Supplementary data

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Supplemental Method: qRT-PCR

All primers used in this study were designed with the Primer3 program (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi) and tested for specificity with NCBI's BLASTs (http://blast.ncbi.nlm.nih.gov/Blast.cgi) to verify that the binding sites were unique for each gene. All primers were ordered from Metabion International (Martinsried, Germany). The size of all targeted genes' amplicon sequence was about 300bp and cross at least one boundary of exon and intron (Table 2).

Real time quantitative RT-PCR. First strand cDNA was synthesized using an oligo-(dT)15 primer and Moloney murine leukemia virus reverse transcriptase (Fermentas, Vilnius, Lithuania) at 42°C for 1 h. The real-time quantitative RT-PCR was carried out using 7900HT Fast Real-Time PCR System (Applied Biosystems) according to the manufacturer's instructions. The protocol of Relative Quantification (2-ΔΔCt) was applied. The thermal cycling program consisted of 2 min at 50 °C, 10 min at 95 °C, followed by 40 cycles of 15 second at 95°C and 60 °C for 1 min. The qRT-PCR was performed using SYBR green PCR master mix (Fermentas, Vilnius, Lithuania) with 25 ng cDNA as template, 0.2μM of final oligos concentration. Real time qPCR was monitored and analyzed by the Sequence Detection System version 2.2.2 (PE Applied Biosystems, California, USA). The reactions were run in triplicate for each sample. Endogenous control gene had the mean cycle threshold (Ct) values as low as 14.6 and a constant expression level in normal lung tissue and tumors. The dissociation curves for all reactions were verified to display a single peak.

Supplemental tables

Table 1. Patients and tumor characteristics

Category	Cases /histology			
	total (N=85)	SCC	BA(AC+BC)	NL
Median (range) of age	68 (38~81)	69 (44~81)	64 (38~79)	70 (53~79)
Gender				
Male	76 (89.41%)	61 (71.7%)	15(17.64%)	20
Female	9 (10.58%)	1 (1.17%)	8 (9.41%)	1
Tobacco use				
>50 packages/year	26	24	7	
35 packages/year	52	40	12	10
<5 packages/year	2	2	0	11
non	5	1	4	
Cancer TNM stage:				
Ia	13 (15.29%)	8 (9.41%)	5 (5.88%)	
Ib	46 (54.11%)	36 (42.35%)	10 (11.76%)	
IIa	3 (3.52%)	2 (2.35%)	1 (1.17%)	
IIb	3 (3.52%)	2 (2.35%)	1 (1.17%)	
IIIa	9 (10.58%)	6 (7.05%)	3 (3.52%)	
IIIb	6 (7.05%)	4 (4.70%)	2 (2.35%)	
IV	5 (5.88%)	4 (4.70%)	1 (1.17%)	

Table 2 Oligos for validation of microarray gene expression by qRT-PCR. Accession number for a given gene is shown in parenthesis. (F: forward oligo, R: reverse oligo)

Up-regulated genes		
CCNB2 (NM_004701.2)	Cyclin B2	F, 5’ actgctctgctcttggcttc R, 5’ ctcggatttgggaactggta
TTK (NM_003318.3)	Dual specificity protein kinase	F, 5’cagcagcaacagcatcaaat R, 5’ttgcttgaacctccacttcc
BUB1B (AF107297)	Budding uninhibited by benzimidazoles 1 homolog beta (yeast)	F, 5’ctcgtggcaatacagcttca R, 5’ccaggctttctggtgcttag
PTTG2 (NP_006598.1)	Pituitary tumor-transforming 2	F, 5’ctgcctcagatgacgcctat R, 5’gagaggcactccactcaagg
Down-regulated genes		
CLIC5 (AF216941)	Chloride intracellular channel protein 5	F, 5’gtctggcaaacacagcttca R, 5’ggcactgcaacaaactgaga
GPR116 (NM_015234)	G-protein coupled receptor 116	F, 5’cagaagctatgccggttctc R, 5’agccatctggagcagactgt
AGER (RAGE) (NP_001127.1)	Advanced glycosylation end product-specific receptor	F, 5’cgtcccaccttctcctgtag R, 5’gctactgctccaccttctgg
TNNC1 (NM_001002862.1)	Troponin C type 1	F, 5’atcgaggagctcatgaagga R, 5’ctgggtgaaggtcagcatc
Internal control genes		
ESD (M13450)	Esterase D/formylglutathione hydrolase	F, 5'atttgctccaatttgcaacc R, 5'tcacaaggtgggtagcatca

Table 3 Genes down-regulated and up-regulated in NSCLC.

Genes down-regulated in NSCLC

Gene ID	adj. p-value	Fold change
SFTPC	7,13E-10	24,43
FCN3	6,77E-17	16,71
FABP4	3,28E-14	13,54
C19ORF59	5,43E-20	12,51
TMEM100	1,65E-21	12,11
CYP4B1	1,35E-12	11,41
CLIC5	9,37E-21	10,99
SFTPD	4,18E-08	10,75
SFTA2_HUMAN	4,02E-07	10,59
CLEC3B	9,66E-22	10,23
GKN2	1,50E-19	9,83
SCGB1A1	1,23E-07	9,65
SFTPA1B	7,00E-15	9,51
MAMDC2	9,55E-17	9,19
CPB2	2,75E-20	9,04
AGER	4,14E-24	8,85
INMT	1,51E-15	8,71
FAM107A	1,41E-20	8,61
CLDN18	7,11E-23	8,17
FHL1	6,23E-18	7,95
ADH1A	9,67E-09	7,57
MARCO	6,55E-12	7,43
SCGB3A2	2,63E-07	7,36
BTNL9	6,09E-23	7,33
LPL	1,82E-16	7,23
HPGD	3,12E-13	7,09
TNNC1	3,91E-20	6,72
SUSD2	4,05E-11	6,64
HBA2	8,44E-11	6,60
C4BPA	5,08E-06	6,59
ABCA3	1,50E-08	6,56
PGC	8,11E-07	6,23
PDK4	5,06E-14	6,14
FMO2	7,06E-16	6,07
SCGB3A1	3,20E-05	5,96
FOLR1	9,50E-07	5,95
AQP4	3,21E-14	5,93
LAMP3	1,17E-11	5,93
MRC1L1	5,14E-13	5,83
CP21A_HUMAN	3,89E-14	5,79
OLR1	6,82E-13	5,78
C10ORF116	7,70E-13	5,75
OGN	1,10E-10	5,67
C7	8,25E-08	5,64
PEBPL_HUMAN	3,83E-14	5,51
ADH1C	8,00E-07	5,45
FBP1	8,13E-11	5,39
HSD17B6	2,10E-15	5,35
NP_689672,3	1,36E-07	5,34
TEK	5,80E-21	5,21

GPR116	5,05E-15	5,19
HBD	3,05E-11	5,15
ABCA8	1,51E-16	5,14
Q8N8N9_HUMAN	1,94E-21	5,11
VIPR1	7,67E-18	5,10
AGR3	2,30E-08	5,07
RETN	6,29E-20	5,05
LRRC36	3,53E-23	5,04
RAMP3	4,16E-22	5,04
TPPP3	6,77E-16	5,02
MFAP4	9,35E-10	5,00
SLC39A8	5,21E-14	5,00
NOSTRIN	1,80E-16	5,00
PLEKHK1	1,15E-25	4,99
PLA2G1B	7,00E-15	4,90
HIGD1B	1,69E-15	4,87
GDF10	1,17E-22	4,86
C13ORF15	1,21E-16	4,82
NP_835466,1	2,17E-15	4,80
CD52	2,32E-12	4,77
KAL1	7,56E-15	4,74
SDPR	1,10E-19	4,73
TCF21	2,24E-20	4,65
ATOH8	6,74E-11	4,65
2B32_HUMAN	3,27E-04	4,62
ABI3BP	4,03E-12	4,61
CACNA2D2	5,80E-14	4,59
LYZ	4,26E-07	4,54
MS4A7	2,77E-13	4,52
CA4	3,75E-25	4,50
CXCL2	8,99E-08	4,50
SLC6A4	1,58E-24	4,48
EDG1	9,39E-15	4,42
SPOCK2	1,27E-11	4,42
CAV1	3,69E-15	4,34
FIGF	6,08E-17	4,31
PLEKHH2	1,51E-16	4,29
ZNF533	2,87E-10	4,25
SLCO2A1	2,30E-10	4,21
VSIG2	5,57E-16	4,20
LMO3	3,41E-05	4,17
CPA3	3,64E-09	4,17
IFT57	3,49E-17	4,16
SELENBP1	4,08E-09	4,16
VSIG4	4,61E-14	4,14
EMP2	1,35E-16	4,14
GLDN	3,51E-18	4,09
CFD	1,16E-14	4,07
NPNT	2,12E-13	4,06
WIF1	1,07E-12	3,99
S100A4	1,04E-12	3,94
A2ABK7_HUMAN	2,13E-05	3,94
CALCRL	4,22E-14	3,91
CGNL1	6,73E-13	3,89

ITLN2	5,16E-21	3,86
AOC3	3,33E-20	3,84
C9ORF61	1,26E-16	3,82
NP_079189,3	1,22E-15	3,81
SLIT2	4,97E-16	3,78
CD300LG	1,30E-22	3,78
FGFR4	1,91E-14	3,76
ANKRD29	6,33E-14	3,74
C9ORF19	2,98E-17	3,74
TMPRSS2	1,75E-07	3,70
CD36	3,57E-12	3,70
CLEC14A	3,67E-13	3,68
LMO7	1,22E-19	3,67
MYH11	7,26E-06	3,66
KLF4	1,51E-10	3,63
GNG11	1,51E-11	3,61
CADM1	1,45E-08	3,60
FBLN5	1,57E-13	3,60
FLRT3	4,47E-07	3,58
CYBB	2,77E-13	3,57
ALOX5	8,35E-12	3,55
C1ORF162	2,01E-12	3,54
NLRC4	2,76E-17	3,53
MNDA	2,75E-12	3,53
ESAM	8,35E-10	3,53
STX11	7,30E-19	3,51
GPRC5A	3,24E-06	3,49
GIMAP7	7,78E-11	3,48
FCN1	8,50E-10	3,48
MSR1	1,10E-19	3,48
LRRN3	1,07E-20	3,46
A2M	4,91E-08	3,46
VEPH1	5,60E-16	3,45
NKX2-1	2,90E-05	3,45
CYBRD1	8,82E-10	3,44
CD97	1,71E-10	3,44
PECAM1	1,31E-11	3,43
ALOX5AP	2,93E-10	3,42
MAOB	1,96E-09	3,42
WWC2	6,66E-14	3,42
HOP_HUMAN	3,70E-06	3,42
LDB2	1,32E-15	3,42
TMEM125	2,48E-07	3,41
AYTL2	4,73E-06	3,40
GRK5	9,39E-15	3,38
GPM6A	6,09E-23	3,36
PTPRB	4,10E-19	3,35
NR4A2	4,06E-09	3,34
CLIC3	2,57E-14	3,32
IL33	6,01E-08	3,31
PTGDS	6,55E-06	3,31
LIMS2	5,53E-14	3,31
FRY	7,67E-18	3,29
CSF3	9,46E-05	3,29

TGFBR3	2,23E-17	3,29
ANXA3	7,03E-13	3,28
ACADL	1,26E-18	3,26
COLEC12	5,01E-09	3,26
CD83	3,90E-11	3,25
AMICA1	1,71E-09	3,24
FGR	5,73E-14	3,23
NM_001002919,2	2,34E-13	3,21
SLC6A14	1,28E-05	3,20
DMBT1	1,35E-03	3,20
FOS	8,10E-09	3,20
MSLN	2,03E-04	3,19
SFTPB	1,47E-02	3,18
NP_689963,2	7,05E-12	3,18
DRAM_HUMAN	2,07E-09	3,18
TBX2	9,97E-09	3,18
GRINL1B	8,63E-24	3,18
RICH2_HUMAN	9,24E-11	3,17
MLPH	3,78E-06	3,16
PID1	3,88E-13	3,16
PLAC8	5,01E-09	3,15
HLA-DRA	5,59E-07	3,14
PLLP	4,72E-13	3,14
AREG	3,18E-05	3,14
DPYSL2	5,20E-11	3,13
PTGD2_HUMAN	7,12E-12	3,12
DUSP1	1,21E-08	3,11
ADAMTSL3	1,26E-18	3,08
CLEC12B	1,11E-17	3,08
CA2	8,21E-10	3,08
TYROBP	4,10E-09	3,07
ALDH2	8,50E-13	3,05
THBD	1,49E-07	3,04
AXUD1	5,86E-09	3,04
ROS1	3,56E-08	3,04
MMP19	1,72E-06	3,04
ADRB2	1,20E-16	3,03
SHROOM4	2,86E-21	3,03
AGTR1	2,10E-15	3,02
NEDD4L	4,05E-14	3,01
GIMAP6	4,42E-12	3,01
MAOA	1,87E-07	3,01
Q8NAF8_HUMAN	1,92E-08	3,01
ALDH3B1	1,60E-09	3,01
EGR2	6,10E-11	3,00
CYP27A1	1,87E-09	3,00
KL	9,68E-24	2,98
SMAD6	4,32E-15	2,98
CD55	3,06E-09	2,97
LTA4H	4,62E-14	2,96
EDNRB	1,26E-17	2,96
SLC46A2	7,00E-15	2,93
PCOLCE2	5,85E-14	2,93
C6ORF60	4,76E-13	2,92

FGD5	1,69E-18	2,92
CCBE1	6,76E-16	2,91
C14ORF132	2,12E-10	2,91
APOC1	8,44E-06	2,91
TIMP3	1,29E-07	2,91
CHI3L2	1,02E-08	2,90
SERPINA1	3,42E-04	2,89
CD93	1,39E-09	2,89
CCDC48	1,65E-21	2,88
SCTR	4,15E-06	2,88
SPARCL1	2,58E-09	2,88
GPD1	1,17E-22	2,87
ASAH1	5,44E-11	2,85
COL4A3	3,00E-10	2,85
DPEP2	1,77E-14	2,85
PHACTR2	5,14E-13	2,85
UBL3	3,62E-15	2,84
NCF2	1,26E-10	2,84
PROS1	4,35E-08	2,84
GIMAP8	3,40E-15	2,84
CYB5A	1,94E-08	2,84
C20ORF46	3,39E-18	2,84
RNASE1	1,81E-05	2,83
HBEGF	5,32E-08	2,82
KLF6	1,71E-11	2,82
SLC1A1	6,04E-13	2,80
MGP	4,99E-06	2,79
SEPP1	3,82E-06	2,78
EFEMP1	1,01E-06	2,78
PAPSS2	3,13E-10	2,78
EMCN	7,32E-17	2,77
ENPP4	3,93E-09	2,77
RNASE4	1,47E-09	2,77
C10ORF128	8,69E-10	2,76
PTGS2	2,79E-05	2,76
METTL7A	4,82E-08	2,74
ANKRD47	1,84E-19	2,74
CTSS	1,36E-08	2,74
SELP	8,68E-08	2,73
CYYR1	5,57E-14	2,73
GMFG	2,82E-10	2,73
ADCY4	3,10E-11	2,73
PLSCR4	1,45E-10	2,73
DNALI1	1,51E-09	2,73
DAPK1	8,63E-10	2,73
HSPA12B	8,25E-13	2,73
FCER1A	2,21E-09	2,72
ALPL	1,39E-04	2,72
EGFL7	9,81E-12	2,72
TREM1	1,38E-05	2,72
C5AR1	1,67E-09	2,71
ANKRD25	1,43E-11	2,71
NEBL	1,56E-10	2,71
SPTBN1	2,23E-19	2,70

LDLR	1,26E-08	2,69
C7ORF41	1,95E-09	2,68
ACP5	1,87E-06	2,67
SULT1A2	3,96E-10	2,66
TMEM47	2,02E-09	2,66
MUC1	7,88E-04	2,66
GYPC	1,05E-09	2,66
IGSF10	1,22E-17	2,66
CAT	7,37E-14	2,65
FOXF1	2,82E-15	2,65
TACC1	3,91E-10	2,65
LTBP2	3,73E-08	2,65
MS4A2	1,14E-12	2,65
DENND3	6,19E-11	2,64
HSD17B11	6,98E-09	2,64
DACH1	2,57E-14	2,64
IL7R	2,27E-07	2,63
KIAA1683	4,67E-14	2,63
STXBP6	6,07E-08	2,63
TBX3	9,26E-14	2,63
H33_HUMAN	3,67E-13	2,62
Q7Z7L8_HUMAN	1,41E-04	2,62
NEDD9	1,53E-09	2,61
SOCS2	4,55E-07	2,60
CRIP2	6,03E-05	2,59
CDH5	4,86E-16	2,59
TRYB2_HUMAN	2,40E-04	2,59
ITM2A	5,40E-06	2,59
NR3C2	9,28E-14	2,59
ZFP36	2,68E-07	2,58
CAMK2N1	3,36E-05	2,58
CITED2	9,23E-10	2,58
BTK	1,38E-09	2,57
ARHGEF6	4,54E-09	2,57
NP_001009555,2	1,42E-11	2,57
GRASP	4,61E-11	2,57
NP_116284,2	1,96E-10	2,56
MMP28	6,35E-10	2,56
FLVCR2	1,45E-11	2,56
ZEB2	4,20E-11	2,56
NP_001093858,1	2,62E-06	2,56
GIMAP5	8,11E-10	2,55
C8ORF4	2,19E-05	2,54
CDO1	1,62E-16	2,54
NP_060761,2	1,59E-09	2,53
LYVE1	8,38E-16	2,53
EDN1	1,44E-08	2,52
KLF9	2,22E-09	2,52
SEMA3G	2,40E-14	2,52
KLF2	6,13E-10	2,52
TRPC6	5,27E-12	2,52
CCRL2	1,62E-09	2,52
CD300C	1,34E-10	2,51
COBL	6,54E-07	2,51

C2ORF40	9,99E-10	2,51
COX7A1	1,38E-10	2,51
ARHGAP18	6,31E-11	2,51
NP_001073160,1	1,33E-12	2,51
PRX	1,84E-19	2,51
NP_443121,1	3,11E-10	2,51
PPP1R15A	5,27E-11	2,51
HECW2	2,73E-12	2,51
SNX25	2,65E-14	2,50
CTSH	1,98E-06	2,50
TRPV2	1,93E-15	2,50
GBP4	1,25E-07	2,50
CEACAM6	8,83E-03	2,48
SVEP1	4,03E-09	2,48
GATA2	6,77E-16	2,48
LAML1_HUMAN	4,89E-08	2,47
LIMCH1	4,20E-08	2,47
NP_079006,1	2,76E-08	2,47
FCER1G	6,22E-08	2,47
GCHFR	7,92E-12	2,46
RBP4	2,60E-10	2,46
SH3BGRL	3,45E-08	2,46
SH2D3C	4,74E-12	2,45
C1QA	8,60E-07	2,45
KCTD12	1,10E-11	2,45
EDG6	3,21E-10	2,45
C9ORF24	2,39E-05	2,44
ITGAM	9,48E-09	2,43
ZBTB16	8,94E-09	2,43
DNASE1L3	3,82E-13	2,43
GATA6	5,98E-09	2,42
PPP1R3C	3,45E-08	2,41
RGS2	1,48E-06	2,41
SLC35A1	2,73E-12	2,41
EGR1	8,86E-08	2,41
RASIP1	1,30E-06	2,41
K0256_HUMAN	5,37E-13	2,40
CLEC1A	3,12E-13	2,40
STOM	3,79E-11	2,40
ITGA8	5,93E-13	2,40
LTBP4	2,47E-07	2,40
SGCG	7,30E-19	2,40
APOH	5,61E-08	2,39
SG269_HUMAN	2,61E-10	2,39
SLPI	4,03E-05	2,39
BMP5	2,44E-06	2,39
LMO2	1,48E-14	2,38
MMRN2	2,92E-09	2,38
LRRC32	9,12E-10	2,37
FAM105A	5,28E-08	2,37
NTNG1	1,15E-18	2,36
ROR1	6,84E-09	2,35
FLI1	6,58E-10	2,35
TRIM22	6,31E-07	2,35

Q8N843_HUMAN	6,25E-05	2,35
ENG	8,91E-07	2,35
IGSF6	2,71E-07	2,35
HOXA5	3,25E-08	2,34
ICAM4	2,97E-08	2,34
LGALS3	1,76E-08	2,34
ARRDC4	1,78E-09	2,34
HK3	3,27E-12	2,33
TSPAN8	1,63E-03	2,33
NP_001073159,1	6,83E-08	2,33
C11ORF9	1,26E-10	2,33
LIPA	3,56E-06	2,33
FAM38B	1,05E-05	2,33
EDNRA	1,13E-08	2,32
KCNK3	7,79E-11	2,32
SLCO2B1	8,00E-07	2,32
JAM2	4,97E-12	2,32
LHFP	6,70E-09	2,32
PDLIM2	1,49E-09	2,32
PRAM1	7,44E-17	2,31
LPHN2	5,74E-10	2,31
GLS	1,09E-05	2,30
ID2	7,54E-08	2,30
MYADM	1,83E-07	2,29
FCGR3A	1,50E-06	2,29
SLC7A7	4,59E-09	2,29
AQP9	2,84E-06	2,29
LY86	3,85E-08	2,29
GPD1L	5,77E-11	2,29
NRGN	9,25E-06	2,29
ACSL5	8,48E-05	2,28
RRAD	3,21E-06	2,28
C7ORF23	3,64E-09	2,28
SPI1	4,05E-10	2,28
MYO5C	9,62E-07	2,28
GADD45B	7,86E-06	2,28
IL18R1	9,07E-09	2,28
FOLR3	6,79E-10	2,28
CCL2	3,35E-04	2,27
EVI2B	1,72E-05	2,27
PAG1	8,56E-09	2,27
RASL12	4,52E-12	2,27
SNX10	5,99E-08	2,27
ALDH1A2	4,13E-06	2,27
NP_689930,1	2,32E-13	2,26
CST6	1,69E-04	2,26
DNHD2	1,38E-08	2,26
MGLL	1,09E-05	2,26
IL8RB	1,99E-09	2,26
ASPA	1,01E-16	2,26
SLC9A3R2	2,10E-06	2,26
TNFSF13	8,17E-11	2,25
TM6SF1	1,66E-13	2,25
GABARAPL3	1,21E-12	2,25

GIMAP4	3,30E-07	2,25
SERINC1	4,85E-10	2,25
RERG	2,14E-10	2,25
CXCL16	1,34E-06	2,25
CYP3A5	3,72E-09	2,25
RASSF2	5,83E-07	2,24
CD69	1,46E-07	2,24
SCEL	1,50E-07	2,24
DYNLRB2	6,75E-07	2,24
HHIP	5,47E-13	2,24
SLC15A3	4,56E-08	2,23
ICAM5	1,03E-07	2,23
SLC11A1	3,62E-13	2,23
C1QTNF7	3,02E-19	2,23
FZD4	1,06E-12	2,23
FAM134B	5,56E-09	2,22
EFCBP1	5,80E-14	2,22
SNRK	3,53E-15	2,22
FRMD3	1,06E-15	2,22
APOL3	4,17E-08	2,21
PER1	1,44E-06	2,21
C1ORF115	2,78E-12	2,21
SH3BGRL2	7,24E-08	2,21
CPVL	7,70E-06	2,20
CNTN6	8,66E-21	2,20
LPXN	5,73E-07	2,20
RCAN2	1,77E-06	2,19
TFPI	6,45E-04	2,19
UNC13B	9,21E-09	2,19
CGN	3,00E-04	2,19
AP1S2	1,95E-07	2,19
CMAH	3,55E-05	2,19
RTN1	7,83E-11	2,19
FAT4	4,06E-09	2,19
PTPRM	1,18E-08	2,18
MACROD2	5,35E-06	2,18
C5	3,79E-04	2,18
KIT	8,17E-05	2,18
KIAA1324L	4,73E-08	2,18
C9ORF5	1,09E-09	2,18
CD300LF	9,46E-12	2,18
TDRD10	3,38E-09	2,18
TM7SF4	9,95E-10	2,18
HRASLS3	1,83E-04	2,17
AKAP13	1,03E-10	2,17
NP_059135,2	1,52E-13	2,17
AK1	8,82E-11	2,17
DAAM2	3,21E-06	2,16
GPC3	3,91E-06	2,16
TSC22D3	1,15E-05	2,16
MICALCL	3,90E-10	2,16
RECK	6,40E-11	2,15
SLC31A2	4,04E-15	2,15
PTPLA	8,80E-06	2,15

TXNIP	5,62E-06	2,15
RAI2	2,18E-12	2,15
SOD3	1,84E-03	2,14
SOX18	2,37E-04	2,14
RSPO2	3,80E-21	2,14
SHE	8,68E-13	2,14
HSPB6	2,02E-06	2,14
C5ORF23	2,86E-07	2,14
RARA	3,58E-06	2,14
TREM2	4,32E-05	2,14
STEAP4	4,89E-08	2,13
HLA-DQB1	4,01E-04	2,13
CTSO	9,39E-09	2,13
DPT	3,00E-04	2,13
SAHH3_HUMAN	9,16E-08	2,13
CCDC85A	2,22E-19	2,13
SASH1	7,59E-15	2,13
SPN	7,77E-11	2,13
DOCK8	2,37E-07	2,13
NP_620419,2	2,24E-06	2,13
ZMYND15	1,11E-10	2,13
C13ORF30	1,50E-07	2,12
SERPING1	3,67E-05	2,12
ANKRD1	4,89E-15	2,12
CTNNAL1	4,24E-08	2,12
WFDC1	1,33E-14	2,12
ARPC3	5,61E-07	2,12
MOSC2	2,20E-10	2,12
FAM82C	3,39E-18	2,12
SLC40A1	1,85E-04	2,11
NEXN	2,38E-08	2,11
ADHFE1	2,12E-09	2,11
SULT1A1	1,44E-09	2,11
CFL2	2,10E-11	2,11
SPATA18	2,88E-08	2,11
SH2B3	9,55E-10	2,11
PRELP	8,12E-05	2,11
STAC	2,08E-14	2,11
GRRP1	9,95E-08	2,10
LOH11CR2A	5,97E-08	2,10
RAMP2	1,28E-14	2,10
CBX7	2,03E-12	2,10
AQP1	8,66E-06	2,10
PCDH17	7,70E-07	2,10
OSCAR	5,23E-12	2,10
REEP5	1,35E-08	2,09
ITPR1	1,94E-07	2,09
CAV2	3,67E-05	2,09
ERP27	2,19E-04	2,09
TMBIM1	1,92E-09	2,09
EPB41L3	7,69E-07	2,09
HSPB8	3,16E-09	2,09
DUOXA1	9,67E-09	2,09
CD53	8,43E-06	2,09

AIF1	1,71E-05	2,09
ALDH1A1	9,79E-03	2,08
C1QB	3,89E-05	2,08
SOSTDC1	9,64E-04	2,08
NFKBIZ	4,85E-06	2,08
NP_694996,3	7,03E-12	2,08
MAP3K8	1,80E-06	2,07
SH3GL3	1,82E-07	2,07
COX4I2	1,41E-09	2,07
SAMD9L	2,34E-09	2,07
APOLD1	4,24E-06	2,07
NP_056410,2	7,88E-13	2,07
ICAM2	1,57E-06	2,06
NP_659495,1	5,21E-13	2,06
KLRB1	2,52E-04	2,06
BCL2A1	2,35E-07	2,06
CASQ2	7,13E-15	2,06
IFIT2	2,30E-06	2,06
CD34	1,72E-05	2,06
C1QC	1,49E-05	2,06
N4BP1_HUMAN	7,20E-11	2,06
ZFP106	1,66E-13	2,05
PRKCZ	2,92E-10	2,05
SEMA3B	1,07E-10	2,05
Q68DG2_HUMAN	2,22E-19	2,05
HCST	2,05E-06	2,05
ZNF331	6,98E-05	2,05
HNMT	4,97E-06	2,05
ID4	1,62E-13	2,05
NP_001025167,1	2,36E-08	2,05
FMO5	2,05E-05	2,05
FCHO2	5,81E-08	2,05
PRICKLE2	1,23E-07	2,04
MMRN1	6,65E-12	2,04
FCGR3B	2,41E-09	2,04
AIF1_HUMAN	2,64E-06	2,04
MT1M	2,53E-04	2,04
ANK3	3,56E-07	2,04
CENTD3	6,78E-11	2,03
SRPX	1,03E-04	2,03
BMP2	1,67E-09	2,03
MAML1	1,07E-07	2,03
HLF	2,83E-11	2,03
DDAH1	2,72E-05	2,03
SIGLEC11	1,57E-11	2,02
IFIT1	1,96E-04	2,02
HEG1	2,59E-07	2,02
SLC27A3	1,46E-06	2,02
PLA2G10	5,44E-04	2,02
GPM6B	4,48E-10	2,02
NPR1	6,03E-10	2,02
TMC5	1,92E-03	2,02
RRAS	4,45E-07	2,02
ST3GAL5	1,09E-04	2,02

CAMP	1,38E-12	2,02
ALOX15B	4,40E-04	2,01
SESN1	1,54E-08	2,01
DPYD	5,16E-06	2,01
DARC	5,29E-04	2,01
DEFA1	7,61E-07	2,01
PLEKHC1	3,31E-06	2,00
CAPSL	1,43E-06	2,00
GRAMD2	4,04E-11	2,00

Genes up-regulated in NSCLC

Gene ID	**adj. p-value**	**Fold change**
SPP1	2,76E-17	14,52
MMP1	5,20E-11	10,74
KRT6A	3,85E-05	10,39
KRT17	1,86E-06	9,44
CTHRC1	2,76E-17	7,62
S100A2	2,21E-05	7,44
MMP11	1,29E-11	7,14
TMPRSS4	1,04E-08	6,85
CDC20	1,59E-13	6,82
KRT6B	7,41E-04	6,15
P11388-2	9,29E-14	6,07
COL7A1	4,99E-09	6,07
GJB2	2,42E-08	5,98
KRT5	5,73E-04	5,86
MMP12	1,47E-08	5,64
SERPINB5	6,48E-05	5,48
AKR1B10	1,35E-03	5,47
PYCR1	1,83E-17	5,43
CALML3	7,23E-04	5,29
KRT6C	1,12E-03	5,13
CCNB2	1,46E-14	5,00
KRT15	1,51E-04	4,96
SLC2A1	2,13E-08	4,89
SULF1	3,22E-13	4,79
C20ORF42	6,65E-09	4,68
IGFBP3	8,95E-11	4,57
MCM2	2,12E-11	4,46
TK1	6,94E-11	4,40
MMP9	3,94E-09	4,37
BIRC5	2,48E-12	4,31
COL1A1	2,94E-07	4,29
AURKB	4,25E-12	4,25
KIF2C	2,97E-13	4,20
ECE2	3,13E-11	4,15
UCHL1	4,06E-06	4,14
CDKN3	2,15E-12	4,08
KRT16	1,20E-03	4,08
TP63	2,17E-04	4,07
COL1A2	3,32E-12	4,04
CCNB1	3,37E-13	4,01
FOXM1	6,28E-11	4,01

KRT14	1,61E-03	3,99
MDK	1,51E-09	3,98
HMGB3	2,31E-10	3,97
THBS2	2,45E-10	3,95
GPR87	3,73E-06	3,92
IQGAP3	3,30E-11	3,84
ASPM	7,46E-12	3,82
NR_003287,1	1,29E-11	3,81
KIAA0101	2,24E-11	3,81
PSAT1	6,23E-12	3,80
LTF	1,42E-03	3,79
PNCK	3,87E-05	3,75
AK3L2	2,64E-11	3,73
LOXL2	7,12E-10	3,72
CDH3	5,45E-08	3,70
MYBL2	4,38E-11	3,65
PI3	1,26E-03	3,63
IGLV3-9	6,61E-04	3,63
PRC1	2,32E-12	3,60
COL10A1	1,09E-09	3,59
CEP55	1,43E-11	3,59
SPAG5	2,70E-13	3,58
TYMS	7,43E-12	3,57
GAPDH	6,77E-17	3,56
MMP3	7,42E-06	3,54
IGKV3D-7	1,29E-03	3,52
MMP10	6,55E-04	3,51
NM_016459,3	5,54E-05	3,50
PTTG2	4,38E-11	3,47
AKR1C2	8,10E-03	3,47
CXCL14	2,43E-04	3,46
IMA2_HUMAN	6,71E-13	3,46
TUBB3	3,12E-08	3,46
WDR72	1,16E-04	3,44
CP	1,66E-04	3,43
NM_006607,2	1,65E-12	3,43
IGHG3	2,05E-03	3,40
S100A7	1,61E-03	3,39
POSTN	3,46E-06	3,38
IGFBP2	6,77E-06	3,38
TUBB2B	1,07E-03	3,37
PPAP2C	5,39E-09	3,37
IGSF9	1,64E-08	3,36
DLG7	3,35E-12	3,36
CDC45L	1,39E-09	3,35
IGF2BP3	4,00E-06	3,34
CLCA2	1,30E-03	3,34
CABYR	2,57E-07	3,31
UBE2S	8,47E-11	3,31
POLQ	4,00E-11	3,30
IGKV3-20	8,79E-04	3,29
SPAG4	6,14E-12	3,29
LEG7_HUMAN	3,20E-03	3,29
CTSL2	3,02E-06	3,28

NME2	9,04E-16	3,27
TTK	8,69E-10	3,27
MLLT11	3,73E-06	3,25
RFC4	9,65E-11	3,24
NCAPG	5,90E-11	3,24
PROM2	2,20E-06	3,20
IGKV2-40	7,11E-04	3,19
SFN	8,15E-05	3,19
FAP	1,55E-08	3,19
COL5A2	4,88E-08	3,17
IGKV1-39	1,39E-03	3,16
TMEM132A	1,95E-12	3,15
EIF4EBP1	6,23E-07	3,14
ALDH3B2	2,97E-06	3,13
AURKA	6,28E-11	3,11
MAGED4	6,33E-10	3,09
MCM4	9,76E-11	3,08
IGKV2D-29	1,17E-03	3,07
MFAP2	4,38E-09	3,06
PBK	4,11E-09	3,06
GYLTL1B	5,53E-09	3,05
CNTNAP2	1,18E-04	3,05
MIF	3,13E-12	3,05
UBE2T	5,13E-11	3,04
SERPINB13	2,10E-03	3,03
SPRR1B	2,06E-03	3,03
GPT2	4,18E-09	2,99
CDCA8	6,33E-10	2,99
HIG2_HUMAN	3,19E-07	2,97
DSG3	2,31E-03	2,96
CENPF	2,17E-09	2,95
KRT80	3,50E-06	2,93
TRIP13	2,60E-08	2,93
IGKV1-6	1,61E-03	2,91
PAFAH1B3	1,81E-08	2,90
C16ORF75	1,94E-10	2,90
GREM1	3,01E-08	2,89
PLAU	4,37E-08	2,89
COL3A1	3,12E-13	2,88
ANLN	7,97E-10	2,88
PERP	3,67E-05	2,87
KIF23	3,21E-10	2,87
DDIT4	5,47E-08	2,86
ECT2	3,86E-08	2,85
HIST2H2AA4	4,13E-08	2,84
SAA2	6,84E-04	2,83
IL4I1	5,90E-11	2,82
SHMT2	2,22E-17	2,81
CA12	4,26E-05	2,80
C18ORF24	1,85E-10	2,80
SERPINE2	1,87E-07	2,79
CENPN	3,38E-09	2,78
FAM83D	8,57E-08	2,78
TPI1	3,17E-08	2,78

MXRA5	9,02E-07	2,77
TIMP1	1,74E-08	2,75
UHRF1	1,83E-10	2,74
PHGDH	3,56E-06	2,73
COL5A1	2,36E-05	2,73
KIF20A	3,29E-11	2,72
GCLC	7,23E-05	2,72
RAD51AP1	9,02E-08	2,71
MAD2L1	1,56E-09	2,71
UCK2	1,29E-11	2,70
KCRU_HUMAN	3,44E-06	2,69
SERPINB3	3,54E-03	2,69
BIK	1,34E-09	2,68
HIST1H2BD	3,30E-10	2,65
HIST2H2AC	1,11E-07	2,65
SCG5	9,80E-08	2,65
NMU	1,65E-05	2,65
ITGB4	5,87E-05	2,64
GGH	1,70E-06	2,64
MELK	3,13E-09	2,64
WDR86	6,85E-08	2,64
CA9	3,20E-05	2,64
C1ORF106	6,65E-07	2,64
TROAP	5,02E-09	2,59
FKBP4	1,52E-07	2,59
NPM3	2,33E-12	2,58
DSC3	3,07E-04	2,58
DAPL1	2,02E-02	2,56
PAICS	1,14E-11	2,56
KIF4A	3,67E-11	2,55
BUB1B	2,08E-11	2,55
BAIAP2L1	1,29E-07	2,55
GPI	1,06E-06	2,54
CKS1B	5,64E-09	2,53
SLC2A5	3,57E-12	2,53
IL20RB	2,02E-04	2,53
ALDH18A1	2,19E-21	2,52
CRABP2	2,54E-05	2,51
HN1	1,86E-08	2,51
FAKTS_HUMAN	1,42E-10	2,50
TPBG	2,41E-09	2,50
TIMELESS	2,97E-10	2,50
PRAME	5,55E-06	2,49
SPRR3	2,07E-02	2,49
TBB5_HUMAN	9,46E-12	2,48
LMNB2	1,53E-08	2,47
NR_002187,2	2,09E-10	2,46
BUB1	1,64E-10	2,45
WDHD1	6,46E-11	2,45
H2AFV	3,55E-03	2,44
S100A16	3,13E-05	2,43
Q4G0D9_HUMAN	1,07E-08	2,43
TNFRSF18	3,65E-08	2,43
NP_001015050,1	2,56E-06	2,43

ZIC2	1,38E-04	2,43
AIM2	2,81E-05	2,42
NCAPD2	4,09E-07	2,42
SORD	1,05E-09	2,41
RPL39L	4,90E-08	2,41
KNTC1	1,16E-12	2,40
CDH2	3,73E-04	2,39
NDC80	1,44E-09	2,39
PRDX4	3,39E-17	2,39
WDR66	2,61E-04	2,39
KIF14	3,87E-10	2,38
CEACAM5	4,76E-02	2,38
ARNTL2	6,36E-07	2,37
CCT5	5,01E-09	2,37
ERO1L	2,32E-07	2,37
PTGFRN	6,26E-09	2,37
HMGA1	5,95E-08	2,37
CD79A	4,12E-04	2,36
HOXC6	1,85E-06	2,35
KDELR3	1,81E-09	2,35
PFKP	4,42E-07	2,35
COCH	6,06E-06	2,34
CCNA2	7,20E-10	2,34
MAGEA3	3,64E-04	2,34
HN1L_HUMAN	3,00E-10	2,34
DTL	4,89E-08	2,34
SRPX2	1,44E-07	2,33
TRIM16L	4,60E-04	2,33
NCAPH	5,93E-09	2,33
ATF5	5,46E-09	2,32
POU2AF1	3,01E-06	2,32
PDIA4	4,51E-13	2,32
CXCL13	1,78E-05	2,32
RBM35A	1,60E-05	2,32
ANKRD22	1,54E-06	2,32
KDELR2	2,82E-14	2,32
PAK1	9,63E-09	2,32
KIF11	9,97E-10	2,31
CENPA	2,53E-08	2,31
OIP5	1,80E-07	2,31
ALDOC	3,74E-06	2,30
GMNN	4,98E-09	2,30
PMAIP1	9,61E-07	2,30
CENPM	7,40E-08	2,30
FAM64A	1,47E-07	2,30
HOXB7	2,18E-06	2,30
RNASEH2A	3,60E-08	2,30
ANGPTL4	4,99E-04	2,29
H2AFX	6,49E-07	2,29
STRA6	1,11E-06	2,29
NO55_HUMAN	1,18E-11	2,29
EGLN3	2,45E-06	2,29
SRD5A1	5,54E-10	2,28
LEPREL2	1,19E-06	2,28

MRPL12	1,90E-11	2,28
NUP155	6,61E-10	2,27
SPINK1	1,28E-02	2,27
ACTL6A	3,07E-06	2,27
TPX2	2,45E-08	2,26
SFRP2	2,25E-03	2,26
CST1	3,64E-04	2,26
HIST1H2BH	5,37E-07	2,25
MAGEA9B	7,16E-03	2,25
STX1A	9,33E-07	2,25
THOC3	1,54E-06	2,25
CHEK1	4,46E-09	2,25
RPS15	1,71E-06	2,25
BXDC2	3,45E-07	2,25
IRF6	3,67E-05	2,24
C15ORF48	1,53E-04	2,24
LSR	2,31E-05	2,24
SPTBN2	1,18E-09	2,23
PKP3	2,05E-05	2,23
DTYMK	2,44E-11	2,22
GCNT3	1,25E-03	2,22
COMP	2,26E-03	2,22
BCL11A	2,32E-04	2,22
MSTO1	1,46E-12	2,22
MRPS12	3,60E-09	2,21
LAPTM4B	7,22E-06	2,21
KIF26B	9,81E-10	2,21
NDRG1	4,18E-06	2,20
CRKRS	7,97E-05	2,20
C6ORF129	1,62E-15	2,20
DERL3	5,19E-07	2,20
KIAA1199	1,48E-04	2,19
RANBP1	5,66E-07	2,19
ITM2C	1,13E-07	2,19
CXCL6	3,49E-03	2,19
LAGE3	2,49E-10	2,19
TCN1	8,37E-03	2,19
SOX4	1,83E-08	2,19
SLC7A5	3,56E-05	2,19
PTPRZ1	2,08E-03	2,19
IDH2	1,54E-09	2,19
SPRR2A	7,67E-03	2,19
SPRR2D	1,34E-02	2,18
FKBP11	1,40E-06	2,18
TPD52L1	4,74E-05	2,18
RAD54L	1,81E-09	2,18
WFDC3	9,23E-04	2,18
HIST1H1C	7,03E-06	2,18
NP_001017964,1	1,65E-09	2,17
CDC2	3,06E-07	2,16
CCNE2	5,70E-08	2,16
OCIAD2	5,48E-07	2,16
Q4KMW4_HUMAN	7,96E-06	2,16
BARX1	7,67E-04	2,16

CKAP4	8,35E-10	2,16
NUDT1	1,91E-09	2,15
HMMR	8,53E-09	2,15
FNDC1	4,69E-06	2,15
GINS2	4,37E-06	2,15
SRM	1,16E-05	2,15
PIM2	2,64E-04	2,15
ADH7	4,37E-02	2,14
RPL22L1	1,48E-07	2,14
EXOSC4	4,68E-10	2,14
TUBG1	4,60E-08	2,13
TMPRSS11E2	1,09E-03	2,13
SESN3	4,63E-04	2,13
ATAD2	3,67E-09	2,13
KIFC1_HUMAN	3,78E-07	2,13
MARCKSL1	3,85E-07	2,12
EEF1A2	8,01E-03	2,12
TNC	2,23E-04	2,12
JUP	1,65E-04	2,12
BTBD11	2,11E-06	2,12
CLDN10	1,72E-03	2,12
COL17A1	2,22E-04	2,11
SLC25A10	1,24E-06	2,11
NDUFA4L2	3,49E-03	2,11
PPIF	1,20E-08	2,11
ALPK2	1,55E-06	2,11
CDCA4	3,58E-08	2,11
MTHFD2	1,66E-07	2,10
CLDN1	1,53E-02	2,10
CKS2	4,58E-06	2,10
C4ORF7	1,79E-02	2,10
C6ORF125	1,56E-10	2,10
GCLM	1,83E-03	2,10
CDCA5	9,55E-10	2,10
HS3ST3A1	1,44E-05	2,10
RGS17	6,83E-05	2,09
PSMD2	1,38E-06	2,09
GMPS	5,48E-08	2,09
RPP40	2,67E-08	2,09
ABCC5	1,87E-04	2,09
MTP18_HUMAN	1,04E-09	2,08
MRPS17	1,90E-08	2,08
SLC39A14	4,70E-08	2,08
CD24L4	1,56E-04	2,08
DKC1	3,06E-10	2,08
SLC9A3R1	2,75E-04	2,08
TMEM79	1,89E-06	2,08
DNAJB11	4,09E-10	2,08
FEN1	9,76E-11	2,07
TMEM45A	2,87E-04	2,07
CARM1	6,63E-08	2,07
SGPL1	1,31E-15	2,07
HIST1H2AB	2,87E-07	2,07
MLZE	8,39E-05	2,07

C3ORF21	1,48E-06	2,07
ADM	6,28E-04	2,07
EYA2	9,16E-05	2,06
POLE2	1,52E-08	2,06
SLC4A11	1,53E-04	2,06
PTTG3	2,23E-07	2,06
CHSS2_HUMAN	2,25E-06	2,06
TRIM29	2,26E-03	2,06
CD27	2,41E-03	2,06
FGFBP1	4,44E-02	2,06
FAM83A	7,37E-04	2,05
TMEM14A	2,24E-04	2,05
HELLS	2,52E-08	2,05
JSRP1	1,47E-05	2,05
HSPB1	2,19E-03	2,04
DSC2	1,90E-03	2,04
ABCA12	5,97E-06	2,04
CDT1	4,13E-07	2,04
SRPRB	3,08E-14	2,04
LOX	8,48E-07	2,03
DDX39	3,70E-11	2,03
RAB26	4,05E-09	2,03
MAGED1	1,57E-07	2,03
FAM83H	1,07E-04	2,03
FAM57A	5,38E-08	2,03
CSTF2	2,04E-11	2,03
PLOD1	4,68E-07	2,03
ENO2	1,15E-05	2,03
WNT5B	3,95E-06	2,03
ARHGEF19	4,32E-09	2,02
RGMA	1,21E-03	2,02
C17ORF53	1,40E-07	2,02
PKM2	3,07E-05	2,02
FST	3,89E-03	2,02
DDR1_HUMAN	2,26E-05	2,01
XTP3A_HUMAN	2,12E-08	2,01
C16ORF33	5,67E-09	2,01

Table 4 Processes up regulated in cancer versus cancer-free tissue

Genes	NGR	NG	Hyp	Hyp*	Annotations
32 genes	191(29095)	32(378)	4.29289e-26	8.80042e-24	GO:0007067 :mitosis (BP)
32 genes	240(29095)	32(378)	6.51952e-23	6.68251e-21	GO:0051301 :cell division (BP)
41 genes	459(29095)	41(378)	2.66984e-22	1.82439e-20	GO:0007049 :cell cycle (BP)
26 genes	162(29095)	26(378)	6.39059e-21	3.27518e-19	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP)
25 genes	155(29095)	25(378)	3.22944e-20	1.32407e-18	GO:0007067 :mitosis (BP) GO:0051301 :cell division (BP)
28 genes	223(29095)	28(378)	1.78282e-19	6.09131e-18	GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP)
23 genes	151(29095)	23(378)	4.01804e-18	1.17671e-16	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP)
14 genes	81(29095)	14(378)	2.54768e-12	6.52843e-11	GO:0008544 :epidermis development (BP)
16 genes	146(29095)	16(378)	9.00685e-11	2.05156e-09	GO:0006260 :DNA replication (BP)
7 genes	13(29095)	7(378)	9.48516e-11	1.94446e-09	GO:0007051 :spindle organization (BP)
6 genes	9(29095)	6(378)	3.75723e-10	7.00212e-09	GO:0007049 :cell cycle (BP) GO:0007051 :spindle organization (BP)

5 genes	7(29095)	5(378)	7.4109e-09	1.16864e-07	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP) GO:0007051 :spindle organization (BP)
5 genes	7(29095)	5(378)	7.4109e-09	1.16864e-07	GO:0007049 :cell cycle (BP) GO:0048015 :phosphoinositide-mediated signaling (BP) GO:0007051 :spindle organization (BP)
8 genes	35(29095)	8(378)	1.30619e-08	1.91264e-07	GO:0048015 :phosphoinositide-mediated signaling (BP)
5 genes	8(29095)	5(378)	1.95514e-08	2.50502e-07	GO:0001568 :blood vessel development (BP) GO:0030199 :collagen fibril organization (BP)
5 genes	8(29095)	5(378)	1.95514e-08	2.50502e-07	GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP) GO:0007051 :spindle organization (BP)
23 genes	452(29095)	23(378)	3.40935e-08	4.11127e-07	GO:0006915 :apoptosis (BP)
6 genes	18(29095)	6(378)	7.5204e-08	8.5649e-07	GO:0051301 :cell division (BP) GO:0031145 :anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process (BP)
5 genes	10(29095)	5(378)	8.61128e-08	9.29111e-07	GO:0007067 :mitosis (BP) GO:0007018 :microtubule-based movement (BP)
4 genes	5(29095)	4(378)	1.38787e-07	1.42257e-06	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP)

					GO:0048015 :phosphoinositide-mediated signaling (BP) GO:0007051 :spindle organization (BP)
7 genes	34(29095)	7(378)	2.35058e-07	2.29461e-06	GO:0030216 :keratinocyte differentiation (BP)
6 genes	22(29095)	6(378)	2.89261e-07	2.69539e-06	GO:0007067 :mitosis (BP) GO:0006468 :protein amino acid phosphorylation (BP)
4 genes	6(29095)	4(378)	4.1208e-07	3.51985e-06	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP) GO:0007051 :spindle organization (BP)
4 genes	6(29095)	4(378)	4.1208e-07	3.51985e-06	GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP) GO:0048015 :phosphoinositide-mediated signaling (BP) GO:0007051 :spindle organization (BP)
6 genes	25(29095)	6(378)	6.6433e-07	5.44751e-06	GO:0030199 :collagen fibril organization (BP)
4 genes	7(29095)	4(378)	9.51639e-07	7.50331e-06	GO:0007067 :mitosis (BP) GO:0051301 :cell division (BP) GO:0007076 :mitotic chromosome condensation (BP)
7 genes	42(29095)	7(378)	1.07803e-06	8.18504e-06	GO:0006096 :glycolysis (BP)
6 genes	27(29095)	6(378)	1.08627e-06	7.95303e-06	GO:0006508 :proteolysis (BP) GO:0008152 :metabolic process (BP)

22 genes	512(29095)	22(378)	1.19441e-06	8.44323e-06	GO:0007155 :cell adhesion (BP)
4 genes	8(29095)	4(378)	1.88373e-06	1.28721e-05	GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP) GO:0007093 :mitotic cell cycle checkpoint (BP)
5 genes	17(29095)	5(378)	1.9617e-06	1.25671e-05	GO:0008544 :epidermis development (BP) GO:0030216 :keratinocyte differentiation (BP)
5 genes	17(29095)	5(378)	1.9617e-06	1.25671e-05	GO:0007049 :cell cycle (BP) GO:0051301 :cell division (BP) GO:0031145 :anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0001501 :skeletal system development (BP) GO:0043589 :skin morphogenesis (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP) GO:0006468 :protein amino acid phosphorylation (BP) GO:0034501 :protein localization to kinetochore (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0001568 :blood vessel development (BP) GO:0030199 :collagen fibril organization (BP) GO:0032964 :collagen biosynthetic process (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0006468 :protein amino acid phosphorylation (BP)

					GO:0007051 :spindle organization (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0007052 :mitotic spindle organization (BP) GO:0007051 :spindle organization (BP)
3 genes	3(29095)	3(378)	2.17576e-06	1.17376e-05	GO:0006915 :apoptosis (BP) GO:0008152 :metabolic process (BP)
9 genes	89(29095)	9(378)	2.44115e-06	1.28317e-05	GO:0007018 :microtubule-based movement (BP)
5 genes	18(29095)	5(378)	2.68728e-06	1.37723e-05	GO:0006508 :proteolysis (BP) GO:0030574 :collagen catabolic process (BP)
5 genes	20(29095)	5(378)	4.75972e-06	2.37986e-05	GO:0007067 :mitosis (BP) GO:0007049 :cell cycle (BP) GO:0006468 :protein amino acid phosphorylation (BP)
12 genes	182(29095)	12(378)	5.11292e-06	2.49559e-05	GO:0006916 :anti-apoptosis (BP)

Table 5 Processes down regulated in NSCLC versus cancer-free normal tissue

Genes	NGR	NG	Hyp	Hyp*	Annotations
25 genes	227(29095)	25(544)	1.41322e-12	4.93214e-10	GO:0006954 :inflammatory response (BP)
76 genes	1871(29095)	76(544)	1.50838e-10	2.63212e-08	GO:0007165 :signal transduction (BP)
19 genes	164(29095)	19(544)	2.92379e-10	3.40134e-08	GO:0007166 :cell surface receptor linked signaling pathway (BP)
32 genes	512(29095)	32(544)	3.49252e-09	3.04723e-07	GO:0007155 :cell adhesion (BP)

31 genes	531(29095)	31(544)	2.96388e-08	2.06879e-06	GO:0055114 :oxidation reduction (BP)
13 genes	99(29095)	13(544)	4.22677e-08	2.45857e-06	GO:0045087 :innate immune response (BP)
8 genes	29(29095)	8(544)	4.31052e-08	2.1491e-06	GO:0006958 :complement activation, classical pathway (BP)
6 genes	17(29095)	6(544)	4.31769e-07	1.88359e-05	GO:0045087 :innate immune response (BP) GO:0006958 :complement activation, classical pathway (BP)
26 genes	459(29095)	26(544)	6.88845e-07	2.67119e-05	GO:0006955 :immune response (BP)
6 genes	19(29095)	6(544)	9.16902e-07	3.19999e-05	GO:0019370 :leukotriene biosynthetic process (BP)
7 genes	30(29095)	7(544)	1.07754e-06	3.41874e-05	GO:0009612 :response to mechanical stimulus (BP)
9 genes	58(29095)	9(544)	1.2331e-06	3.31041e-05	GO:0051384 :response to glucocorticoid stimulus (BP)
9 genes	58(29095)	9(544)	1.2331e-06	3.31041e-05	GO:0007165 :signal transduction (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP)
5 genes	12(29095)	5(544)	1.59414e-06	3.97395e-05	GO:0045730 :respiratory burst (BP)
4 genes	6(29095)	4(544)	1.75999e-06	4.09492e-05	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0006898 :receptor-mediated endocytosis (BP)
5 genes	13(29095)	5(544)	2.55059e-06	5.56348e-05	GO:0010744 :positive regulation of macrophage derived foam cell differentiation (BP)
38 genes	898(29095)	38(544)	3.03717e-06	6.23513e-05	GO:0007275 :multicellular organismal development (BP)
6 genes	23(29095)	6(544)	3.20112e-06	6.20661e-05	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP)

4 genes	7(29095)	4(544)	4.04574e-06	7.43139e-05	GO:0042493 :response to drug (BP) GO:0032570 :response to progesterone stimulus (BP) GO:0009612 :response to mechanical stimulus (BP)
9 genes	67(29095)	9(544)	4.2657e-06	7.44365e-05	GO:0016337 :cell-cell adhesion (BP)
3 genes	3(29095)	3(544)	6.50111e-06	9.86473e-05	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP) GO:0030593 :neutrophil chemotaxis (BP)
3 genes	3(29095)	3(544)	6.50111e-06	9.86473e-05	GO:0043065 :positive regulation of apoptosis (BP) GO:0006979 :response to oxidative stress (BP) GO:0032355 :response to estradiol stimulus (BP)
3 genes	3(29095)	3(544)	6.50111e-06	9.86473e-05	GO:0010552 :positive regulation of gene-specific transcription from RNA polymerase II promoter (BP) GO:0006644 :phospholipid metabolic process (BP)
8 genes	54(29095)	8(544)	6.93242e-06	0.000100809	GO:0032355 :response to estradiol stimulus (BP)
5 genes	16(29095)	5(544)	8.26321e-06	0.000115354	GO:0001937 :negative regulation of endothelial cell proliferation (BP)
7 genes	41(29095)	7(544)	9.96006e-06	0.000133695	GO:0006898 :receptor-mediated endocytosis (BP)
5 genes	17(29095)	5(544)	1.15263e-05	0.000148988	GO:0032870 :cellular response to hormone stimulus (BP)
6 genes	29(29095)	6(544)	1.36943e-05	0.000170689	GO:0007585 :respiratory gaseous exchange (BP)
5 genes	18(29095)	5(544)	1.57143e-05	0.000189114	GO:0030593 :neutrophil chemotaxis (BP)

4 genes	10(29095)	4(544)	2.32115e-05	0.000270028	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0006954 :inflammatory response (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP)
17 genes	280(29095)	17(544)	2.42188e-05	0.000272657	GO:0008284 :positive regulation of cell proliferation (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0007507 :heart development (BP) GO:0001569 :patterning of blood vessels (BP) GO:0001666 :response to hypoxia (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0008284 :positive regulation of cell proliferation (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0007204 :elevation of cytosolic calcium ion concentration (BP) GO:0042310 :vasoconstriction (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0010552 :positive regulation of gene-specific transcription from RNA polymerase II promoter (BP) GO:0001570 :vasculogenesis (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0007186 :G-protein coupled receptor protein signaling pathway (BP) GO:0007204 :elevation of cytosolic calcium ion concentration (BP) GO:0051482 :elevation of cytosolic calcium ion concentration during G-protein signaling, coupled to IP3 second messenger (phospholipase C activating) (BP)

3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0045944 :positive regulation of transcription from RNA polymerase II promoter (BP) GO:0051789 :response to protein stimulus (BP)
3 genes	4(29095)	3(544)	2.56418e-05	0.000235499	GO:0010744 :positive regulation of macrophage derived foam cell differentiation (BP) GO:0010886 :positive regulation of cholesterol storage (BP)
5 genes	21(29095)	5(544)	3.56294e-05	0.000318837	GO:0032570 :response to progesterone stimulus (BP)
6 genes	34(29095)	6(544)	3.58176e-05	0.000312509	GO:0006959 :humoral immune response (BP)
4 genes	11(29095)	4(544)	3.59356e-05	0.000298608	GO:0006935 :chemotaxis (BP) GO:0007166 :cell surface receptor linked signaling pathway (BP)

Figure 1 Heatmap with differentially expressed genes in NSCLC. Color on the heatmap depicts $\log_2$-expression value: red- high expression, green- low expression. Sidebar presents tissue type: blue – normal control, red – tumor tissue.

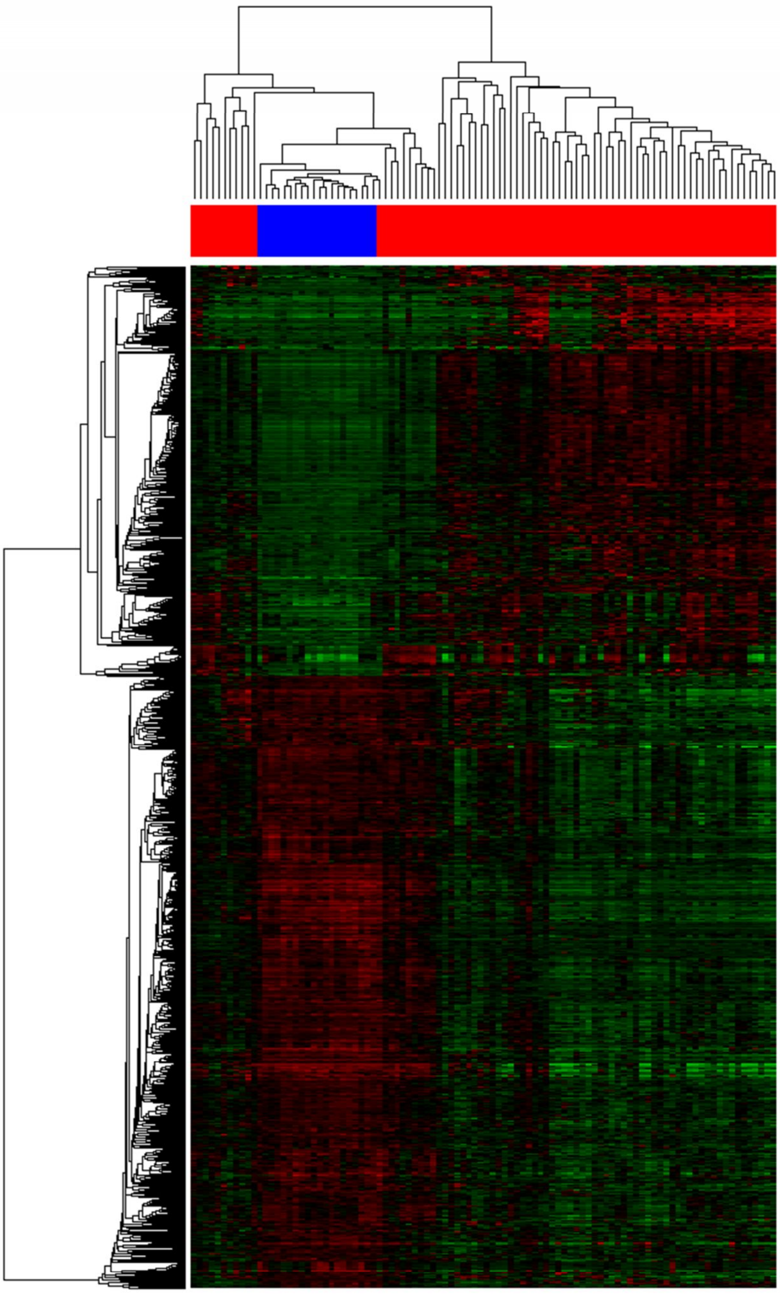

Figure 2 Heatmap with differentially expressed genes between SCC and other subtypes. Color on the heatmap depicts $\log_2$-expression value: red- high expression, green- low expression. Sidebar presents different subtypes: red – SCC, pink – BAC, orange – AC.