Supplemental Material

Analysis of the Indacaterol-Regulated Transcriptome in Human Airway Epithelial Cells Implicates Gene Expression Changes in the Adverse and Therapeutic Effects of β_2-Adrenoceptor Agonists

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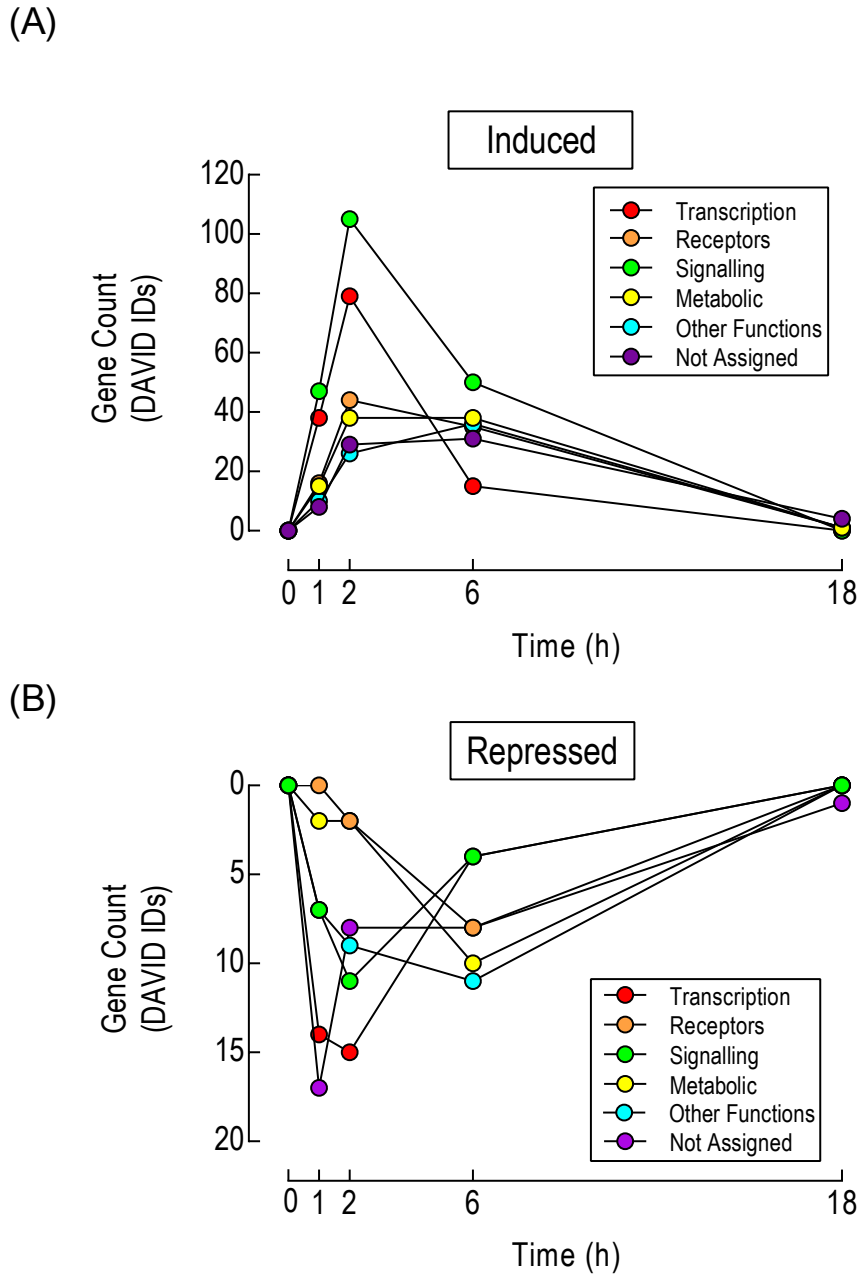
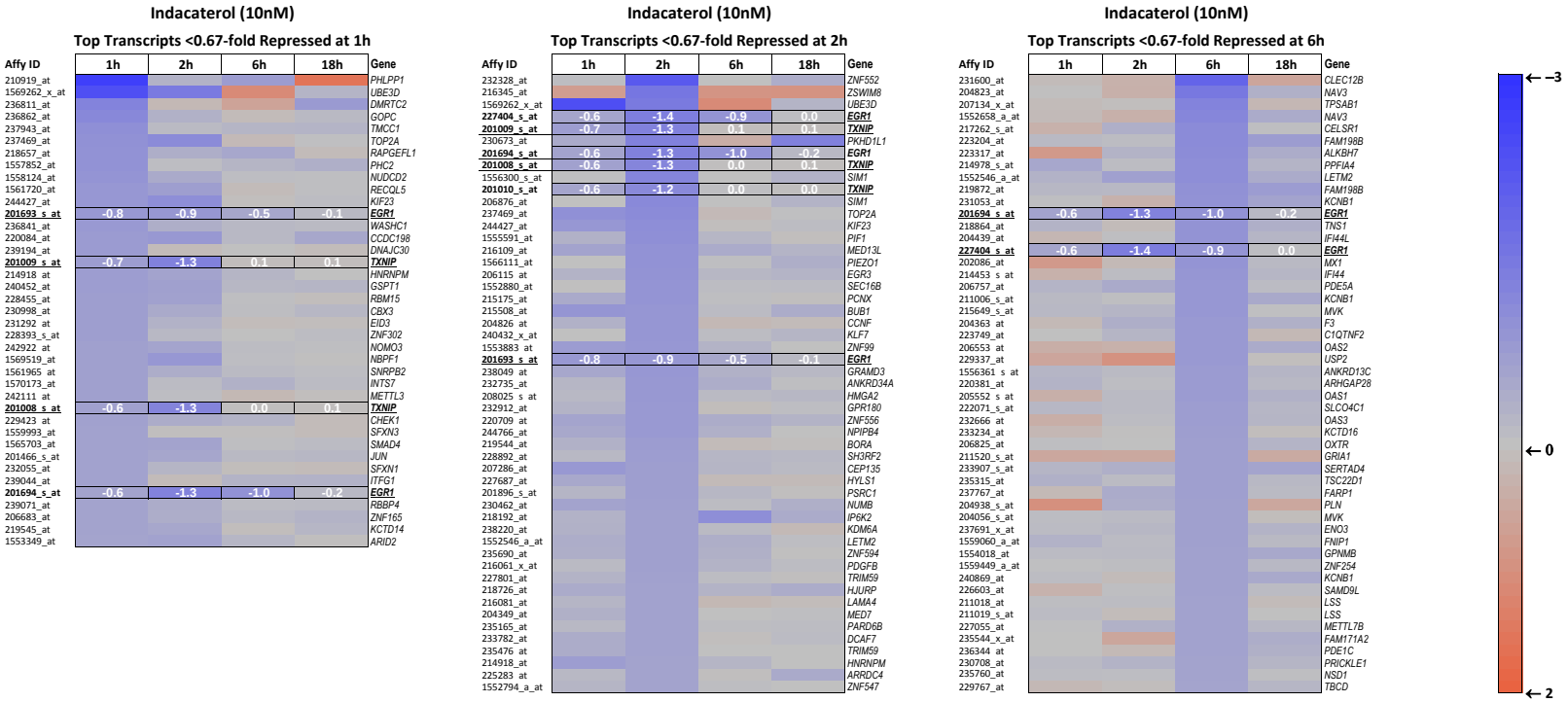


Supplemental Fig. 1. Effect of indacaterol on the number of significantly induced and repressed genes (panels A and B respectively) at 1h, 2h, 6h and 18h that were annotated with one of the six broad GO terms used in figure 4.

Supplemental Fig. 2. Heats maps showing the effect of indacaterol on gene induction in BEAS-2B cells treated with indacaterol (10nM) for 1h, 2h and 6h. The top induced transcripts by probe set that were statistically different from time-matched, vehicle-treated cells at each time-point (FDR *P*-value <0.1) were ranked highest to lowest and presented as heat maps relative to changes of the same transcripts at the other two time-points. The colour scale is logarithmic (base 2) with the most intense red and blue colours representing a 128-fold increase ($\log_2 = 7$) and an 2-fold decrease ($\log_2 = -1$) in gene expression respectively. The right hand-side and left hand-side of every row in each heat map shows the gene name and corresponding Affymetrix identification number (Affy ID). Genes validated by PCR are underlined and bolded in black, and their expression level changes are shown in each cell in $\log_2$ format. At 2h, *DMBT1* was the 128th highest transcript induced by indacaterol.



Supplemental Fig. 3. Heats maps showing the effect of indacaterol on gene repression in BEAS-2B cells treated with indacaterol (10nM) for 1h, 2h and 6h. The top repressed transcripts by probe set that were statistically different from time-matched, vehicle-treated cells at each time-point (FDR *P* value <0.1) were ranked highest to lowest and presented as heat maps relative to changes of the same transcripts at the other two time-points. The colour scale is logarithmic (base 2) with the most intense blue and red colours representing a 8-fold decrease ($\log_2 = -3$) and an 4-fold increase ($\log_2 = 2$) in gene expression respectively. The right hand-side and left hand-side of every row in each heat map shows the gene name and corresponding Affymetrix identification number (Affy ID). Genes validated by PCR are underlined and bolded in black, and their expression level changes are shown in each cell in log2 format.

Supplemental TABLE 1. Donor demographics.

Donor ID#	Age	Gender	Ethnicity	Smoker	Cause of Death	Source of Epithelial Cells
p42	18	Male	Caucasian	No	Head Trauma	Right Lung
p48	22	Male	Caucasian	Yes	Anoxia	Left Lung
p72	62	Male	Caucasian	No	Intracerebral Haemorrhage	Right Lung
p78	60	Male	Hispanic	Yes	Head Trauma	Left Lung
p82	42	Male	Caucasian	Yes	Intracerebral Haemorrhage	Right Lung

Supplemental TABLE 2. Primer pairs for real-time PCR. Official HGNC gene symbols are shown. When appropriate common gene symbols are provided in parentheses. Generic primers were used for genes that encode multiple isoforms.

Gene	Oligonucleotides	Accession Number(s)
AVPI1		NM_021732.2
Forward	5′-AAGGCTGTGGAAGAGGTTGG-3′	
Reverse	5′-TGTGGATGCTCACACTGAAGG-3′	
BDNF		NM_001352269.1, NM_001352270.1, NM_001352267.1, NM_001352271, NM_020734.4, NM_001352268.1, NM_001297776.1, XM_017019690.1, XM_017019683.1, XM_017019684.1, XM_017019685.1, XM_017019686.1 XM_017019687.1, XM_017019688.1, XM_017019689.1
Forward	5′-GGCGGCAGACAAAAAGACTG-3′	
Reverse	5′-TGGGATTGCACTTGGTCTCG-3′	
C5AR1		NM_001736.3
Forward	5′-TCCTCCGGAACGTGTTGACT-3′	
Reverse	5′-AGCGCGTGAATGACTTGCT-3′	
CD200		NM_005944.5, NM_001004196.2
Forward	5′-GGACTGTGACCGACTTTAAGCAA-3′	
Reverse	5′-AGCAATAGCGGAACTGAAAACC-3′	
***CDKN1C* (*p57^{kip2}*)**		NM_000076.2, NM_001122630.1, NM_001122631.1
Forward	5′-CTGTCCGGGCCTCTGATCT-3′	
Reverse	5′-CATCGCCCGACGACTTCT-3′	
CEBPD		NM_005195
Forward	5′-GGAGATGCAGCAGAAGTTGGT-3′	
Reverse	5′-CGCGCTGGTGCAGCTT-3′	
DEPDC7		NM_139160.2, NM_001077242.1
Forward	5′-GACTCTCAGGAAGATGAGTGG-3′	
Reverse	5′-GTCTGGTTGCTCAGGAAAGC-3′	
DMBT1		NM_004406.2, NM_007329.2, NM_017579.2, NM_001320644.1
Forward	5′-GGTGGCATCCAACAACTACAA-3′	
Reverse	5′-GTAGGATGGGCTGGAGAATGT-3′	
***DUSP1* (*MKP1*)**		NM_004417.3
Forward	5′-CGCGCAAGTCTTCTTCCTCA-3′	
Reverse	5′-GATGCTTCGCCTCTGCTTCA-3′	
EDN1		NM_001955.4, NM_001168319.1
Forward	5′-TGATTTTCTCTCTGCTGTTTGTGG-3′	
Reverse	5′-GCGCCTAAGACTGCTGTTTCT-3′	

Gene	Oligonucleotides	Accession Number(s)
EGR1		NM_001964.2
Forward	5′-ACCTGACCGCAGAGTCTTTT-3′	
Reverse	5′-GAGTGGTTTGGCTGGGGTAA-3′	
EPHA4		NM_001304537.1, NM_001304536.1, NM_004438.4, XM_005246374.2
Forward	5′-GGATCATTGGAGATGGGGCT-3′	
Reverse	5′-GTATTTACTCCGTCTCCGGCT-3′	
FGFR2		NM_000141.4, NM_022970.3, NM_001144913.1, NM_023029.2
Forward	5′-CATCGCATTGGAGGCTACAAG-3′	NM_001144914.1, NM_001144915.1, NM_001144916.1,
Reverse	5′-GGGACCACACTTTCCATAATGAG-3′	NM_001144917.1, NM_001144918.1, NM_001144919.1.
GAPDH		NM_002046.5, NM_001256799.2
Forward	5′-ATGGAAATCCCATCACCATCTT-3′	
Reverse	5′-CAGCATCGCCCCACTTG-3′	
GAS1		NM_002048.2
Forward	5′-CAGATTGTCGCCAGTGAGGA-3′	
Reverse	5′-TCTGGGCCGCAGATACAAACA-3′	
IL6		NM_000600.4, NM_001318095.1
Forward	5′-GAGTAGTGAGGAACAAGCCAG-3′	
Reverse	5′-GTCAGGGGTGGTTATTGCATC-3′	
IL11		NM_000641.3, NM_001267718.1
Forward	5′-GGGACCACAACCTGGATTC-3′	
Reverse	5′-CGCAGGTAGGACAGTAGGT-3′	
NR4A1		NM_002135.4, NM_173157.2, NM_001202233.1, NM_001202234.1
Forward	5′-GCATGGTGAAGGAAGTTGTCCG-3′	
Reverse	5′-GGGGCTGCTTGGGTTTTGAA-3′	
NR4A2		NM_006186.3
Forward	5′-GGCCCATGTCGACTCCAA-3′	
Reverse	5′-GTCAGGGTTCGCCTGGAA-3′	
NR4A3		NM_006981.3, NM_173200.2, NM_173199.2
Forward	5′-GTAGACAAGAGACGTCGAAACC-3′	
Reverse	5′-CCTCTCCTCCCTTTCAGACTAT-3′	
PDE4D		NM_006203.4, NM_001104631.1, NM_001165899.1, NM_001197218.1,
Forward	5′-CTCTCTGAAATGAGTCGGTCTG-3′	NM_001197219.1, NM_001197220.1, NM_001197221.1, NM_001197222.1,
Reverse	5′-CCTTCTGAGTTGGAGAAGGAAT-3′	NM_001197223.1

Gene	Oligonucleotides	Accession Number(s)
PDK4		NM_002612.3
Forward	5′-GCTGTCCATGAAGCAGCTACTG-3′	
Reverse	5′-CGCAAAAATGCAAAAGAAGTTCT-3′	
PPP1R3C		NM_005398.6
Forward	5′-CCTAATGAGCTGCACCAGAATG-3′	
Reverse	5′-TCACAGGTGGTGAATGTGCC-3′	
RGS2		NM_002923
Forward	5′-CCTCAAAAGCAAGGAAAATATATACTGA-3′	
Reverse	5′-AGTTGTAAAGCAGCCACTTGTAGCT-3′	
RIMKLB		NM_001352269.1, NM_001352270.1, NM_001352267.1, NM_001352271,
Forward	5′-GCGGGGTCACAGAGGTAAAG-3′	NM_020734.4, NM_001352268.1, NM_001297776.1, XM_017019690.1,
Reverse	5′-GGAACAGGTATGGCGCTTCA-3′	XM_017019683.1, XM_017019684.1, XM_017019685.1,
		XM_017019686.1, XM_017019687.1, XM_017019688.1
SGK1		NM_001291995.1, NM_001143676.1, NM_001143677.1, NM_001143678.1
Forward	5′-ATGGCCTGCCGCCTTTTTAT-3′	NM_005627.3, XM_011536071.1
Reverse	5′-CAGGAGGTGTCTTGCGGAAT-3′	
SLC7A2		NM_001164771.1, NM_001008539.3, NM_003046.5, XM_017013747,
Forward	5′-GGATTCCTAGCTTTCCTCGTG-3′	XM_005273610.4, XM_005273611.4, XM_005273612.4
Reverse	5′-GCCTGGTGATGGCATGAACT-3′	
SMOC1		NM_022137.5, NM_001034852.2, XM_005267995.1, XM_005267996.1
Forward	5′-GGCGTTTCACCGACTACTGT-3′	
Reverse	5′-AGGCGTCCTACTTCTTTGCT-3′	
SOCS3		NM_003955.3
Forward	5′-GATTCTCCTTCAATTCCTCAGCTT-3′	
Reverse	5′-ATTAGTTCAGCATTCCCGAAGTGT-3′	
STEAP4		NM_001205316.1, NM_001205315.1, NM_024636.3
Forward	5′-GTTCCGATTTGTCCAGTCCA-3′	
Reverse	5′-GGCTGAGGAATCTCTTCCCAC-3′	
TXNIP		NM_006472.5, XM_017000085.1
Forward	5′-AGACCAGCCAACAGGTGAGA-3′	
Reverse	5′-AGGAAGCTCAAAGCCGAACT-3′	

Supplemental TABLE 3. Indacaterol-induced transcripts with expression level changes >1.5-fold (*FDR* < 0.10) at 1h, 2h, 6h and 18h.

Transcriptional Regulators
Transporters, Ion Channels and Membrane Receptors
Metabolic Proteins
General Signalling Molecules, including Translational Regulators
Other Functions
Not Assigned

Indacaterol (1h)
(173 Probe Sets ≡ 134 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
204621_s_at	**4929**	***NR4A2***	**2.10E-03**	**25.34**	**nuclear receptor subfamily 4, group A, member 2**	
207978_s_at	8013	*NR4A3*	2.40E-03	21.95	nuclear receptor subfamily 4, group A, member 3	
216248_s_at	**4929**	***NR4A2***	**1.40E-03**	**21.76**	**nuclear receptor subfamily 4, group A, member 2**	
204622_x_at	**4929**	***NR4A2***	**1.60E-03**	**20.56**	**nuclear receptor subfamily 4, group A, member 2**	
209959_at	8013	*NR4A3*	2.80E-03	18.20	nuclear receptor subfamily 4, group A, member 3	
205207_at	3569	*IL6*	5.78E-05	11.20	interleukin 6	
205476_at	6364	*CCL20*	1.93E-02	7.04	chemokine (C-C motif) ligand 20	
239145_at	84330	*ZNF414*	1.00E-01	6.62	zinc finger protein 414	
228964_at	639	*PRDM1*	5.78E-05	6.48	PR domain containing 1, with ZNF domain	
208078_s_at	150094 102724428	*SIK1* *LOC102724428*	2.00E-04	5.07	salt-inducible kinase 1 serine/threonine-protein kinase SIK1	
209774_x_at	2920	*CXCL2*	5.78E-05	4.91	chemokine (C-X-C motif) ligand 2	
233972_s_at	55079	*FEZF2*	8.52E-02	4.90	FEZ family zinc finger 2	
239818_x_at	10221	*TRIB1*	5.00E-04	4.71	tribbles pseudokinase 1	
232470_at	150094 102724428	*SIK1* *LOC102724428*	3.00E-04	4.65	salt-inducible kinase 1 serine/threonine-protein kinase SIK1	
238378_at	285513	*GPRIN3*	1.10E-02	4.48	GPRIN family member 3	
202241_at	10221	*TRIB1*	5.78E-05	4.46	tribbles pseudokinase 1	
201739_at	**6446**	***SGK1***	**1.00E-04**	**4.42**	**serum/glucocorticoid regulated kinase 1**	
205960_at	**5166**	***PDK4***	**1.00E-04**	**4.41**	**pyruvate dehydrogenase kinase, isozyme 4**	
202388_at	**5997**	***RGS2***	**6.58E-05**	**4.33**	**regulator of G-protein signaling 2**	
1557285_at	374	*AREG*	1.88E-02	3.79	amphiregulin	
225207_at	**5166**	***PDK4***	**2.90E-03**	**3.78**	**pyruvate dehydrogenase kinase, isozyme 4**	
218995_s_at	1906	*EDN1*	2.00E-04	3.63	endothelin 1	
201044_x_at	**1843**	***DUSP1***	**2.00E-04**	**3.49**	**dual specificity phosphatase 1**	
222802_at	1906	*EDN1*	2.00E-04	3.47	endothelin 1	
1555585_a_at	153745	*FAM71B*	8.10E-03	3.42	family with sequence similarity 71, member B	
227613_at	55422	*ZNF331*	2.60E-03	3.39	zinc finger protein 331	
201169_s_at	8553	*BHLHE40*	2.00E-04	3.37	basic helix-loop-helix family, member e40	
202340_x_at	3164	*NR4A1*	3.40E-03	3.35	nuclear receptor subfamily 4, group A, member 1	
211143_x_at	3164	*NR4A1*	1.30E-03	3.28	nuclear receptor subfamily 4, group A, member 1	
213139_at	6591	*SNAI2*	6.58E-05	3.24	snail family zinc finger 2	
219228_at	55422	*ZNF331*	3.40E-03	3.22	zinc finger protein 331	
244025_at	85450	*ITPRIP*	6.00E-04	3.17	inositol 1,4,5-trisphosphate receptor interacting protein	
201170_s_at	8553	*BHLHE40*	7.07E-05	3.07	basic helix-loop-helix family, member e40	
224797_at	57561	*ARRDC3*	9.10E-03	2.88	arrestin domain containing 3	
205764_at	1452	*CSNK1A1*	2.51E-02	2.78	casein kinase 1, alpha 1	
203395_s_at	3280	*HES1*	1.40E-02	2.77	hes family bHLH transcription factor 1	
221841_s_at	9314	*KLF4*	3.50E-03	2.75	Kruppel-like factor 4 (gut)	
225582_at	85450	*ITPRIP*	3.00E-04	2.66	inositol 1,4,5-trisphosphate receptor interacting protein	
203394_s_at	3280	*HES1*	4.70E-03	2.65	hes family bHLH transcription factor 1	
239530_at	119	*ADD2*	6.44E-02	2.64	adducin 2 (beta)	
238987_at	2683	*B4GALT1*	1.16E-02	2.48	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	
205239_at	374	*AREG*	1.76E-02	2.41	amphiregulin	
240413_at	149628	*PYHIN1*	2.32E-02	2.38	pyrin and HIN domain family, member 1	
203313_s_at	7050	*TGIF1*	7.00E-04	2.37	TGFB-induced factor homeobox 1	
210632_s_at	6442	*SGCA*	9.68E-02	2.35	sarcoglycan alpha	
227337_at	353322	*ANKRD37*	7.00E-03	2.34	ankyrin repeat domain 37	
220088_at	**728**	***C5AR1***	**2.60E-03**	**2.30**	**complement component 5a receptor 1**	
36711_at	23764	*MAFF*	4.70E-03	2.29	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	
205290_s_at	650	*BMP2*	7.04E-02	2.27	bone morphogenetic protein 2	
1559987_at	124540	*MSI2*	8.27E-02	2.27	musashi RNA binding protein 2	
201939_at	10769	*PLK2*	2.60E-03	2.23	polo-like kinase 2	
209582_s_at	**4345**	***CD200***	**6.90E-03**	**2.21**	**CD200 molecule**	
1566901_at	7050	*TGIF1*	3.12E-02	2.21	TGFB induced factor homeobox 1	
202935_s_at	6662	*SOX9*	9.00E-04	2.19	SRY box 9	
242543_at	284948	*SH2D6*	8.83E-02	2.19	SH2 domain containing 6	
205193_at	23764	*MAFF*	1.49E-02	2.17	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	
229152_at	260436	*FDCSP*	4.70E-02	2.17	follicular dendritic cell secreted protein	
1555118_at	956	*ENTPD3*	7.24E-02	2.15	ectonucleoside triphosphate diphosphohydrolase 3	
209583_s_at	**4345**	***CD200***	**5.00E-04**	**2.12**	**CD200 molecule**	
204011_at	10253	*SPRY2*	8.00E-04	2.11	sprouty RTK signaling antagonist 2	
204491_at	**5144**	***PDE4D***	**1.67E-02**	**2.11**	**phosphodiesterase 4D, cAMP-specific**	
239367_at	627	*BDNF*	1.30E-03	2.10	brain-derived neurotrophic factor	
220125_at	27019	*DNAI1*	5.65E-02	2.10	dynein, axonemal, intermediate chain 1	
228962_at	**5144**	***PDE4D***	**2.49E-02**	**2.06**	**phosphodiesterase 4D, cAMP-specific**	
204456_s_at	**2619**	***GAS1***	**3.50E-02**	**2.05**	**growth arrest-specific 1**	
205466_s_at	9957	*HS3ST1*	2.92E-02	2.04	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	
203574_at	4783	*NFIL3*	1.33E-02	2.02	nuclear factor, interleukin 3 regulated	
218177_at	57132	*CHMP1B*	1.63E-02	2.02	charged multivesicular body protein 1B	
209457_at	1847	*DUSP5*	2.00E-03	2.01	dual specificity phosphatase 5	
216604_s_at	23428	*SLC7A8*	6.90E-03	2.01	solute carrier family 7 (amino acid transporter light chain, L system), member 8	
212977_at	57007	*ACKR3*	2.20E-03	1.99	atypical chemokine receptor 3	
205027_s_at	1326	*MAP3K8*	2.29E-02	1.99	mitogen-activated protein kinase kinase kinase 8	
206758_at	1907	*EDN2*	1.88E-02	1.98	endothelin 2	
206382_s_at	627	*BDNF*	3.60E-03	1.97	brain-derived neurotrophic factor	
230748_at	9120	*SLC16A6*	2.20E-02	1.96	solute carrier family 16, member 6	
207826_s_at	3399	*ID3*	5.10E-03	1.95	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	
206706_at	4908	*NTF3*	8.00E-04	1.94	neurotrophin 3	
218631_at	60370	*AVPI1*	9.00E-04	1.93	arginine vasopressin-induced 1	
218178_s_at	57132	*CHMP1B*	1.80E-03	1.93	charged multivesicular body protein 1B	
202936_s_at	6662	*SOX9*	1.90E-03	1.93	SRY box 9	

	1139	*CHRFAM7A*	3.12E-02		CHRNA7 (Exons 5-10) And FAM7A (Exons A-E) Fusion	
236385_at	89832	*CHRNA7*	3.12E-02	1.93	cholinergic receptor, nicotinic alpha 7	
	101929970	*LOC101929970*	3.12E-02		CHRNA7-FAM7A fusion protein	
229110_at	25769	*SLC24A2*	5.09E-02	1.93	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	
202672_s_at	467	*ATF3*	5.76E-02	1.93	activating transcription factor 3	
208937_s_at	3397	*ID1*	1.21E-02	1.91	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	
218810_at	80149	*ZC3H12A*	9.20E-03	1.90	zinc finger CCCH-type containing 12A	
208960_s_at	1316	*KLF6*	6.00E-04	1.88	Kruppel-like factor 6	
202023_at	1942	*EFNA1*	3.00E-04	1.86	ephrin-A1	
215111_s_at	8848	*TSC22D1*	1.03E-02	1.85	TSC22 domain family, member 1	
218723_s_at	28984	*RGCC*	1.33E-02	1.85	regulator of cell cycle	
239058_at	2303	*FOXC2*	1.49E-02	1.85	forkhead box C2	
232746_at	57007	*ACKR3*	4.43E-02	1.84	atypical chemokine receptor 3	
225557_at	64651	*CSRNP1*	2.20E-03	1.83	cysteine-serine-rich nuclear protein 1	
207850_at	2921	*CXCL3*	9.80E-03	1.83	chemokine (C-X-C motif) ligand 3	
234583_at	10752	*CHL1*	6.34E-02	1.83	cell adhesion molecule L1-like	
1552948_at	148870	*CCDC27*	9.80E-03	1.82	coiled-coil domain containing 27	
220987_s_at	56672	*AKIP1*	2.00E-03	1.81	A kinase (PRKA) interacting protein 1	
	81788	*NUAK2*	2.00E-03	1.81	NUAK family, SNF1-like kinase, 2	
202149_at	4739	*NEDD9*	8.40E-03	1.81	neural precursor cell expressed, developmentally down-regulated 9	
202431_s_at	4609	*MYC*	6.00E-04	1.80	v-myc avian myelocytomatosis viral oncogene homolog	
220266_s_at	9314	*KLF4*	4.10E-02	1.80	Kruppel-like factor 4 (gut)	
205815_at	5068	*REG3A*	8.98E-02	1.79	regenerating islet-derived 3 alpha	
202499_s_at	6515	*SLC2A3*	3.34E-02	1.78	solute carrier family 2 (facilitated glucose transporter), member 3	
204014_at	1846	*DUSP4*	1.20E-02	1.77	dual specificity phosphatase 4	
210836_x_at	**5144**	***PDE4D***	**1.90E-02**	**1.77**	**phosphodiesterase 4D, cAMP-specific**	
1555832_s_at	1316	*KLF6*	1.40E-03	1.76	Kruppel-like factor 6	
203708_at	5142	*PDE4B*	1.96E-02	1.76	phosphodiesterase 4B, cAMP-specific	
226034_at	1846	*DUSP4*	6.90E-03	1.75	dual specificity phosphatase 4	
230472_at	79192	*IRX1*	6.90E-03	1.75	iroquois homeobox 1	
202150_s_at	4739	*NEDD9*	2.18E-02	1.74	neural precursor cell expressed, developmentally down-regulated 9	
231035_s_at	220213	*OTUD1*	3.90E-02	1.74	OTU deubiquitinase 1	
211962_s_at	677	*ZFP36L1*	9.92E-02	1.73	ZFP36 ring finger protein-like 1	
235849_at	286133	*SCARA5*	6.63E-02	1.71	scavenger receptor class A, member 5	
1553422_s_at	54715	*RBFOX1*	5.93E-02	1.70	RNA binding protein, fox-1 homolog (C. elegans) 1	
1553613_s_at	2296	*FOXC1*	1.60E-03	1.69	forkhead box C1	
233379_at	79899	*PRR5L*	8.33E-02	1.69	proline rich 5 like	
1554980_a_at	467	*ATF3*	1.80E-02	1.68	activating transcription factor 3	
215990_s_at	604	*BCL6*	1.90E-02	1.68	B-cell CLL/lymphoma 6	
222162_s_at	9510	*ADAMTS1*	2.20E-02	1.68	ADAM metallopeptidase with thrombospondin type 1 motif 1	
202497_x_at	6515	*SLC2A3*	2.97E-02	1.68	solute carrier family 2 (facilitated glucose transporter), member 3	
216236_s_at	6515	*SLC2A14*	2.98E-02		solute carrier family 2 (facilitated glucose transporter), member 14	
	144195	*SLC2A3*	2.98E-02	1.68	solute carrier family 2 (facilitated glucose transporter), member 3	
213170_at	2882	*GPX7*	4.29E-02		glutathione peroxidase 7	
224606_at	1316	*KLF6*	2.30E-03	1.67	Kruppel-like factor 6	
203140_at	604	*BCL6*	2.60E-03	1.67	B-cell CLL/lymphoma 6	
207981_s_at	2104	*ESRRG*	4.29E-02	1.67	estrogen-related receptor gamma	
213284_at	677	*ZFP36L1*	5.24E-02	1.66	ZFP36 ring finger protein-like 1	
224657_at	54206	*ERRFI1*	1.45E-02	1.65	ERBB receptor feedback inhibitor 1	
204931_at	6943	*TCF21*	1.88E-02	1.65	transcription factor 21	
204284_at	5507	*PPP1R3C*	5.76E-02	1.65	protein phosphatase 1, regulatory subunit 3C	
201041_s_at	**1843**	***DUSP1***	**6.00E-04**	**1.64**	**dual specificity phosphatase 1**	
221766_s_at	55603	*FAM46A*	5.09E-02	1.64	family with sequence similarity 46, member A	
227443_at	286343	*LURAP1L*	7.04E-02	1.64	leucine rich adaptor protein 1-like	
229373_at	3274	*HRH2*	1.63E-02	1.63	histamine receptor H2	
222088_s_at	6515	*SLC2A14*	6.27E-02	1.63	solute carrier family 2 (facilitated glucose transporter), member 14	
	144195	*SLC2A3*	6.27E-02	1.63	solute carrier family 2 (facilitated glucose transporter), member 3	
205929_at	10223	*GPA33*	6.88E-02	1.62	glycoprotein A33 (transmembrane)	
1554420_at	467	*ATF3*	9.65E-02	1.62	activating transcription factor 3	
222379_at	23704	*KCNE4*	1.88E-02	1.61	potassium channel, voltage gated subfamily E regulatory beta subunit 4	
219371_s_at	10365	*KLF2*	4.72E-02	1.61	Kruppel-like factor 2	
225720_at	171024	*SYNPO2*	8.98E-02	1.61	synaptopodin 2	
208961_s_at	1316	*KLF6*	1.80E-03	1.60	Kruppel-like factor 6	
225606_at	10018	*BCL2L11*	2.32E-02	1.60	BCL2-like 11 (apoptosis facilitator)	
1553378_a_at	256957	*HEATR9*	5.39E-02	1.60	HEAT repeat containing 9	
234928_x_at	864	*RUNX3*	6.63E-02	1.60	runt-related transcription factor 3	
206374_at	1850	*DUSP8*	2.31E-02	1.59	dual specificity phosphatase 8	
1431_at	1571	*CYP2E1*	1.67E-02	1.58	cytochrome P450, family 2, subfamily E, polypeptide 1	
218880_at	2355	*FOSL2*	4.79E-02	1.58	FOS-like antigen 2	
211302_s_at	5142	*PDE4B*	8.43E-02	1.58	phosphodiesterase 4B, cAMP-specific	
239381_at	5650	*KLK7*	9.47E-02	1.58	kallikrein related peptidase 7	
203438_at	8614	*STC2*	1.63E-02	1.57	stanniocalcin 2	
226140_s_at	220213	*OTUD1*	8.90E-03	1.56	OTU deubiquitinase 1	
229552_at	8739	*HRK*	8.49E-02	1.56	harakiri, BCL2 interacting protein	
	283454	*LOC283454*	8.49E-02		uncharacterized LOC283454	
201328_at	2114	*ETS2*	7.00E-03	1.55	v-ets avian erythroblastosis virus E26 oncogene homolog 2	
228325_at	23514	*SPIDR*	1.03E-02	1.55	scaffolding protein involved in DNA repair	
228462_at	153572	*IRX2*	1.33E-02	1.55	iroquois homeobox 2	
212143_s_at	3486	*IGFBP3*	3.90E-02	1.55	insulin like growth factor binding protein 3	
228188_at	2355	*FOSL2*	8.83E-02	1.55	FOS-like antigen 2	
230493_at	387914	*SHISA2*	8.30E-03	1.54	shisa family member 2	
207980_s_at	10370	*CITED2*	1.11E-02	1.54	Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 2	
212230_at	8613	*PLPP3*	3.27E-02	1.54	phospholipid phosphatase 3	
202704_at	10140	*TOB1*	5.18E-02	1.54	transducer of ERBB2, 1	
209101_at	1490	*CTGF*	5.89E-02	1.54	connective tissue growth factor	
202628_s_at	5054	*SERPINE1*	2.60E-03	1.53	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	
203973_s_at	1052	*CEBPD*	7.00E-03	1.53	CCAAT/enhancer binding protein (C/EBP), delta	
231958_at	132001	*TAMM41*	3.78E-02	1.53	TAM41 mitochondrial translocator assembly and maintenance homolog	
228167_at	89857	*KLHL6*	7.24E-02	1.53	kelch-like family member 6	
229800_at	9201	*DCLK1*	1.63E-02	1.52	doublecortin-like kinase 1	
212226_s_at	8613	*PLPP3*	1.72E-02	1.52	phospholipid phosphatase 3	
206999_at	3595	*IL12RB2*	4.25E-02	1.52	interleukin 12 receptor, beta 2	
206170_at	154	*ADRB2*	1.63E-02	1.51	adrenoceptor beta 2, surface	
229004_at	170689	*ADAMTS15*	1.88E-02	1.51	ADAM metallopeptidase with thrombospondin type 1 motif 15	

230372_at	3037	*HAS2*	2.25E-02	1.51	hyaluronan synthase 2	
204015_s_at	1846	*DUSP4*	2.41E-02	1.51	dual specificity phosphatase 4	
230773_at	79750	*ZNF385D*	3.60E-02	1.51	zinc finger protein 385D	
208293_x_at	1444	*CSHL1*	6.70E-02	1.51	chorionic somatomammotropin hormone-like 1	
235182_at	140862	*ISM1*	9.00E-02	1.51	isthmin 1, angiogenesis inhibitor	

Indacaterol (2h)
(515 Probe Sets ≡ 321 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
209959_at	8013	*NR4A3*	6.05E-05	66.19	nuclear receptor subfamily 4, group A, member 3	
207978_s_at	8013	*NR4A3*	4.57E-05	38.53	nuclear receptor subfamily 4, group A, member 3	
216248_s_at	**4929**	***NR4A2***	**7.00E-04**	**28.71**	**nuclear receptor subfamily 4, group A, member 2**	
204622_x_at	**4929**	***NR4A2***	**2.00E-04**	**24.49**	**nuclear receptor subfamily 4, group A, member 2**	
204621_s_at	**4929**	***NR4A2***	**1.70E-03**	**24.45**	**nuclear receptor subfamily 4, group A, member 2**	
203639_s_at	**2263**	***FGFR2***	**1.51E-02**	**13.55**	**fibroblast growth factor receptor 2**	
205289_at	650	*BMP2*	1.45E-02	11.62	bone morphogenetic protein 2	
221541_at	**83716**	***CRISPLD2***	**5.25E-06**	**8.50**	**cysteine-rich secretory protein LCCL domain containing 2**	
225207_at	**5166**	***PDK4***	**1.00E-04**	**8.30**	**pyruvate dehydrogenase kinase, isozyme 4**	
205476_at	6364	*CCL20*	3.00E-04	7.94	chemokine (C-C motif) ligand 20	
205207_at	3569	*IL6*	1.90E-03	7.75	interleukin 6	
234511_at	140731	*ANKRD60*	1.08E-01	7.53	ankyrin repeat domain 60	
205960_at	**5166**	***PDK4***	**3.00E-03**	**6.74**	**pyruvate dehydrogenase kinase, isozyme 4**	
232470_at	150094 102724428	*SIK1* *LOC102724428*	2.00E-04	6.56	salt-inducible kinase 1 serine/threonine-protein kinase SIK1	
208078_s_at	150094 102724428	*SIK1* *LOC102724428*	1.11E-05	6.31	salt-inducible kinase 1 serine/threonine-protein kinase SIK1	
218541_s_at	56892	*C8orf4*	1.81E-02	6.12	chromosome 8 open reading frame 4	
228962_at	**5144**	***PDE4D***	**8.63E-05**	**6.12**	**phosphodiesterase 4D, cAMP-specific**	
201739_at	**6446**	***SGK1***	**6.05E-05**	**5.78**	**serum/glucocorticoid regulated kinase 1**	
206359_at	**9021**	***SOCS3***	**1.44E-02**	**5.73**	**suppressor of cytokine signaling 3**	
209582_s_at	**4345**	***CD200***	**2.00E-04**	**5.71**	**CD200 molecule**	
203638_s_at	**2263**	***FGFR2***	**1.20E-03**	**5.67**	**fibroblast growth factor receptor 2**	
228964_at	639	*PRDM1*	1.11E-05	5.50	PR domain containing 1, with ZNF domain	
211401_s_at	**2263**	***FGFR2***	**5.23E-02**	**5.37**	**fibroblast growth factor receptor 2**	
204491_at	**5144**	***PDE4D***	**5.15E-05**	**5.25**	**phosphodiesterase 4D, cAMP-specific**	
227697_at	**9021**	***SOCS3***	**2.11E-02**	**5.04**	**suppressor of cytokine signaling 3**	
225582_at	85450	*ITPRIP*	1.35E-05	4.75	inositol 1,4,5-trisphosphate receptor interacting protein	
210837_s_at	**5144**	***PDE4D***	**2.00E-04**	**4.75**	**phosphodiesterase 4D, cAMP-specific**	
202388_at	**5997**	***RGS2***	**9.78E-05**	**4.75**	**regulator of G-protein signaling 2**	
210836_x_at	**5144**	***PDE4D***	**9.33E-05**	**4.52**	**phosphodiesterase 4D, cAMP-specific**	
244025_at	85450	*ITPRIP*	3.00E-04	4.49	inositol 1,4,5-trisphosphate receptor interacting protein	
205290_s_at	650	*BMP2*	1.20E-03	4.45	bone morphogenetic protein 2	
209774_x_at	2920	*CXCL2*	1.80E-03	4.40	chemokine (C-X-C motif) ligand 2	
205330_at	4330	*MN1*	1.20E-03	4.40	meningioma (disrupted in balanced translocation) 1	
1562321_at	**5166**	***PDK4***	**1.34E-01**	**4.35**	**pyruvate dehydrogenase kinase, isozyme 4**	
230748_at	9120	*SLC16A6*	1.00E-04	4.32	solute carrier family 16, member 6	
209583_s_at	**4345**	***CD200***	**1.11E-05**	**4.30**	**CD200 molecule**	
227613_at	55422	*ZNF331*	2.00E-04	4.30	zinc finger protein 331	
207038_at	9120	*SLC16A6*	3.20E-03	4.29	solute carrier family 16, member 6	
220088_at	**728**	***C5AR1***	**5.00E-04**	**4.23**	**complement component 5a receptor 1**	
211143_x_at	3164	*NR4A1*	5.00E-04	4.17	nuclear receptor subfamily 4, group A, member 1	
219228_at	55422	*ZNF331*	3.00E-04	4.12	zinc finger protein 331	
229552_at	8739 283454	*HRK* *LOC283454*	3.00E-04	4.08	harakiri, BCL2 interacting protein uncharacterized LOC283454	
239367_at	627	*BDNF*	3.74E-05	4.05	brain-derived neurotrophic factor	
208083_s_at	3694 100505984	*ITGB6* *LOC100505984*	7.49E-02	4.05	integrin beta 6 uncharacterized LOC100505984	
213182_x_at	1028	*CDKN1C*	2.68E-02	4.02	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
202340_x_at	3164	*NR4A1*	1.60E-03	3.97	nuclear receptor subfamily 4, group A, member 1	
219911_s_at	28231	*SLCO4A1*	2.40E-03	3.84	solute carrier organic anion transporter family, member 4A1	
1559141_s_at	157693 400728	*FAM87A* *FAM87B*	8.00E-03	3.81	family with sequence similarity 87, member A family with sequence similarity 87, member B	
219534_x_at	1028	*CDKN1C*	1.81E-02	3.76	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
224828_at	80315	*CPEB4*	3.00E-04	3.74	cytoplasmic polyadenylation element binding protein 4	
229709_at	483	*ATP1B3*	6.20E-03	3.73	ATPase, Na+/K+ transporting, beta 3 polypeptide	
206382_s_at	627	*BDNF*	1.00E-04	3.72	brain-derived neurotrophic factor	
219682_s_at	6926	*TBX3*	9.99E-05	3.59	T-box 3	
203549_s_at	4023	*LPL*	2.00E-04	3.57	lipoprotein lipase	
224829_at	80315	*CPEB4*	2.00E-04	3.53	cytoplasmic polyadenylation element binding protein 4	
216894_x_at	1028	*CDKN1C*	7.80E-03	3.47	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
206865_at	8739	*HRK*	2.00E-04	3.47	harakiri, BCL2 interacting protein	
239818_x_at	10221	*TRIB1*	2.00E-04	3.46	tribbles pseudokinase 1	
218177_at	57132	*CHMP1B*	2.00E-04	3.39	charged multivesicular body protein 1B	
218995_s_at	1906	*EDN1*	8.59E-05	3.36	endothelin 1	
1552755_at	157983	*C9orf66*	8.11E-02	3.35	chromosome 9 open reading frame 66	
216236_s_at	6515 144195	*SLC2A14* *SLC2A3*	9.78E-05	3.35	solute carrier family 2 (facilitated glucose transporter), member 14 solute carrier family 2 (facilitated glucose transporter), member 3	
213348_at	1028	*CDKN1C*	8.70E-03	3.32	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
213006_at	1052	*CEBPD*	8.00E-04	3.32	CCAAT/enhancer binding protein (C/EBP), delta	
202241_at	10221	*TRIB1*	3.74E-05	3.31	tribbles pseudokinase 1	
209631_s_at	2861	*GPR37*	2.00E-04	3.30	G protein-coupled receptor 37 (endothelin receptor type B-like)	
202497_x_at	6515	*SLC2A3*	2.00E-04	3.30	solute carrier family 2 (facilitated glucose transporter), member 3	
228128_x_at	5069	*PAPPA*	4.00E-04	3.28	pregnancy-associated plasma protein A, pappalysin 1	
201981_at	5069	*PAPPA*	2.68E-02	3.21	pregnancy-associated plasma protein A, pappalysin 1	
203548_s_at	4023	*LPL*	2.00E-04	3.18	lipoprotein lipase	
224831_at	80315	*CPEB4*	2.00E-04	3.17	cytoplasmic polyadenylation element binding protein 4	
222088_s_at	6515 144195	*SLC2A14* *SLC2A3*	3.00E-04	3.16	solute carrier family 2 (facilitated glucose transporter), member 14 solute carrier family 2 (facilitated glucose transporter), member 3	
228325_at	23514	*SPIDR*	8.00E-04	3.16	scaffolding protein involved in DNA repair	
220483_s_at	25897	*RNF19A*	5.00E-04	3.13	ring finger protein 19A, RBR E3 ubiquitin protein ligase	
202499_s_at	6515	*SLC2A3*	5.00E-04	3.11	solute carrier family 2 (facilitated glucose transporter), member 3	
224942_at	5069	*PAPPA*	7.00E-04	3.09	pregnancy-associated plasma protein A, pappalysin 1	

202498_s_at	6515	*SLC2A3*	1.00E-03	3.04	solute carrier family 2 (facilitated glucose transporter), member 3
224940_s_at	5069	*PAPPA*	8.00E-04	3.03	pregnancy-associated plasma protein A, pappalysin 1
239123_at	8848	*TSC22D1*	1.21E-02	3.03	TSC22 domain family, member 1
218178_s_at	57132	*CHMP1B*	1.77E-05	3.00	charged multivesicular body protein 1B
203984_s_at	842	*CASP9*	4.80E-03	2.99	caspase 9
222802_at	1906	*EDN1*	8.34E-05	2.98	endothelin 1
226614_s_at	83648	*FAM167A*	5.00E-04	2.96	family with sequence similarity 167, member A
205027_s_at	1326	*MAP3K8*	1.70E-03	2.93	mitogen-activated protein kinase kinase kinase 8
204456_s_at	**2619**	***GAS1***	**5.50E-03**	**2.91**	**growth arrest-specific 1**
212226_s_at	8613	*PLPP3*	6.82E-05	2.90	phospholipid phosphatase 3
218723_s_at	28984	*RGCC*	1.02E-02	2.89	regulator of cell cycle
212977_at	57007	*ACKR3*	9.84E-05	2.87	atypical chemokine receptor 3
208228_s_at	**2263**	***FGFR2***	**1.00E-04**	**2.86**	**fibroblast growth factor receptor 2**
225516_at	6542	*SLC7A2*	1.00E-04	2.84	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
209355_s_at	8613	*PLPP3*	7.59E-05	2.83	phospholipid phosphatase 3
225544_at	6926	*TBX3*	1.00E-04	2.82	T-box 3
230472_at	79192	*IRX1*	7.00E-04	2.81	iroquois homeobox 1
210775_x_at	842	*CASP9*	5.20E-03	2.77	caspase 9
237187_at	8739	*HRK*	3.20E-03	2.77	harakiri, BCL2 interacting protein
224941_at	5069	*PAPPA*	2.60E-03	2.77	pregnancy-associated plasma protein A, pappalysin 1
225606_at	10018	*BCL2L11*	1.00E-04	2.76	BCL2-like 11 (apoptosis facilitator)
219316_s_at	55640	*FLVCR2*	2.20E-03	2.72	feline leukemia virus subgroup C cellular receptor family, member 2
228340_at	7090	*TLE3*	5.60E-02	2.69	transducin-like enhancer of split 3
1553613_s_at	2296	*FOXC1*	1.54E-05	2.67	forkhead box C1
209681_at	10560	*SLC19A2*	4.50E-03	2.67	solute carrier family 19 (thiamine transporter), member 2
235085_at	157285	*PRAG1*	5.20E-03	2.65	homolog of rat pragma of Rnd2
214446_at	22936	*ELL2*	1.02E-02	2.63	elongation factor, RNA polymerase II, 2
209189_at	2353	*FOS*	6.00E-03	2.63	FBJ murine osteosarcoma viral oncogene homolog
223085_at	25897	*RNF19A*	2.00E-04	2.62	ring finger protein 19A, RBR E3 ubiquitin protein ligase
222015_at	1454	*CSNK1E*	5.00E-04	2.61	casein kinase 1, epsilon
	102800317	*LOC400927-CSNK1E*			LOC400927-CSNK1E readthrough
227443_at	286343	*LURAP1L*	1.36E-02	2.61	leucine rich adaptor protein 1-like
205239_at	374	*AREG*	4.20E-03	2.60	amphiregulin
218880_at	2355	*FOSL2*	3.00E-04	2.60	FOS-like antigen 2
224325_at	8325	*FZD8*	9.00E-03	2.60	frizzled class receptor 8
227099_s_at	387763	*C11orf96*	6.76E-02	2.59	chromosome 11 open reading frame 96
227188_at	59271	*EVA1C*	8.50E-03	2.59	eva-1 homolog C (C. elegans)
206924_at	3589	*IL11*	3.00E-03	2.59	interleukin 11
229004_at	170689	*ADAMTS15*	9.99E-05	2.58	ADAM metallopeptidase with thrombospondin type 1 motif 15
214438_at	3142	*HLX*	3.38E-02	2.57	H2.0-like homeobox
36711_at	23764	*MAFF*	1.00E-04	2.57	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
205193_at	23764	*MAFF*	7.00E-04	2.57	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
227337_at	353322	*ANKRD37*	3.00E-04	2.56	ankyrin repeat domain 37
220225_at	50805	*IRX4*	6.60E-03	2.56	iroquois homeobox 4
218631_at	60370	*AVPI1*	6.05E-05	2.55	arginine vasopressin-induced 1
225987_at	79689	*STEAP4*	4.00E-04	2.54	STEAP family member 4
230398_at	84951	*TNS4*	1.11E-02	2.54	tensin 4
215111_s_at	8848	*TSC22D1*	4.60E-03	2.53	TSC22 domain family, member 1
205409_at	2355	*FOSL2*	5.70E-03	2.52	FOS-like antigen 2
1553133_at	203228	*C9orf72*	2.60E-03	2.51	chromosome 9 open reading frame 72
212230_at	8613	*PLPP3*	3.26E-05	2.51	phospholipid phosphatase 3
201044_x_at	**1843**	***DUSP1***	**2.00E-04**	**2.50**	**dual specificity phosphatase 1**
208250_s_at	**1755**	***DMBT1***	**8.63E-05**	**2.48**	**deleted in malignant brain tumors 1**
236911_at	57494	*RIMKLB*	2.53E-02	2.48	ribosomal modification protein rimK-like family member B
202150_s_at	4739	*NEDD9*	4.00E-04	2.47	neural precursor cell expressed, developmentally down-regulated 9
202723_s_at	2308	*FOXO1*	3.20E-03	2.46	forkhead box O1
202768_at	2354	*FOSB*	7.40E-03	2.43	FBJ murine osteosarcoma viral oncogene homolog B
206404_at	2254	*FGF9*	4.00E-04	2.42	fibroblast growth factor 9
213221_s_at	23235	*SIK2*	3.30E-03	2.42	salt-inducible kinase 2
205466_s_at	9957	*HS3ST1*	2.21E-02	2.40	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
201169_s_at	8553	*BHLHE40*	5.60E-03	2.39	basic helix-loop-helix family, member e40
210136_at	4155	*MBP*	7.00E-04	2.39	myelin basic protein
202149_at	4739	*NEDD9*	3.00E-04	2.38	neural precursor cell expressed, developmentally down-regulated 9
203574_at	4783	*NFIL3*	5.00E-04	2.38	nuclear factor, interleukin 3 regulated
223379_s_at	26524	*LATS2*	3.00E-04	2.37	large tumor suppressor kinase 2
207626_s_at	6542	*SLC7A2*	3.00E-04	2.37	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
213139_at	6591	*SNAI2*	5.20E-03	2.37	snail family zinc finger 2
224797_at	57561	*ARRDC3*	5.80E-03	2.36	arrestin domain containing 3
215990_s_at	604	*BCL6*	9.30E-03	2.36	B-cell CLL/lymphoma 6
224480_s_at	84803	*GPAT3*	1.27E-01	2.36	glycerol-3-phosphate acyltransferase 3
231035_s_at	220213	*OTUD1*	3.70E-03	2.36	OTU deubiquitinase 1
226858_at	1454	*CSNK1E*	4.00E-04	2.34	casein kinase 1, epsilon
	102800317	*LOC400927-CSNK1E*			LOC400927-CSNK1E readthrough
209101_at	1490	*CTGF*	3.00E-04	2.34	connective tissue growth factor
231067_s_at	9590	*AKAP12*	1.51E-02	2.33	A kinase (PRKA) anchor protein 12
220335_x_at	23491	*CES3*	1.70E-03	2.33	carboxylesterase 3
216627_s_at	2683	*B4GALT1*	6.80E-03	2.32	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
218881_s_at	2355	*FOSL2*	3.00E-03	2.32	FOS-like antigen 2
237252_at	7056	*THBD*	1.58E-02	2.32	thrombomodulin
208606_s_at	54361	*WNT4*	9.27E-02	2.32	wingless-type MMTV integration site family, member 4
208536_s_at	10018	*BCL2L11*	2.11E-02	2.28	BCL2-like 11 (apoptosis facilitator)
203796_s_at	605	*BCL7A*	4.00E-04	2.28	B-cell CLL/lymphoma 7A
212099_at	388	*RHOB*	4.00E-04	2.28	ras homolog family member B
203313_s_at	7050	*TGIF1*	6.00E-04	2.28	TGFB-induced factor homeobox 1
223484_at	84419	*C15orf48*	1.32E-01	2.27	chromosome 15 open reading frame 48
229720_at	573	*BAG1*	1.50E-03	2.25	BCL2-associated athanogene
1558143_a_at	10018	*BCL2L11*	5.00E-03	2.25	BCL2-like 11 (apoptosis facilitator)
219195_at	10891	*PPARGC1A*	1.14E-02	2.24	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
223430_at	23235	*SIK2*	1.84E-02	2.23	salt-inducible kinase 2
207213_s_at	9099	*USP2*	3.00E-03	2.23	ubiquitin specific peptidase 2
238987_at	2683	*B4GALT1*	8.84E-02	2.22	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
228625_at	163732	*CITED4*	4.00E-04	2.22	Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 4
225955_at	284207	*METRNL*	1.00E-04	2.22	meteorin, glial cell differentiation regulator-like
1554544_a_at	4155	*MBP*	7.00E-04	2.21	myelin basic protein

200731_s_at	7803	*PTP4A1*	1.09E-02	2.21	protein tyrosine phosphatase type IVA, member 1
203887_s_at	7056	*THBD*	1.69E-02	2.21	thrombomodulin
202023_at	1942	*EFNA1*	2.00E-04	2.20	ephrin-A1
221841_s_at	9314	*KLF4*	9.90E-03	2.20	Kruppel-like factor 4 (gut)
206472_s_at	7090	*TLE3*	8.63E-02	2.19	transducin-like enhancer of split 3
201170_s_at	8553	*BHLHE40*	4.00E-04	2.18	basic helix-loop-helix family, member e40
202672_s_at	467	*ATF3*	8.00E-04	2.17	activating transcription factor 3
228188_at	2355	*FOSL2*	8.00E-04	2.17	FOS-like antigen 2
221011_s_at	81606	*LBH*	3.00E-04	2.17	limb bud and heart development
222784_at	64093	*SMOC1*	3.10E-02	2.17	SPARC related modular calcium binding 1
226575_at	58499	*ZNF462*	1.00E-03	2.17	zinc finger protein 462
219433_at	54880	*BCOR*	1.35E-02	2.16	BCL6 corepressor
205870_at	624	*BDKRB2*	3.27E-02	2.16	bradykinin receptor B2
204014_at	1846	*DUSP4*	5.20E-03	2.16	dual specificity phosphatase 4
225262_at	2355	*FOSL2*	1.00E-04	2.16	FOS-like antigen 2
209184_s_at	8660	*IRS2*	7.00E-04	2.15	insulin receptor substrate 2
213260_at	2296	*FOXC1*	5.34E-05	2.14	forkhead box C1
234804_at	283571	*PROX2*	1.29E-01	2.14	prospero homeobox 2
200732_s_at	7803	*PTP4A1*	2.30E-03	2.14	protein tyrosine phosphatase type IVA, member 1
206035_at	5966	*REL*	2.90E-03	2.13	v-rel avian reticuloendotheliosis viral oncogene homolog
205896_at	6583	*SLC22A4*	2.08E-02	2.13	solute carrier family 22 (organic cation/zwitterion transporter), member 4
203290_at	3117	*HLA-DQA1*	3.73E-02	2.12	major histocompatibility complex, class II, DQ alpha 1
1553962_s_at	388	*RHOB*	1.40E-03	2.12	ras homolog family member B
1556185_a_at	79689	*STEAP4*	3.99E-02	2.12	STEAP family member 4
212143_s_at	3486	*IGFBP3*	1.70E-03	2.11	insulin like growth factor binding protein 3
204032_at	8412	*BCAR3*	4.00E-03	2.10	breast cancer anti-estrogen resistance 3
211631_x_at	2683	*B4GALT1*	3.66E-02	2.09	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
209772_s_at	100133941	*CD24*	3.00E-04	2.09	CD24 molecule
224572_s_at	359948	*IRF2BP2*	3.00E-04	2.09	interferon regulatory factor 2 binding protein 2
233002_at	57718	*PPP4R4*	1.53E-02	2.09	protein phosphatase 4, regulatory subunit 4
207826_s_at	3399	*ID3*	1.10E-03	2.08	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
233379_at	79899	*PRR5L*	1.35E-02	2.08	proline rich 5 like
225999_at	57494	*RIMKLB*	3.10E-03	2.08	ribosomal modification protein rimK-like family member B
203140_at	604	*BCL6*	9.00E-04	2.07	B-cell CLL/lymphoma 6
223566_s_at	54880	*BCOR*	5.30E-03	2.07	BCL6 corepressor
227458_at	29126	*CD274*	3.20E-03	2.07	CD274 molecule
202724_s_at	2308	*FOXO1*	1.80E-03	2.07	forkhead box O1
205051_s_at	3815	*KIT*	2.70E-03	2.07	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
205157_s_at	3872	*KRT17*	3.12E-02	2.07	keratin 17, type I
225407_at	4155	*MBP*	8.00E-04	2.07	myelin basic protein
223834_at	29126	*CD274*	5.60E-03	2.06	CD274 molecule
209457_at	1847	*DUSP5*	1.90E-03	2.06	dual specificity phosphatase 5
230348_at	26524	*LATS2*	7.70E-03	2.06	large tumor suppressor kinase 2
204284_at	5507	*PPP1R3C*	2.53E-02	2.06	protein phosphatase 1, regulatory subunit 3C
218113_at	23670	*TMEM2*	7.00E-04	2.06	transmembrane protein 2
227529_s_at	9590	*AKAP12*	9.90E-03	2.05	A kinase (PRKA) anchor protein 12
203795_s_at	605	*BCL7A*	3.50E-03	2.05	B-cell CLL/lymphoma 7A
219383_at	79899	*PRR5L*	1.70E-03	2.05	proline rich 5 like
223916_s_at	54880	*BCOR*	3.60E-02	2.04	BCL6 corepressor
216598_s_at	6347	*CCL2*	2.10E-03	2.03	chemokine (C-C motif) ligand 2
201925_s_at	1604	*CD55*	1.99E-02	2.03	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
228462_at	153572	*IRX2*	6.00E-04	2.03	iroquois homeobox 2
220540_at	60598	*KCNK15*	7.93E-02	2.03	potassium channel, two pore domain subfamily K, member 15
231798_at	9241	*NOG*	6.00E-04	2.03	noggin
217584_at	4864	*NPC1*	2.11E-02	2.03	Niemann-Pick disease, type C1
228284_at	7088	*TLE1*	4.00E-03	2.03	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
241547_at	29974	*A1CF*	4.11E-02	2.02	APOBEC1 complementation factor
203708_at	5142	*PDE4B*	2.22E-02	2.02	phosphodiesterase 4B, cAMP-specific
225919_s_at	203228	*C9orf72*	3.44E-02	2.01	chromosome 9 open reading frame 72
225626_at	55824	*PAG1*	5.80E-02	2.01	phosphoprotein membrane anchor with glycosphingolipid microdomains 1
1554980_a_at	467	*ATF3*	8.00E-04	2.00	activating transcription factor 3
1555950_a_at	1604	*CD55*	6.90E-03	2.00	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
213844_at	3202	*HOXA5*	9.00E-03	2.00	homeobox A5
206864_s_at	8739	*HRK*	5.00E-04	2.00	harakiri, BCL2 interacting protein
1555486_a_at	79899	*PRR5L*	2.00E-04	2.00	proline rich 5 like
204654_s_at	7020	*TFAP2A*	6.70E-03	2.00	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
239178_at	2254	*FGF9*	2.11E-02	1.99	fibroblast growth factor 9
203108_at	9052	*GPRC5A*	6.00E-04	1.99	G protein-coupled receptor, class C, group 5, member A
220187_at	79689	*STEAP4*	9.40E-03	1.99	STEAP family member 4
229337_at	9099	*USP2*	2.33E-02	1.99	ubiquitin specific peptidase 2
236352_at	245806	*VGLL2*	1.53E-02	1.99	vestigial-like family member 2
242162_at	164781	*DAW1*	1.51E-02	1.98	dynein assembly factor with WDR repeat domains 1
226206_at	7975	*MAFK*	3.00E-04	1.98	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K
235421_at	1326	*MAP3K8*	4.99E-02	1.98	mitogen-activated protein kinase kinase kinase 8
224570_s_at	359948	*IRF2BP2*	3.20E-03	1.97	interferon regulatory factor 2 binding protein 2
229889_at	388341	*LRRC75A*	1.78E-02	1.97	leucine rich repeat containing 75A
228293_at	91614	*DEPDC7*	1.70E-03	1.96	DEP domain containing 7
201328_at	2114	*ETS2*	7.00E-04	1.96	v-ets avian erythroblastosis virus E26 oncogene homolog 2
210162_s_at	4772	*NFATC1*	8.00E-04	1.96	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
219737_s_at	5101	*PCDH9*	6.30E-03	1.96	protocadherin 9
218691_s_at	8572	*PDLIM4*	1.00E-01	1.96	PDZ and LIM domain 4
212444_at	9052	*GPRC5A*	8.00E-04	1.95	G protein-coupled receptor, class C, group 5, member A
228812_at	5966	*REL*	6.90E-03	1.95	v-rel avian reticuloendotheliosis viral oncogene homolog
222343_at	10018	*BCL2L11*	5.00E-03	1.94	BCL2-like 11 (apoptosis facilitator)
224826_at	56261	*GPCPD1*	2.40E-03	1.94	glycerophosphocholine phosphodiesterase 1
203372_s_at	8835	*SOCS2*	6.82E-02	1.94	suppressor of cytokine signaling 2
226034_at	1846	*DUSP4*	1.60E-03	1.93	dual specificity phosphatase 4
224835_at	56261	*GPCPD1*	4.20E-03	1.93	glycerophosphocholine phosphodiesterase 1
201473_at	3726	*JUNB*	1.15E-01	1.93	jun B proto-oncogene
215034_s_at	4071	*TM4SF1*	2.90E-02	1.93	transmembrane 4 L six family member 1
227530_at	9590	*AKAP12*	1.16E-02	1.92	A kinase (PRKA) anchor protein 12
208650_s_at	100133941	*CD24*	4.10E-03	1.92	CD24 molecule
225408_at	4155	*MBP*	1.00E-03	1.92	myelin basic protein
206036_s_at	5966	*REL*	6.80E-03	1.92	v-rel avian reticuloendotheliosis viral oncogene homolog

205074_at	6584	*SLC22A5*	4.20E-03	1.92	solute carrier family 22 (organic cation/carnitine transporter), member 5
231183_s_at	128710	*SLX4IP*	3.54E-02	1.92	SLX4 interacting protein
205286_at	7022	*TFAP2C*	3.09E-02	1.92	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)
209185_s_at	8660	*IRS2*	2.00E-04	1.91	insulin receptor substrate 2
238419_at	90102	*PHLDB2*	8.17E-02	1.91	pleckstrin homology-like domain, family B, member 2
210095_s_at	3486	*IGFBP3*	9.00E-04	1.90	insulin like growth factor binding protein 3
216268_s_at	182	*JAG1*	8.50E-03	1.90	jagged 1
212236_x_at	3872	*KRT17*	2.53E-02	1.90	keratin 17, type I
201416_at	6659	*SOX4*	1.80E-03	1.90	SRY box 4
204597_x_at	6781	*STC1*	8.49E-02	1.90	stanniocalcin 1
231899_at	85463	*ZC3H12C*	2.80E-03	1.90	zinc finger CCCH-type containing 12C
204679_at	3775	*KCNK1*	1.20E-03	1.89	potassium channel, two pore domain subfamily K, member 1
235242_at	5966	*REL*	5.90E-03	1.89	v-rel avian reticuloendotheliosis viral oncogene homolog
230493_at	387914	*SHISA2*	2.70E-03	1.89	shisa family member 2
203888_at	7056	*THBD*	4.19E-02	1.89	thrombomodulin
227405_s_at	8325	*FZD8*	5.57E-02	1.88	frizzled class receptor 8
205992_s_at	3600	*IL15*	4.20E-03	1.88	interleukin 15
224571_at	359948	*IRF2BP2*	4.20E-03	1.88	interferon regulatory factor 2 binding protein 2
206706_at	4908	*NTF3*	3.80E-03	1.88	neurotrophin 3
231823_s_at	285590	*SH3PXD2B*	3.06E-02	1.88	SH3 and PX domains 2B
203373_at	8835	*SOCS2*	1.21E-02	1.88	suppressor of cytokine signaling 2
213003_s_at	23514	*SPIDR*	6.71E-02	1.88	scaffolding protein involved in DNA repair
226208_at	57688	*ZSWIM6*	5.20E-03	1.88	zinc finger, SWIM-type containing 6
203003_at	4209	*MEF2D*	1.05E-02	1.87	myocyte enhancer factor 2D
226140_s_at	220213	*OTUD1*	3.00E-04	1.87	OTU deubiquitinase 1
242329_at	9586	*CREB5*	9.69E-02	1.86	cAMP responsive element binding protein 5
	401317	*LOC401317*			uncharacterized LOC401317
204015_s_at	1846	*DUSP4*	4.30E-03	1.86	dual specificity phosphatase 4
239058_at	2303	*FOXC2*	2.21E-02	1.86	forkhead box C2
201939_at	10769	*PLK2*	9.00E-04	1.86	polo-like kinase 2
1553965_x_at	388	*RHOB*	1.53E-02	1.86	ras homolog family member B
222783_s_at	64093	*SMOC1*	1.05E-02	1.86	SPARC related modular calcium binding 1
244007_at	58499	*ZNF462*	1.60E-03	1.86	zinc finger protein 462
211302_s_at	5142	*PDE4B*	1.39E-01	1.85	phosphodiesterase 4B, cAMP-specific
235849_at	286133	*SCARA5*	6.50E-03	1.85	scavenger receptor class A, member 5
202897_at	140885	*SIRPA*	2.18E-02	1.85	signal-regulatory protein alpha
229529_at	6943	*TCF21*	9.40E-03	1.85	transcription factor 21
216379_x_at	100133941	*CD24*	8.00E-04	1.84	CD24 molecule
204602_at	22943	*DKK1*	5.26E-02	1.84	dickkopf WNT signaling pathway inhibitor 1
227354_at	55824	*PAG1*	7.54E-02	1.84	phosphoprotein membrane anchor with glycosphingolipid microdomains 1
222258_s_at	23677	*SH3BP4*	1.10E-03	1.84	SH3-domain binding protein 4
202935_s_at	6662	*SOX9*	2.55E-02	1.84	SRY box 9
224963_at	1836	*SLC26A2*	1.60E-03	1.83	solute carrier family 26 (anion exchanger), member 2
205294_at	10458	*BAIAP2*	1.30E-03	1.82	BAI1-associated protein 2
209099_x_at	182	*JAG1*	4.50E-03	1.82	jagged 1
206765_at	3759	*KCNJ2*	3.48E-02	1.82	potassium channel, inwardly rectifying subfamily J, member 2
203180_at	220	*ALDH1A3*	6.85E-02	1.81	aldehyde dehydrogenase 1 family, member A3
208651_x_at	100133941	*CD24*	3.60E-02	1.81	CD24 molecule
232026_at	26091	*HERC4*	1.44E-01	1.81	HECT and RLD domain containing E3 ubiquitin protein ligase 4
229800_at	9201	*DCLK1*	1.00E-03	1.80	doublecortin-like kinase 1
228501_at	117248	*GALNT15*	1.84E-02	1.80	polypeptide N-acetylgalactosaminyltransferase 15
204698_at	3669	*ISG20*	2.75E-02	1.80	interferon stimulated exonuclease gene 20kDa
212831_at	1955	*MEGF9*	8.50E-03	1.80	multiple EGF-like-domains 9
217678_at	23657	*SLC7A11*	6.00E-04	1.80	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
202936_s_at	6662	*SOX9*	7.10E-03	1.80	SRY box 9
204908_s_at	602	*BCL3*	2.90E-02	1.79	B-cell CLL/lymphoma 3
201926_s_at	1604	*CD55*	3.07E-02	1.79	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
204678_s_at	3775	*KCNK1*	5.08E-02	1.79	potassium channel, two pore domain subfamily K, member 1
1557578_at	90102	*PHLDB2*	1.27E-01	1.79	pleckstrin homology-like domain, family B, member 2
1554822_at	57157	*PHTF2*	8.10E-03	1.79	putative homeodomain transcription factor 2
224973_at	55603	*FAM46A*	7.89E-02	1.78	family with sequence similarity 46, member A
204472_at	2669	*GEM*	6.90E-03	1.78	GTP binding protein overexpressed in skeletal muscle
203394_s_at	3280	*HES1*	5.78E-02	1.78	hes family bHLH transcription factor 1
226164_x_at	57494	*RIMKLB*	8.37E-02	1.78	ribosomal modification protein rimK-like family member B
266_s_at	100133941	*CD24*	4.13E-02	1.77	CD24 molecule
228759_at	64764	*CREB3L2*	1.74E-02	1.77	cAMP responsive element binding protein 3-like 2
221766_s_at	55603	*FAM46A*	4.30E-03	1.77	family with sequence similarity 46, member A
223380_s_at	26524	*LATS2*	1.10E-03	1.77	large tumor suppressor kinase 2
237724_at	162333	*MARCH10*	5.94E-02	1.76	membrane associated ring finger 10
203044_at	22856	*CHSY1*	5.00E-04	1.76	chondroitin sulfate synthase 1
227755_at	2081	*ERN1*	1.50E-03	1.76	endoplasmic reticulum to nucleus signaling 1
219889_at	10023	*FRAT1*	1.05E-02	1.76	frequently rearranged in advanced T-cell lymphomas 1
227032_at	5362	*PLXNA2*	5.04E-02	1.76	plexin A2
204197_s_at	864	*RUNX3*	9.90E-03	1.76	runt-related transcription factor 3
238029_s_at	151473	*SLC16A14*	3.00E-03	1.76	solute carrier family 16, member 14
202387_at	573	*BAG1*	7.00E-04	1.75	BCL2-associated athanogene
236361_at	117248	*GALNT15*	1.73E-02	1.75	polypeptide N-acetylgalactosaminyltransferase 15
218469_at	26585	*GREM1*	1.60E-03	1.75	gremlin 1, DAN family BMP antagonist
224569_s_at	359948	*IRF2BP2*	3.70E-03	1.75	interferon regulatory factor 2 binding protein 2
204684_at	4884	*NPTX1*	6.04E-02	1.75	neuronal pentraxin I
202861_at	5187	*PER1*	2.77E-02	1.75	period circadian clock 1
209771_x_at	100133941	*CD24*	6.00E-04	1.74	CD24 molecule
225978_at	57494	*RIMKLB*	1.50E-03	1.74	ribosomal modification protein rimK-like family member B
201418_s_at	6659	*SOX4*	1.02E-02	1.74	SRY box 4
230824_at	162333	*MARCH10*	1.79E-02	1.73	membrane associated ring finger 10
206374_at	1850	*DUSP8*	2.83E-02	1.73	dual specificity phosphatase 8
218696_at	9451	*EIF2AK3*	6.98E-02	1.73	eukaryotic translation initiation factor 2-alpha kinase 3
201329_s_at	2114	*ETS2*	1.50E-03	1.73	v-ets avian erythroblastosis virus E26 oncogene homolog 2
218468_s_at	26585	*GREM1*	9.00E-04	1.73	gremlin 1, DAN family BMP antagonist
226333_at	3570	*IL6R*	4.04E-02	1.73	interleukin 6 receptor
209098_s_at	182	*JAG1*	1.89E-02	1.73	jagged 1
220266_s_at	9314	*KLF4*	7.49E-02	1.73	Kruppel-like factor 4 (gut)
206750_at	7975	*MAFK*	2.02E-02	1.73	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K
200730_s_at	7803	*PTP4A1*	8.50E-03	1.73	protein tyrosine phosphatase type IVA, member 1

203439_s_at	8614	*STC2*	1.00E-03	1.73	stanniocalcin 2
218182_s_at	9076	*CLDN1*	1.06E-01	1.72	claudin 1
205035_at	9150	*CTDP1*	1.08E-02	1.72	CTD phosphatase subunit 1
224657_at	54206	*ERRFI1*	4.10E-03	1.72	ERBB receptor feedback inhibitor 1
204011_at	10253	*SPRY2*	1.69E-02	1.72	sprouty RTK signaling antagonist 2
220400_at	157680	*VPS13B*	1.17E-01	1.72	vacuolar protein sorting 13 homolog B (yeast)
222549_at	9076	*CLDN1*	4.70E-03	1.71	claudin 1
210350_x_at	3621	*ING1*	4.14E-02	1.71	inhibitor of growth family member 1
231559_at	4837	*NNMT*	1.79E-02	1.71	nicotinamide N-methyltransferase
202679_at	4864	*NPC1*	3.00E-03	1.71	Niemann-Pick disease, type C1
222662_at	79660	*PPP1R3B*	3.79E-02	1.71	protein phosphatase 1, regulatory subunit 3B
239615_at	6584	*SLC22A5*	6.40E-03	1.71	solute carrier family 22 (organic cation/carnitine transporter), member 5
209921_at	23657	*SLC7A11*	6.00E-04	1.71	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
238542_at	80328	*ULBP2*	1.60E-03	1.71	UL16 binding protein 2
202628_s_at	5054	*SERPINE1*	1.50E-03	1.70	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
213624_at	10924	*SMPDL3A*	4.45E-02	1.70	sphingomyelin phosphodiesterase, acid-like 3A
213668_s_at	6659	*SOX4*	3.35E-02	1.70	SRY box 4
218810_at	80149	*ZC3H12A*	3.60E-02	1.70	zinc finger CCCH-type containing 12A
203973_s_at	1052	*CEBPD*	4.00E-04	1.69	CCAAT/enhancer binding protein (C/EBP), delta
242767_at	29995	*LMCD1*	1.65E-02	1.69	LIM and cysteine-rich domains 1
202431_s_at	4609	*MYC*	3.90E-03	1.69	v-myc avian myelocytomatosis viral oncogene homolog
230330_at	8493	*PPM1D*	2.06E-02	1.69	protein phosphatase, Mg2+/Mn2+ dependent, 1D
204595_s_at	6781	*STC1*	3.52E-02	1.69	stanniocalcin 1
221577_x_at	9518	*GDF15*	1.00E-02	1.68	growth differentiation factor 15
201195_s_at	8140	*SLC7A5*	2.11E-02	1.68	solute carrier family 7 (amino acid transporter light chain, L system), member 5
202181_at	9766	*SUSD6*	2.70E-03	1.68	sushi domain containing 6
227195_at	84858	*ZNF503*	1.87E-02	1.68	zinc finger protein 503
204039_at	1050	*CEBPA*	7.58E-02	1.67	CCAAT/enhancer binding protein (C/EBP), alpha
241985_at	133746	*JMY*	1.35E-02	1.67	junction mediating and regulatory protein, p53 cofactor
201810_s_at	9467	*SH3BP5*	3.00E-03	1.67	SH3-domain binding protein 5 (BTK-associated)
211475_s_at	573	*BAG1*	9.00E-04	1.66	BCL2-associated athanogene
1552487_a_at	646	*BNC1*	5.20E-03	1.66	basonuclin 1
212830_at	1955	*MEGF9*	4.30E-03	1.66	multiple EGF-like-domains 9
203438_at	8614	*STC2*	2.02E-02	1.66	stanniocalcin 2
204931_at	6943	*TCF21*	3.10E-03	1.66	transcription factor 21
209386_at	4071	*TM4SF1*	7.20E-03	1.66	transmembrane 4 L six family member 1
1559140_at	157693 400728	*FAM87A* *FAM87B*	7.49E-02	1.65	family with sequence similarity 87, member A family with sequence similarity 87, member B
206997_s_at	9394	*HS6ST1*	1.30E-01	1.65	heparan sulfate 6-O-sulfotransferase 1
204198_s_at	864	*RUNX3*	2.13E-02	1.65	runt-related transcription factor 3
206511_s_at	10736	*SIX2*	1.55E-02	1.65	SIX homeobox 2
224126_at	84068	*SLC10A7*	9.42E-02	1.65	solute carrier family 10, member 7
225615_at	126917	*IFFO2*	1.04E-01	1.64	intermediate filament family orphan 2
204967_at	357	*SHROOM2*	1.18E-01	1.64	shroom family member 2
204653_at	7020	*TFAP2A*	3.10E-03	1.64	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
235404_at	84159	*ARID5B*	1.09E-01	1.63	AT rich interactive domain 5B (MRF1-like)
214445_at	22936	*ELL2*	1.34E-01	1.63	elongation factor, RNA polymerase II, 2
209864_at	23401	*FRAT2*	1.43E-02	1.63	frequently rearranged in advanced T-cell lymphomas 2
204512_at	3096	*HIVEP1*	9.40E-03	1.63	human immunodeficiency virus type I enhancer binding protein 1
212641_at	3097	*HIVEP2*	2.27E-02	1.63	human immunodeficiency virus type I enhancer binding protein 2
225263_at	9394	*HS6ST1*	9.40E-03	1.63	heparan sulfate 6-O-sulfotransferase 1
202464_s_at	5209	*PFKFB3*	6.30E-03	1.63	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
225056_at	57568	*SIPA1L2*	6.39E-02	1.63	signal-induced proliferation-associated 1 like 2
212614_at	84159	*ARID5B*	2.20E-03	1.62	AT rich interactive domain 5B (MRF1-like)
219825_at	56603	*CYP26B1*	1.48E-01	1.62	cytochrome P450, family 26, subfamily B, polypeptide 1
235122_at	59269	*HIVEP3*	3.98E-02	1.62	human immunodeficiency virus type I enhancer binding protein 3
217371_s_at	3600	*IL15*	8.39E-02	1.62	interleukin 15
205945_at	3570	*IL6R*	1.99E-02	1.62	interleukin 6 receptor
209808_x_at	3621	*ING1*	5.60E-03	1.62	inhibitor of growth family member 1
33304_at	3669	*ISG20*	2.93E-02	1.62	interferon stimulated exonuclease gene 20kDa
225688_s_at	90102	*PHLDB2*	9.83E-02	1.62	pleckstrin homology-like domain, family B, member 2
204286_s_at	5366	*PMAIP1*	9.50E-02	1.62	phorbol-12-myristate-13-acetate-induced protein 1
205097_at	1836	*SLC26A2*	5.20E-03	1.62	solute carrier family 26 (anion exchanger), member 2
227867_at	129293	*TRABD2A*	3.98E-02	1.62	TraB domain containing 2A
210511_s_at	3624	*INHBA*	5.57E-02	1.61	inhibin beta A
211205_x_at	8394	*PIP5K1A*	1.60E-02	1.61	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
229344_x_at	57494	*RIMKLB*	3.63E-02	1.61	ribosomal modification protein rimK-like family member B
201417_at	6659	*SOX4*	3.80E-03	1.61	SRY box 4
203220_s_at	7088	*TLE1*	5.26E-02	1.61	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
243259_at	6314	*ATXN7*	5.79E-02	1.60	ataxin 7
233506_at	9689	*BZW1*	4.39E-02	1.60	basic leucine zipper and W2 domains 1
214595_at	3755	*KCNG1*	5.38E-02	1.60	potassium channel, voltage gated modifier subfamily G, member 1
202883_s_at	5519	*PPP2R1B*	2.33E-02	1.60	protein phosphatase 2, regulatory subunit A, beta
226101_at	5581	*PRKCE*	7.10E-03	1.60	protein kinase C, epsilon
213988_s_at	6303	*SAT1*	7.21E-02	1.60	spermidine/spermine N1-acetyltransferase 1
226492_at	80031	*SEMA6D*	3.05E-02	1.60	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
207332_s_at	7037	*TFRC*	1.09E-02	1.60	transferrin receptor
209387_s_at	4071	*TM4SF1*	4.82E-02	1.60	transmembrane 4 L six family member 1
1555007_s_at	144406	*WDR66*	2.10E-03	1.60	WD repeat domain 66
1553096_s_at	10018	*BCL2L11*	2.70E-02	1.59	BCL2-like 11 (apoptosis facilitator)
206581_at	646	*BNC1*	5.90E-03	1.59	basonuclin 1
203628_at	3480	*IGF1R*	2.33E-02	1.59	insulin-like growth factor 1 receptor
1554833_at	55784	*MCTP2*	1.37E-02	1.59	multiple C2 domains, transmembrane 2
213963_s_at	8819	*SAP30*	1.30E-01	1.59	Sin3A associated protein 30kDa
208234_x_at	**2263**	***FGFR2***	**1.16E-01**	**1.58**	**fibroblast growth factor receptor 2**
202838_at	2517	*FUCA1*	6.90E-03	1.58	fucosidase, alpha-L- 1, tissue
205227_at	3556	*IL1RAP*	3.40E-02	1.58	interleukin 1 receptor accessory protein
219657_s_at	51274	*KLF3*	5.04E-02	1.58	Kruppel-like factor 3 (basic)
229092_at	7026	*NR2F2*	9.40E-03	1.58	nuclear receptor subfamily 2, group F, member 2
202886_s_at	5519	*PPP2R1B*	3.98E-02	1.58	protein phosphatase 2, regulatory subunit A, beta
237215_s_at	7037	*TFRC*	1.11E-01	1.58	transferrin receptor
228404_at	153572	*IRX2*	1.39E-01	1.57	iroquois homeobox 2
212272_at	23175	*LPIN1*	6.14E-02	1.57	lipin 1
209758_s_at	8076	*MFAP5*	3.33E-02	1.57	microfibrillar associated protein 5

202238_s_at	4837	*NNMT*	1.05E-02	1.57	nicotinamide N-methyltransferase	
36829_at	5187	*PER1*	6.70E-03	1.57	period circadian clock 1	
216074_x_at	23286	*WWC1*	1.21E-02	1.57	WW and C2 domain containing 1	
241969_at	84159	*ARID5B*	8.15E-02	1.56	AT rich interactive domain 5B (MRF1-like)	
200920_s_at	694	*BTG1*	5.60E-03	1.56	B-cell translocation gene 1, anti-proliferative	
1553134_s_at	203228	*C9orf72*	8.79E-02	1.56	chromosome 9 open reading frame 72	
224822_at	10395	*DLC1*	4.00E-03	1.56	DLC1 Rho GTPase activating protein	
222866_s_at	55640	*FLVCR2*	1.17E-02	1.56	feline leukemia virus subgroup C cellular receptor family, member 2	
230492_s_at	56261	*GPCPD1*	6.02E-02	1.56	glycerophosphocholine phosphodiesterase 1	
212642_s_at	3097	*HIVEP2*	1.19E-02	1.56	human immunodeficiency virus type I enhancer binding protein 2	
204952_at	27076	*LYPD3*	1.04E-01	1.56	LY6/PLAUR domain containing 3	
223218_s_at	64332	*NFKBIZ*	1.27E-01	1.56	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	
201811_x_at	9467	*SH3BP5*	2.90E-03	1.56	SH3-domain binding protein 5 (BTK-associated)	
228181_at	7779	*SLC30A1*	1.08E-01	1.56	solute carrier family 30 (zinc transporter), member 1	
203221_at	7088	*TLE1*	3.05E-02	1.56	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	
224978_s_at	57602	*USP36*	9.13E-02	1.56	ubiquitin specific peptidase 36	
226982_at	22936	*ELL2*	2.12E-02	1.55	elongation factor, RNA polymerase II, 2	
200879_s_at	2034	*EPAS1*	1.09E-01	1.55	endothelial PAS domain protein 1	
214212_x_at	10979	*FERMT2*	1.64E-02	1.55	fermitin family member 2	
243358_at	3480	*IGF1R*	4.20E-03	1.55	insulin-like growth factor 1 receptor	
217489_s_at	3570	*IL6R*	1.34E-01	1.55	interleukin 6 receptor	
203542_s_at	687	*KLF9*	2.90E-03	1.55	Kruppel-like factor 9	
226844_at	79817	*MOB3B*	6.55E-02	1.55	MOB kinase activator 3B	
238919_at	5101	*PCDH9*	1.46E-01	1.55	protocadherin 9	
204285_s_at	5366	*PMAIP1*	2.30E-02	1.55	phorbol-12-myristate-13-acetate-induced protein 1	
213280_at	23108	*RAP1GAP2*	6.00E-03	1.55	RAP1 GTPase activating protein 2	
220924_s_at	54407	*SLC38A2*	1.30E-03	1.55	solute carrier family 38, member 2	
225033_at	6482	*ST3GAL1*	4.92E-02	1.55	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	
204596_s_at	6781	*STC1*	8.05E-02	1.55	stanniocalcin 1	
202644_s_at	7128	*TNFAIP3*	7.49E-02	1.55	tumor necrosis factor, alpha-induced protein 3	
209946_at	7424	*VEGFC*	1.51E-02	1.55	vascular endothelial growth factor C	
209964_s_at	6314	*ATXN7*	1.17E-01	1.54	ataxin 7	
214014_at	10435	*CDC42EP2*	2.21E-02	1.54	CDC42 effector protein (Rho GTPase binding) 2	
208072_s_at	8527	*DGKD*	1.62E-02	1.54	diacylglycerol kinase, delta 130kDa	
1554966_a_at	11259	*FILIP1L*	2.75E-02	1.54	filamin A interacting protein 1-like	
230788_at	2651	*GCNT2*	1.74E-02	1.54	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	
203821_at	1839	*HBEGF*	7.30E-03	1.54	heparin-binding EGF-like growth factor	
208960_s_at	1316	*KLF6*	2.30E-03	1.54	Kruppel-like factor 6	
210805_x_at	861	*RUNX1*	8.70E-03	1.54	runt-related transcription factor 1	
	100506403	*LOC100506403*			uncharacterized LOC100506403	
202896_s_at	140885	*SIRPA*	1.09E-02	1.54	signal-regulatory protein alpha	
212290_at	6541	*SLC7A1*	6.23E-02	1.54	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	
221291_at	80328	*ULBP2*	3.12E-02	1.54	UL16 binding protein 2	
236557_at	253461	*ZBTB38*	2.75E-02	1.54	zinc finger and BTB domain containing 38	
218865_at	64757	*MARC1*	5.90E-03	1.53	mitochondrial amidoxime reducing component 1	
212974_at	22898	*DENND3*	1.23E-01	1.53	DENN/MADD domain containing 3	
203592_s_at	10272	*FSTL3*	7.79E-02	1.53	follistatin-like 3 (secreted glycoprotein)	
203097_s_at	9693	*RAPGEF2*	2.30E-03	1.53	Rap guanine nucleotide exchange factor 2	
203096_s_at	9693	*RAPGEF2*	1.59E-02	1.53	Rap guanine nucleotide exchange factor 2	
209481_at	54861	*SNRK*	3.00E-03	1.53	SNF related kinase	
203759_at	6484	*ST3GAL4*	2.19E-02	1.53	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	
205990_s_at	7474	*WNT5A*	2.83E-02	1.53	wingless-type MMTV integration site family, member 5A	
210517_s_at	9590	*AKAP12*	1.14E-02	1.52	A kinase (PRKA) anchor protein 12	
201508_at	3487	*IGFBP4*	3.82E-02	1.52	insulin like growth factor binding protein 4	
208415_x_at	3621	*ING1*	8.80E-03	1.52	inhibitor of growth family member 1	
231849_at	144501	*KRT80*	8.60E-03	1.52	keratin 80, type II	
212823_s_at	26030	*PLEKHG3*	6.70E-02	1.52	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	
227093_at	57602	*USP36*	1.17E-01	1.52	ubiquitin specific peptidase 36	
241950_at	23286	*WWC1*	1.27E-01	1.52	WW and C2 domain containing 1	
210762_s_at	10395	*DLC1*	8.60E-03	1.51	DLC1 Rho GTPase activating protein	
203627_at	3480	*IGF1R*	6.88E-02	1.51	insulin-like growth factor 1 receptor	
233487_s_at	56262	*LRRC8A*	6.00E-03	1.51	leucine rich repeat containing 8 family, member A	
210845_s_at	5329	*PLAUR*	4.00E-03	1.51	plasminogen activator, urokinase receptor	
216049_at	22836	*RHOBTB3*	6.50E-02	1.51	Rho-related BTB domain containing 3	
226563_at	4087	*SMAD2*	3.93E-02	1.51	SMAD family member 2	
235598_at	4087	*SMAD2*	6.82E-02	1.51	SMAD family member 2	
213873_at	10402	*ST3GAL6*	7.38E-02	1.51	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	
229812_at	84196	*USP48*	4.92E-02	1.51	ubiquitin specific peptidase 48	

Indacaterol (6h)
(320 Probe Sets ≡ 205 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
209959_at	8013	*NR4A3*	5.00E-04	14.13	nuclear receptor subfamily 4, group A, member 3	
221541_at	**83716**	***CRISPLD2***	**5.31E-08**	**8.05**	**cysteine-rich secretory protein LCCL domain containing 2**	
1565657_at	54918	*CMTM6*	9.35E-02	6.78	CKLF-like MARVEL transmembrane domain containing 6	
219049_at	55790	*CSGALNACT1*	3.00E-04	6.58	chondroitin sulfate N-acetylgalactosaminyltransferase 1	
228128_x_at	5069	*PAPPA*	1.00E-04	6.16	pregnancy-associated plasma protein A, pappalysin 1	
222784_at	64093	*SMOC1*	1.00E-04	5.62	SPARC related modular calcium binding 1	
225207_at	**5166**	***PDK4***	**7.00E-04**	**5.41**	**pyruvate dehydrogenase kinase, isozyme 4**	
239461_at	117248	*GALNT15*	4.05E-02	5.02	polypeptide N-acetylgalactosaminyltransferase 15	
222783_s_at	64093	*SMOC1*	1.00E-04	4.93	SPARC related modular calcium binding 1	
243438_at	27115	*PDE7B*	8.50E-03	4.85	phosphodiesterase 7B	
205421_at	6581	*SLC22A3*	5.51E-02	4.77	solute carrier family 22 (organic cation transporter), member 3	
1556185_a_at	79689	*STEAP4*	5.00E-04	4.73	STEAP family member 4	
224942_at	5069	*PAPPA*	3.00E-04	4.69	pregnancy-associated plasma protein A, pappalysin 1	
224940_s_at	5069	*PAPPA*	3.00E-04	4.68	pregnancy-associated plasma protein A, pappalysin 1	
203638_s_at	**2263**	***FGFR2***	**1.40E-03**	**4.65**	**fibroblast growth factor receptor 2**	
224941_at	5069	*PAPPA*	5.00E-04	4.64	pregnancy-associated plasma protein A, pappalysin 1	
228962_at	**5144**	***PDE4D***	**1.30E-03**	**4.51**	**phosphodiesterase 4D, cAMP-specific**	
230109_at	27115	*PDE7B*	3.00E-04	4.31	phosphodiesterase 7B	
201981_at	5069	*PAPPA*	7.00E-04	4.10	pregnancy-associated plasma protein A, pappalysin 1	
238649_at	26207	*PITPNC1*	2.20E-03	4.10	phosphatidylinositol transfer protein, cytoplasmic 1	

228501_at	117248	*GALNT15*	1.60E-03	4.02	polypeptide N-acetylgalactosaminyltransferase 15	
203549_s_at	4023	*LPL*	3.00E-04	3.99	lipoprotein lipase	
211401_s_at	**2263**	***FGFR2***	**4.96E-02**	**3.85**	**fibroblast growth factor receptor 2**	
203548_s_at	4023	*LPL*	1.00E-03	3.82	lipoprotein lipase	
213050_at	23242	*COBL*	5.00E-04	3.79	cordon-bleu WH2 repeat protein	
220088_at	**728**	***C5AR1***	**9.00E-04**	**3.65**	**complement component 5a receptor 1**	
225987_at	79689	*STEAP4*	3.00E-04	3.44	STEAP family member 4	
211119_at	2100	*ESR2*	3.77E-02	3.44	estrogen receptor 2 (ER beta)	
236361_at	117248	*GALNT15*	6.20E-03	3.41	polypeptide N-acetylgalactosaminyltransferase 15	
237804_at	8701	*DNAH11*	4.79E-02	3.41	dynein, axonemal, heavy chain 11	
205960_at	**5166**	***PDK4***	**2.24E-02**	**3.40**	**pyruvate dehydrogenase kinase, isozyme 4**	
229709_at	483	*ATP1B3*	8.00E-03	3.39	ATPase, Na+/K+ transporting, beta 3 polypeptide	
216248_s_at	**4929**	***NR4A2***	**6.53E-02**	**3.39**	**nuclear receptor subfamily 4, group A, member 2**	
225516_at	6542	*SLC7A2*	1.00E-04	3.33	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	
208606_s_at	54361	*WNT4*	6.96E-02	3.27	wingless-type MMTV integration site family, member 4	
213182_x_at	1028	*CDKN1C*	3.10E-03	3.14	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
205501_at	10846	*PDE10A*	5.43E-05	3.00	phosphodiesterase 10A	
220540_at	60598	*KCNK15*	2.79E-02	2.93	potassium channel, two pore domain subfamily K, member 15	
219093_at	55022	*PID1*	3.90E-03	2.86	phosphotyrosine interaction domain containing 1	
204491_at	**5144**	***PDE4D***	**1.03E-02**	**2.82**	**phosphodiesterase 4D, cAMP-specific**	
219534_x_at	1028	*CDKN1C*	1.40E-03	2.75	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
216894_x_at	1028	*CDKN1C*	3.00E-04	2.74	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
213348_at	1028	*CDKN1C*	9.00E-04	2.73	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
220187_at	79689	*STEAP4*	7.00E-04	2.70	STEAP family member 4	
223484_at	84419	*C15orf48*	9.39E-02	2.69	chromosome 15 open reading frame 48	
239650_at	344148	*NCKAP5*	1.11E-02	2.68	NCK-associated protein 5	
237939_at	2044	*EPHA5*	3.00E-04	2.64	EPH receptor A5	
230748_at	9120	*SLC16A6*	1.63E-02	2.55	solute carrier family 16, member 6	
207038_at	9120	*SLC16A6*	1.72E-02	2.49	solute carrier family 16, member 6	
222015_at	1454	*CSNK1E*	5.00E-04	2.45	casein kinase 1, epsilon	
	102800317	*LOC400927-CSNK1E*			LOC400927-CSNK1E readthrough	
216627_s_at	2683	*B4GALT1*	2.40E-03	2.44	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	
210102_at	4013	*VWA5A*	2.93E-02	2.41	von Willebrand factor A domain containing 5A	
229093_at	4846	*NOS3*	6.78E-02	2.38	nitric oxide synthase 3	
228132_at	84448	*ABLIM2*	3.00E-04	2.36	actin binding LIM protein family, member 2	
236300_at	5139	*PDE3A*	1.30E-03	2.35	phosphodiesterase 3A, cGMP-inhibited	
238029_s_at	151473	*SLC16A14*	1.90E-03	2.35	solute carrier family 16, member 14	
210836_x_at	**5144**	***PDE4D***	**1.06E-02**	**2.35**	**phosphodiesterase 4D, cAMP-specific**	
1555007_s_at	144406	*WDR66*	3.00E-04	2.34	WD repeat domain 66	
228507_at	5139	*PDE3A*	2.20E-03	2.34	phosphodiesterase 3A, cGMP-inhibited	
208228_s_at	**2263**	***FGFR2***	**2.60E-03**	**2.32**	**fibroblast growth factor receptor 2**	
209583_s_at	**4345**	***CD200***	**2.80E-03**	**2.32**	**CD200 molecule**	
229414_at	26207	*PITPNC1*	3.25E-02	2.32	phosphatidylinositol transfer protein, cytoplasmic 1	
1553199_at	138009	*DCAF4L2*	6.02E-02	2.31	DDB1 and CUL4 associated factor 4-like 2	
224071_at	50604	*IL20*	6.00E-02	2.30	interleukin 20	
225978_at	57494	*RIMKLB*	3.00E-04	2.29	ribosomal modification protein rimK-like family member B	
1555006_at	144406	*WDR66*	1.11E-02	2.28	WD repeat domain 66	
221305_s_at	54576	*UGT1A8*	9.20E-02	2.27	UDP glucuronosyltransferase 1 family, polypeptide A8	
	54600	*UGT1A9*			UDP glucuronosyltransferase 1 family, polypeptide A9	
229552_at	8739	*HRK*	1.20E-03	2.24	harakiri, BCL2 interacting protein	
	283454	*LOC283454*			uncharacterized LOC283454	
208425_s_at	26115	*TANC2*	1.20E-03	2.24	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	
209582_s_at	**4345**	***CD200***	**1.20E-03**	**2.22**	**CD200 molecule**	
232267_at	283383	*ADGRD1*	8.60E-03	2.22	adhesion G protein-coupled receptor D1	
206616_s_at	53616	*ADAM22*	2.07E-02	2.22	ADAM metallopeptidase domain 22	
1552736_a_at	81832	*NETO1*	3.00E-04	2.21	neuropilin (NRP) and tolloid (TLL)-like 1	
1554199_at	5800	*PTPRO*	4.44E-02	2.20	protein tyrosine phosphatase, receptor type, O	
218177_at	57132	*CHMP1B*	2.94E-02	2.18	charged multivesicular body protein 1B	
205003_at	9732	*DOCK4*	1.92E-02	2.17	dedicator of cytokinesis 4	
227099_s_at	387763	*C11orf96*	1.80E-03	2.16	chromosome 11 open reading frame 96	
206389_s_at	5139	*PDE3A*	2.40E-03	2.16	phosphodiesterase 3A, cGMP-inhibited	
209772_s_at	100133941	*CD24*	1.00E-04	2.15	CD24 molecule	
206356_s_at	2774	*GNAL*	1.20E-03	2.15	guanine nucleotide binding protein, alpha activating activity polypeptide, olfactory type	
218589_at	10161	*LPAR6*	1.13E-02	2.15	lysophosphatidic acid receptor 6	
228325_at	23514	*SPIDR*	4.55E-02	2.15	scaffolding protein involved in DNA repair	
235367_at	84665	*MYPN*	9.00E-04	2.13	myopalladin	
213006_at	1052	*CEBPD*	7.22E-02	2.13	CCAAT/enhancer binding protein (C/EBP), delta	
224952_at	26115	*TANC2*	3.00E-04	2.12	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	
203628_at	3480	*IGF1R*	9.00E-04	2.10	insulin-like growth factor 1 receptor	
213436_at	1268	*CNR1*	1.30E-03	2.10	cannabinoid receptor 1 (brain)	
218865_at	64757	*MARC1*	3.00E-04	2.09	mitochondrial amidoxime reducing component 1	
207626_s_at	6542	*SLC7A2*	1.55E-02	2.09	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	
220335_x_at	23491	*CES3*	3.00E-04	2.08	carboxylesterase 3	
205157_s_at	3872	*KRT17*	1.63E-02	2.08	keratin 17, type I	
230398_at	84951	*TNS4*	4.36E-02	2.07	tensin 4	
205896_at	6583	*SLC22A4*	9.20E-03	2.06	solute carrier family 22 (organic cation/zwitterion transporter), member 4	
208078_s_at	150094	*SIK1*	7.78E-02	2.06	salt-inducible kinase 1	
	102724428	*LOC102724428*			serine/threonine-protein kinase SIK1	
208651_x_at	100133941	*CD24*	2.05E-02	2.05	CD24 molecule	
1568949_at	26207	*PITPNC1*	8.20E-03	2.03	phosphatidylinositol transfer protein, cytoplasmic 1	
206359_at	**9021**	***SOCS3***	**4.68E-02**	**2.03**	**suppressor of cytokine signaling 3**	
207430_s_at	4477	*MSMB*	9.32E-02	2.03	microseminoprotein, beta-	
208650_s_at	100133941	*CD24*	8.00E-03	2.02	CD24 molecule	
201810_s_at	9467	*SH3BP5*	1.20E-03	2.01	SH3-domain binding protein 5 (BTK-associated)	
226858_at	1454	*CSNK1E*	5.00E-04	2.00	casein kinase 1, epsilon	
	102800317	*LOC400927-CSNK1E*			LOC400927-CSNK1E readthrough	
224963_at	1836	*SLC26A2*	9.00E-04	2.00	solute carrier family 26 (anion exchanger), member 2	
236440_at	81832	*NETO1*	1.30E-03	2.00	neuropilin (NRP) and tolloid (TLL)-like 1	
211631_x_at	2683	*B4GALT1*	3.50E-03	1.99	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	
206864_s_at	8739	*HRK*	3.00E-04	1.98	harakiri, BCL2 interacting protein	
236087_at	84448	*ABLIM2*	1.20E-03	1.98	actin binding LIM protein family, member 2	
266_s_at	100133941	*CD24*	2.84E-02	1.98	CD24 molecule	
210837_s_at	**5144**	***PDE4D***	**7.29E-02**	**1.98**	**phosphodiesterase 4D, cAMP-specific**	
237724_at	162333	*MARCH10*	2.61E-02	1.97	membrane associated ring finger 10	

206388_at	5139	*PDE3A*	5.00E-04	1.96	phosphodiesterase 3A, cGMP-inhibited	
226865_at	84898	*PLXDC2*	1.40E-03	1.96	plexin domain containing 2	
242444_at	114904	*C1QTNF6*	1.31E-02	1.96	C1q and tumor necrosis factor related protein 6	
238919_at	5101	*PCDH9*	3.88E-02	1.95	protocadherin 9	
200731_s_at	7803	*PTP4A1*	5.85E-02	1.95	protein tyrosine phosphatase type IVA, member 1	
224393_s_at	27439	*TMEM121B*	8.80E-02	1.95	transmembrane Protein 121B	
225728_at	8470	*SORBS2*	1.57E-02	1.94	sorbin and SH3 domain containing 2	
203627_at	3480	*IGF1R*	9.00E-04	1.93	insulin-like growth factor 1 receptor	
213438_at	23114	*NFASC*	1.30E-03	1.93	neurofascin	
215703_at	1080	*CFTR*	8.96E-02	1.92	cystic fibrosis transmembrane conductance regulator	
213765_at	8076	*MFAP5*	1.20E-03	1.91	microfibrillar associated protein 5	
202952_s_at	8038	*ADAM12*	3.00E-04	1.90	ADAM metallopeptidase domain 12	
220343_at	27115	*PDE7B*	3.00E-04	1.89	phosphodiesterase 7B	
214807_at	84898	*PLXDC2*	1.63E-02	1.89	plexin domain containing 2	
219155_at	26207	*PITPNC1*	1.93E-02	1.89	phosphatidylinositol transfer protein, cytoplasmic 1	
206865_at	8739	*HRK*	3.31E-02	1.89	harakiri, BCL2 interacting protein	
1559997_x_at	201191	*SAMD14*	6.77E-02	1.89	sterile alpha motif domain containing 14	
216379_x_at	100133941	*CD24*	3.10E-03	1.88	CD24 molecule	
210397_at	1672	*DEFB1*	7.30E-03	1.88	defensin, beta 1	
228964_at	639	*PRDM1*	1.71E-02	1.88	PR domain containing 1, with ZNF domain	
225330_at	3480	*IGF1R*	4.50E-02	1.88	insulin-like growth factor 1 receptor	
214595_at	3755	*KCNG1*	7.60E-03	1.87	potassium channel, voltage gated modifier subfamily G, member 1	
223571_at	114904	*C1QTNF6*	1.35E-02	1.87	C1q and tumor necrosis factor related protein 6	
226614_s_at	83648	*FAM167A*	3.00E-04	1.86	family with sequence similarity 167, member A	
213924_at	2774	*GNAL*	8.20E-03	1.86	guanine nucleotide binding protein, alpha activating activity polypeptide, olfactory type	
213764_s_at	8076	*MFAP5*	1.82E-02	1.86	microfibrillar associated protein 5	
221272_s_at	81563	*C1orf21*	3.20E-03	1.85	chromosome 1 open reading frame 21	
242162_at	164781	*DAW1*	8.60E-03	1.85	dynein assembly factor with WDR repeat domains 1	
237187_at	8739	*HRK*	9.00E-04	1.84	harakiri, BCL2 interacting protein	
227529_s_at	9590	*AKAP12*	1.72E-02	1.84	A kinase (PRKA) anchor protein 12	
227276_at	84898	*PLXDC2*	1.30E-03	1.83	plexin domain containing 2	
206355_at	2774	*GNAL*	1.60E-03	1.83	guanine nucleotide binding protein, alpha activating activity polypeptide, olfactory type	
208250_s_at	**1755**	***DMBT1***	**3.10E-03**	**1.83**	**deleted in malignant brain tumors 1**	
212236_x_at	3872	*KRT17*	4.52E-02	1.83	keratin 17, type I	
1563933_a_at	200150	*PLD5*	5.00E-04	1.82	phospholipase D family, member 5	
229180_at	23286	*WWC1*	1.30E-03	1.82	WW and C2 domain containing 1	
209771_x_at	100133941	*CD24*	2.20E-03	1.82	CD24 molecule	
237217_at	92949	*ADAMTSL1*	8.20E-03	1.82	ADAMTS like 1	
219743_at	23493	*HEY2*	5.53E-02	1.82	hes-related family bHLH transcription factor with YRPW motif 2	
202388_at	**5997**	***RGS2***	**7.25E-02**	**1.82**	**regulator of G-protein signaling 2**	
201811_x_at	9467	*SH3BP5*	2.10E-03	1.81	SH3-domain binding protein 5 (BTK-associated)	
225999_at	57494	*RIMKLB*	2.48E-02	1.81	ribosomal modification protein rimK-like family member B	
218178_s_at	57132	*CHMP1B*	3.03E-02	1.81	charged multivesicular body protein 1B	
209016_s_at	3855	*KRT7*	9.00E-04	1.80	keratin 7, type II	
1562713_a_at	81832	*NETO1*	3.30E-03	1.80	neuropilin (NRP) and tolloid (TLL)-like 1	
208335_s_at	2532	*ACKR1*	1.03E-02	1.80	atypical chemokine receptor 1 (Duffy blood group)	
229403_at	2683	*B4GALT1*	7.27E-02	1.80	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	
243243_at	2719	*GPC3*	1.48E-02	1.79	glypican 3	
221577_x_at	9518	*GDF15*	2.43E-02	1.79	growth differentiation factor 15	
1554744_at	114769	*CARD16*	2.64E-02	1.79	caspase recruitment domain family, member 16	
200732_s_at	7803	*PTP4A1*	2.92E-02	1.79	protein tyrosine phosphatase type IVA, member 1	
213425_at	7474	*WNT5A*	7.78E-02	1.79	wingless-type MMTV integration site family, member 5A	
205139_s_at	10090	*UST*	8.29E-02	1.79	uronyl-2-sulfotransferase	
1560253_at	56956	*LHX9*	8.92E-02	1.79	LIM homeobox 9	
229529_at	6943	*TCF21*	9.00E-04	1.78	transcription factor 21	
226777_at	8038	*ADAM12*	1.30E-03	1.78	ADAM metallopeptidase domain 12	
225328_at	114907	*FBXO32*	1.70E-03	1.78	F-box protein 32	
226834_at	79827	*CLMP*	6.30E-03	1.78	CXADR-like membrane protein	
223475_at	83690	*CRISPLD1*	1.20E-03	1.77	cysteine-rich secretory protein LCCL domain containing 1	
205097_at	1836	*SLC26A2*	1.50E-03	1.77	solute carrier family 26 (anion exchanger), member 2	
215189_at	3892	*KRT86*	2.00E-03	1.77	keratin 86, type II	
227752_at	55304	*SPTLC3*	3.10E-03	1.77	serine palmitoyltransferase, long chain base subunit 3	
228748_at	966	*CD59*	1.56E-02	1.77	CD59 molecule, complement regulatory protein	
236297_at	84898	*PLXDC2*	2.91E-02	1.77	plexin domain containing 2	
227660_at	84168	*ANTXR1*	3.00E-04	1.76	anthrax toxin receptor 1	
209921_at	23657	*SLC7A11*	2.07E-02	1.76	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	
209387_s_at	4071	*TM4SF1*	2.22E-02	1.76	transmembrane 4 L six family member 1	
236038_at	57484	*RNF150*	3.89E-02	1.76	ring finger protein 150	
214842_s_at	213	*ALB*	4.74E-02	1.76	albumin	
220092_s_at	84168	*ANTXR1*	7.00E-04	1.75	anthrax toxin receptor 1	
229720_at	573	*BAG1*	1.10E-03	1.75	BCL2-associated athanogene	
203710_at	3708	*ITPR1*	6.40E-03	1.75	inositol 1,4,5-trisphosphate receptor, type 1	
215303_at	9201	*DCLK1*	2.60E-03	1.74	doublecortin-like kinase 1	
219383_at	79899	*PRR5L*	3.10E-03	1.74	proline rich 5 like	
228731_at	2977	*GUCY1A2*	8.87E-02	1.74	guanylate cyclase 1, soluble, alpha 2	
212143_s_at	3486	*IGFBP3*	3.80E-03	1.73	insulin like growth factor binding protein 3	
230962_at	9201	*DCLK1*	7.30E-03	1.72	doublecortin-like kinase 1	
225520_at	25902	*MTHFD1L*	8.00E-03	1.72	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	
238455_at	84898	*PLXDC2*	1.15E-02	1.72	plexin domain containing 2	
227530_at	9590	*AKAP12*	2.20E-02	1.72	A kinase (PRKA) anchor protein 12	
236201_at	55304	*SPTLC3*	6.71E-02	1.72	serine palmitoyltransferase, long chain base subunit 3	
241950_at	23286	*WWC1*	8.80E-03	1.71	WW and C2 domain containing 1	
217678_at	23657	*SLC7A11*	1.40E-02	1.71	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	
202478_at	28951	*TRIB2*	2.78E-02	1.71	tribbles pseudokinase 2	
212906_at	57476	*GRAMD1B*	9.87E-02	1.71	GRAM domain containing 1B	
202897_at	140885	*SIRPA*	6.80E-03	1.70	signal-regulatory protein alpha	
209277_at	7980	*TFPI2*	2.12E-02	1.70	tissue factor pathway inhibitor 2	
231559_at	4837	*NNMT*	2.35E-02	1.70	nicotinamide N-methyltransferase	
203180_at	220	*ALDH1A3*	1.20E-03	1.69	aldehyde dehydrogenase 1 family, member A3	
224959_at	1836	*SLC26A2*	4.50E-03	1.69	solute carrier family 26 (anion exchanger), member 2	
219911_s_at	28231	*SLCO4A1*	1.35E-02	1.69	solute carrier organic anion transporter family, member 4A1	
202238_s_at	4837	*NNMT*	1.57E-02	1.69	nicotinamide N-methyltransferase	
209758_s_at	8076	*MFAP5*	3.00E-04	1.68	microfibrillar associated protein 5	
202679_at	4864	*NPC1*	9.00E-04	1.68	Niemann-Pick disease, type C1	

205399_at	9201	*DCLK1*	2.00E-03	1.68	doublecortin-like kinase 1
230493_at	387914	*SHISA2*	2.70E-03	1.68	shisa family member 2
213849_s_at	5521	*PPP2R2B*	3.10E-03	1.68	protein phosphatase 2, regulatory subunit B, beta
227867_at	129293	*TRABD2A*	1.50E-02	1.68	TraB domain containing 2A
215034_s_at	4071	*TM4SF1*	2.07E-02	1.68	transmembrane 4 L six family member 1
203984_s_at	842	*CASP9*	6.44E-02	1.68	caspase 9
226281_at	92737	*DNER*	6.89E-02	1.68	delta/notch like EGF repeat containing
201925_s_at	1604	*CD55*	7.41E-02	1.68	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
203865_s_at	104	*ADARB1*	9.00E-04	1.67	adenosine deaminase, RNA-specific, B1
216074_x_at	23286	*WWC1*	4.90E-03	1.67	WW and C2 domain containing 1
219825_at	56603	*CYP26B1*	6.80E-03	1.67	cytochrome P450, family 26, subfamily B, polypeptide 1
206707_x_at	9750	*FAM65B*	1.36E-02	1.67	family with sequence similarity 65, member B
228461_at	344558	*SH3RF3*	1.20E-03	1.66	SH3 domain containing ring finger 3
209676_at	7035	*TFPI*	2.22E-02	1.66	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
214199_at	6441	*SFTPD*	5.72E-02	1.66	surfactant protein D
209829_at	9750	*FAM65B*	7.78E-02	1.66	family with sequence similarity 65, member B
206866_at	1002	*CDH4*	1.20E-03	1.65	cadherin 4, type 1, R-cadherin (retinal)
223125_s_at	81563	*C1orf21*	2.00E-03	1.65	chromosome 1 open reading frame 21
1555486_a_at	79899	*PRR5L*	2.90E-03	1.65	proline rich 5 like
213258_at	7035	*TFPI*	2.90E-03	1.65	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
222073_at	1285	*COL4A3*	3.90E-03	1.65	collagen, type IV, alpha 3 (Goodpasture antigen)
204456_s_at	**2619**	***GAS1***	**4.60E-03**	**1.65**	**growth arrest-specific 1**
208108_s_at	554	*AVPR2*	4.26E-02	1.65	arginine vasopressin receptor 2
215646_s_at	1462	*VCAN*	7.22E-02	1.65	versican
213085_s_at	23286	*WWC1*	8.00E-04	1.64	WW and C2 domain containing 1
213988_s_at	6303	*SAT1*	2.49E-02	1.64	spermidine/spermine N1-acetyltransferase 1
217546_at	4499	*MT1M*	3.96E-02	1.64	metallothionein 1M
219737_s_at	5101	*PCDH9*	7.13E-02	1.64	protocadherin 9
224783_at	283991	*UBALD2*	9.00E-04	1.63	UBA-like domain containing 2
225540_at	4133	*MAP2*	1.20E-03	1.63	microtubule associated protein 2
202723_s_at	2308	*FOXO1*	4.30E-03	1.63	forkhead box O1
232206_at	54986	*ULK4*	3.00E-04	1.62	unc-51 like kinase 4
219714_s_at	55799	*CACNA2D3*	5.00E-04	1.62	calcium channel, voltage-dependent, alpha 2/delta subunit 3
229585_at	92949	*ADAMTSL1*	3.40E-03	1.62	ADAMTS like 1
216598_s_at	6347	*CCL2*	6.70E-03	1.62	chemokine (C-C motif) ligand 2
205795_at	9369	*NRXN3*	9.80E-03	1.62	neurexin 3
209355_s_at	8613	*PLPP3*	1.17E-02	1.62	phospholipid phosphatase 3
216944_s_at	3708	*ITPR1*	3.78E-02	1.62	inositol 1,4,5-trisphosphate receptor, type 1
238419_at	90102	*PHLDB2*	4.08E-02	1.62	pleckstrin homology-like domain, family B, member 2
206002_at	10149	*ADGRG2*	7.00E-04	1.61	adhesion G protein-coupled receptor G2
226506_at	79875	*THSD4*	1.80E-03	1.61	thrombospondin type 1 domain containing 4
36711_at	23764	*MAFF*	2.14E-02	1.61	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
231067_s_at	9590	*AKAP12*	2.39E-02	1.61	A kinase (PRKA) anchor protein 12
210775_x_at	842	*CASP9*	4.69E-02	1.61	caspase 9
229228_at	9586	*CREB5*	6.56E-02	1.61	cAMP responsive element binding protein 5
225803_at	114907	*FBXO32*	4.60E-03	1.60	F-box protein 32
207826_s_at	3399	*ID3*	9.50E-03	1.60	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
209278_s_at	7980	*TFPI2*	1.71E-02	1.60	tissue factor pathway inhibitor 2
201508_at	3487	*IGFBP4*	9.00E-04	1.59	insulin like growth factor binding protein 4
209276_s_at	2745	*GLRX*	1.80E-03	1.59	glutaredoxin
225989_at	26091	*HERC4*	3.10E-03	1.59	HECT and RLD domain containing E3 ubiquitin protein ligase 4
229649_at	9369	*NRXN3*	3.90E-03	1.59	neurexin 3
210592_s_at	6303	*SAT1*	1.97E-02	1.59	spermidine/spermine N1-acetyltransferase 1
238877_at	2070	*EYA4*	2.67E-02	1.59	EYA transcriptional coactivator and phosphatase 4
213624_at	10924	*SMPDL3A*	3.36E-02	1.59	sphingomyelin phosphodiesterase, acid-like 3A
211682_x_at	54490	*UGT2B28*	4.95E-02	1.59	UDP glucuronosyltransferase 2 family, polypeptide B28
204039_at	1050	*CEBPA*	5.67E-02	1.59	CCAAT/enhancer binding protein (C/EBP), alpha
204288_s_at	8470	*SORBS2*	5.74E-02	1.59	sorbin and SH3 domain containing 2
226931_at	83857	*TMTC1*	7.00E-04	1.58	transmembrane and tetratricopeptide repeat containing 1
209386_at	4071	*TM4SF1*	1.38E-02	1.58	transmembrane 4 L six family member 1
224480_s_at	84803	*GPAT3*	2.18E-02	1.58	glycerol-3-phosphate acyltransferase 3
202479_s_at	28951	*TRIB2*	8.42E-02	1.58	tribbles pseudokinase 2
205074_at	6584	*SLC22A5*	2.60E-03	1.57	solute carrier family 22 (organic cation/carnitine transporter), member 5
238733_at	4193	*MDM2*	5.00E-03	1.57	MDM2 proto-oncogene, E3 ubiquitin protein ligase
212226_s_at	8613	*PLPP3*	8.80E-03	1.57	phospholipid phosphatase 3
221731_x_at	1462	*VCAN*	1.31E-02	1.57	versican
33304_at	3669	*ISG20*	1.46E-02	1.57	interferon stimulated exonuclease gene 20kDa
232124_at	729085	*FAM198A*	2.16E-02	1.57	family with sequence similarity 198, member A
228293_at	91614	*DEPDC7*	4.93E-02	1.57	DEP domain containing 7
228933_at	4810	*NHS*	6.40E-02	1.57	Nance-Horan syndrome (congenital cataracts and dental anomalies)
203108_at	9052	*GPRC5A*	5.00E-04	1.56	G protein-coupled receptor, class C, group 5, member A
230193_at	144406	*WDR66*	3.20E-03	1.56	WD repeat domain 66
207528_s_at	23657	*SLC7A11*	6.60E-03	1.56	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
204698_at	3669	*ISG20*	1.29E-02	1.56	interferon stimulated exonuclease gene 20kDa
205870_at	624	*BDKRB2*	4.44E-02	1.56	bradykinin receptor B2
223402_at	54935	*DUSP23*	1.50E-03	1.55	dual specificity phosphatase 23
202387_at	573	*BAG1*	1.60E-03	1.55	BCL2-associated athanogene
209087_x_at	4162	*MCAM*	4.60E-03	1.55	melanoma cell adhesion molecule
242624_at	84448	*ABLIM2*	8.00E-03	1.55	actin binding LIM protein family, member 2
217623_at	91807	*MYLK3*	1.30E-02	1.55	myosin light chain kinase 3
202724_s_at	2308	*FOXO1*	1.57E-02	1.55	forkhead box O1
200730_s_at	7803	*PTP4A1*	5.37E-02	1.55	protein tyrosine phosphatase type IVA, member 1
210869_s_at	4162	*MCAM*	2.10E-03	1.54	melanoma cell adhesion molecule
210095_s_at	3486	*IGFBP3*	2.90E-03	1.54	insulin like growth factor binding protein 3
226431_at	150864	*FAM117B*	3.70E-03	1.54	family with sequence similarity 117, member B
228625_at	163732	*CITED4*	1.01E-02	1.54	Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 4
202237_at	4837	*NNMT*	1.36E-02	1.54	nicotinamide N-methyltransferase
228813_at	9759	*HDAC4*	1.57E-02	1.54	histone deacetylase 4
213790_at	8038	*ADAM12*	2.61E-02	1.54	ADAM metallopeptidase domain 12
243358_at	3480	*IGF1R*	2.64E-02	1.54	insulin-like growth factor 1 receptor
213508_at	171546	*SPTSSA*	4.14E-02	1.54	serine palmitoyltransferase, small subunit A
225496_s_at	54843	*SYTL2*	5.37E-02	1.54	synaptotagmin-like 2
211475_s_at	573	*BAG1*	1.40E-03	1.53	BCL2-associated athanogene
202254_at	26037	*SIPA1L1*	5.70E-03	1.53	signal-induced proliferation-associated 1 like 1

201858_s_at	5552	*SRGN*	6.80E-03	1.53	serglycin	
1555950_a_at	1604	*CD55*	1.74E-02	1.53	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	
227657_at	57484	*RNF150*	3.90E-02	1.53	ring finger protein 150	
229812_at	84196	*USP48*	4.12E-02	1.53	ubiquitin specific peptidase 48	
231015_at	28999	*KLF15*	7.74E-02	1.53	Kruppel-like factor 15	
218113_at	23670	*TMEM2*	9.95E-02	1.53	transmembrane protein 2	
226322_at	83857	*TMTC1*	1.70E-03	1.52	transmembrane and tetratricopeptide repeat containing 1	
219501_at	55068	*ENOX1*	2.20E-03	1.52	ecto-NOX disulfide-thiol exchanger 1	
210015_s_at	4133	*MAP2*	2.60E-03	1.52	microtubule associated protein 2	
208055_s_at	26091	*HERC4*	2.69E-02	1.52	HECT and RLD domain containing E3 ubiquitin protein ligase 4	
226811_at	54855	*FAM46C*	8.29E-02	1.52	family with sequence similarity 46, member C	
203455_s_at	6303	*SAT1*	9.47E-02	1.52	spermidine/spermine N1-acetyltransferase 1	
220227_at	1002	*CDH4*	1.30E-03	1.51	cadherin 4, type 1, R-cadherin (retinal)	
229310_at	114818	*KLHL29*	1.00E-02	1.51	kelch-like family member 29	
210664_s_at	7035	*TFPI*	2.43E-02	1.51	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	
209683_at	81553	*FAM49A*	4.80E-02	1.51	family with sequence similarity 49, member A	
228796_at	131034	*CPNE4*	5.13E-02	1.51	copine IV	
205193_at	23764	*MAFF*	8.39E-02	1.51	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	
205462_s_at	3241	*HPCAL1*	1.30E-03	1.50	hippocalcin-like 1	
239352_at	55117	*SLC6A15*	4.30E-03	1.50	solute carrier family 6 (neutral amino acid transporter), member 15	
213280_at	23108	*RAP1GAP2*	2.18E-02	1.50	RAP1 GTPase activating protein 2	
220148_at	64577	*ALDH8A1*	4.05E-02	1.50	aldehyde dehydrogenase 8 family, member A1	
233506_at	9689	*BZW1*	9.02E-02	1.50	basic leucine zipper and W2 domains 1	

Indacaterol (18h)
(9 Probe Sets ≡ 9 Gene IDs)

Affy Probe Set ID	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
237328_at	55195	*C14orf105*	9.76E-02	3.27	chromosome 14 open reading frame 105	
1556420_s_at	388403	*YPEL2*	4.21E-02	2.24	yippee like 2	
216639_at	27286	*SRPX2*	7.81E-02	2.02	sushi-repeat containing protein, X-linked 2	
220006_at	79825	*EFCC1*	4.21E-02	1.98	EF-hand and coiled-coil domain containing 1	
237222_at	123722	*FSD2*	9.76E-02	1.85	fibronectin type III and SPRY domain containing 2	
208335_s_at	2532	*ACKR1*	3.93E-02	1.59	atypical chemokine receptor 1 (Duffy blood group)	
220227_at	1002	*CDH4*	3.67E-02	1.55	cadherin 4, type 1, R-cadherin (retinal)	
1554202_x_at	57010	*CABP4*	9.76E-02	1.54	calcium binding protein 4	
220335_x_at	23491	*CES3*	3.53E-02	1.53	carboxylesterase 3	

Transcripts used for real-time PCR validation are bolded and underlined.

*Some genes are recognised by more than one probe set and some probe sets recognise more than one gene.

Supplemental TABLE 4. Indacaterol-repressed transcripts with expression level changes <0.67-fold (*FDR* < 0.10) at 1h, 2h, 6h and 18h.

Transcriptional Regulators
Transporters, Ion Channels and Membrane Receptors
Metabolic Proteins
General Signalling Molecules, including Translational Regulators
Other Functions
Not Assigned

Indacaterol (1h)
(39 Probe Sets ≡ 46 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
210919_at	23239	*PHLPP1*	7.23E-02	0.15	PH domain and leucine rich repeat protein phosphatase 1	
1569262_x_at	90025	*UBE3D*	5.12E-02	0.19	ubiquitin protein ligase E3D	
236811_at	63946	*DMRTC2*	9.40E-02	0.41	DMRT-like family C2	
236862_at	57120	*GOPC*	7.67E-02	0.44	golgi-associated PDZ and coiled-coil motif containing	
237943_at	23023	*TMCC1*	1.26E-02	0.49	transmembrane and coiled-coil domain family 1	
237469_at	7153	*TOP2A*	7.00E-03	0.50	topoisomerase (DNA) II alpha	
218657_at	51195	*RAPGEFL1*	8.58E-02	0.51	Rap guanine nucleotide exchange factor like 1	
1557852_at	1912	*PHC2*	7.80E-03	0.51	polyhomeotic homolog 2 (Drosophila)	
1558124_at	134492	*NUDCD2*	5.91E-02	0.53	NudC domain containing 2	
244427_at	9493	*KIF23*	6.70E-03	0.55	kinesin family member 23	
1561720_at	9400	*RECQL5*	5.67E-02	0.55	RecQ helicase-like 5	
201693_s_at	**1958**	***EGR1***	**7.00E-03**	**0.56**	**early growth response 1**	
236841_at	100287171	*WASHC1*	3.27E-02	0.57	WAS protein family homolog 1	
220084_at	55195	*CCDC198*	5.65E-02	0.58	coiled-Coil Domain Containing 198	
239194_at	84277	*DNAJC30*	9.91E-02	0.58	DnaJ (Hsp40) homolog, subfamily C, member 30	
214918_at	4670	*HNRNPM*	8.11E-02	0.60	heterogeneous nuclear ribonucleoprotein M	
201009_s_at	**10628**	***TXNIP***	**1.02E-02**	**0.60**	**thioredoxin interacting protein**	
240452_at	2935	*GSPT1*	5.04E-02	0.60	G1 to S phase transition 1	
230998_at	11335	*CBX3*	9.92E-02	0.61	chromobox homolog 3	
231292_at	493861	*EID3*	9.51E-02	0.61	EP300 interacting inhibitor of differentiation 3	
228455_at	64783	*RBM15*	3.95E-02	0.61	RNA binding motif protein 15	
228393_s_at	55900	*ZNF302*	4.43E-02	0.61	zinc finger protein 302	
242922_at	408050	*NOMO3*	7.19E-02	0.63	NODAL modulator 3	
	55672	*NBPF1*			neuroblastoma breakpoint family member 1	
	728841	*NBPF8*			neuroblastoma breakpoint family, member 8	
	400818	*NBPF9*			neuroblastoma breakpoint family, member 9	
	100132406	*NBPF10*			neuroblastoma breakpoint family, member 10	
	200030	*NBPF11*			neuroblastoma breakpoint family, member 11	
1569519_at	149013	*NBPF12*	8.16E-02	0.63	neuroblastoma breakpoint family, member 12	
	25832	*NBPF14*			neuroblastoma breakpoint family, member 14	
	101060226	*NBPF19*			neuroblastoma breakpoint family, member 19	
	101060684	*NBPF26*			neuroblastoma breakpoint family, member 26	
	100996763	*LOC100996763*			notch Homolog 2 N-Terminal-Like Protein	
	102724250	*LOC102724250*			neuroblastoma breakpoint family member 1	
1570173_at	25896	*INTS7*	3.50E-02	0.63	integrator complex subunit 7	
242111_at	56339	*METTL3*	3.50E-03	0.63	methyltransferase like 3	
1561965_at	6629	*SNRPB2*	2.30E-02	0.63	small nuclear ribonucleoprotein polypeptide B	
229423_at	1111	*CHEK1*	9.47E-02	0.64	checkpoint kinase 1	
201008_s_at	**10628**	***TXNIP***	**2.90E-03**	**0.64**	**thioredoxin interacting protein**	
1559993_at	81855	*SFXN3*	8.94E-02	0.65	sideroflexin 3	
1565703_at	4089	*SMAD4*	6.24E-02	0.65	SMAD family member 4	
201466_s_at	3725	*JUN*	3.80E-02	0.65	jun proto-oncogene	
232055_at	94081	*SFXN1*	8.11E-02	0.65	sideroflexin 1	
239044_at	81533	*ITFG1*	2.20E-03	0.65	integrin alpha FG-GAP repeat containing 1	
201694_s_at	**1958**	***EGR1***	**1.17E-02**	**0.66**	**early growth response 1**	
239071_at	5928	*RBBP4*	7.29E-02	0.66	retinoblastoma binding protein 4	
219545_at	65987	*KCTD14*	8.43E-02	0.66	potassium channel tetramerization domain containing 14	
	100532726	*NDUFC2-KCTD14*			NDUFC2-KCTD14 readthrough	
206683_at	7718	*ZNF165*	9.17E-02	0.66	zinc finger protein 165	
1553349_at	196528	*ARID2*	9.47E-02	0.67	AT rich interactive domain 2 (ARID, RFX-like)	

Indacaterol (2h)
(51 Probe Sets ≡ 47 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
232328_at	79818	*ZNF552*	1.70E-03	0.22	zinc finger protein 552	
216345_at	23053	*ZSWIM8*	5.53E-02	0.34	zinc finger, SWIM-type containing 8	
1569262_x_at	90025	*UBE3D*	6.85E-02	0.36	ubiquitin protein ligase E3D	
227404_s_at	**1958**	***EGR1***	**7.00E-04**	**0.38**	**early growth response 1**	
201009_s_at	**10628**	***TXNIP***	**7.00E-04**	**0.40**	**thioredoxin interacting protein**	
230673_at	93035	*PKHD1L1*	9.18E-02	0.40	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	
201694_s_at	**1958**	***EGR1***	**3.00E-04**	**0.40**	**early growth response 1**	
201008_s_at	**10628**	***TXNIP***	**3.00E-04**	**0.42**	**thioredoxin interacting protein**	
1556300_s_at	6492	*SIM1*	2.20E-03	0.42	single-minded family bHLH transcription factor 1	
201010_s_at	**10628**	***TXNIP***	**3.00E-04**	**0.45**	**thioredoxin interacting protein**	
206876_at	6492	*SIM1*	5.20E-03	0.45	single-minded family bHLH transcription factor 1	
237469_at	7153	*TOP2A*	2.00E-04	0.46	topoisomerase (DNA) II alpha	
244427_at	9493	*KIF23*	1.50E-03	0.48	kinesin family member 23	
1555591_at	80119	*PIF1*	6.70E-02	0.49	PIF1 5'-to-3' DNA helicase	
216109_at	23389	*MED13L*	1.30E-02	0.51	mediator complex subunit 13-like	
1566111_at	9780	*PIEZO1*	1.20E-03	0.51	piezo-type mechanosensitive ion channel component 1	
206115_at	1960	*EGR3*	5.78E-02	0.52	early growth response 3	
1552880_at	89866	*SEC16B*	2.49E-02	0.53	SEC16 homolog B, endoplasmic reticulum export factor	
215175_at	22990	*PCNX*	1.12E-02	0.53	pecanex homolog (Drosophila)	
215508_at	699	*BUB1*	7.38E-02	0.54	BUB1 mitotic checkpoint serine/threonine kinase	
204826_at	899	*CCNF*	3.40E-03	0.54	cyclin F	
240432_x_at	8609	*KLF7*	1.02E-02	0.54	Kruppel-like factor 7 (ubiquitous)	
1553883_at	7652	*ZNF99*	4.47E-02	0.55	zinc finger protein 99	
201693_s_at	**1958**	***EGR1***	**1.95E-02**	**0.55**	**early growth response 1**	
238049_at	65983	*GRAMD3*	4.99E-02	0.55	GRAM domain containing 3	
232735_at	284615	*ANKRD34A*	4.00E-03	0.56	ankyrin repeat domain 34A	

208025_s_at	8091	*HMGA2*	1.30E-03	0.56	high mobility group AT-hook 2	
232912_at	160897	*GPR180*	8.34E-02	0.57	G protein-coupled receptor 180	
220709_at	80032	*ZNF556*	7.18E-02	0.57	zinc finger protein 556	
	23049	*NPIPB4*			nuclear pore complex interacting protein family, member B4	
	440345	*NPIPB5*			nuclear pore complex interacting protein family, member B5	
	440354	*SMG1*			SMG1 phosphatidylinositol 3-kinase-related kinase	
	595101	*SMG1P1*			SMG1 pseudogene 1	
	641298	*SMG1P2*			SMG1 pseudogene 2	
244766_at	100132247	*SMG1P3*	6.15E-02	0.57	SMG1 pseudogene 3	
	100271836	*SMG1P5*			SMG1 pseudogene 5	
	100506060	*SMG1P7*			SMG1 pseudogene 7	
	101060596	*LOC101060596*			serine/threonine-protein kinase SMG1-Like	
	105369244	*LOC105369244*			serine/threonine-protein kinase SMG1-like	
	105369278	*LOC105369278*			serine/threonine-protein kinase SMG1-Like	
219544_at	79866	*BORA*	2.80E-03	0.59	bora, aurora kinase A activator	
228892_at	153769	*SH3RF2*	9.78E-02	0.60	SH3 domain containing ring finger 2	
207286_at	9662	*CEP135*	2.57E-02	0.61	centrosomal protein 135kDa	
227687_at	219844	*HYLS1*	2.40E-03	0.61	hydrolethalus syndrome 1	
201896_s_at	84722	*PSRC1*	9.00E-04	0.61	proline/serine-rich coiled-coil 1	
230462_at	8650	*NUMB*	3.38E-02	0.62	numb homolog (Drosophila)	
218192_at	51447	*IP6K2*	5.40E-03	0.63	inositol hexakisphosphate kinase 2	
238220_at	7403	*KDM6A*	7.53E-02	0.63	lysine (K)-specific demethylase 6A	
1552546_a_at	137994	*LETM2*	2.06E-02	0.63	leucine zipper-EF-hand containing transmembrane protein 2	
235690_at	84622	*ZNF594*	7.49E-02	0.63	zinc finger protein 594	
216061_x_at	5155	*PDGFB*	1.13E-02	0.63	platelet-derived growth factor beta polypeptide	
227801_at	286827	*TRIM59*	7.00E-03	0.64	tripartite motif containing 59	
218726_at	55355	*HJURP*	9.20E-03	0.65	Holliday junction recognition protein	
216081_at	3910	*LAMA4*	6.14E-02	0.65	laminin, alpha 4	
204349_at	9443	*MED7*	3.98E-02	0.65	mediator complex subunit 7	
235165_at	84612	*PARD6B*	7.48E-02	0.65	par-6 family cell polarity regulator beta	
233782_at	10238	*DCAF7*	1.69E-02	0.65	DDB1 and CUL4 associated factor 7	
235476_at	286827	*TRIM59*	8.20E-03	0.65	tripartite motif containing 59	
214918_at	4670	*HNRNPM*	6.42E-02	0.66	heterogeneous nuclear ribonucleoprotein M	
225283_at	91947	*ARRDC4*	4.50E-03	0.66	arrestin domain containing 4	
1552794_a_at	284306	*ZNF547*	6.66E-02	0.66	zinc finger protein 547	

Indacaterol (6h)
(51 Probe Sets ≡ 47 Gene IDs)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
231600_at	387837	*CLEC12B*	3.31E-02	0.26	C-type lectin domain family 12, member B	
204823_at	89795	*NAV3*	8.00E-04	0.35	neuron navigator 3	
207134_x_at	7177	*TPSAB1*	7.04E-02	0.41	tryptase alpha/beta 1	
	64499	*TPSB2*			tryptase beta 2 (gene/pseudogene)	
1552658_a_at	89795	*NAV3*	7.00E-04	0.43	neuron navigator 3	
217262_s_at	9620	*CELSR1*	6.07E-02	0.46	cadherin, EGF LAG seven-pass G-type receptor 1	
223204_at	51313	*FAM198B*	1.31E-02	0.46	family with sequence similarity 198, member B	
223317_at	84266	*ALKBH7*	4.09E-02	0.47	alkB homolog 7	
214978_s_at	8497	*PPFIA4*	6.39E-02	0.48	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	
1552546_a_at	137994	*LETM2*	1.82E-02	0.48	leucine zipper-EF-hand containing transmembrane protein 2	
219872_at	51313	*FAM198B*	3.00E-04	0.50	family with sequence similarity 198, member B	
231053_at	3745	*KCNB1*	5.67E-02	0.51	potassium channel, voltage gated Shab related subfamily B, member 1	
201694_s_at	**1958**	***EGR1***	**1.74E-02**	**0.51**	**early growth response 1**	
218864_at	7145	*TNS1*	4.60E-03	0.52	tensin 1	
204439_at	10964	*IFI44L*	1.67E-02	0.52	interferon-induced protein 44-like	
227404_s_at	**1958**	***EGR1***	**1.33E-02**	**0.53**	**early growth response 1**	
202086_at	4599	*MX1*	7.05E-02	0.53	MX dynamin-like GTPase 1	
214453_s_at	10561	*IFI44*	9.90E-03	0.54	interferon-induced protein 44	
206757_at	8654	*PDE5A*	9.95E-02	0.55	phosphodiesterase 5A, cGMP-specific	
211006_s_at	3745	*KCNB1*	2.14E-02	0.55	potassium channel, voltage gated Shab related subfamily B, member 1	
215649_s_at	4598	*MVK*	1.80E-03	0.55	mevalonate kinase	
204363_at	2152	*F3*	5.74E-02	0.57	coagulation factor III (thromboplastin, tissue factor)	
223749_at	114898	*C1QTNF2*	2.83E-02	0.57	C1q and tumor necrosis factor related protein 2	
206553_at	4939	*OAS2*	8.63E-02	0.57	2'-5'-oligoadenylate synthetase 2	
229337_at	9099	*USP2*	7.04E-02	0.57	ubiquitin specific peptidase 2	
1556361_s_at	81573	*ANKRD13C*	1.51E-02	0.58	ankyrin repeat domain 13C	
220381_at	79822	*ARHGAP28*	7.11E-02	0.58	Rho GTPase activating protein 28	
205552_s_at	4938	*OAS1*	7.12E-02	0.58	2'-5'-oligoadenylate synthetase 1	
232666_at	4940	*OAS3*	4.19E-02	0.60	2'-5'-oligoadenylate synthetase 3	
222071_s_at	353189	*SLCO4C1*	3.53E-02	0.60	solute carrier organic anion transporter family, member 4C1	
233234_at	57528	*KCTD16*	6.71E-02	0.61	potassium channel tetramerization domain containing 16	
211520_s_at	2890	*GRIA1*	6.15E-02	0.62	glutamate receptor, ionotropic, AMPA 1	
206825_at	5021	*OXTR*	1.60E-03	0.62	oxytocin receptor	
237767_at	10160	*FARP1*	5.51E-02	0.62	FERM, ARH/RhoGEF and pleckstrin domain protein 1	
233907_s_at	56256	*SERTAD4*	9.00E-03	0.62	SERTA domain containing 4	
235315_at	8848	*TSC22D1*	6.53E-02	0.62	TSC22 domain family, member 1	
204938_s_at	5350	*PLN*	6.15E-02	0.63	phospholamban	
237691_x_at	2027	*ENO3*	1.51E-02	0.63	enolase 3 (beta, muscle)	
204056_s_at	4598	*MVK*	1.60E-03	0.63	mevalonate kinase	
1559060_a_at	96459	*FNIP1*	5.54E-02	0.63	folliculin interacting protein 1	
1554018_at	10457	*GPNMB*	8.38E-02	0.64	glycoprotein (transmembrane) nmb	
240869_at	3745	*KCNB1*	6.88E-02	0.64	potassium channel, voltage gated Shab related subfamily B, member 1	
1559449_a_at	9534	*ZNF254*	5.51E-02	0.64	zinc finger protein 254	
226603_at	219285	*SAMD9L*	1.40E-02	0.64	sterile alpha motif domain containing 9-like	
211018_at	4047	*LSS*	6.70E-03	0.65	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	
211019_s_at	4047	*LSS*	1.70E-03	0.65	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	
227055_at	196410	*METTL7B*	2.79E-02	0.65	methyltransferase like 7B	
235544_x_at	284069	*FAM171A2*	7.04E-02	0.65	family with sequence similarity 171, member A2	
236344_at	5137	*PDE1C*	1.40E-02	0.65	phosphodiesterase 1C, calmodulin-dependent 70kDa	
235760_at	64324	*NSD1*	4.41E-02	0.66	nuclear receptor binding SET domain protein 1	
230708_at	144165	*PRICKLE1*	2.70E-02	0.66	prickle homolog 1	
229767_at	6904	*TBCD*	1.07E-02	0.67	tubulin folding cofactor D	

Indacaterol (18h)
(1 Probe Set ≡ 1 Gene ID)

Affy Probe Set ID*	Entrez Gene ID	*Official Gene Symbol*	*FDR P-Value*	Fold change	UniGene Name	Function
240876_x_at	145645	*C15orf43*	9.51E-02	0.51	chromosome 15 open reading frame 43	

Transcripts used for real-time PCR validation are bolded and underlined.
*Some genes are recognised by more than one probe set and some probe sets recognise more than one gene.

Supplemental TABLE 5. Functional Annotation Clustering of Genes Significantly Induced by Indacaterol in BEAS-2B Cells at 1h, 2h and 6h.

Indacaterol (1h)

Annotation Cluster 1	Enrichment Score: 4.48	Genes	Count	*P*-Value	Benjamini
GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter	*ATF3, BCL6, BHLHE40, BMP2, CITED2, EDN1, EFNA1, ETS2, FEZF2, FOXC2, HES1, ID1, ID3, KLF4, MYC, NFIL3, NR4A2, NR4A3, PRDM1, RUNX3, SNAI2, TCF21, TGIF1*	23	4.30E-09	5.70E-06
GOTERM_MF_DIRECT	sequence-specific DNA binding	*ATF3, BCL6, CSRNP1, ESRRG, ETS2, FOSL2, FOXC1, FOXC2, HES1, IRX1, IRX2, KLF2, MAFF, MYC, NFIL3, NR4A1, NR4A2, NR4A3, SNAI2*	19	1.10E-08	3.40E-06
GOTERM_BP_DIRECT	positive regulation of transcription from RNA polymerase II promoter	*ADRB2, ATF3, BMP2, CEBPD, CITED2, CSRNP1, EDN1, ESRRG, ETS2, FEZF2, FOSL2, FOXC1, FOXC2, HES1, IL6, KLF2, KLF4, MAFF, MYC, NR4A1, NR4A2, NR4A3, RGCC, SERPINE1, SOX9, TCF21*	26	1.30E-08	8.40E-06
GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	*ATF3, BCL6, BHLHE40, CEBPD, CITED2, CSRNP1, ESRRG, ETS2, FOSL2, FOXC1, FOXC2, HES1, ID1, ID3, KLF2, KLF4, MAFF, MYC, NFIL3, PRDM1, RUNX3, SOX9, TGIF1, TSC22D1, ZFP36L1*	25	2.00E-08	3.10E-06
GOTERM_MF_DIRECT	transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	*ATF3, BHLHE40, ETS2, HES1, NFIL3, PRDM1, SNAI2, TCF21, TGIF1*	9	8.40E-07	8.40E-05
GOTERM_BP_DIRECT	transcription from RNA polymerase II promoter	*ATF3, CEBPD, SRNP1, FEZF2, FOXC1, FOXC2, KLF4, MAFF, MYC, NFIL3, RUNX3, SOX9, TCF21, TSC22D1*	14	5.90E-05	7.80E-03
GOTERM_CC_DIRECT	nucleus	*AKIP1, ANKRD37, ATF3, BCL6, BHLHE40, CEBPD, CITED2, CSNK1A1, CSRNP1, DUSP1, DUSP4, DUSP5, ERRFI1, ESRRG, ETS2, FAM71B, FEZF2, FOSL2, FOXC1, FOXC2, HES1, ID1, ID3, IRX1, IRX2, KLF2, KLF4, KLF6, MAFF, MYC, NEDD9, NFIL3, NR4A1, NR4A2, NR4A3, PRDM1, PYHIN1, RBFOX1, RGCC, RGS2, RUNX3, SGK1, SIK1, SNAI2, SOX9, SPIDR, SYNPO2, TCF21, TGIF1, TOB1, TSC22D1, ZFP36L1, ZNF331, ZNF385D, ZNF414*	55	1.60E-04	2.00E-02
GOTERM_BP_DIRECT	transcription, DNA-templated	*BBCL6, BHLHE40, CEBPD, CITED2, ESRRG, ETS2, FOSL2, HES1, ID1, ID3, KLF2, KLF6, NR4A1, NR4A2, NR4A3, PRDM1, SNAI2, TGIF1, ZNF331, ZNF414*	20	8.30E-02	6.90E-01
GOTERM_CC_DIRECT	nucleoplasm	*AKIP1, ATF3, BCL6, DUSP4, DUSP5, ESRRG, ETS2, FOSL2, FOXC1, HES1, ID1, ID3, KLF4, MAFF, MYC, NR4A1, NR4A2, NR4A3, PRDM1 SGK1, SOX9, SPIDR, TGIF1*	23	1.80E-01	9.40E-01
Annotation Cluster 2	**Enrichment Score: 3.49**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cellular response to interleukin-1	*CCL20, EDN1, KLF2, HAS2, IL6, MYC, SOX9*	7	1.00E-05	2.20E-03
GOTERM_BP_DIRECT	cellular response to tumor necrosis factor	*CCL20, EDN1, KLF2, HAS2, IL6, ZNF36L1*	6	1.00E-03	6.30E-02
GOTERM_BP_DIRECT	positive regulation of nitric oxide biosynthetic process	*EDN1, KLF2, KLF4, IL6*	4	3.30E-03	1.10E-01
Annotation Cluster 3	**Enrichment Score: 3.24**		**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	neural crest cell development	*EDN1, FOXC1, FOXC2, SNAI2, SOX9*	5	1.50E-06	6.70E-04
GOTERM_BP_DIRECT	Notch signaling pathway	*BMP2, FOXC1, FOXC2, HES1, MYC, SNAI2, SOX9*	7	1.50E-04	1.50E-02
GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding	*BHLHE40, FOXC1, FOXC2, SNAI2, SOX9*	5	1.00E-03	3.80E-02
GOTERM_BP_DIRECT	ossification	*CTGF, FOXC1, FOXC2, RUNX3, SOX9*	5	2.40E-03	9.30E-02
GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, sequence-specific DNA binding	*BHLHE40, FOXC1, RUNX3, SOX9*	4	1.10E-01	7.10E-01
Annotation Cluster 4	**Enrichment Score: 3.17**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter	*ATL3, FASL2, MAFF, RUNX3*	4	6.00E-01	1.00E+00
Annotation Cluster 5	**Enrichment Score: 2.52**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	positive regulation of epithelial cell proliferation	*C5AR1, ID1, IL6, MYC, NR4A3, SOX9*	6	6.10E-05	7.30E-03
GOTERM_BP_DIRECT	positive regulation of smooth muscle cell proliferation	*EDN1, IL6, MYC, NR4A3*	4	8.50E-03	2.00E-01
Annotation Cluster 6	**Enrichment Score: 2.18**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cell-cell signaling	*ADRB2, AREG, BDNF, BMP2, CCL20, CTGF, EFNA1, EDN1, NTF3*	9	4.00E-04	3.30E-02
GOTERM_MF_DIRECT	growth factor activity	*AREG, BDNF, BMP2, CTGF, IL6, NTF3*	6	4.90E-03	1.10E-01
GOTERM_MF_DIRECT	cytokine activity	*AREG, EDN1, IL6, BMP2*	4	1.20E-01	7.10E-01
Annotation Cluster 7	**Enrichment Score: 2.14**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	Notch signaling pathway	*BMP2, FOXC1, FOXC2, HES1, MYC, SNAI2, SOX9*	7	1.50E-04	1.50E-02
GOTERM_BP_DIRECT	epithelial to mesenchymal transition	*BMP2, SNAI2, SOX9*	3	2.30E-02	3.90E-01
GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	*BMP2, CSNK1A1, SNAI2, SOX9*	4	1.10E-01	7.50E-01
Annotation Cluster 8	**Enrichment Score: 2.12**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cellular response to corticotropin-releasing hormone stimulus	*NR4A1, NR4A2, NR4A3*	3	7.10E-04	4.80E-02
GOTERM_BP_DIRECT	fat cell differentiation	*CEBPD, KLF4, NR4A1, NR4A2, NR4A3*	5	1.70E-03	7.60E-02
GOTERM_MF_DIRECT	steroid hormone receptor activity	*ESRRG, NR4A1, NR4A2, NR4A3*	4	6.40E-03	1.40E-01
GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	*ESRRG, NR4A1, NR4A2, NR4A3*	4	7.30E-03	1.90E-01
GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	*CTGF, ESRRG, NR4A1, NR4A2, NR4A3*	5	2.20E-02	3.80E-01
GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	*NR4A1, NR4A2, NR4A3*	3	2.50E-02	3.30E-01
GOTERM_BP_DIRECT	intracellular receptor signaling pathway	*NR4A1, NR4A2, NR4A3*	3	2.90E-02	4.30E-01
GOTERM_MF_DIRECT	zinc ion binding	*ADAMTS1, ADAMTS15, ESRRG, KLF4, NR4A1, NR4A2, NR4A3, ZNF331, ZNF385D*	9	5.40E-01	1.00E+00
Annotation Cluster 9	**Enrichment Score: 2.08**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	negative regulation of sequence-specific DNA binding transcription factor activity	*BHLHE40, ID1, ID3, TRIB1*	4	8.50E-03	2.00E-01
GOTERM_MF_DIRECT	E-box binding	*BHLHE40, TCF21, MYC*	3	2.20E-02	3.10E-01
GOTERM_MF_DIRECT	transcription factor binding	*ID1, ID3, FOXC1, HES1, MYC, TRIB1*	6	4.40E-02	4.30E-01
GOTERM_MF_DIRECT	protein dimerization activity	*ID3, MYC, SLC24A2, TRIB1*	4	8.10E-02	6.40E-01
Annotation Cluster 10	**Enrichment Score: 1.66**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	*DUSP1, DUSP4, DUSP5*	3	2.50E-03	9.40E-02
GOTERM_BP_DIRECT	endoderm formation	*DUSP1, DUSP4, DUSP5*	3	3.00E-03	1.10E-01
GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine phosphatase activity	*DUSP1, DUSP4, DUSP5*	3	3.40E-03	8.80E-02
GOTERM_BP_DIRECT	inactivation of MAPK activity	*DUSP1, DUSP4, DUSP5*	3	1.30E-02	2.80E-01
GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	*DUSP1, DUSP4, DUSP5*	3	1.50E-01	8.50E-01
GOTERM_MF_DIRECT	protein tyrosine phosphatase activity	*DUSP1, DUSP4, DUSP5*	3	1.50E-01	7.70E-01
Annotation Cluster 11	**Enrichment Score: 1.51**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	positive regulation of ERK1 and ERK2 cascade	*ACKR3, BMP3, C5AR1, CCL20, CTGF, IL6, SPRY2*	7	1.40E-03	7.00E-02
GOTERM_BP_DIRECT	response to lipopolysaccharide	*C5AR1, CXCL2, CXCL3, EDN1, IL12RB2, TRIB1*	6	5.80E-03	1.60E-01
GOTERM_BP_DIRECT	positive regulation of neutrophil chemotaxis	*C5AR1, CXCL2, CXCL3*	3	1.00E-02	2.30E-01
GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	*ACKR3, CCL20, CXCL2, CXCL3*	4	1.30E-02	2.80E-01
GOTERM_MF_DIRECT	chemokine activity	*CCL20, CXCL2, CXCL3*	3	4.30E-02	4.40E-01
GOTERM_BP_DIRECT	inflammatory response	*BCL6, BMP2, C5AR1, CCL20, CXCL2, CXCL3, IL6,*	7	4.90E-02	5.60E-01
GOTERM_BP_DIRECT	chemotaxis	*ACKR3, C5AR1, CXCL2, CCL20,*	4	5.40E-02	5.80E-01
GOTERM_BP_DIRECT	immune response	*C5AR1, CCL20, CXCL2, CXCL3, IL6, NFIL3, SH2D6*	7	7.40E-02	6.60E-01
GOTERM_BP_DIRECT	cell chemotaxis	*C5AR1, CCL20, CXCL2*	3	7.50E-02	6.60E-01
GOTERM_BP_DIRECT	G-protein coupled receptor signaling pathway	*ACKR3, AREG, CCL20, CXCL2, CXCL3, EDN1*	6	7.60E-01	1.00E+00

Indacaterol (2h)

Annotation Cluster 1	Enrichment Score: 7.64	Genes	Count	*P* -Value	Benjamini
UP_SEQ_FEATURE	DNA-binding region:Basic motif	*ATF3, BHLHE40, CEBPA, CEBPD, CREB3L2, EPAS1, FOS, FOSB, FOSL2, HES1, JUNB, MAFF, MAFK, MYC, NFIL3, PHTF2, TCF21*	17	4.90E-09	4.60E-06
Annotation Cluster 2	**Enrichment Score: 6.81**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_BP_DIRECT	positive regulation of transcription from RNA polymerase II promoter	*ATF3, ATXN7, BMP2, CEBPA, CEBPD, CITED4, CREB3L2, EDN1, EPAS1, ETS2, FGFR2, FOS, FOSB, FOSL2, FOXC1, FOXC2, FOXO1, FSTL3, GREM1, HES1, HOXA5, IL6, IL11, INHBA, JAG1, JUNB, KLF4, LPIN1, MAFF, MAFK, MEF2D, MYC, NFATC1, NOG, NR4A1, NR4A2, NR4A3, PPARGC1A, PROX2, REL, RGCC, SERPINE1, SIX2, SMAD2, SOX4, SOX9, TCF21, TFAP2A, TFAP2C, VGLL2, WNT5A, ZBTB38, ZNF462*	53	3.20E-13	7.50E-10
GOTERM_MF_DIRECT	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	*CEBPA, CEBPD, CREB3L2, EPAS1, FOS, FOSB, FOXC2, HOXA5, JUNB, KLF4, MEF2D, MYC, NR4A1, NR4A2, NR4A3, SIX2, SMAD2, SOX4, SOX9, TCF21, TFAP2A, TFAP2C*	22	8.60E-10	4.40E-07
GOTERM_BP_DIRECT	transcription from RNA polymerase II promoter	*ATF3, CEBPA, CEBPD, CREB3L2, CTDP1, EPAS1, FOS, FOSB, FOXC1, FOXC2, HIVEP1, HIVEP2, HIVEP3, HOXA5, JUNB, KLF4, MAFF, MAFK, MEF2D, MYC, NFATC1, NFIL3, REL, RUNX3, SIX2, SMAD2, SOX4, SOX9, TCF21, TFAP2A, TFAP2C, TSC22D1*	32	1.40E-09	1.10E-06
GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	*ATF3, BCL6, BHLHE40, BNC1, CEBPA, CEBPD, CREB3L2, EPAS1, ETS2, FOS, FOSB, FOSL2, FOXC1, FOXC2, HES1, HIVEP2, HIVEP3, HOXA5, ID3, KLF3, KLF4, KLF9, MAFF, MAFK, MEF2D, MYC, NFATC1, NFIL3, NR2F2, PRDM1, REL, RUNX3, SIX2, SMAD2, SOX4, SOX9, TBX3, TFAP2A, TFAP2C, TGIF1, TSC22D1, WNT5A, ZBTB38*	43	2.50E-08	4.30E-06
GOTERM_CC_DIRECT	nucleus	*ANKRD37, AREG, ARID5B, ATF3, ATXN7, BAG1, BCL6, BCOR, BHLHE40, BNC1, BTG1, C8orf4, C9orf72, C15orf48, CASP9, CDKN1C, CEBPA, CEBPD, CITED4, CPEB4, CREB3L2, CSNK1E, CTDP1, DGKD, DLC1, DUSP1, DUSP4, EPAS1, ERRFI1, ETS2, FERMT2, FGFR2, FILIP1L, FOS, FOSB, FOSL2, FOXC1, FOXC2, FOXO1, FSTL3, GDF15, GEM, HERC4, HES1, HIVEP1, HIVEP2, HIVEP3, HLX, HOXA5, ID3, IGFBP3, ING1, IRF2BP2, IRX1, IRX2, IRX4, ISG20, JMY, JUP, KLF3, KLF6, KLF9, LATS2, LBH, LMCD1, LPIN1, MAFF, MAFK, MBP, MEF2D, MYC, NEDD9, NFATC1, NFIL3, NFKBIZ, NR2F2, NR4A1, NR4A2, NR4A3, PHTF2, PIP5K1A, PMAIP1, PPARGC1A, PPM1D, PRDM1, PRKCE, PROX2, PTP4A1, REL, RGCC, RGS2, RHOB, RUNX3, SGK1, SH3BP4, SIK1, SIK2, SIX2, SLC2A14, SMAD2, SNAI2, SNRK, SOX4, SOX9, SPRY2, STC1, TBX3, TCF21, TFAP2A, TFAP2C, TGIF1, TLE1, TLE3, TNFAIP3, TRIB1, TSC22D1, USP36, VGLL2, WWC1, ZBTB38, ZNF331, ZNF462, ZNF503*	123	2.90E-06	7.10E-04
GOTERM_CC_DIRECT	nucleoplasm	*A1CF, ARID5B, ATF3, ATXN7, BCL6, BNC1, C9orf72, CREB3L2, CSNK1E, CTDP1, DUSP4, DUSP5, ELL2, EPAS1, ETS2, FERMT2, FGFR2, FOS, FOSL2, FOXC1, FOXO1, FSTL3, HES1, HIVEP2, ID3, IL15, ING1, ISG20, JMY, JUNB, KLF4, KLF9, LMCD1, LPIN1, MAFF, MAFK, MCTP2, MEF2D, MYC, NFATC1, NR4A1, NR4A2, NR4A3, PFKFB3, PIP5K1A, PPARGC1A, PRDM1, REL, SAP30, SGK1, SIX2, SMAD2, SOX4, SOX9, SPIDR, TFAP2A, TFAP2C, TGIF1, TLE1, TLE3, USP2, USP48*	62	4.30E-03	1.40E-01
GOTERM_BP_DIRECT	transcription, DNA-templated	*ARID5B, ATXN7, BCL6, BCOR, BHLHE40, BNC1, CEBPA, CEBPD, CITED4, EPAS1, ERN1, ETS2, FOSL2, FOXO1, FSTL3, HES1, HLX, ID3, IRF2BP2, KLF3, KLF6, KLF9, LBH, LMCD1, LPIN1, MAFK, MEF2D, MN1, NFKBIZ, NR2F2, NR4A1, NR4A2, NR4A3, PHTF2, PRDM1, PROX2, SAP30, SMAD2, SNAI2, TBX3, TGIF1, TLE1, TLE3, VGLL2, WWC1. ZBTB38. ZNF331. ZNF462. ZNF503*	49	7.50E-03	1.80E-01
Annotation Cluster 3	**Enrichment Score: 3.73**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_BP_DIRECT	neural crest cell development	*EDN1, FOXC1, FOXC2, SNAI2, SOX9*	5	5.50E-05	7.40E-03
GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding	*BHLHE40, CEBPA, FOXC1, FOXC2, NFATC1, SNAI2, SOX9, VGLL2*	8	1.40E-04	7.00E-03
GOTERM_BP_DIRECT	Notch signaling pathway	*BMP2, CEBPA, FOXC1, FOXC2, HES1, JAG1, MYC, SNAI2, SOX9*	9	8.60E-04	3.80E-02
Annotation Cluster 4	**Enrichment Score: 3.41**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_MF_DIRECT	growth factor activity	*AREG, BDNF, BMP2, CTGF, DKK1, FGF9, DF15, HBEGF, IL6, IL11, INHBA, JAG1, NTF3, VEGFC*	14	4.80E-06	4.90E-04
GOTERM_BP_DIRECT	cell-cell signaling	*AREG, BDNF, BMP2, CCL20, CTGF, EDN1, EFNA1, FGF9, FGFR2, GDF15, GREM1, IL11, IL15, INHBA, NTF3, TFAP2C*	16	3.70E-05	5.70E-03
GOTERM_MF_DIRECT	cytokine activity	*AREG, BMP2, EDN1, GDF15, GREM1, IL6, IL11, IL15, INHBA, WNT5A*	10	3.50E-03	1.10E-01
Annotation Cluster 5	**Enrichment Score: 3.34**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_BP_DIRECT	cell fate commitment	*BMP2, FGFR2, GAS1, PRDM1, SMAD2, SPRY2, WNT4, WNT5A*	8	1.30E-05	2.90E-03
GOTERM_BP_DIRECT	epithelial to mesenchymal transition	*BMP2, FGFR2, NOG, SNAI2, SOX9, WNT4, WNT5A*	7	2.30E-05	4.00E-03
Annotation Cluster 6	**Enrichment Score: 2.16**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_CC_DIRECT	integral component of plasma membrane	*BDKRB2, C5AR1, CD200, CD55, CLDN1, DLCK1, EFNA1, FGFR2, GPRC5A, GPR37, HBEGF, HLA-DQA1, HS6ST1, IGF1R, IL15, IL1RAP, JAG1, KCNJ2, KCNK1, KCNK15, NPC1, PAG1, PLAUR, PLPP3, PLXNA2, RAPGEF2, SCARA5, SEMA6D, SLC2A3, SLC7A1, SLC7A2, SLC7A5, SLC7A11, SLC16A6, SLC19A2, SLC22A4, SLC22A5, SLC26A2, SLC38A2, SLCO4A1, STEAP4, TFRC, THBD, TRABD2A, TM4SF1*	45	1.20E-05	1.40E-03
GOTERM_CC_DIRECT	extracellular space	*ADAMTS15, AREG, B4GALT1, BMP2, C9orf72, CCL2, CCL20, CES3, CTGF, CXCL2, DKK1, DMBT1, EDN1, FGF9, FSTL3, GDF15, GREM1, HBEGF, IGFBP3, IGFBP4, IL6, IL6R, IL11, IL15, KIT, LMCD1, LPL, LYPD3, METRNL, NOG, PAPPA, SERPINE1, SMPDL3A, STC1, STC2, TFRC, THBD, ULBP2, VEGFC, WNT4, WNT5A*	41	8.30E-05	6.70E-03
GOTERM_CC_DIRECT	extracellular region	*BDNF, BMP2, CCL2, CCL20, CD55, CHSY1, CRISPLD2, CTGF, CXCL2, DKK1, DMBT1, EDN1, EFNA1, FGF9, FGFR2, FSTL3, GDF15, HBEGF, IGFBP3, IGFBP4, IL6, IL6R, IL11, IL15, IL1RAP, INHBA, JAG1, LPL, MFAP5, NOG, NPC1, NTF3, PAPPA, SERPINE1, STC2, TFRC, VEGFC, WNT4. WNT5A*	39	8.20E-03	2.00E-01

GOTERM_CC_DIRECT	integral component of membrane	*ACKR3, AREG, B4GALT1, BDKRB2, BDNF, C15orf48, CD200, CD274, CHSY1, CLDN1, CREB3L2, EVA1C, FAM87A, FGFR2, FLVCR2, GALNT15, GAS1, GCNT2, GPAT3, GPRC5A, HLA-DQA1, HRK, HS3ST1, HS6ST1, IGF1R, IL1RAP, IL6R, JAG1, KCNK1, KIT, LRRC8A, LYPD3, MARC1, MCTP2, MEGF9, NPC1, PAPPA, PCDH9, PHLDB2, PHTF2, PLAUR, RNF19A, SEMA6D, SHISA2, SIRPA, SLC2A3, SLC2A14, SLC7A1, SLC7A5, SLC7A11, SLC10A7, SLC16A6, SLC16A14, SLC19A2, SLC22A4, SLC22A5, SLC26A2, SLC30A1, SLC38A2, SLCO4A1, SMAD2, ST3GAL1, ST3GAL4, ST3GAL6, STEAP4, SUSD6, TFRC, TM4SF1, TMEM2, WNT5A*	70	9.60E-01	1.00E+00
Annotation Cluster 7	**Enrichment Score: 2.05**		**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	amino acid transport	*MYC, SLC7A1, SLC7A2, SLC7A5, SLC7A11, SLC38A2*	6	3.20E-04	2.10E-02
GOTERM_MF_DIRECT	amino acid transmembrane transporter activity	*SLC7A1, SLC7A2, SLC7A5, SLC7A11, SLC38A2*	5	8.60E-03	2.30E-01
GOTERM_MF_DIRECT	antiporter activity	*SLC7A1, SLC7A2, SLC7A5*	3	5.00E-02	5.30E-01
GOTERM_BP_DIRECT	transport	*ATP1B3, NPTX1, SLC7A1, SLC7A2, SLC7A5, SLC19A2,*	6	7.20E-01	1.00E+00
Annotation Cluster 8	**Enrichment Score: 1.98**	**Genes**	**Count**	***P*-Value**	**Benjamini**
KEGG_PATHWAY	TNF signaling pathway	*CCL2, CCL20, CREB3L2, CXCL2, EDN1, FOS, IL6, IL15, JUNB, MAP3K8, SOCS3, TNFAIP3*	12	1.80E-05	3.40E-03
KEGG_PATHWAY	Rheumatoid arthritis	*CCL2, CCL20, FOS, IL6, IL11, IL15, HLA-DQA1*	7	1.20E-02	2.00E-01
Annotation Cluster 9	**Enrichment Score: 1.80**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	neutrophil chemotaxis	*C5AR1, CCL2, CCL20, EDN1, PDE4B, PDE4D*	6	5.60E-03	1.50E-01
GOTERM_BP_DIRECT	cellular response to interleukin-1	*CCL2, CCL20, END1, IL6, MYC, SOX9*	6	7.60E-03	1.80E-01
GOTERM_BP_DIRECT	response to amino acid	*CCL2, CTGF, EDN1, IL6*	4	1.60E-02	2.80E-01
GOTERM_BP_DIRECT	cellular response to interferon-gamma	*CCL2, CCL20, EDN1, MYC, WNT5A*	5	1.70E-02	2.90E-01
GOTERM_BP_DIRECT	cellular response to drug	*CCL2, EDN1, MYC, PDE4B, TFRC*	5	3.10E-02	4.10E-01
GOTERM_BP_DIRECT	cellular response to tumor necrosis factor	*CEBPA, CCL2, CCL20, EDN1, IL6, PPARGC1A*	6	4.20E-02	4.80E-01
Annotation Cluster 10	**Enrichment Score: 1.75**	**Genes**	**Count**	***P*-Value**	**Benjamini**
INTERPRO	Major facilitator superfamily domain	*FLVCR2, SLC2A3, SLC2A14, SLC16A6, SLC16A14, SLC19A2, SLC22A4, SLC22A5, SLCO4A1*	9	1.70E-03	1.80E-01
GOTERM_MF_DIRECT	transmembrane transporter activity	*SLC2A3, SLC2A14, SLC22A5*	3	2.10E-01	8.40E-01
Annotation Cluster 11	**Enrichment Score: 1.52**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cellular response to corticotropin-releasing hormone stimulus	*NR4A1, NR4A2, NR4A3*	3	4.30E-03	1.30E-01
GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	*NR2F2, NR4A1, NR4A2, NR4A3*	4	2.40E-02	3.90E-01
GOTERM_BP_DIRECT	intracellular receptor signaling pathway	*NR2F2, NR4A1, NR4A2, NR4A3*	4	2.80E-02	3.80E-01
GOTERM_MF_DIRECT	steroid hormone receptor activity	*NR2F2, NR4A1, NR4A2, NR4A3*	4	7.20E-02	5.90E-01
GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	*NR2F2, NR4A1, NR4A2, NR4A3*	4	7.60E-02	6.50E-01
GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	*CTGF, NR4A1, NR4A2, NR4A3, PPARGC1A*	5	2.70E-01	9.50E-01
Annotation Cluster 12	**Enrichment Score: 1.52**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	regulation of cell growth	*CTGF, IGFBP3, IGFBP4, SGK1, SOCS2, TFRC*	6	1.20E-02	2.40E-01
Annotation Cluster 13	**Enrichment Score: 1.52**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_CC_DIRECT	anchored component of plasma membrane	*EFNA1, GAS1, LYPD3, ULBP2*	4	9.60E-03	2.10E-01
Annotation Cluster 14	**Enrichment Score: 1.52**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	monocyte chemotaxis	*CCL2, CCL20, IL6, IL6R*	4	3.60E-02	4.40E-01
Annotation Cluster 15	**Enrichment Score: 1.49**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cellular response to transforming growth factor beta stimulus	*EDN1, PPARGC1A, SOX9, WNT4, WNT5A*	5	1.00E-02	2.10E-01
GOTERM_BP_DIRECT	cartilage development	*CREB3L2, EDN1, NOG, SOX9, WNT5A*	5	1.90E-02	3.10E-01
Annotation Cluster 16	**Enrichment Score: 1.47**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	protein phosphorylation	*BMP2, CSNK1E, CCL2, DCLK1, ERN1, EIF2AK3, IGFBP3, LATS2, MAP3K8, PLK2, PRKCE, PDK4, RUNX3, SIK1, SIK2, SGK1, SMAD2, SNRK, ST3GAL1, TRIB1*	20	3.80E-04	2.40E-02
GOTERM_BP_DIRECT	peptidyl-serine phosphorylation	*CSNK1E, DCLK1, EIF2AK3, LATS2, PLK2, PRKCE, SGK1*	7	2.10E-02	3.40E-01
GOTERM_MF_DIRECT	protein serine/threonine kinase activity	*CSNK1E, DCLK1, EIF2AK3, ERN1, LATS2, MAP3K8, PLK2, PRKCE, SGK1, SIK1, SIK2, SNRK*	12	6.20E-02	5.70E-01
GOTERM_MF_DIRECT	protein kinase activity	*CCL2, CSNK1E, DCLK1, EIF2AK3, MAP3K8, PDK4, PRKCE, SGK223, SNRK, SOX9, TRIB1*	11	9.30E-02	6.30E-01
GOTERM_MF_DIRECT	magnesium ion binding	*ERN1, GEM, MAP3K8, SIK1, SIK2, SNRK*	6	2.80E-01	8.90E-01
GOTERM_MF_DIRECT	ATP binding	*CSNK1E, DCLK1, DGKD, EIF2AK3, ERN1, FGFR2, IGF1R, KIT, LATS2, MAP3K8, PDK4, PFKFB3, PIP5K1A, PLK2, PRKCE, RHOBTB3, RIMKLB, RUNX3, SGK1, SGK223, SIK1, SIK2, SLC22A4, SLC22A5, SNRK, TRIB1*	26	5.90E-01	1.00E+00
Annotation Cluster 17	**Enrichment Score: 1.43**		**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cellular response to dexamethasone stimulus	*CCL2, CASP9, ERRFI1, FOXO1, IL6*	5	1.50E-03	5.70E-02
GOTERM_BP_DIRECT	response to antibiotic	*CCL2, CASP9, IL6*	3	1.10E-01	7.30E-01
Annotation Cluster 18	**Enrichment Score: 1.42**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	endoderm formation	*DKK, DUSP1, DUSP4, DUSP5, NOG, SMAD2*	6	1.10E-06	3.50E-04
GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	*DUSP1, DUSP4, DUSP5, PPM1D*	4	7.60E-04	3.50E-02
GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine phosphatase activity	*DKK, DUSP1, DUSP4, DUSP5, NOG, SMAD2*	3	2.00E-02	3.80E-01
GOTERM_BP_DIRECT	inactivation of MAPK activity	*DUSP1, DUSP4, DUSP5*	3	6.90E-02	6.20E-01
GOTERM_MF_DIRECT	phosphatase activity	*DUSP4, DUSP5, PTP4A1*	3	1.50E-01	7.60E-01
GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	*DUSP1, DUSP4, DUSP5, PTP4A1*	4	2.40E-01	9.30E-01
GOTERM_MF_DIRECT	protein tyrosine phosphatase activity	*DUSP1, DUSP4, DUSP5, PTP4A1*	4	2.50E-01	8.80E-01
Annotation Cluster 19	**Enrichment Score: 1.37**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_MF_DIRECT	symporter activity	*SLC10A7, SLC16A6, SLC16A14, SLC22A4, SLC22A5, SLC38A2*	6	1.80E-03	7.40E-02
GOTERM_BP_DIRECT	sodium ion transport	*ATP13B, SGK1, SLC10A7, SLC22A4, SLC22A5, SLC38A2*	6	1.30E-02	2.40E-01
GOTERM_BP_DIRECT	transmembrane transport	*FLVCR2, SLC10A7, SLC16A6, SLC16A14*	4	8.00E-01	1.00E+00
Annotation Cluster 20	**Enrichment Score: 1.31**	**Genes**	**Count**	***P*-Value**	**Benjamini**
UP_SEQ_FEATURE	DNA-binding region:Homeobox; TALE-type	*IRX1, IRX2, IRX4, TGIF1*	4	3.40E-03	3.30E-01
INTERPRO	Iroquois-class homeodomain protein	*IRX1, IRX2, IRX4*	3	3.70E-03	3.00E-01

Indacaterol (6h)

Annotation Cluster 1	**Enrichment Score: 4.86**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_CC_DIRECT	extracellular space	*ALB, B4GALT1, C1QTNF6, CCL2, CD59, CES3, CMTM6, DEFB1, DMBT1, ENOX1, GDF15, GPC3, IGFBP3, IGFBP4, IL20, KRT86, LPL, MCAM, MSMB, PAPPA, SFTPD, SMPDL3A, SRGN, TFPI, VCAN, WNT4, WNT5A*	27	1.20E-03	5.50E-02
GOTERM_CC_DIRECT	extracellular region	*ADAM12, ALB, CCL2, CD55, COL4A3, CRISPLD1, CRISPLD2, DEFB1, DMBT1, ESR2, FAM198A, FGFR2, GDF15, IGFBP3, IGFBP4, IL20, LPL, MFAP5, NETO1, NPC1, PAPPA, SFTPD, SRGN, TFPI, VCAN, WNT4, WNT5A*	27	1.20E-02	2.60E-01
Annotation Cluster 2	**Enrichment Score: 3.77**	**Genes**	**Count**	***P*-Value**	**Benjamini**

GOTERM_CC_DIRECT	integral component of plasma membrane	*ADGRG2, AVPR2, BDKRB2, C5AR1, CD200, CD55, CDH4, CNR1, DCLK1, EPHA5, FGFR2, GPC3, GPRC5A, IGF1R, KCNK15, LPAR6, NPC1, NRXN3, PLPP3, PTPRO, SLC6A15, SLC7A2, SLC7A11, SLC16A6, SLC22A3, SLC22A4, SLC22A5, SLC26A2, STEAP4, TM4SF1,*	32	3.70E-05	7.30E-03
GOTERM_CC_DIRECT	plasma membrane	*ACKR1, ADAM12, ADAM22, ADGRD1, AKAP12, ANTXR1, ATP1B3, AVPR2, B4GALT1, BDKRB2, C5AR1, CACNA2D3, CD55, CD59, CD200, CDH4, CFTR, CLMP, CNR1, COBL, DNER, DOCK4, ENOX1, EPHA5, FGFR2, GAS1, GNAL, GPC3, GPRC5A, GUCY1A2, IGF1R, ITPR1, JUP, KCNG1, KCNK15, LPAR6, LPL, MCAM, MDM2, NFASC, NOS3, PCDH9, PHLDB2, PLPP3, PTPRO, RAP1GAP2, RGS2, SIRPA, SLC6A15, SLC7A2, SLC7A11, SLC16A14, SLC22A3, SLC22A4, SLC22A5, SLC26A2, SLCO4A1, STEAP4, SYTL2, TFPI, WNT4, WNT5A*	62	7.60E-04	7.20E-02
GOTERM_CC_DIRECT	integral component of membrane	*ACKR1, ADAM12, ADAM22, ADGRD1, ADGRG2, ANTXR1, AVPR2, B4GALT1, BDKRB2, C15orf48, C1QTNF6, CD200, CDH4, CFTR, CLMP, CMTM6, CNR1, DNER, EPHA5, FGFR2, GALNT15, GAS1, GPAT3, GPRC5A, GRAMD1B, HRK, IGF1R, ITPR1, LPAR6, MARC1, MCAM, NETO1, NFASC, NPC1, NRXN3, PAPPA, PCDH9, PDE3A, PHLDB2, PLD5, PLXDC2, PTPRO, RNF150, SHISA2, SIRPA, SLC6A15, SLC7A11, SLC16A6, SLC16A14, SLC22A3, SLC22A4, SLC22A5, SLC26A2, SLCO4A1, SPTLC3, SPTSSA, STEAP4, TM4SF1, TMEM2, TMTC1, UGT1A8, UGT2B28, UST, WNT5A*	64	5.10E-02	5.20E-01
Annotation Cluster 3	**Enrichment Score: 2.10**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cell fate commitment	*FGFR2, GAS1, HEY1, PRDM1, WNT4, WNT5A*	6	1.10E-04	7.70E-02
GOTERM_BP_DIRECT	epithelial to mesenchymal transition	*FGFR2, WNT4, WNT5A*	3	4.90E-02	9.10E-01
Annotation Cluster 4	**Enrichment Score: 2.10**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	cAMP catabolic process	*PDE3A, PDE4D, PDE7B, PDE10A*	4	4.60E-04	2.00E-01
GOTERM_MF_DIRECT	3',5'-cyclic-AMP phosphodiesterase activity	*PDE3A, PDE4D, PDE7B, PDE10A*	4	4.90E-04	1.80E-01
GOTERM_MF_DIRECT	3',5'-cyclic-nucleotide phosphodiesterase activity	*PDE3A, PDE4D, PDE10A*	3	2.50E-02	7.60E-01
GOTERM_MF_DIRECT	cAMP binding	*PDE3A, PDE4D, PDE10A*	3	2.70E-02	7.40E-01
Annotation Cluster 5	**Enrichment Score: 2.08**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_BP_DIRECT	quaternary ammonium group transport	*SLC22A3, SLC22A4, SLC22A5*	3	1.10E-03	3.10E-01
GOTERM_MF_DIRECT	quaternary ammonium group transmembrane transporter activity	*SLC22A3, SLC22A4, SLC22A5*	3	1.10E-03	2.00E-01
Annotation Cluster 6	**Enrichment Score: 2.02**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_CC_DIRECT	proteinaceous extracellular matrix	*ADAMTSL1, COL4A3, CRISPLD2, GPC3, SFTPD, SMOC1, TFPI2, VCAN, WNT4, WNT5A*	10	1.70E-03	6.50E-02
GOTERM_CC_DIRECT	endoplasmic reticulum lumen	*ADAMTSL1, CES3, COL4A3, WNT4, WNT5A*	5	1.30E-01	7.70E-01
Annotation Cluster 7	**Enrichment Score: 1.73**	**Genes**	**Count**	***P*-Value**	**Benjamini**
GOTERM_MF_DIRECT	symporter activity	*SLC16A6, SLC16A14, SLC22A4, SLC22A5*	4	1.70E-02	6.80E-01
Annotation Cluster 8	**Enrichment Score: 1.56**	**Genes**	**Count**	***P*-Value**	**Benjamini**
KEGG_PATHWAY	Pathways in cancer	*BDKRB2, CASP9, CEBPA, COL4A3, FGFR2, FOXO1, IGF1R, JUP, LPAR6, MDM2, WNT4, WNT5A*	12	7.60E-03	4.80E-01

Indacaterol-induced genes (defined by using Affymetrix probe sets) with significant expression level changes of >1.5-fold (based on a FDR *P*-value of <0.1) were subjected to functional annotation clustering using DAVID (default parameters). Clusters with enrichment scores >1.3 are shown.

Supplemental TABLE 6. Functional Annotation Clustering of Genes Significantly Repressed by Indacaterol in BEAS-2B Cells at 1h, 2h and 6h.

Indacaterol (1h)

Annotation Cluster 1	Enrichment Score: 1.35	Genes	Count	*P* -Value	Benjamini
GOTERM_BP_DIRECT	DNA repair	*CHEK1, EID3, RECQL5*	3	5.40E-02	8.90E-01

Indacaterol (2h)

Annotation Cluster 1	Enrichment Score: 2.72	Genes	Count	*P* -Value	Benjamini
GOTERM_BP_DIRECT	cell division	*BUB1, BORA, CCNF, HMGA2, PARD6B, PSRC1*	6	1.20E-03	3.20E-01
GOTERM_BP_DIRECT	mitotic nuclear division	*BUB1, BORA, CCNF, HMGA2*	4	2.00E-02	7.80E-01
GOTERM_CC_DIRECT	cytosol	*BORA, BUB1, CEP135, KIF23, PARD6B, PKHD1L1, PSRC1, SEC16B, TXNIP*	9	5.30E-01	1.00E+00
Annotation Cluster 2	**Enrichment Score: 1.91**	**Genes**	**Count**	***P* -Value**	**Benjamini**
GOTERM_MF_DIRECT	DNA binding	*EGR1, EGR3, HJURP, HMGA2, KLF7, SIM1, TOP2A, ZNF99, ZNF547, ZNF556, ZNF594, ZNF738*	12	1.40E-03	1.30E-01
GOTERM_BP_DIRECT	transcription, DNA-templated	*EGR3, KLF7, MED13L, SIM1, TXNIP, ZNF99, ZNF547, ZNF552, ZNF556, ZNF594, ZNF738*	11	1.20E-02	7.10E-01
GOTERM_CC_DIRECT	nucleus	*CCNF, EGR1, EGR3, HJURP, HMGA2, HYLS1, IP6K2, KDM6A, KIF23, KLF7, NUMB, PARD6B, SIM1, TOP2A, TXNIP, ZNF99, ZNF547, ZNF552, ZNF556, ZNF594, ZNF738*	21	1.50E-02	7.20E-01
GOTERM_MF_DIRECT	nucleic acid binding	*KLF7, ZNF99, ZNF552, ZNF547, ZNF556, ZNF594, ZNF738*	7	2.70E-02	7.70E-01
GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	*EGR3, HMGA2, ZNF99, ZNF552, ZNF547, ZNF556, ZNF594, ZNF738*	8	5.60E-02	8.90E-01
GOTERM_CC_DIRECT	intracellular	*KIF23, TRIM59, ZNF99, ZNF547, ZNF552, ZNF556, ZNF738*	7	9.10E-02	8.10E-01
GOTERM_MF_DIRECT	metal ion binding	*EGR1, EGR3, KDM6A, KLF7, ZNF99, ZNF547, ZNF552, ZNF556, ZNF594*	9	1.10E-01	9.80E-01
GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	*EGR1, EGR3, KLF7, SIM1, ZNF552*	5	1.90E-01	1.00E+00
GOTERM_MF_DIRECT	zinc ion binding	*EGR1, KLF7, SH3RF2, TRIM59, ZSWIM8*	5	3.00E-01	1.00E+00

Indacaterol (6h)

Annotation Cluster 1	Enrichment Score: 2.31	Genes	Count	*P* -Value	Benjamini
GOTERM_BP_DIRECT	type I interferon signaling pathway	*EGR1, MX1, OAS1, OAS2, OAS3*	5	1.30E-05	3.70E-03
GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthetase activity	*OAS1, OAS2, OAS3*	3	2.80E-05	2.70E-03
GOTERM_BP_DIRECT	response to virus	*IFI44, MX1, OAS1, OAS2, OAS3*	5	1.10E-04	1.60E-02
GOTERM_BP_DIRECT	defense response to virus	*IFI44L, MX1, OAS1, OAS2, OAS3*	5	5.10E-04	4.90E-02
GOTERM_MF_DIRECT	nucleotidyltransferase activity	*OAS1, OAS2, OAS3*	3	1.60E-03	7.50E-02
GOTERM_BP_DIRECT	negative regulation of viral genome replication	*MX1, OAS1, OAS3*	3	3.70E-03	2.40E-01
GOTERM_MF_DIRECT	double-stranded RNA binding	*OAS1, OAS2, OAS3*	3	7.90E-03	2.30E-01
GOTERM_BP_DIRECT	interferon-gamma-mediated signaling pathway	*OAS1, OAS2, OAS3*	3	1.10E-02	4.20E-01
GOTERM_MF_DIRECT	transferase activity	*OAS1, OAS2, OAS3*	3	1.90E-02	3.70E-01
GOTERM_BP_DIRECT	immune response	*OAS1, OAS2, OAS3*	3	2.50E-01	1.00E+00
GOTERM_MF_DIRECT	ATP binding	*MVK, NAV3, OAS1, OAS2, OAS3*	5	4.20E-01	1.00E+00

Indacaterol-induced genes (defined by using Affymetrix probe sets) with significant expression level changes of <0.67-fold (based on a FDR *P* -value of <0.1) were subjected to functional annotation clustering using DAVID (default parameters). Clusters with enrichment scores >1.3 are shown.