



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 in signal 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, each array 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 work under 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-171Z.

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-171Z) 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 Automatic selection from full panel 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 $2^{(-\text{delta delta } C_T)}$ 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

RT² Profiler™ PCR Array Human Macular Degeneration

Position	RefSeq Number	Symbol	Description
A01	NM_005502	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
A02	NM_000350	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4
A03	NM_000789	ACE	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1
A04	NM_000477	ALB	Albumin
A05	NM_001154	ANXA5	Annexin A5
A06	NM_000041	APOE	Apolipoprotein E
A07	NM_001099667	ARMS2	Age-related maculopathy susceptibility 2
A08	NM_000063	C2	Complement component 2
A09	NM_000064	C3	Complement component 3
A10	NM_001735	C5	Complement component 5
A11	NM_001737	C9	Complement component 9
A12	NM_002986	CCL11	Chemokine (C-C motif) ligand 11
B01	NM_002982	CCL2	Chemokine (C-C motif) ligand 2
B02	NM_000078	CETP	Cholesteryl ester transfer protein, plasma
B03	NM_001710	CFB	Complement factor B
B04	NM_000186	CFH	Complement factor H
B05	NM_021023	CFHR3	Complement factor H-related 3
B06	NM_000204	CFI	Complement factor I
B07	NM_001831	CLU	Clusterin
B08	NM_021110	COL14A1	Collagen, type XIV, alpha 1
B09	NM_000096	CP	Ceruloplasmin (ferroxidase)
B10	NM_000567	CRP	C-reactive protein, pentraxin-related
B11	NM_000394	CRYAA	Crystallin, alpha A
B12	NM_001885	CRYAB	Crystallin, alpha B
C01	NM_006891	CRYGD	Crystallin, gamma D
C02	NM_000099	CST3	Cystatin C
C03	NM_001901	CTGF	Connective tissue growth factor
C04	NM_001909	CTSD	Cathepsin D
C05	NM_001337	CX3CR1	Chemokine (C-X3-C motif) receptor 1
C06	NM_000609	CXCL12	Chemokine (C-X-C motif) ligand 12
C07	NM_177438	DICER1	Dicer 1, ribonuclease type III
C08	NM_004105	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1
C09	NM_000501	ELN	Elastin
C10	NM_000124	ERCC6	Excision repair cross-complementing rodent repair deficiency, complementation group 6
C11	NM_004629	FANCG	Fanconi anemia, complementation group G
C12	NM_000639	FASLG	Fas ligand (TNF superfamily, member 6)
D01	NM_006329	FBLN5	Fibulin 5
D02	NM_002026	FN1	Fibronectin 1
D03	NM_002055	GFAP	Glial fibrillary acidic protein
D04	NM_000561	GSTM1	Glutathione S-transferase mu 1
D05	NM_000852	GSTP1	Glutathione S-transferase pi 1
D06	NM_001530	HIF1A	Hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
D07	NM_031935	HMCN1	Hemicentin 1
D08	NM_002133	HMOX1	Heme oxygenase (decycling) 1
D09	NM_002134	HMOX2	Heme oxygenase (decycling) 2
D10	NM_002775	HTRA1	HtrA serine peptidase 1

Position	RefSeq Number	Symbol	Description
D11	NM_000201	ICAM1	Intercellular adhesion molecule 1
D12	NM_000618	IGF1	Insulin-like growth factor 1 (somatomedin C)
E01	NM_000600	IL6	Interleukin 6 (interferon, beta 2)
E02	NM_000584	CXCL8	Interleukin 8
E03	NM_000230	LEP	Leptin
E04	NM_000236	LIPC	Lipase, hepatic
E05	NM_000237	LPL	Lipoprotein lipase
E06	NM_004530	MMP2	Matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
E07	NM_004994	MMP9	Matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
E08	NM_000620	NOS1	Nitric oxide synthase 1 (neuronal)
E09	NM_000603	NOS3	Nitric oxide synthase 3 (endothelial cell)
E10	NM_000301	PLG	Plasminogen
E11	NM_000446	PON1	Paraoxonase 1
E12	NM_000539	RHO	Rhodopsin
F01	NM_000326	RLBP1	Retinaldehyde binding protein 1
F02	NM_000329	RPE65	Retinal pigment epithelium-specific protein 65kDa
F03	NM_000541	SAG	S-antigen; retina and pineal gland (arrestin)
F04	NM_005505	SCARB1	Scavenger receptor class B, member 1
F05	NM_000602	SERPINE1	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
F06	NM_002615	SERPINF1	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
F07	NM_000062	SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
F08	NM_000342	SLC4A1	Solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)
F09	NM_000636	SOD2	Superoxide dismutase 2, mitochondrial
F10	NM_003118	SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)
F11	NM_005563	STMN1	Stathmin 1
F12	NM_001063	TF	Transferrin
G01	NM_000660	TGFB1	Transforming growth factor, beta 1
G02	NM_006288	THY1	Thy-1 cell surface antigen
G03	NM_003254	TIMP1	TIMP metalloproteinase inhibitor 1
G04	NM_000362	TIMP3	TIMP metalloproteinase inhibitor 3
G05	NM_003265	TLR3	Toll-like receptor 3
G06	NM_138554	TLR4	Toll-like receptor 4
G07	NM_001078	VCAM1	Vascular cell adhesion molecule 1
G08	NM_003376	VEGFA	Vascular endothelial growth factor A
G09	NM_003380	VIM	Vimentin
G10	NM_003383	VLDLR	Very low density lipoprotein receptor
G11	NM_000638	VTN	Vitronectin
G12	NM_000552	VWF	Von Willebrand factor
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

Control Group	Group 1	Group 2	Group 3	Group 4	Group 5
	VEGFA	CXCL12	CRYAA+CRYAB	IGF-1	ELN

Pre-amplification

A pre-amplification using the appropriate species- and pathway-specific RT² PreAMP Primer Mix was not performed and the appropriate corrections were made during the data analysis procedure.

Lower limit of detection

The C_T cut-off was set to 40

Data quality control (QC)

Quality checks performed and results

Test Performed	Test Result
1. PCR Array Reproducibility	All Samples Passed
2. RT Efficiency	Check Samples: VEGFA
3. Genomic DNA Contamination	All Samples Passed

Test Performed	VEGF A
PCR Array Reproducibility	
Average C_T (PPC)	18.92
Result	Pass
Reverse Transcription Control (RTC)	
Delta C_T (Average RTC - Average PPC)	5.76
Result	Inquiry
Genomic DNA Contamination (GDC)	
C_T (GDC)	35.00
Result	Pass

Criteria for Reverse Transcription Control (RTC): If Delta C_T (AVG RTC - AVG PPC) ≤ 5 , RT Efficiency reports 'Pass'; otherwise, RT Efficiency reports 'Inquiry'.

See the Troubleshooting Guide of the PCR Array User Manual/Handbook or Contact Technical Support at 888-503-3187 regarding samples with control(s) labeled 'Inquiry'.

Normalization analysis

Automatic selection from full panel

Groups	Samples	CCL11	COL14A1	GFAP	Geometric Mean	Average Geometric Mean
Control Group		35.020145	35.96433	33.91843	34.96	34.96
Group 1	VEGFA	35.34998	36.05205	33.111675	34.82	34.82
Group 2	CXCL12	35.51936	35.363888	33.76946	34.88	34.88
Group 3	CRYAA+CRYAB	35.011074	35.66257	33.624146	34.76	34.76
Group 4	IGF-1	34.83242	35.738873	34.12071	34.89	34.89
Group 5	ELN	35.775642	36.31992	33.874344	35.31	35.31

This method automatically selects an optimal set of internal control / housekeeping / normalization genes for the analysis from the full plate on the PCR Array. The software measures and identifies the genes with the most stable expression via a non-normalized calculation. The C_T values for these genes are then geometrically averaged and used for the $\Delta\Delta C_T$ calculations.

Results

Fold regulation comparison and p-value

Control Group	Test Group	Fold Regulation cut off	p-Value cut off
Control Group	Group 1	2	0.05

Position	Gene Symbol	Fold Regulation	p-Value	Comments
A01	ABCA1	-46.92	0.000000	
A02	ABCA4	5.06	0.000000	
A05	ANXA5	27.02	0.000000	
A06	APOE	2.74	0.000000	
A07	ARMS2	-2.32	0.000000	
A11	C9	11.94	0.000000	
B01	CCL2	3.30	0.000000	
B02	CETP	2.19	0.000000	
B11	CRYAA	27.94	0.000000	
C04	CTSD	2.31	0.000000	
C05	CX3CR1	-2.42	0.000000	
C08	EFEMP1	14.59	0.000000	
C09	ELN	2.64	0.000000	
D04	GSTM1	6.05	0.000000	
D05	GSTP1	36.03	0.000000	
D07	HMCN1	3.47	0.000000	
D08	HMOX1	2.70	0.000000	
D11	ICAM1	2.56	0.000000	
E01	IL6	12.04	0.000000	
E04	LIPC	63.35	0.000000	
E11	PON1	3.40	0.000000	
F04	SCARB1	3.74	0.000000	
F05	SERPINE1	6.49	0.000000	
F06	SERPINF1	4.85	0.000000	
F07	SERPING1	4.21	0.000000	
F11	STMN1	11.63	0.000000	
G07	VCAM1	-25.82	0.000000	
G09	VIM	2.21	0.000000	
H01	ACTB	32.53	0.000000	
H03	GAPDH	35.41	0.000000	A

Control Group	Test Group	Fold Regulation cut off	p-Value cut off
Control Group	Group 2	2	0.05

Position	Gene Symbol	Fold Regulation	p-Value	Comments
A01	ABCA1	-6.73	0.000000	
A02	ABCA4	-2.01	0.000000	
A04	ALB	5.91	0.000000	
A05	ANXA5	268.82	0.000000	
A07	ARMS2	-2.23	0.000000	
A09	C3	89.58	0.000000	
A10	C5	2.45	0.000000	
B01	CCL2	211.02	0.000000	
B03	CFB	288.55	0.000000	
B04	CFH	44.58	0.000000	
B05	CFHR3	38.47	0.000000	
B06	CFI	5.71	0.000000	
B07	CLU	34.09	0.000000	A
B09	CP	5.84	0.000000	
B11	CRYAA	23.90	0.000000	
B12	CRYAB	37.75	0.000000	
C02	CST3	53.80	0.000000	
C03	CTGF	148.72	0.000000	
C04	CTSD	6.20	0.000000	
C05	CX3CR1	-8.74	0.000000	
C06	CXCL12	64.91	0.000000	
C07	DICER1	82.29	0.000000	
C08	EFEMP1	266.42	0.000000	
C09	ELN	12.78	0.000000	
C12	FASLG	-3.23	0.000000	
D01	FBLN5	55.09	0.000000	
D02	FN1	4.43	0.000000	
D05	GSTP1	388.64	0.000000	
D06	HIF1A	285.94	0.000000	
D08	HMOX1	8.85	0.000000	
D10	HTRA1	60.25	0.000000	
D11	ICAM1	65.20	0.000000	
E01	IL6	2172.79	0.000000	A
E02	CXCL8	19.96	0.000000	
E04	LIPC	32.23	0.000000	
E05	LPL	36.56	0.000000	
E06	MMP2	57.47	0.000000	
E07	MMP9	7.88	0.000000	
E09	NOS3	24.66	0.000000	
E11	PON1	15.84	0.000000	
E12	RHO	133.33	0.000000	
F01	RLBP1	-3.20	0.000000	
F02	RPE65	29.25	0.000000	
F03	SAG	122.39	0.000000	
F04	SCARB1	4.25	0.000000	
F05	SERPINE1	36.72	0.000000	
F06	SERPINF1	216.81	0.000000	
F07	SERPING1	85.65	0.000000	
F09	SOD2	40.70	0.000000	A
F10	SPARC	5.74	0.000000	
F11	STMN1	37.79	0.000000	
F12	TF	129.27	0.000000	
G01	TGFB1	12.42	0.000000	
G02	THY1	21.62	0.000000	

Position	Gene Symbol	Fold Regulation	p-Value	Comments
G03	TIMP1	18.69	0.000000	
G04	TIMP3	47.20	0.000000	A
G06	TLR4	4.56	0.000000	
G07	VCAM1	11.97	0.000000	
G08	VEGFA	6.24	0.000000	
G09	VIM	176.80	0.000000	A
G11	VTN	41.68	0.000000	
G12	VWF	123.03	0.000000	
H01	ACTB	2116.99	0.000000	A
H02	B2M	79.61	0.000000	A
H03	GAPDH	35.50	0.000000	A
H04	HPRT1	30.61	0.000000	
H05	RPLP0	36.59	0.000000	A

Control Group	Test Group	Fold Regulation cut off	p-Value cut off
Control Group	Group 3	2	0.05

Position	Gene Symbol	Fold Regulation	p-Value	Comments
A01	ABCA1	-34.74	0.000000	
A02	ABCA4	7.80	0.000000	
A05	ANXA5	29.21	0.000000	
A10	C5	-6.26	0.000000	
B01	CCL2	5.29	0.000000	
B05	CFHR3	3.90	0.000000	
B06	CFI	5.45	0.000000	
B07	CLU	2.63	0.000000	
B09	CP	-2.61	0.000000	
B11	CRYAA	28.92	0.000000	
B12	CRYAB	5.59	0.000000	
C02	CST3	3.31	0.000000	
C05	CX3CR1	-2.72	0.000000	
C06	CXCL12	-2.12	0.000000	
D02	FN1	-8.38	0.000000	
D05	GSTP1	8.22	0.000000	
D08	HMOX1	-2.02	0.000000	
E01	IL6	3.02	0.000000	
E11	PON1	3.49	0.000000	
E12	RHO	233.05	0.000000	
F02	RPE65	-2.67	0.000000	
F03	SAG	165.68	0.000000	
F06	SERPINF1	32.46	0.000000	
F07	SERPING1	3.34	0.000000	
F08	SLC4A1	-4.19	0.000000	
F10	SPARC	-2.13	0.000000	
F11	STMN1	3.88	0.000000	
G04	TIMP3	3.03	0.000000	
G07	VCAM1	-26.91	0.000000	
G09	VIM	7.11	0.000000	
G10	VLDLR	2.76	0.000000	
H01	ACTB	15.19	0.000000	
H02	B2M	-21.16	0.000000	
H03	GAPDH	2.24	0.000000	
H05	RPLP0	3.60	0.000000	

Control Group	Test Group	Fold Regulation cut off	p-Value cut off
Control Group	Group 4	2	0.05

Position	Gene Symbol	Fold Regulation	p-Value	Comments
A01	ABCA1	-20.53	0.000000	
A04	ALB	-2.78	0.000000	
A06	APOE	-2.00	0.000000	
A10	C5	-2.81	0.000000	
B01	CCL2	-3.40	0.000000	
B07	CLU	-37.45	0.000000	
B12	CRYAB	14.02	0.000000	
C02	CST3	-5.89	0.000000	
C06	CXCL12	-2.16	0.000000	
C11	FANCG	-2.45	0.000000	
C12	FASLG	-2.64	0.000000	
D02	FN1	-6.12	0.000000	
D07	HMCN1	26.10	0.000000	
D09	HMOX2	2.91	0.000000	
E02	CXCL8	-3.40	0.000000	
E06	MMP2	10.78	0.000000	
E10	PLG	3.51	0.000000	
F01	RLBP1	-2.10	0.000000	
F02	RPE65	-3.20	0.000000	
F06	SERPINF1	24.98	0.000000	
F07	SERPING1	-6.85	0.000000	
F08	SLC4A1	-2.14	0.000000	
F09	SOD2	-7.41	0.000000	
F10	SPARC	-2.06	0.000000	
G03	TIMP1	-6.47	0.000000	
G07	VCAM1	-17.79	0.000000	
G09	VIM	-9.72	0.000000	
H02	B2M	-19.26	0.000000	
H03	GAPDH	-35.74	0.000000	
H05	RPLP0	-99.34	0.000000	

Control Group	Test Group	Fold Regulation cut off	p-Value cut off
Control Group	Group 5	2	0.05

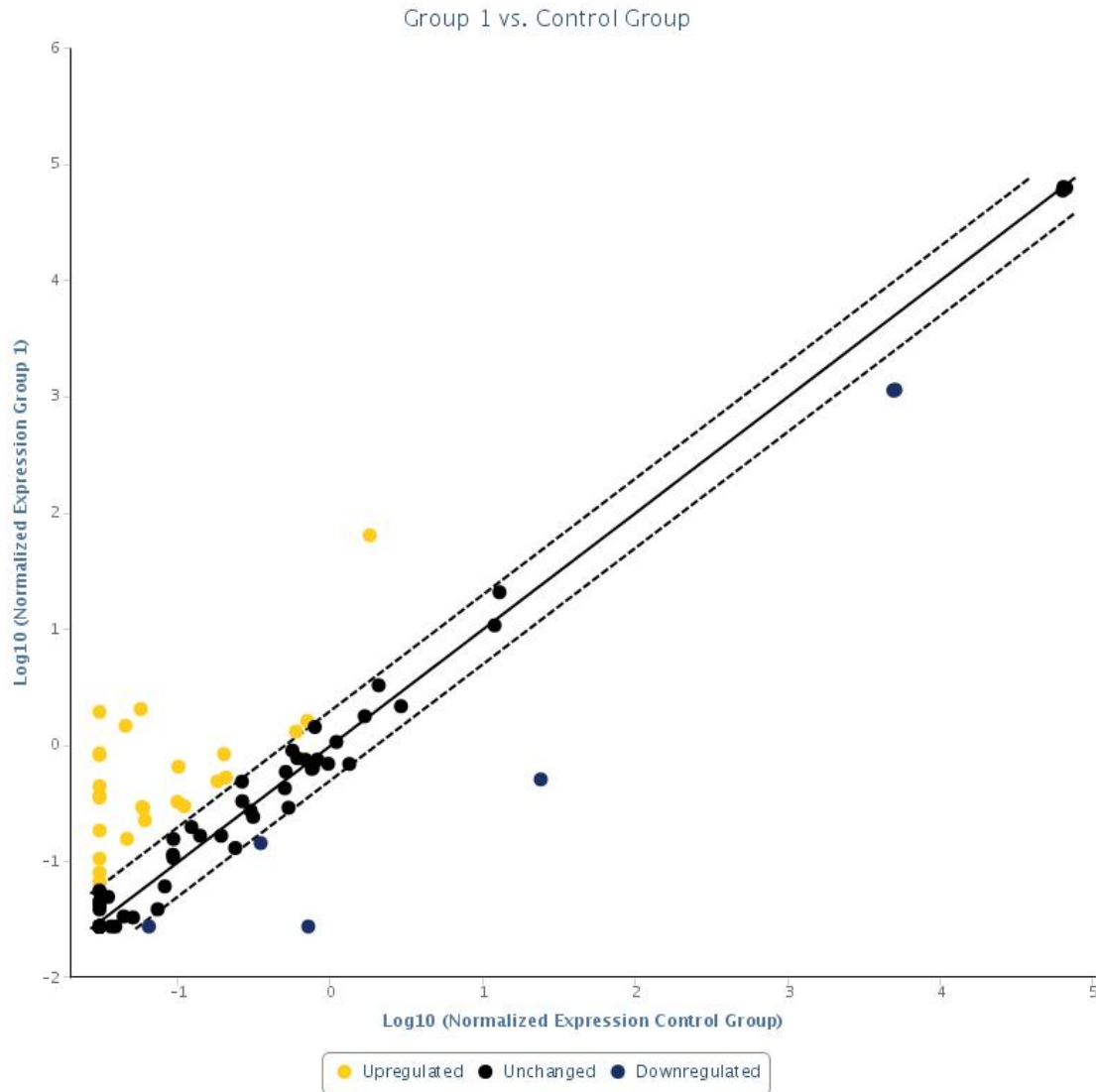
Position	Gene Symbol	Fold Regulation	p-Value	Comments
A06	APOE	3.31	0.000000	
A09	C3	2.75	0.000000	
B01	CCL2	5.70	0.000000	
B04	CFH	3.34	0.000000	
B07	CLU	-28.06	0.000000	
C02	CST3	-2.42	0.000000	
C08	EFEMP1	22.57	0.000000	
D08	HMOX1	3.76	0.000000	
E01	IL6	91.29	0.000000	
E04	LIPC	16.49	0.000000	
E12	RHO	13.77	0.000000	
F01	RLBP1	-2.17	0.000000	
F02	RPE65	-2.39	0.000000	
F03	SAG	23.10	0.000000	
F06	SERPINF1	47.35	0.000000	
F07	SERPING1	-5.13	0.000000	
F08	SLC4A1	-3.03	0.000000	
G07	VCAM1	-18.35	0.000000	
G09	VIM	5.53	0.000000	
G11	VTN	2.83	0.000000	
G12	VWF	2.42	0.000000	
H01	ACTB	42.94	0.000000	
H03	GAPDH	-9.85	0.000000	
H04	HPRT1	2.91	0.000000	

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.

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 array between the two selected groups by plotting them against one another to quickly visualize large gene expression changes. The central line indicates unchanged gene expression. The dotted lines indicate the selected fold regulation threshold. Data points beyond the dotted lines in the upper left and lower right sections meet the selected fold regulation threshold.

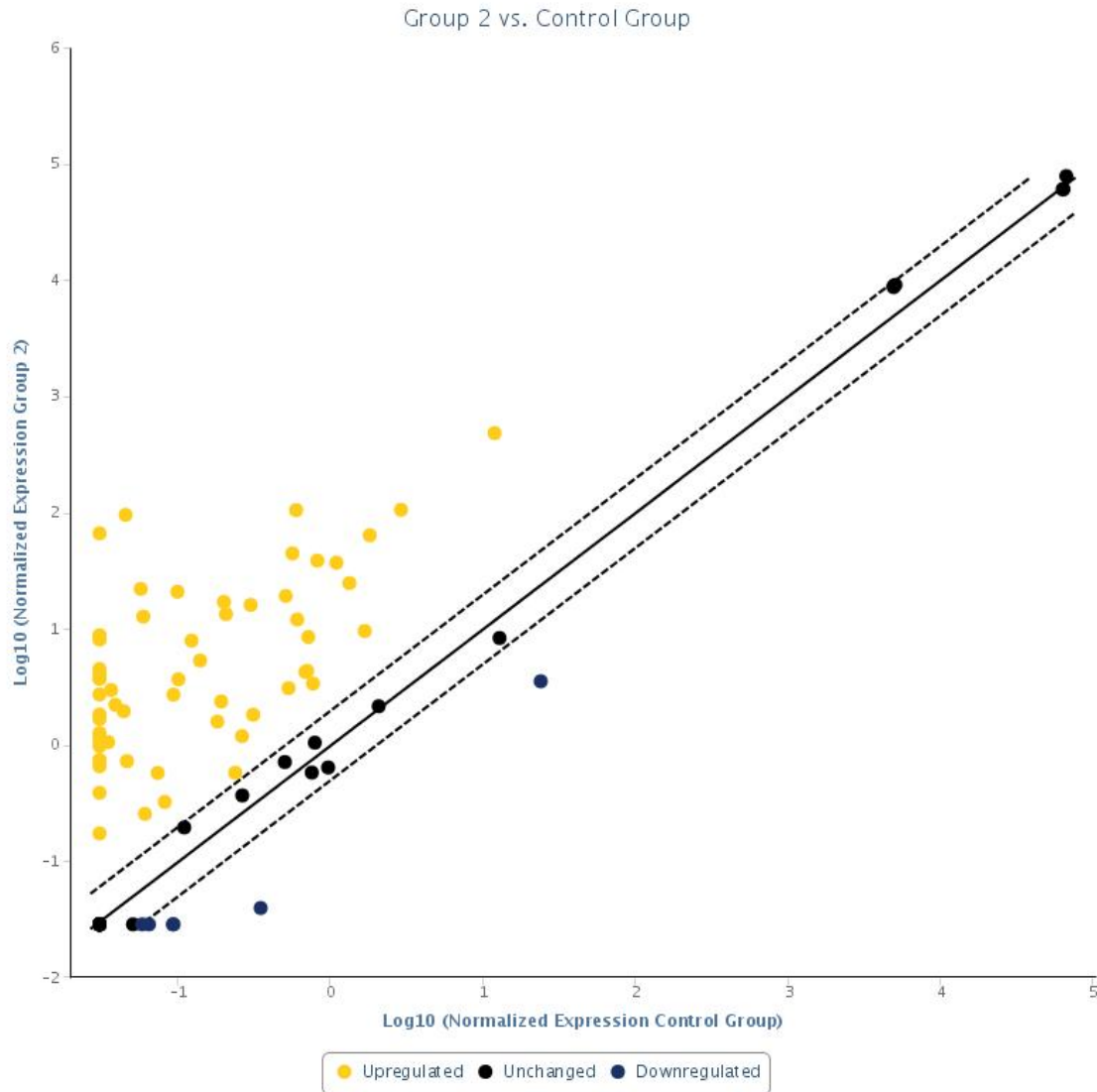
Genes Over-Expressed in Group 1 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
E04	LIPC	63.35		PPH01743A
D05	GSTP1	36.03		PPH00318F
H03	GAPDH	35.41	A	PPH00150F
H01	ACTB	32.53		PPH00073G
B11	CRYAA	27.94		PPH01703A
A05	ANXA5	27.02		PPH00304F
C08	EFEMP1	14.59		PPH10012A
E01	IL6	12.04		PPH00560C
A11	C9	11.94		PPH07065B
F11	STMN1	11.63		PPH14448B
F05	SERPINE1	6.49		PPH00215F
D04	GSTM1	6.05		PPH00501B
A02	ABCA4	5.06		PPH06925F
F06	SERPINF1	4.85		PPH00805A
F07	SERPING1	4.21		PPH18747F
F04	SCARB1	3.74		PPH02121F
D07	HMCN1	3.47		PPH17142E
E11	PON1	3.40		PPH05940F
B01	CCL2	3.30		PPH00192F
A06	APOE	2.74		PPH01366D
D08	HMOX1	2.70		PPH00161E
C09	ELN	2.64		PPH06895F
D11	ICAM1	2.56		PPH00640F
C04	CTSD	2.31		PPH00112F
G09	VIM	2.21		PPH00417F
B02	CETP	2.19		PPH01386F

Genes Under-Expressed in Group 1 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
A01	ABCA1	-46.92		PPH02595A
G07	VCAM1	-25.82		PPH00623E
H09	RTC	-4.44		PPX63340A
H07	RTC	-4.37		PPX63340A
H08	RTC	-4.35		PPX63340A
C05	CX3CR1	-2.42		PPH00620A
A07	ARMS2	-2.32		PPH17120E

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



The scatter plot compares the normalized expression of every gene on the array between the two selected groups by plotting them against one another to quickly visualize large gene expression changes. The central line indicates unchanged gene expression. The dotted lines indicate the selected fold regulation threshold. Data points beyond the dotted lines in the upper left and lower right sections meet the selected fold regulation threshold.

Genes Over-Expressed in Group 2 vs. Control Group

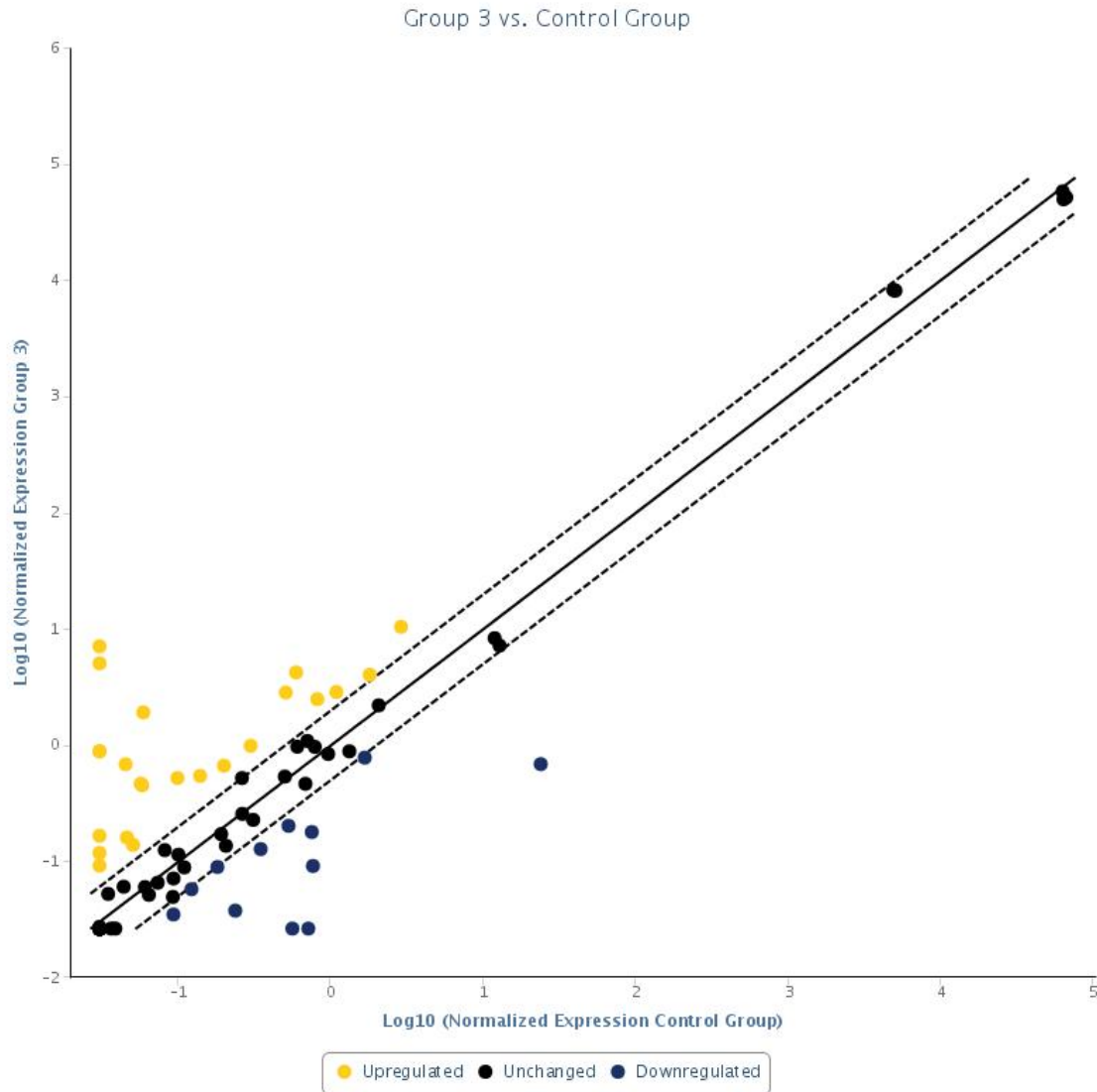
Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
E01	IL6	2172.79	A	PPH00560C
H01	ACTB	2116.99	A	PPH00073G
D05	GSTP1	388.64		PPH00318F
B03	CFB	288.55		PPH02001A
D06	HIF1A	285.94		PPH01361B
A05	ANXA5	268.82		PPH00304F
C08	EFEMP1	266.42		PPH10012A
F06	SERPINF1	216.81		PPH00805A
B01	CCL2	211.02		PPH00192F
G09	VIM	176.80	A	PPH00417F
C03	CTGF	148.72		PPH00550G
E12	RHO	133.33		PPH02351A
F12	TF	129.27		PPH01712A
G12	VWF	123.03		PPH02567F
F03	SAG	122.39		PPH08974A
A09	C3	89.58		PPH01185E
F07	SERPING1	85.65		PPH18747F
C07	DICER1	82.29		PPH10383A
H02	B2M	79.61	A	PPH01094E
D11	ICAM1	65.20		PPH00640F
C06	CXCL12	64.91		PPH00528B
D10	HTRA1	60.25		PPH09932A
E06	MMP2	57.47		PPH00151B
D01	FBLN5	55.09		PPH07793A
C02	CST3	53.80		PPH01359C
G04	TIMP3	47.20	A	PPH00762B
B04	CFH	44.58		PPH15684E
G11	VTN	41.68		PPH00253F
F09	SOD2	40.70	A	PPH01716B
B05	CFHR3	38.47		PPH07154A
F11	STMN1	37.79		PPH14448B
B12	CRYAB	37.75		PPH00123B
F05	SERPINE1	36.72		PPH00215F
H05	RPLP0	36.59	A	PPH21138F
E05	LPL	36.56		PPH00023C
H03	GAPDH	35.50	A	PPH00150F
B07	CLU	34.09	A	PPH00243F
E04	LIPC	32.23		PPH01743A
H04	HPRT1	30.61		PPH01018C
F02	RPE65	29.25		PPH07121A
E09	NOS3	24.66		PPH01298F
B11	CRYAA	23.90		PPH01703A
G02	THY1	21.62		PPH02406G
E02	CXCL8	19.96		PPH00568A
G03	TIMP1	18.69		PPH00771C
E11	PON1	15.84		PPH05940F
C09	ELN	12.78		PPH06895F
G01	TGFB1	12.42		PPH00508A
G07	VCAM1	11.97		PPH00623E
D08	HMOX1	8.85		PPH00161F
E07	MMP9	7.88		PPH00152E
G08	VEGFA	6.24		PPH00251C
C04	CTSD	6.20		PPH00112F

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
A04	ALB	5.91		PPH19822E
B09	CP	5.84		PPH02042B
F10	SPARC	5.74		PPH01175A
B06	CFI	5.71		PPH16784E
G06	TLR4	4.56		PPH01795F
D02	FN1	4.43		PPH00143B
F04	SCARB1	4.25		PPH02121F
H06	HGDC	3.98		
A10	C5	2.45		PPH07062C

Genes Under-Expressed in Group 2 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
C05	CX3CR1	-8.74		PPH00620A
A01	ABCA1	-6.73		PPH02595A
C12	FASLG	-3.23		PPH00142C
F01	RLBP1	-3.20		PPH07106A
A07	ARMS2	-2.23		PPH17120E
A02	ABCA4	-2.01		PPH06925F

Test Group	Control Group	Fold Regulation Threshold
Group 3	Control Group	2



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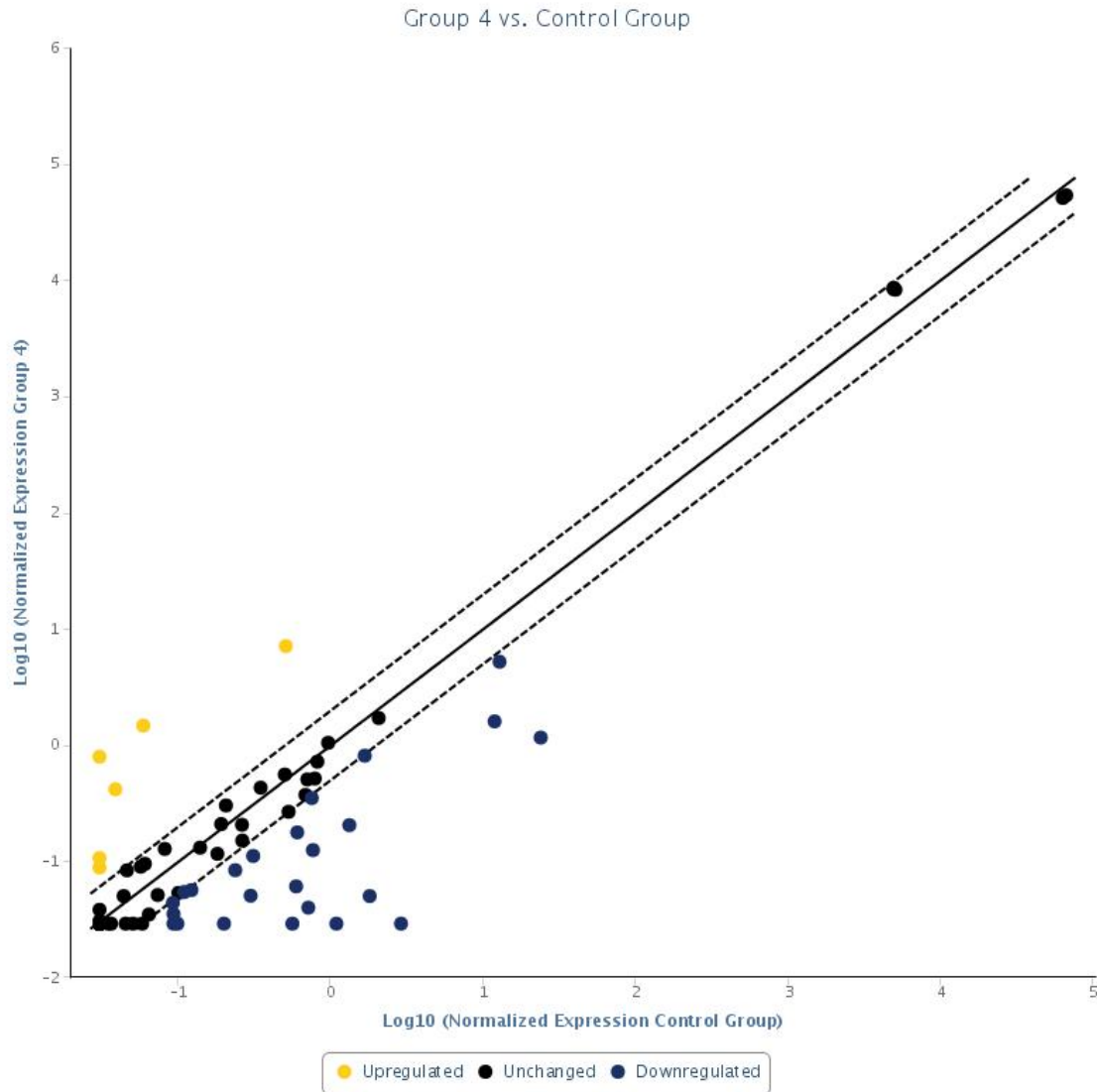
Genes Over-Expressed in Group 3 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
E12	RHO	233.05		PPH02351A
F03	SAG	165.68		PPH08974A
F06	SERPINF1	32.46		PPH00805A
A05	ANXA5	29.21		PPH00304E
B11	CRYAA	28.92		PPH01703A
H01	ACTB	15.19		PPH00073G
D05	GSTP1	8.22		PPH00318F
A02	ABCA4	7.80		PPH06925E
G09	VIM	7.11		PPH00417F
B12	CRYAB	5.59		PPH00123B
B06	CFI	5.45		PPH16784E
B01	CCL2	5.29		PPH00192E
B05	CFHR3	3.90		PPH07154A
F11	STMN1	3.88		PPH14448B
H05	RPLP0	3.60		PPH21138F
E11	PON1	3.49		PPH05940F
F07	SERPING1	3.34		PPH18747E
C02	CST3	3.31		PPH01359C
G04	TIMP3	3.03		PPH00762B
E01	IL6	3.02		PPH00560C
G10	VLDLR	2.76		PPH06222A
B07	CLU	2.63		PPH00243E
H03	GAPDH	2.24		PPH00150F

Genes Under-Expressed in Group 3 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
A01	ABCA1	-34.74		PPH02595A
G07	VCAM1	-26.91		PPH00623E
H02	B2M	-21.16		PPH01094E
D02	FN1	-8.38		PPH00143B
A10	C5	-6.26		PPH07062C
F08	SLC4A1	-4.19		PPH00836A
C05	CX3CR1	-2.72		PPH00620A
F02	RPE65	-2.67		PPH07121A
B09	CP	-2.61		PPH02042B
F10	SPARC	-2.13		PPH01175A
C06	CXCL12	-2.12		PPH00528B
D08	HMOX1	-2.02		PPH00161E

Test Group	Control Group	Fold Regulation Threshold
Group 4	Control Group	2



The scatter plot compares the normalized expression of every gene on the array between the two selected groups by plotting them against one another to quickly visualize large gene expression changes. The central line indicates unchanged gene expression. The dotted lines indicate the selected fold regulation threshold. Data points beyond the dotted lines in the upper left and lower right sections meet the selected fold regulation threshold.

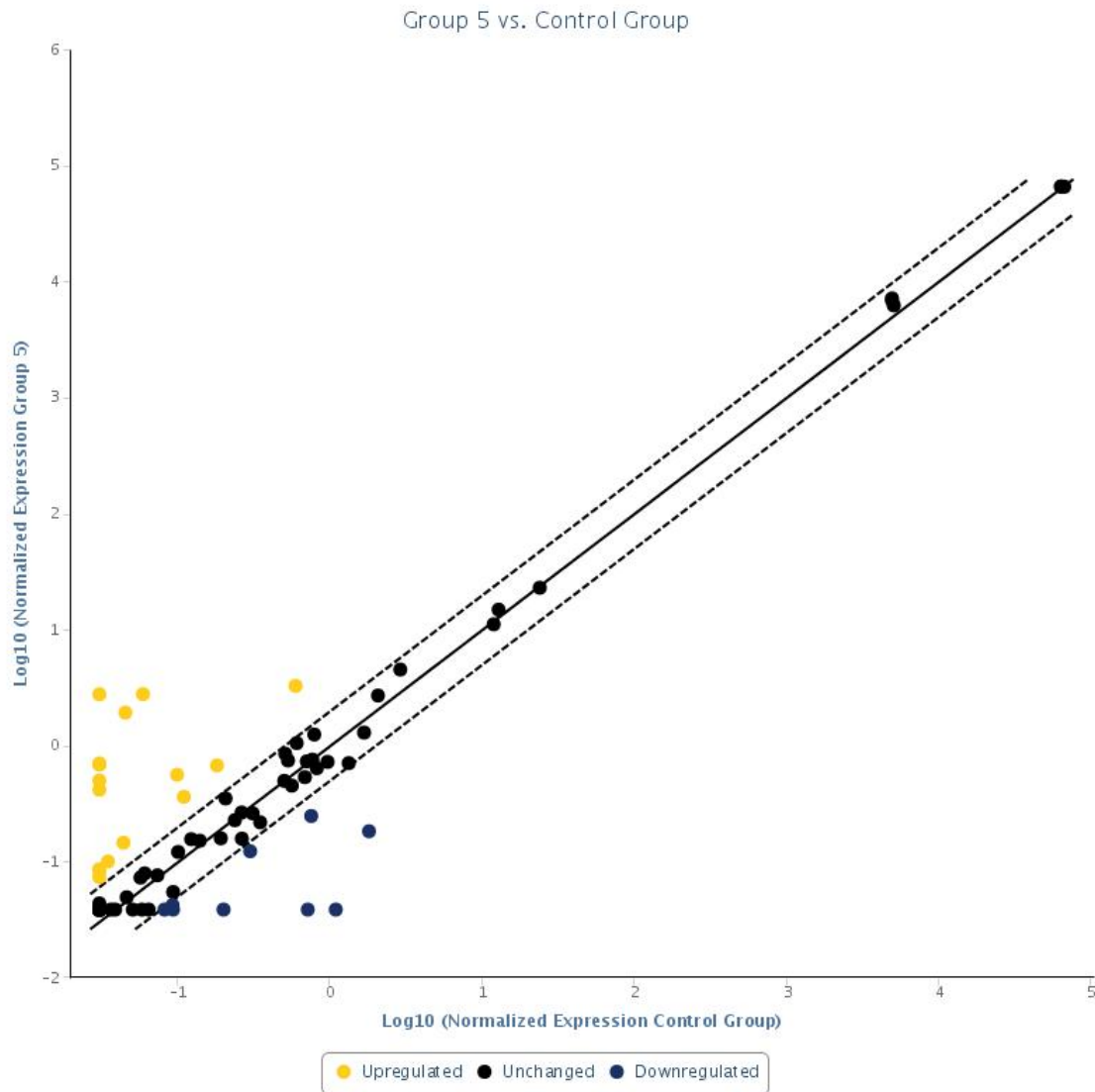
Genes Over-Expressed in Group 4 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
D07	HMCN1	26.10		PPH17142E
F06	SERPINF1	24.98		PPH00805A
B12	CRYAB	14.02		PPH00123B
E06	MMP2	10.78		PPH00151B
E10	PLG	3.51		PPH02587G
D09	HMOX2	2.91		PPH00162G

Genes Under-Expressed in Group 4 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
H05	RPLP0	-99.34		PPH21138F
B07	CLU	-37.45		PPH00243F
H03	GAPDH	-35.74		PPH00150F
A01	ABCA1	-20.53		PPH02595A
H02	B2M	-19.26		PPH01094E
G07	VCAM1	-17.79		PPH00623E
G09	VIM	-9.72		PPH00417F
F09	SOD2	-7.41		PPH01716B
F07	SERPING1	-6.85		PPH18747F
G03	TIMP1	-6.47		PPH00771C
D02	FN1	-6.12		PPH00143B
C02	CST3	-5.89		PPH01359C
B01	CCL2	-3.40		PPH00192F
E02	CXCL8	-3.40		PPH00568A
F02	RPE65	-3.20		PPH07121A
A10	C5	-2.81		PPH07062C
A04	ALB	-2.78		PPH19822E
C12	FASLG	-2.64		PPH00142C
C11	FANCG	-2.45		PPH20387A
C06	CXCL12	-2.16		PPH00528B
F08	SLC4A1	-2.14		PPH00836A
F01	RLBP1	-2.10		PPH07106A
F10	SPARC	-2.06		PPH01175A
A06	APOE	-2.00		PPH01366D

Test Group	Control Group	Fold Regulation Threshold
Group 5	Control Group	2



The scatter plot compares the normalized expression of every gene on the array between the two selected groups by plotting them against one another to quickly visualize large gene expression changes. The central line indicates unchanged gene expression. The dotted lines indicate the selected fold regulation threshold. Data points beyond the dotted lines in the upper left and lower right sections meet the selected fold regulation threshold.

Genes Over-Expressed in Group 5 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
E01	IL6	91.29		PPH00560C
F06	SERPINF1	47.35		PPH00805A
H01	ACTB	42.94		PPH00073G
F03	SAG	23.10		PPH08974A
C08	EFEMP1	22.57		PPH10012A
E04	LIPC	16.49		PPH01743A
E12	RHO	13.77		PPH02351A
B01	CCL2	5.70		PPH00192E
G09	VIM	5.53		PPH00417F
D08	HMOX1	3.76		PPH00161F
B04	CFH	3.34		PPH15684E
A06	APOE	3.31		PPH01366D
H04	HPRT1	2.91		PPH01018C
G11	VTN	2.83		PPH00253F
A09	C3	2.75		PPH01185E
G12	VWF	2.42		PPH02567F

Genes Under-Expressed in Group 5 vs. Control Group

Position	Gene Symbol	Fold Regulation	Comments	RT2 Catalog
B07	CLU	-28.06		PPH00243F
G07	VCAM1	-18.35		PPH00623E
H03	GAPDH	-9.85		PPH00150F
F07	SERPING1	-5.13		PPH18747E
F08	SLC4A1	-3.03		PPH00836A
C02	CST3	-2.42		PPH01359C
F02	RPE65	-2.39		PPH07121A
F01	RLBP1	-2.17		PPH07106A
H06	HGDC	-2.10		

Next steps

After using QIAGEN's RT² Profiler PCR array, use the upregulated or downregulated qPCR assays to further validate your hypothesis.

You can use individual qPCR RT² assays or create custom RT² PCR arrays.

Further, you can use the assay and other products discussed above in the "What's next?" section to design additional studies on the expression and function of miRNAs regulating the differentially expressed genes, somatic mutations in those genes, epigenetic marks (such as modified histones, transcription factor binding, and DNA methylation) at the promoters of those genes, or study the genes' function using gene-specific siRNA.

Glossary

Comments

A: This gene's average threshold cycle is relatively high (> 30) in either the control or the test sample, and is reasonably low in the other sample (< 30). These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result. This fold-change result may also have greater variations if p value > 0.05 ; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

B: This gene's average threshold cycle is relatively high (> 30), meaning that its relative expression level is low, in both control and test samples, and the p -value for the fold-change is either unavailable or relatively high ($p > 0.05$). This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biological replicates to validate the result for this gene.

C: This gene's average threshold cycle is either not determined or greater than the defined cut-off (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and un-interpretable.