TABLE 1S - TOP 100 GENES UPREGULATED BY 9-AMINAOACRIDINE IN CFBE41o- CELLS

			fold-increase	
	Gene symbol	Description	CFBE41o-	BE *
1	CXCR4	chemokine (C-X-C motif) receptor 4	2383.0	
2	PCDH10	protocadherin 10	1111.1	
3	INSM2	insulinoma-associated 2	1000.4	
4	C20orf160	chromosome 20 open reading frame 160	913.9	
5	NPTX2	neuronal pentraxin II	815.9	
6	SLC16A10	solute carrier family 16 (monocarboxylic acid transporters), member 10	772.9	
7	PCDH8	protocadherin 8	745.6	
8	ARC	activity-regulated cytoskeleton-associated protein	737.6	
9	C11orf43	chromosome 11 open reading frame 43	690.0	
10	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	652.3	
11	NEFH	neurofilament, heavy polypeptide 200kDa	650.2	
12	HBA1	hemoglobin, alpha 1	622.6	
13	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	600.3	
14	PCDH17	protocadherin 17	560.5	
15	HIST1H4H	histone 1, H4h	553.2	9.8
16	DLX2	distal-less homeobox 2	548.5	
17	ETV7	ets variant gene 7 (TEL2 oncogene)	500.9	2.2
18	DIO3	deiodinase, iodothyronine, type III	498.4	
19	HBA2	hemoglobin, alpha 2	488.5	
20	IL17RB	interleukin 17 receptor B	471.9	
21	TAC1	tachykinin, precursor 1	470.1	
22	DDIT4L	DNA-damage-inducible transcript 4-like	463.5	
23	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	463.1	
24	RGS16	regulator of G-protein signalling 16	433.9	
25	NEF3	neurofilament 3 (150kDa medium)	423.0	
26	PRIMA1	proline rich membrane anchor 1	413.3	
27	EOMES	eomesodermin homolog (Xenopus laevis)	408.0	
28	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	382.9	3.2
29	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	382.1	
30	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	372.4	4.1
31	GFPT2	glutamine-fructose-6-phosphate transaminase 2	366.8	
32	CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	361.1	
33	ZCCHC12	zinc finger, CCHC domain containing 12	354.8	
34	CLU	clusterin	343.3	
35	TEX14	testis expressed sequence 14	342.6	
36	EGR4	early growth response 4	336.2	
37	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	328.9	
38	BMP2	bone morphogenetic protein 2	325.7	
39	SNAI1	snail homolog 1 (Drosophila)	322.8	2.2
40	IGF2	insulin-like growth factor 2 (somatomedin A)	311.4	
41	FGF19	fibroblast growth factor 19	300.9	
42	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	295.0	2.1
43	NRIP3	nuclear receptor interacting protein 3	285.3	2.1
44	HOXD1	homeobox D1	275.3	
45	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	274.5	
46	RND1	Rho family GTPase 1	271.4	
47	PCDH9	protocadherin 9	262.3	
48	HAS3	hyaluronan synthase 3	257.5	
49	HIST1H2AE	histone 1, H2ae	253.5	5.2
50	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygena	253.2	
51	C19orf30	chromosome 19 open reading frame 30	251.3	
52	EPHA4	EPH receptor A4	240.2	
53	AQP1	aquaporin 1 (Colton blood group)	239.6	
54	CRYBA2	crystallin, beta A2	237.3	
55	SH3GL2	SH3-domain GRB2-like 2	221.8	
56	ERO1LB	ERO1-like beta (S. cerevisiae)	220.5	
57	MSX1	msh homeobox homolog 1 (Drosophila)	212.5	
58	SBSN	NA	212.2	
59	OLIG2	oligodendrocyte lineage transcription factor 2	207.4	
60	UCN	urocortin	205.2	
61	RASD1	RAS, dexamethasone-induced 1	199.4	
62	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death d	198.8	
63	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	197.5	3.6
64	CTH	cystathionase (cystathionine gamma-lyase)	195.6	
65	KRT14	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	187.7	
66	NHLH2	nescient helix loop helix 2	185.7	
67	HAMP	hepcidin antimicrobial peptide	182.1	

68	C10orf10	chromosome 10 open reading frame 10	181.2	
69	RGC32	NA	178.1	
70	RGS2	regulator of G-protein signalling 2, 24kDa	175.5	
71	ATF3	activating transcription factor 3	171.3	2.4
72	TNNC1	troponin C type 1 (slow)	170.6	
73	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	169.1	2.4
74	SPON2	spondin 2, extracellular matrix protein	168.8	
75	VIM	vimentin	167.2	
76	HAND1	heart and neural crest derivatives expressed 1	165.0	
77	KRTAP2-1	keratin associated protein 2-1	160.6	
78	SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	158.9	
79	HBZ	hemoglobin, zeta	156.8	
80	STC1	stanniocalcin 1	155.1	
81	SOST	sclerosteosis	154.7	
82	COMP	cartilage oligomeric matrix protein	151.9	2.1
83	SHOX2	short stature homeobox 2	151.4	
84	SOX8	SRY (sex determining region Y)-box 8	150.0	
85	JAG1	jagged 1 (Alagille syndrome)	145.4	
86	HIST1H3J	histone 1, H3j	141.0	
87	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	139.4	
88	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)	139.4	
89	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	138.2	
90	CSH2	chorionic somatomammotropin hormone 2	137.6	
91	NPY	neuropeptide Y	137.3	
92	FAM90A1	family with sequence similarity 90, member A1	134.7	
93	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	133.8	
94	IRF4	interferon regulatory factor 4	132.9	
95	KRTAP1-5	keratin associated protein 1-5	132.8	
96	HSPA6	heat shock 70kDa protein 6 (HSP70B')	130.8	
97	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	129.9	
98	SOX2	SRY (sex determining region Y)-box 2	125.6	
99	KCTD12	potassium channel tetramerisation domain containing 12	123.7	
100	HIST1H2AM	histone 1, H2am	123.1	

* BE: fold-increase in primary bronchial epithelial cells (genes with > 2-fold increase)

TABLE 2S - TOP 100 GENES UPREGULATED BY CICLOPIROX IN CFBE41o- CELLS

			fold-increase	
	Gene symbol	Description	CFBE41o-	BE *
1	GLS2	glutaminase 2 (liver, mitochondrial)	241.4	
2	FAM13C1	family with sequence similarity 13, member C1	211.4	
3	RASAL1	RAS protein activator like 1 (GAP1 like)	202.5	
4	COL2A1	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congen	197.3	
5	DPYSL4	dihydropyrimidinase-like 4	196.3	2.1
6	CLCA2	chloride channel, calcium activated, family member 2	171.9	
7	LCE1B	late cornified envelope 1B	170.6	
8	MYO10	myosin X	165.8	5.6
9	XDH	xanthine dehydrogenase	153.1	2.3
10	CDH10	cadherin 10, type 2 (T2-cadherin)	152.5	
11	ATF3	activating transcription factor 3	135.5	4.2
12	PVT1	Pvt1 oncogene homolog, MYC activator (mouse)	133.4	
13	BTG2	BTG family, member 2	118.7	
14	PGAP1	NA	115.8	
15	GNAS	GNAS complex locus	112.4	
16	C4orf9	chromosome 4 open reading frame 9	109.8	
17	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	109.6	
18	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	103.2	
19	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	99.7	
20	CRYAB	crystallin, alpha B	97.3	
21	KIAA1324	KIAA1324	95.1	
22	POLH	polymerase (DNA directed), eta	89.1	
23	RGS2	regulator of G-protein signalling 2, 24kDa	89.0	
24	PANK1	pantothenate kinase 1	82.8	
25	GDF9	growth differentiation factor 9	80.0	
26	DSC3	desmocollin 3	78.0	
27	IKIP	NA	75.3	
28	CSTA	cystatin A (stefin A)	75.0	
29	UNQ2541	NA	73.6	
30	JAG1	jagged 1 (Alagille syndrome)	67.7	
31	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygena	66.9	
32	WDR66	WD repeat domain 66	64.1	
33	ADRB2	adrenergic, beta-2-, receptor, surface	62.2	
34	CENTG3	centaurin, gamma 3	61.6	
35	NHLH2	nescient helix loop helix 2	61.4	
36	KCTD12	potassium channel tetramerisation domain containing 12	61.3	
37	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	60.2	
38	GRHL3	grainyhead-like 3 (Drosophila)	59.0	2.2
39	IBRDC2	IBR domain containing 2	58.9	
40	RAB38	RAB38, member RAS oncogene family	56.8	
41	CIAS1	cold autoinflammatory syndrome 1	56.6	
42	SIPA1L2	signal-induced proliferation-associated 1 like 2	56.1	
43	GDF15	growth differentiation factor 15	55.2	
44	ZNF654	zinc finger protein 654	53.8	
45	SLCO4A1	solute carrier organic anion transporter family, member 4A1	53.8	9.5
46	DNAH5	dynein, axonemal, heavy polypeptide 5	53.2	
47	PNLIPRP2	pancreatic lipase-related protein 2	51.9	
48	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	51.1	
49	NDRG1	N-myc downstream regulated gene 1	50.4	
50	RNASE7	ribonuclease, RNase A family, 7	50.2	3.1
51	COBLL1	COBL-like 1	50.2	
52	ETNK1	ethanolamine kinase 1	50.1	
53	NPPB	natriuretic peptide precursor B	49.8	
54	MAK	male germ cell-associated kinase	48.0	
55	MR1	major histocompatibility complex, class I-related	47.6	
56	NALP1	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1	46.8	
57	DUSP5	dual specificity phosphatase 5	46.5	5.6
58	RORA	RAR-related orphan receptor A	45.5	3.8
59	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucos	45.1	2.2
60	SCN3B	sodium channel, voltage-gated, type III, beta	45.0	
61	C1orf183	chromosome 1 open reading frame 183	44.0	
62	NRG1	neuregulin 1	43.8	
63	GGT6	gamma-glutamyltransferase 6 homolog (rat)	43.7	
64	TREM2	triggering receptor expressed on myeloid cells 2	43.7	
65	CNTNAP3B	contactin associated protein-like 3B	43.4	
66	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	43.2	
67	KITLG	KIT ligand	43.2	
68	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	42.7	

69	CNTNAP3	contactin associated protein-like 3	42.4	
70	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	42.4	
71	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	41.9	
72	HSPA4L	heat shock 70kDa protein 4-like	41.8	
73	AREG	amphiregulin (schwannoma-derived growth factor)	41.7	
74	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	41.1	
75	IRF6	interferon regulatory factor 6	41.0	
76	SLC35E4	solute carrier family 35, member E4	40.4	
77	SESN1	sestrin 1	40.3	
78	COL27A1	collagen, type XXVII, alpha 1	40.0	
79	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	39.8	
80	PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	39.7	2.6
81	FAS	Fas (TNF receptor superfamily, member 6)	39.7	
82	TAB3	NA	39.4	2.1
83	LRDD	leucine-rich repeats and death domain containing	39.1	
84	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	38.6	3.1
85	FLG	filaggrin	38.1	6.4
86	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	38.1	
87	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	37.9	
88	HBEGF	heparin-binding EGF-like growth factor	37.5	
89	PDK1	pyruvate dehydrogenase kinase, isozyme 1	36.7	2.9
90	STS-1	NA	36.2	
91	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	35.8	
92	KCTD12	potassium channel tetramerisation domain containing 12	35.7	
93	FDXR	ferredoxin reductase	35.7	
94	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	35.5	
95	DUSP13	dual specificity phosphatase 13	35.4	
96	FAM46C	family with sequence similarity 46, member C	35.1	
97	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	34.9	
98	LMCD1	LIM and cysteine-rich domains 1	34.8	
99	BMP2	bone morphogenetic protein 2	34.5	2.6
100	SOX7	SRY (sex determining region Y)-box 7	34.3	

* BE: fold-increase in primary bronchial epithelial cells (genes with > 2-fold increase)

TABLE 3S - TOP 100 GENES UPREGULATED BY LOW TEMPERATURE IN CFBE41o- CELLS

			fold-increase	
	Gene symbol	Description	CFBE41o-	BE *
1	MYO10	myosin X	411.6	18.8
2	ZBTB24	zinc finger and BTB domain containing 24	83.5	16.7
3	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	73.0	
4	ATXN1	ataxin 1	67.5	6.7
5	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	61.6	25.9
6	ETNK1	ethanolamine kinase 1	55.1	
7	C6orf114	chromosome 6 open reading frame 114	55.0	5.3
8	CNNM2	cyclin M2	42.8	8.0
9	EPC1	enhancer of polycomb homolog 1 (Drosophila)	40.3	
10	IFNB1	interferon, beta 1, fibroblast	35.4	
11	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	35.3	
12	PANK1	pantothenate kinase 1	33.8	
13	RHOBTB3	Rho-related BTB domain containing 3	33.2	11.1
14	BTG1	B-cell translocation gene 1, anti-proliferative	32.9	
15	HMGA2	high mobility group AT-hook 2	32.2	20.9
16	IL28A	interleukin 28A (interferon, lambda 2)	30.3	
17	IL28B	interleukin 28B (interferon, lambda 3)	30.1	
18	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	28.4	2.3
19	ZNF638	zinc finger protein 638	27.2	2.6
20	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme	25.8	19.1
21	TPM3	tropomyosin 3	25.5	5.4
22	PPARD	peroxisome proliferative activated receptor, delta	24.9	
23	BCL10	B-cell CLL/lymphoma 10	24.3	7.5
24	MNAB	membrane associated DNA binding protein	23.8	
25	H3F3B	H3 histone, family 3B (H3.3B)	23.3	5.9
26	ST7	suppression of tumorigenicity 7	22.6	
27	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	21.6	
28	EIF5A2	eukaryotic translation initiation factor 5A2	20.6	4.1
29	IL29	interleukin 29 (interferon, lambda 1)	20.4	
30	CUL1	cullin 1	20.3	8.1
31	AMMECR1	Alport syndrome, gene 1	19.7	
32	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	18.9	2.6
33	STARD13	START domain containing 13	18.6	
34	GNAS	GNAS complex locus	18.1	3.5
35	INA	internexin neuronal intermediate filament protein, alpha	18.1	
36	FOSL1	FOS-like antigen 1	18.0	
37	PTHLH	parathyroid hormone-like hormone	17.9	
38	USP15	ubiquitin specific peptidase 15	17.7	5.1
39	SP8	Sp8 transcription factor	17.6	4.5
40	ING3	inhibitor of growth family, member 3	16.9	4.9
41	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	16.9	
42	C20orf155	chromosome 20 open reading frame 155	16.7	
43	WIBG	within bgcn homolog (Drosophila)	16.7	6.3
44	C20orf67	chromosome 20 open reading frame 67	16.1	
45	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	15.8	4.0
46	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	15.8	5.2
47	DUSP5	dual specificity phosphatase 5	15.6	
48	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	15.5	
49	KLF4	Kruppel-like factor 4 (gut)	15.4	2.7
50	POLB	polymerase (DNA directed), beta	15.2	
51	THBS1	thrombospondin 1	15.2	5.2
52	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	14.8	4.3
53	IFIH1	interferon induced with helicase C domain 1	14.6	2.4
54	ELL2	elongation factor, RNA polymerase II, 2	14.4	2.2
55	ARIH2	ariadne homolog 2 (Drosophila)	14.3	5.0
56	RUNX1	c("runt-related transcription factor 1 (acute myeloid leukemia 1", " aml1 oncogene)")	14.1	3.0
57	HERC3	hect domain and RLD 3	14.1	13.5
58	OSMR	oncostatin M receptor	14.0	3.2
59	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	13.8	
60	PRO0149	NA	13.6	
61	RNF103	ring finger protein 103	13.6	6.4
62	KRTAP2-1	keratin associated protein 2-1	13.6	
63	C1orf116	chromosome 1 open reading frame 116	13.5	
64	TMEM68	transmembrane protein 68	13.5	4.7
65	C10orf89	chromosome 10 open reading frame 89	13.1	
66	GOLPH3	golgi phosphoprotein 3 (coat-protein)	12.9	
67	SLC22A5	solute carrier family 22 (organic cation transporter), member 5	12.9	

68	THRAP1	thyroid hormone receptor associated protein 1	12.8	
69	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	12.4	8.2
70	MPHOSPH6	M-phase phosphoprotein 6	12.4	8.5
71	SLC30A1	solute carrier family 30 (zinc transporter), member 1	12.3	2.7
72	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	12.2	5.6
73	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	12.2	
74	KIAA0804	KIAA0804	12.1	
75	LIMS3	LIM and senescent cell antigen-like domains 3	12.0	3.4
76	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygena	12.0	
77	PER2	period homolog 2 (Drosophila)	11.8	2.1
78	PCDH7	BH-protocadherin (brain-heart)	11.8	3.2
79	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	11.8	2.9
80	KLHDC5	kelch domain containing 5	11.8	3.0
81	CTGF	connective tissue growth factor	11.6	
82	SPHK1	sphingosine kinase 1	11.6	2.1
83	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	11.4	
84	MAX	MYC associated factor X	11.4	2.7
85	CCDC50	coiled-coil domain containing 50	11.3	3.1
86	ATF3	activating transcription factor 3	11.2	
87	DUSP6	dual specificity phosphatase 6	11.1	
88	MFSD2	major facilitator superfamily domain containing 2	11.1	
89	NR4A2	nuclear receptor subfamily 4, group A, member 2	11.0	
90	FAM105B	family with sequence similarity 105, member B	11.0	4.1
91	SPRY4	sprouty homolog 4 (Drosophila)	11.0	
92	MICALCL	MICAL C-terminal like	10.9	
93	CUL4A	cullin 4A	10.7	12.3
94	PCGF5	polycomb group ring finger 5	10.5	3.9
95	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	10.2	4.8
96	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	10.2	8.4
97	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	10.1	
98	SP3	Sp3 transcription factor	10.1	3.0
99	LARP2	La ribonucleoprotein domain family, member 2	10.1	6.3
100	USP36	ubiquitin specific peptidase 36	10.0	2.4

* BE: fold-increase in primary bronchial epithelial cells (genes with > 2-fold increase)

TABLE 4S - TOP 100 GENES UPREGULATED BY CORR-4a IN CFBE41o- CELLS

			fold-increase	
	Gene symbol	Description	CFBE41o-	BE *
1	DUSP5	dual specificity phosphatase 5	8.2	
2	HSPA6	heat shock 70kDa protein 6 (HSP70B')	7.6	2.2
3	DUSP6	dual specificity phosphatase 6	6.5	
4	COL8A1	collagen, type VIII, alpha 1	6.3	
5	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	5.8	
6	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	5.4	
7	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	5.3	
8	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygena	5.3	
9	CLIC5	chloride intracellular channel 5	5.2	
10	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	4.8	
11	HDAC9	histone deacetylase 9	4.5	
12	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	4.3	
13	PLAT	plasminogen activator, tissue	4.3	
14	HBEGF	heparin-binding EGF-like growth factor	4.3	
15	FOSL1	FOS-like antigen 1	4.3	
16	ADRB2	adrenergic, beta-2-, receptor, surface	4.2	
17	FAM107B	family with sequence similarity 107, member B	4.1	
18	SLCO4A1	solute carrier organic anion transporter family, member 4A1	4.0	
19	CDH4	cadherin 4, type 1, R-cadherin (retinal)	4.0	
20	DUSP7	dual specificity phosphatase 7	4.0	
21	CUGBP2	CUG triplet repeat, RNA binding protein 2	3.9	
22	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	3.9	
23	GOLT1A	golgi transport 1 homolog A (S. cerevisiae)	3.8	
24	PRR6	proline rich 6	3.8	
25	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	3.8	
26	TMEM45A	transmembrane protein 45A	3.8	
27	HIST1H4H	histone 1, H4h	3.8	
28	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	3.8	
29	MYEOV	c("myeloma overexpressed gene (in a subset of t(11", "14) positive multiple myelomas	3.8	
30	VEZT	vezatin, adherens junctions transmembrane protein	3.7	
31	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	3.7	
32	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	3.7	
33	GRHL1	grainyhead-like 1 (Drosophila)	3.7	
34	ASNS	asparagine synthetase	3.6	
35	TSPAN5	tetraspanin 5	3.6	
36	WT1	Wilms tumor 1	3.6	
37	CXCL5	chemokine (C-X-C motif) ligand 5	3.6	2.7
38	CREM	cAMP responsive element modulator	3.5	
39	C6orf155	chromosome 6 open reading frame 155	3.4	
40	COL13A1	collagen, type XIII, alpha 1	3.4	
41	IL24	interleukin 24	3.4	
42	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	3.4	
43	TLR4	toll-like receptor 4	3.4	
44	STYK1	serine/threonine/tyrosine kinase 1	3.4	
45	ARHGAP18	Rho GTPase activating protein 18	3.4	
46	SPRY4	sprouty homolog 4 (Drosophila)	3.4	
47	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	3.3	
48	HIST1H2BD	histone 1, H2bd	3.3	
49	ITGB5	integrin, beta 5	3.3	
50	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	3.2	
51	FST	follistatin	3.2	
52	C1orf24	chromosome 1 open reading frame 24	3.2	
53	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	3.2	
54	C1orf116	chromosome 1 open reading frame 116	3.2	
55	TMEM16A	transmembrane protein 16A	3.2	
56	EIF5A2	eukaryotic translation initiation factor 5A2	3.2	
57	MALL	mal, T-cell differentiation protein-like	3.2	
58	BICD2	bicaudal D homolog 2 (Drosophila)	3.1	
59	WHSC1	Wolf-Hirschhorn syndrome candidate 1	3.1	
60	STAMBPL1	STAM binding protein-like 1	3.1	
61	TGFA	transforming growth factor, alpha	3.1	
62	KIAA1826	KIAA1826	3.1	
63	PHLDA1	pleckstrin homology-like domain, family A, member 1	3.1	
64	PI3	peptidase inhibitor 3, skin-derived (SKALP)	3.1	
65	CCND2	cyclin D2	3.0	
66	STC1	stanniocalcin 1	3.0	
67	C12orf24	chromosome 12 open reading frame 24	3.0	

68	MCM3AP	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	3.0
69	RUNX2	runt-related transcription factor 2	3.0
70	STC2	stanniocalcin 2	3.0
71	GPR160	G protein-coupled receptor 160	3.0
72	NT5E	5'-nucleotidase, ecto (CD73)	3.0
73	FAIM3	Fas apoptotic inhibitory molecule 3	3.0
74	BOP1	block of proliferation 1	3.0
75	FOXA1	forkhead box A1	3.0
76	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	2.9
77	ACPL2	acid phosphatase-like 2	2.9
78	HINT3	histidine triad nucleotide binding protein 3	2.9
79	C3orf58	chromosome 3 open reading frame 58	2.9
80	KIAA0368	KIAA0368	2.9
81	ETV5	ets variant gene 5 (ets-related molecule)	2.9
82	IL1R2	interleukin 1 receptor, type II	2.9
83	ANKH	ankylosis, progressive homolog (mouse)	2.9
84	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	2.9
85	SLC43A3	solute carrier family 43, member 3	2.9
86	LPIN1	lipin 1	2.9
87	PLAGL1	pleiomorphic adenoma gene-like 1	2.8
88	PDCD1LG2	programmed cell death 1 ligand 2	2.8
89	CKB	creatine kinase, brain	2.8
90	VEGF	vascular endothelial growth factor	2.8
91	RAB3B	RAB3B, member RAS oncogene family	2.8
92	FRMD4A	FERM domain containing 4A	2.8
93	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-lik	2.8
94	CD44	CD44 antigen (Indian blood group)	2.8
95	ZBED2	zinc finger, BED-type containing 2	2.8
96	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	2.8
97	ANAPC7	anaphase promoting complex subunit 7	2.8
98	CCDC22	coiled-coil domain containing 22	2.8
99	SPHK1	sphingosine kinase 1	2.8
100	EREG	epiregulin	2.8

* BE: fold-increase in primary bronchial epithelial cells (genes with > 2-fold increase)

TABLE 5S - MOST DOWNREGULATED GENES BY 9-AMINAOACRIDINE IN CFBE41o- CELLS

			fold-change	
	Gene symbol	Description	CFBE41o-	BE *
1	SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	0.02	
2	ANXA8	annexin A8	0.02	
3	CDCA7	cell division cycle associated 7	0.02	
4	PYCARD	PYD and CARD domain containing	0.02	0.42
5	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	0.02	
6	EXOC2	exocyst complex component 2	0.02	
7	TRIM14	tripartite motif-containing 14	0.02	
8	SP110	SP110 nuclear body protein	0.03	
9	SFXN1	sideroflexin 1	0.03	0.49
10	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	0.03	
11	MYO5C	myosin VC	0.03	
12	ZNF512	zinc finger protein 512	0.03	0.50
13	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	0.03	
14	SP100	SP100 nuclear antigen	0.03	
15	AGGF1	angiogenic factor with G patch and FHA domains 1	0.03	
16	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.03	
17	COMMD2	COMM domain containing 2	0.03	
18	AP3S2	adaptor-related protein complex 3, sigma 2 subunit	0.03	
19	C1orf144	chromosome 1 open reading frame 144	0.04	
20	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	0.04	0.28
21	VPS72	vacuolar protein sorting 72 (yeast)	0.04	
22	SAR1B	SAR1 gene homolog B (S. cerevisiae)	0.04	
23	GPR110	G protein-coupled receptor 110	0.04	
24	SLC25A37	solute carrier family 25, member 37	0.04	
25	ICMT	isoprenylcysteine carboxyl methyltransferase	0.04	
26	HIP2	huntingtin interacting protein 2	0.04	
27	SRI	sorcin	0.04	0.50
28	FN1	fibronectin 1	0.04	0.48
29	GSTO2	glutathione S-transferase omega 2	0.04	0.31
30	C1orf19	chromosome 1 open reading frame 19	0.04	
31	NR6A1	nuclear receptor subfamily 6, group A, member 1	0.04	
32	ORC5L	origin recognition complex, subunit 5-like (yeast)	0.04	
33	BHLHB2	basic helix-loop-helix domain containing, class B, 2	0.04	
34	DPH5	DPH5 homolog (S. cerevisiae)	0.04	0.39
35	MKL2	MKL/myocardin-like 2	0.04	
36	KIAA0974	KIAA0974	0.04	
37	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	0.04	0.48
38	GRAMD3	GRAM domain containing 3	0.04	0.33
39	GBP3	guanylate binding protein 3	0.04	
40	BBS2	Bardet-Biedl syndrome 2	0.04	
41	VGLL1	vestigial like 1 (Drosophila)	0.04	
42	SAAL1	serum amyloid A-like 1	0.04	0.37
43	NECAP1	NECAP endocytosis associated 1	0.04	
44	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	0.04	
45	NPEPPS	aminopeptidase puromycin sensitive	0.04	
46	LSM6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.04	
47	MULK	multiple substrate lipid kinase	0.05	
48	MPHOSPH9	M-phase phosphoprotein 9	0.05	0.46
49	MBTPS2	membrane-bound transcription factor peptidase, site 2	0.05	
50	NMI	N-myc (and STAT) interactor	0.05	
51	SCCPDH	saccharopine dehydrogenase (putative)	0.05	
52	CCL28	chemokine (C-C motif) ligand 28	0.05	0.49
53	TRIM16	tripartite motif-containing 16	0.05	
54	CXorf39	chromosome X open reading frame 39	0.05	
55	ZNF22	zinc finger protein 22 (KOX 15)	0.05	0.44
56	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	0.05	
57	EPRS	glutamyl-prolyl-tRNA synthetase	0.05	0.27
58	TNRC5	trinucleotide repeat containing 5	0.05	
59	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	0.05	
60	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	0.05	
61	FCMD	Fukuyama type congenital muscular dystrophy (fukutin)	0.05	
62	C8orf55	chromosome 8 open reading frame 55	0.05	
63	ZYG11B	zyg-11 homolog B (C. elegans)	0.05	0.37
64	TBC1D2B	TBC1 domain family, member 2B	0.05	
65	IFI44	interferon-induced protein 44	0.05	0.38
66	BTN3A3	butyrophilin, subfamily 3, member A3	0.05	
67	PARP12	poly (ADP-ribose) polymerase family, member 12	0.05	

68	NCOA5	nuclear receptor coactivator 5	0.05	
69	C6orf108	chromosome 6 open reading frame 108	0.05	
70	SAMD9L	sterile alpha motif domain containing 9-like	0.05	
71	RNF141	ring finger protein 141	0.05	
72	PDZK1IP1	PDZK1 interacting protein 1	0.05	
73	STRN	striatin, calmodulin binding protein	0.05	
74	KCTD18	potassium channel tetramerisation domain containing 18	0.05	
75	SFRS4	splicing factor, arginine/serine-rich 4	0.05	
76	THUMPD3	THUMP domain containing 3	0.06	
77	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	0.06	
78	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37	0.06	
79	CRTAP	cartilage associated protein	0.06	0.35
80	SLC30A9	solute carrier family 30 (zinc transporter), member 9	0.06	
81	ARL4C	ADP-ribosylation factor-like 4C	0.06	
82	CD58	CD58 antigen, (lymphocyte function-associated antigen 3)	0.06	
83	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	0.06	
84	CUTC	cutC copper transporter homolog (E. coli)	0.06	
85	TMBIM4	transmembrane BAX inhibitor motif containing 4	0.06	0.49
86	BCAT1	branched chain aminotransferase 1, cytosolic	0.06	
87	CST6	cystatin E/M	0.06	
88	CDC91L1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	0.06	
89	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	0.06	
90	RFP	ret finger protein	0.06	
91	DOCK5	dedicator of cytokinesis 5	0.06	
92	C1orf112	chromosome 1 open reading frame 112	0.06	
93	YTHDC2	YTH domain containing 2	0.06	0.44
94	CRBN	cereblon	0.06	
95	DPP8	dipeptidyl-peptidase 8	0.06	
96	PIGB	phosphatidylinositol glycan, class B	0.06	0.32
97	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	0.06	
98	C16orf44	chromosome 16 open reading frame 44	0.06	
99	ORC3L	origin recognition complex, subunit 3-like (yeast)	0.06	
100	RABIF	RAB interacting factor	0.06	

* BE: fold-change in primary bronchial epithelial cells (genes with > 2-fold decrease)

TABLE 6S - MOST DOWNREGULATED GENES BY CICLOPIROX IN CFBE41o- CELLS

			fold-change	
	Gene symbol	Description	CFBE41o-	BE *
1	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.02	
2	IGFBP5	insulin-like growth factor binding protein 5	0.02	
3	BCAT1	branched chain aminotransferase 1, cytosolic	0.04	
4	KLK6	kallikrein 6 (neurosin, zyme)	0.04	
5	FZD2	frizzled homolog 2 (Drosophila)	0.05	0.44
6	PPAP2C	phosphatidic acid phosphatase type 2C	0.05	0.5
7	GPR110	G protein-coupled receptor 110	0.05	
8	KYNU	kynureninase (L-kynurenine hydrolase)	0.05	
9	GRHL2	grainyhead-like 2 (Drosophila)	0.06	
10	HIST1H2AC	histone 1, H2ac	0.06	
11	ANKRD38	ankyrin repeat domain 38	0.06	
12	PCDHB5	protocadherin beta 5	0.06	
13	SORBS2	sorbin and SH3 domain containing 2	0.06	
14	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.06	
15	NS4ATP2	NA	0.06	
16	PRTFDC1	phosphoribosyl transferase domain containing 1	0.07	0.26
17	HIST1H2BD	histone 1, H2bd	0.07	
18	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	0.07	
19	STEAP4	STEAP family member 4	0.07	
20	TMTC4	transmembrane and tetratricopeptide repeat containing 4	0.07	
21	RHOBTB3	Rho-related BTB domain containing 3	0.08	
22	VTCN1	V-set domain containing T cell activation inhibitor 1	0.08	0.48
23	HIST1H3H	histone 1, H3h	0.08	
24	TRIM16	tripartite motif-containing 16	0.08	
25	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.08	
26	HYLS1	hydrolethalus syndrome 1	0.08	
27	CCNB1	cyclin B1	0.08	0.3
28	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	0.08	
29	WNT5A	wingless-type MMTV integration site family, member 5A	0.08	
30	PSRC1	proline/serine-rich coiled-coil 1	0.08	0.48
31	SAMD9L	sterile alpha motif domain containing 9-like	0.09	
32	TRIM4	tripartite motif-containing 4	0.09	
33	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	0.09	
34	JPH2	junctophilin 2	0.09	
35	FRAS1	Fraser syndrome 1	0.09	0.46
36	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme	0.09	
37	EPSTI1	epithelial stromal interaction 1 (breast)	0.09	0.44
38	PBX1	pre-B-cell leukemia transcription factor 1	0.10	0.49
39	ACOT4	acyl-CoA thioesterase 4	0.10	
40	HIST2H2BE	histone 2, H2be	0.10	
41	HIST1H2BF	histone 1, H2bf	0.10	
42	RTN4IP1	reticulon 4 interacting protein 1	0.10	
43	HIST1H2BH	histone 1, H2bh	0.10	
44	KLK10	kallikrein 10	0.10	
45	MAML2	mastermind-like 2 (Drosophila)	0.10	
46	PGRMC2	progesterone receptor membrane component 2	0.10	
47	PHF23	PHD finger protein 23	0.10	
48	BMF	Bcl2 modifying factor	0.10	
49	C1QTNF6	C1q and tumor necrosis factor related protein 6	0.10	
50	BTN3A3	butyrophilin, subfamily 3, member A3	0.11	0.46
51	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	0.11	
52	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-lik	0.11	
53	MAN2C1	mannosidase, alpha, class 2C, member 1	0.11	
54	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	0.11	
55	C8orf4	chromosome 8 open reading frame 4	0.11	
56	TRIM6	tripartite motif-containing 6	0.11	
57	MPHOSPH9	M-phase phosphoprotein 9	0.12	
58	C9orf3	chromosome 9 open reading frame 3	0.12	
59	BTN3A2	butyrophilin, subfamily 3, member A2	0.12	
60	TMPO	thymopoietin	0.12	
61	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	0.12	
62	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal	0.12	
63	DEPDC1	DEP domain containing 1	0.12	0.31
64	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0.12	0.37
65	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	0.12	
66	B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	0.12	
67	MXRA5	matrix-remodelling associated 5	0.12	

68	C14orf93	chromosome 14 open reading frame 93	0.12	
69	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.13	
70	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.13	
71	LEPR	leptin receptor	0.13	
72	TEF	thyrotrophic embryonic factor	0.13	
73	H2BFS	H2B histone family, member S	0.13	
74	VANGL1	vang-like 1 (van gogh, Drosophila)	0.13	
75	TRERF1	transcriptional regulating factor 1	0.13	
76	FIGN	fidgetin	0.13	
77	HOXA9	homeobox A9	0.14	
78	ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae)	0.14	
79	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.14	0.46
80	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	0.14	
81	MAL	mal, T-cell differentiation protein	0.14	
82	DHRS1	dehydrogenase/reductase (SDR family) member 1	0.14	0.44
83	NAPE-PLD	NA	0.14	
84	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	0.14	
85	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.14	
86	HIST1H2BG	histone 1, H2bg	0.15	
87	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	0.15	0.45
88	HIST1H2BE	histone 1, H2be	0.15	
89	OPN3	opsin 3 (encephalopsin, panopsin)	0.15	
90	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	0.15	
91	SLITRK6	SLIT and NTRK-like family, member 6	0.15	
92	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	0.15	
93	ANTXR1	anthrax toxin receptor 1	0.15	0.33
94	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.15	
95	MARCKS	myristoylated alanine-rich protein kinase C substrate	0.15	
96	VGCNL1	voltage gated channel like 1	0.15	
97	TNS3	tensin 3	0.15	
98	ZNF302	zinc finger protein 302	0.15	
99	CBR4	NA	0.15	
100	HIST2H2AA	histone 2, H2aa	0.15	

* BE: fold-change in primary bronchial epithelial cells (genes with > 2-fold decrease)

TABLE 7S - MOST DOWNREGULATED GENES BY LOW TEMPERATURE IN CFBE41o- CELLS

			fold-change	
	Gene symbol	Description	CFBE41o-	BE *
1	SLC39A10	solute carrier family 39 (zinc transporter), member 10	0.03	
2	RAD54B	RAD54 homolog B (S. cerevisiae)	0.04	0.28
3	C14orf125	chromosome 14 open reading frame 125	0.05	
4	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozym	0.05	0.50
5	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0.05	0.27
6	STARD13	START domain containing 13	0.05	
7	HERC4	hect domain and RLD 4	0.06	0.08
8	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	0.06	0.21
9	FANCL	Fanconi anemia, complementation group L	0.07	0.28
10	NAPE-PLD	NA	0.07	
11	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.07	0.19
12	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.07	0.30
13	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	0.07	0.17
14	SMEK2	NA	0.08	0.06
15	FAM69A	family with sequence similarity 69, member A	0.08	
16	RBM4B	RNA binding motif protein 4B	0.08	0.25
17	LYST	lysosomal trafficking regulator	0.08	0.13
18	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.08	
19	PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) m	0.08	0.38
20	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	0.08	0.22
21	TXNDC5	thioredoxin domain containing 5	0.08	
22	C17orf80	chromosome 17 open reading frame 80	0.09	0.23
23	ENO2	enolase 2 (gamma, neuronal)	0.09	0.22
24	EYA3	eyes absent homolog 3 (Drosophila)	0.09	0.39
25	C11orf54	chromosome 11 open reading frame 54	0.09	0.17
26	FAM36A	family with sequence similarity 36, member A	0.09	0.45
27	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homo	0.09	
28	FLJ13305	NA	0.09	
29	C1orf25	chromosome 1 open reading frame 25	0.09	0.09
30	MOSPD2	motile sperm domain containing 2	0.10	0.18
31	SYTL4	synaptotagmin-like 4 (granuphilin-a)	0.10	0.25
32	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	0.10	0.24
33	FSHPRH1	FSH primary response (LRPR1 homolog, rat) 1	0.10	
34	C9orf40	chromosome 9 open reading frame 40	0.10	
35	CAMTA1	calmodulin binding transcription activator 1	0.10	0.35
36	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	0.10	0.32
37	DOC1	NA	0.10	
38	ZF	NA	0.10	
39	CCDC77	coiled-coil domain containing 77	0.11	
40	C11orf30	chromosome 11 open reading frame 30	0.11	0.47
41	C10orf137	chromosome 10 open reading frame 137	0.11	
42	CCDC15	coiled-coil domain containing 15	0.11	0.47
43	TMEM22	transmembrane protein 22	0.11	
44	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	0.11	0.21
45	NUDCD1	NudC domain containing 1	0.11	0.35
46	C8orf4	chromosome 8 open reading frame 4	0.11	0.33
47	CARD8	caspase recruitment domain family, member 8	0.11	0.12
48	CLDND1	claudin domain containing 1	0.11	0.17
49	MGA	MAX gene associated	0.12	0.26
50	MBD5	methyl-CpG binding domain protein 5	0.12	0.15
51	FN5	NA	0.12	
52	LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	0.12	0.47
53	ZNF177	zinc finger protein 177	0.12	
54	SKP2	S-phase kinase-associated protein 2 (p45)	0.12	
55	FLJ32363	NA	0.12	
56	LFNG	lunatic fringe homolog (Drosophila)	0.12	0.42
57	TRIP11	thyroid hormone receptor interactor 11	0.12	0.25
58	ARL13B	ADP-ribosylation factor-like 13B	0.12	
59	METTL3	methyltransferase like 3	0.12	0.32
60	DOPEY1	dopey family member 1	0.12	
61	FZD2	frizzled homolog 2 (Drosophila)	0.12	0.39
62	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	0.12	
63	RNF146	ring finger protein 146	0.13	
64	TRERF1	transcriptional regulating factor 1	0.13	0.34
65	FLJ22531	NA	0.13	
66	OIP5	Opa interacting protein 5	0.13	
67	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth fac	0.13	

68	EXOC6	exocyst complex component 6	0.13	0.41
69	ZNF512	zinc finger protein 512	0.13	0.30
70	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypep	0.13	0.26
71	ZNF692	zinc finger protein 692	0.13	0.35
72	MRPS30	mitochondrial ribosomal protein S30	0.13	0.39
73	SOS1	son of sevenless homolog 1 (Drosophila)	0.13	0.22
74	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.13	
75	GJA7	gap junction protein, alpha 7, 45kDa (connexin 45)	0.13	
76	S100PBP	S100P binding protein	0.13	0.38
77	SBF2	SET binding factor 2	0.13	
78	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.13	
79	MAK	male germ cell-associated kinase	0.13	
80	C18orf54	chromosome 18 open reading frame 54	0.13	0.41
81	IER5L	immediate early response 5-like	0.14	
82	APAF1	apoptotic peptidase activating factor	0.14	0.31
83	C1orf63	chromosome 1 open reading frame 63	0.14	0.23
84	PANK1	pantothenate kinase 1	0.14	0.39
85	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	0.14	0.20
86	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	0.14	0.42
87	ETNK1	ethanolamine kinase 1	0.14	0.16
88	NOX1	NADPH oxidase 1	0.14	
89	MECP2	methyl CpG binding protein 2 (Rett syndrome)	0.14	
90	RAB4B	RAB4B, member RAS oncogene family	0.14	
91	C10orf6	chromosome 10 open reading frame 6	0.14	
92	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	0.15	
93	ZNF610	zinc finger protein 610	0.15	0.26
94	WDR76	WD repeat domain 76	0.15	
95	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	0.15	0.35
96	JARID1A	Jumonji, AT rich interactive domain 1A (RBBP2-like)	0.15	
97	CIRBP	cold inducible RNA binding protein	0.15	0.37
98	EFHC1	EF-hand domain (C-terminal) containing 1	0.15	0.48
99	SPOP	speckle-type POZ protein	0.15	0.50
100	TMTC4	transmembrane and tetratricopeptide repeat containing 4	0.15	0.36

* BE: fold-change in primary bronchial epithelial cells (genes with > 2-fold decrease)

TABLE 8S - MOST DOWNREGULATED GENES BY CORR-4a IN CFBE41o- CELLS

			fold-change	
	Gene symbol	Description	CFBE41o-	BE *
1	RNU71B	RNA, U71B small nucleolar	0.27	
2	C8orf4	chromosome 8 open reading frame 4	0.32	
3	CABP4	calcium binding protein 4	0.32	
4	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hor	0.33	
5	TCF15	transcription factor 15 (basic helix-loop-helix)	0.36	
6	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.36	
7	REST	RE1-silencing transcription factor	0.38	
8	IQGAP2	IQ motif containing GTPase activating protein 2	0.39	
9	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	0.42	
10	EGR1	early growth response 1	0.42	
11	VTCN1	V-set domain containing T cell activation inhibitor 1	0.43	
12	ZFP64	zinc finger protein 64 homolog (mouse)	0.44	
13	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.45	
14	EHD4	EH-domain containing 4	0.45	
15	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	0.45	
16	CRIP2	cysteine-rich protein 2	0.45	
17	ALPP	alkaline phosphatase, placental (Regan isozyme)	0.46	
18	DLEU2	deleted in lymphocytic leukemia, 2	0.46	
19	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	0.46	
20	TCTE3	t-complex-associated-testis-expressed 3	0.46	
21	PRX	periaxin	0.47	
22	TXNIP	thioredoxin interacting protein	0.47	
23	SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	0.47	
24	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth fac	0.47	
25	SCN2B	sodium channel, voltage-gated, type II, beta	0.48	
26	ADCY1	adenylate cyclase 1 (brain)	0.48	
27	BTBD3	BTB (POZ) domain containing 3	0.48	
28	IGFBP3	insulin-like growth factor binding protein 3	0.48	
29	ALPPL2	alkaline phosphatase, placental-like 2	0.49	
30	NCOA2	nuclear receptor coactivator 2	0.49	
31	SEC15L2	SEC15-like 2 (S. cerevisiae)	0.49	
32	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	0.49	
33	TFRC	transferrin receptor (p90, CD71)	0.49	
34	SYNJ2	synaptojanin 2	0.49	
35	GPR153	G protein-coupled receptor 153	0.49	
36	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	0.49	
37	PLCE1	phospholipase C, epsilon 1	0.50	
38	ASB12	ankyrin repeat and SOCS box-containing 12	0.50	
39	PTGER3	prostaglandin E receptor 3 (subtype EP3)	0.50	
40	ZNF230	zinc finger protein 230	0.50	
41	RFFL	ring finger and FYVE-like domain containing 1	0.50	
42	STAC3	SH3 and cysteine rich domain 3	0.50	
43	C20orf58	chromosome 20 open reading frame 58	0.51	
44	BDH1	3-hydroxybutyrate dehydrogenase, type 1	0.51	
45	CAGE1	cancer antigen 1	0.51	
46	C8orf42	chromosome 8 open reading frame 42	0.52	
47	MLLT7	c("myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)", " tra	0.52	
48	POU6F1	POU domain, class 6, transcription factor 1	0.52	
49	CRLF1	cytokine receptor-like factor 1	0.52	
50	PNPLA2	patatin-like phospholipase domain containing 2	0.52	
51	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.52	
52	PI16	peptidase inhibitor 16	0.52	
53	MKL2	MKL/myocardin-like 2	0.52	
54	EMID2	EMI domain containing 2	0.53	
55	CNOT4	CCR4-NOT transcription complex, subunit 4	0.53	
56	WWOX	WW domain containing oxidoreductase	0.53	
57	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.54	
58	CFB	complement factor B	0.54	
59	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0.54	
60	C14orf159	chromosome 14 open reading frame 159	0.54	
61	BTNL3	butyrophilin-like 3	0.54	
62	PREB	prolactin regulatory element binding	0.54	
63	RPL7	ribosomal protein L7	0.54	
64	ZNF606	zinc finger protein 606	0.54	
65	WDR62	WD repeat domain 62	0.54	
66	KLC3	kinesin light chain 3	0.54	
67	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)	0.54	

68	HEG1	HEG homolog 1 (zebrafish)	0.55
69	RBL1	retinoblastoma-like 1 (p107)	0.55
70	DLX2	distal-less homeobox 2	0.55
71	PPP4R1L	protein phosphatase 4, regulatory subunit 1-like	0.55
72	ZNF720	zinc finger protein 720	0.55
73	GLUL	glutamate-ammonia ligase (glutamine synthetase)	0.55
74	MTMR11	myotubularin related protein 11	0.55
75	PQBP1	polyglutamine binding protein 1	0.55
76	WNT6	wingless-type MMTV integration site family, member 6	0.55
77	ZNF148	zinc finger protein 148 (pHZ-52)	0.56
78	NRG1	neuregulin 1	0.56
79	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.56
80	C1orf69	chromosome 1 open reading frame 69	0.56
81	SHPRH	SNF2 histone linker PHD RING helicase	0.56
82	ZNF696	zinc finger protein 696	0.56
83	RGS12	regulator of G-protein signalling 12	0.56
84	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	0.56
85	SMOX	spermine oxidase	0.57
86	SFTPC	surfactant, pulmonary-associated protein C	0.57
87	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0.57
88	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	0.57
89	SRCRB4D	scavenger receptor cysteine rich domain containing, group B (4 domains)	0.57
90	CABC1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	0.57
91	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	0.57
92	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	0.57
93	ANKRD38	ankyrin repeat domain 38	0.57
94	ZFPM1	zinc finger protein, multitype 1	0.57
95	TFR2	transferrin receptor 2	0.57
96	LZTR1	leucine-zipper-like transcription regulator 1	0.58
97	RNF38	ring finger protein 38	0.58
98	RORA	RAR-related orphan receptor A	0.58
99	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	0.58
100	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	0.58

* none of the listed genes was downregulated by corr-4a in primary bronchial epithelial cells