SUPPLEMENTARY MATERIAL on "Networks inferred from biochemical data reveal profound differences in TLR and inflammatory signaling between normal and transformed hepatocytes"

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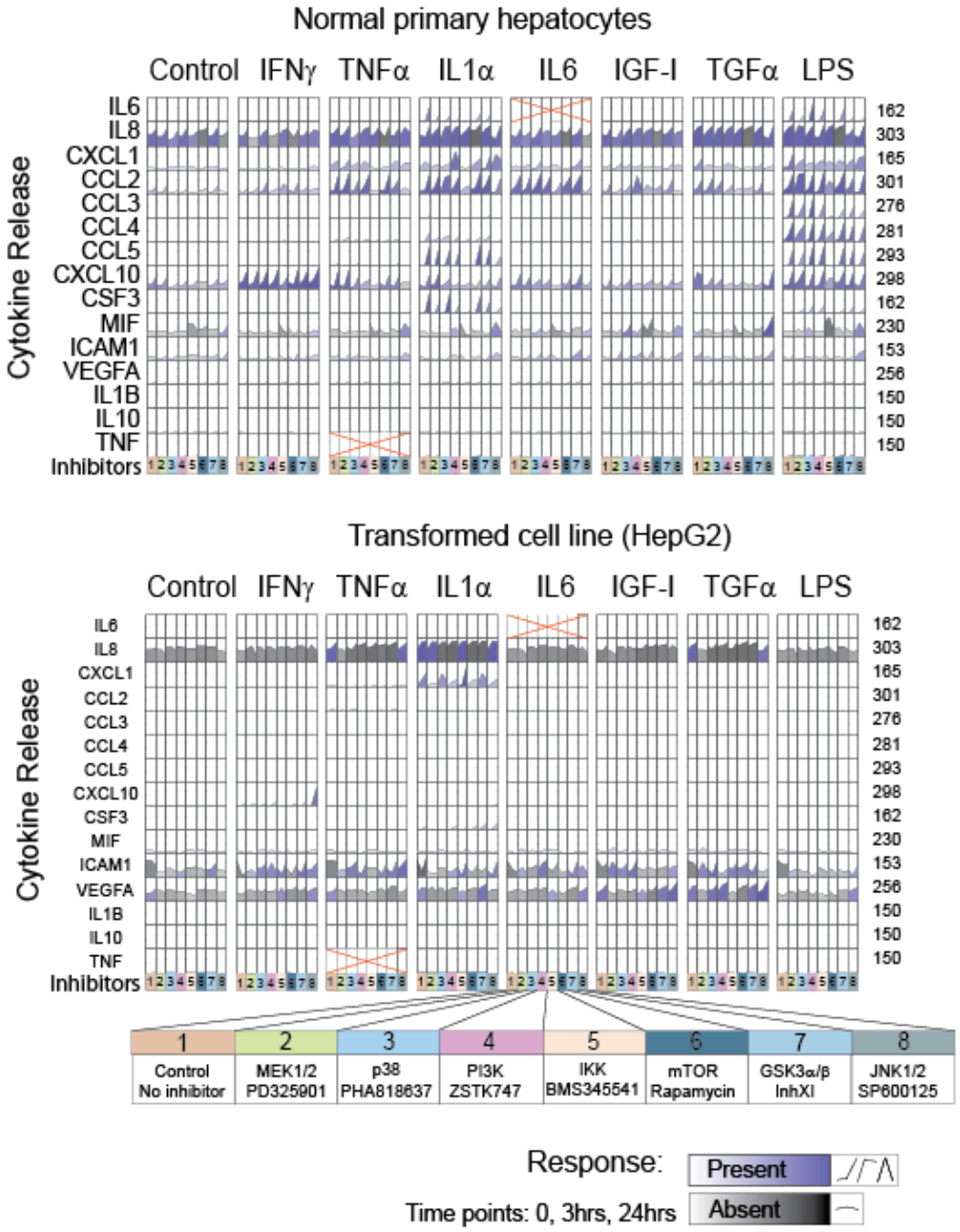
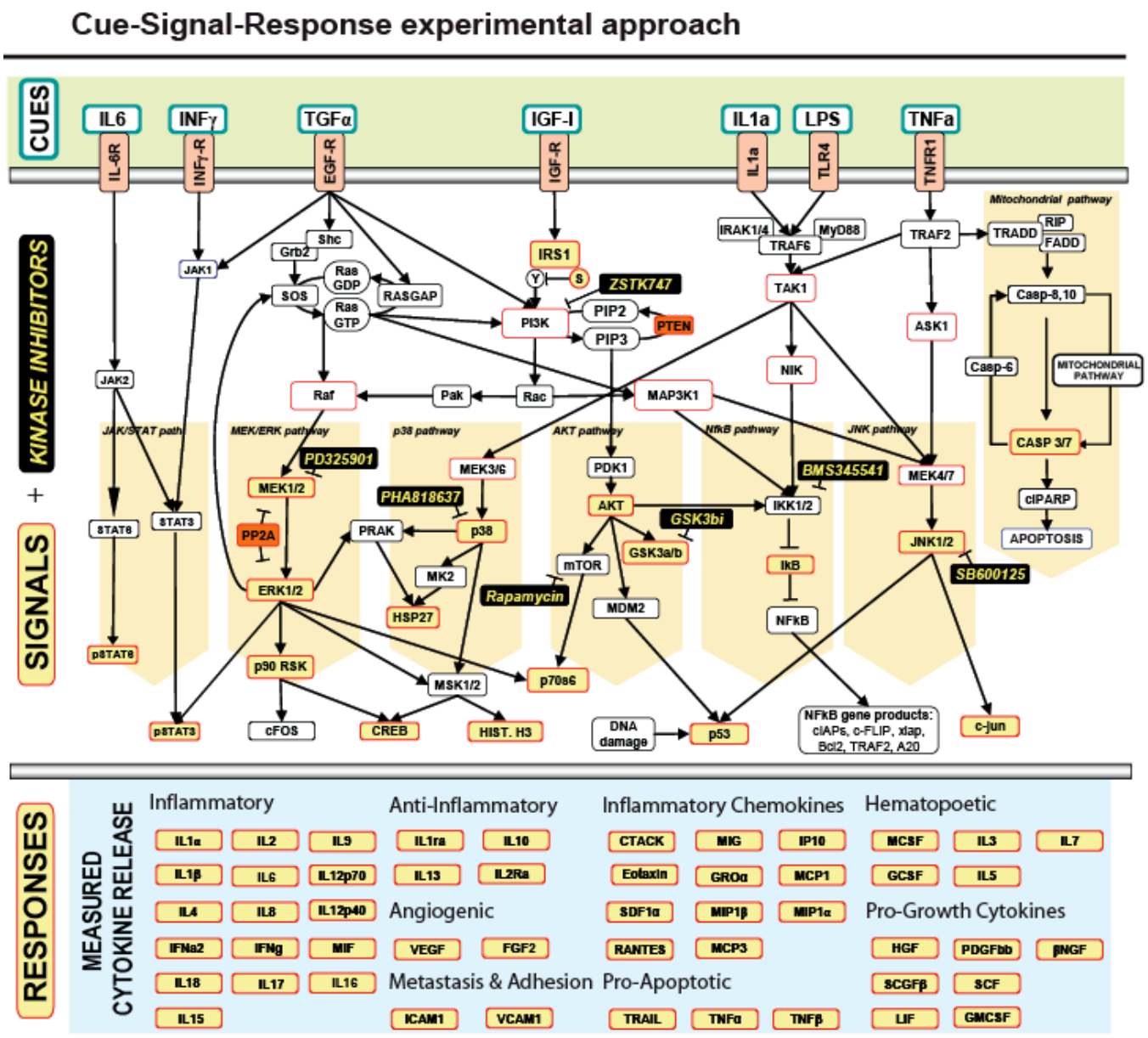
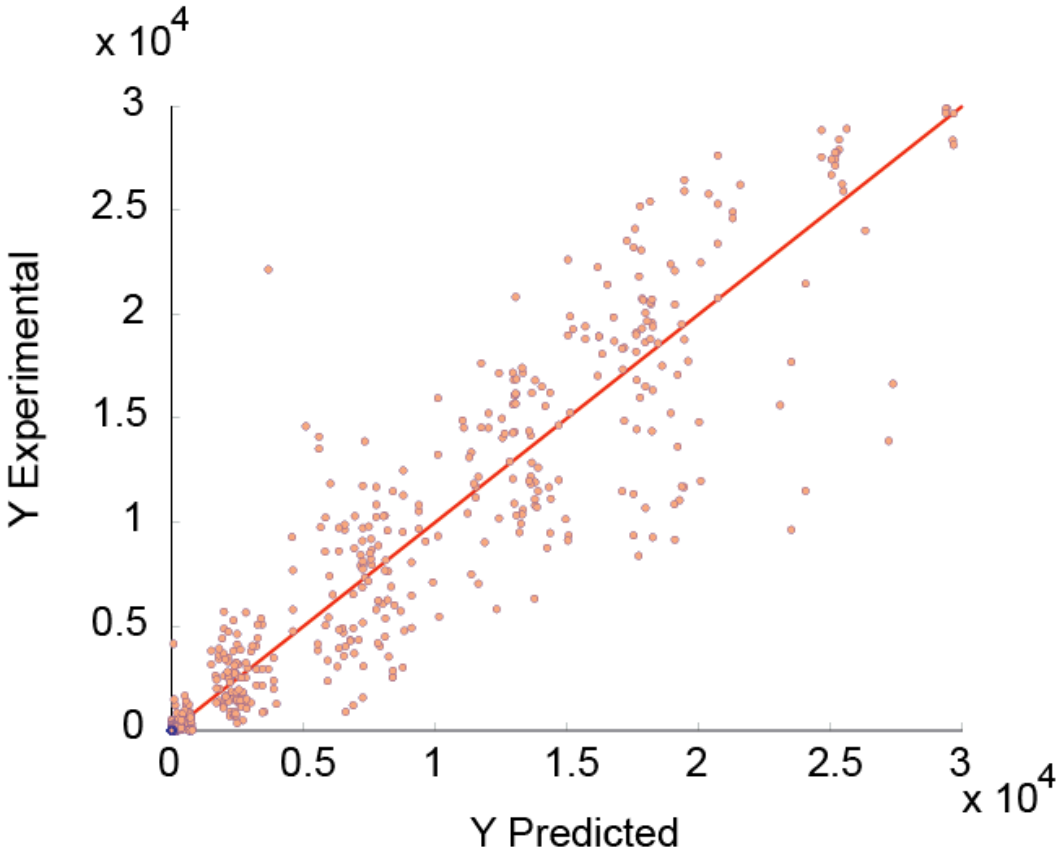
Supplemental Figure 1. Cytokine levels at 0, 3hr and 24hr after addition of ligand cues. In each column, one of seven small molecules kinase inhibitors were added, following the format of Figure 1. Red "X" denotes measurements that are not meaningful because they correspond to exogenously added ligand. Only non-zero cytokines were plotted except for IL1B, IL10, and TNF that are left for demonstrating the hepatocyte purity (see Supplementary Supplemental Figure 6b for additional information on hepatocyte purity).



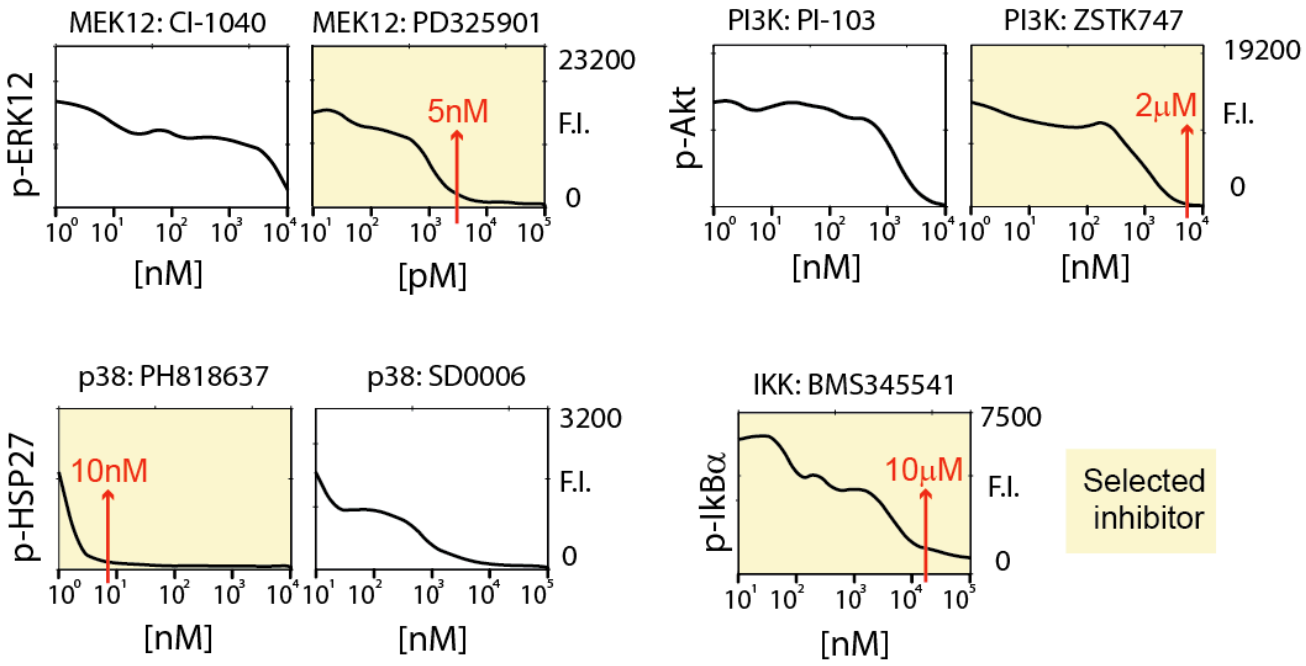
Supplemental Figure 2. Schematic of signaling pathways studied in this proposal. Pathways are redrawn from Ingenuity Systems.



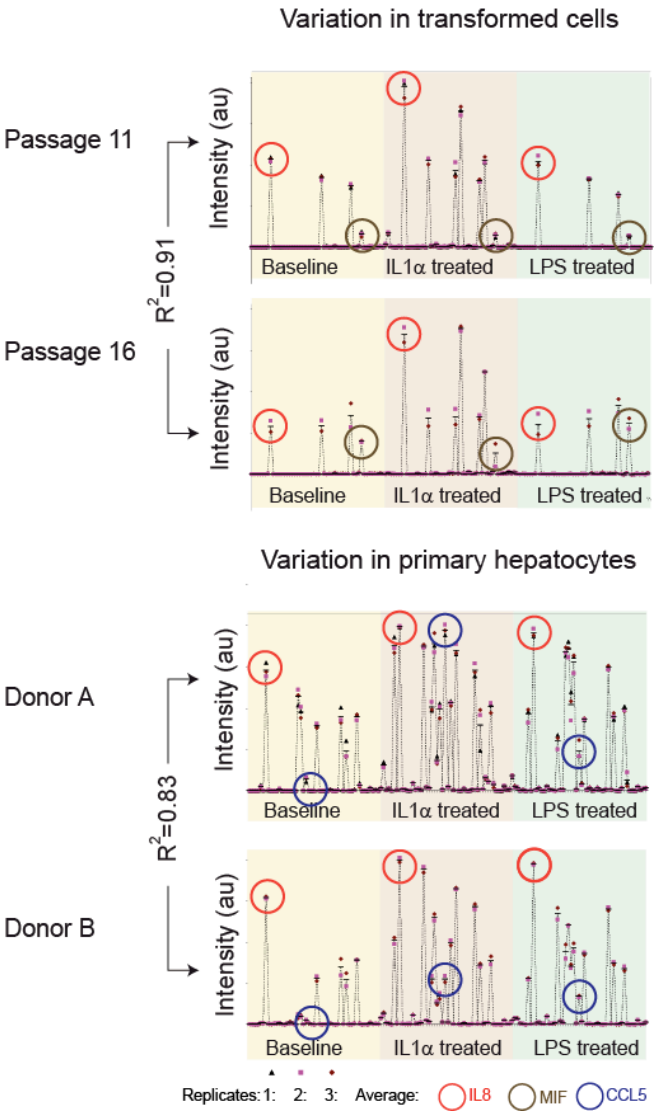
Supplemental Figure 3. Evaluation of the performance of Multiple Linear Regression modeling by cross-correlation analysis. Cross-correlation analysis was performed by omitting randomly ~15% of the original dataset (omitting 8 out of the 64 cases in each cell type), calculate the correlation coefficients from the remaining ~85% of the data, and then attempting to predict the omitted data. The procedure was repeated iteratively 100 times with different omitted cases each time.



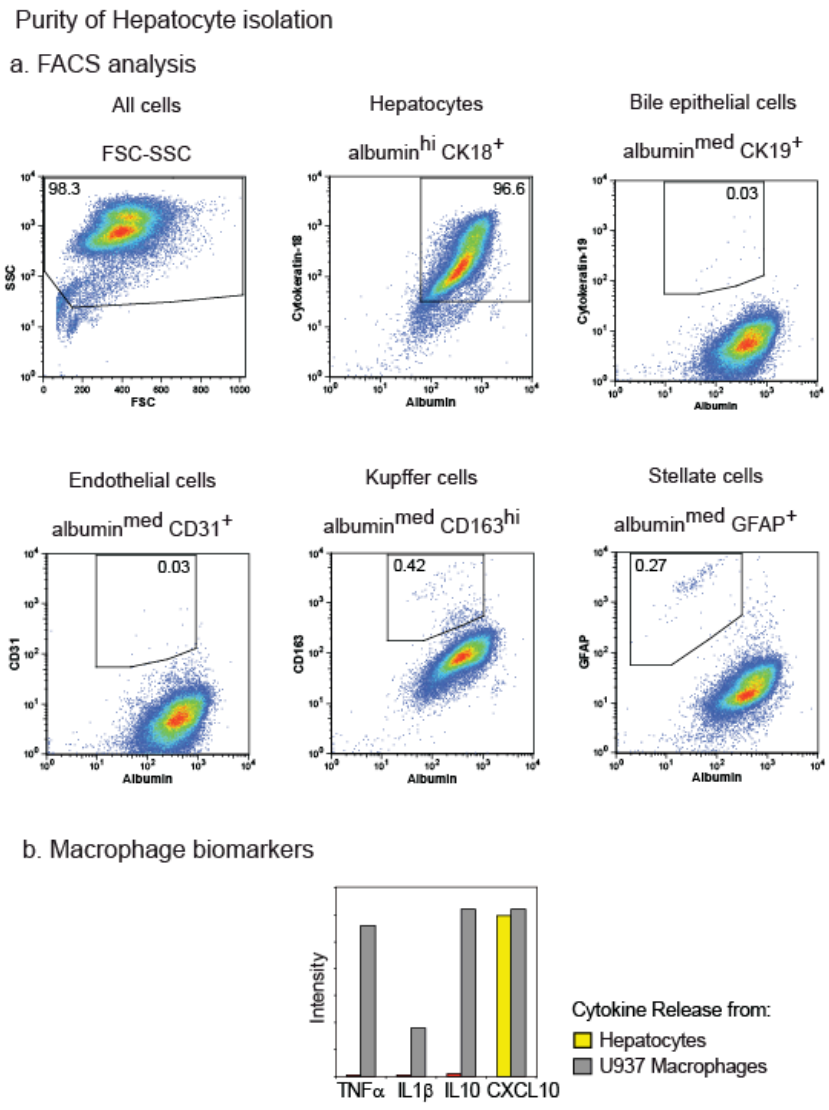
Supplemental Figure 4. Determining optimal concentrations of kinase inhibitors targeting Mek, PI3K, P38 and IKK. Experiments were performed in HepG2 cell lines; vertical axes represent fluorescence units as determined using the relevant xMAP assays.



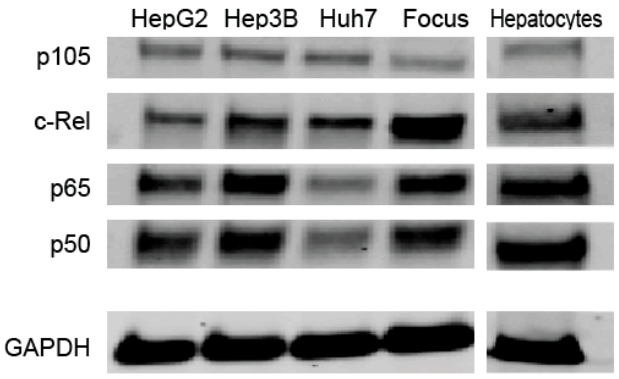
Supplemental Figure 5. Evaluation of preparation-to-preparation and donor-to-donor variability. We evaluated variation of cytokine levels in supernatants from HepG2 cells at different passage numbers and from hepatocytes from different donors. Successive cytokine measurements 24 hours after ligand addition are arrayed along the horizontal axis in three successive blocks representing baseline, IL1α and LPS-stimulation. The intensity of the signal is depicted by the height of the vertical axis. Replicate assays (replicated 1, 2, and 3) of a single biological sample are shown as small triangles, squares and circles; the typical coefficient of variation for such repeat measurements was 0.08. Data from passage 11 (upper panel) and passage 16 (lower panel) HepG2 cells correlated with R^2=0.91. Large open circles highlight selected cytokines that were observed to vary the most (MIF) or the least (IL8) with passage number. (**b**) Analysis similar to that in (a) but for hepatocytes from two human donors. Large circles highlight CCL5, which varied dramatically from donor to donor, and IL8, which did not. Data from two donors correlated with R^2=0.83.

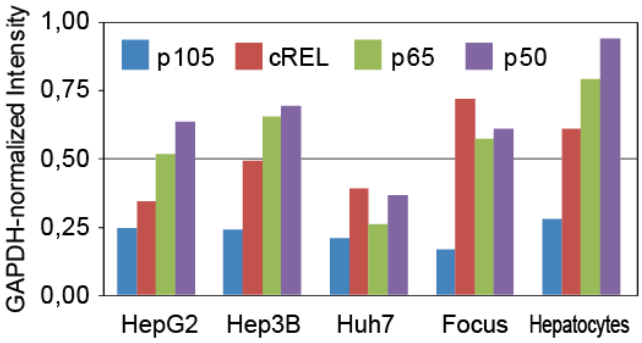


Supplemental Figure 6. Evaluation of hepatocyte purity. **(a)** To assess the purity of hepatocyte preparations we used flow cytometry with biomarkers specific for hepatocytes (albumin and cytokeratin-18), bile epithelial cells (cytokeratin-19), liver endothelial cells (CD31), Kupffer cells (CD163), and stellate cells (GFAP) and analyzed by flow cytometry. Hepatocyte isolations showed levels of contaminating cells to be very low. **(b)** To ensure that contamination with Kupffer cells was not a confounding factor in interpreting cytokine secretion results we assayed for responses characteristic of Kupffer cells: LPS and IFNγ induced secretion of TNFα , IL-1β, and IL-10. Bar graph show results of an activity-based assay for Kupffer cells in which LPS or INFγ -induced cytokine levels were measured for hepatocyte preparations and a U937 macrophage cell line served as a positive control. Induced secretion of TNFα, IL1β and IL10 typical of Kupffer cells was observed in U937 controls and its absence in hepatocyte preparations is consistent with flow cytometry data showing very few Kupffer cells to be present.

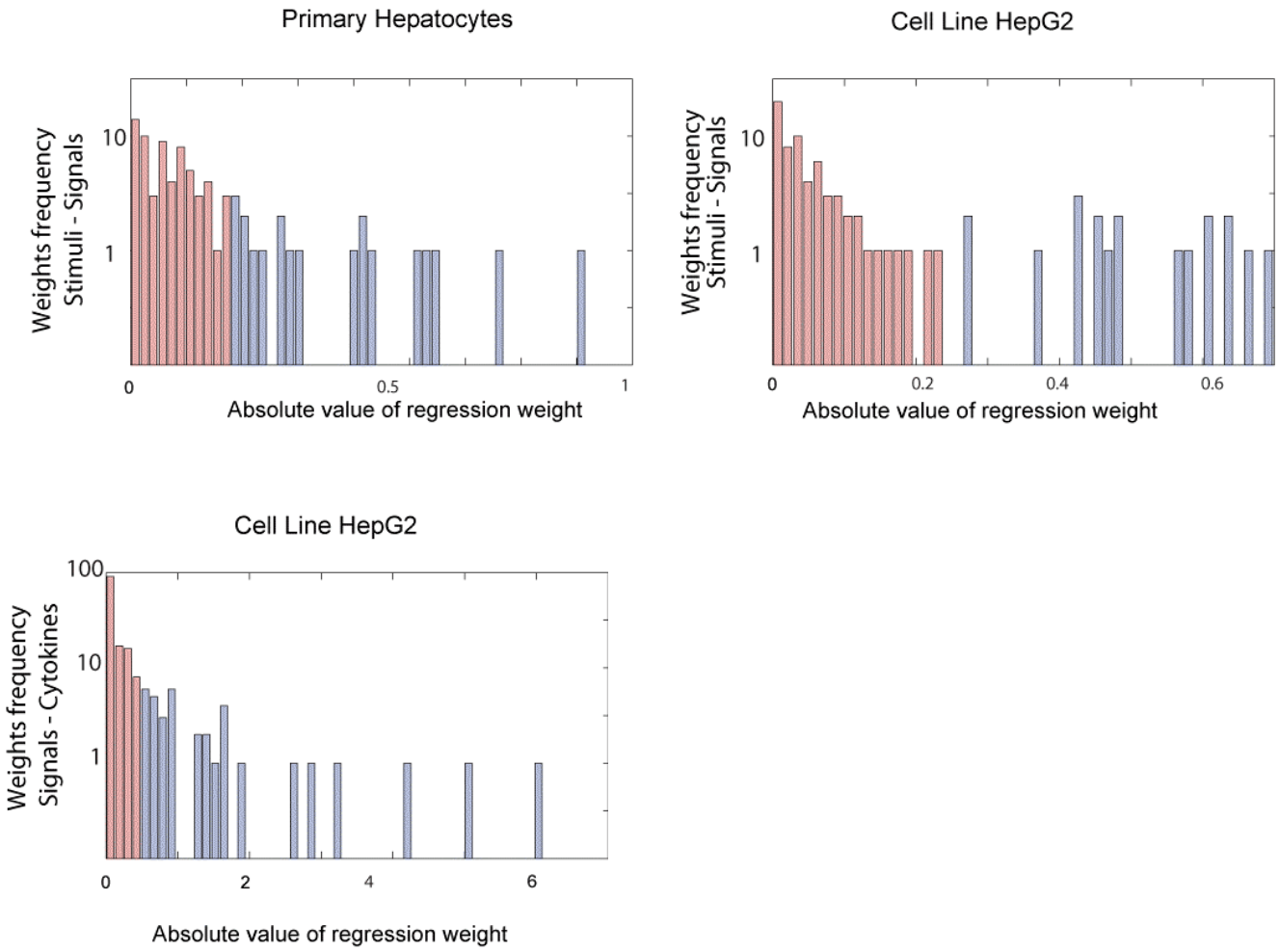


Supplemental Figure 7. Levels of NF-κB family members in hepatocytes and HCC cell lysates. Immunoblotting was used to identify NF-κB family members p105, c-Rel, p65, and p50 in four HCC cell lines and primary hepatocytes (as indicated). GAPDH serves as a loading control.





Supplemental Figure 8. Histograms of MLR weights for regression of signals against simuli (upper panels) and signals against cytokines (lower panels). The blue bars represent the 25% strongest weights, which are plotted in Figure 3c-d.



Supplemental Table 1. Subsets of data contained in this manuscript used in DREAM3 and DREAM4 competitions. http://wiki.c2b2.columbia.edu/dream/index.php/The_DREAM_Project

Cell Type	Data type	Dream 3 Project	Dream 4 Project	Current Manuscript
Primary Human	Phosphoproteins	80%	X	full set
Primary Human	Cytokine Release	80%	X	full set
HCC- HepG2	Phosphoproteins	80%	30%	full set
HCC- HepG2	Cytokine Release	80%	X	full set
HCC- Huh7	Cytokine Release	X	X	full set
HCC- Focus	Cytokine Release	X	X	full set
HCC- Hep3B	Cytokine Release	X	X	full set

Supplemental Table 2. Identities of signals for CSR analysis. Intracellular signals assayed using a Luminex 200 system from 50µl of whole cell extract prepared from a single well of a 96 well plate Protocols were as described by the bead manufacturer BioRad (Hercules, CA).

A: xMAP Assays
p-IRS-1 (Ser636/Ser639)
p-Akt (Ser473)
p-MEK1 (Ser217/Ser221)
p-ERK1/2 (Thr202/Tyr204, Thr185/Tyr187)
p-p90RSK (Thr359/Ser363)
p-CREB (Ser133)
p-p70 S6 kinase (Thr421/Ser424)
p-p38 MAPK (Thr180/Tyr182)
p-HSP27 (Ser78)
p-IκB-α (Ser32/Ser36)
p-JNK (Thr183/Tyr185)
p-c-Jun (Ser63)
p-p53 (Ser15)
p-GSK-3α/β (Ser21/Ser9)
p-Histone H3 (Ser10)
p-STAT3 (Tyr705)
p-STAT6 (Tyr641)

Supplemental Table 3. Cytokines assayed using xMAP assays. 50 cytokines were measured using a Luminex 200 system from 100 μl of supernatant from a single well of a 96 well plate following protocols provided by the bead manufacturer (Bio-Rad, Hercules CA).

Cytokine xMAP assays			
IL1A	interleukin-1α	CXCL1	chemokine (C-X-C motif) ligand 1
IL1RA	interleukin-1 receptor antagonist	CCL2	chemokine (C-C motif) ligand 2
IL1B	interleukin-1β	CCL3	chemokine (C-C motif) ligand 3
IL1-10,13,15-18	interleukin-2 to 10, 13, and 15 to 18	CCL4	chemokine (C-C motif) ligand 4
IL2RA	interleukin-2 receptor,α	CCL5	chemokine (C-C motif) ligand 5
IL12A	interleukin-12 p70 heterodimer	CCL7	chemokine (C-C motif) ligand 7
IL12B	interleukin-12B p40	CXCL9	chemokine (C-X-C motif) ligand 9
IFNA2	interferon-α2	CXCL10	chemokine (C-X-C motif) ligand 10
IFNG	interferon-γ	CCL11	chemokine (C-C motif) ligand 11
MIF	macrophage migration inhibitory factor	CXCL12	chemokine (C-X-C motif) ligand 12
ICAM1	intercellular adhesion molecule-1 (CD54)	CCL27	chemokine (C-C motif) ligand 27
VCAM1	vascular cell adhesion molecule-1	TRAIL	tumor necrosis factor, member 10
VEGFA	vascular endothelial growth factor A	TNFα	tumor necrosis factor, member 2
FGF2	fibroblast growth factor 2 (basic)	TNFβ	lymphotoxin alpha, member 1
CSF1	colony stimulating factor 1	CLEC11A	C-type lectin domain family 11, member A
CSF3	colony stimulating factor 3	KITLG	KIT ligand
HGF	hepatocyte growth factor	LIF	leukemia inhibitory factor
PDGFB	platelet-derived growth factor β	CSF2	colony stimulating factor 2
NGF	nerve growth factor (β)		

Supplemental Table 4. Expression levels of TLR receptors and downstream proteins in hepatocytes vs HCC cell. PCR Arrays by SABiosciences were used as instructed by the vendor. Green background denotes overexpression in primary hepatocytes whereas red background denotes overexpression in HCC cells. The proteins have been grouped according to their function and ranked from "highly expressed in hepatocytes" to "highly expressed in HCC cells". The first 4 data rows present gene expression levels (number of cell cycle where the gene expression level is detectable: CT-cycle threshold), whereas the next 4 rows (with red/green color in background) are difference of cell cycles between the 4 HCC cell types and hepatocytes normalized to the Actin Beta housekeeping gene (ΔΔCT). As a general guideline, 1 unit corresponds to what corresponds to the *log2* fold-difference in mRNA levels, The "Average" row contains the average normalized gene expression levels between hepatocytes and HCC cells. Expression level of TLR in all HCC cell lines are significantly lower when compared to hepatocytes, but differences in RNA levels do not necessarily correlate with changes in protein levels (de Sousa Abreu et al., *Mol. Biosystems*, 5(12):1512-26, 2009).

	ALL CELL TYPES					HCC vs. HEPATOCYTES						
	Hepatocytes	HepG2	HUH7	FOCUS	Hep3B	HepG2	HUH7	FOCUS	Hep3B		Average	
	Expression levels [cycle number]					Normalized gene expression levels [HCC-Hepatocytes]						
RECEPTORS												
TLR2	25,3	30,2	32,9	36,6	21,5	**4,8**	**7,7**	**10,6**	**7,9**		7,75	Toll-like receptor 2
TLR3	24,5	31,2	31,5	29,8	21,6	**6,6**	**7,2**	**4,1**	**8,9**		6,68	Toll-like receptor 3
TLR1	25,1	31,6	32,7	31,7	19,5	**6,4**	**7,8**	**5,2**	**5,2**		6,13	Toll-like receptor 1
TLR4	26,3	31,0	32,3	32,0	21,5	**4,7**	**6,2**	**4,4**	**7,0**		5,56	Toll-like receptor 4
TLR8	29,3	32,0	31,4	35,4	22,6	**2,7**	**2,2**	**5,2**	**5,6**		3,91	Toll-like receptor 8
TLR5	28,8	31,6	30,6	34,9	21,0	**2,9**	**2,0**	**5,3**	**3,8**		3,48	Toll-like receptor 5
TLR10	30,4	32,5	32,5	34,8	21,1	**2,0**	**2,2**	**3,4**	**2,3**		2,46	Toll-like receptor 10
CD180	27,7	30,3	30,0	27,5	21,1	**2,6**	**2,4**	**-1,1**	**4,9**		2,19	CD180 molecule
TLR7	31,8	33,2	31,6	34,8	23,3	**1,5**	**0,0**	**1,6**	**4,2**		1,81	Toll-like receptor 7
TLR9	29,7	30,4	30,7	32,8	20,4	**0,8**	**1,4**	**2,4**	**2,1**		1,65	Toll-like receptor 9
TLR6	28,2	28,9	30,3	26,7	19,7	**0,8**	**2,4**	**-2,3**	**2,5**		0,84	Toll-like receptor 6
TNFRSF1A	22,7	23,2	23,6	22,1	15,2	**0,4**	**1,0**	**-2,0**	**1,0**		0,11	Tumor necrosis factor receptor superfamily, member 1A
NR2C2	26,0	24,2	24,2	25,8	16,6	**-1,9**	**-1,7**	**-1,7**	**-0,2**		-1,36	Nuclear receptor subfamily 2, group C, member 2
EXTRACELLULAR ADAPTORS												
CLEC4E	26,3	31,6	31,6	34,8	21,6	**5,5**	**5,7**	**7,3**	**7,4**		6,46	C-type lectin domain family 4, member E
CD14	21,8	26,0	26,2	33,0	18,3	**4,2**	**4,5**	**9,8**	**6,6**		6,26	CD14 molecule
CD86	27,1	30,8	31,0	32,5	21,1	**3,8**	**4,2**	**4,7**	**5,6**		4,55	CD86 molecule
LY86	29,0	30,3	31,1	34,9	20,9	**1,2**	**2,3**	**4,8**	**3,4**		2,90	Lymphocyte antigen 86
CD80	28,2	29,5	30,6	30,1	20,4	**1,3**	**2,6**	**0,7**	**3,5**		2,03	CD80 molecule
SIGIRR	26,4	27,1	30,5	29,9	17,2	**0,7**	**4,2**	**2,0**	**0,4**		1,81	Single immunoglobulin and toll-interleukin 1 receptor (TIR) domain
LY96	28,5	27,3	31,9	27,1	21,5	-	**3,5**	**-2,6**	**4,7**		1,09	Lymphocyte antigen 96

						1,3						
INTRACELLULAR ADAPTORS												
TICAM2	24,5	27,6	26,1	26,5	18,3	**3,1**	**1,7**	**0,6**	**4,0**		2,33	Toll-like receptor adaptor molecule 2
TICAM1	22,3	24,9	24,5	24,2	15,3	**2,5**	**2,4**	**0,4**	**1,6**		1,71	Toll-like receptor adaptor molecule 1
TIRAP	24,9	26,3	26,0	27,5	17,7	**1,3**	**1,2**	**1,3**	**2,7**		1,61	Toll-interleukin 1 receptor (TIR) domain containing adaptor protein
TRAF6	24,0	25,0	25,1	26,4	16,9	**1,1**	**1,4**	**1,1**	**2,4**		1,48	TNF receptor-associated factor 6
MYD88	22,6	22,7	23,4	25,3	15,9	**0,3**	**1,2**	**1,5**	**2,5**		1,34	*Myeloid differentiation primary response gene (88)*
TOLLIP	25,4	25,5	26,2	27,4	17,0	**0,1**	**1,0**	**0,6**	**1,1**		0,66	Toll interacting protein
ECSIT	23,8	22,8	22,8	23,7	16,2	**-0,8**	**-0,6**	**-0,9**	**1,7**		-0,15	ECSIT homolog (Drosophila)
PELI1	23,2	22,7	22,7	24,2	13,4	**-0,4**	**-0,2**	**-0,2**	**-2,0**		-0,69	Pellino homolog 1 (Drosophila)
CYTOKINES												
IL8	20,1	26,3	26,3	28,4	16,7	**6,1**	**6,4**	**7,2**	**5,9**		6,39	Interleukin 8
CCL2	24,4	30,3	30,8	27,3	20,9	**6,1**	**6,7**	**2,0**	**8,1**		5,70	Chemokine (C-C motif) ligand 2
CXCL10	27,0	31,6	31,0	34,2	19,9	**4,8**	**4,3**	**6,3**	**4,0**		4,84	Chemokine (C-X-C motif) ligand 10
IL1B	25,1	27,8	29,5	24,4	20,7	**2,8**	**4,7**	**-1,9**	**7,0**		3,11	Interleukin 1, beta
IL10	30,7	32,5	33,0	36,4	21,9	**1,8**	**2,4**	**4,8**	**3,1**		3,00	Interleukin 10
IFNG	31,4	32,2	33,1	36,4	22,3	**0,8**	**1,9**	**4,4**	**3,1**		2,56	Interferon, gamma
IFNA1	29,8	31,3	32,0	33,8	20,9	**1,7**	**2,6**	**2,8**	**2,9**		2,49	Interferon, alpha 1
IL2	31,6	32,7	32,3	37,2	22,6	**1,1**	**0,9**	**4,3**	**3,3**		2,40	Interleukin 2
CSF2	31,1	32,8	33,4	32,7	22,7	**1,6**	**2,5**	**0,2**	**3,9**		2,03	Colony stimulating factor 2 (granulocyte-macrophage)
LTA	30,8	31,5	32,2	32,9	21,6	**0,9**	**1,7**	**1,4**	**2,7**		1,66	Lymphotoxin alpha (TNF superfamily, member 1)
IFNB1	30,4	31,4	32,2	31,7	21,6	**1,0**	**1,9**	**0,0**	**3,0**		1,46	Interferon, beta 1, fibroblast
TNF	30,5	31,0	31,5	33,8	21,0	**0,4**	**1,2**	**1,9**	**1,9**		1,34	Tumor necrosis factor (TNF superfamily, member 2)
CSF3	31,6	30,7	31,9	30,1	21,2	**-0,9**	**0,5**	**-2,3**	**1,2**		-0,38	Colony stimulating factor 3 (granulocyte)
IL6	30,3	31,1	31,1	25,0	20,6	**0,7**	**0,9**	**-6,6**	**1,5**		-0,85	Interleukin 6 (interferon, beta 2)
IL12A	29,3	28,5	28,1	27,0	19,3	**-0,8**	**-0,9**	**-3,6**	**0,7**		-1,16	Interleukin 12A
IL1A	28,9	27,0	29,0	23,1	19,3	**-2,0**	**0,3**	**-7,0**	**1,0**		-1,93	Interleukin 1, alpha
INTRACELLULAR SIGNALS												
HSPA1A	17,4	23,1	23,7	26,4	18,0	**5,7**	**6,5**	**7,7**	**10,7**		7,65	Heat shock 70kDa protein 1A
FOS	22,1	25,9	26,5	23,8	18,0	**3,9**	**4,6**	**0,5**	**5,9**		3,71	V-fos FBJ murine osteosarcoma viral oncogene homolog
JUN	18,8	22,0	22,7	21,0	14,2	**3,2**	**4,2**	**1,2**	**3,5**		3,01	Jun oncogene
MAPK8	23,6	24,2	24,9	27,0	18,1	**0,6**	**1,6**	**2,1**	**4,7**		2,24	Mitogen-activated protein kinase 8
PTGS2	30,4	31,9	32,5	33,9	20,2	**1,5**	**2,3**	**2,9**	**0,9**		1,91	(prostaglandin G/H synthase and cyclooxygenase)
SARM1	26,2	27,8	29,2	27,7	17,7	**1,7**	**3,3**	**0,9**	**1,5**		1,85	Sterile alpha and TIR motif containing 1
PPARA	23,0	22,4	24,2	25,9	17,3	**-0,3**	**1,6**	**1,8**	**4,2**		1,81	Peroxisome proliferative activated receptor, alpha
MAP2K3	22,2	22,6	23,1	24,8	16,5	**0,5**	**1,2**	**1,5**	**3,8**		1,74	Mitogen-activated protein kinase kinase 3
RIPK2	22,0	23,5	23,8	23,9	15,8	**1,4**	**2,0**	**0,6**	**2,6**		1,64	Receptor-interacting serine-threonine kinase 2
BTK	30,3	32,5	31,4	28,8	22,0	**2,3**	**1,3**	**-2,8**	**3,8**		1,13	Bruton agammaglobulinemia tyrosine kinase
EIF2AK2	23,1	22,7	24,8	23,3	16,7	**-0,2**	**2,0**	**-0,7**	**3,1**		1,03	Eukaryotic translation initiation factor 2-alpha kinase 2
HSPD1	17,7	17,2	18,5	19,9	12,9	**-0,5**	**1,0**	**0,8**	**2,7**		1,01	Heat shock 60kDa protein 1 (chaperonin)
MAP4K4	22,9	20,8	22,9	26,2	17,0	**-2,1**	**0,3**	**2,0**	**3,6**		0,95	Mitogen-activated protein kinase kinase kinase kinase 4
MAPK8IP3	23,9	23,4	24,3	24,5	17,0	**-0,4**	**0,8**	**-0,2**	**2,7**		0,71	Mitogen-activated protein kinase 8 interacting protein 3
MAP2K4	24,3	24,0	24,5	26,1	16,5	**-0,3**	**0,4**	**0,7**	**1,5**		0,58	Mitogen-activated protein kinase kinase 4

CASP8	27,0	26,4	26,9	27,9	18,3	**-0,7**	**0,0**	**0,2**	**1,4**		0,21	Caspase 8, apoptosis-related cysteine peptidase
FADD	22,7	22,9	21,9	23,4	14,6	**0,3**	**-0,5**	**0,0**	**0,3**		0,04	Fas (TNFRSF6)-associated via death domain
MAP3K7IP1	24,3	23,6	23,8	25,5	16,1	**-0,7**	**-0,3**	**-0,1**	**0,9**		-0,02	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1
PRKRA	28,4	26,6	27,1	29,5	19,0	**-1,6**	**-0,8**	**0,0**	**1,3**		-0,29	Protein kinase, interferon-inducible double stranded RNA dependent activator
ELK1	28,3	28,5	27,2	27,5	18,9	**0,1**	**-1,0**	**-1,9**	**1,0**		-0,44	ELK1, member of ETS oncogene family
HMGB1	27,1	26,5	24,2	29,7	17,3	**-0,6**	**-2,7**	**1,5**	**-0,1**		-0,46	High-mobility group box 1
UBE2V1	28,4	26,6	27,1	28,2	19,1	**-1,9**	**-1,2**	**-1,2**	**1,2**		-0,75	Ubiquitin-conjugating enzyme E2 variant 1
UBE2N	23,3	21,8	22,2	23,6	14,9	**-1,6**	**-1,0**	**-0,9**	**0,1**		-0,85	Ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)
MAP3K1	24,7	22,5	24,1	24,5	16,1	**-2,3**	**-0,4**	**-1,2**	**0,4**		-0,89	Mitogen-activated protein kinase kinase kinase 1
HRAS	26,2	24,1	25,8	25,6	16,4	**-1,9**	**0,0**	**-1,7**	**-0,3**		-0,97	V-Ha-ras Harvey rat sarcoma viral oncogene homolog
MAP3K7	26,0	24,6	24,4	26,1	15,8	**-1,5**	**-1,5**	**-1,4**	**-1,4**		-1,43	Mitogen-activated protein kinase kinase kinase 7
NFkB RELATED SIGNALS												
IRF1	23,3	26,3	28,3	24,7	18,1	**3,1**	**5,2**	**0,1**	**4,9**		3,30	Interferon regulatory factor 1
NFKBIA	24,2	24,0	26,1	28,2	18,4	**0,0**	**2,3**	**3,1**	**4,7**		2,53	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
REL	24,9	25,6	26,2	28,6	18,5	**0,9**	**1,6**	**3,0**	**4,0**		2,35	V-rel reticuloendotheliosis viral oncogene homolog (avian)
NFKB1	24,8	25,3	26,2	27,6	18,2	**0,4**	**1,6**	**1,5**	**3,5**		1,74	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
IRAK2	22,3	23,0	24,0	25,0	15,8	**0,8**	**2,0**	**1,5**	**2,4**		1,65	Interleukin-1 receptor-associated kinase 2
RELA	21,2	21,9	22,6	23,0	14,6	**0,7**	**1,6**	**0,6**	**1,8**		1,16	V-rel reticuloendotheliosis viral oncogene homolog A
NFKB2	27,1	27,1	27,1	28,1	18,6	**0,1**	**0,4**	**0,5**	**2,0**		0,73	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
NFKBIL1	21,7	21,5	21,7	23,3	15,3	**-0,2**	**0,2**	**0,4**	**2,2**		0,61	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1
IRAK1	22,7	22,2	23,1	23,2	15,8	**-0,6**	**0,6**	**-0,9**	**2,0**		0,26	Interleukin-1 receptor-associated kinase 1
TBK1	26,4	26,5	25,9	26,3	18,0	**0,2**	**-0,2**	**-1,3**	**1,8**		0,11	TANK-binding kinase 1
CHUK	27,1	26,8	26,2	27,8	18,1	**-0,1**	**-0,5**	**-0,4**	**1,4**		0,11	Conserved helix-loop-helix ubiquitous kinase
IKBKB	26,3	25,9	26,7	26,5	17,6	**-0,5**	**0,5**	**-0,9**	**1,1**		0,05	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
IRF3	24,7	23,8	23,1	26,8	15,9	**-0,6**	**-1,2**	**1,1**	**0,4**		-0,06	Interferon regulatory factor 3
NFRKB	25,6	23,5	23,9	26,0	16,2	**-1,9**	**-1,3**	**-0,8**	**-0,1**		-0,99	Nuclear factor related to kappaB binding protein
HOUSE KEEPING GENES												
B2M	17,2	17,3	19,0	19,9	19,9	**2,5**	**3,5**	**1,5**	**5,0**		3,11	Beta-2-microglobulin
HPRT1	27,6	27,6	27,2	26,5	26,5	**-0,8**	**0,1**	**4,2**	**6,1**		2,41	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
RPL13A	20,9	20,9	19,8	19,3	19,3	**-1,1**	**-1,0**	**0,0**	**3,3**		0,29	Ribosomal protein L13a
ACTB	15,0	15,3	15,3	15,0	14,7	**0,0**	**0,0**	**0,0**	**0,0**		0,00	Actin, beta
GAPDH	21,0	21,0	19,9	19,3	19,2	**-1,4**	**-1,8**	**-1,7**	**0,7**		-1,03	Glyceraldehyde-3-phosphate dehydrogenase