Supplemental Data

Immature DC efficiently take up Listeria and are bactericidal

To study regulation of IDO in DC we established an in vitro model previously described (1). Human monocytes, immature monocyte-derived DC (immDC) and mature DC (matDC) were infected with FITC-labeled wild type *L.monocytogenes* (strain EGD) at different multiplicities of infection (MOI) and infection efficiency was assessed by flow cytometry (**Figure S2A**) and confocal microscopy (**Figure S2B**). As previously reported, FITC labeling does not alter the phagocytosis and intracellular survival of listeria (2). Intracellular localization of phagocytosed bacteria was clearly demonstrated by confocal microscopy (**Figure S2B**). Phagosomal escape and cytosolic localization of listeria were seen within 2 hours after infection as shown by co-localization of actin condensation around intracellularly residing *L.monocytogenes.* Monocytes and immature DC were infected very efficiently (more than 95% resp. 75% of the cells at MOI ≥ 10) while infection rates for matDC were significantly lower and never reached comparable rates even at higher MOI (**Figure S2C**). For subsequent experiments we used immDC as they resemble features of those DC first encountering *L.monocytogenes* in vivo. In addition, we also infected in vitro generated macrophages and could demonstrate that infection efficiency was comparable to immature DC (**Figure S2C**).

Infected immDC exhibited a profound bactericidal effect reducing bacterial burden by 60 to 75% within the first 30 minutes post infection (p.i.) (**Figure S2D**). The bactericidal effect of DC demonstrated here is in accordance with previously reported data (3).

Changes of gene expression in immDC following L.monocytogenes infection

To address the transcriptional changes, induced in human DC during listeria infection, we conducted a set of experiments, in which immDC were infected with virulent *L.monocytogenes* (strain EGD) at a MOI of 10. Subsequently, transcriptional changes of infected DC were determined at 2 hrs (immediate response) and 6 hrs (early response) p.i. using the Affymetrix HG-U133A microarray with appropriate non-infected controls (two independent mo-DC preparations resp. infections were used for 2 hrs time point, at 6 hrs p.i. four independent mo-DC preparations and four independent infection experiments were analysed, resulting in 12 independent microarray hybridizations). Scanned GeneChip® DAT Files were analyzed with Affymetrix Microarray Suite 5.0 and resulting CEL files were subsequently analyzed with dChip® 2005 and R software package 2.2.1 (Bioconductor project). Variable transcripts across the Affymetrix dataset (total of 12 microarrays) were defined in dChip using the following variation filter: 0.5 < standard deviation / mean < 10, the resulting list of 1189 genes was used for hierarchical clustering in dChip (**Figure 2A**). For comparison of transcriptional changes after infection of immDC with virulent *L.monocytogenes* vs heat-killed listeria we also performed a screening experiment including three time-points (2, 6, and 24 hrs) using the newly introduced Illumina human whole-genome Sentrix Human-6 Expression BeadChip array.

Comparison of infected and non-infected immDC using stringent filtering criteria (lower bound of the 90% confidence interval of the fold change > 2, absolute difference in signal intensity between group means > 100, and present call % ≥ 50), revealed 159 transcripts significantly changed already 2 hrs after *L.monocytogenes* infection. Expression levels of 833 transcripts were significantly modified after 6 hours of infection. Time-course analysis of *L.monocytogenes* infection, performed with GeneSpring 7.2 software, resulted in the definition of 3 different temporal patterns of gene expression in infected mo-DC (**Figure 2B, Table S2**). A set of 29 transcripts was significantly regulated at the early stages of infection ("immediate response", **Table S2**), whereas 703 transcripts were regulated after 6 hours ("early response", **Table S2**). Another 130 transcripts were regulated throughout the infection course both at 2 and 6 hrs time points ("immediate-early response", **Table S2**). Interestingly, most of the genes, defined as immediate (2 hrs) and immediate-early response targets (2 and 6 hrs), were upregulated, whereas more than 50% of the "early response" genes (6 hrs) were downregulated. The infection of human DC with *L.monocytogenes* was dominated by two main functional gene groups, namely NF-κB target genes (represented with 241 transcripts) and interferon-sensitive genes (ISG, 560 transcripts). Among the NF-κB target genes, 6 transcripts were regulated at 2 hrs, 50 transcripts at 2 and 6 hrs, and 30 transcripts only at 6 hrs, respectively; the most significantly regulated genes among the NF-κB targets at 2 hrs were *CSF1*, *REL* and *SOD2*, the most significantly regulated genes at the later time-point were *PTGS2*, *BCL2A1*, *CXCL1*, *CXCL10*, *CXCL11*, *CCL20*, *IL1B*, *IL6*, *IL8*, *IL10*, *IL12B*, *IL1RN*, *IL2RA*, and *IL15RA*. From a list of 560 transcripts derived from the Interferon Stimulated Gene Database (http://www.lerner.ccf.org/labs/williams/xchip-html.cgi), 3 transcripts were regulated at 2 hrs (immediate response), 26 transcripts at 2 and 6 hrs (immediate to early response) and 69 transcripts only at 6 hrs (early response). Among the most significantly changed genes of the ISG-group were *INDO*, *ISG20*, *TNFSF10*, *GBP1*, *G1P2*, *INHBA*, *PDGFRL*, *PBEF1*, *PMAIP1*, *IFIT2*, *IFIT3*, and *IFITM1*.

Interestingly, assessment of infection-induced transcriptional changes in the context of DC maturation demonstrated that less than 40% of genes, defined as DC maturation targets in immDC stimulated with TNFα and α-CD40 mAbs (A.Popov, unpublished results), were significantly regulated 6 hrs after listeria infection, suggesting that the majority of transcriptional changes post infection are not related to maturation. All transcriptional data are presented in detail in **Table S2**.

Immunohistological assessment of other infectious and non-infectious diseases

To assess whether IDO-expressing DC might also play a role in other granulomatous infectious diseases caused by intracellular bacteria we analyzed lymph node samples from patients with granuloma-associated diseases such as cat scratch disease, tuberculosis, sarcoidosis and compared those to infectious diseases lacking granuloma including malakoplakia, mycobacterial histiocytosis, and Morbus Whipple. We first analyzed lymph nodes from patients with cat scratch disease (CSD) (**Figure S3A**). CSD is caused by *Bartonella henselae*, a facultative intracellular Gram-negative bacterium. Regional lymphadenopathy is the most common clinical manifestation of CSD in humans (4). Histologically, lymph nodes in CSD are characterized - similar to suppurative granulomatous listeriosis - by formation of granuloma surrounded by concentric layers of reticulohistiocytic cells and lymphocytes (**Figure S3A**). In contrast to listeriosis, the ring wall observed in CSD contained more CD68$^+$ macrophages and less S100$^+$ DC. However, similar to listeriosis, the majority of cells within the ring wall structure strongly expressed IDO suggesting an important role for this enzyme in infectious diseases characterized by granuloma formation.

Next we analyzed granuloma in tuberculosis (**Figure S3B**). Even in immunocompetent individuals infection with *Mycobacterium tuberculosis* is not eliminated by suppurative inflammation (5). Lymph node specimens from patients with genetically verified *M.tuberculosis* infection are characterized by multiple granuloma consisting of specialized macrophages (epitheloid cells and Langerhans giant cells) and central caseating necrosis surrounded by a T-cell rich area and collagen rich fibers. CD68$^+$ macrophages were identified as the major cellular component of the center of the granuloma, while S100$^+$ DC were mainly located along the border of the granuloma. Interestingly, although at low numbers, IDO$^+$ cells were observed at the edge of the granuloma (**Figure S3B**) marking a border between the granuloma and surrounding tissue.

In addition to tuberculosis we studied sarcoidosis as another granulomatous disease associated with enrichment of extracellular fibers, however, for which no infectious origin is known (6). Shown here is a lymph node from a patient with sarcoidosis (**Figure S3C**). Granuloma consisting of epitheloid cells and some giant cells are characteristic. A prominent circular enrichment of extracellular fibers surrounding the granuloma markedly distinguishes these lesions from classical tuberculosis (van Gieson, data not shown). As expected, granuloma forming cells are mostly CD68 positive. In contrast to tuberculosis associated granuloma, S100$^+$ cells in sarcoidosis are obviously around the granuloma but also within the center of the granuloma. IDO positive cells are surrounding the granuloma and are found in the area between granulomas.

To determine if IDO is also expressed in infectious diseases lacking granuloma, we assessed IDO expression in malakoplakia (7), mycobacterial histiocytosis, and M. Whipple (**Figure S4**). Patients with malakoplakia show defective phagolysosomal activity in macrophages and monocytes, which is associated with intracellular storage of bacteria, mostly *Escherichia coli* (**Figure S4A**). Multi-lamellar vesicles harboring *E.coli* are visible by ultrastructural analysis. Large numbers of CD68$^+$ macrophages were dispersed throughout the diseased tissue. However, among the significant numbers of S100$^+$ DC virtually no cells staining for IDO were detectable.

Mycobacterial histiocytosis (8) and M. Whipple (9) (**Figures S4B** and **S4C**) were analyzed as two additional examples of bacterial infections characterized by numerous phagocytic stored pathogens and lack of granuloma formation. Intracellularly accumulated acid-proofed rods are visible in a case of mycobacterial histiocytosis (lymph node, Ziehl-Neelson, x 1000). Intracellularly stored regressive pathogens are nicely seen in a small intestine biopsy in a patient with M. Whipple (PAS reaction, x 1000). CD68 immunostaining demonstrates macrophage origin of the pathogen-storing cells. In both diseases, S100$^+$ DC are rather rare. Either no or only very rare cells expressing IDO can be detected (magnification x200).

Taken together, these data strongly suggest that the induction and enrichment of IDO$^+$ DC is a response to specific pathogen signals, particularly in infections caused by intracellular bacteria associated with suppurative granuloma formation.

References within Supplemental Data

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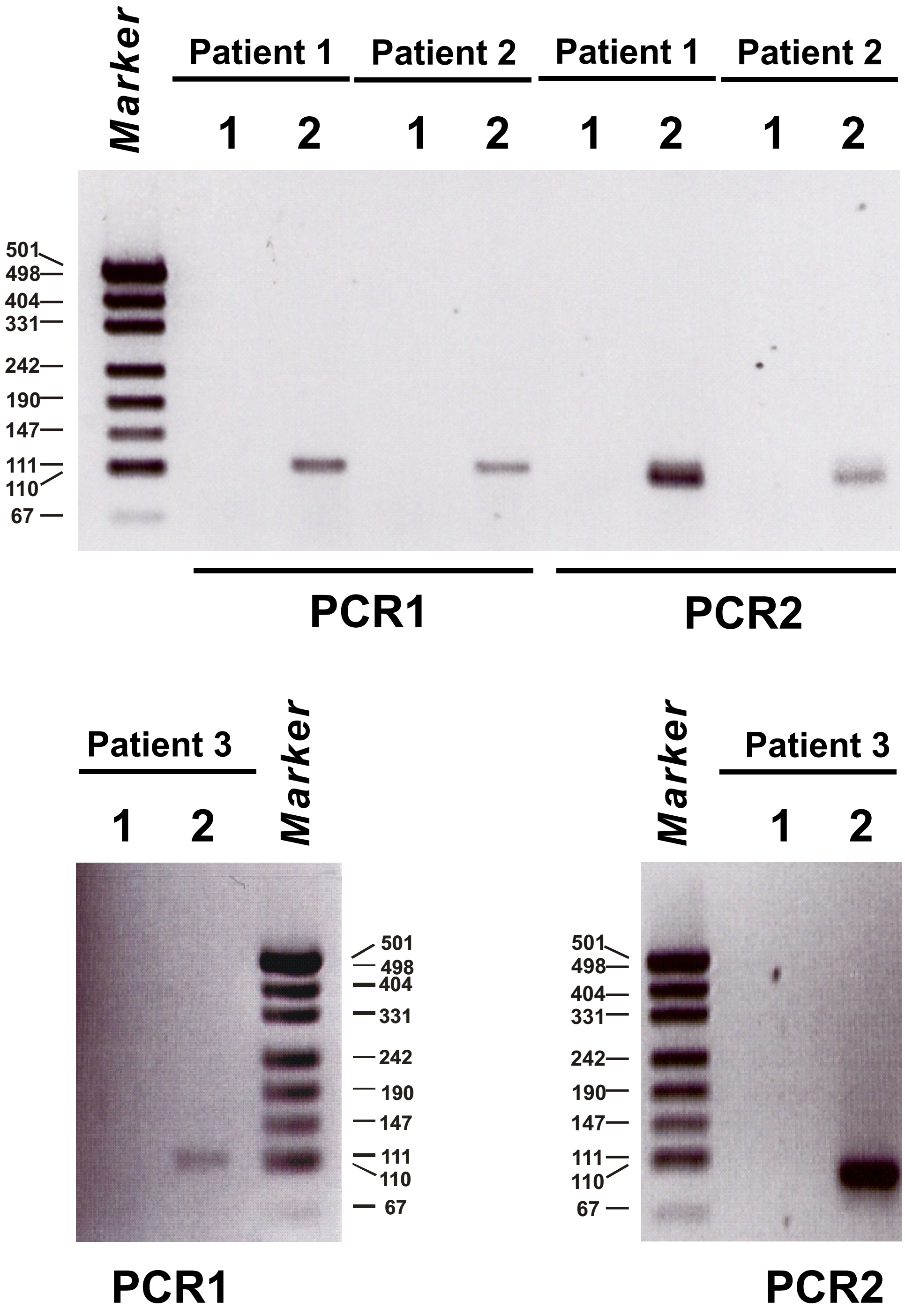
Figure S1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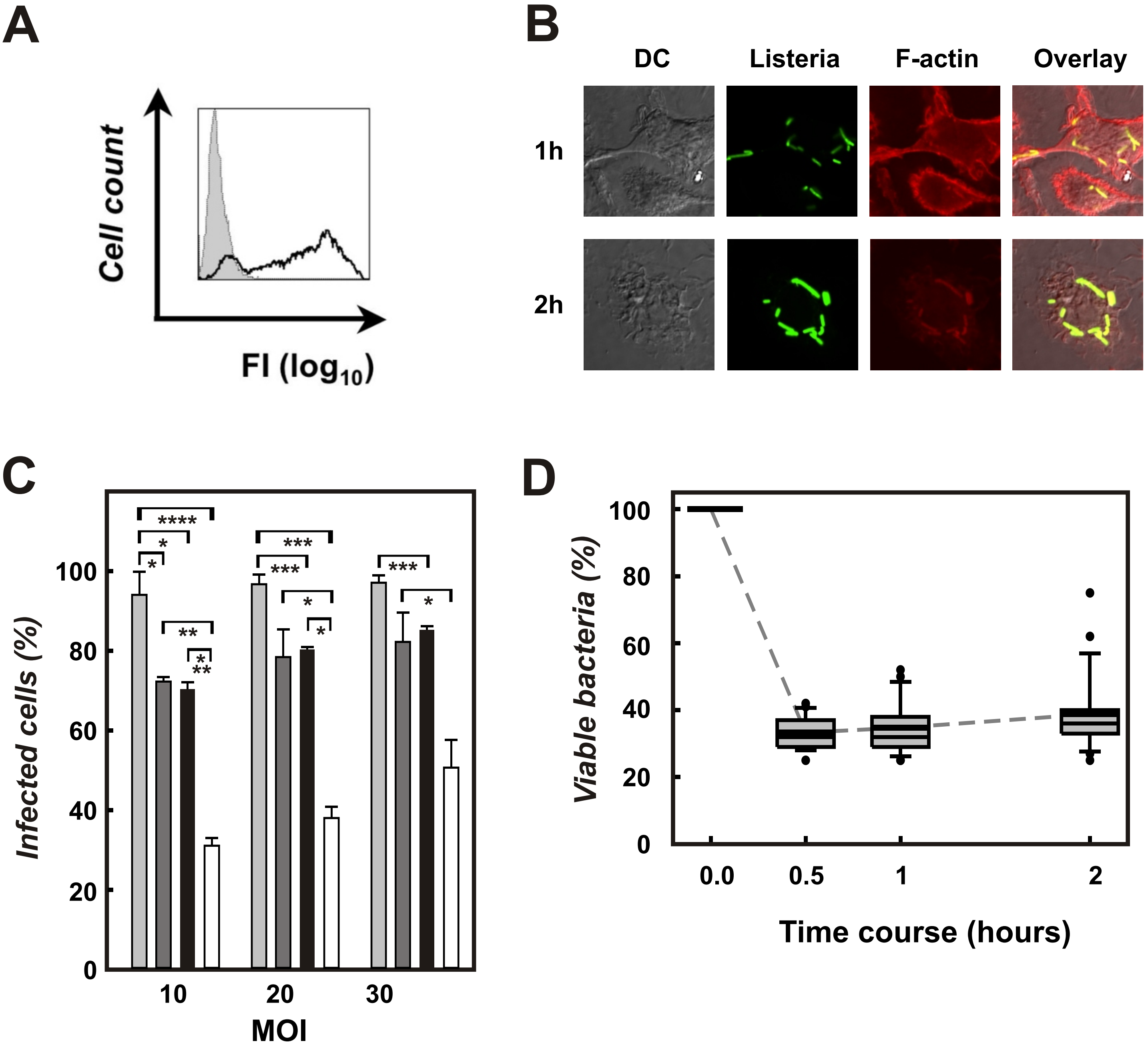
PCR2

Figure S2


A
Cell count
FI ($\log_{10}$)
B
DC
Listeria
F-actin
Overlay
1h
2h
C
Infected cells (%)
0
20
40
60
80
100
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*
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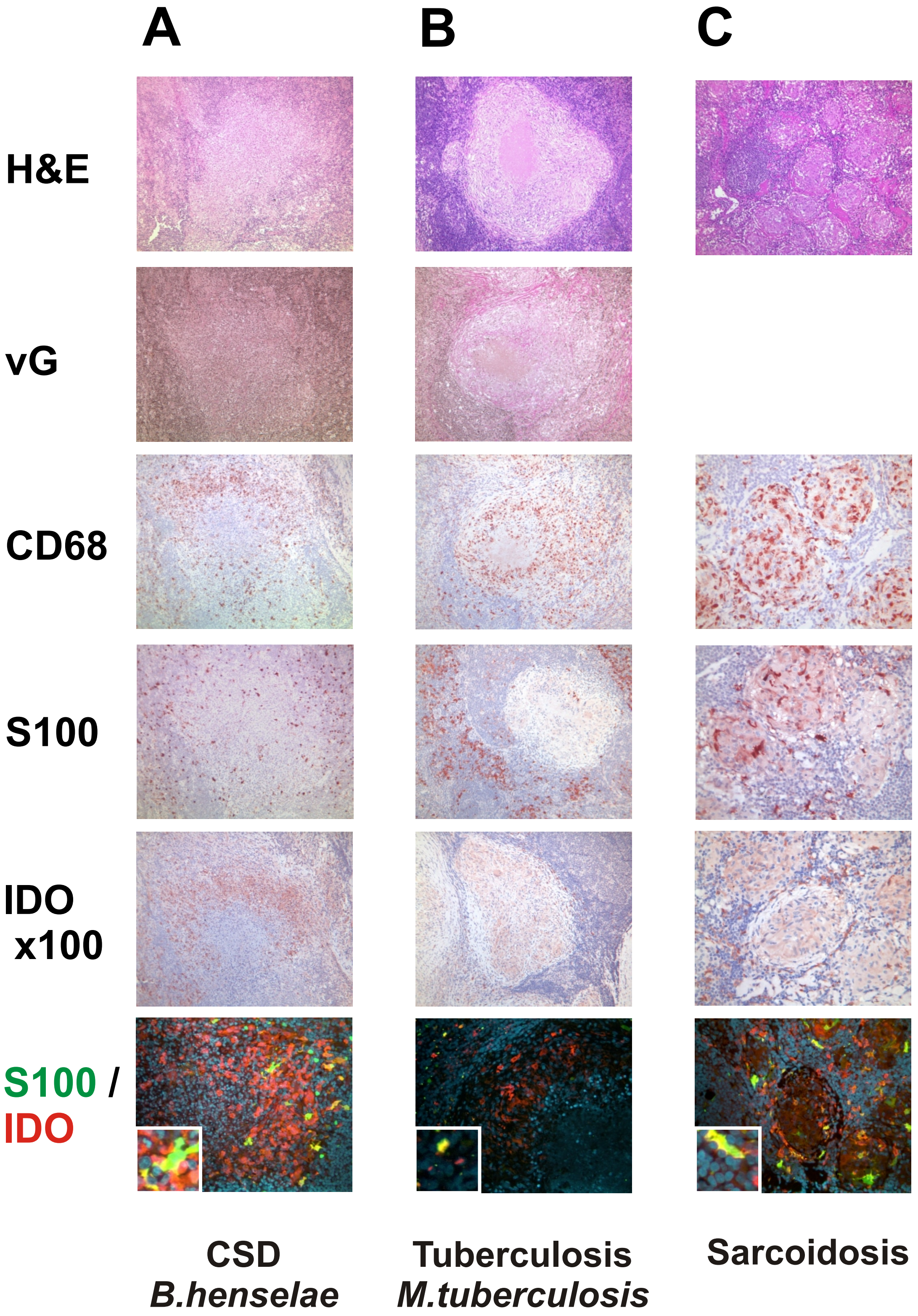
*
*
*
10
20
30
MOI
D
Viable bacteria (%)
0
20
40
60
80
100
0.0
0.5
1
2
Time course (hours)

Figure S3


A
B
C
H&E
vG
CD68
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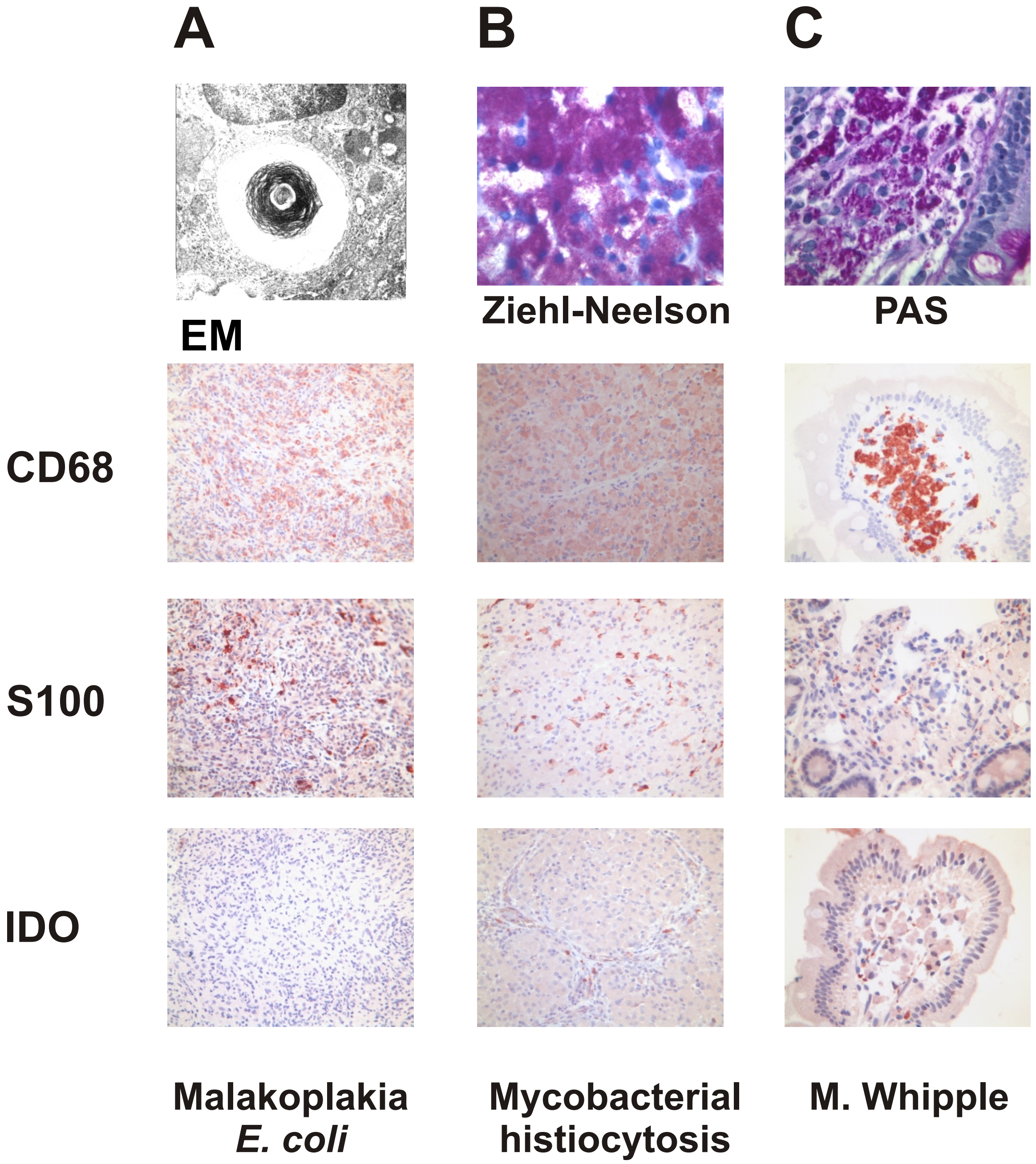
IDO
x100
S100 /
IDO
CSD
B.henselae
Tuberculosis
M.tuberculosis
Sarcoidosis

Figure S4


A
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C
EM
Ziehl-Neelson
PAS
CD68
S100
IDO
Malakoplakia
E. coli
Mycobacterial
histiocytosis
M. Whipple

Supplemental Figure legends

Figure S1:

Confirmation of human dendritic cells' infection by *Listeria monocytogenes*

Confirmation of listeria persistence in lymph node samples. Nested PCR utilizing primer for transcript AJ132543 (*L.monocytogenes* fibronectin binding protein gene) was used to confirm listeria infection in analyzed samples. Bacterial DNA was derived from lymph node specimens of three patients with serologically confirmed cervicoglandular type infection with *L.monocytogenes*. 1 – negative control; 2-specific PCR products (PCR1 113 bp, PCR2 – 95 bp), marker - pUC19 DNA/MspI marker 23 (MBI Fermentas).

Figure S2:

In vitro Infection of human DC with *L.monocytogenes*

(A) Phagocytosis of *L.monocytogenes* by human DC in vitro. Immature mo-DC were infected with FITC-labeled *L.monocytogenes* at MOI 10, and the infection efficiency was controlled by flow cytometry. Uninfected control is shown as grey area underneath the dotted line, fluorescence of cells infected with FITC-labeled bacteria is depicted by the thick black line. A representative experiment from twenty independent infections is shown.

(B) Localization of phagocytosed listeria in mo-DC. Subcellular localization of phagocytosed bacteria and the phagosomal escape of the virulent strain followed by actin condensation were confirmed by confocal microscopy using FITC-labeled listeria and staining for F-actin after fixation. Microscopy was performed with Olympus FluoView FV1000 Confocal Microscope (60x) followed by digital magnification (7x) 1 and 2 hours after infection. Condensation of actin (red) colocalizing with FITC-labeled listeria (green) can be observed (yellow combination color on the overlay).

(C) Infection rates of monocytes, macrophages, immature and mature dendritic cells. Cells were infected with indicated multiplicities of infection (MOI) for 30 min and infection rate was assessed by flow cytometry after the extracellular bacteria were removed. At least 3 experiments for each cell type and condition were performed and data are expressed as mean ± SD; asterisks highlight the statistically significant comparisons (* $p<0.05$, ** $p<0.01$, *** $p<0.005$, **** $p<0.001$). Monocytes: light grey bars, macrophages: dark grey bars, immature DC: black bars, mature DC: white bars.

(D) Assessment of bactericidal activity of human immDC infected with *L.monocytogenes* at MOI of 10. Time-point t=0 hrs is defined as the time, when the infection period of 30 min was terminated and DC were washed to remove extracellular bacteria. Box plots' graph represents the number of intracellular viable bacteria at specified time-point normalized to the initial time-point (t=0) set to 100%. Shown are median, 75 percentile (box), standard deviation (whiskers), thick black line represents mean, and outliers are identified by black dots, gray dashed line represents the kinetics. Number of viable bacteria was assessed as described in Methods. A total of n=18 experiments was performed.

Figure S3:

Ring wall formation containing IDO$^+$ DC in diseases, associated with granuloma formation

Histomorphology and immunohistochemistry of **(A)** cat scratch disease (CSD, *Bartonella henselae*), **(B)** tuberculosis (*Mycobacterium tuberculosis*) and **(C)** sarcoidosis. H&E: Hematoxylin-eosin staining, (x100), vG: Van Gieson reaction, (x100). Photographs of samples stained with CD68 and S100 were taken at a magnification x100, and of samples stained with IDO at magnifications x100 and x400. Representative cases are depicted for each disease. Photographs were taken by a JVC digital camera connected to a Zeiss Axiophot microscope. Lower row: to assess expression of IDO by DC, immunofluorescence analysis of IDO was combined with S100; all photos were taken at magnification x250. In each right corner an enlarged section of the photo is shown for more detail.

Figure S4:

Assessment of IDO in infectious diseases lacking granuloma formation

Histomorphology and immunohistochemistry of **(A)** malakoplakia (here *Escherichia coli*), **(B)** mycobacterial histiocytosis, and **(C)** M. Whipple. Photographs were taken by a JVC digital camera connected to a Zeiss Axiophot microscope. H&E: Hematoxylin-eosin staining (x100), Ziehl-Neelson (x1000), PAS reaction (x1000). For malakoplakia an ultrastructural analysis from a renal biopsy was performed to demonstrate engulfment of *E.coli* by macrophages (electron microscopy (EM), magnification x 14.000). Photographs for stainings with CD68, S100 and IDO were taken at a magnification x100, IDO additionally with a magnification x400.

Table S1*:* PCR Primer

PCR Primer for the detection of bacteria within histological specimens

Bacterium to be detected	Gene	Accession Nr.	PCR #	Forward Primer	Reverse Primer
Mycobacterium tuberculosis	probable transposase	AJ242907	1	TGG CCA TCG TGG AAG CGA CG	GAC CAA ACT CGG CCT GTC CG
			2	TGC GAG CGT AGG CGT CGG TGA	GAT CGC GTC CAG CGC CGC TTC
Bartonella haenselae	serine protease	L20127	1	GGT TCA GAT TCA GCC TGT AAC AA	AAC TCC TAA GGT TAC TGT TTC TCC TG
			2	CTG ATT CAA TTG GTT TGA AGG A	CAA TAC GCT TTG CTA GAT CAC G
Listeria monocytogenes	fibronectin binding protein (*fbp*) gene	AJ132543	1	CCC GCC TGG TCT AAA CTG GAT TTG	TGT ACG CCG ACC AAA TTT CCA TCC
			2	CCC GCC TGG TCT AAA CTG GAT TTG	CCATCCTCG TAA GTC ACG ATA TAC

Primer for the detection of IDO and COX-2 transcripts by real-time PCR

Gene symbol	Gene	Accession Nr.	Forward Primer	Reverse Primer	Universal ProbeLibrary probes (Roche)
INDO	indoleamine-pyrrole 2,3 dioxygenase	M34455	TTC AGT GCT TTG ACG TCC TG	TGG AGG AAC TGA GCA GCA T	22
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963	TGG GAA GCC TTC TCT AAC CTC	TCA GGA AGC TGC TTT TCC T	69
B2M	beta-2-microglobulin	NM_004048	TTC TGG CCT GGA GGC TAT	TCA GGA AAT TTG ACT TTC CAT TC	42

Table S2: List of genes found to be significantly changed after the infection of human mo-DC with virulent strain of *Listeria monocytogenes*. Fold changes between the means of average expression signals in listeria-infected and mock-infected DC are shown. Positive values indicate upregulated genes, negative values indicate downregulated genes. Values in bold highlight the genes, which expression was significantly changed (**Supplemental Data**), green color hallmarks the upregulated and red color hallmarks the downregulated genes, respectively.

Immediate response: genes, regulated immediately (whithin first 2 hours) after infection

Probe Set ID	Gene Symbol	Gene Title	GenBank ID	Fold change	
				2h	6h
209716_at	*CSF1*	colony stimulating factor 1 (macrophage)	M37435	**10.14**	2.36
201694_s_at	*EGR1*	early growth response 1	NM_001964	**5.86**	1.96
213146_at	---	---	AA521267	**4.9**	2.27
206115_at	*EGR3*	early growth response 3	NM_004430	**4.87**	3.2
219045_at	*RHOF*	ras homolog gene family, member F (in filopodia)	NM_019034	**4.23**	2.23
203397_s_at	*GALNT3*	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	BF063271	**4.2**	5.53
210557_x_at	*CSF1*	colony stimulating factor 1 (macrophage)	M76453	**4.1**	1.67
206036_s_at	*REL*	v-rel reticuloendotheliosis viral oncogene homolog (avian)	NM_002908	**3.94**	3.27
203821_at	*HBEGF*	heparin-binding EGF-like growth factor	NM_001945	**3.89**	2.1
216056_at	*CD44*	CD44 antigen (homing function and Indian blood group system)	AW851559	**3.6**	2.25
217523_at	*CD44*	CD44 antigen (homing function and Indian blood group system)	AV700298	**3.6**	2.7
41386_i_at	---	---	AB002344	**3.32**	1.68
208370_s_at	*DSCR1*	Down syndrome critical region gene 1	NM_004414	**3.17**	1.77
201235_s_at	*BTG2*	BTG family, member 2	BG339064	**3.15**	2.16
201631_s_at	*IER3*	immediate early response 3	NM_003897	**3.03**	1.93
211668_s_at	*PLAU*	plasminogen activator, urokinase	K03226	**3**	-2
211839_s_at	*CSF1*	colony stimulating factor 1 (macrophage)	U22386	**2.99**	1.38
222292_at	*CD40*	CD40 antigen (TNF receptor superfamily member 5)	AW298127	**2.96**	2.94
207667_s_at	*MAP2K3*	mitogen-activated protein kinase kinase 3	NM_002756	**2.9**	2.5
205479_s_at	*PLAU*	plasminogen activator, urokinase	NM_002658	**2.88**	-2.15
201236_s_at	*BTG2*	BTG family, member 2	NM_006763	**2.83**	1.89
202071_at	*SDC4*	syndecan 4 (amphiglycan, ryudocan)	NM_002999	**2.71**	2.49
200644_at	*MARCKSL1*	MARCKS-like 1	NM_023009	**2.68**	2.12
203124_s_at	*SLC11A2*	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NM_000617	**2.66**	2.53
209921_at	*SLC7A11*	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AB040875	**2.44**	2.52
214047_s_at	*MBD4*	methyl-CpG binding domain protein 4	AI913365	**-2.58**	-1.67
203445_s_at	*CTDSP2*	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NM_005730	**-2.67**	-1.64
212907_at	*SLC30A1*	Solute carrier family 30 (zinc transporter), member 1	AI972416	**-3.02**	-1.13
202769_at	*CCNG2*	Cyclin G2	AW134535	**-3.53**	-2.6

Immediate-early response: genes, regulated immediately to early (2 and 6 hours) after infection

Probe Set ID	Gene Symbol	Gene Title	GenBank ID	Fold change	
				2h	6h
204748_at	*PTGS2*	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963	**9.02**	**109.31**
205067_at	*IL1B*	interleukin 1, beta	NM_000576	**42.81**	**66.68**
205681_at	*BCL2A1*	BCL2-related protein A1	NM_004049	**22.72**	**67.67**
39402_at	*IL1B*	interleukin 1, beta	M15330	**29.11**	**54.79**
205207_at	*IL6*	interleukin 6 (interferon, beta 2)	NM_000600	**19.41**	**58.48**
204614_at	*SERPINB2*	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	NM_002575	**21.48**	**56.29**
206026_s_at	*TNFAIP6*	tumor necrosis factor, alpha-induced protein 6	NM_007115	**12.79**	**64.57**
204470_at	*CXCL1*	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511	**19.33**	**55.18**
211506_s_at	*IL8*	interleukin 8	AF043337	**41.44**	**26.84**

209774_x_at	*CXCL2*	chemokine (C-X-C motif) ligand 2	M57731	**40.44**	**24.92**
204655_at	*CCL5*	chemokine (C-C motif) ligand 5	NM_002985	**14.35**	**47.98**
206025_s_at	*TNFAIP6*	tumor necrosis factor, alpha-induced protein 6	AW188198	**8.35**	**50.77**
210118_s_at	*IL1A*	interleukin 1, alpha	M15329	**20.13**	**35.99**
207113_s_at	*TNF*	tumor necrosis factor (TNF superfamily, member 2)	NM_000594	**25.09**	**28.69**
210511_s_at	*INHBA*	inhibin, beta A (activin A, activin AB alpha polypeptide)	M13436	**14.14**	**36.6**
1405_i_at	*CCL5*	chemokine (C-C motif) ligand 5	M21121	**9.06**	**41.68**
205476_at	*CCL20*	chemokine (C-C motif) ligand 20	NM_004591	**8.47**	**40.57**
207850_at	*CXCL3*	chemokine (C-X-C motif) ligand 3	NM_002090	**19.8**	**28.41**
206157_at	*PTX3*	pentraxin-related gene, rapidly induced by IL-1 beta	NM_002852	**8.81**	**29.41**
215223_s_at	*SOD2*	superoxide dismutase 2, mitochondrial	W46388	**10.6**	**22.8**
216841_s_at	*SOD2*	superoxide dismutase 2, mitochondrial	X15132	**9.32**	**21.22**
204103_at	*CCL4*	chemokine (C-C motif) ligand 4	NM_002984	**14.55**	**14.31**
205114_s_at	*CCL3 /// CCL3L1 /// CCL3L3*	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1	NM_002983	**12.06**	**16.24**
213524_s_at	*G0S2*	putative lymphocyte G0/G1 switch gene	NM_015714	**9.61**	**18.36**
204794_at	*DUSP2*	dual specificity phosphatase 2	NM_004418	**7.98**	**19.92**
209037_s_at	*EHD1*	EH-domain containing 1	AW182860	**10.91**	**16.9**
217502_at	*IFIT2*	interferon-induced protein with tetratricopeptide repeats 2	BE888744	**4.26**	**22.7**
204286_s_at	*PMAIP1*	phorbol-12-myristate-13-acetate-induced protein 1	NM_021127	**5.17**	**21.12**
207536_s_at	*TNFRSF9*	tumor necrosis factor receptor superfamily, member 9	NM_001561	**7.99**	**17.85**
206359_at	*SOCS3*	suppressor of cytokine signaling 3	BG035761	**6.27**	**19.56**
210873_x_at	*APOBEC3A*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	U03891	**4.76**	**20.6**
202860_at	*KIAA0476*	KIAA0476	NM_014856	**13.89**	**10.2**
209039_x_at	*EHD1*	EH-domain containing 1	AF001434	**10.91**	**13.09**
213797_at	*RSAD2*	radical S-adenosyl methionine domain containing 2	AI337069	**4.93**	**18.88**
222221_x_at	*EHD1*	EH-domain containing 1	AY007161	**9.93**	**13.68**
204285_s_at	*PMAIP1*	phorbol-12-myristate-13-acetate-induced protein 1	AI857639	**3.73**	**19.36**
205599_at	*TRAF1*	TNF receptor-associated factor 1	NM_005658	**9.66**	**13.13**
215078_at	*SOD2*	superoxide dismutase 2, mitochondrial	AL050388	**10.28**	**12.36**
208112_x_at	*EHD1*	EH-domain containing 1	NM_006795	**8.71**	**12.53**
205660_at	*OASL*	2'-5'-oligoadenylate synthetase-like	NM_003733	**3.28**	**17.21**
221477_s_at	*MGC5618*	hypothetical protein MGC5618	BF575213	**9.53**	**10.67**
204747_at	*IFIT3*	interferon-induced protein with tetratricopeptide repeats 3	NM_001549	**3.81**	**16.07**
206181_at	*SLAMF1*	signaling lymphocytic activation molecule family member 1	NM_003037	**3.54**	**14.72**
212659_s_at	*IL1RN*	interleukin 1 receptor antagonist	AW083357	**3.68**	**14.57**
205483_s_at	*G1P2*	interferon, alpha-inducible protein (clone IFI-15K)	NM_005101	**3.89**	**14.03**
202643_s_at	*TNFAIP3*	tumor necrosis factor, alpha-induced protein 3	AI738896	**8.55**	**8.47**
216243_s_at	*IL1RN*	interleukin 1 receptor antagonist	BE563442	**3.43**	**13.45**
205013_s_at	*ADORA2A*	adenosine A2a receptor	NM_000675	**3.61**	**12.84**
202644_s_at	*TNFAIP3*	tumor necrosis factor, alpha-induced protein 3	NM_006290	**8.16**	**7.3**
222303_at	---	---	AV700891	**8.02**	**7.27**
202988_s_at	*RGS1*	regulator of G-protein signalling 1	NM_002922	**7.29**	**7.55**

205153_s_at	*CD40*	CD40 antigen (TNF receptor superfamily member 5)	NM_001250	**5.12**	**8.76**
202760_s_at	*AKAP2 /// PALM2-AKAP2*	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein	NM_007203	**3.62**	**10.21**
202759_s_at	*PALM2-AKAP2*	PALM2-AKAP2 protein	BE879367	**3.52**	**9.71**
218627_at	*FLJ11259*	hypothetical protein FLJ11259	NM_018370	**5.58**	**7.41**
215346_at	*CD40*	CD40 antigen (TNF receptor superfamily member 5)	BF664114	**5.42**	**7.54**
218810_at	*ZC3H12A*	zinc finger CCCH-type containing 12A	NM_025079	**3.74**	**9.11**
204897_at	*PTGER4*	prostaglandin E receptor 4 (subtype EP4)	AA897516	**6.71**	**5.92**
216834_at	*RGS1*	regulator of G-protein signalling 1	S59049	**6.37**	**6.13**
210285_x_at	*WTAP*	Wilms tumor 1 associated protein	BC000383	**4.24**	**8.16**
205306_x_at	*KMO*	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	AI074145	**5.88**	**6.42**
206765_at	*KCNJ2*	potassium inwardly-rectifying channel, subfamily J, member 2	AF153820	**5.48**	**6.54**
212458_at	*SPRED2*	sprouty-related, EVH1 domain containing 2	H97931	**3.95**	**7.96**
209305_s_at	*GADD45B*	growth arrest and DNA-damage-inducible, beta	AF078077	**3.96**	**7.78**
209304_x_at	*GADD45B*	growth arrest and DNA-damage-inducible, beta	AF087853	**3.96**	**7.73**
211138_s_at	*KMO*	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	BC005297	**5.26**	**6.42**
35150_at	*CD40*	CD40 antigen (TNF receptor superfamily member 5)	X60592	**3.89**	**7.43**
204896_s_at	*PTGER4*	prostaglandin E receptor 4 (subtype EP4)	AI675173	**4.18**	**6.77**
36711_at	*MAFF*	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	AL021977	**6.03**	**4.68**
209239_at	*NFKB1*	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	M55643	**3.3**	**6.94**
202014_at	*PPP1R15A*	protein phosphatase 1, regulatory (inhibitor) subunit 15A	NM_014330	**4.18**	**5.98**
220882_at	---	---	NM_018612	**6.25**	**3.86**
207978_s_at	*NR4A3*	nuclear receptor subfamily 4, group A, member 3	NM_006981	**3.26**	**6.84**
211924_s_at	*PLAUR*	plasminogen activator, urokinase receptor	AY029180	**4.66**	**5.25**
221485_at	*B4GALT5*	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	AL035683	**3.23**	**6.66**
220865_s_at	*TPRT*	trans-prenyltransferase	NM_014317	**4.31**	**5.44**
205027_s_at	*MAP3K8*	mitogen-activated protein kinase kinase kinase 8	NM_005204	**5.73**	**4**
201566_x_at	*ID2 /// ID2B*	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	D13891	**3.79**	**5.86**
209939_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF005775	**2.9**	**6.72**
209038_s_at	*EHD1*	EH-domain containing 1	AL579035	**4.16**	**5.42**
207528_s_at	*SLC7A11*	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	NM_014331	**3.51**	**5.8**
210564_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF009619	**3.06**	**6.19**
203137_at	*WTAP*	Wilms tumor 1 associated protein	NM_004906	**3.73**	**5.51**
202637_s_at	*ICAM1*	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	AI608725	**3.94**	**5.23**
219209_at	*IFIH1*	interferon induced with helicase C domain 1	NM_022168	**3.67**	**5.48**
210538_s_at	*BIRC3*	baculoviral IAP repeat-containing 3	U37546	**3.2**	**5.91**
211434_s_at	*CCRL2*	chemokine (C-C motif) receptor-like 2	AF015524	**3.29**	**5.81**
203936_s_at	*MMP9*	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	NM_004994	**4.39**	**4.63**
201565_s_at	*ID2*	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_002166	**3.12**	**5.87**
210563_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	U97075	**2.53**	**6.44**
205193_at	*MAFF*	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	NM_012323	**5.55**	**3.37**
205798_at	*IL7R*	interleukin 7 receptor	NM_002185	**4.73**	**4.13**

202638_s_at	*ICAM1*	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	NM_000201	**4.24**	**4.6**
210229_s_at	*CSF2*	colony stimulating factor 2 (granulocyte-macrophage)	M11734	**4.43**	**4.35**
37028_at	*PPP1R15A*	protein phosphatase 1, regulatory (inhibitor) subunit 15A	U83981	**3.82**	**4.89**
207992_s_at	*AMPD3*	adenosine monophosphate deaminase (isoform E)	NM_000480	**3.49**	**5.13**
204440_at	*CD83*	CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)	NM_004233	**2.75**	**5.72**
215485_s_at	*ICAM1*	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	AA284705	**3.99**	**4.39**
200920_s_at	*BTG1*	B-cell translocation gene 1, anti-proliferative	AL535380	**3.08**	**5.27**
203725_at	*GADD45A*	growth arrest and DNA-damage-inducible, alpha	NM_001924	**4.24**	**4.06**
204924_at	*TLR2*	toll-like receptor 2	NM_003264	**3.4**	**4.8**
201502_s_at	*NFKBIA*	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	AI078167	**3.68**	**4.24**
219631_at	*LRP12*	low density lipoprotein-related protein 12	NM_024937	**2.51**	**5.2**
211317_s_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF041461	**2.74**	**4.91**
213113_s_at	*SLC43A3*	solute carrier family 43, member 3	AI630178	**2.79**	**4.61**
220091_at	*SLC2A6*	solute carrier family 2 (facilitated glucose transporter), member 6	NM_017585	**2.82**	**4.4**
214486_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF041459	**2.84**	**4.27**
203045_at	*NINJ1*	ninjurin 1	NM_004148	**2.6**	**4.43**
207196_s_at	*TNIP1*	TNFAIP3 interacting protein 1	NM_006058	**3.02**	**4**
206756_at	*CHST7*	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	NM_019886	**3.41**	**3.57**
221140_s_at	*GPR132*	G protein-coupled receptor 132	NM_013345	**2.77**	**3.96**
215499_at	*MAP2K3*	mitogen-activated protein kinase kinase 3	AA780381	**3.45**	**3.23**
209959_at	*NR4A3*	nuclear receptor subfamily 4, group A, member 3	U12767	**2.7**	**3.94**
215498_s_at	*MAP2K3*	mitogen-activated protein kinase kinase 3	AA780381	**3.13**	**3.32**
202085_at	*TJP2*	tight junction protein 2 (zona occludens 2)	NM_004817	**3.37**	**3.04**
215253_s_at	*DSCR1*	Down syndrome critical region gene 1	AL049369	**3.31**	**2.89**
209508_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF005774	**2.75**	**3.42**
209034_at	*PNRC1*	proline-rich nuclear receptor coactivator 1	AF279899	**3.01**	**2.76**
211316_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF009616	**2.45**	**3.11**
217678_at	*SLC7A11*	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AA488687	**2.49**	**3.04**
217192_s_at	*PRDM1*	PR domain containing 1, with ZNF domain	AL022067	**2.73**	**2.77**
210260_s_at	*TNFAIP8*	tumor necrosis factor, alpha-induced protein 8	BC005352	**2.8**	**2.51**
48531_at	*TNIP2*	TNFAIP3 interacting protein 2	AA522816	**2.56**	**2.58**
218917_s_at	*ARID1A*	AT rich interactive domain 1A (SWI- like)	NM_018450	**-2.71**	**-2.48**
204336_s_at	*RGS19*	regulator of G-protein signalling 19	NM_005873	**-2.66**	**-2.85**
218589_at	*P2RY5*	purinergic receptor P2Y, G-protein coupled, 5	NM_005767	**-3.28**	**-3.98**
204923_at	*CXorf9*	chromosome X open reading frame 9	AL023653	**-2.47**	**-5.04**
207826_s_at	*ID3*	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_002167	**-3.67**	**-5.14**
210220_at	*FZD2*	frizzled homolog 2 (Drosophila)	L37882	**-5.72**	**-4.79**
205579_at	*HRH1*	histamine receptor H1	NM_000861	**-4.18**	**-10.04**

Early response: genes, regulated early (6 hours) after infection

Probe Set ID	**Gene Symbol**	**Gene Title**	**GenBank ID**	**Fold change**	
				2h	**6h**
205767_at	*EREG*	epiregulin	NM_001432	8.89	**53.74**

207901_at	*IL12B*	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	NM_002187	7.9	**44.32**
210163_at	*CXCL11*	chemokine (C-X-C motif) ligand 11	AF030514	1.71	**42.03**
211122_s_at	*CXCL11*	chemokine (C-X-C motif) ligand 11	AF002985	1.43	**39.42**
204224_s_at	*GCH1*	GTP cyclohydrolase 1 (dopa-responsive dystonia)	NM_000161	2.37	**38.56**
220655_at	*TNIP3*	TNFAIP3 interacting protein 3	NM_024873	1.42	**38.47**
210029_at	*INDO*	indoleamine-pyrrole 2,3 dioxygenase	M34455	1.1	**36.84**
33304_at	*ISG20*	interferon stimulated exonuclease gene 20kDa	U88964	2.22	**32.74**
204698_at	*ISG20*	interferon stimulated exonuclease gene 20kDa	NM_002201	2.47	**31.74**
204533_at	*CXCL10*	chemokine (C-X-C motif) ligand 10	NM_001565	5.62	**28.79**
203708_at	*PDE4B*	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_002600	7.72	**23.49**
209722_s_at	*SERPINB9*	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	L40378	3.9	**20.66**
216244_at	*IL1RN*	interleukin 1 receptor antagonist	BE563442	3.77	**19.27**
219159_s_at	*SLAMF7*	SLAM family member 7	NM_021181	1.83	**18.19**
211269_s_at	*IL2RA*	interleukin 2 receptor, alpha	K03122	1.34	**17.5**
202269_x_at	*GBP1*	guanylate binding protein 1, interferon-inducible, 67kDa	BC002666	1.97	**17.45**
208173_at	*IFNB1*	interferon, beta 1, fibroblast	NM_002176	2.46	**16.48**
219911_s_at	*SLCO4A1*	solute carrier organic anion transporter family, member 4A1	NM_016354	3.13	**16.42**
202687_s_at	*TNFSF10*	tumor necrosis factor (ligand) superfamily, member 10	U57059	-1.05	**15.85**
220322_at	*IL1F9*	interleukin 1 family, member 9	NM_019618	2.61	**15.82**
202688_at	*TNFSF10*	tumor necrosis factor (ligand) superfamily, member 10	NM_003810	1.17	**15.7**
209723_at	*SERPINB9*	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	BC002538	8.11	**15.01**
201860_s_at	*PLAT*	plasminogen activator, tissue	NM_000930	2.99	**14.7**
202270_at	*GBP1*	guanylate binding protein 1, interferon-inducible, 67kDa	NM_002053	1.68	**14.63**
206341_at	*IL2RA*	interleukin 2 receptor, alpha	NM_000417	1.11	**14.33**
207275_s_at	*ACSL1*	acyl-CoA synthetase long-chain family member 1	NM_001995	1.11	**14.02**
207375_s_at	*IL15RA*	interleukin 15 receptor, alpha	NM_002189	1.73	**13.55**
201963_at	*ACSL1*	acyl-CoA synthetase long-chain family member 1	NM_021122	-1	**13.39**
214022_s_at	*IFITM1*	interferon induced transmembrane protein 1 (9-27)	AA749101	1.28	**13.32**
44790_s_at	*C13orf18*	chromosome 13 open reading frame 18	AI129310	4.22	**12.93**
205239_at	*AREG*	amphiregulin (schwannoma-derived growth factor)	NM_001657	4.95	**12.7**
206881_s_at	*LILRA3*	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	NM_006865	1.53	**12.65**
202801_at	*PRKACA*	protein kinase, cAMP-dependent, catalytic, alpha	NM_002730	2.08	**12.37**
205226_at	*PDGFRL*	platelet-derived growth factor receptor-like	NM_006207	1.35	**12.21**
214038_at	*CCL8*	chemokine (C-C motif) ligand 8	AI984980	4.66	**12.12**
210797_s_at	*OASL*	2'-5'-oligoadenylate synthetase-like	AF063612	2.01	**11.94**
204439_at	*IFI44L*	interferon-induced protein 44-like	NM_006820	1.3	**11.8**
205965_at	*BATF*	basic leucine zipper transcription factor, ATF-like	NM_006399	2	**11.73**
202357_s_at	*BF*	B-factor, properdin	NM_001710	1.06	**11.49**
214329_x_at	*TNFSF10*	Tumor necrosis factor (ligand) superfamily, member 10	AW474434	-1.22	**11.47**

207030_s_at	*CSRP2*	cysteine and glycine-rich protein 2	NM_001321	2.02	**11.45**
202672_s_at	*ATF3*	activating transcription factor 3	NM_001674	2.17	**11.33**
215806_x_at	*TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP*	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT-gamma-1/2	M13231	1.14	**11.02**
209813_x_at	*TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP*	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT-gamma-1/2	M16768	1.06	**11.01**
218943_s_at	*DDX58*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_014314	2.03	**10.84**
207433_at	*IL10*	interleukin 10	NM_000572	1.84	**10.81**
219863_at	*HERC5*	hect domain and RLD 5	NM_016323	1.31	**10.68**
201329_s_at	*ETS2*	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	NM_005239	4.16	**10.6**
219869_s_at	*SLC39A8*	solute carrier family 39 (zinc transporter), member 8	NM_022154	1.28	**10.17**
204715_at	*PANX1*	pannexin 1	NM_015368	1.78	**9.83**
215411_s_at	*TRAF3IP2*	TRAF3 interacting protein 2	AL008730	1.93	**9.83**
203153_at	*IFIT1*	interferon-induced protein with tetratricopeptide repeats 1	NM_001548	2.52	**9.8**
202446_s_at	*PLSCR1*	phospholipid scramblase 1	AI825926	1.53	**9.53**
203535_at	*S100A9*	S100 calcium binding protein A9 (calgranulin B)	NM_002965	1.14	**9.21**
206907_at	*TNFSF9*	tumor necrosis factor (ligand) superfamily, member 9	NM_003811	2.35	**9.16**
209193_at	*PIM1*	pim-1 oncogene	M24779	1.94	**9.14**
209545_s_at	*RIPK2*	receptor-interacting serine-threonine kinase 2	AF064824	2.33	**8.93**
217738_at	*PBEF1*	pre-B-cell colony enhancing factor 1	BF575514	1.7	**8.93**
216920_s_at	*TRGC2 /// TRGV9 /// LOC442532 /// LOC442670 /// TARP*	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT-gamma-1/2	M27331	1.18	**8.88**
214446_at	*ELL2*	elongation factor, RNA polymerase II, 2	NM_012081	1.8	**8.77**
202086_at	*MX1*	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	NM_002462	3.29	**8.55**
204639_at	*ADA*	adenosine deaminase	NM_000022	1.59	**8.51**
212641_at	*HIVEP2*	human immunodeficiency virus type I enhancer binding protein 2	AL023584	1.94	**8.41**
202430_s_at	*PLSCR1*	phospholipid scramblase 1	NM_021105	1.48	**8.37**
219211_at	*USP18*	ubiquitin specific protease 18	NM_017414	1.29	**8.36**
201195_s_at	*SLC7A5*	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	AB018009	1.77	**8.24**
207574_s_at	*GADD45B*	growth arrest and DNA-damage-inducible, beta	NM_015675	4.19	**7.95**
209457_at	*DUSP5*	dual specificity phosphatase 5	U16996	2.75	**7.84**
202464_s_at	*PFKFB3*	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	NM_004566	2.51	**7.82**

219558_at	*ATP13A3*	ATPase type 13A3	NM_024524	2.33	**7.82**
207332_s_at	*TFRC*	transferrin receptor (p90, CD71)	NM_003234	1.53	**7.72**
210190_at	*STX11*	syntaxin 11	AF071504	2.61	**7.71**
220253_s_at	*LRP12*	low density lipoprotein-related protein 12	NM_013437	2.63	**7.69**
206467_x_at	*TNFRSF6B /// RTEL1*	tumor necrosis factor receptor superfamily, member 6b, decoy /// regulator of telomere elongation helicase 1	NM_003823	1.16	**7.66**
211144_x_at	*TRGC2*	T cell receptor gamma constant 2	M30894	1.01	**7.63**
201490_s_at	*PPIF*	peptidylprolyl isomerase F (cyclophilin F)	NM_005729	2.88	**7.57**
211267_at	*HESX1*	homeo box (expressed in ES cells) 1	U82811	1.11	**7.43**
205552_s_at	*OAS1*	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_002534	1.77	**7.36**
206337_at	*CCR7*	chemokine (C-C motif) receptor 7	NM_001838	2.18	**7.36**
201041_s_at	*DUSP1*	dual specificity phosphatase 1	NM_004417	3.1	**7.33**
202391_at	*BASP1*	brain abundant, membrane attached signal protein 1	NM_006317	1.93	**7.28**
209928_s_at	*MSC*	musculin (activated B-cell factor-1)	AF060154	2.58	**7.14**
212185_x_at	*MT2A*	metallothionein 2A	NM_005953	1.09	**7.11**
212657_s_at	*IL1RN*	interleukin 1 receptor antagonist	U65590	2.92	**7.08**
201601_x_at	*IFITM1*	interferon induced transmembrane protein 1 (9-27)	NM_003641	1.18	**7.05**
205676_at	*CYP27B1*	cytochrome P450, family 27, subfamily B, polypeptide 1	NM_000785	1.57	**7.03**
217739_s_at	*PBEF1*	pre-B-cell colony enhancing factor 1	NM_005746	1.51	**6.98**
204994_at	*MX2*	myxovirus (influenza virus) resistance 2 (mouse)	NM_002463	2.27	**6.96**
219677_at	*SSB1*	SPRY domain-containing SOCS box protein SSB-1	NM_025106	1.33	**6.83**
204972_at	*OAS2*	2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_016817	2.37	**6.77**
220491_at	*HAMP*	hepcidin antimicrobial peptide	NM_021175	-1.15	**6.76**
204057_at	*IRF8*	interferon regulatory factor 8	AI073984	3.15	**6.73**
200628_s_at	*WARS*	tryptophanyl-tRNA synthetase	M61715	1.05	**6.56**
205548_s_at	*BTG3*	BTG family, member 3	NM_006806	2.09	**6.54**
218400_at	*OAS3*	2'-5'-oligoadenylate synthetase 3, 100kDa	NM_006187	1.78	**6.51**
219471_at	*C13orf18*	chromosome 13 open reading frame 18	NM_025113	2.95	**6.4**
219716_at	*APOL6*	apolipoprotein L, 6	NM_030641	1.59	**6.36**
206553_at	*OAS2*	2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_002535	2.08	**6.35**
201328_at	*ETS2*	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	AL575509	4.13	**6.29**
203508_at	*TNFRSF1B*	tumor necrosis factor receptor superfamily, member 1B	NM_001066	1.46	**6.28**
214228_x_at	*TNFRSF4*	tumor necrosis factor receptor superfamily, member 4	AJ277151	2.89	**6.21**
207176_s_at	*CD80*	CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)	NM_005191	2.16	**6.15**
208092_s_at	*FAM49A*	family with sequence similarity 49, member A	NM_030797	1.42	**6.03**
200629_at	*WARS*	tryptophanyl-tRNA synthetase	NM_004184	1.08	**6**
202906_s_at	*NBN*	nibrin	AF049895	1.24	**5.98**
220104_at	*ZC3HAV1*	zinc finger CCCH-type, antiviral 1	NM_020119	1.34	**5.97**

209267_s_at	*SLC39A8*	solute carrier family 39 (zinc transporter), member 8	AB040120	1.18	**5.9**
211101_x_at	*LILRA2*	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	U82276	1.35	**5.9**
204118_at	*CD48*	CD48 antigen (B-cell membrane protein)	NM_001778	1.62	**5.78**
205568_at	*AQP9*	aquaporin 9	NM_020980	1.89	**5.74**
221087_s_at	*APOL3*	apolipoprotein L, 3	NM_014349	-1.07	**5.74**
217897_at	*FXYD6*	FXYD domain containing ion transport regulator 6	NM_022003	2.82	**5.72**
202531_at	*IRF1*	interferon regulatory factor 1	NM_002198	2.18	**5.7**
213134_x_at	*BTG3*	BTG family, member 3	AI765445	1.9	**5.64**
201044_x_at	*DUSP1*	dual specificity phosphatase 1	AA530892	2.27	**5.63**
202510_s_at	*TNFAIP2*	tumor necrosis factor, alpha-induced protein 2	NM_006291	2.3	**5.58**
201489_at	*PPIF*	peptidylprolyl isomerase F (cyclophilin F)	BC005020	2.56	**5.56**
210146_x_at	*LILRB2*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	AF004231	1.26	**5.55**
211302_s_at	*PDE4B*	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	L20966	2	**5.52**
221484_at	*B4GALT5*	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	BF691447	2.43	**5.52**
206877_at	*MXD1*	MAX dimerization protein 1	NM_002357	1.15	**5.51**
204926_at	*INHBA*	inhibin, beta A (activin A, activin AB alpha polypeptide)	NM_002192	2.12	**5.49**
207697_x_at	*LILRB2*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	NM_005874	1.47	**5.42**
201315_x_at	*IFITM2*	interferon induced transmembrane protein 2 (1-8D)	NM_006435	1.33	**5.39**
205569_at	*LAMP3*	lysosomal-associated membrane protein 3	NM_014398	1.94	**5.35**
208691_at	*TFRC*	transferrin receptor (p90, CD71)	BC001188	1.57	**5.35**
218182_s_at	*CLDN1*	claudin 1	NM_021101	3.26	**5.34**
202411_at	*IFI27*	interferon, alpha-inducible protein 27	NM_005532	1.04	**5.31**
221765_at	---	---	AI378044	1.23	**5.26**
212642_s_at	*HIVEP2*	human immunodeficiency virus type I enhancer binding protein 2	AL023584	1.55	**5.25**
216565_x_at	*LOC391020*	similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U)	AL121994	-1.05	**5.23**
203395_s_at	*HES1*	hairy and enhancer of split 1, (Drosophila)	NM_005524	1.78	**5.22**
214453_s_at	*IFI44*	interferon-induced protein 44	NM_006417	2.16	**5.18**
204326_x_at	*MT1X*	metallothionein 1X	NM_002450	1.04	**5.17**
210692_s_at	*SLC43A3*	solute carrier family 43, member 3	BC003163	2.33	**5.16**
55081_at	*MICAL-L1*	MICAL-like 1	W46406	1.31	**5.16**
204881_s_at	*UGCG*	UDP-glucose ceramide glucosyltransferase	NM_003358	1.12	**5.15**
208594_x_at	*LILRA6*	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	NM_024318	1.39	**5.15**
217848_s_at	*PP*	pyrophosphatase (inorganic)	NM_021129	-1.22	**5.15**
205992_s_at	*IL15*	interleukin 15	NM_000585	1	**5.08**
219352_at	*HERC6*	hect domain and RLD 6	NM_017912	1.12	**5.08**
221432_s_at	*SLC25A28*	solute carrier family 25, member 28	NM_031212	-1.21	**5.07**

221081_s_at	*FLJ22457*	hypothetical protein FLJ22457	NM_024901	1.23	**5.06**
207104_x_at	*LILRB1*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	NM_006669	1.43	**5.02**
204415_at	*G1P3*	interferon, alpha-inducible protein (clone IFI-6-16)	NM_022873	1.06	**5**
205872_x_at	*PDE4DIP*	phosphodiesterase 4D interacting protein (myomegalin)	NM_022359	2.09	**5**
218507_at	*HIG2*	hypoxia-inducible protein 2	NM_013332	1.76	**4.99**
205990_s_at	*WNT5A*	wingless-type MMTV integration site family, member 5A	NM_003392	1.41	**4.96**
217299_s_at	*NBN*	nibrin	AK001017	1.24	**4.95**
212203_x_at	*IFITM3*	interferon induced transmembrane protein 3 (1-8U)	BF338947	1.25	**4.93**
218032_at	*SNN*	stannin	AF070673	1.36	**4.93**
200921_s_at	*BTG1*	B-cell translocation gene 1, anti-proliferative	NM_001731	2.57	**4.89**
202509_s_at	*TNFAIP2*	tumor necrosis factor, alpha-induced protein 2	AI862445	1.93	**4.89**
203372_s_at	*SOCS2*	suppressor of cytokine signaling 2	AB004903	-1.07	**4.89**
203921_at	*CHST2*	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	NM_004267	2.98	**4.89**
211336_x_at	*LILRB1*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	AF009007	1.42	**4.89**
209288_s_at	*CDC42EP3*	CDC42 effector protein (Rho GTPase binding) 3	AL136842	2.51	**4.87**
213629_x_at	*MT1F*	metallothionein 1F (functional)	BF246115	1.02	**4.86**
202716_at	*PTPN1*	protein tyrosine phosphatase, non-receptor type 1	NM_002827	1.44	**4.82**
206118_at	*STAT4*	signal transducer and activator of transcription 4	NM_003151	1.96	**4.75**
202912_at	*ADM*	adrenomedullin	NM_001124	1.6	**4.72**
212501_at	*CEBPB*	CCAAT/enhancer binding protein (C/EBP), beta	AL564683	1.14	**4.71**
202905_x_at	*NBN*	nibrin	AI796269	1.36	**4.68**
211527_x_at	*VEGF*	vascular endothelial growth factor	M27281	1.96	**4.65**
221779_at	*MICAL-L1*	MICAL-like 1	BC001090	1.08	**4.65**
202307_s_at	*TAP1*	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000593	1.45	**4.63**
208485_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	NM_003879	2.69	**4.63**
210784_x_at	*LILRB2 /// LILRB3*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009634	1.38	**4.63**
211862_x_at	*CFLAR*	CASP8 and FADD-like apoptosis regulator	AF015451	2.62	**4.62**
208436_s_at	*IRF7*	interferon regulatory factor 7	NM_004030	1.86	**4.6**
210663_s_at	*KYNU*	kynureninase (L-kynurenine hydrolase)	BC000879	2.38	**4.58**
200796_s_at	*MCL1*	myeloid cell leukemia sequence 1 (BCL2-related)	BF594446	1.42	**4.55**
203097_s_at	*RAPGEF2*	Rap guanine nucleotide exchange factor (GEF) 2	NM_014247	1.46	**4.51**
210225_x_at	*LILRB2 /// LILRB3*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	AF009635	1.36	**4.5**
212859_x_at	*MT1E*	metallothionein 1E (functional)	BF217861	-1.11	**4.47**
202087_s_at	*CTSL*	cathepsin L	NM_001912	1.92	**4.46**
206360_s_at	*SOCS3*	suppressor of cytokine signaling 3	NM_003955	2.19	**4.39**
209417_s_at	*IFI35*	interferon-induced protein 35	BC001356	1.16	**4.38**
203542_s_at	*KLF9*	Kruppel-like factor 9	AI690205	1.35	**4.35**
214430_at	*GLA*	galactosidase, alpha	NM_000169	2.25	**4.33**
215977_x_at	*GK*	glycerol kinase	X68285	-1.08	**4.31**
211456_x_at	---	Similar to 60S ribosomal protein L35	AF333388	-1.09	**4.3**
216705_s_at	*ADA*	adenosine deaminase	X02189	1.14	**4.28**

218319_at	*PELI1*	pellino homolog 1 (Drosophila)	NM_020651	1.48	**4.27**
208581_x_at	*MT1X*	metallothionein 1X	NM_005952	1.03	**4.26**
211864_s_at	*FER1L3*	fer-1-like 3, myoferlin (C. elegans)	AF207990	1.83	**4.19**
219424_at	*EBI3*	Epstein-Barr virus induced gene 3	NM_005755	1.39	**4.19**
203276_at	*LMNB1*	lamin B1	NM_005573	1.24	**4.18**
206513_at	*AIM2*	absent in melanoma 2	NM_004833	1.42	**4.14**
209761_s_at	*SP110*	SP110 nuclear body protein	AA969194	1.16	**4.13**
202734_at	*TRIP10*	thyroid hormone receptor interactor 10	NM_004240	1.58	**4.12**
207387_s_at	*GK*	glycerol kinase	NM_000167	-1.03	**4.12**
216316_x_at	---	PREDICTED: Homo sapiens similar to GKP3 protein (LOC201989), mRNA	X78713	-1.04	**4.08**
217165_x_at	*MT1F*	metallothionein 1F (functional)	M10943	-1.02	**4.08**
202917_s_at	*S100A8*	S100 calcium binding protein A8 (calgranulin A)	NM_002964	-1.11	**4.04**
209762_x_at	*SP110*	SP110 nuclear body protein	AF280094	-1.04	**3.99**
206911_at	*TRIM25*	tripartite motif-containing 25	NM_005082	1.35	**3.98**
212268_at	*SERPINB1*	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	NM_030666	1.39	**3.98**
210305_at	*PDE4DIP*	phosphodiesterase 4D interacting protein (myomegalin)	AB042557	1.9	**3.95**
203543_s_at	*KLF9*	Kruppel-like factor 9	NM_001206	1.18	**3.93**
211367_s_at	*CASP1*	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	U13699	1.57	**3.93**
215966_x_at	*GK*	glycerol kinase	AA292874	-1.06	**3.92**
219684_at	*IFRG28*	28kD interferon responsive protein	NM_022147	1.37	**3.91**
202907_s_at	*NBN*	nibrin	NM_002485	1.21	**3.9**
204088_at	*P2RX4*	purinergic receptor P2X, ligand-gated ion channel, 4	NM_002560	1.5	**3.9**
217167_x_at	*GK*	glycerol kinase	AJ252550	-1.17	**3.88**
203120_at	*TP53BP2*	tumor protein p53 binding protein, 2	NM_005426	1.6	**3.87**
219257_s_at	*SPHK1*	sphingosine kinase 1	NM_021972	2.16	**3.86**
204620_s_at	*CSPG2*	chondroitin sulfate proteoglycan 2 (versican)	NM_004385	-1.1	**3.79**
207610_s_at	*EMR2*	egf-like module containing, mucin-like, hormone receptor-like 2	NM_013447	1.16	**3.79**
213361_at	*TDRD7*	tudor domain containing 7	AW129593	-1.08	**3.71**
204385_at	*KYNU*	kynureninase (L-kynurenine hydrolase)	NM_003937	2.03	**3.7**
210845_s_at	*PLAUR*	plasminogen activator, urokinase receptor	U08839	2.6	**3.69**
209875_s_at	*SPP1*	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	M83248	1.77	**3.68**
203887_s_at	*THBD*	thrombomodulin	NM_000361	3.81	**3.64**
217388_s_at	*KYNU*	kynureninase (L-kynurenine hydrolase)	D55639	1.98	**3.63**
201798_s_at	*FER1L3*	fer-1-like 3, myoferlin (C. elegans)	NM_013451	2.32	**3.58**
211366_x_at	*CASP1*	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	U13698	1.58	**3.58**
200706_s_at	*LITAF*	lipopolysaccharide-induced TNF factor	NM_004862	1.6	**3.57**
201749_at	*ECE1*	Endothelin converting enzyme 1	BF969352	2.4	**3.56**
202878_s_at	*C1QR1*	complement component 1, q subcomponent, receptor 1	NM_012072	2.14	**3.56**

208012_x_at	*SP110*	SP110 nuclear body protein	NM_004509	-1.03	**3.53**
216336_x_at	*MT1K*	Metallothionein 1K	AL031602	1.06	**3.51**
212390_at	*PDE4DIP*	phosphodiesterase 4D interacting protein (myomegalin)	AB007923	1.8	**3.5**
213497_at	*ABTB2*	ankyrin repeat and BTB (POZ) domain containing 2	AL050374	1.23	**3.5**
202879_s_at	*PSCD1*	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	AI798823	1.73	**3.49**
203044_at	*CHSY1*	carbohydrate (chondroitin) synthase 1	NM_014918	1.27	**3.49**
210754_s_at	*LYN*	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	M79321	1.38	**3.49**
204141_at	*TUBB2*	tubulin, beta 2	NM_001069	1.78	**3.48**
220254_at	*LRP12*	low density lipoprotein-related protein 12	NM_013437	1.81	**3.47**
204211_x_at	*EIF2AK2*	eukaryotic translation initiation factor 2-alpha kinase 2	NM_002759	1.9	**3.45**
209544_at	*RIPK2*	receptor-interacting serine-threonine kinase 2	AF027706	1.75	**3.45**
202074_s_at	*OPTN*	optineurin	NM_021980	1.36	**3.44**
203408_s_at	*SATB1*	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	NM_002971	1.05	**3.43**
205692_s_at	*CD38*	CD38 antigen (p45)	NM_001775	1.03	**3.43**
202834_at	*AGT*	angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)	NM_000029	1.2	**3.42**
205899_at	*CCNA1*	cyclin A1	NM_003914	-1.17	**3.42**
206571_s_at	*MAP4K4*	mitogen-activated protein kinase kinase kinase kinase 4	NM_004834	1.47	**3.41**
214681_at	*GK*	glycerol kinase	AI830490	-1.05	**3.4**
204137_at	*TM7SF1*	transmembrane 7 superfamily member 1 (upregulated in kidney)	NM_003272	1.43	**3.36**
217933_s_at	*LAP3*	leucine aminopeptidase 3	NM_015907	-1.01	**3.36**
209970_x_at	*CASP1*	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	M87507	1.52	**3.35**
211368_s_at	*CASP1*	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	U13700	1.54	**3.35**
203066_at	*GALNAC4S-6ST*	B cell RAG associated protein	NM_014863	2.06	**3.34**
205016_at	*TGFA*	transforming growth factor, alpha	NM_003236	1.13	**3.34**
208864_s_at	*TXN*	thioredoxin	AF313911	1.88	**3.34**
202748_at	*GBP2*	guanylate binding protein 2, interferon-inducible	NM_004120	1.24	**3.31**
207091_at	*P2RX7*	purinergic receptor P2X, ligand-gated ion channel, 7	NM_002562	2.53	**3.31**
210818_s_at	*BACH1*	BTB and CNC homology 1, basic leucine zipper transcription factor 1	AF026199	-1.1	**3.31**
211135_x_at	*LILRB2 /// LILRB3*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009644	1.15	**3.3**
209286_at	*CDC42EP3*	CDC42 effector protein (Rho GTPase binding) 3	AI754416	2.3	**3.27**
212561_at	*RAB6IP1*	RAB6 interacting protein 1	AA349595	1.18	**3.27**
212297_at	*ATP13A3*	ATPase type 13A3	BF218804	2.03	**3.25**
218404_at	*SNX10*	sorting nexin 10	NM_013322	1.59	**3.25**
204745_x_at	*MT1G*	metallothionein 1G	NM_005950	1.12	**3.24**
202626_s_at	*LYN*	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	NM_002350	1.15	**3.23**
209893_s_at	*FUT4*	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	M58596	1.41	**3.22**

212665_at	*TIPARP*	TCDD-inducible poly(ADP-ribose) polymerase	AL556438	-1.08	**3.22**
213051_at	*ZC3HAV1*	zinc finger CCCH-type, antiviral 1	AI133727	1.18	**3.22**
209684_at	*RIN2*	Ras and Rab interactor 2	AL136924	1.56	**3.21**
36564_at	*IBRDC3*	IBR domain containing 3	W27419	1.29	**3.2**
204401_at	*KCNN4*	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	NM_002250	1.33	**3.19**
201999_s_at	*TCTEL1*	t-complex-associated-testis-expressed 1-like 1	NM_006519	-1.04	**3.18**
202551_s_at	*CRIM1*	cysteine rich transmembrane BMP regulator 1 (chordin-like)	BG546884	1.04	**3.18**
202552_s_at	*CRIM1*	cysteine rich transmembrane BMP regulator 1 (chordin-like)	NM_016441	1.06	**3.18**
202763_at	*CASP3*	caspase 3, apoptosis-related cysteine protease	NM_004346	-1.42	**3.17**
213038_at	*IBRDC3*	IBR domain containing 3	AL031602	1.21	**3.17**
213572_s_at	*SERPINB1*	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	AI554300	1.08	**3.17**
214435_x_at	*RALA*	v-ral simian leukemia viral oncogene homolog A (ras related)	NM_005402	-1.07	**3.13**
200798_x_at	*MCL1*	myeloid cell leukemia sequence 1 (BCL2-related)	NM_021960	1.36	**3.11**
207535_s_at	*NFKB2*	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_002502	2.07	**3.11**
210916_s_at	*CD44*	CD44 antigen (homing function and Indian blood group system)	AF098641	1.66	**3.11**
219210_s_at	*RAB8B*	RAB8B, member RAS oncogene family	NM_016530	-1.19	**3.11**
221185_s_at	*IQCG*	IQ motif containing G	NM_025111	2	**3.11**
201627_s_at	*INSIG1*	insulin induced gene 1	NM_005542	2.59	**3.1**
221881_s_at	*CLIC4*	chloride intracellular channel 4	AI638420	1.4	**3.09**
201668_x_at	*MARCKS*	myristoylated alanine-rich protein kinase C substrate	AW163148	1.44	**3.07**
217371_s_at	*IL15*	interleukin 15	Y09908	-1	**3.07**
222068_s_at	*LRRC50*	leucine rich repeat containing 50	AW663632	1.52	**3.06**
201266_at	*TXNRD1*	thioredoxin reductase 1	NM_003330	1.2	**3.05**
208066_s_at	*GTF2B*	general transcription factor IIB	NM_001514	-1.2	**3.05**
210087_s_at	*MPZL1*	myelin protein zero-like 1	AF095727	1.17	**3.05**
201531_at	*ZFP36*	zinc finger protein 36, C3H type, homolog (mouse)	NM_003407	1.85	**3.04**
211012_s_at	*PML /// LOC161527*	promyelocytic leukemia /// hypothetical protein LOC161527	BC000080	1.03	**3.03**
201625_s_at	*INSIG1*	insulin induced gene 1	BE300521	2.41	**3.01**
201952_at	*ALCAM*	activated leukocyte cell adhesion molecule	AA156721	1.63	**3.01**
204908_s_at	*BCL3*	B-cell CLL/lymphoma 3	NM_005178	1.38	**3.01**
203358_s_at	*EZH2*	enhancer of zeste homolog 2 (Drosophila)	NM_004456	1.71	**2.98**
209765_at	*ADAM19*	a disintegrin and metalloproteinase domain 19 (meltrin beta)	Y13786	1.62	**2.97**
212902_at	*SEC24A*	SEC24 related gene family, member A (S. cerevisiae)	BE645231	2.01	**2.96**
203149_at	*PVRL2*	poliovirus receptor-related 2 (herpesvirus entry mediator B)	NM_002856	1.16	**2.95**
207616_s_at	*TANK*	TRAF family member-associated NFKB activator	NM_004180	1.89	**2.94**
203595_s_at	*IFIT5*	interferon-induced protein with tetratricopeptide repeats 5	N47725	1.71	**2.93**
201670_s_at	*MARCKS*	myristoylated alanine-rich protein kinase C substrate	M68956	1.55	**2.92**
213191_at	*TICAM1*	toll-like receptor adaptor molecule 1	AF070530	1.98	**2.91**
207181_s_at	*CASP7*	caspase 7, apoptosis-related cysteine protease	NM_001227	-1.22	**2.89**

211133_x_at	*LILRB2 /// LILRB3*	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /// leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009643	1.11	**2.88**
214866_at	*PLAUR*	plasminogen activator, urokinase receptor	X74039	1.83	**2.87**
204194_at	*BACH1*	BTB and CNC homology 1, basic leucine zipper transcription factor 1	NM_001186	-1.12	**2.86**
213618_at	*CENTD1*	centaurin, delta 1	AB011152	-1.19	**2.86**
205322_s_at	*MTF1*	metal-regulatory transcription factor 1	AW182367	-1.06	**2.85**
218995_s_at	*EDN1*	endothelin 1	NM_001955	1.56	**2.84**
204512_at	*HIVEP1*	human immunodeficiency virus type I enhancer binding protein 1	NM_002114	1.72	**2.81**
213457_at	*MFHAS1*	malignant fibrous histiocytoma amplified sequence 1	BF739959	1.74	**2.78**
203125_x_at	*SLC11A2*	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AF046997	1.81	**2.77**
203925_at	*GCLM*	glutamate-cysteine ligase, modifier subunit	NM_002061	1.08	**2.71**
201649_at	*UBE2L6*	ubiquitin-conjugating enzyme E2L 6	NM_004223	-1.19	**2.7**
208992_s_at	*STAT3*	signal transducer and activator of transcription 3 (acute-phase response factor)	BC000627	1.06	**2.7**
202043_s_at	*SMS*	spermine synthase	NM_004595	1.71	**2.68**
213988_s_at	*SAT*	spermidine/spermine N1-acetyltransferase	BE971383	1.46	**2.67**
209640_at	*PML*	promyelocytic leukemia	M79462	1.19	**2.64**
212201_at	*KIAA0692*	KIAA0692 protein	AW274877	1.35	**2.64**
212014_x_at	*CD44*	CD44 antigen (homing function and Indian blood group system)	AI493245	1.51	**2.63**
208296_x_at	*TNFAIP8*	tumor necrosis factor, alpha-induced protein 8	NM_014350	2.56	**2.61**
213546_at	---	---	AL050378	1.73	**2.61**
208805_at	*PSMA6*	proteasome (prosome, macropain) subunit, alpha type, 6	BC002979	1.46	**2.6**
217986_s_at	*BAZ1A*	bromodomain adjacent to zinc finger domain, 1A	NM_013448	1.49	**2.6**
200881_s_at	*DNAJA1*	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_001539	1.37	**2.57**
201858_s_at	*PRG1*	proteoglycan 1, secretory granule	J03223	1.67	**2.57**
202625_at	*LYN*	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	AI356412	1.23	**2.56**
203010_at	*STAT5A*	signal transducer and activator of transcription 5A	NM_003152	2.11	**2.55**
202466_at	*POLS*	polymerase (DNA directed) sigma	NM_006999	-1.07	**2.51**
217966_s_at	*C1orf24*	chromosome 1 open reading frame 24	NM_022083	1.35	**2.47**
202925_s_at	*PLAGL2*	pleiomorphic adenoma gene-like 2	NM_002657	1.53	**2.4**
209015_s_at	*DNAJB6*	DnaJ (Hsp40) homolog, subfamily B, member 6	BC002446	-1	**2.39**
204559_s_at	*LSM7*	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_016199	-1.2	**-2.34**
218165_at	*C1orf149*	chromosome 1 open reading frame 149	NM_022756	-1.95	**-2.34**
221937_at	---	CDNA FLJ34482 fis, clone HLUNG2004067	AI472320	-1.64	**-2.34**
201092_at	*RBBP7*	retinoblastoma binding protein 7	NM_002893	-1.49	**-2.38**
200027_at	*NARS*	asparaginyl-tRNA synthetase /// asparaginyl-tRNA synthetase	NM_004539	-1.4	**-2.39**
211988_at	*SMARCE1*	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	BG289800	-1.48	**-2.39**
64418_at	---	CDNA FLJ34482 fis, clone HLUNG2004067	AI472320	-1.85	**-2.39**
209075_s_at	*NIFUN*	NifU-like N-terminal domain containing	AY009128	-1.63	**-2.4**
211747_s_at	*LSM5*	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	BC005938	-1.34	**-2.45**

207168_s_at	*H2AFY*	H2A histone family, member Y	NM_004893	-1.33	**-2.46**
221688_s_at	*IMP3*	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	AL136913	-1.4	**-2.46**
202117_at	*ARHGAP1*	Rho GTPase activating protein 1	BG468434	-1.43	**-2.47**
218042_at	*COPS4*	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	NM_016129	-1.56	**-2.47**
200883_at	*UQCRC2*	ubiquinol-cytochrome c reductase core protein II	NM_003366	-1.24	**-2.48**
206989_s_at	*SFRS2IP*	splicing factor, arginine/serine-rich 2, interacting protein	NM_004719	-1.33	**-2.48**
213154_s_at	*BICD2*	bicaudal D homolog 2 (Drosophila)	AI934125	-2.14	**-2.49**
221689_s_at	*DSCR5*	Down syndrome critical region gene 5	AB035745	-1.16	**-2.49**
208669_s_at	*CRI1*	CREBBP/EP300 inhibitor 1	AF109873	-1.39	**-2.5**
219279_at	*DOCK10*	dedicator of cytokinesis 10	NM_017718	-1.34	**-2.51**
219597_s_at	*DUOX1*	dual oxidase 1	NM_017434	-1.22	**-2.51**
204192_at	*CD37*	CD37 antigen	NM_001774	-1.28	**-2.52**
213566_at	*RNASE6*	ribonuclease, RNase A family, k6	NM_005615	1.14	**-2.52**
217736_s_at	*EIF2AK1*	eukaryotic translation initiation factor 2-alpha kinase 1	NM_014413	-1.39	**-2.52**
201306_s_at	*ANP32B*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	NM_006401	-1.77	**-2.53**
208986_at	*TCF12*	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	AL559478	-1.35	**-2.53**
200847_s_at	*TMEM66*	transmembrane protein 66	NM_016127	-1.19	**-2.54**
209615_s_at	*PAK1*	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	U51120	-1.47	**-2.55**
210027_s_at	*APEX1*	APEX nuclease (multifunctional DNA repair enzyme) 1	M80261	-1.47	**-2.55**
212585_at	*OSBPL8*	oxysterol binding protein-like 8	BF970829	-1.55	**-2.55**
212632_at	*STX7*	Syntaxin 7	N32035	-2	**-2.55**
214730_s_at	*GLG1*	golgi apparatus protein 1	AK025457	-1.59	**-2.55**
209111_at	*RNF5*	ring finger protein 5	BC004155	-1.43	**-2.56**
216044_x_at	*LOC388650*	hypothetical LOC388650	AK027146	-2.4	**-2.56**
218048_at	*COMMD3*	COMM domain containing 3	NM_012071	-1.35	**-2.56**
221532_s_at	*WDR61*	WD repeat domain 61	AF309553	-1.48	**-2.56**
203739_at	*ZNF217*	zinc finger protein 217	NM_006526	-1.22	**-2.57**
212904_at	*LRRC47*	leucine rich repeat containing 47	AB033011	-2.01	**-2.57**
210980_s_at	*ASAH1*	N-acylsphingosine amidohydrolase (acid ceramidase) 1	U47674	-1.26	**-2.58**
222127_s_at	*SEC3L1*	SEC3-like 1 (S. cerevisiae)	AK023461	-1.69	**-2.58**
202306_at	*POLR2G*	polymerase (RNA) II (DNA directed) polypeptide G	NM_002696	-1.15	**-2.59**
202778_s_at	*ZNF198*	zinc finger protein 198	NM_003453	-1.69	**-2.59**
208764_s_at	*ATP5G2*	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	D13119	-1.15	**-2.59**
208890_s_at	*PLXNB2*	plexin B2	BC004542	-1.45	**-2.59**
209787_s_at	*HMGN4*	high mobility group nucleosomal binding domain 4	BC001282	-1.52	**-2.59**
212251_at	*MTDH*	metadherin	AI972475	-1.5	**-2.59**
201515_s_at	*TSN*	translin	NM_004622	-1.8	**-2.6**
214383_x_at	*KLHDC3*	kelch domain containing 3	BF063121	-1.76	**-2.6**
218014_at	*PCNT1*	pericentrin 1	NM_024844	-1.88	**-2.6**
220094_s_at	*C6orf79*	chromosome 6 open reading frame 79	NM_022102	-1.3	**-2.6**
202802_at	*DHPS*	deoxyhypusine synthase	NM_001930	-1.28	**-2.61**

217792_at	*SNX5*	sorting nexin 5	NM_014426	-1.47	**-2.61**
217797_at	*UFC1*	ubiquitin-fold modifier conjugating enzyme 1	NM_016406	-1.21	**-2.63**
212593_s_at	*PDCD4*	programmed cell death 4 (neoplastic transformation inhibitor)	N92498	-1.51	**-2.64**
203932_at	*HLA-DMB*	major histocompatibility complex, class II, DM beta	NM_002118	-1.12	**-2.65**
204834_at	*FGL2*	fibrinogen-like 2	NM_006682	-1.04	**-2.66**
208964_s_at	*FADS1*	fatty acid desaturase 1	AL512760	-1.14	**-2.66**
209385_s_at	*PROSC*	proline synthetase co-transcribed homolog (bacterial)	AL136616	-1.4	**-2.66**
218366_x_at	*FLJ20859*	FLJ20859 gene	NM_022734	-1.83	**-2.66**
204690_at	*STX8*	syntaxin 8	NM_004853	-1.21	**-2.67**
203909_at	*SLC9A6*	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	NM_006359	-1.9	**-2.68**
211974_x_at	*RBPSUH*	recombining binding protein suppressor of hairless (Drosophila)	AL513759	-1.19	**-2.68**
214281_s_at	*RCHY1*	ring finger and CHY zinc finger domain containing 1	AA524525	-1.76	**-2.68**
219947_at	*CLEC4A*	C-type lectin domain family 4, member A	NM_016184	1.01	**-2.68**
202809_s_at	*C1orf60*	chromosome 1 open reading frame 60	NM_023015	-1.38	**-2.69**
212552_at	*HPCAL1*	hippocalcin-like 1	BE617588	-1.45	**-2.69**
219007_at	*NUP43*	nucleoporin 43kDa	NM_024647	-1.82	**-2.69**
221565_s_at	*FAM26B*	family with sequence similarity 26, member B	BC000039	-2.64	**-2.69**
221637_s_at	*MGC2477*	hypothetical protein MGC2477	BC001434	-1.39	**-2.69**
201730_s_at	*TPR*	translocated promoter region (to activated MET oncogene)	BF110993	-1.46	**-2.7**
217945_at	*BTBD1*	BTB (POZ) domain containing 1	NM_025238	-1.66	**-2.71**
218205_s_at	*MKNK2*	MAP kinase interacting serine/threonine kinase 2	NM_017572	-1.39	**-2.73**
202218_s_at	*FADS2*	fatty acid desaturase 2	NM_004265	-1.12	**-2.74**
209565_at	*RNF113A*	ring finger protein 113A	BC000832	-2.27	**-2.74**
212880_at	*WDR7*	WD repeat domain 7	AB011113	-1.43	**-2.74**
201288_at	*ARHGDIB*	Rho GDP dissociation inhibitor (GDI) beta	NM_001175	1.09	**-2.75**
202848_s_at	*GRK6*	G protein-coupled receptor kinase 6	BG423052	-1.52	**-2.75**
210580_x_at	*SULT1A3 /// SULT1A4*	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	L25275	-1.44	**-2.75**
212829_at	---	CDNA FLJ13267 fis, clone OVARC1000964	BE878277	-1.33	**-2.75**
217870_s_at	*CMPK*	cytidylate kinase	NM_016308	-1.34	**-2.76**
218167_at	*LOC51321*	hypothetical protein LOC51321	NM_016627	-1.22	**-2.76**
219329_s_at	*C2orf28*	chromosome 2 open reading frame 28	NM_016085	1.02	**-2.76**
201632_at	*EIF2B1*	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	NM_001414	-1.81	**-2.78**
204438_at	*MRC1 /// MRC1L1*	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	NM_002438	-1.05	**-2.78**
221223_x_at	*CISH*	cytokine inducible SH2-containing protein	NM_013324	-1.55	**-2.78**
203621_at	*NDUFB5*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	NM_002492	-1.03	**-2.79**
217989_at	*DHRS8*	dehydrogenase/reductase (SDR family) member 8	NM_016245	-1.22	**-2.79**
219191_s_at	*BIN2*	bridging integrator 2	NM_016293	-1.61	**-2.8**

201570_at	*CGI-51*	CGI-51 protein	NM_015380	-1.54	**-2.81**
202060_at	*SH2BP1*	SH2 domain binding protein 1 (tetratricopeptide repeat containing)	NM_014633	-1.38	**-2.81**
203831_at	*KIAA1002*	KIAA1002 protein	NM_014925	-1.37	**-2.81**
201938_at	*CDK2AP1*	CDK2-associated protein 1	NM_004642	-1.25	**-2.82**
202395_at	*NSF*	N-ethylmaleimide-sensitive factor	NM_006178	-1.7	**-2.82**
202003_s_at	*ACAA2*	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	NM_006111	-1.26	**-2.83**
202944_at	*NAGA*	N-acetylgalactosaminidase, alpha-	NM_000262	-1.43	**-2.83**
201338_x_at	*GTF3A*	general transcription factor IIIA	NM_002097	-1.44	**-2.84**
201998_at	*ST6GAL1*	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	AI743792	-1.5	**-2.84**
203166_at	*CFDP1*	craniofacial development protein 1	NM_006324	-1.28	**-2.84**
208982_at	*PECAM1*	Platelet/endothelial cell adhesion molecule (CD31 antigen)	AW574504	-1.1	**-2.84**
211987_at	*TOP2B*	topoisomerase (DNA) II beta 180kDa	NM_001068	-1.56	**-2.84**
202546_at	*VAMP8*	vesicle-associated membrane protein 8 (endobrevin)	NM_003761	-1.1	**-2.85**
209152_s_at	*TCF3*	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	AI655986	-1.4	**-2.85**
202382_s_at	*GNPDA1*	glucosamine-6-phosphate deaminase 1	NM_005471	-1.22	**-2.86**
218421_at	*CERK*	ceramide kinase	NM_022766	-1.57	**-2.86**
201990_s_at	*CREBL2*	cAMP responsive element binding protein-like 2	NM_001310	-1.05	**-2.87**
213160_at	*DOCK2*	dedicator of cytokinesis 2	D86964	-1.23	**-2.87**
213564_x_at	*LDHB*	lactate dehydrogenase B	BE042354	-1.13	**-2.87**
201740_at	*NDUFS3*	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NM_004551	-1.72	**-2.88**
210046_s_at	*IDH2*	isocitrate dehydrogenase 2 (NADP+), mitochondrial	U52144	1.27	**-2.88**
212399_s_at	*VGLL4*	vestigial like 4 (Drosophila)	D50911	-1.74	**-2.88**
219157_at	*KLHL2*	kelch-like 2, Mayven (Drosophila)	NM_007246	-1.69	**-2.88**
200098_s_at	*ANAPC5*	anaphase promoting complex subunit 5	T33068	-1.62	**-2.89**
201576_s_at	*GLB1*	galactosidase, beta 1	NM_000404	-1.56	**-2.89**
202449_s_at	*RXRA*	retinoid X receptor, alpha	NM_002957	-1.93	**-2.89**
209154_at	*TAX1BP3*	Tax1 (human T-cell leukemia virus type I) binding protein 3	AF234997	-1.37	**-2.89**
212631_at	*STX7*	Syntaxin 7	AI566082	-1.96	**-2.89**
202736_s_at	*LSM4*	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	AA112507	-1.26	**-2.9**
209444_at	*RAP1GDS1*	RAP1, GTP-GDP dissociation stimulator 1	BC001851	-1.38	**-2.9**
213689_x_at	*LOC388650*	Hypothetical LOC388650	AL137958	-2.01	**-2.9**
203615_x_at	*SULT1A1*	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	NM_001055	-1.38	**-2.91**
203747_at	*AQP3*	aquaporin 3	NM_004925	-1.5	**-2.91**
217887_s_at	*EPS15*	epidermal growth factor receptor pathway substrate 15	NM_001981	-1.3	**-2.91**
212155_at	*RNF187*	ring finger protein 187	AA085748	-1.6	**-2.92**
212675_s_at	---	---	AB011154	-1.83	**-2.92**
219002_at	*FLJ21901*	hypothetical protein FLJ21901	NM_024622	-1.8	**-2.92**
202468_s_at	*CTNNAL1*	catenin (cadherin-associated protein), alpha-like 1	NM_003798	-1.28	**-2.93**
218102_at	*DERA*	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	NM_015954	-1.1	**-2.93**

221058_s_at	*CKLF*	chemokine-like factor	NM_016326	-1.33	**-2.93**
217914_at	*TPCN1*	two pore segment channel 1	NM_017901	-1.24	**-2.94**
200617_at	*KIAA0152*	KIAA0152	NM_014730	-1.43	**-2.95**
204386_s_at	*MRP63*	mitochondrial ribosomal protein 63	BF303597	-1.56	**-2.95**
209218_at	*SQLE*	squalene epoxidase	AF098865	1.22	**-2.95**
39249_at	*AQP3*	aquaporin 3	AB001325	-1.74	**-2.95**
201202_at	*PCNA*	proliferating cell nuclear antigen	NM_002592	-2.08	**-2.96**
218454_at	*FLJ22662*	hypothetical protein FLJ22662	NM_024829	-1.15	**-2.96**
213400_s_at	*TBL1X*	transducin (beta)-like 1X-linked	AV753028	-1.29	**-2.98**
214937_x_at	*PCM1*	pericentriolar material 1	AI924817	-1.43	**-2.99**
222014_x_at	*MTO1*	mitochondrial translation optimization 1 homolog (S. cerevisiae)	AI249752	-1.53	**-2.99**
218179_s_at	*FLJ12716*	FLJ12716 protein	NM_021942	-1.97	**-3**
218716_x_at	*MTO1*	mitochondrial translation optimization 1 homolog (S. cerevisiae)	NM_012123	-1.67	**-3**
201612_at	*ALDH9A1*	aldehyde dehydrogenase 9 family, member A1	NM_000696	-1.82	**-3.01**
201816_s_at	*GBAS*	glioblastoma amplified sequence	NM_001483	-1.32	**-3.01**
210891_s_at	*GTF2I /// GTF2IP1*	general transcription factor II, i /// general transcription factor II, i, pseudogene 1	AF035737	-1.36	**-3.02**
212625_at	*STX10*	syntaxin 10	NM_003765	-1.24	**-3.02**
36030_at	*HOM-TES-103*	HOM-TES-103 tumor antigen-like	AL080214	-1.77	**-3.02**
204153_s_at	*MFNG*	manic fringe homolog (Drosophila)	NM_002405	-1.33	**-3.03**
210658_s_at	*GGA2*	golgi associated, gamma adaptin ear containing, ARF binding protein 2	BC000284	-1.53	**-3.03**
221770_at	*RPE*	ribulose-5-phosphate-3-epimerase	BE964473	-1.38	**-3.03**
202950_at	*CRYZ*	crystallin, zeta (quinone reductase)	NM_001889	-1.26	**-3.04**
206120_at	*CD33*	CD33 antigen (gp67)	NM_001772	-1.28	**-3.04**
217846_at	*QARS*	glutaminyl-tRNA synthetase	NM_005051	-1.21	**-3.05**
218250_s_at	*CNOT7*	CCR4-NOT transcription complex, subunit 7	NM_013354	-1.78	**-3.05**
200726_at	*PPP1CC*	protein phosphatase 1, catalytic subunit, gamma isoform	NM_002710	-1.61	**-3.06**
208983_s_at	*PECAM1*	platelet/endothelial cell adhesion molecule (CD31 antigen)	M37780	-1.16	**-3.06**
221984_s_at	*C2orf17*	chromosome 2 open reading frame 17	AL040896	-2.12	**-3.07**
202603_at	*ADAM10*	A disintegrin and metalloproteinase domain 10	N51370	-1.33	**-3.09**
212638_s_at	*WWP1*	WW domain containing E3 ubiquitin protein ligase 1	BF131791	-1.56	**-3.09**
218133_s_at	*NIF3L1*	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	NM_021824	-1.46	**-3.1**
218606_at	*ZDHHC7*	zinc finger, DHHC-type containing 7	NM_017740	-1.72	**-3.1**
209607_x_at	*SULT1A3 /// SULT1A4*	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	U08032	-1.39	**-3.11**
213465_s_at	*PPP1R7*	protein phosphatase 1, regulatory subunit 7	BF718769	-1.36	**-3.11**
209734_at	*HEM1*	hematopoietic protein 1	BC001604	-1.37	**-3.12**
211557_x_at	*SLCO2B1*	solute carrier organic anion transporter family, member 2B1	AF205073	-1.49	**-3.12**
203190_at	*NDUFS8*	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NM_002496	-1.2	**-3.13**
204861_s_at	*BIRC1*	baculoviral IAP repeat-containing 1	NM_004536	-2.33	**-3.13**

212248_at	*LYRIC*	LYRIC/3D3	AI886796	-1.68	**-3.13**
220952_s_at	*PLEKHA5*	pleckstrin homology domain containing, family A member 5	NM_019012	-1.88	**-3.13**
209083_at	*CORO1A*	coronin, actin binding protein, 1A	U34690	-1.64	**-3.14**
209585_s_at	*MINPP1*	multiple inositol polyphosphate histidine phosphatase, 1	AF084943	-1.75	**-3.14**
214198_s_at	*DGCR2*	DiGeorge syndrome critical region gene 2	AU150824	-2.07	**-3.14**
201305_x_at	*ANP32B*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	AV712577	-1.75	**-3.15**
202326_at	*EHMT2*	euchromatic histone-lysine N-methyltransferase 2	NM_006709	-1.61	**-3.16**
203007_x_at	*LYPLA1*	lysophospholipase I	AF077198	-1.38	**-3.16**
205147_x_at	*NCF4*	neutrophil cytosolic factor 4, 40kDa	NM_000631	-1.42	**-3.16**
207540_s_at	*SYK*	spleen tyrosine kinase	NM_003177	-1.41	**-3.16**
214118_x_at	*PCM1*	pericentriolar material 1	AI205598	-1.22	**-3.16**
222148_s_at	*RHOT1*	ras homolog gene family, member T1	BF688108	-1.7	**-3.16**
201043_s_at	*ANP32A*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	NM_006305	-1.1	**-3.17**
202593_s_at	*MIR16*	membrane interacting protein of RGS16	NM_016641	-1.52	**-3.17**
205090_s_at	*NAGPA*	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	NM_016256	-1.81	**-3.17**
202174_s_at	*PCM1*	pericentriolar material 1	NM_006197	-1.53	**-3.18**
209143_s_at	*CLNS1A /// C3orf4*	chloride channel, nucleotide-sensitive, 1A /// chromosome 3 open reading frame 4	AF005422	-1.53	**-3.18**
214735_at	*PIP3-E*	phosphoinositide-binding protein PIP3-E	AW166711	-1.88	**-3.18**
218298_s_at	*C14orf159*	chromosome 14 open reading frame 159	NM_024952	-1.44	**-3.18**
202265_at	*PCGF4*	polycomb group ring finger 4	NM_005180	-1.72	**-3.19**
206206_at	*CD180*	CD180 antigen	NM_005582	-1.99	**-3.19**
218138_at	*MKKS*	McKusick-Kaufman syndrome	NM_018848	-1.96	**-3.19**
209717_at	*EVI5*	ecotropic viral integration site 5	AF008915	-1.79	**-3.21**
212360_at	*AMPD2*	adenosine monophosphate deaminase 2 (isoform L)	AI916249	-1.6	**-3.21**
220079_s_at	*USP48*	ubiquitin specific protease 48	NM_018391	-1.98	**-3.21**
221539_at	*EIF4EBP1*	eukaryotic translation initiation factor 4E binding protein 1	AB044548	-1.3	**-3.21**
208787_at	*MRPL3*	mitochondrial ribosomal protein L3	BC003375	-1.57	**-3.22**
214949_at	---	Similar to family with sequence similarity 9, member C	AL050136	-2.28	**-3.23**
209780_at	*PHTF2*	putative homeodomain transcription factor 2	AL136883	-1.38	**-3.24**
221830_at	*RAP2A*	RAP2A, member of RAS oncogene family	AI302106	-1.83	**-3.24**
201413_at	*HSD17B4*	hydroxysteroid (17-beta) dehydrogenase 4	NM_000414	-1.34	**-3.25**
203472_s_at	*SLCO2B1*	solute carrier organic anion transporter family, member 2B1	AB026256	-1.37	**-3.25**
215338_s_at	*NKTR*	natural killer-tumor recognition sequence	AI688640	-1.7	**-3.25**
201432_at	*CAT*	catalase	NM_001752	-1.21	**-3.26**
215091_s_at	*GTF3A*	general transcription factor IIIA	BE542815	-1.5	**-3.26**
208796_s_at	*CCNG1*	cyclin G1	BC000196	-1.51	**-3.27**
210950_s_at	*FDFT1*	farnesyl-diphosphate farnesyltransferase 1	BC003573	-1.6	**-3.27**
214054_at	*DOK2*	docking protein 2, 56kDa	AI828929	-1.67	**-3.27**
202823_at	*TCEB1*	Transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	N89607	-1.24	**-3.28**
203182_s_at	*SRPK2*	SFRS protein kinase 2	NM_003138	-1.71	**-3.28**
204392_at	*CAMK1*	calcium/calmodulin-dependent protein kinase I	NM_003656	-1.67	**-3.29**
213083_at	*SLC35D2*	solute carrier family 35, member D2	AJ005866	-1.5	**-3.29**
211922_s_at	*CAT*	catalase	AY028632	-1.23	**-3.31**
212897_at	*CDC2L6*	cell division cycle 2-like 6 (CDK8-like)	AI738802	-1.42	**-3.31**

221724_s_at	*CLEC4A*	C-type lectin domain family 4, member A	AF200738	-1.03	**-3.31**
203836_s_at	*MAP3K5*	mitogen-activated protein kinase kinase kinase 5	D84476	-1.38	**-3.32**
212449_s_at	*LYPLA1*	lysophospholipase I	BG288007	-1.07	**-3.34**
217802_s_at	*NUCKS1*	nuclear casein kinase and cyclin-dependent kinase substrate 1	NM_022731	-1.32	**-3.35**
200789_at	*ECH1*	enoyl Coenzyme A hydratase 1, peroxisomal	NM_001398	-1.21	**-3.36**
202664_at	*WASPIP*	Wiskott-Aldrich syndrome protein interacting protein	AW058622	-1.6	**-3.36**
202119_s_at	*CPNE3*	copine III	NM_003909	-1.2	**-3.37**
204646_at	*DPYD*	dihydropyrimidine dehydrogenase	NM_000110	-1.53	**-3.37**
208911_s_at	*PDHB*	pyruvate dehydrogenase (lipoamide) beta	M34055	-1.89	**-3.37**
212830_at	*EGFL5*	EGF-like-domain, multiple 5	W68084	-1.97	**-3.37**
201010_s_at	*TXNIP*	thioredoxin interacting protein	NM_006472	-1.59	**-3.38**
37170_at	*BMP2K*	BMP2 inducible kinase	AB015331	-1.59	**-3.39**
202206_at	*ARL7*	ADP-ribosylation factor-like 7	AW450363	-1.38	**-3.4**
219607_s_at	*MS4A4A*	membrane-spanning 4-domains, subfamily A, member 4	NM_024021	-1.05	**-3.4**
209484_s_at	*C1orf48*	chromosome 1 open reading frame 48	AF201941	-2.07	**-3.41**
217886_at	*EPS15*	epidermal growth factor receptor pathway substrate 15	BF213575	-1.93	**-3.41**
221824_s_at	*MARCH8*	membrane-associated ring finger (C3HC4) 8	AA770170	-1.74	**-3.42**
202737_s_at	*LSM4*	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_012321	-1.49	**-3.44**
208808_s_at	*HMGB2*	high-mobility group box 2	BC000903	-1.47	**-3.44**
217122_s_at	*SLC35E2*	solute carrier family 35, member E2	AL031282	-2.1	**-3.44**
39248_at	*AQP3*	aquaporin 3	N74607	-1.57	**-3.44**
207785_s_at	*RBPSUH*	recombining binding protein suppressor of hairless (Drosophila)	NM_015874	-1.03	**-3.45**
208647_at	*FDFT1*	farnesyl-diphosphate farnesyltransferase 1	AA872727	-1.75	**-3.45**
218094_s_at	*C20orf35*	chromosome 20 open reading frame 35	NM_018478	-1.6	**-3.45**
220162_s_at	*CARD9*	caspase recruitment domain family, member 9	NM_022352	-1.41	**-3.47**
208661_s_at	*TTC3*	tetratricopeptide repeat domain 3	AW510696	-1.39	**-3.48**
208963_x_at	*FADS1*	fatty acid desaturase 1	BG165833	-1.31	**-3.49**
204640_s_at	*SPOP*	speckle-type POZ protein	NM_003563	-2.09	**-3.51**
209357_at	*CITED2*	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	AF109161	-1.89	**-3.51**
209337_at	*PSIP1*	PC4 and SFRS1 interacting protein 1	AF063020	-1.36	**-3.54**
212640_at	*PTPLB*	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	AV712602	-1.35	**-3.55**
214948_s_at	*TMF1*	TATA element modulatory factor 1 /// Similar to family with sequence similarity 9, member C	AL050136	-1.78	**-3.55**
218195_at	*C6orf211*	chromosome 6 open reading frame 211	NM_024573	-1.74	**-3.55**
222129_at	*C2orf17*	Chromosome 2 open reading frame 17	AK026155	-1.92	**-3.55**
201278_at	*DAB2*	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	N21202	-1.99	**-3.57**
218493_at	*C16orf33*	chromosome 16 open reading frame 33	NM_024571	-1.44	**-3.57**
202207_at	*ARL7*	ADP-ribosylation factor-like 7	BG435404	-1.37	**-3.58**
222217_s_at	*SLC27A3*	solute carrier family 27 (fatty acid transporter), member 3	BC003654	-1.37	**-3.58**
201214_s_at	*PPP1R7*	protein phosphatase 1, regulatory subunit 7	NM_002712	-1.29	**-3.59**
209285_s_at	*RAP140*	retinoblastoma-associated protein 140	N38985	-1.58	**-3.6**
202741_at	*PRKACB*	protein kinase, cAMP-dependent, catalytic, beta	AA130247	-1.64	**-3.62**
203741_s_at	*ADCY7*	adenylate cyclase 7	NM_001114	-2.22	**-3.64**
204044_at	*QPRT*	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	NM_014298	-1.29	**-3.64**
201887_at	*IL13RA1*	interleukin 13 receptor, alpha 1	NM_001560	-1.26	**-3.65**

210024_s_at	*UBE2E3*	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	AB017644	-1.8	**-3.65**
209879_at	*SELPLG*	selectin P ligand	AI741056	-1.52	**-3.66**
217317_s_at	*D15F37 /// LOC440248*	D15F37 gene /// hypothetical LOC440248	AB002391	-1.86	**-3.67**
205128_x_at	*PTGS1*	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962	-1.21	**-3.68**
210555_s_at	*NFATC3*	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	U85430	-2.58	**-3.68**
212160_at	*XPOT*	exportin, tRNA (nuclear export receptor for tRNAs)	AI984005	-1.43	**-3.68**
218263_s_at	*LOC58486*	transposon-derived Buster1 transposase-like protein gene	NM_021211	-1.99	**-3.69**
201529_s_at	*RPA1*	replication protein A1, 70kDa	NM_002945	-1.54	**-3.7**
203837_at	*MAP3K5*	mitogen-activated protein kinase kinase kinase 5	NM_005923	-1.57	**-3.7**
214500_at	*H2AFY*	H2A histone family, member Y	AF044286	-1.23	**-3.7**
211742_s_at	*EVI2B*	ecotropic viral integration site 2B	BC005926	-1.92	**-3.71**
207677_s_at	*NCF4*	neutrophil cytosolic factor 4, 40kDa	NM_013416	-1.45	**-3.72**
201051_at	*ANP32A*	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	BE560202	-1.68	**-3.74**
208956_x_at	*DUT*	dUTP pyrophosphatase	U62891	-1.55	**-3.74**
208962_s_at	*FADS1*	fatty acid desaturase 1	BE540552	-1.54	**-3.74**
218019_s_at	*PDXK*	pyridoxal (pyridoxine, vitamin B6) kinase	NM_021941	-1.34	**-3.74**
219892_at	*TM6SF1*	transmembrane 6 superfamily member 1	NM_023003	-1.62	**-3.76**
218341_at	*PPCS*	phosphopantothenoylcysteine synthetase	NM_024664	-1.76	**-3.78**
201384_s_at	*NBR1*	neighbor of BRCA1 gene 1	NM_005899	-1.76	**-3.8**
210987_x_at	*TPM1*	tropomyosin 1 (alpha)	M19267	-1.57	**-3.8**
219161_s_at	*CKLF*	chemokine-like factor	NM_016951	-1.37	**-3.81**
201253_s_at	*CDIPT*	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	NM_006319	-1.54	**-3.82**
204112_s_at	*HNMT*	histamine N-methyltransferase	NM_006895	-1.35	**-3.82**
212276_at	*LPIN1*	lipin 1	D80010	-1.25	**-3.82**
201193_at	*IDH1*	isocitrate dehydrogenase 1 (NADP+), soluble	NM_005896	-1.46	**-3.83**
202169_s_at	*AASDHPPT*	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AF302110	-2.08	**-3.83**
202594_at	*LEPROTL1*	leptin receptor overlapping transcript-like 1	NM_015344	-1.98	**-3.86**
203704_s_at	*RREB1*	ras responsive element binding protein 1	AW118862	-1.51	**-3.86**
204759_at	*RCBTB2*	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	NM_001268	-1.96	**-3.87**
208927_at	*SPOP*	speckle-type POZ protein	BF673888	-2.01	**-3.9**
202530_at	*MAPK14*	mitogen-activated protein kinase 14	NM_001315	-1.89	**-3.92**
202039_at	*TIAF1 /// MYO18A*	TGFB1-induced anti-apoptotic factor 1 /// myosin XVIIIA	NM_004740	-1.71	**-3.93**
218530_at	*FHOD1*	formin homology 2 domain containing 1	NM_013241	-1.82	**-3.93**
202727_s_at	*IFNGR1*	interferon gamma receptor 1	NM_000416	-1.52	**-3.95**
213016_at	*BBX*	Bobby sox homolog (Drosophila)	AA573805	-1.47	**-3.95**
217838_s_at	*EVL*	Enah/Vasp-like	NM_016337	-1.56	**-3.97**
201008_s_at	*TXNIP*	thioredoxin interacting protein	AA812232	-1.85	**-3.98**
201518_at	*CBX1*	chromobox homolog 1 (HP1 beta homolog Drosophila)	NM_006807	-1.82	**-3.98**

208121_s_at	*PTPRO*	protein tyrosine phosphatase, receptor type, O	NM_002848	-2.23	**-3.99**
221666_s_at	*PYCARD*	PYD and CARD domain containing	BC004470	-1.39	**-3.99**
218304_s_at	*OSBPL11*	oxysterol binding protein-like 11	NM_022776	-2.35	**-4**
219043_s_at	*PDCL3 /// LOC285359*	phosducin-like 3 /// hypothetical protein FLJ12205	NM_024065	-1.38	**-4.01**
200931_s_at	*VCL*	vinculin	NM_014000	-1.41	**-4.04**
213737_x_at	*LOC283768 /// LOC388080 /// LOC388189 /// LOC390535 /// LOC400304 /// LOC440234 /// DKFZp434P162*	hypothetical LOC283768 /// similar to hypothetical protein /// golgi autoantigen, golgin family member /// hypothetical protein DKFZp434P162	AI620911	-1.4	**-4.06**
218456_at	*C1QDC1*	C1q domain containing 1	NM_023925	-1.59	**-4.06**
201009_s_at	*TXNIP*	thioredoxin interacting protein	AI439556	-1.99	**-4.11**
202151_s_at	*UBADC1*	ubiquitin associated domain containing 1	NM_016172	-1.69	**-4.11**
211023_at	*PDHB*	pyruvate dehydrogenase (lipoamide) beta	AL117618	-1.74	**-4.11**
201729_s_at	*KIAA0100*	KIAA0100 gene product	NM_014680	-1.49	**-4.13**
201935_s_at	*EIF4G3*	eukaryotic translation initiation factor 4 gamma, 3	AI768122	-1.39	**-4.13**
203402_at	*KCNAB2*	potassium voltage-gated channel, shaker-related subfamily, beta member 2	AL520102	-1.42	**-4.16**
202641_at	*ARL3*	ADP-ribosylation factor-like 3	NM_004311	-1.43	**-4.17**
206682_at	*CLEC10A*	C-type lectin domain family 10, member A	NM_006344	-1.03	**-4.17**
201528_at	*RPA1*	replication protein A1, 70kDa	BG398414	-1.83	**-4.19**
209479_at	*C6orf80*	chromosome 6 open reading frame 80	BC000758	-1.35	**-4.19**
205743_at	*STAC*	SH3 and cysteine rich domain	NM_003149	-1.23	**-4.22**
211676_s_at	*IFNGR1*	interferon gamma receptor 1	AF056979	-1.45	**-4.26**
206171_at	*ADORA3*	adenosine A3 receptor	NM_000677	-2.02	**-4.28**
221804_s_at	*FAM45B /// FAM45A*	family with sequence similarity 45, member B /// family with sequence similarity 45, member A	BE565675	-1.81	**-4.29**
215813_s_at	*PTGS1*	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	S36219	-1.53	**-4.33**
218218_at	*DIP13B*	DIP13 beta	NM_018171	-1.8	**-4.35**
63825_at	*ABHD2*	abhydrolase domain containing 2	AI557319	-1.55	**-4.35**
202839_s_at	*NDUFB7*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NM_004146	-1.56	**-4.4**
218697_at	*NCKIPSD*	NCK interacting protein with SH3 domain	NM_016453	-1.73	**-4.42**
218918_at	*MAN1C1*	mannosidase, alpha, class 1C, member 1	NM_020379	-1.71	**-4.44**
205684_s_at	*C9orf55*	chromosome 9 open reading frame 55	NM_017925	-1.67	**-4.46**
203241_at	*UVRAG*	UV radiation resistance associated gene	NM_003369	-1.6	**-4.48**
212616_at	*CHD9*	chromodomain helicase DNA binding protein 9	BF668950	-1.79	**-4.48**
205505_at	*GCNT1*	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	NM_001490	-2.41	**-4.49**

208662_s_at	*TTC3*	tetratricopeptide repeat domain 3	AI885338	-1.17	**-4.49**
208858_s_at	*FAM62A*	family with sequence similarity 62 (C2 domain containing), member A	BC004998	-1.59	**-4.54**
203104_at	*CSF1R*	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /// colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	NM_005211	-1.26	**-4.59**
221692_s_at	*MRPL34*	mitochondrial ribosomal protein L34	AB049652	-1.87	**-4.6**
212706_at	*RASA4 /// FLJ21767*	RAS p21 protein activator 4 /// hypothetical protein FLJ21767	AB011110	-1.84	**-4.63**
203799_at	*CD302*	CD302 antigen	NM_014880	-1.02	**-4.64**
204172_at	*CPOX*	coproporphyrinogen oxidase	NM_000097	-1.46	**-4.65**
218631_at	*AVPI1*	arginine vasopressin-induced 1	NM_021732	-2.32	**-4.65**
218323_at	*RHOT1*	ras homolog gene family, member T1	NM_018307	-1.83	**-4.71**
210645_s_at	*TTC3*	tetratricopeptide repeat domain 3	D83077	-1.32	**-4.81**
212846_at	*KIAA0179*	KIAA0179	AA811192	-1.49	**-4.87**
201368_at	*ZFP36L2*	zinc finger protein 36, C3H type-like 2	U07802	-2.57	**-4.88**
203286_at	*RNF44*	ring finger protein 44	NM_014901	-2.08	**-4.9**
212500_at	*C10orf22*	chromosome 10 open reading frame 22	AL049319	-1.69	**-4.91**
206542_s_at	*SMARCA2*	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	AV725365	-1.52	**-4.93**
205721_at	*GFRA2*	GDNF family receptor alpha 2	U97145	-1.17	**-4.96**
218351_at	*COMMD8*	COMM domain containing 8	NM_017845	-1.49	**-4.96**
201819_at	*SCARB1*	scavenger receptor class B, member 1	NM_005505	-1.34	**-5.03**
212331_at	*RBL2*	retinoblastoma-like 2 (p130)	X76061	-1.02	**-5.03**
219694_at	*FLJ11127*	hypothetical protein FLJ11127	NM_019018	-1.96	**-5.08**
208073_x_at	*TTC3*	tetratricopeptide repeat domain 3	NM_003316	-1.52	**-5.13**
215764_x_at	*AP2A2*	adaptor-related protein complex 2, alpha 2 subunit	AA877641	-1.42	**-5.17**
202191_s_at	*GAS7*	growth arrest-specific 7	BE439987	-1.58	**-5.27**
209748_at	*SPAST*	spastin	AB029006	-3.97	**-5.32**
217906_at	*KLHDC2*	kelch domain containing 2	NM_014315	-2.03	**-5.35**
221210_s_at	*NPL*	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NM_030769	-1.5	**-5.35**
204039_at	*CEBPA*	CCAAT/enhancer binding protein (C/EBP), alpha	NM_004364	-2.15	**-5.37**
205101_at	*MHC2TA*	MHC class II transactivator	NM_000246	-1.36	**-5.53**
210136_at	*MBP*	myelin basic protein	AW070431	-1.69	**-5.53**
203332_s_at	*INPP5D*	inositol polyphosphate-5-phosphatase, 145kDa	NM_005541	-1.39	**-5.55**
212856_at	*DIP*	death-inducing-protein	AB018310	-1.38	**-5.56**
211779_x_at	*AP2A2*	adaptor-related protein complex 2, alpha 2 subunit	BC006155	-1.38	**-5.77**
208771_s_at	*LTA4H*	leukotriene A4 hydrolase	J02959	-1.22	**-5.82**
201462_at	*SCRN1*	secernin 1	NM_014766	-1.68	**-5.86**
203156_at	*AKAP11*	A kinase (PRKA) anchor protein 11	NM_016248	-1.92	**-5.89**
214807_at	---	MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	AI278204	-1.24	**-6.01**
201034_at	*ADD3*	adducin 3 (gamma)	BE545756	-1.53	**-6.18**
212159_x_at	*AP2A2*	adaptor-related protein complex 2, alpha 2 subunit	AI125280	-1.42	**-6.35**
209933_s_at	*CD300A*	CD300A antigen	AF020314	-1.31	**-6.46**
201697_s_at	*DNMT1*	DNA (cytosine-5-)-methyltransferase 1	NM_001379	-1.99	**-7.1**
214719_at	*LOC283537*	hypothetical protein LOC283537	AK026720	-1.54	**-7.6**

217047_s_at	*FAM13A1*	family with sequence similarity 13, member A1	AK027138	-1.25	**-7.64**
201753_s_at	*ADD3*	adducin 3 (gamma)	NM_019903	-1.22	**-7.79**
205052_at	*AUH*	AU RNA binding protein/enoyl-Coenzyme A hydratase	NM_001698	-1.67	**-7.83**
215933_s_at	*HHEX*	hematopoietically expressed homeobox	Z21533	-2.24	**-7.91**
207761_s_at	*DKFZP586A0522*	DKFZP586A0522 protein	NM_014033	-1.43	**-8.2**
204446_s_at	*ALOX5*	arachidonate 5-lipoxygenase	NM_000698	-1.36	**-8.37**
218197_s_at	*OXR1*	oxidation resistance 1	NM_018002	-1.86	**-8.47**
210986_s_at	*TPM1*	tropomyosin 1 (alpha)	Z24727	-1.79	**-8.66**
207655_s_at	*BLNK*	B-cell linker	NM_013314	-2.3	**-9.9**
203473_at	*SLCO2B1*	solute carrier organic anion transporter family, member 2B1	NM_007256	-1.45	**-9.95**
202973_x_at	*FAM13A1*	family with sequence similarity 13, member A1	NM_014883	1.11	**-10.01**
208944_at	*TGFBR2*	transforming growth factor, beta receptor II (70/80kDa)	D50683	-2.13	**-10.64**
202364_at	*MXI1*	MAX interactor 1	NM_005962	-1.54	**-11.12**
209348_s_at	*MAF*	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	AF055376	-1.61	**-12.73**
206363_at	*MAF*	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_005360	-1.77	**-12.88**
219666_at	*MS4A6A*	membrane-spanning 4-domains, subfamily A, member 6A	NM_022349	-1.75	**-15.74**

Table S3: Kinetics of the transcriptional changes of genes, associated with the induction of IDO, during the infection of human mo-DC with virulent strain of *Listeria monocytogenes*. Fold changes in average expression strength between listeria-infected and mock-infected DC are shown. Positive values indicate upregulated genes, negative values indicate downregulated genes. Values in bold highlight the genes, which expression was significantly changed (**Supplemental Data**), green color hallmarks the upregulated and red color hallmarks the downregulated genes, respectively.

#	Gene Symbol	GenBank ID	2 hrs		6 hrs			
			DC1	DC2	DC1	DC2	DC3	DC4
1	*TNF*	NM_000594	**25.96**	**24.14**	**16.32**	**33.83**	**36.50**	**40.98**
2	*PTGS2*	NM_000963	**7.47**	**10.54**	**53.80**	**110.52**	**136.48**	**132.37**
3	*PTGER4*	AA897516	**7.23**	**6.12**	**5.37**	**8.08**	**5.02**	**5.60**
4	*IFNB1*	NM_002176	1.93	2.94	**3.96**	**22.38**	**18.45**	**19.79**
5	*IFNA1*	NM_024013	2.85	1.23	1.17	-1.15	1.33	1.69
6	*IFNG*	M29383	2.50	1.37	**3.38**	**3.93**	**2.87**	1.54
7	*IFNGR2*	NM_005534	1.63	2.02	-1.09	1.10	1.46	1.10
8	*TNFRSF1B*	NM_001066	1.46	1.45	**6.29**	**6.75**	**5.44**	**6.75**
9	*IFNA17*	M38289	1.64	1.08	1.31	-1.06	1.05	1.24
10	*IFNA5*	NM_002169	1.54	1.17	-1.45	1.19	1.41	1.87
11	*IFNA13*	NM_006900	1.14	1.56	1.36	1.30	0.96	1.20
12	*IFNA10*	NM_002171	1.28	1.35	1.12	1.58	1.04	1.33
13	*IFNA4*	NM_021068	1.13	1.42	3.48	0.96	-2.05	1.07
14	*PTGER2*	NM_000956	1.42	1.12	1.18	1.24	1.19	-1.06
15	*IFNA14*	NM_002172	1.18	1.28	1.11	0.97	-1.24	0.96
16	*IFNA16*	NM_002173	1.13	1.32	1.39	-1.16	2.05	-1.53
17	*IFNA21*	M12350	1.48	-1.09	-1.07	0.97	1.24	1.21
18	*IFNA6*	NM_021002	1.35	0.95	1.01	1.09	-1.32	1.07
19	*IFNA7*	NM_021057	1.26	-1.24	1.00	1.02	-1.20	1.11
20	*IFNA8*	NM_002170	-1.29	1.19	1.08	-1.09	-1.18	1.15
21	*IFNAR1*	NM_000629	0.97	-1.21	-1.05	-1.10	1.10	0.97
22	*IFNA2*	M54886	-1.37	1.07	-1.88	1.02	-1.25	1.29
23	*IFNAR2*	L41944	-1.25	-1.24	-1.41	-1.24	1.07	-1.09
24	*IFNGR1*	AF056979	-1.37	-1.49	**-3.82**	**-4.74**	**-5.19**	**-3.57**
25	*TNFRSF1A*	NM_001065	-1.81	-1.50	-1.22	1.12	1.05	1.35