RT² Profiler PCR Array Gene Expression Analysis Report

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Introduction

Cataloged arrays

RT² Profiler PCR Arrays are highly reliable and sensitive gene expression profiling tools for analyzing focused panels of genes insignal transduction, biological processes or disease research pathways using real-time PCR. Each cataloged RT² Profiler PCR Array contains a list of the pathway-focused genes as well as five housekeeping (reference) genes on the array. In addition, eacharray contains a panel of proprietary controls to monitor genomic DNA contamination (GDC) as well as the first strand synthesis (RTC) and real-time PCR efficiency (PPC). The qPCR Assays used in PCR Arrays are laboratory-verified and optimized to workunder standard conditions enabling a large number of genes to be assayed simultaneously. Their specificity is guaranteed when RT² SYBR Green qPCR Master Mixes are used as part of the complete PCR Array System protocol.

In this study, 96 genes were profiled on 6 samples with the PAHS-148Z.

Summary and workflow

Cataloged arrays

1. Mature RNA was isolated using an RNA extraction kit according to the manufacturer's instructions.
2. RNA quality was determined using a spectrophotometer and was reverse transcribed using a cDNA conversion kit.
3. The cDNA was used on the real-time RT² Profiler PCR Array (QIAGEN, Cat. no. PAHS-148Z) in combination with RT² SYBR® Green qPCR Mastermix (Cat. no. 330529).

C_T values were exported to an Excel file to create a table of C_T values. This table was then uploaded on to the data analysis web portal at http://www.qiagen.com/geneglobe. Samples were assigned to controls and test groups. C_T values were normalized based on a/an Manual Selection of reference genes.

The data analysis web portal calculates fold change/regulation using delta delta C_T method, in which delta C_T is calculated between gene of interest (GOI) and an average of reference genes (HKG), followed by delta-delta C_T calculations (delta C_T (Test Group)-delta C_T (Control Group)). Fold Change is then calculated using 2 ^ (-delta delta C_T) formula. The data analysis web portal also plots scatter plot, volcano plot, clustergram, and heat map.

This data analysis report was exported from the QIAGEN web portal at GeneGlobe.

Gene Table

Position	RefSeq Number	Symbol	Description
A01	NM_005163	AKT1	V-akt murine thymoma viral oncogene homolog 1
A02	NM_001639	APCS	Amyloid P component, serum
A03	NM_001165	BIRC3	Baculoviral IAP repeat containing 3
A04	NM_001725	BPI	Bactericidal/permeability-increasing protein
A05	NM_004345	CAMP	Cathelicidin antimicrobial peptide
A06	NM_032587	CARD6	Caspase recruitment domain family, member 6
A07	NM_052813	CARD9	Caspase recruitment domain family, member 9
A08	NM_033292	CASP1	Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
A09	NM_001228	CASP8	Caspase 8, apoptosis-related cysteine peptidase
A10	NM_002983	CCL3	Chemokine (C-C motif) ligand 3
A11	NM_002985	CCL5	Chemokine (C-C motif) ligand 5
A12	NM_000591	CD14	CD14 molecule
B01	NM_001278	CHUK	Conserved helix-loop-helix ubiquitous kinase
B02	NM_000567	CRP	C-reactive protein, pentraxin-related
B03	NM_001911	CTSG	Cathepsin G
B04	NM_001511	CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
B05	NM_002089	CXCL2	Chemokine (C-X-C motif) ligand 2
B06	NM_004406	DMBT1	Deleted in malignant brain tumors 1
B07	NM_003824	FADD	Fas (TNFRSF6)-associated via death domain
B08	NM_001017963	HSP90AA1	Heat shock protein 90kDa alpha (cytosolic), class A member 1
B09	NM_024013	IFNA1	Interferon, alpha 1
B10	NM_002176	IFNB1	Interferon, beta 1, fibroblast
B11	NM_001556	IKBKB	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
B12	NM_000882	IL12A	Interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
C01	NM_002187	IL12B	Interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)
C02	NM_001562	IL18	Interleukin 18 (interferon-gamma-inducing factor)
C03	NM_000576	IL1B	Interleukin 1, beta
C04	NM_000600	IL6	Interleukin 6 (interferon, beta 2)
C05	NM_000584	CXCL8	Interleukin 8
C06	NM_001569	IRAK1	Interleukin-1 receptor-associated kinase 1
C07	NM_007199	IRAK3	Interleukin-1 receptor-associated kinase 3
C08	NM_001098629	IRF5	Interferon regulatory factor 5
C09	NM_001572	IRF7	Interferon regulatory factor 7
C10	NM_002228	JUN	Jun proto-oncogene

Position	RefSeq Number	Symbol	Description
C11	NM_004139	LBP	Lipopolysaccharide binding protein
C12	NM_005564	LCN2	Lipocalin 2
D01	NM_002343	LTF	Lactotransferrin
D02	NM_015364	LY96	Lymphocyte antigen 96
D03	NM_000239	LYZ	Lysozyme
D04	NM_002755	MAP2K1	Mitogen-activated protein kinase kinase 1
D05	NM_002756	MAP2K3	Mitogen-activated protein kinase kinase 3
D06	NM_003010	MAP2K4	Mitogen-activated protein kinase kinase 4
D07	NM_003188	MAP3K7	Mitogen-activated protein kinase kinase kinase 7
D08	NM_002745	MAPK1	Mitogen-activated protein kinase 1
D09	NM_001315	MAPK14	Mitogen-activated protein kinase 14
D10	NM_002746	MAPK3	Mitogen-activated protein kinase 3
D11	NM_002750	MAPK8	Mitogen-activated protein kinase 8
D12	NM_000243	MEFV	Mediterranean fever
E01	NM_000250	MPO	Myeloperoxidase
E02	NM_002468	MYD88	Myeloid differentiation primary response gene (88)
E03	NM_004536	NAIP	NLR family, apoptosis inhibitory protein
E04	NM_003998	NFKB1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
E05	NM_020529	NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
E06	NM_021209	NLRC4	NLR family, CARD domain containing 4
E07	NM_033004	NLRP1	NLR family, pyrin domain containing 1
E08	NM_183395	NLRP3	NLR family, pyrin domain containing 3
E09	NM_006092	NOD1	Nucleotide-binding oligomerization domain containing 1
E10	NM_022162	NOD2	Nucleotide-binding oligomerization domain containing 2
E11	NM_006218	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
E12	NM_002777	PRTN3	Proteinase 3
F01	NM_003978	PSTPIP1	Proline-serine-threonine phosphatase interacting protein 1
F02	NM_013258	PYCARD	PYD and CARD domain containing
F03	NM_006908	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
F04	NM_021975	RELA	V-rel reticuloendotheliosis viral oncogene homolog A (avian)
F05	NM_003804	RIPK1	Receptor (TNFRSF)-interacting serine-threonine kinase 1
F06	NM_003821	RIPK2	Receptor-interacting serine-threonine kinase 2
F07	NM_000578	SLC11A1	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
F08	NM_003064	SLPI	Secretory leukocyte peptidase inhibitor
F09	NM_006704	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
F10	NM_182919	TICAM1	Toll-like receptor adaptor molecule 1
F11	NM_021649	TICAM2	Toll-like receptor adaptor molecule 2

Position	RefSeq Number	Symbol	Description
F12	NM_001039661	TIRAP	Toll-interleukin 1 receptor (TIR) domain containing adaptor protein
G01	NM_003263	TLR1	Toll-like receptor 1
G02	NM_003264	TLR2	Toll-like receptor 2
G03	NM_138554	TLR4	Toll-like receptor 4
G04	NM_003268	TLR5	Toll-like receptor 5
G05	NM_006068	TLR6	Toll-like receptor 6
G06	NM_017442	TLR9	Toll-like receptor 9
G07	NM_000594	TNF	Tumor necrosis factor
G08	NM_001065	TNFRSF1A	Tumor necrosis factor receptor superfamily, member 1A
G09	NM_019009	TOLLIP	Toll interacting protein
G10	NM_004620	TRAF6	TNF receptor-associated factor 6
G11	NM_001167	XIAP	X-linked inhibitor of apoptosis
G12	NM_030776	ZBP1	Z-DNA binding protein 1
H01	NM_001101	ACTB	Actin, beta
H02	NM_004048	B2M	Beta-2-microglobulin
H03	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H04	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H05	NM_001002	RPLP0	Ribosomal protein, large, P0
H06	SA_00105	HGDC	Human Genomic DNA Contamination
H07	SA_00104	RTC	Reverse Transcription Control
H08	SA_00104	RTC	Reverse Transcription Control
H09	SA_00104	RTC	Reverse Transcription Control
H10	SA_00103	PPC	Positive PCR Control
H11	SA_00103	PPC	Positive PCR Control
H12	SA_00103	PPC	Positive PCR Control

Data analysis setup

Sample management

Sample ID	Sample Name	Group
1	IC M1 UPEC	Group 1
2	IC M2 UPEC	Group 1
3	IC M4 UPEC	Group 1
4	IC M1 Saline	Control Group
5	IC M2 Saline	Control Group
6	IC M3 Saline	Control Group

Pre-amplification

A pre-amplification using the appropriate species- and pathway-specific RT^2 PreAMP Primer Mix was performed and the appropriate corrections were made during the data analysis procedure.

Lower limit of detection

The C_T cut-off was set to 35

Data quality control (QC)

Quality checks performed and results

Test Performed	**Test Result**
1. PCR Array Reproducibility	All Samples Passed
2. Reverse Transcription Efficiency	All Samples Passed
3. Genomic DNA Contamination	All Samples Passed

Normalization analysis

Manual Selection

Groups	Samples	ACTB	B2M	GAPDH	HPRT1	RPLP0	Arithmetic Mean	Average Arithmetic Mean
Control Group	IC M1 Saline	15.55	18.53	15.49	20.70	15.39	17.13	16.29
Control Group	IC M2 Saline	15.41	17.97	15.52	20.62	15.33	16.97	
Control Group	IC M3 Saline	13.50	15.60	12.94	18.47	13.30	14.76	
Group 1	IC M1 UPEC	27.32	28.96	26.41	26.78	25.74	27.04	24.44
Group 1	IC M2 UPEC	25.05	28.20	24.98	27.78	24.42	26.09	
Group 1	IC M4 UPEC	19.90	24.01	18.49	20.95	17.61	20.19	

In the Manual Selection method, the arithmetic or geometric means of the data from the assays for the housekeeping / reference genes listed in the table were used to normalize the raw data.

Result

Fold regulation and p-value

Test Group	Control Group	Fold Regulation Threshold	p-Value Threshold
Group 1	Control Group	2	0.05

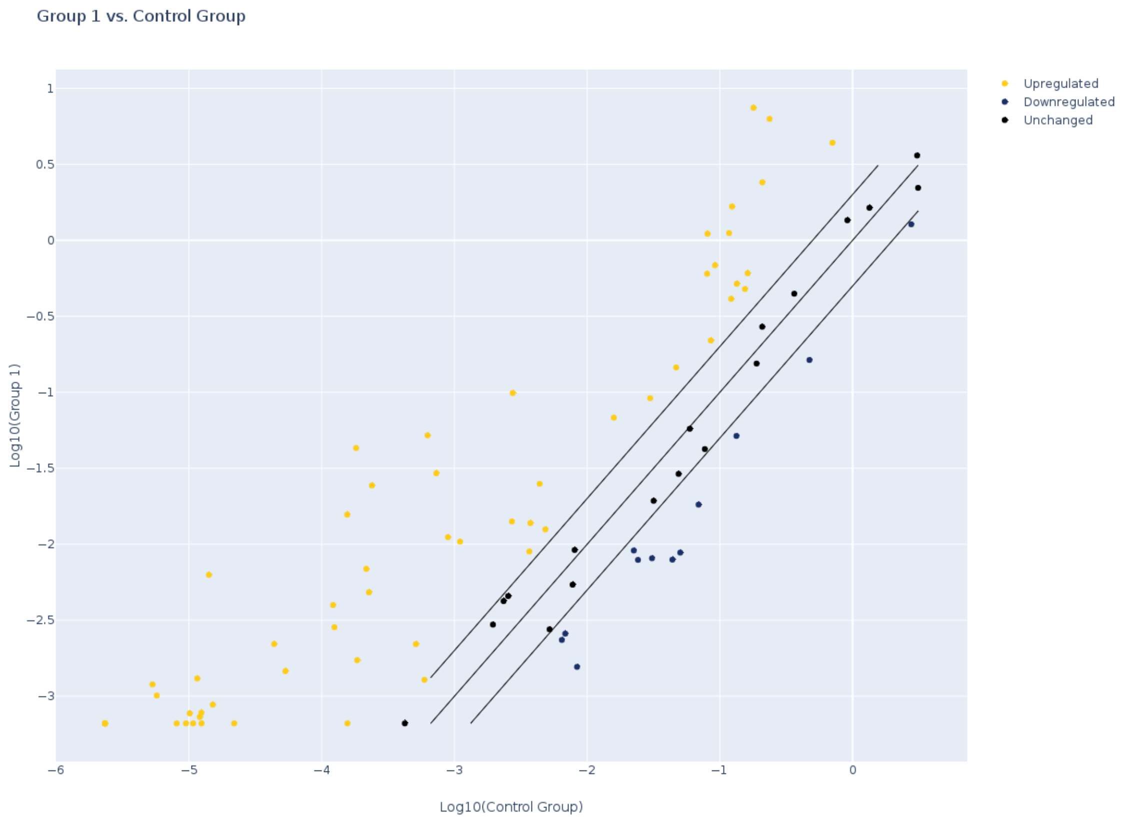
Position	Gene Symbol	Fold Regulation	p-Value	Comments
B08	HSP90AA1	13.51	0.005036	
B12	IL12A	13.68	0.005460	
C01	IL12B	50.35	0.047669	
C03	IL1B	5.70	0.007394	
D02	LY96	4.28	0.020612	
D07	MAP3K7	9.50	0.000014	
D08	MAPK1	6.21	0.000031	
D10	MAPK3	3.75	0.020362	
D11	MAPK8	3.11	0.000313	
E11	PIK3CA	2.57	0.029412	
F02	PYCARD	26.57	0.025879	
F09	SUGT1	11.52	0.000558	
G04	TLR5	22.82	0.039230	A
G09	TOLLIP	41.53	0.041028	
G11	XIAP	7.45	0.037814	
A09	CASP8	-5.71	0.011765	A
E02	MYD88	-5.38	0.011814	A
F05	RIPK1	-2.47	0.010605	A
G08	TNFRSF1A	-2.58	0.009846	
G10	TRAF6	-5.54	0.011066	A
H01	ACTB	-2.17	0.026279	
H02	B2M	-2.90	0.022013	

Fold-Change (2 ^ (-Delta Delta C_T)) is the normalized gene expression (2 ^ (- Delta C_T)) in the Test Sample divided the normalized gene expression (2 ^ (- Delta C_T)) in the Control Sample. Fold-Regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicates a positive- or an up-regulation, and the fold-regulation is equal to the fold-change. Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change.

The p values are calculated based on a Student's t-test of the replicate 2 ^ (- Delta C_T) values for each gene in the control group and treatment groups, and p values less than 0.05 are indicated in red. The p-value calculation used is based on parametric, unpaired, two-sample equal variance, two-tailed distribution – a method widely accepted in scientific literature.

Scatter Plot

Test Group	Control Group	Fold Regulation Threshold
Group 1	Control Group	2



The Scatter Plot compares the normalized expression of every gene on the PCR Array between the two selected groups by plotting them against one another to quickly visualize large gene expression changes. The center diagonal line indicates unchanged gene expression, while the outer diagonal lines indicate the selected fold regulation threshold. Genes with data points beyond the outer lines in the upper left and lower right corners are up-regulated or down-regulated, respectively, by more than the fold regulation threshold in the y-axis Group relative to the x-axis Group.

Genes Over-Expressed in Group 1 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT² qPCR Assay Catalog #
A02	APCS	82.10	B	PPH07107A
A04	BPI	284.40	C	PPH16561B
A05	CAMP	76.13	B	PPH09430A
A07	CARD9	2.58	A	PPH06127F
A08	CASP1	100.62	A	PPH00105C
A10	CCL3	101.94		PPH00566F
A11	CCL5	40.11		PPH00703B
A12	CD14	5.21	A	PPH05723A
B03	CTSG	60.62	B	PPH01358A
B04	CXCL1	225.51	B	PPH00696C
B05	CXCL2	284.40	C	PPH00552F
B06	DMBT1	444.85	B	PPH15755A
B07	FADD	284.40	C	PPH00367A
B08	HSP90AA1	13.51		PPH63391B
B10	IFNB1	284.40	C	PPH00384F
B11	IKBKB	113.41	B	PPH00780C
B12	IL12A	13.68		PPH00544B
C01	IL12B	50.35		PPH00545A
C02	IL18	53.29	B	PPH00580C
C03	IL1B	5.70		PPH00171C
C05	CXCL8	69.80	B	PPH00568A
C06	IRAK1	3.86		PPH00835A
C07	IRAK3	4.24	A	PPH06041A
C08	IRF5	2.45	A	PPH02870A
C11	LBP	12.44	A	PPH01424F
C12	LCN2	3.69	A	PPH00446E
D01	LTF	61.65	B	PPH05751A
D02	LY96	4.28		PPH06052A
D06	MAP2K4	3.39		PPH00195C
D07	MAP3K7	9.50		PPH00749C
D08	MAPK1	6.21		PPH00715B
D09	MAPK14	3.09		PPH00750B
D10	MAPK3	3.75		PPH00721F
D11	MAPK8	3.11		PPH00720B
D12	MEFV	176.56	B	PPH13601A
E01	MPO	284.40	C	PPH06082F

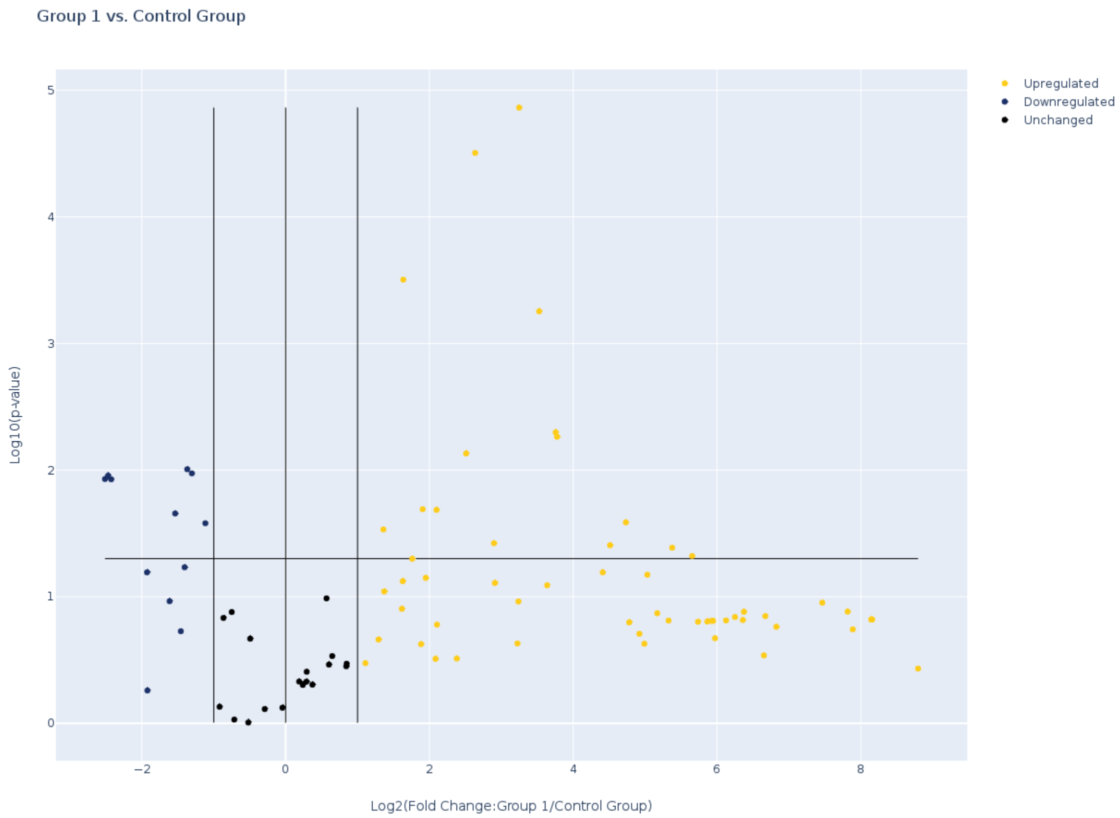
Position	**Gene Symbol**	**Fold Regulation**	**Comments**	**RT² qPCR Assay Catalog #**
E03	NAIP	62.78	B	PPH00909E
E06	NLRC4	58.26	B	PPH06124A
E07	NLRP1	284.40	C	PPH06155E
E08	NLRP3	2.16	A	PPH13170A
E10	NOD2	82.95		PPH06126F
E11	PIK3CA	2.57		PPH01355A
E12	PRTN3	236.88		PPH07029A
F01	PSTPIP1	31.76	A	PPH11981A
F02	PYCARD	26.57		PPH00907A
F08	SLPI	32.68	A	PPH02863A
F09	SUGT1	11.52		PPH05871A
F11	TICAM2	30.27	B	PPH06042A
F12	TIRAP	3.06		PPH06246B
G02	TLR2	9.43	A	PPH01808A
G03	TLR4	21.26	A	PPH01795F
G04	TLR5	22.82	A	PPH01793F
G05	TLR6	4.30	A	PPH01798E
G06	TLR9	9.34	A	PPH01809A
G07	TNF	27.44	B	PPH00341F
G09	TOLLIP	41.53		PPH05844C
G11	XIAP	7.45		PPH00323A
G12	ZBP1	35.97		PPH16531C
H04	HPRT1	7.52		PPH01018C

Genes Under-Expressed in Group 1 vs. Control Group

Position	**Gene Symbol**	**Fold Regulation**	**Comments**	**RT² qPCR Assay Catalog #**
A09	CASP8	-5.71	A	PPH00359F
B01	CHUK	-2.75	A	PPH00649C
B02	CRP	-3.79	A	PPH02632A
E02	MYD88	-5.38	A	PPH00911B
E05	NFKBIA	-3.81	A	PPH00170F
F05	RIPK1	-2.47	A	PPH00335C
F06	RIPK2	-2.65	A	PPH00881C
F10	TICAM1	-3.06	A	PPH06044A
G08	TNFRSF1A	-2.58		PPH00346C
G10	TRAF6	-5.54	A	PPH00329B
H01	ACTB	-2.17		PPH00073G
H02	B2M	-2.90		PPH01094E

Volcano Plot

Test Group	Control Group	Fold Regulation Threshold	p-Value Threshold
Group 1	Control Group	2	0.05



The Volcano Plot identifies significant gene expression changes by plotting the log2 of the fold changes in gene expression on the x-axis versus their statistical significance on the y-axis. The center vertical line indicates unchanged gene expression, while the two outer vertical lines indicate the selected fold regulation threshold. The horizontal line indicates the selected p-value threshold. Genes with data points in the far upper left (down-regulated) and far upper right (up-regulated) sections meet the selected fold regulation and p-value thresholds. By combining the fold change results with the p-value statistical test results, genes with both large and small expression changes that are statistically significant are easily visualized.

Genes Over-Expressed in Group 1 vs. Control Group

Position	Gene Symbol	Fold Regulation	p-Value	Comments	RT² qPCR Assay Catalog #
A02	APCS	82.10	0.152817	B	PPH07107A
A04	BPI	284.40	0.151122	C	PPH16561B
A05	CAMP	76.13	0.144655	B	PPH09430A
A07	CARD9	2.58	0.091009	A	PPH06127F
A08	CASP1	100.62	0.290793	A	PPH00105C
A10	CCL3	101.94	0.142366		PPH00566F
A11	CCL5	40.11	0.154224		PPH00703B
A12	CD14	5.21	0.307835	A	PPH05723A
B03	CTSG	60.62	0.155123	B	PPH01358A
B04	CXCL1	225.51	0.131080	B	PPH00696C
B05	CXCL2	284.40	0.151122	C	PPH00552F
B06	DMBT1	444.85	0.369415	B	PPH15755A
B07	FADD	284.40	0.151122	C	PPH00367A
B08	HSP90AA1	13.51	0.005036		PPH63391B
B10	IFNB1	284.40	0.151122	C	PPH00384F
B11	IKBKB	113.41	0.172864	B	PPH00780C
B12	IL12A	13.68	0.005460		PPH00544B
C01	IL12B	50.35	0.047669		PPH00545A
C02	IL18	53.29	0.157678	B	PPH00580C
C03	IL1B	5.70	0.007394		PPH00171C
C05	CXCL8	69.80	0.153932	B	PPH00568A
C06	IRAK1	3.86	0.071011		PPH00835A
C07	IRAK3	4.24	0.309664	A	PPH06041A
C08	IRF5	2.45	0.217979	A	PPH02870A
C11	LBP	12.44	0.081246	A	PPH01424F
C12	LCN2	3.69	0.237004	A	PPH00446E
D01	LTF	61.65	0.155264	B	PPH05751A
D02	LY96	4.28	0.020612		PPH06052A
D06	MAP2K4	3.39	0.050188		PPH00195C
D07	MAP3K7	9.50	0.000014		PPH00749C
D08	MAPK1	6.21	0.000031		PPH00715B
D09	MAPK14	3.09	0.075421		PPH00750B
D10	MAPK3	3.75	0.020362		PPH00721F
D11	MAPK8	3.11	0.000313		PPH00720B
D12	MEFV	176.56	0.111528	B	PPH13601A
E01	MPO	284.40	0.151122	C	PPH06082F

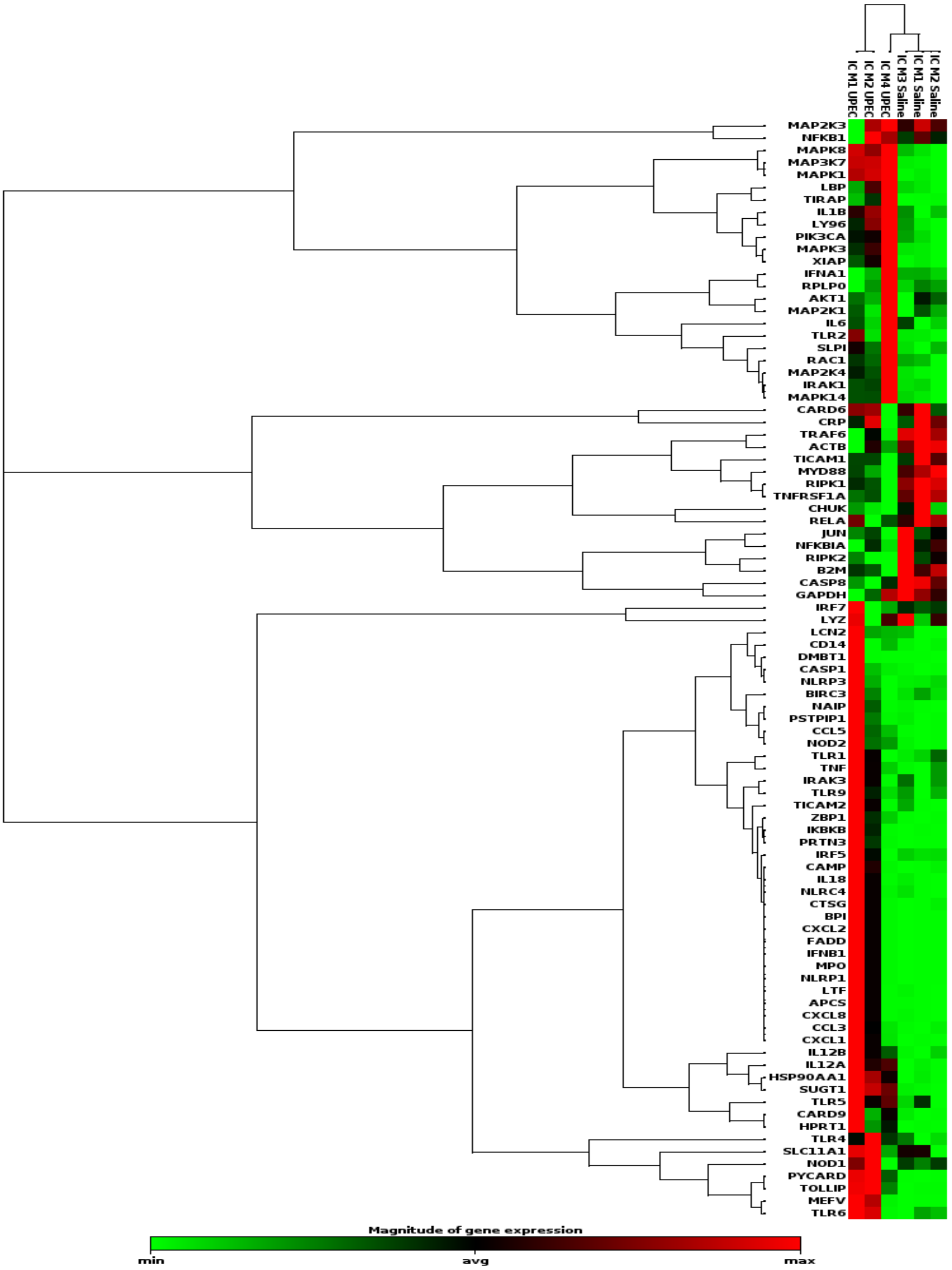
Position	Gene Symbol	Fold Regulation	p-Value	Comments	RT² qPCR Assay Catalog #
E03	NAIP	62.78	0.212859	B	PPH00909E
E06	NLRC4	58.26	0.157054	B	PPH06124A
E07	NLRP1	284.40	0.151122	C	PPH06155E
E08	NLRP3	2.16	0.334714	A	PPH13170A
E10	NOD2	82.95	0.131628		PPH06126F
E11	PIK3CA	2.57	0.029412		PPH01355A
E12	PRTN3	236.88	0.181103		PPH07029A
F01	PSTPIP1	31.76	0.235284	A	PPH11981A
F02	PYCARD	26.57	0.025879		PPH00907A
F08	SLPI	32.68	0.067081	A	PPH02863A
F09	SUGT1	11.52	0.000558		PPH05871A
F11	TICAM2	30.27	0.196212	B	PPH06042A
F12	TIRAP	3.06	0.124674		PPH06246B
G02	TLR2	9.43	0.109141	A	PPH01808A
G03	TLR4	21.26	0.064220	A	PPH01795F
G04	TLR5	22.82	0.039230	A	PPH01793F
G05	TLR6	4.30	0.166207	A	PPH01798E
G06	TLR9	9.34	0.233951	A	PPH01809A
G07	TNF	27.44	0.159485	B	PPH00341F
G09	TOLLIP	41.53	0.041028		PPH05844C
G11	XIAP	7.45	0.037814		PPH00323A
G12	ZBP1	35.97	0.135086		PPH16531C
H04	HPRT1	7.52	0.077954		PPH01018C

Genes Under-Expressed in Group 1 vs. Control Group

Position	**Gene Symbol**	**Fold Regulation**	**p-Value**	**Comments**	**RT² qPCR Assay Catalog #**
A09	CASP8	-5.71	0.011765	A	PPH00359F
B01	CHUK	-2.75	0.187327	A	PPH00649C
B02	CRP	-3.79	0.550285	A	PPH02632A
E02	MYD88	-5.38	0.011814	A	PPH00911B
E05	NFKBIA	-3.81	0.064225	A	PPH00170F
F05	RIPK1	-2.47	0.010605	A	PPH00335C
F06	RIPK2	-2.65	0.058542	A	PPH00881C
F10	TICAM1	-3.06	0.108474	A	PPH06044A
G08	TNFRSF1A	-2.58	0.009846		PPH00346C
G10	TRAF6	-5.54	0.011066	A	PPH00329B
H01	ACTB	-2.17	0.026279		PPH00073G
H02	B2M	-2.90	0.022013		PPH01094E

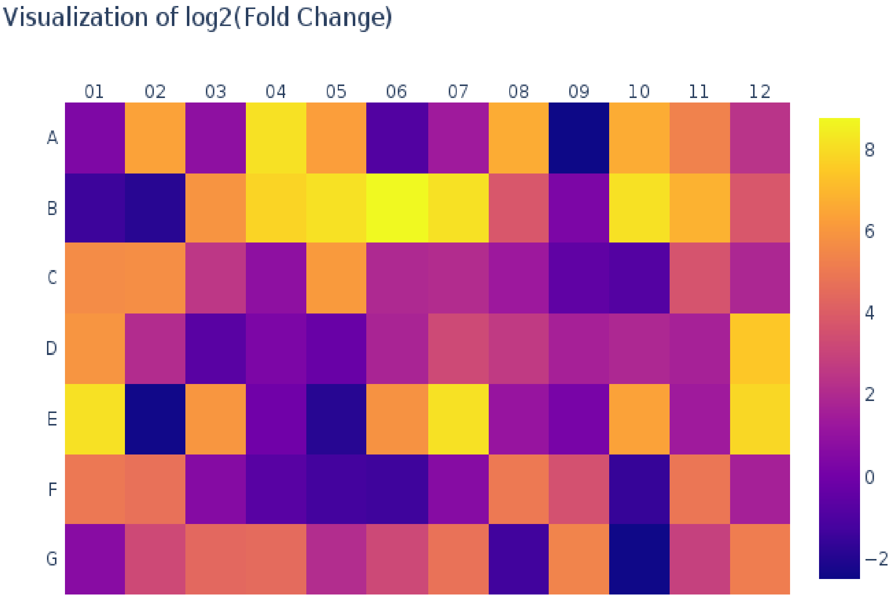
Clustergram

Sample	Dimension	Join Type	Color Coded
Array	2-D	Average	Genes



Heat Map

Test Group	**Control Group**
Group 1	Control Group



Layout	**01**	**02**	**03**	**04**	**05**	**06**	**07**	**08**	**09**	**10**	**11**	**12**
A	AKT1 / 1.29	APCS / 82.1 / B	BIRC3 / 1.79 / A	BPI / 284.4 / C	CAMP / 76.13 / B	CARD6 / -1.89 / A	CARD9 / 2.58 / A	CASP1 / 100.62 / A	CASP8 / -5.71 / A	CCL3 / 101.94	CCL5 / 40.11	CD14 / 5.21 / A
B	CHUK / -2.75 / A	CRP / -3.79 / A	CTSG / 60.62 / B	CXCL1 / 225.51 / B	CXCL2 / 284.4 / C	DMBT1 / 444.85 / B	FADD / 284.4 / C	HSP90AA1 / 13.51	IFNA1 / 1.22	IFNB1 / 284.4 / C	IKBKB / 113.41 / B	IL12A / 13.68
C	IL12B / 50.35	IL18 / 53.29 / B	IL1B / 5.7	IL6 / 1.8 / A	CXCL8 / 69.8 / B	IRAK1 / 3.86	IRAK3 / 4.24 / A	IRF5 / 2.45 / A	IRF7 / -1.43 / A	JUN / -1.82	LBP / 12.44 / A	LCN2 / 3.69 / A
D	LTF / 61.65 / B	LY96 / 4.28	LYZ / -1.64 / A	MAP2K1 / 1.22	MAP2K3 / -1.22	MAP2K4 / 3.39	MAP3K7 / 9.5	MAPK1 / 6.21	MAPK14 / 3.09	MAPK3 / 3.75	MAPK8 / 3.11	MEFV / 176.56 / B
E	MPO / 284.4 / C	MYD88 / -5.38 / A	NAIP / 62.78 / B	NFKB1 / -1.03	NFKBIA / -3.81 / A	NLRC4 / 58.26 / B	NLRP1 / 284.4 / C	NLRP3 / 2.16 / A	NOD1 / 1.14 / A	NOD2 / 82.95	PIK3CA / 2.57	PRTN3 / 236.88
F	PSTPIP1 / 31.76 / A	PYCARD / 26.57	RAC1 / 1.48	RELA / -1.68	RIPK1 / -2.47 / A	RIPK2 / -2.65 / A	SLC11A1 / 1.52 / A	SLPI / 32.68 / A	SUGT1 / 11.52	TICAM1 / -3.06 / A	TICAM2 / 30.27 / B	TIRAP / 3.06
G	TLR1 / 1.57 / A	TLR2 / 9.43 / A	TLR4 / 21.26 / A	TLR5 / 22.82 / A	TLR6 / 4.3 / A	TLR9 / 9.34 / A	TNF / 27.44 / B	TNFRSF1A / -2.58	TOLLIP / 41.53	TRAF6 / -5.54 / A	XIAP / 7.45	ZBP1 / 35.97