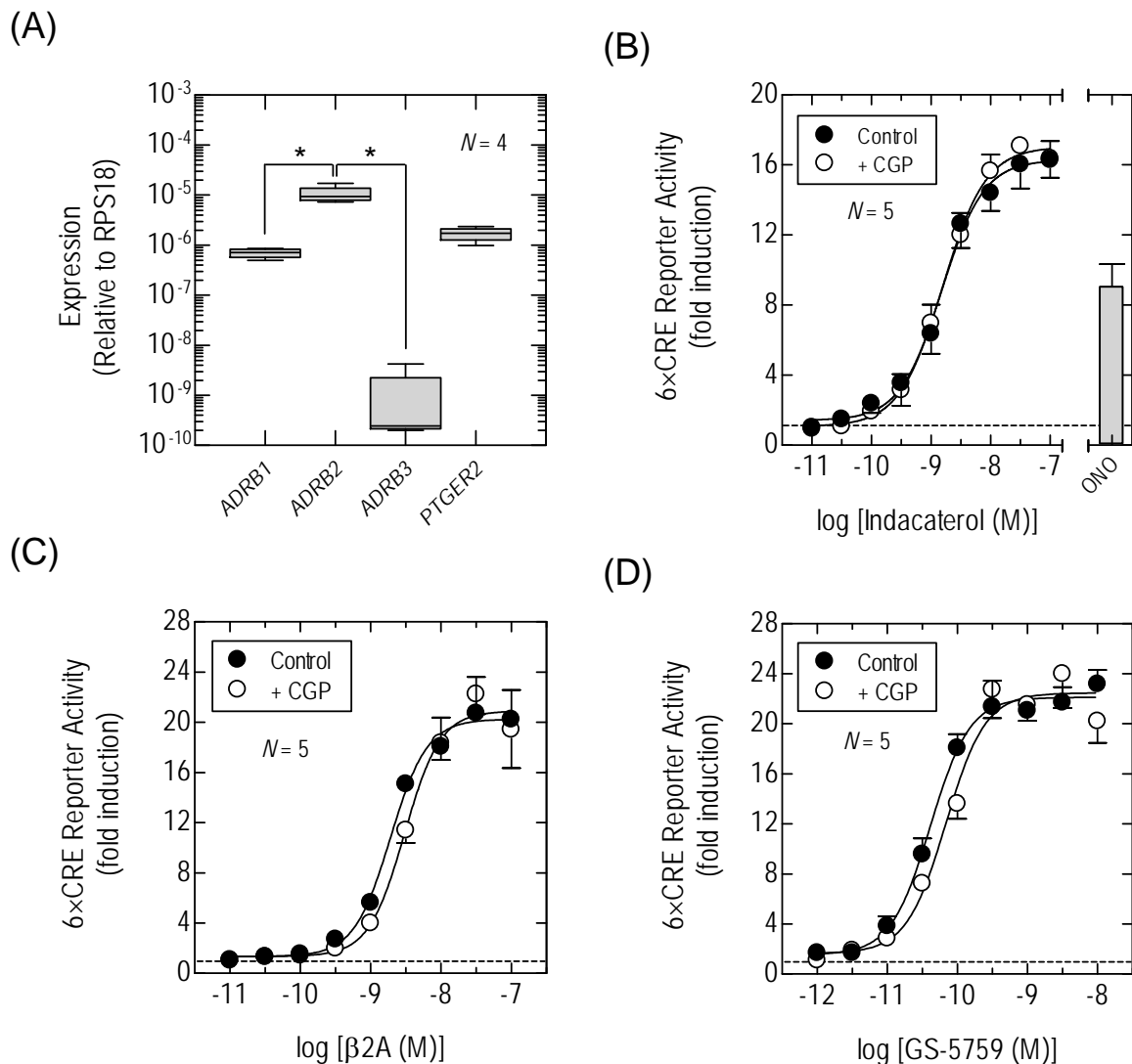


Supplemental Material

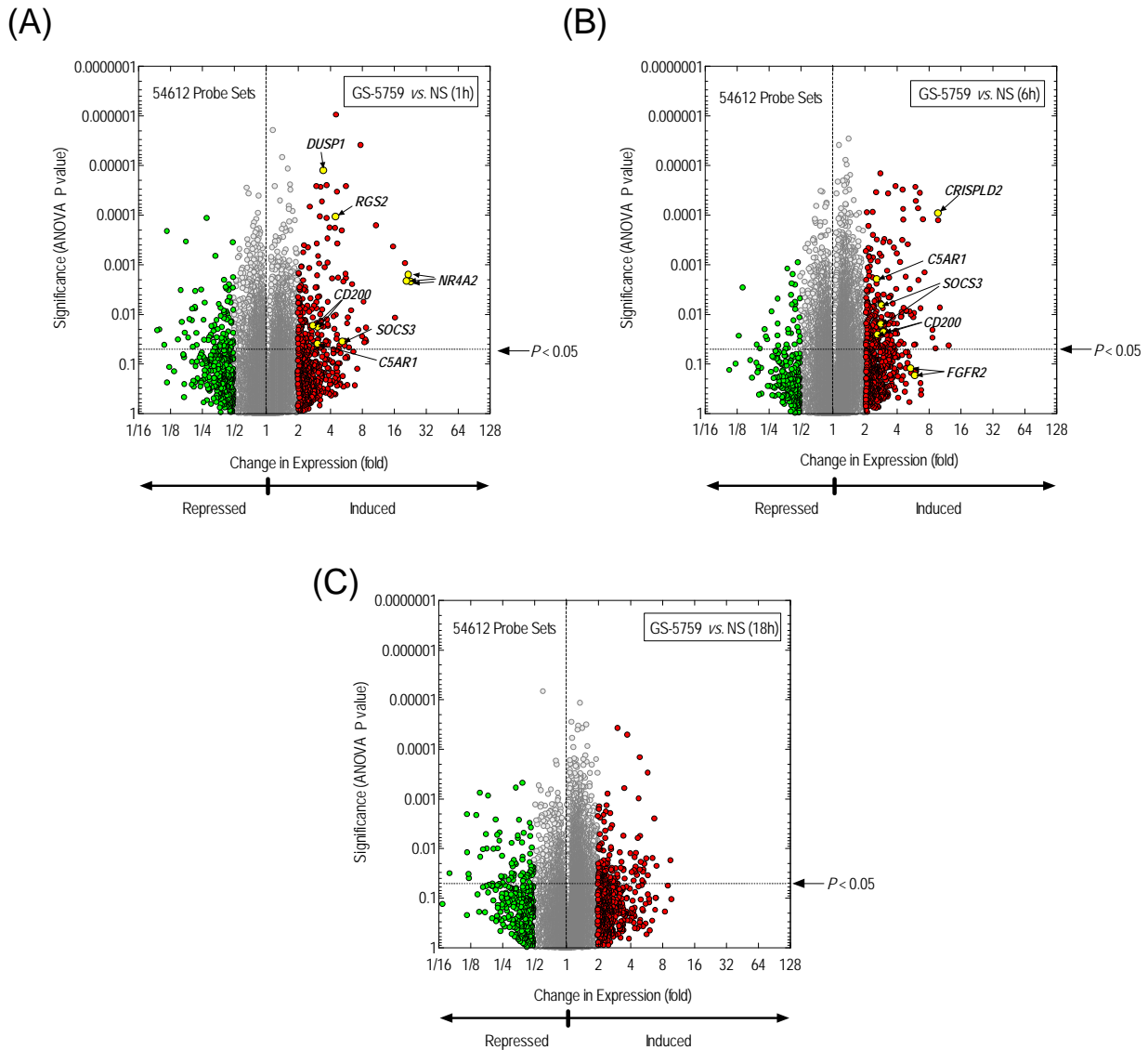
GS-5759, a Bifunctional β_2 -Adrenoceptor Agonist and Phosphodiesterase 4 Inhibitor for Chronic Obstructive Pulmonary Disease with a Unique Mode of Action: Effects on Gene Expression in Human Airway Epithelial Cells

Taruna Joshi, Dong Yan, Omar Hamed, Stacey L. Tannheimer, Gary B. Phillips, Musong Kim, Clifford D. Wright, Michael Salmon, Robert Newton & Mark A. Giembycz

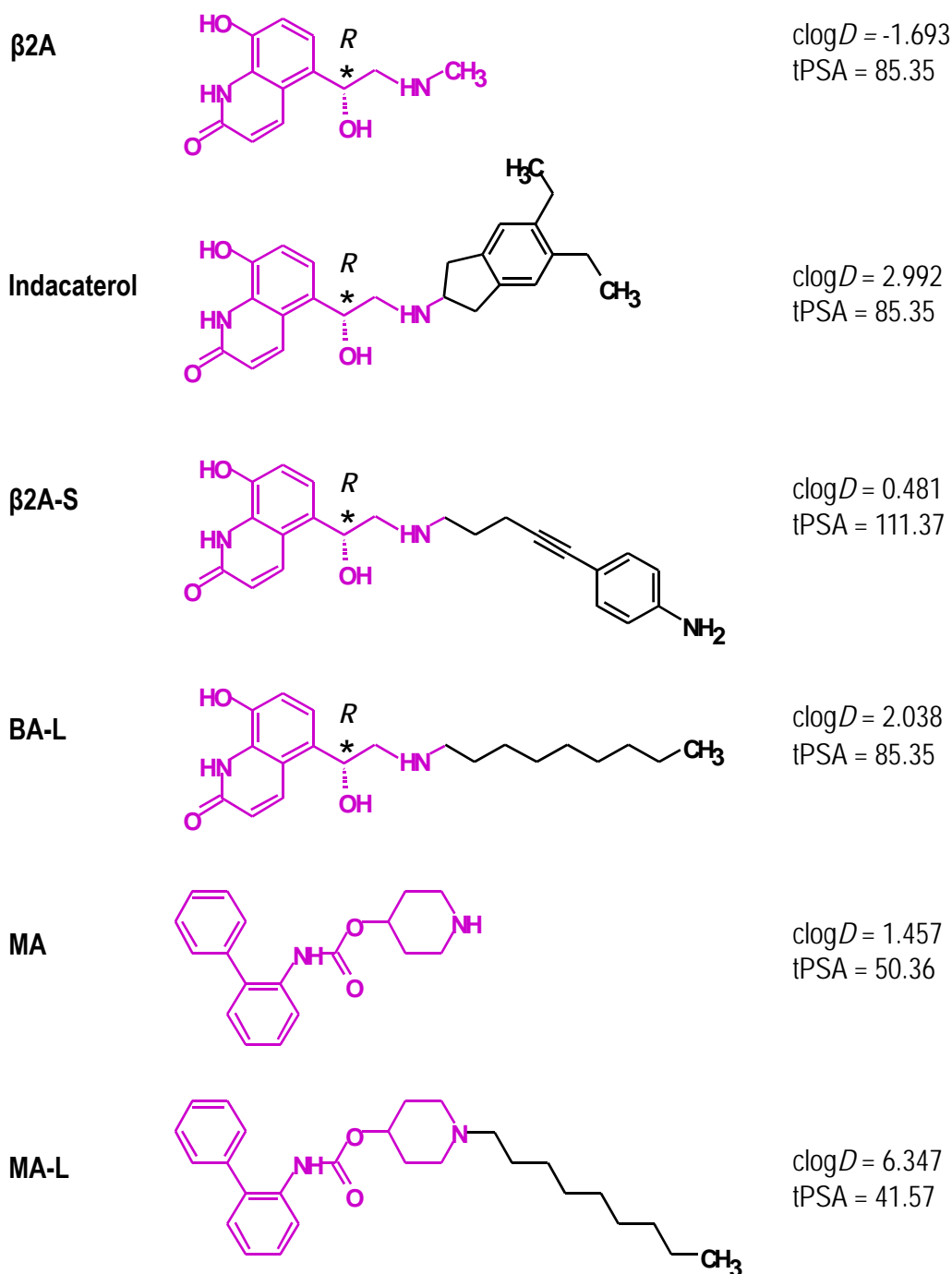
Departments of Physiology & Pharmacology (T.J., D.Y., O.H., M.A.G.) and Cell Biology & Anatomy (R.N.), Snyder Institute for Chronic Diseases, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada and Translational Medicine, Biomarkers (S.L.T.), Inflammation Research (M.S., C.D.W.) and Medicinal Chemistry (M.H., G.B.P.), Gilead Sciences Inc., Seattle, Washington, USA.



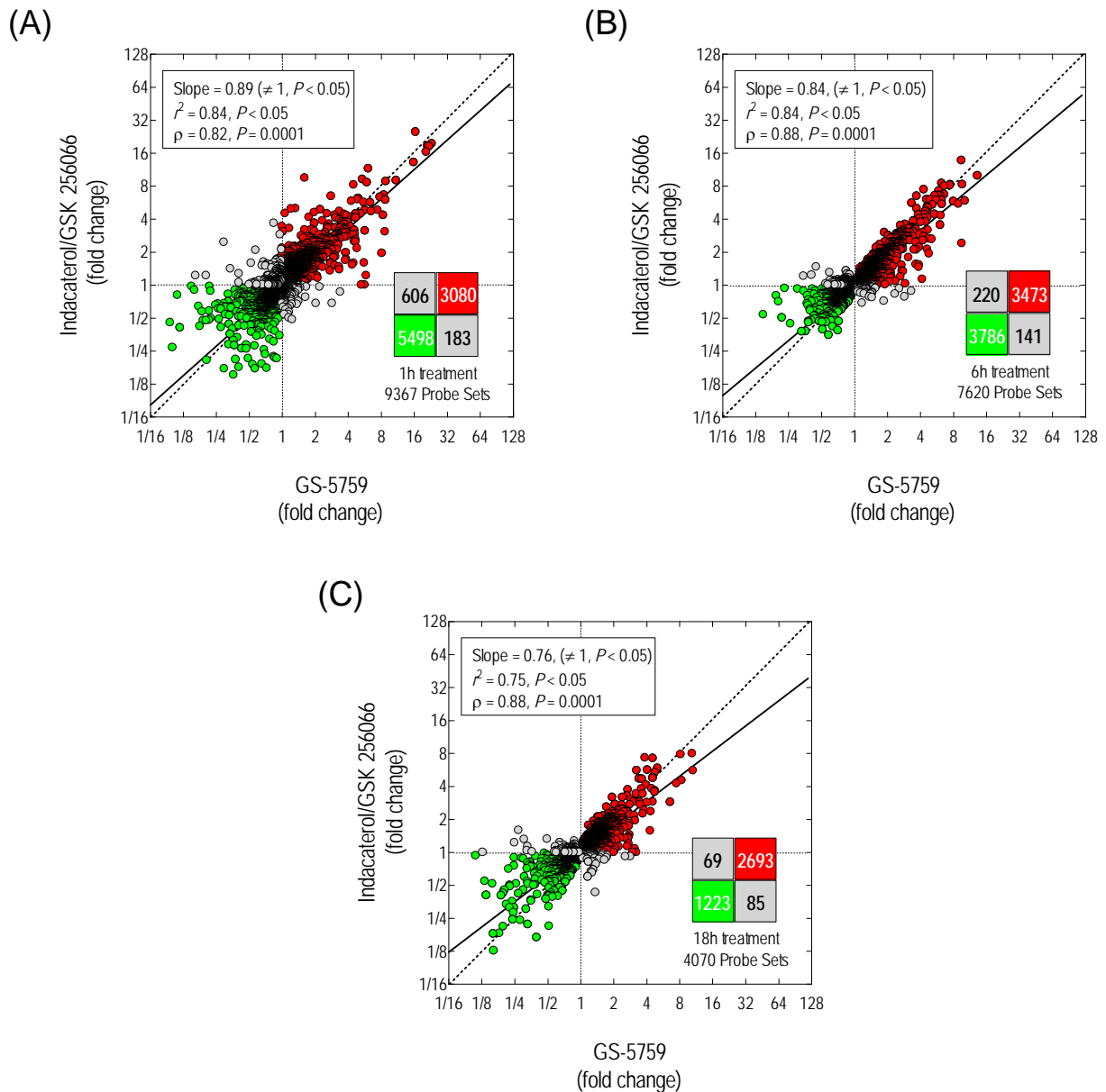
Supplemental Fig. 1. β -Adrenoceptor expression and function in BEAS-2B cells. Panel A. cDNA from untreated BEAS-2B cells was subjected to TaqMan PCR using a human GPCR array. β -Adrenoceptor mRNA transcripts, expressed as a ratio to *RPS18*, are presented as Box and Whisker plots in log₁₀ format and are compared to transcripts encoding the prostanoid EP₂-receptor. Panels B-D. Effect of the selective β ₁-adrenoceptor antagonist, CGP 20712A (CGP), on indacaterol-, β 2A- and GS-5759-induced reporter activation. 6xCRE BEAS-2B reporter cells were treated with GS-5759, β 2A and indacaterol alone and after pre-treatment (30min) with CGP (500nM). GSK 256066 (10nM) was present throughout the GS-5759 experiments to eliminate the contribution that PDE4 inhibition could make to reporter activation. At 6h, cells were lysed, luciferase activity measured and $E/[A]$ curves constructed. The effect of selective EP₂-receptor agonist, ONO-AE1-259 (ONO; 1 μ M), is shown for comparison. The horizontal dashed lines represent baseline luciferase activity. In all panels, data represent the mean \pm s.e. mean of *N* independent observations. **P* < 0.05, one-way ANOVA followed by Tukey's multiple comparison test.



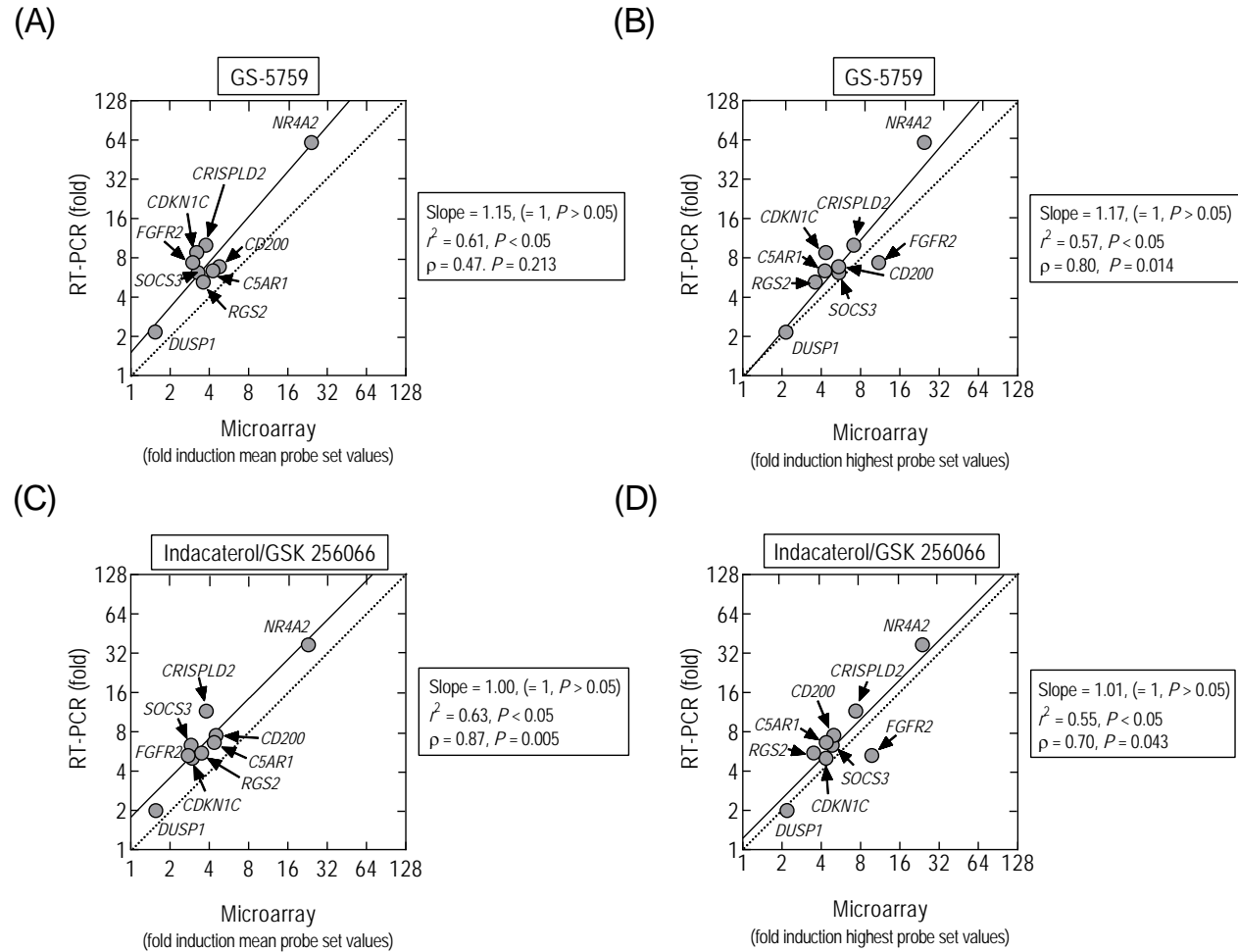
Supplemental Fig. 2. Volcano plots showing global gene expression changes induced in BEAS-2B cells by GS-5759. Total RNA was extracted from cells treated with GS-5759 (10nM) or vehicle for 1h, 6h or 18h (panels A-C respectively) and processed for gene expression changes by microarray. Expression levels of all 47,400+ transcripts (by probe set) are shown relative to time-matched, vehicle-treated cells (NS). Each probe set is represented by a circle coloured grey (transcript changes ≤ 2 -fold), red or green (corresponding to transcript that are induced and repressed by > 2 -fold respectively). Yellow circles show GS-5759-induced genes (> 2 -fold) that were validated by real-time PCR (Fig 9; Table 5). Values above the horizontal dashed line represent transcript level expression changes that were significantly different from vehicle ($P < 0.05$ unadjusted, one-way ANOVA). The vertical dashed lines indicate baseline gene expression.



Supplemental Fig. 3. Structures of the quinolinone- and biphenyl-containing orthosteres that confer β_2 -adrenoceptor agonism (β 2A) and muscarinic receptor antagonism (MA) respectively. Indacaterol is an analogue of β 2A in which the methyl group of the secondary amine is replaced with 5,6-diethyl-2,3-dihydro-1*H*-indene. β 2A-S and BA-L represent the same quinolinone-containing orthostere linked to 4-(pent-1-yn-1-yl)aniline (this study) and nonane (Steinfeld et al., 2011) respectively. MA and MA-L represent the biphenyl-containing orthostere with and without nonane (Steinfeld et al., 2011). The distribution coefficients ($\text{clog}D$) and total polar surface area (tPSA) values were calculated using MedChem Designer, Simulations Plus Inc (Lancaster, CA). The asterisks indicate chiral centres.

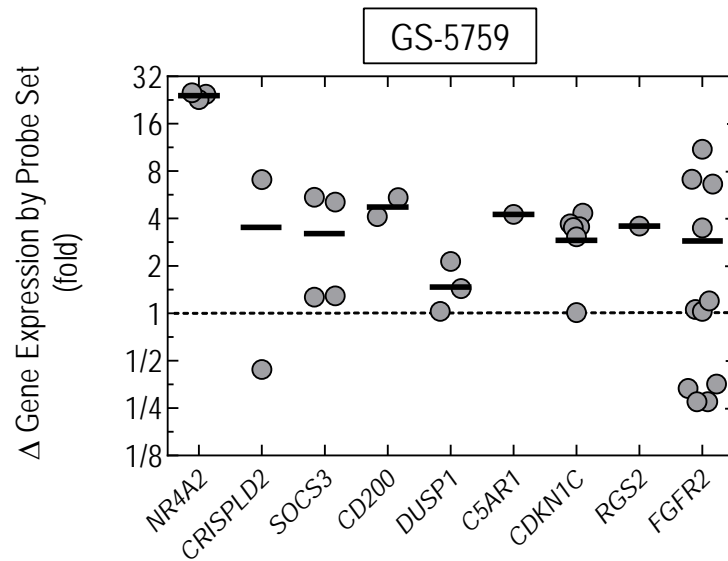


Supplemental Fig. 4. Relationship between gene expression changes in BEAS-2B cells induced by GS-5759 and Ind/GSK. Total RNA was extracted from cells treated with GS-5759 (10nM), Ind/GSK (both at 10nM) or vehicle for 1h, 6h or 18h (panels A, B and C respectively) and processed for gene expression changes by microarray. Transcripts (by probe set) with expression level changes that were statistically different ($P < 0.05$ unadjusted, one-way ANOVA) from time-matched, vehicle-treated cells were subjected to rank order and linear correlations. The values in the red and green coloured quadrants correspond to the number of probes sets indicating gene induction and repression by both treatments respectively. The numbers in the grey quadrants indicate genes (by probe set) that were induced by GS-5759 and repressed by Ind/GSK and *vice versa* although these changes were not validated. The solid and dashed diagonal lines represent linear regression and the line of identity respectively.

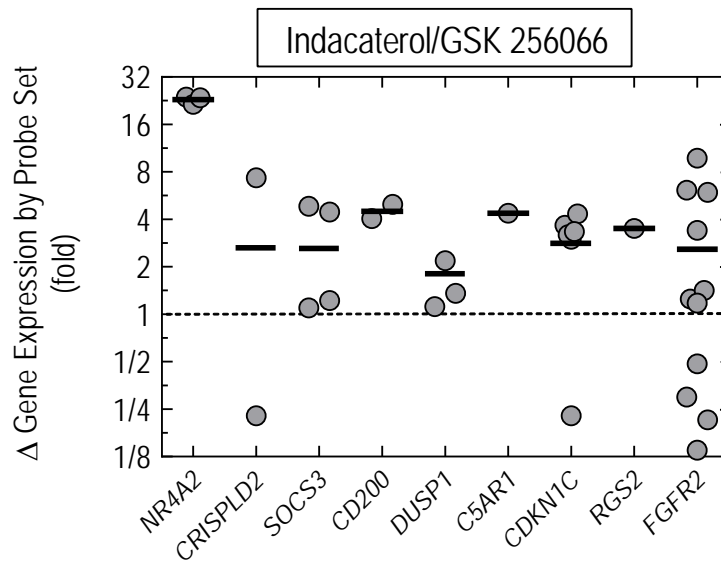


Supplemental Fig. 5. Relationship between gene expression changes determined by microarray and RT-PCR. Total RNA was extracted from cells treated for 2h with GS-5759 (10nM), Ind/GSK (both 10nM) or vehicle and processed for gene expression changes by microarray. The induction of nine genes on the array was then validated by RT-PCR (Fig. 9; Table 5). Changes in expression detected by both methods were subjected to rank order and linear correlations under conditions where the fold induction on the microarray was calculated from the mean of all probe set values (panels A & B) and the highest probe set value (panels C & D). The solid and dashed diagonal lines represent linear regression and the line of identity respectively.

(A)



(B)



Supplemental Fig. 6. Effect of probe set on the assessment of gene expression changes in BEAS-2B cells. Total RNA was extracted from cells treated with GS-5759 (10nM), Ind/GSK (both 10nM) or vehicle for 2h and processed for gene expression changes by microarray. The panels show the effect of treatments relative to vehicle on the expression of nine genes for which there is one or more probe set on each Affymetrix® U133plus2.0 human gene chip. Each probe set is represented by a grey circle and each black horizontal line is the gene expression change calculated using the mean data of all probe sets for that gene. The dashed horizontal line represents baseline gene expression.

Supplemental Table 1. Primer pairs for real-time PCR.

Gene	Oligonucleotide	Accession Number(s)
<i>SOCS3</i>		NM_003955.3
Forward	5' -GAT TCT CCT TCA ATT CCT CAG CTT-3'	
Reverse	5' -ATT AGT TCA GCA TTC CCG AAG TGT-3'	
<i>CRISPLD2</i>		NM_031476.3
Forward	5' -CAA ACC TTC CAG CTC ATT CAT G-3'	
Reverse	5' -GGT CGT GTA GCA GTC CAA ATC C-3'	
<i>C5AR1</i>		NM_001736.3
Forward	5' -TCC TCC GGA ACG TGT TGA CT-3'	
Reverse	5' -AGC GCG TGA ATG ACT TGC T-3'	
<i>FGFR2</i>		NM_000141.4, NM_022970.3, NM_001144913.1, NM_023029.2 NM_001144914.1, NM_001144915.1, NM_001144916.1, NM_001144917.1, NM_001144918.1, NM_001144919.1.
Forward	5' -CAT CGC ATT GGA GGC TAC AAG-3'	
Reverse	5' -GGG ACC ACA CTT TCC ATA ATG AG-3'	
<i>CD200</i>		NM_005944.5, NM_001004196.2
Forward	5' -GGA CTG TGA CCG ACT TTA AGC AA-3'	
Reverse	5' -AGC AAT AGC GGA ACT GAA AAC C-3'	
<i>DUSP1 (MKP1)</i>		NM_004417.3
Forward	5' -CGC GCA AGT CTT CTT CCT CA-3'	
Reverse	5' -GAT GCT TCG CCT CTG CTT CA-3'	
<i>NR4A2</i>		NM_006186.3
Forward	5' -GGC CCA TGT CGA CTC CAA-3'	
Reverse	5' -GTC AGG GTT CGC CTG GAA-3'	
<i>RGS2</i>		NM_002923
Forward	5' -CCT CAA AAG CAA GGA AAA TAT ATA CTG A-3'	
Reverse	5' -AGT TGT AAA GCA GCC ACT TGT AGC T-3'	
<i>CDKN1C (p57^{kip2})</i>		NM_000076.2, NM_001122630.1, NM_001122631.1
Forward	5' -CTG TCC GGG CCT CTG ATC T-3'	
Reverse	5' -CAT CGC CCG ACG ACT TCT-3'	
<i>GAPDH</i>		NM_002046.5, NM_001256799.2
Forward	5' -ATG GAA ATC CCA TCA CCA TCT T-3'	
Reverse	5' -CAG CAT CGC CCC ACT TG-3'	

Forward and reverse primers for each gene are listed. Official HGNC gene symbols are shown and, where appropriate, common genes symbols are provided in parentheses. Generic primers were used for genes that can encode multiple isoforms.

Supplemental Table 2. DAVID-derived functional clusters of related GO terms from all GS-5759-induced genes with expression level changes >2 fold at 1h, 2h, 6h and 18h.

1h GS-5759

<u>Annotation Cluster 1</u>	<u>Enrichment Score: 2.76</u>	<u>Count</u>	<u>P-Value</u>
GOTERM_BP_FAT	behavior	12	1.50E-04
GOTERM_BP_FAT	locomotory behavior	9	2.90E-04
SP_PIR_KEYWORDS	chemotaxis	5	7.20E-04
GOTERM_BP_FAT	chemotaxis	6	3.20E-03
GOTERM_BP_FAT	taxis	6	3.20E-03
GOTERM_BP_FAT	defense response	8	8.70E-02
<u>Annotation Cluster 2</u>	<u>Enrichment Score: 1.89</u>	<u>Count</u>	<u>P-Value</u>
GOTERM_BP_FAT	positive regulation of cellular biosynthetic process	13	1.00E-03
GOTERM_BP_FAT	positive regulation of biosynthetic process	13	1.20E-03
GOTERM_BP_FAT	positive regulation of nitrogen compound metabolic process	12	2.10E-03
GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	9	2.10E-03
GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	14	2.30E-03
GOTERM_BP_FAT	positive regulation of macromolecule biosynthetic process	12	2.30E-03
GOTERM_BP_FAT	positive regulation of gene expression	11	3.10E-03
GOTERM_BP_FAT	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	11	5.20E-03
GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	12	5.20E-03
GOTERM_BP_FAT	positive regulation of transcription	10	8.20E-03
GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	9	9.40E-03
GOTERM_BP_FAT	positive regulation of RNA metabolic process	9	9.90E-03
GOTERM_MF_FAT	transcription regulator activity	18	1.10E-02
SP_PIR_KEYWORDS	transcription regulation	20	1.70E-02
GOTERM_MF_FAT	transcription factor activity	13	1.70E-02
SP_PIR_KEYWORDS	transcription	20	2.10E-02
GOTERM_MF_FAT	transcription activator activity	7	4.30E-02
GOTERM_BP_FAT	regulation of transcription	24	4.30E-02
GOTERM_BP_FAT	regulation of transcription, DNA-dependent	18	4.30E-02
GOTERM_BP_FAT	regulation of RNA metabolic process	18	5.20E-02
GOTERM_BP_FAT	transcription	20	5.50E-02
SP_PIR_KEYWORDS	dna-binding	17	5.70E-02
GOTERM_MF_FAT	sequence-specific DNA binding	8	8.40E-02
SP_PIR_KEYWORDS	nucleus	30	1.50E-01
GOTERM_MF_FAT	DNA binding	18	2.80E-01
<u>Annotation Cluster 3</u>	<u>Enrichment Score: 1.24</u>	<u>Count</u>	<u>P-Value</u>
SP_PIR_KEYWORDS	cytokine	6	3.60E-03
GOTERM_MF_FAT	cytokine activity	6	7.40E-03
GOTERM_BP_FAT	immune response	11	1.00E-02
GOTERM_BP_FAT	inflammatory response	7	1.60E-02
GOTERM_BP_FAT	cell-cell signaling	9	3.20E-02
GOTERM_BP_FAT	response to wounding	8	4.60E-02
KEGG_PATHWAY	cytokine-cytokine receptor interaction	5	8.00E-02
GOTERM_BP_FAT	defense response	8	8.70E-02
GOTERM_CC_FAT	extracellular space	7	1.50E-01
GOTERM_CC_FAT	extracellular region part	7	3.90E-01
GOTERM_CC_FAT	extracellular region	11	6.20E-01
SP_PIR_KEYWORDS	secreted	9	7.40E-01

2h GS-5759

<u>Annotation Cluster 1</u>	<u>Enrichment Score: 3.73</u>	<u>Count</u>	<u>P-Value</u>
GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	26	4.10E-08
GOTERM_MF_FAT	transcription regulator activity	36	4.70E-07
GOTERM_MF_FAT	transcription factor activity	26	5.20E-06
GOTERM_BP_FAT	regulation of transcription, DNA-dependent	38	5.70E-06
GOTERM_BP_FAT	regulation of RNA metabolic process	38	9.60E-06
GOTERM_MF_FAT	sequence-specific DNA binding	19	2.00E-05
GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	16	7.50E-05
GOTERM_BP_FAT	positive regulation of RNA metabolic process	16	8.30E-05
GOTERM_BP_FAT	positive regulation of gene expression	17	2.00E-04
GOTERM_BP_FAT	positive regulation of nitrogen compound metabolic process	18	2.10E-04
SP_PIR_KEYWORDS	transcription regulation	34	2.40E-04
GOTERM_BP_FAT	regulation of transcription	44	2.60E-04
GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	13	3.20E-04
GOTERM_BP_FAT	positive regulation of cellular biosynthetic process	18	4.30E-04
GOTERM_BP_FAT	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	17	4.50E-04
GOTERM_BP_FAT	positive regulation of transcription	16	4.60E-04
GOTERM_BP_FAT	positive regulation of biosynthetic process	18	5.00E-04
GOTERM_BP_FAT	positive regulation of macromolecule biosynthetic process	17	7.40E-04
SP_PIR_KEYWORDS	transcription	33	7.70E-04

GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	19	2.00E-03
GOTERM_MF_FAT	transcription activator activity	12	2.00E-03
SP_PIR_KEYWORDS	nucleus	54	2.50E-03
GOTERM_BP_FAT	transcription	33	7.30E-03
SP_PIR_KEYWORDS	dna-binding	27	9.90E-03
GOTERM_MF_FAT	DNA binding	31	5.30E-02

Annotation Cluster 2

Enrichment Score: 3.47

Count

P-Value

GOTERM_BP_FAT	tube development	14	2.70E-07
GOTERM_BP_FAT	tube morphogenesis	9	3.70E-05
GOTERM_BP_FAT	embryonic morphogenesis	13	5.40E-05
GOTERM_BP_FAT	chordate embryonic development	13	1.10E-04
GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	13	1.20E-04
GOTERM_BP_FAT	embryonic organ development	9	3.10E-04
GOTERM_BP_FAT	sensory organ development	10	4.60E-04
GOTERM_BP_FAT	embryonic organ morphogenesis	7	2.10E-03
GOTERM_BP_FAT	skeletal system development	10	4.50E-03
GOTERM_BP_FAT	pattern specification process	8	1.70E-02
GOTERM_BP_FAT	regionalization	6	4.60E-02

Annotation Cluster 3

Enrichment Score: 3.17

Count

P-Value

GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	26	4.10E-08
GOTERM_BP_FAT	negative regulation of gene expression	15	4.70E-04
GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	12	8.20E-04
GOTERM_BP_FAT	negative regulation of RNA metabolic process	12	9.40E-04
GOTERM_MF_FAT	transcription repressor activity	11	9.50E-04
GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	15	1.00E-03
GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	15	1.30E-03
SP_PIR_KEYWORDS	repressor	12	1.40E-03
GOTERM_BP_FAT	negative regulation of biosynthetic process	15	1.60E-03
GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	14	1.70E-03
GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process	14	1.90E-03
GOTERM_BP_FAT	negative regulation of transcription	13	2.00E-03
GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	17	2.40E-03
GOTERM_BP_FAT	negative regulation of transcription from RNA polymerase II promoter	9	5.00E-03

Annotation Cluster 4

Enrichment Score: 3.17

Count

P-Value

GOTERM_BP_FAT	regulation of apoptosis	24	3.70E-06
GOTERM_BP_FAT	regulation of programmed cell death	24	4.40E-06
GOTERM_BP_FAT	regulation of cell death	24	4.70E-06
GOTERM_BP_FAT	negative regulation of apoptosis	14	4.90E-05
GOTERM_BP_FAT	negative regulation of programmed cell death	14	5.70E-05
GOTERM_BP_FAT	negative regulation of cell death	14	5.90E-05
GOTERM_BP_FAT	anti-apoptosis	10	2.10E-04
GOTERM_BP_FAT	positive regulation of apoptosis	10	2.70E-02
GOTERM_BP_FAT	positive regulation of programmed cell death	10	2.80E-02
GOTERM_BP_FAT	positive regulation of cell death	10	2.90E-02
GOTERM_BP_FAT	induction of apoptosis	5	3.90E-01
GOTERM_BP_FAT	induction of programmed cell death	5	3.90E-01

Annotation Cluster 5

Enrichment Score: 2.71

Count

P-Value

GOTERM_BP_FAT	development of primary male sexual characteristics	6	4.50E-04
GOTERM_BP_FAT	sex differentiation	8	7.60E-04
GOTERM_BP_FAT	male sex differentiation	6	7.70E-04
GOTERM_BP_FAT	reproductive developmental process	10	1.20E-03
GOTERM_BP_FAT	development of primary sexual characteristics	7	1.60E-03
GOTERM_BP_FAT	reproductive structure development	6	8.30E-03
GOTERM_BP_FAT	gonad development	5	2.50E-02

Annotation Cluster 6

Enrichment Score: 2.42

Count

P-Value

GOTERM_MF_FAT	heparin binding	7	4.70E-04
GOTERM_MF_FAT	glycosaminoglycan binding	7	2.30E-03
GOTERM_MF_FAT	polysaccharide binding	7	3.70E-03
GOTERM_MF_FAT	pattern binding	7	3.70E-03
GOTERM_MF_FAT	carbohydrate binding	10	7.20E-03
GOTERM_CC_FAT	extracellular matrix	8	2.70E-02

Annotation Cluster 7

Enrichment Score: 2.08

Count

P-Value

GOTERM_BP_FAT	response to endogenous stimulus	12	2.30E-03
GOTERM_BP_FAT	response to hormone stimulus	11	3.50E-03
GOTERM_BP_FAT	response to organic substance	16	5.10E-03
GOTERM_BP_FAT	cellular response to hormone stimulus	6	1.00E-02
GOTERM_BP_FAT	response to peptide hormone stimulus	6	1.90E-02
GOTERM_BP_FAT	response to steroid hormone stimulus	6	4.20E-02

Annotation Cluster 8

Enrichment Score: 1.99

Count

P-Value

SP_PIR_KEYWORDS	signal	43	3.80E-03
UP_SEQ_FEATURE	signal peptide	43	4.20E-03
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNac...)	51	6.20E-03

SP_PIR_KEYWORDS	glycoprotein	52	8.20E-03
UP_SEQ_FEATURE	disulfide bond	37	1.00E-02
SP_PIR_KEYWORDS	disulfide bond	37	1.60E-02
GOTERM_CC_FAT	extracellular region	26	2.70E-02
SP_PIR_KEYWORDS	secreted	23	3.40E-02

Annotation Cluster 9		Enrichment Score: 1.94	Count	P-Value
GOTERM_BP_FAT	regulation of protein kinase activity	11	2.30E-03	
GOTERM_BP_FAT	regulation of phosphorylation	13	2.30E-03	
GOTERM_BP_FAT	regulation of kinase activity	11	2.90E-03	
GOTERM_BP_FAT	regulation of phosphate metabolic process	13	3.20E-03	
GOTERM_BP_FAT	regulation of phosphorus metabolic process	13	3.20E-03	
GOTERM_BP_FAT	regulation of transferase activity	11	3.90E-03	
GOTERM_BP_FAT	regulation of MAP kinase activity	6	1.30E-02	
GOTERM_BP_FAT	positive regulation of MAP kinase activity	5	1.90E-02	
GOTERM_BP_FAT	positive regulation of protein kinase activity	7	2.40E-02	
GOTERM_BP_FAT	positive regulation of kinase activity	7	2.70E-02	
GOTERM_BP_FAT	positive regulation of transferase activity	7	3.20E-02	
GOTERM_BP_FAT	positive regulation of molecular function	10	1.30E-01	
GOTERM_BP_FAT	positive regulation of catalytic activity	9	1.40E-01	

Annotation Cluster 10		Enrichment Score: 1.68	Count	P-Value
GOTERM_BP_FAT	death	15	1.30E-02	
SP_PIR_KEYWORDS	apoptosis	9	1.80E-02	
GOTERM_BP_FAT	programmed cell death	13	1.80E-02	
GOTERM_BP_FAT	cell death	14	2.60E-02	
GOTERM_BP_FAT	apoptosis	12	3.70E-02	

Annotation Cluster 11		Enrichment Score: 1.66	Count	P-Value
GOTERM_BP_FAT	reproductive developmental process	10	1.20E-03	
GOTERM_BP_FAT	multicellular organism reproduction	12	9.00E-03	
GOTERM_BP_FAT	reproductive process in a multicellular organism	12	9.00E-03	
GOTERM_BP_FAT	sexual reproduction	11	1.60E-02	
GOTERM_BP_FAT	gamete generation	9	4.30E-02	
GOTERM_BP_FAT	male gamete generation	6	1.90E-01	
GOTERM_BP_FAT	spermatogenesis	6	1.90E-01	

Annotation Cluster 12		Enrichment Score: 1.39	Count	P-Value
GOTERM_CC_FAT	extracellular region part	17	6.60E-03	
GOTERM_BP_FAT	response to wounding	12	1.60E-02	
SP_PIR_KEYWORDS	cytokine	6	2.10E-02	
GOTERM_MF_FAT	cytokine activity	6	4.00E-02	
GOTERM_BP_FAT	immune response	13	4.10E-02	
GOTERM_BP_FAT	inflammatory response	8	4.30E-02	
KEGG_PATHWAY	cytokine-cytokine receptor interaction	6	9.90E-02	
GOTERM_CC_FAT	extracellular space	10	1.20E-01	
GOTERM_BP_FAT	defense response	10	1.60E-01	

Annotation Cluster 13		Enrichment Score: 1.38	Count	P-Value
GOTERM_BP_FAT	positive regulation of lymphocyte activation	5	1.60E-02	
GOTERM_BP_FAT	positive regulation of leukocyte activation	5	2.10E-02	
GOTERM_BP_FAT	positive regulation of cell activation	5	2.40E-02	
GOTERM_BP_FAT	regulation of T cell activation	5	2.90E-02	
GOTERM_BP_FAT	regulation of lymphocyte activation	5	5.90E-02	
GOTERM_BP_FAT	regulation of leukocyte activation	5	8.30E-02	
GOTERM_BP_FAT	positive regulation of immune system process	6	8.80E-02	
GOTERM_BP_FAT	regulation of cell activation	5	9.60E-02	

6h GS-5759

Annotation Cluster 1		Enrichment Score: 3.23	Count	P-Value
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	49	4.60E-05	
SP_PIR_KEYWORDS	glycoprotein	49	1.30E-04	
UP_SEQ_FEATURE	disulfide bond	36	2.20E-04	
SP_PIR_KEYWORDS	disulfide bond	36	3.90E-04	
SP_PIR_KEYWORDS	signal	34	8.90E-03	
UP_SEQ_FEATURE	signal peptide	34	9.80E-03	

Annotation Cluster 2		Enrichment Score: 2.27	Count	P-Value
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	49	4.60E-05	
SP_PIR_KEYWORDS	glycoprotein	49	1.30E-04	
GOTERM_CC_FAT	intrinsic to plasma membrane	19	1.40E-03	
GOTERM_CC_FAT	integral to plasma membrane	17	6.70E-03	
SP_PIR_KEYWORDS	membrane	57	7.40E-03	
GOTERM_CC_FAT	plasma membrane	38	8.20E-03	
UP_SEQ_FEATURE	topological domain:Extracellular	30	8.30E-03	
UP_SEQ_FEATURE	topological domain:Cytoplasmic	35	9.70E-03	
UP_SEQ_FEATURE	transmembrane region	46	1.50E-02	

SP_PIR_KEYWORDS	transmembrane	46	1.60E-02
GOTERM_CC_FAT	intrinsic to membrane	49	1.80E-02
GOTERM_CC_FAT	plasma membrane part	23	4.10E-02
GOTERM_CC_FAT	integral to membrane	45	6.40E-02

Annotation Cluster 3		Enrichment Score: 1.6	Count	P-Value
GOTERM_BP_FAT	regulation of phosphorylation	10	5.00E-03	
GOTERM_BP_FAT	regulation of phosphorus metabolic process	10	6.50E-03	
GOTERM_BP_FAT	regulation of phosphate metabolic process	10	6.50E-03	
GOTERM_BP_FAT	regulation of protein kinase activity	6	9.20E-02	
GOTERM_BP_FAT	regulation of kinase activity	6	1.00E-01	
GOTERM_BP_FAT	regulation of transferase activity	6	1.20E-01	

Annotation Cluster 4		Enrichment Score: 2.13	Count	P-Value
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	5	1.20E-02	
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	5	1.20E-02	
INTERPRO	fibronectin, type III-like fold	5	4.10E-02	
INTERPRO	fibronectin, type III	5	4.50E-02	
SMART	FN3	5	7.50E-02	

18h GS-5759

Annotation Cluster 1		Enrichment Score: 1.29	Count	P-Value
GOTERM_CC_FAT	cytoskeletal part	10	9.30E-03	
GOTERM_CC_FAT	cytoskeleton	12	1.40E-02	
SP_PIR_KEYWORDS	cytoskeleton	6	8.60E-02	
GOTERM_CC_FAT	non-membrane-bounded organelle	14	1.80E-01	
GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	14	1.80E-01	

DAVID IDs of genes induced by GS-5759 determined by microarray with significant expression level changes of > 2-fold (based on *P*-value) were used for functional clustering with the following parameters: similarity term overlap = 5; similarity threshold = 0.5; initial group membership = 5; final group membership = 5; multiple linkage threshold = 0.5. Clusters with enrichment scores > 1.2 are shown, which were considered to be significant.

Supplemental Table 3. GS-5759-induced transcripts with expression level changes >2-fold ($P < 0.05$) at 1h, 2h, 6h and 18h used for GO analysis to generate functional clusters

1h GS-5759		<i>139 probe sets are listed correspondinmg to 117 DEGs</i>		
Probe Set ID	Gene Symbol	UniGene Name	Fold Change	P-Value
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	23.35	2.25E-03
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	22.07	1.64E-03
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	21.30	2.20E-03
209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	20.63	9.65E-04
231667_at	SLC39A5	solute carrier family 39 (metal ion transporter), member 5	16.61	1.21E-02
207978_s_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	15.89	4.47E-04
205207_at	IL6	interleukin 6 (interferon, beta 2)	10.99	1.66E-04
208193_at	IL9	interleukin 9	8.81	1.91E-02
1553629_a_at	FAM71B	family with sequence similarity 71, member B	8.71	3.33E-02
233280_at	NEBL	nebullette	8.51	3.82E-02
218541_s_at	C8orf4	chromosome 8 open reading frame 4	8.39	5.75E-03
228964_at	PRDM1	PR domain containing 1, with ZNF domain	7.83	4.00E-06
237648_x_at	SLC9B2	Na ⁺ /H ⁺ exchanger domain containing 2	7.45	2.11E-02
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	6.52	2.56E-03
205476_at	CCL20	chemokine (C-C motif) ligand 20	6.41	8.53E-03
1557660_s_at	FAM170B-AS1	FAM170B antisense RNA 1	6.12	4.79E-02
232570_s_at	ADAM33	ADAM metallopeptidase domain 33	5.86	1.57E-02
236610_at	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	5.73	1.93E-03
239818_x_at	TRIB1	tribbles homolog 1 (Drosophila)	5.71	2.70E-05
244048_x_at	DISC1	disrupted in schizophrenia 1	5.67	1.59E-03
242170_at	ZNF154	zinc finger protein 154	5.60	3.58E-02
240558_at	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila); similar to roundabout 1 isoform b	5.57	4.40E-02
235739_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	5.28	3.65E-02
208078_s_at	SIK1	salt-inducible kinase 1	5.23	2.12E-04
1560788_at	MYO3B	myosin IIIB	4.97	4.31E-02
241796_x_at	DIAPH2	diaphanous homolog 2 (Drosophila)	4.82	1.88E-03
232470_at	SIK1	salt-inducible kinase 1	4.74	3.89E-04
201739_at	SGK1	serum/glucocorticoid regulated kinase 1	4.71	3.50E-05
1562250_at	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	4.68	3.20E-02
202241_at	TRIB1	tribbles homolog 1 (Drosophila)	4.62	9.82E-07
1561200_at	VWA3B	von Willebrand factor A domain containing 3B	4.59	1.06E-02
239145_at	ZNF414	zinc finger protein 414	4.56	1.11E-03
220461_at	PCNXL2	pecanex-like 2 (Drosophila)	4.51	1.87E-04
200951_s_at	CCND2	cyclin D2	4.45	2.03E-02
202340_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1	4.23	1.95E-03
202388_at	RGS2	regulator of G-protein signaling 2, 24kDa	4.01	1.85E-04
217031_at	KRT84	keratin 84	3.87	1.76E-02
202989_at	RGS1	regulator of G-protein signaling 1	3.86	5.77E-03
1555585_a_at	FAM71B	family with sequence similarity 71, member B	3.85	9.40E-04
241207_at	MLK1	megakaryoblastic leukemia (translocation) 1	3.85	4.28E-02
218995_s_at	EDN1	endothelin 1	3.75	2.60E-05
244025_at	ITPR1	inositol 1,4,5-trisphosphate receptor interacting protein	3.75	1.19E-04
226913_s_at	SOX8	SRY (sex determining region Y)-box 8	3.73	3.48E-02
215635_at	PDE8A	phosphodiesterase 8A	3.68	3.66E-02
211143_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1	3.61	1.17E-03
1564044_at	KNCN	kinocilin	3.51	1.83E-02
232746_at	CXCR7	chemokine (C-X-C motif) receptor 7	3.49	1.30E-05
241188_at	IPCEF1	interaction protein for cytohesin exchange factors 1	3.41	8.21E-03
235668_at	PRDM1	PR domain containing 1, with ZNF domain	3.40	5.50E-05
239589_at	RNF43	ring finger protein 43	3.35	1.38E-02
233793_at	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	3.33	1.47E-02
1557285_at	AREG, AREGB	amphiregulin; amphiregulin B	3.32	1.77E-02
201044_x_at	DUSP1	dual specificity phosphatase 1	3.31	2.80E-05
231961_at	RBPMS	RNA binding protein with multiple splicing	3.28	1.03E-02
219243_at	GIMAP4	GTPase, IMAP family member 4	3.27	4.81E-02
237646_x_at	PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	3.26	4.90E-02
201169_s_at	BHLHE40	basic helix-loop-helix family, member e40	3.20	4.51E-03
227613_at	ZNF331	zinc finger protein 331	3.20	9.75E-04
233681_at	KRTAP3-3	keratin associated protein 3-3	3.19	4.42E-02
229039_at	SYN2	synapsin II	3.15	3.28E-02
215289_at	ZNF749	zinc finger protein 749	3.13	6.95E-04
233127_at	ZNF133	zinc finger protein 331	3.12	4.66E-03
242085_at	C2orf18	chromosome 2 open reading frame 18	3.09	1.86E-02
211794_at	FYB	FYN binding protein	3.08	3.37E-02
219228_at	ZNF331	zinc finger protein 331	3.06	1.70E-03
244503_at	BDNF	brain-derived neurotrophic factor	3.04	3.87E-04
238987_at	B4GALNT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	3.03	2.93E-03
234694_at	CNTROB	centrobin, centrosomal BRCA2 interacting protein	3.03	4.37E-02

201170_s_at	<i>BHLHE40</i>	basic helix-loop-helix family, member e40	3.01	5.84E-03
234243_at	<i>RPF1</i>	ribosome production factor 1 homolog (S. cerevisiae)	3.01	2.70E-05
222261_at	<i>TLDC1</i>	TBC/LysM-associated domain containing 1	3.01	7.75E-03
242836_at	<i>ATP1B3</i>	ATPase, Na+/K+ transporting, beta 3 polypeptide	2.96	2.99E-03
237194_at	<i>TSPAN5</i>	tetraspanin 5	2.83	3.61E-02
231678_s_at	<i>ADH4</i>	alcohol dehydrogenase 4 (class II), pi polypeptide	2.79	1.74E-02
217616_at	<i>SIK1</i>	salt-inducible kinase 1	2.79	1.19E-02
1556287_a_at	<i>C6orf182</i>	chromosome 6 open reading frame 182	2.75	4.92E-02
238051_x_at	<i>PWWP2B</i>	PWWP domain containing 2B	2.74	1.79E-02
220088_at	<i>CSAR1</i>	complement component 5a receptor 1	2.73	8.14E-03
1567575_at	<i>BDNF</i>	brain-derived neurotrophic factor	2.71	2.81E-02
1564160_at	<i>DTHD1</i>	death domain containing 1	2.64	1.91E-02
230333_at	<i>SAT1</i>	spermidine/spermine N1-acetyltransferase 1	2.64	1.75E-02
205027_s_at	<i>MAP3K8</i>	mitogen-activated protein kinase kinase kinase 8	2.61	7.00E-05
1561181_at	<i>ARID5B</i>	AT rich interactive domain 5B (MRF1-like)	2.57	9.11E-03
1563040_s_at	<i>LARGE-AS1</i>	LARGE antisense RNA 1	2.57	4.46E-02
233309_at	<i>TMEM2</i>	transmembrane protein 2	2.57	1.20E-03
225582_at	<i>ITPRIP</i>	inositol 1,4,5-trisphosphate receptor interacting protein	2.51	4.61E-04
238317_x_at	<i>RBMS1</i>	RNA binding motif, single stranded interacting protein 1	2.49	2.66E-02
234854_at	<i>MDN1</i>	MDN1, midasin homolog (yeast)	2.47	6.93E-03
221062_at	<i>HS3ST3B1</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	2.45	3.50E-02
1552691_at	<i>ARL11</i>	ADP-ribosylation factor-like 11	2.42	3.66E-02
217425_at	<i>MC2R</i>	melanocortin 2 receptor (adrenocorticotrophic hormone)	2.41	3.05E-02
205239_at	<i>AREG; AREGB</i>	amphiregulin; amphiregulin B	2.40	3.52E-03
241518_at	<i>HTR2C</i>	5-hydroxytryptamine (serotonin) receptor 2C	2.38	3.17E-02
233136_at	<i>PABPC5</i>	poly(A) binding protein, cytoplasmic 5	2.37	4.78E-02
209924_at	<i>CCL18</i>	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated); c-C motif chemokine 18-like	2.36	2.54E-02
222802_at	<i>EDN1</i>	endothelin 1	2.35	2.93E-03
201939_at	<i>PLK2</i>	polo-like kinase 2	2.35	7.96E-03
241691_at	<i>SCARF2</i>	scavenger receptor class F, member 2	2.35	1.35E-02
210082_at	<i>ABCA4</i>	ATP-binding cassette, sub-family A (ABC1), member 4	2.34	1.41E-02
227337_at	<i>ANKRD37</i>	ankyrin repeat domain 37	2.34	4.65E-02
203313_s_at	<i>TGIF1</i>	TGFB-induced factor homeobox 1	2.31	4.19E-04
228962_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	2.29	3.84E-02
210833_at	<i>PTGER3</i>	prostaglandin E receptor 3 (subtype EP3)	2.29	3.27E-03
223801_s_at	<i>APOL4</i>	apolipoprotein L, 4	2.28	3.61E-02
1559987_at	<i>MSI2</i>	musashi homolog 2 (Drosophila)	2.28	1.48E-02
36711_at	<i>MAFF</i>	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.27	5.82E-04
230784_at	<i>PRAC</i>	prostate cancer susceptibility candidate	2.27	9.55E-03
204491_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	2.26	3.21E-02
238808_at	<i>HOXA13</i>	homeobox A13	2.25	2.14E-03
214511_x_at	<i>FCGR1B</i>	Fc fragment of IgG, high affinity Ib, receptor (CD64)	2.22	1.52E-02
234855_at	<i>ORF1</i>	uncharacterized protein, clone pT-Adv JuaX22	2.20	7.16E-03
1562301_at	<i>C8orf34</i>	chromosome 8 open reading frame 34	2.19	4.45E-02
235614_at	<i>TMEM151A</i>	transmembrane protein 151A	2.19	1.83E-02
205193_at	<i>MAFF</i>	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.18	1.12E-03
210836_x_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	2.18	2.94E-02
244026_at	<i>ELL2</i>	elongation factor, RNA polymerase II, 2	2.17	1.14E-03
209582_s_at	<i>CD200</i>	CD200 molecule	2.16	2.14E-02
204011_at	<i>SPRY2</i>	sprouty homolog 2 (Drosophila)	2.16	2.68E-03
229424_s_at	<i>ARHGAP27</i>	Rho GTPase activating protein 27	2.15	2.75E-02
235592_at	<i>ELL2</i>	elongation factor, RNA polymerase II, 2	2.14	1.35E-02
234097_s_at	<i>ZNRD1-AS1</i>	ZNRD1 antisense RNA 1	2.14	3.20E-02
202935_s_at	<i>SOX9</i>	SRY (sex determining region Y)-box 9	2.13	1.98E-02
231445_at	<i>PAX1</i>	paired box 1	2.12	1.09E-02
224039_at	<i>FAM186B</i>	family with sequence similarity 186, member B	2.11	3.40E-03
242659_at	<i>ELF4</i>	E74-like factor 4 (ets domain transcription factor)	2.10	6.34E-02
218177_at	<i>CHMP1B</i>	charged multivesicular body protein 1B	2.09	3.21E-03
222299_x_at	<i>PEX13</i>	peroxisomal biogenesis factor 13	2.09	7.95E-03
210632_s_at	<i>SGCA</i>	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	2.09	2.93E-03
1566901_at	<i>TGIF1</i>	TGFB-induced factor homeobox 1	2.07	5.22E-03
209583_s_at	<i>CD200</i>	CD200 molecule	2.06	1.85E-02
232756_at	<i>KALRN</i>	kalirin, RhoGEF kinase	2.06	1.59E-03
208960_s_at	<i>KLF6</i>	Kruppel-like factor 6	2.05	1.52E-03
1557459_at	<i>SIK2</i>	salt-inducible kinase 2	2.05	2.35E-02
218631_at	<i>AVPI1</i>	arginine vasopressin-induced 1	2.03	4.63E-03
233157_x_at	<i>CCDC114</i>	coiled-coil domain containing 114	2.03	3.04E-02
234792_x_at	<i>IGHA1; IGHV4-31</i>	immunoglobulin heavy constant alpha 1; immunoglobulin heavy variable 4-31	2.03	4.04E-02
237484_at	<i>SMCO3</i>	single-pass membrane protein with coiled-coil domains 3	2.03	6.08E-03
233979_s_at	<i>ESPN</i>	espin	2.01	3.20E-02
243652_at	<i>EYA2</i>	eyes absent homolog 2 (Drosophila)	2.01	9.63E-03

2h GS-5759		<i>252 probe sets are listed corresponding to 152 DEGs</i>		
Probe Set ID	Gene Symbol	UniGene Name	Fold Change	P-Value
209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	77.25	2.70E-05
207978_s_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	32.75	2.50E-05
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	25.22	7.47E-04
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	24.66	1.12E-03
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	22.74	5.89E-04
203639_s_at	FGFR2	fibroblast growth factor receptor 2	11.04	4.25E-02
1556683_x_at	AUTS2	autism susceptibility candidate 2	10.41	4.97E-02
205207_at	IL6	interleukin 6 (interferon, beta 2)	8.88	1.79E-03
234511_at	ANKRD60	ankyrin repeat domain 60	8.56	1.84E-03
218541_s_at	C8orf4	chromosome 8 open reading frame 4	8.48	1.83E-02
232470_at	SIK1	salt-inducible kinase 1	8.20	1.07E-04
206202_at	MEOX2	mesenchyme homeobox 2	7.74	1.51E-03
211401_s_at	FGFR2	fibroblast growth factor receptor 2	7.10	1.79E-02
221541_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	7.08	3.10E-05
228964_at	PRDM1	PR domain containing 1, with ZNF domain	6.98	8.50E-05
203638_s_at	FGFR2	fibroblast growth factor receptor 2	6.63	3.43E-02
208078_s_at	SIK1	salt-inducible kinase 1	6.35	1.10E-05
205476_at	CCL20	chemokine (C-C motif) ligand 20	6.27	7.80E-04
228962_at	PDE4D	phosphodiesterase 4D, cAMP-specific	6.25	1.46E-03
236610_at	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	6.25	1.27E-03
217505_at	KLHL23	kelch-like family member 23	6.08	1.97E-02
244586_x_at	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	5.97	4.21E-02
1557713_at	DIS3L2	DIS3 mitotic control homolog (S. cerevisiae)-like 2	5.55	2.43E-03
201739_at	SGK1	serum/glucocorticoid regulated kinase 1	5.55	1.41E-04
204491_at	PDE4D	phosphodiesterase 4D, cAMP-specific	5.47	5.79E-04
206359_at	SOCS3	suppressor of cytokine signaling 3	5.46	1.33E-02
209582_s_at	CD200	CD200 molecule	5.44	1.98E-04
241099_at	RLP4	elongation protein 4 homolog (S. cerevisiae)	5.30	1.07E-02
210837_s_at	PDE4D	phosphodiesterase 4D, cAMP-specific	5.19	4.66E-04
230081_at	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	5.17	2.33E-02
227697_at	SOCS3	suppressor of cytokine signaling 3	5.11	3.20E-03
244025_at	ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	5.10	2.70E-05
235841_at	MAML3	mastermind-like 3 (Drosophila)	5.09	1.15E-03
211143_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1	5.02	3.42E-04
207038_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	5.00	1.16E-02
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	4.98	5.49E-03
210836_x_at	PDE4D	phosphodiesterase 4D, cAMP-specific	4.70	1.37E-03
243486_at	SND1	staphylococcal nuclease and tudor domain containing 1	4.51	8.60E-05
202340_x_at	NR4A1	nuclear receptor subfamily 4, group A, member 1	4.42	7.52E-04
210997_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	4.41	3.53E-02
220088_at	CSAR1	complement component 5a receptor 1	4.26	2.40E-05
225582_at	ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	4.25	5.00E-06
239604_at	RBMS3	RNA binding motif, single stranded interacting protein	4.17	8.32E-03
209583_s_at	CD200	CD200 molecule	4.12	4.48E-04
230333_at	SAT1	spermidine/spermine N1-acetyltransferase 1	4.12	1.95E-03
230748_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	4.03	1.56E-02
227613_at	ZNF331	zinc finger protein 331	4.03	7.40E-05
203548_s_at	LPL	lipoprotein lipase	3.88	1.79E-02
237479_at	SPAG16	sperm associated antigen 16	3.84	3.46E-02
239367_at	BDNF	brain-derived neurotrophic factor	3.83	1.07E-03
228128_x_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.81	3.00E-05
203549_s_at	LPL	lipoprotein lipase	3.80	1.14E-02
234419_x_at	IGHA1; IGHG1; IGHG3; IGHM; IGHV4-31	immunoglobulin heavy constant alpha 1; gamma 1 (G1m marker); gamma 3 (G3m marker); mu; heavy variable 4-31	3.79	8.69E-03
206382_s_at	BDNF	brain-derived neurotrophic factor	3.78	8.78E-04
239818_x_at	TRIB1	tribbles homolog 1 (Drosophila)	3.78	1.42E-04
206546_at	SYCP2	synaptonemal complex protein 2	3.77	2.89E-02
224828_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	3.76	6.52E-04
219682_s_at	TBX3	T-box 3	3.73	1.00E-05
202241_at	TRIB1	tribbles homolog 1 (Drosophila)	3.72	6.40E-05
237593_at	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	3.71	1.59E-02
1552908_at	GCSAML	germinal center-associated, signaling and motility-like	3.68	5.65E-03
219228_at	ZNF331	zinc finger protein 331	3.65	1.11E-04
209631_s_at	GPR37; SEL1L2	G protein-coupled receptor 37 (endothelin receptor type B-like); sel-1 suppressor of lin-12-like 2 (C. elegans)	3.62	1.50E-05
218177_at	CHMP1B	charged multivesicular body protein 1B	3.60	8.40E-04
202388_at	RGS2	regulator of G-protein signaling 2, 24kDa	3.59	2.39E-04
242840_at	DAB1	disabled homolog 1 (Drosophila)	3.56	4.04E-02
220483_s_at	RNF19A	ring finger protein 19A, E3 ubiquitin protein ligase	3.56	1.79E-03
1564718_at	ZHX2	zinc fingers and homeoboxes 2	3.56	4.55E-02
229552_at	HRK; LOC283454	harakiri, BCL2 interacting protein (contains only BH3 domain); uncharacterized LOC283454	3.55	3.84E-03
229709_at	ATP1B3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	3.52	6.24E-03
213006_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	3.50	5.31E-03

208228_s_at	FGFR2	fibroblast growth factor receptor 2	3.49	4.86E-02
1567656_at	OR2H1	olfactory receptor, family 2, subfamily H, member 1	3.49	2.37E-02
1569042_at	LRP1	low density lipoprotein receptor-related protein 1	3.48	3.93E-03
224940_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.47	3.00E-06
224942_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.45	8.23E-04
205239_at	AREG; AREGB	amphiregulin; amphiregulin B	3.44	4.41E-04
206865_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	3.43	3.43E-03
224831_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	3.35	1.14E-04
224941_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.33	4.20E-05
224829_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	3.30	1.66E-04
201981_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.29	6.41E-04
219316_s_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	3.24	2.97E-02
228325_at	SPDR	Scaffolding Protein Involved In DNA Repair	3.22	6.70E-03
242009_at	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	3.20	3.63E-03
238987_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	3.13	5.37E-03
218995_s_at	EDN1	endothelin 1	3.04	3.60E-05
218178_s_at	CHMP1B	charged multivesicular body protein 1B	3.03	8.44E-04
204456_s_at	GAS1	growth arrest-specific 1	3.01	2.52E-02
205027_s_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8	2.99	4.00E-06
1559141_s_at	FAM87A; FAM87B	family with sequence similarity 87, member A; family with sequence similarity 87, member B	2.98	5.59E-03
209355_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	2.97	7.44E-04
1557285_at	AREG, AREGB	amphiregulin; amphiregulin B	2.96	1.20E-02
225606_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	2.95	2.87E-02
230986_at	KLF8	Kruppel-like factor 8	2.94	4.73E-02
227337_at	ANKRD37	ankyrin repeat domain 37	2.91	1.84E-03
225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.91	1.30E-05
212977_at	CXCR7	chemokine (C-X-C motif) receptor 7	2.90	2.63E-02
205466_s_at	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.90	3.94E-02
216236_s_at	SLC2A14; SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 14; solute carrier family 2 (facilitated glucose transporter), member 3	2.88	1.24E-03
205193_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.85	4.50E-05
1553036_at	GPR111	G protein-coupled receptor 111	2.82	4.99E-02
203984_s_at	CASP9	caspase 9, apoptosis-related cysteine peptidase	2.81	4.74E-03
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.81	4.00E-05
224917_at	MIR21	microRNA 21	2.79	6.16E-03
222802_at	EDN1	endothelin 1	2.78	1.21E-04
225544_at	TBX3	T-box 3	2.77	5.10E-05
227443_at	LURAP1L	leucine rich adaptor protein 1-like	2.76	1.86E-02
226614_s_at	FAM167A	family with sequence similarity 167, member A	2.75	1.41E-04
225987_at	STEAP4	STEAP family member 4	2.73	1.74E-02
241340_at	CASP4	caspase 4, apoptosis-related cysteine peptidase	2.72	1.19E-02
236911_at	RIMKLB	ribosomal modification protein rimK-like family member B	2.72	1.31E-03
244277_at	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	2.71	2.83E-02
1567303_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	2.68	2.01E-02
228187_at	GAS1	growth arrest-specific 1	2.68	3.71E-02
202497_x_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	2.68	1.38E-03
223484_at	C15orf48	chromosome 15 open reading frame 48	2.67	1.03E-02
216627_s_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	2.66	6.77E-03
212226_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	2.65	9.57E-04
235668_at	PRDM1	PR domain containing 1, with ZNF domain	2.65	1.48E-02
218880_at	FOSL2	FOS-like antigen 2	2.64	2.44E-04
1553133_at	C9orf72	chromosome 9 open reading frame 72	2.63	4.38E-04
214438_at	HLX	H2.0-like homeobox	2.63	2.30E-03
242870_at	RIMKLB	ribosomal modification protein rimK-like family member B	2.61	1.88E-03
229004_at	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	2.60	1.40E-02
227099_s_at	C11orf96	chromosome 11 open reading frame 96	2.59	8.32E-03
202499_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	2.59	1.61E-03
210775_x_at	CASP9	caspase 9, apoptosis-related cysteine peptidase	2.58	5.36E-03
209101_at	CTGF	connective tissue growth factor	2.56	7.20E-05
237187_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.55	8.35E-03
235421_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8	2.55	3.44E-03
231035_s_at	OTUD1	OTU domain containing 1	2.55	8.13E-04
231367_s_at	FNDC3A	fibronectin type III domain containing 3A	2.54	1.46E-03
223379_s_at	LATS2	large tumor suppressor kinase 2	2.54	9.70E-03
217616_at	SIK1	salt-inducible kinase 1	2.54	1.84E-02
222088_s_at	SLC2A14; SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 14; solute carrier family 2 (facilitated glucose transporter), member 3	2.54	1.39E-03
1558143_a_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	2.53	2.78E-02
239123_at	TSC22D1	TSC22 domain family, member 1	2.52	4.00E-03
224797_at	ARRDC3	arrestin domain containing 3	2.51	4.93E-02
218631_at	AVPI1	arginine vasopressin-induced 1	2.50	8.90E-05
229720_at	BAG1	BCL2-associated athanogene	2.49	1.64E-02
203795_s_at	BCL7A	B-cell CLL/lymphoma 7A	2.49	4.06E-03
227188_at	EVA1C	eva-1 homolog C (C. elegans)	2.49	4.17E-02
218881_s_at	FOSL2	FOS-like antigen 2	2.49	2.61E-04
212099_at	RHOB	ras homolog family member B	2.49	2.63E-03
240845_at	EVI5	ecotropic viral integration site 5	2.48	1.27E-02

212230_at	<i>PPAP2B</i>	phosphatidic acid phosphatase type 2B	2.48	1.47E-03
223085_at	<i>RNF19A</i>	ring finger protein 19A, E3 ubiquitin protein ligase	2.48	1.54E-03
237252_at	<i>THBD</i>	thrombomodulin	2.48	6.28E-03
215111_s_at	<i>TSC22D1</i>	TSC22 domain family, member 1	2.47	9.28E-03
237512_at	<i>NAV2</i>	neuron navigator 2	2.46	4.92E-04
202498_s_at	<i>SLC2A3</i>	solute carrier family 2 (facilitated glucose transporter), member 3	2.46	2.29E-03
237451_x_at	<i>CASP9</i>	caspase 9, apoptosis-related cysteine peptidase	2.45	1.16E-02
214446_at	<i>ELL2</i>	elongation factor, RNA polymerase II, 2	2.45	2.20E-03
224325_at	<i>FZD8</i>	frizzled family receptor 8	2.45	2.03E-02
203574_at	<i>NFIL3</i>	nuclear factor, interleukin 3 regulated	2.45	1.62E-02
1553962_s_at	<i>RHOB</i>	ras homolog family member B	2.45	2.04E-03
1568644_at	<i>ZNF208</i>	zinc finger protein 208	2.45	2.04E-02
215990_s_at	<i>BCL6</i>	B-cell CLL/lymphoma 6	2.43	4.29E-03
205409_at	<i>FOSL2</i>	FOS-like antigen 2	2.43	3.90E-04
218723_s_at	<i>RGCC</i>	regulator of cell cycle	2.42	4.14E-03
203796_s_at	<i>BCL7A</i>	B-cell CLL/lymphoma 7A	2.39	5.89E-03
202723_s_at	<i>FOXO1</i>	forkhead box O1	2.38	2.96E-02
239461_at	<i>GALNT15</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15	2.38	3.00E-02
214586_at	<i>GPR37</i>	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.38	6.43E-04
209681_at	<i>SLC19A2</i>	solute carrier family 19 (thiamine transporter), member 2	2.38	1.45E-04
220335_x_at	<i>CES3</i>	carboxylesterase 3	2.37	3.81E-03
1555585_a_at	<i>FAM71B</i>	family with sequence similarity 71, member B	2.37	6.79E-03
233379_at	<i>PRR5L</i>	proline rich 5 like	2.37	2.66E-03
224480_s_at	<i>AGPAT9</i>	1-acylglycerol-3-phosphate O-acyltransferase 9	2.36	8.71E-03
208536_s_at	<i>BCL2L11</i>	BCL2-like 11 (apoptosis facilitator)	2.36	3.98E-02
222015_at	<i>CSNK1E</i>	casein kinase 1, epsilon	2.36	4.39E-04
209480_at	<i>HLA-DQB1</i>	major histocompatibility complex, class II, DQ beta 1	2.36	7.92E-03
243969_at	<i>SLC24A4</i>	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	2.36	3.76E-03
1553613_s_at	<i>FOXO1</i>	forkhead box C1	2.34	1.11E-03
214520_at	<i>FOXO2</i>	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	2.34	9.33E-03
207626_s_at	<i>SLC7A2</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.34	6.74E-04
203313_s_at	<i>TGIF1</i>	TGF-beta-induced factor homeobox 1	2.34	2.38E-04
228834_at	<i>TOB1</i>	transducer of ERBB2, 1	2.34	3.50E-05
244503_at	<i>BDNF</i>	brain-derived neurotrophic factor	2.33	8.83E-04
208250_s_at	<i>DMBT1</i>	deleted in malignant brain tumors 1	2.33	4.81E-03
226858_at	<i>CSNK1E</i>	casein kinase 1, epsilon	2.32	8.99E-04
210136_at	<i>MBP</i>	myelin basic protein	2.30	3.58E-04
209772_s_at	<i>CD24</i>	CD24 molecule	2.29	3.64E-02
237978_at	<i>COL8A1</i>	collagen, type VIII, alpha 1	2.29	1.19E-02
201169_s_at	<i>BHLHE40</i>	basic helix-loop-helix family, member e40	2.27	5.23E-03
1555777_at	<i>POSTN</i>	periostin, osteoblast specific factor	2.27	5.36E-03
200771_s_at	<i>PTP4A1</i>	protein tyrosine phosphatase type IVA, member 1	2.27	6.40E-03
1554544_a_at	<i>MBP</i>	myelin basic protein	2.26	8.44E-04
210409_at	<i>MLLT4-AS1</i>	MLLT4 antisense RNA 1 (head to head)	2.26	1.16E-03
219737_s_at	<i>PCDH9</i>	protocadherin 9	2.26	4.62E-02
208606_s_at	<i>WNT4</i>	wingless-type MMTV integration site family, member 4	2.26	1.44E-03
202023_at	<i>EFNA1</i>	ephrin-A1	2.24	1.74E-04
241404_at	<i>EPHA5</i>	EPH receptor A5	2.22	2.76E-04
205896_at	<i>SLC22A4</i>	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	2.22	1.04E-02
237006_at	<i>AFF1</i>	AF4/FMR2 family, member 1	2.21	3.43E-04
225407_at	<i>MBP</i>	myelin basic protein	2.21	1.19E-04
231798_at	<i>NOG</i>	noggin	2.21	3.11E-03
203888_at	<i>THBD</i>	thrombomodulin	2.21	3.88E-03
228188_at	<i>FOSL2</i>	FOS-like antigen 2	2.20	2.02E-04
213221_s_at	<i>SIK2</i>	salt-inducible kinase 2	2.20	2.71E-03
203140_at	<i>BCL6</i>	B-cell CLL/lymphoma 6	2.19	9.44E-03
222343_at	<i>BCL2L11</i>	BCL2-like 11 (apoptosis facilitator)	2.18	2.98E-02
244026_at	<i>ELL2</i>	elongation factor, RNA polymerase II, 2	2.18	1.72E-02
225262_at	<i>FOSL2</i>	FOS-like antigen 2	2.18	8.70E-05
202149_at	<i>NEDD9</i>	neural precursor cell expressed, developmentally down-regulated 9	2.18	3.65E-02
217584_at	<i>NPC1</i>	Niemann-Pick disease, type C1	2.18	3.83E-04
211631_x_at	<i>B4GALT1</i>	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	2.17	6.10E-03
224572_s_at	<i>IRF2BP2</i>	interferon regulatory factor 2 binding protein 2	2.17	2.09E-02
225955_at	<i>METRNL</i>	meteorin, glial cell differentiation regulator-like	2.17	6.43E-03
203887_s_at	<i>THBD</i>	thrombomodulin	2.17	2.88E-03
1569003_at	<i>VMP1</i>	vacuole membrane protein 1	2.17	1.19E-02
201170_s_at	<i>BHLHE40</i>	basic helix-loop-helix family, member e40	2.15	1.83E-03
201044_x_at	<i>DUSP1</i>	dual specificity phosphatase 1	2.14	3.21E-04
202768_at	<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	2.14	1.71E-02
201473_at	<i>JUNB</i>	jun B proto-oncogene	2.14	4.79E-02
228293_at	<i>DEPDC7</i>	DEP domain containing 7	2.13	1.00E-02
213260_at	<i>FOXO1</i>	forkhead box C1	2.13	1.85E-03
219433_at	<i>BCOR</i>	BCL6 corepressor	2.12	1.38E-02
216598_s_at	<i>CCL2</i>	chemokine (C-C motif) ligand 2	2.12	7.52E-03
238432_at	<i>DLGAP1-AS1</i>	DLGAP1 antisense RNA 1	2.12	4.50E-03
202150_s_at	<i>NEDD9</i>	neural precursor cell expressed, developmentally down-regulated 9	2.12	2.74E-02
226140_s_at	<i>OTUD1</i>	OTU domain containing 1	2.12	8.22E-03

204654_s_at	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	2.12	4.98E-04
1567575_at	BDNF	brain-derived neurotrophic factor	2.11	6.43E-03
225999_at	RIMKLB	ribosomal modification protein rimK-like family member B	2.10	2.51E-04
223566_s_at	BCOR	BCL6 corepressor	2.09	1.01E-02
204602_at	DKK1	dickkopf WNT signaling pathway inhibitor 1	2.09	9.02E-03
207826_s_at	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	2.09	2.73E-02
223430_at	SIK2	salt-inducible kinase 2	2.09	6.67E-03
201925_s_at	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	2.08	7.31E-04
229889_at	FAM211A	family with sequence similarity 211, member A	2.08	9.43E-04
217371_s_at	IL15	interleukin 15	2.08	3.39E-04
226444_at	SLC39A10	solute carrier family 39 (zinc transporter), member 10	2.07	1.18E-02
231067_s_at	AKAP12	A kinase (PRKA) anchor protein 12	2.06	5.27E-03
206864_s_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.06	6.55E-03
235085_at	SGK223	homolog of rat pragra of Rnd2	2.06	3.77E-03
202935_s_at	SOX9	SRY (sex determining region Y)-box 9	2.06	1.16E-02
228284_at	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	2.06	2.10E-02
205177_at	TNNT1	troponin I type 1 (skeletal, slow)	2.06	2.02E-02
204014_at	DUSP4	dual specificity phosphatase 4	2.05	1.22E-04
1566901_at	TGIF1	TGFB-induced factor homeobox 1	2.05	1.82E-03
226575_at	ZNF462	zinc finger protein 462	2.05	3.73E-04
242836_at	ATP1B3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	2.04	1.66E-02
223916_s_at	BCOR	BCL6 corepressor	2.04	1.72E-02
1569153_at	GRAMD4	GRAM domain containing 4	2.04	6.51E-03
226034_at	DUSP4	dual specificity phosphatase 4	2.02	7.70E-05
217875_s_at	PMEPA1	prostate transmembrane protein, androgen induced 1	2.02	4.53E-02
215992_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	2.02	8.45E-03
236352_at	VGLL2	vestigial like 2 (Drosophila)	2.02	1.46E-02
206035_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	2.01	1.88E-02
202936_s_at	SOX9	SRY (sex determining region Y)-box 9	2.01	2.25E-02

6h GS-5759		<i>178 probe sets are listed corresponding to 134 DEGs</i>		
Probe Set ID	Gene Symbol	UniGene Name	Fold Change	P-Value
218541_s_at	C8orf4	chromosome 8 open reading frame 4	10.24	7.50E-05
221541_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	9.72	9.60E-05
230189_x_at	NSMF	NMDA receptor synaptonuclear signaling and neuronal migration factor	9.61	4.51E-02
209959_at	NRA43	nuclear receptor subfamily 4, group A, member 3	9.49	1.75E-03
1570422_at	SNTG2	syntrophin, gamma 2	8.93	4.44E-02
215912_at	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	7.53	3.34E-02
219049_at	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	7.49	3.10E-05
228128_x_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	6.62	1.47E-04
231961_at	RBPMS	RNA binding protein with multiple splicing	6.62	1.04E-02
224941_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	6.29	7.50E-05
1569693_at	BTBD8	BTB (POZ) domain containing 8	6.16	3.93E-02
222784_at	SMOC1	SPARC related modular calcium binding 1	6.14	8.75E-03
224940_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	5.94	5.40E-05
224942_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	5.84	2.70E-05
1558654_at	PPM1H	protein phosphatase, Mg2+/Mn2+ dependent, 1H	5.61	2.93E-02
243438_at	PDE7B	phosphodiesterase 7B	5.43	1.91E-04
244434_at	GPR82	G protein-coupled receptor 82	5.42	1.05E-02
222783_s_at	SMOC1	SPARC related modular calcium binding 1	5.20	9.77E-03
243275_at	BMPR1A	bone morphogenetic protein receptor, type IA; similar to ALK-3	5.09	1.99E-02
239461_at	GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15	4.93	8.45E-03
215382_x_at	TPSAB1	trypsin alpha/beta 1	4.81	1.58E-03
234129_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	4.78	3.85E-02
228962_at	PDE4D	phosphodiesterase 4D, cAMP-specific	4.72	9.72E-03
216951_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	4.67	1.22E-02
1564580_at	DAB1	disabled homolog 1 (Drosophila)	4.62	1.91E-03
203549_s_at	LPL	lipoprotein lipase	4.61	8.52E-03
201981_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	4.60	1.03E-04
230109_at	PDE7B	phosphodiesterase 7B	4.45	3.30E-05
203548_s_at	LPL	lipoprotein lipase	4.38	1.15E-02
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	4.33	1.10E-02
206519_x_at	SIGLEC6	sialic acid binding Ig-like lectin 6	4.16	1.01E-02
238649_at	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	4.04	6.09E-04
1569262_x_at	UBE3D	ubiquitin protein ligase E3D	3.95	4.50E-02
243273_at	PPFIA2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	3.93	2.72E-02
234587_at	IL1RAPL1	interleukin 1 receptor accessory protein-like 1	3.90	2.84E-02
1553938_a_at	STK32A	serine/threonine kinase 32A	3.89	1.45E-02
225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	3.86	2.90E-05
228501_at	GALNT15	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15	3.72	4.80E-04
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	3.72	1.61E-02
233502_at	CNTN3	contactin 3 (plasmacytoma associated)	3.70	1.50E-02
220461_at	PCNXL2	pecanex-like 2 (Drosophila)	3.67	2.94E-02

237280_at	<i>TCTE1</i>	t-complex-associated-testis-expressed 1	3.67	1.62E-02
216167_at	<i>LRRN2</i>	leucine rich repeat neuronal 2	3.66	3.18E-02
208606_s_at	<i>WNT4</i>	wingless-type MMTV integration site family, member 4	3.59	6.95E-03
1557538_at	<i>MED13L</i>	mediator complex subunit 13-like	3.51	3.80E-03
241119_at	<i>ANGPT1</i>	angiopoietin 1	3.50	3.15E-02
220190_s_at	<i>GTF2A1L</i>	general transcription factor IIA, 1-like	3.49	1.97E-02
236361_at	<i>GALNT15</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15	3.46	9.98E-04
229709_at	<i>ATP1B3</i>	ATPase, Na+/K+ transporting, beta 3 polypeptide	3.45	5.02E-03
239622_at	<i>TRAP1</i>	TNF receptor-associated protein 1	3.43	4.55E-02
219093_at	<i>PID1</i>	phosphotyrosine interaction domain containing 1	3.42	1.12E-02
204622_x_at	<i>NR4A2</i>	nuclear receptor subfamily 4, group A, member 2	3.34	1.42E-02
225987_at	<i>STEAP4</i>	STEAP family member 4	3.34	4.29E-04
204491_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	3.27	2.31E-03
220187_at	<i>STEAP4</i>	STEAP family member 4	3.26	4.30E-05
1553199_at	<i>DCAF4L2</i>	DDB1 and CUL4 associated factor 4-like 2	3.23	6.81E-03
213182_x_at	<i>CDKN1C</i>	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	3.14	4.60E-02
1569850_at	<i>LPHN2</i>	latrophilin 2	3.14	4.59E-02
224098_at	<i>ABAT</i>	4-aminobutyrate aminotransferase	3.13	1.70E-03
224071_at	<i>IL20</i>	interleukin 20	3.05	1.13E-02
205501_at	<i>PDE10A</i>	phosphodiesterase 10A	3.04	4.61E-04
228507_at	<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	3.03	1.95E-02
1560516_at	<i>TMEM26</i>	transmembrane protein 26	2.95	3.82E-02
210982_s_at	<i>HLA-DRA</i>	major histocompatibility complex, class II, DR alpha	2.93	1.17E-02
239650_at	<i>NCKAP5</i>	NCK-associated protein 5	2.93	4.34E-03
207038_at	<i>SLC16A6</i>	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	2.92	8.09E-03
216894_x_at	<i>CDKN1C</i>	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.89	4.93E-02
1555585_a_at	<i>FAM71B</i>	family with sequence similarity 71, member B	2.89	4.47E-04
220540_at	<i>KCNK15</i>	potassium channel, subfamily K, member 15	2.86	8.51E-04
37020_at	<i>CRP</i>	C-reactive protein, pentraxin-related	2.83	3.21E-02
236300_at	<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	2.83	1.64E-02
207768_at	<i>EGR4</i>	early growth response 4	2.80	2.31E-02
237939_at	<i>EPHA5</i>	EPH receptor A5	2.79	2.00E-05
241404_at	<i>EPHA5</i>	EPH receptor A5	2.79	7.38E-03
213348_at	<i>CDKN1C</i>	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.78	4.71E-02
244272_s_at	<i>TC2N</i>	tandem C2 domains, nuclear	2.74	2.92E-02
216627_s_at	<i>B4GALT1</i>	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	2.73	6.56E-04
210836_x_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	2.73	6.57E-03
226913_s_at	<i>SOX8</i>	SRY (sex determining region Y)-box 8	2.73	3.23E-02
231773_at	<i>ANGPTL1</i>	angiopoietin-like 1	2.71	1.48E-03
213183_s_at	<i>CDKN1C</i>	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.70	4.80E-02
242202_at	<i>INTS4</i>	integrator complex subunit 4	2.69	1.01E-02
206389_s_at	<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	2.68	2.70E-02
220492_s_at	<i>OTOF</i>	otoferlin	2.67	1.56E-02
210837_s_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific	2.66	4.04E-03
230748_at	<i>SLC16A6</i>	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	2.66	5.40E-03
230714_s_at	<i>UBE2S</i>	ubiquitin-conjugating enzyme E2S	2.66	7.44E-03
1558489_at	<i>RCL1</i>	RNA terminal phosphate cyclase-like 1	2.65	9.33E-03
235770_at	<i>MASP1</i>	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	2.64	2.21E-02
220088_at	<i>CSAR1</i>	complement component 5a receptor 1	2.63	2.50E-03
1555006_at	<i>WDR66</i>	WD repeat domain 66	2.59	3.55E-02
209583_s_at	<i>CD200</i>	CD200 molecule	2.58	2.01E-02
217201_at	<i>RASAL2</i>	RAS protein activator like 2	2.58	3.90E-02
208425_s_at	<i>TANC2</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	2.58	2.03E-03
206947_at	<i>B3GALT5</i>	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	2.57	3.34E-02
1560172_at	<i>INTS10</i>	integrator complex subunit 10	2.55	5.15E-03
218177_at	<i>CHMP1B</i>	charged multivesicular body protein 1B	2.54	2.37E-03
207626_s_at	<i>SLC7A2</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.53	3.71E-04
225801_at	<i>FBXO32</i>	F-box protein 32	2.51	1.40E-03
209582_s_at	<i>CD200</i>	CD200 molecule	2.50	1.82E-02
1552993_at	<i>DYDC1</i>	DPY30 domain containing 1	2.50	3.90E-02
222015_at	<i>CSNK1E</i>	casein kinase 1, epsilon	2.48	4.80E-05
229552_at	<i>HRK</i>	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.48	3.90E-02
1566931_at	<i>TFB2M</i>	transcription factor B2, mitochondrial	2.48	4.00E-02
223484_at	<i>C15orf48</i>	chromosome 15 open reading frame 48	2.47	1.54E-02
1558387_at	<i>NKAIN3</i>	Na+/K+ Transporting ATPase interacting 3	2.47	1.33E-02
216289_at	<i>GPR144</i>	G protein-coupled receptor 144	2.46	2.03E-02
240362_at	<i>MPC1</i>	mitochondrial pyruvate carrier 1	2.46	1.68E-02
213006_at	<i>CEBPD</i>	CCAAT/enhancer binding protein (C/EBP), delta	2.44	7.78E-03
1555994_at	<i>DIAPH3-AS1</i>	DIAPH3 antisense RNA 1	2.44	3.03E-02
238919_at	<i>PCDH9</i>	protocadherin 9	2.44	2.91E-02
208078_s_at	<i>SIK1</i>	salt-inducible kinase 1	2.44	1.17E-02
208400_at	<i>GLP1R</i>	glucagon-like peptide 1 receptor	2.43	1.92E-03
227697_at	<i>SQCS3</i>	suppressor of cytokine signaling 3	2.41	8.20E-03
227173_s_at	<i>BACH2</i>	BTB and CNC homology 1, basic leucine zipper transcription factor 2	2.38	2.13E-02
1555007_s_at	<i>WDR66</i>	WD repeat domain 66	2.38	3.18E-02
228132_at	<i>ABLIM2</i>	actin binding LIM protein family, member 2	2.37	7.86E-03
203628_at	<i>IGF1R</i>	insulin-like growth factor 1 receptor	2.35	1.05E-04

201810_s_at	<i>SH3BP5</i>	SH3-domain binding protein 5 (BTK-associated)	2.35	2.90E-04
236610_at	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	2.34	4.56E-02
228964_at	<i>PRDM1</i>	PR domain containing 1, with ZNF domain	2.34	3.46E-02
209772_s_at	<i>CD24</i>	CD24 molecule	2.31	3.20E-02
235367_at	<i>MYPN</i>	myopalladin	2.31	7.22E-03
1552736_a_at	<i>NETO1</i>	neuropilin (NRP) and tolloid (TLL)-like 1	2.30	1.14E-02
230439_at	<i>RBAK</i>	RB-associated KRAB zinc finger	2.29	4.37E-02
228325_at	<i>SPDR</i>	scaffolding Protein Involved In DNA Repair	2.29	3.62E-03
211631_x_at	<i>B4GALT1</i>	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	2.25	5.42E-04
221140_s_at	<i>GPR132</i>	G protein-coupled receptor 132	2.25	1.02E-03
238029_s_at	<i>SLC16A14</i>	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	2.24	1.03E-03
229414_at	<i>PITPNC1</i>	phosphatidylinositol transfer protein, cytoplasmic 1	2.22	8.71E-03
225978_at	<i>RIMKLB</i>	ribosomal modification protein rimK-like family member B	2.22	1.25E-03
232470_at	<i>SIK1</i>	salt-inducible kinase 1	2.21	2.52E-02
235650_at	<i>CDHR3</i>	cadherin-related family member 3	2.20	2.80E-02
218865_at	<i>MARC1</i>	mitochondrial amidoxime reducing component 1	2.19	3.36E-03
203627_at	<i>IGF1R</i>	insulin-like growth factor 1 receptor	2.17	1.68E-03
1558552_s_at	<i>C3orf55</i>	chromosome 3 open reading frame 55	2.16	2.40E-02
208651_x_at	<i>CD24</i>	CD24 molecule	2.16	2.95E-02
226858_at	<i>CSNK1E</i>	casein kinase 1, epsilon	2.16	2.02E-04
236440_at	<i>NETO1</i>	neuropilin (NRP) and tolloid (TLL)-like 1	2.16	2.23E-02
224952_at	<i>TANC2</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	2.16	2.13E-03
231367_s_at	<i>FNDC3A</i>	fibronectin type III domain containing 3A	2.14	3.42E-03
225999_at	<i>RIMKLB</i>	ribosomal modification protein rimK-like family member B	2.14	8.04E-03
206616_s_at	<i>ADAM22</i>	ADAM metallopeptidase domain 22	2.13	3.09E-03
213436_at	<i>CNR1</i>	cannabinoid receptor 1 (brain)	2.12	1.49E-03
241717_at	<i>MOBP</i>	myelin-associated oligodendrocyte basic protein	2.12	4.84E-03
1564022_at	<i>ZNF804B</i>	zinc finger protein 804B	2.12	2.43E-02
208650_s_at	<i>CD24</i>	CD24 molecule	2.11	3.48E-02
220335_x_at	<i>CES3</i>	carboxylesterase 3	2.11	2.99E-02
238455_at	<i>PLXDC2</i>	plexin domain containing 2	2.11	7.15E-03
207864_at	<i>SCN7A</i>	sodium channel, voltage-gated, type VII, alpha subunit	2.11	2.65E-02
205896_at	<i>SLC22A4</i>	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	2.11	8.33E-03
200731_s_at	<i>PTP4A1</i>	protein tyrosine phosphatase type IVA, member 1	2.10	4.14E-03
218723_s_at	<i>RGCC</i>	regulator of cell cycle	2.10	1.49E-02
220006_at	<i>EFCC1</i>	EF-hand and coiled-coil domain containing 1	2.09	3.51E-02
206864_s_at	<i>HRK</i>	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.08	2.61E-02
219155_at	<i>PITPNC1</i>	phosphatidylinositol transfer protein, cytoplasmic 1	2.08	1.17E-02
221305_s_at	<i>UGT1A8; UGT1A9</i>	UDP glucuronosyltransferase 1 family, polypeptide A8; UDP glucuronosyltransferase 1 family, polypeptide A9	2.08	1.66E-03
1568949_at	<i>PITPNC1</i>	phosphatidylinositol transfer protein, cytoplasmic 1	2.07	9.42E-03
236297_at	<i>C10orf112</i>	chromosome 10 open reading frame 112	2.06	5.55E-03
1564690_at	<i>C9orf41</i>	chromosome 9 open reading frame 41	2.06	3.20E-02
206633_at	<i>CHRNA1</i>	cholinergic receptor, nicotinic, alpha 1 (muscle)	2.06	4.29E-02
206915_at	<i>NKX2-2</i>	NK2 homeobox 2	2.06	3.80E-03
207978_s_at	<i>NR4A3</i>	nuclear receptor subfamily 4, group A, member 3	2.06	1.91E-02
211274_at	<i>TBX1</i>	T-box 1	2.06	3.90E-02
224917_at	<i>MIR21</i>	microRNA 21	2.05	4.12E-02
206388_at	<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	2.05	7.39E-03
205092_x_at	<i>ZBTB1</i>	zinc finger and BTB domain containing 1	2.05	5.11E-03
202238_s_at	<i>NNMT</i>	nicotinamide N-methyltransferase	2.04	7.08E-04
266_s_at	<i>CD24</i>	CD24 molecule	2.03	4.53E-02
242659_at	<i>ELF4</i>	E74-like factor 4 (ets domain transcription factor)	2.03	2.46E-02
220343_at	<i>PDE7B</i>	phosphodiesterase 7B	2.03	1.03E-04
236348_at	<i>TMEM176B</i>	transmembrane protein 176B	2.03	1.14E-02
1552325_at	<i>CCDC11</i>	coiled-coil domain containing 11	2.02	1.50E-02
214292_at	<i>ITGB4</i>	integrin, beta 4	2.02	3.06E-03
1561654_at	<i>LIMK2</i>	LIM domain kinase 2	2.02	2.94E-02
228748_at	<i>CD59</i>	CD59 molecule, complement regulatory protein	2.01	2.44E-03
240709_at	<i>SEZ6L</i>	seizure related 6 homolog (mouse)-like	2.01	1.56E-03
224963_at	<i>SLC26A2</i>	solute carrier family 26 (sulfate transporter), member 2	2.01	2.66E-03

18h GS-5759		<i>75 probe sets are listed corresponding to 75 DEGs</i>		
Probe Set ID	Gene Symbol	UniGene Name	Fold Change	P-Value
233973_at	<i>LYZL1</i>	lysozyme-like 1	10.64	7.35E-03
220645_at	<i>NXPE4</i>	neurexophilin and PC-esterase domain family, member 4	10.43	4.15E-02
216122_at	<i>NAV1</i>	neuron navigator 1	8.23	1.27E-02
220065_at	<i>TNMD</i>	tenomodulin	6.60	1.39E-04
231799_at	<i>TANC2</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	5.07	4.67E-02
239931_at	<i>MYC</i>	v-myc myelocytomatosis viral oncogene homolog (avian)	4.81	2.67E-02
1553573_s_at	<i>EFNA2</i>	ephrin-A2	4.60	5.28E-04
231667_at	<i>SLC39A5</i>	solute carrier family 39 (metal ion transporter), member 5	4.58	3.95E-02
236028_at	<i>IBSP</i>	integrin-binding sialoprotein	4.57	3.70E-03

231336_at	<u>CPNE4</u>	copine IV	4.38	4.09E-02
242952_at	<u>HDAC9</u>	histone deacetylase 9	4.32	3.63E-02
217417_at	<u>MYO5A</u>	myosin VA (heavy chain 12, myosin)	4.08	1.44E-02
240093_x_at	<u>GOLSYN</u>	Golgi-localized protein	3.87	1.26E-03
241369_at	<u>ADAMTS9</u>	ADAM metalloproteinase with thrombospondin type 1 motif, 9	3.72	2.21E-02
243167_at	<u>ABCB5</u>	ATP-binding cassette, sub-family B (MDR/TAP), member 5	3.71	3.76E-02
1553355_at	<u>TMPRSS6</u>	transmembrane protease, serine 6	3.51	5.07E-03
216167_at	<u>LRRN2</u>	leucine rich repeat neuronal 2	3.44	1.42E-02
207523_at	<u>C6orf10</u>	chromosome 6 open reading frame 10	3.41	3.94E-02
240679_at	<u>STK32B</u>	serine/threonine kinase 32B	3.10	4.22E-02
214770_at	<u>MSR1</u>	macrophage scavenger receptor 1	3.05	4.43E-02
1560642_at	<u>ESPN</u>	espin	3.00	4.40E-05
1568902_at	<u>ARL8A</u>	ADP-ribosylation factor-like 8A	2.92	3.85E-02
214122_at	<u>PDLIM7</u>	PDZ and LIM domain 7 (enigma)	2.86	4.12E-02
239183_at	<u>ANGPTL1</u>	angiopoietin-like 1	2.85	2.60E-02
209480_at	<u>HLA-DQB1</u>	major histocompatibility complex, class II, DQ beta 1	2.82	1.26E-02
237720_at	<u>ASB4</u>	ankyrin repeat and SOCS box containing 4	2.79	1.22E-03
215593_at	<u>GCNT2</u>	glucosaminyl (N-acetyl) transferase 2, l-branching enzyme (I blood group)	2.78	2.83E-02
236735_at	<u>C3orf63</u>	chromosome 3 open reading frame 63	2.76	3.57E-02
220394_at	<u>FGF20</u>	fibroblast growth factor 20	2.73	2.30E-02
237328_at	<u>C14orf105</u>	chromosome 14 open reading frame 105	2.71	2.88E-03
215612_at	<u>TBC1D5</u>	TBC1 domain family, member 5	2.69	2.86E-02
207599_at	<u>MMP20</u>	matrix metalloproteinase 20	2.68	3.27E-02
230061_at	<u>TM4SF18</u>	transmembrane 4 L six family member 18	2.68	4.55E-02
1561280_at	<u>LEMD1-AS1</u>	LEMD1 antisense RNA 1	2.57	2.90E-03
1558452_at	<u>TMEM144</u>	transmembrane protein 144	2.54	1.34E-03
220899_at	<u>COPG2</u>	coatamer protein complex, subunit gamma 2	2.49	1.12E-02
215853_at	<u>SDCCAG8</u>	serologically defined colon cancer antigen 8	2.45	1.56E-03
223524_s_at	<u>TMEM108</u>	transmembrane protein 108	2.45	2.73E-02
214206_at	<u>PP1L6</u>	peptidylprolyl isomerase (cyclophilin)-like 6	2.42	8.64E-04
241839_at	<u>DLG3-AS1</u>	DLG3 antisense RNA 1; NULL	2.41	1.67E-02
1569570_at	<u>AGBL4</u>	ATP/GTP binding protein-like 4	2.39	4.62E-02
1566948_at	<u>DLG2</u>	discs, large homolog 2 (Drosophila)	2.39	3.73E-02
1566284_at	<u>REV3L</u>	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	2.36	3.27E-02
240388_at	<u>KRT27</u>	keratin 27	2.33	2.42E-02
234772_s_at	<u>KRTAP2-1; KRTAP2-2</u>	keratin associated protein 2-1; keratin associated protein 2-2	2.32	4.08E-02
243003_at	<u>MLLT10</u>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	2.30	2.30E-02
232578_at	<u>CLDN18</u>	claudin 18	2.29	4.59E-02
240839_at	<u>MAU2</u>	MAU2 sister chromatid cohesion factor	2.29	2.20E-02
1553765_a_at	<u>KLHL32</u>	kelch-like family member 32	2.28	2.93E-02
241518_at	<u>HTR2C</u>	5-hydroxytryptamine (serotonin) receptor 2C	2.26	1.91E-02
241509_at	<u>PLEKHA5</u>	pleckstrin homology domain containing, family A member 5	2.26	4.37E-02
209855_s_at	<u>KLK2</u>	kallikrein-related peptidase 2	2.24	1.54E-02
1553905_at	<u>CXorf22</u>	chromosome X open reading frame 22	2.22	2.44E-02
1569978_x_at	<u>GPR172A</u>	G protein-coupled receptor 172A	2.22	1.99E-02
241026_at	<u>ADAM12</u>	ADAM metalloproteinase domain 12	2.19	4.49E-02
239608_at	<u>LPCAT4</u>	lysophosphatidylcholine acyltransferase 4	2.19	3.48E-03
239530_at	<u>ADD2</u>	adducin 2 (beta)	2.18	2.79E-03
1562573_at	<u>CYP17A1</u>	cytochrome P450, family 17, subfamily A, polypeptide 1	2.18	4.31E-02
220224_at	<u>HAO1</u>	hydroxyacid oxidase (glycolate oxidase) 1	2.16	4.91E-02
211154_at	<u>THPO</u>	thrombopoietin	2.16	3.26E-02
207848_at	<u>AVP</u>	arginine vasopressin	2.15	4.12E-02
1557057_a_at	<u>C5orf47</u>	chromosome 5 open reading frame 47	2.15	1.21E-02
216502_at	<u>ISG20L2</u>	interferon stimulated exonuclease gene 20kDa-like 2	2.13	2.07E-02
1563040_s_at	<u>LARGE-AS1</u>	LARGE antisense RNA 1	2.13	3.62E-03
239328_at	<u>RCS1</u>	RCS1 domain containing 1	2.12	7.03E-03
220006_at	<u>EFCC1</u>	EF-hand and coiled-coil domain containing 1	2.10	1.79E-03
220540_at	<u>KCNK15</u>	potassium channel, subfamily K, member 15	2.10	1.11E-02
1552675_at	<u>DNAJB7</u>	DnaJ (Hsp40) homolog, subfamily B, member 7	2.09	2.71E-02
233884_at	<u>HIVEP3</u>	human immunodeficiency virus type I enhancer binding protein 3	2.09	3.10E-02
220626_at	<u>SERPINA10</u>	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 10	2.07	3.45E-02
1569461_at	<u>KCNT1</u>	potassium channel, subfamily T, member 1	2.06	1.92E-02
240254_at	<u>TNIK</u>	TRAF2 and NCK interacting kinase	2.06	3.66E-02
215784_at	<u>CD1E</u>	CD1e molecule	2.01	3.82E-02
207393_at	<u>HCRTR2</u>	hypocretin (orexin) receptor 2	2.01	1.02E-02
232992_at	<u>SAYS1</u>	SAYS1 motif domain containing 1	2.01	4.01E-02

Transcripts used for RT-PCR validation are bolded and underlined.