40	1.44E-04		
FITM2	128486	fat storage inducing transmembrane protein 2	-2.33	3.75E-10		
FMDV		Foot-and-mouth disease virus genome	17.76	6.46E-35		
FOXS1	2307	forkhead box S1	4.80	4.12E-05		
GBP2	2634	guanylate binding protein 2	6.25	2.03E-44	3.16	8.70E-07
GBP4	115361	guanylate binding protein 4	9.44	8.43E-36	7.58	2.83E-21
GBP5	115362	guanylate binding protein 5	6.39	1.50E-30	3.57	3.88E-06
GMIP	51291	GEM interacting protein	2.84	2.52E-08		
GPR63	81491	G protein-coupled receptor 63	3.41	2.35E-04		
GPR65	8477	G protein-coupled receptor 65	2.70	5.10E-04		
GRINA	2907	glutamate ionotropic receptor NMDA type subunit associated protein 1	2.64	4.05E-13		
GTF2B	2959	general transcription factor IIB	4.44	1.31E-40		
HBEGF	1839	heparin binding EGF like growth factor	3.63	2.88E-10		
HECTD2	143279	HECT domain E3 ubiquitin protein ligase 2	3.96	2.16E-17		
HERC5	51191	HECT and RLD domain containing E3 ubiquitin protein ligase 5	4.83	2.25E-23	2.77	2.57E-04
HERC6	55008	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	5.42	3.58E-48	3.87	9.44E-20
HOMER	57594	homeobox and leucine zipper encoding	2.11	2.49E-11		
HS3ST1	9957	heparan sulfate-glucosamine 3-sulfotransferase 1	4.31	4.36E-09		
HTRA3	94031	HtrA serine peptidase 3			-3.21	2.93E-07
IDO1	3620	indoleamine 2,3-dioxygenase 1	11.56	2.47E-47		
IER2	9592	immediate early response 2	2.17	7.38E-05		
IFI16	3428	interferon gamma inducible protein 16	3.84	5.81E-19	2.53	7.33E-05
IFI27	3429	interferon alpha inducible protein 27	8.11	2.71E-101	8.18	1.95E-92
IFI35	3430	interferon induced protein 35	3.40	1.05E-19	2.31	4.96E-05
IFI44	10561	interferon induced protein 44	6.70	2.33E-20	5.52	3.24E-12
IFI44L	10964	interferon induced protein 44 like	5.74	7.25E-67	3.89	2.65E-24
IFI6	2537	interferon alpha inducible protein 6	6.00	8.16E-20	5.85	3.98E-18
IFIH1	64135	interferon induced with helicase C domain 1	6.49	9.33E-60	4.30	5.93E-21
IFIT2	3433	interferon induced protein with tetratricopeptide repeats 2	10.98	7.92E-89	5.94	5.93E-21
IFIT3	3437	interferon induced protein with tetratricopeptide repeats 3	6.74	1.38E-22		
IFIT5	24138	interferon induced protein with tetratricopeptide repeats 5	2.83	5.12E-13		
IFITM1	8519	interferon induced transmembrane protein 1	4.12	4.96E-19	3.58	2.05E-12
IFITM2	10581	interferon induced transmembrane protein 2	9.76	1.90E-36		
IFNB1	3456	interferon beta 1	10.47	5.67E-53		
IL15RA	3601	interleukin 15 receptor subunit alpha	4.04	1.76E-15		
IL18	3606	interleukin 18	2.95	1.05E-12		
IL18BP	10068	interleukin 18 binding protein	2.42	2.05E-07		
IL3RA	3563	interleukin 3 receptor subunit alpha	6.19	2.65E-17		
IL4I1	259307	interleukin 4 induced 1	4.04	5.43E-13		
IL6	3569	interleukin 6	6.21	2.15E-09		
IP6K1	9807	inositol hexakisphosphate kinase 1	2.10	5.69E-10		
IQCD	115811	IQ motif containing D	3.81	1.82E-08		
IRF1	3659	interferon regulatory factor 1	3.60	4.93E-07		

IRF3	3661	interferon regulatory factor 3	2.06	7.33E-05		
IRF5	3663	interferon regulatory factor 5	3.46	4.08E-04		
IRF7	3665	interferon regulatory factor 7	4.99	9.68E-22	2.85	4.52E-04
IRF9	10379	interferon regulatory factor 9	3.10	3.76E-32	1.99	2.61E-06
ISG15	9636	ISG15 ubiquitin-like modifier	11.18	3.46E-80	8.99	8.10E-47
ITPR2	3709	inositol 1,4,5-trisphosphate receptor type 2	2.32	6.00E-14		
JAKMIP3	282973	Janus kinase and microtubule interacting protein 3	4.23	5.42E-22		
KIF5C	3800	kinesin family member 5C	9.89	5.28E-32		
KIFC3	3801	kinesin family member C3	2.73	3.48E-04		
LAYN	143903	layilin	3.38	4.51E-06		
LEKR1	389170	leucine, glutamate and lysine rich 1	4.93	4.45E-20		
LGALS3BP	3959	galectin 3 binding protein	2.52	1.63E-04		
LGALS9	3965	galectin 9	4.37	1.06E-04		
LOC100139670	100139670	interferon-induced protein with tetratricopeptide repeats 1	5.81	6.09E-21	3.58	2.32E-05
LOC100298356	100298356	bone marrow stromal antigen 2	9.04	7.68E-34	6.48	4.52E-15
LOC100336669	100336669	guanylate-binding protein 4	5.96	1.91E-50	3.25	1.25E-09
LOC101902757	101902757	uncharacterized LOC101902757	4.32	4.04E-05		
LOC101903126	101903126	interferon-induced very large GTPase 1-like	5.94	3.92E-04		
LOC101903326	101903326	zinc finger protein 485	-2.20	5.86E-04		
LOC101903473	101903473	uncharacterized LOC101903473	4.07	9.72E-24	2.43	3.46E-04
LOC101905355	101905355	uncharacterized LOC101905355	5.49	3.05E-11		
LOC101907348	101907348	uncharacterized LOC101907348	3.47	1.61E-09		
LOC101907799	101907799	uncharacterized LOC101907799	13.48	2.47E-29	8.67	3.94E-11
LOC101907813	101907813	uncharacterized LOC101907813	3.39	3.77E-08		
LOC101908206	101908206	uncharacterized LOC101908206	-2.64	8.82E-05		
LOC104968925	104968925	uncharacterized LOC104968925	5.14	1.55E-25		
LOC104970162	104970162	uncharacterized LOC104970162	3.31	1.48E-07		
LOC104970840	104970840	uncharacterized LOC104970840	4.02	5.55E-10		
LOC104971726	104971726	uncharacterized LOC104971726	7.96	8.45E-16		
LOC104972593	104972593	uncharacterized LOC104972593	10.67	1.83E-16	7.17	5.19E-06
LOC104973892	104973892	uncharacterized LOC104973892	3.51	5.51E-15		
LOC104975716	104975716	leukocyte elastase inhibitor pseudogene	2.23	6.64E-05		
LOC107131142	107131142	tumor necrosis factor ligand superfamily member 13B-like	5.70	8.21E-08	4.79	2.57E-04
LOC107131199	107131199	cysteine/serine-rich nuclear protein 2	2.14	4.04E-04		
LOC107131472	107131472	vomeroneasal type-1 receptor 4-like	3.20	1.20E-05		
LOC107131864	107131864	eukaryotic translation initiation factor 4E pseudogene	4.91	1.77E-17	3.04	3.87E-04
LOC107132217	107132217	uncharacterized LOC107132217	8.54	1.06E-29	6.48	1.59E-14
LOC107132617	107132617	uncharacterized LOC107132617	3.97	7.61E-09		
LOC107132911	107132911	uncharacterized LOC107132911	2.32	2.84E-04		
LOC507055	507055	guanylate-binding protein 4	7.60	1.28E-73	4.54	2.18E-20
LOC508153	508153	uncharacterized LOC508153	3.47	1.54E-07	2.96	8.43E-04
LOC509283	509283	E3 ubiquitin-protein ligase RNF213	4.76	1.55E-80	2.87	2.50E-19
LOC510382	510382	guanylate-binding protein 6-like	6.29	1.08E-54	3.19	1.01E-08
LOC511531	511531	guanylate-binding protein 1	5.70	1.00E-38	2.63	5.14E-04

LOC511936	511936	cytochrome P450, family 2, subfamily J	6.32	4.29E-06		
LOC512486	512486	interferon-induced guanylate-binding protein 1	5.51	2.37E-42	4.13	3.23E-19
LOC512672	512672	major histocompatibility complex, class I	2.44	6.07E-09		
LOC513659	513659	guanylate-binding protein 6	7.06	2.17E-10		
LOC613699	613699	interferon-induced transmembrane protein 1	3.42	4.20E-05		
LOC616948	616948	tripartite motif-containing protein 5-like	3.41	1.65E-12		
LOC618409	618409	interferon regulatory factor 4	7.12	1.45E-49	3.40	3.07E-07
LOC618737	618737	bone marrow stromal antigen 2	10.33	8.38E-119	8.70	7.29E-46
LOC781710	781710	guanylate-binding protein 2	7.78	1.45E-49	6.10	9.04E-20
LOC783920	783920	interferon-induced very large GTPase 1-like	5.14	3.14E-14		
LOC786073	786073	interferon-induced transmembrane protein 1-like	4.04	5.67E-04		
LOC786372	786372	golgin subfamily A member 6-like protein 22	5.33	2.84E-18		
LY6E	4061	lymphocyte antigen 6 family member E			3.45	2.61E-06
MAD2L2	10459	mitotic arrest deficient 2 like 2	3.14	3.33E-14		
MANF	7873	mesencephalic astrocyte derived neurotrophic factor	2.25	2.84E-04		
MAP1LC3C	440738	microtubule associated protein 1 light chain 3 gamma	7.76	1.03E-05		
MAP3K8	1326	mitogen-activated protein kinase kinase kinase 8	2.31	4.65E-04		
MARCKSL1	65108	MARCKS like 1	3.00	1.65E-08		
MASTL	84930	microtubule associated serine/threonine kinase like	3.21	9.94E-10		
MAT2B	27430	methionine adenosyltransferase 2B	2.00	5.83E-04		
MB21D1	782472	Mab-21 domain containing 1	6.72	5.14E-38	3.32	1.60E-05
MCHR1	2847	melanin concentrating hormone receptor 1	6.14	3.85E-22		
MED17	9440	mediator complex subunit 17	2.12	2.89E-07		
MIC1	533051	major histocompatibility class I related protein	3.41	2.31E-15		
MITD1	129531	microtubule interacting and trafficking domain containing 1	2.39	5.63E-06		
MOV10	4343	Mov10 RISC complex RNA helicase	2.98	6.40E-08		
MSC	9242	musculin	2.03	2.05E-04		
MTFP1	51537	mitochondrial fission process 1	2.35	1.85E-05		
MUC5B	727897	mucin 5B, oligomeric mucus/gel-forming	4.71	1.41E-11		
MX1	4599	MX dynamin like GTPase 1	8.04	4.06E-164	6.87	4.53E-112
MX2	4600	MX dynamin like GTPase 2	13.02	3.92E-122	10.00	1.56E-66
MYLK	4638	myosin light chain kinase			-3.26	9.60E-07
NAMPT	10135	nicotinamide phosphoribosyltransferase	2.99	5.70E-06		
NCAM1	4684	neural cell adhesion molecule 1			-4.48	3.34E-04
NECTIN2	5819	nectin cell adhesion molecule 2	2.40	6.67E-12		
NFKBIA	4792	NFKB inhibitor alpha	3.75	1.02E-07		
NFKBIB	4793	NFKB inhibitor beta	2.17	1.29E-05		
NFKBIE	4794	NFKB inhibitor epsilon	2.70	4.20E-05		
NLRC5	84166	NLR family CARD domain containing 5	4.40	1.17E-07		
NMES1	84419	Normal Mucosa Of Esophagus Specific 1	3.43	3.23E-23		
NOTCH3	4854	notch 3	3.68	5.25E-05		
NR3C1	2908	nuclear receptor subfamily 3 group C member 1	2.09	9.67E-09		

NR4A3	8013	nuclear receptor subfamily 4 group A member 3	4.71	4.15E-08		
NUB1	51667	negative regulator of ubiquitin like proteins 1	2.01	2.04E-04		
OAS1X	347699	2',5'-oligoadenylate synthetase 1, 40/46kDa	6.41	3.86E-81	5.82	1.47E-60
OAS1Y	654488	2',5'-oligoadenylate synthetase 1, 40/46kDa	6.70	1.35E-61	5.84	1.77E-43
OAS1Z	519922	2',5'-oligoadenylate synthetase 1, 40/46kDa	6.99	9.33E-60	6.78	2.30E-49
OAS2	4939	2'-5'-oligoadenylate synthetase 2	9.15	5.93E-80	6.01	2.45E-28
OLR1	4973	oxidized low density lipoprotein receptor 1	4.20	5.44E-08		
ONECUT2	9480	one cut homeobox 2	4.03	4.78E-04		
PARM1	25849	prostate androgen-regulated mucin-like protein 1	4.76	1.93E-11		
PARP10	84875	poly(ADP-ribose) polymerase family member 10	4.30	7.31E-19		
PARP12	64761	poly(ADP-ribose) polymerase family member 12	4.65	2.49E-40	3.32	1.35E-15
PARP14	54625	poly(ADP-ribose) polymerase family member 14	4.51	1.34E-55	3.03	4.57E-18
PARP9	83666	poly(ADP-ribose) polymerase family member 9	3.53	7.94E-43	3.44	1.50E-38
PDE12	201626	phosphodiesterase 12	1.90	9.11E-05		
PDK1	5163	pyruvate dehydrogenase kinase 1	-2.43	7.00E-05		
PELI1	57162	pellino E3 ubiquitin protein ligase 1	1.97	7.84E-04		
PHLDA1	22822	pleckstrin homology like domain family A member 1	3.39	5.96E-05		
PLAC8	51316	placenta specific 8	8.34	1.87E-14	8.80	4.74E-11
PLEKHA4	57664	pleckstrin homology domain containing A4	3.50	8.77E-36		
PLSCR2	57047	phospholipid scramblase 2	3.43	1.93E-11		
PMAIP1	5366	phorbol-12-myristate-13-acetate-induced protein 1	2.69	1.31E-08		
PML	5371	promyelocytic leukemia	4.11	1.53E-30		
PNPT1	87178	polyribonucleotide nucleotidyltransferase 1	3.65	2.83E-20		
POLH	5429	DNA polymerase eta	2.46	2.07E-07		
PPA1	5464	pyrophosphatase (inorganic) 1	2.23	1.55E-05		
PPP1R15A	23645	protein phosphatase 1 regulatory subunit 15A	2.98	3.88E-11		
PPP2R3C	55012	protein phosphatase 2 regulatory subunit B"gamma	3.46	8.19E-13		
PRICKLE3	4007	prickle planar cell polarity protein 3	2.72	2.84E-08		
PSMB10	5699	proteasome subunit beta 10	2.41	2.18E-04		
PSMB8	5696	proteasome subunit beta 8	3.30	2.94E-09		
PSMB9	5698	proteasome subunit beta 9	4.31	2.05E-06		
PSME2	5721	proteasome activator subunit 2	2.22	2.29E-04		
PSMF1	9491	proteasome inhibitor subunit 1	2.87	7.13E-07		
PTGIR	5739	prostaglandin I2 receptor	5.60	1.56E-05		
RAB37	326624	RAB37, member RAS oncogene family	5.82	3.56E-04		
RAB3IL1	5866	RAB3A interacting protein like 1	-1.91	9.57E-04		
RAB8B	51762	RAB8B, member RAS oncogene family	2.45	3.39E-06		
RASSF1	11186	Ras association domain family member 1	2.96	1.32E-10		
RBCK1	10616	RANBP2-type and C3HC4-type zinc finger containing 1	1.82	3.60E-04		
RBM43	375287	RNA binding motif protein 43	2.95	4.71E-04		
RBMS2	5939	RNA binding motif single stranded interacting protein 2	2.42	3.38E-06		

RHBDF2	79651	rhomboid 5 homolog 2	2.64	2.36E-04		
RIPK3	11035	receptor interacting serine/threonine kinase 3	2.64	4.33E-06		
RNASEL	6041	ribonuclease L	2.54	2.33E-06		
RNF114	55905	ring finger protein 114	2.48	4.07E-06		
RNF19B	127544	ring finger protein 19B	3.30	2.92E-13		
RSAD2	91543	radical S-adenosyl methionine domain containing 2	12.17	1.59E-81	9.44	4.70E-42
RSL1D1	26156	ribosomal L1 domain containing 1	1.92	1.03E-09		
RTP4	64108	receptor transporter protein 4	4.15	5.96E-30	2.47	8.65E-06
SALL2	6297	spalt like transcription factor 2	-3.44	7.68E-06		
SAMD9	54809	sterile alpha motif domain containing 9	4.50	5.85E-08		
SAT1	6303	spermidine/spermine N1-acetyltransferase 1	2.50	2.07E-04		
SCLY	51540	selenocysteine lyase	3.47	2.62E-12		
SCRN1	9805	secernin 1	-3.68	1.07E-05		
SFRP2	6423	secreted frizzled related protein 2			-4.16	3.30E-05
SLC15A3	51296	solute carrier family 15 member 3	6.42	2.05E-45		
SLC25A19	60386	solute carrier family 25 member 19	3.23	3.66E-32		
SLC25A28	81894	solute carrier family 25 member 28	2.37	4.49E-05		
SLFN11	91607	schlafen family member 11	6.08	4.79E-21	3.71	2.64E-05
SLFN12	55106	schlafen family member 12	3.30	1.03E-05		
SMAGP	57228	small cell adhesion glycoprotein	2.44	6.06E-05		
SOCS1	8651	suppressor of cytokine signaling 1	3.64	7.36E-05		
SP100	6672	SP100 nuclear antigen	4.95	1.30E-21	3.07	3.31E-05
SP110	3431	SP110 nuclear body protein	4.49	4.04E-40		
SP140	11262	SP140 nuclear body protein	4.06	3.53E-10		
SP140L	93349	SP140 nuclear body protein like	2.38	2.03E-07		
SPTLC2	9517	serine palmitoyltransferase long chain base subunit 2	2.08	5.88E-05		
STARD5	80765	StAR related lipid transfer domain containing 5	1.94	1.62E-04		
STARD8	9754	StAR related lipid transfer domain containing 8	2.72	5.98E-09		
STAT2	6773	signal transducer and activator of transcription 2	2.42	1.47E-11		
STK17A	9263	serine/threonine kinase 17a	2.66	7.14E-05		
SVIL	6840	supervillin	2.13	7.22E-06		
SYNM	23336	synemin	2.37	7.00E-05		
SYTL3	94120	synaptotagmin like 3	4.13	1.08E-10		
TAF3	83860	TATA-box binding protein associated factor 3	2.46	1.08E-05		
TAF4B	6875	TATA-box binding protein associated factor 4b	3.62	6.19E-17		
TAP1	6890	transporter 1, ATP binding cassette subfamily B member	4.46	5.65E-04		
TDRD7	23424	tudor domain containing 7	2.91	4.02E-24		
TIFA	92610	TRAF interacting protein with forkhead associated domain	5.63	6.96E-17		
TMEM106A	113277	transmembrane protein 106A	3.61	1.05E-24		
TMEM140	55281	transmembrane protein 140	2.96	2.88E-10		
TMEM268	203197	transmembrane protein 268	2.07	4.79E-04		
TMPRSS2	7113	transmembrane protease, serine 2	3.08	2.52E-04		
TNFAIP1	7126	TNF alpha induced protein 1	1.95	9.12E-04		

TNFAIP3	7128	TNF alpha induced protein 3	4.58	3.34E-17		
TNFSF10	8743	TNF superfamily member 10	6.44	2.09E-32	3.79	2.22E-08
TNFSF4	7292	TNF superfamily member 4	3.48	3.76E-10		
TRANK1	9881	tetratricopeptide repeat and ankyrin repeat containing 1	3.37	2.09E-23		
TREX1	11277	three prime repair exonuclease 1	3.80	2.81E-26		
TRIM14	9830	tripartite motif containing 14	3.83	2.26E-04		
TRIM16	10626	tripartite motif containing 16	2.33	1.63E-09		
TRIM21	6737	tripartite motif containing 21	4.10	2.79E-34		
TRIM25	7706	tripartite motif containing 25	2.29	9.35E-14		
TRIM34	53840	tripartite motif containing 34	3.77	1.94E-10		
TRIM38	10475	tripartite motif containing 38	3.01	9.76E-16		
TRIM56	81844	tripartite motif containing 56	1.98	4.54E-05		
TSKU	25987	tsukushi, small leucine rich proteoglycan	2.51	3.14E-07		
TWISTNB	221830	TWIST neighbor	1.94	1.46E-04		
UBA7	7318	ubiquitin like modifier activating enzyme 7	5.31	3.66E-24	3.64	2.33E-08
UNC93B1	81622	unc-93 homolog B1, TLR signaling regulator	1.91	8.06E-06		
USP18	11274	ubiquitin specific peptidase 18	6.91	4.84E-61	5.00	8.63E-27
USP25	29761	ubiquitin specific peptidase 25	2.35	2.58E-06		
WARS	7453	tryptophanyl-tRNA synthetase	3.24	4.42E-04		
WDCP	80304	WD repeat and coiled coil containing	1.96	5.89E-05		
XAF1	54739	XIAP associated factor 1	7.06	2.28E-61	5.63	1.79E-35
XRN2	22803	5'-3' exoribonuclease 2	1.96	2.79E-05		
ZBP1	81030	Z-DNA binding protein 1	8.48	7.27E-122	7.17	2.65E-70
ZCCHC18	644353	zinc finger CCHC-type containing 18	2.56	2.18E-04		
ZMYM5	9205	zinc finger MYM-type containing 5	2.16	4.62E-04		
ZNFX1	57169	zinc finger NFX1-type containing 1	4.15	9.33E-60	2.76	4.05E-18