

Supplementary Materials Table 1: PANTHER Analysis of Pathways Targeted by DAC in Primary Lung Cancers

A. Potentially ($p < 0.05$) enriched functional groups among the genes suppressed in tumor, but activated by DAC treatment

Groups	Genes in the database	Genes in the dataset	Expected genes in the dataset	p value
<i>By biological process</i>				
Asymmetric protein localization	21	2	0	8.48E-04
Cation transport	491	5	1	3.07E-03
Ion transport	628	5	1	8.54E-03
Protein targeting and localization	213	3	0	9.12E-03
Cell adhesion	556	4	1	2.55E-02
Other protein targeting and localization	13	1	0	2.57E-02
DNA replication	126	2	0	2.67E-02
Protein-lipid modification	16	1	0	3.16E-02
Proteolysis	891	5	2	3.30E-02
Nucleoside, nucleotide and nucleic acid metabolism	3056	11	6	3.89E-02
Cell cycle	935	5	2	3.94E-02
<i>By molecular function</i>				
Serine protease inhibitor	71	2	0	9.09E-03
RNA helicase	90	2	0	1.43E-02
Cell junction protein	110	2	0	2.08E-02
Protease inhibitor	119	2	0	2.40E-02
Exodeoxyribonuclease	14	1	0	2.77E-02
Storage protein	14	1	0	2.77E-02
Select regulatory molecule	1154	6	2	2.78E-02
Nucleic acid binding	2605	10	5	3.34E-02
Glutamate receptor	20	1	0	3.93E-02
Metalloprotease	164	2	0	4.31E-02
G-protein modulator	393	3	1	4.45E-02
Helicase	170	2	0	4.60E-02
<i>By pathway</i>				
Metabotropic glutamate receptor group III pathway	63	2	0	7.23E-03
PDGF signaling pathway	208	3	0	8.55E-03

B. Potentially ($p < 0.05$) enriched functional groups among the genes up-regulated in tumor but suppressed by DAC treatment

Groups	Genes in the database	Genes in the dataset	Expected genes in the dataset	p value
<i>By biological process</i>				
Signal transduction	3278	58	31	3.36E-06
Protein modification	1117	27	11	1.30E-05
Protein metabolism and modification	2828	46	27	2.91E-04
Carbohydrate metabolism	572	14	5	1.45E-03
Intracellular signaling cascade	848	18	8	1.60E-03
Developmental processes	2040	33	20	2.43E-03
Cell adhesion-mediated signaling	353	10	3	2.45E-03
Cell communication	1148	21	11	3.93E-03
Protein biosynthesis	526	0	5	6.17E-03
Other carbon metabolism	84	4	1	9.17E-03
Other polysaccharide metabolism	135	5	1	1.03E-02
Protein phosphorylation	658	13	6	1.19E-02
Proteolysis	891	16	9	1.31E-02
Cell structure and motility	1127	19	11	1.33E-02
Carbohydrate transport	51	3	0	1.35E-02
Other developmental process	101	4	1	1.69E-02
Cell motility	340	8	3	1.79E-02
Cell structure	703	13	7	1.94E-02
Cell adhesion	556	11	5	1.97E-02
Cell proliferation and differentiation	1019	17	10	2.04E-02
Biological process unclassified	5807	70	56	2.17E-02
Fatty acid beta-oxidation	24	2	0	2.27E-02
Receptor mediated endocytosis	112	4	1	2.36E-02
Protein acetylation	25	2	0	2.45E-02
Other neuronal activity	125	4	1	3.33E-02
Miscellaneous	129	4	1	3.67E-02
Other homeostasis activities	76	3	1	3.75E-02
JAK-STAT cascade	82	3	1	4.52E-02
Fatty acid desaturation	5	1	0	4.68E-02
Homeostasis	204	5	2	4.82E-02
Ectoderm development	644	11	6	4.83E-02
<i>By molecular function</i>				
Protein phosphatase	141	6	1	2.62E-03
Cell adhesion molecule	358	10	3	2.70E-03
Phosphatase	255	8	2	3.55E-03
Protease	528	12	5	5.53E-03
Myelin protein	12	2	0	6.11E-03
Transferase	866	16	8	1.02E-02
Molecular function unclassified	5425	67	52	1.52E-02
Oxidoreductase	610	12	6	1.59E-02
Ribosomal protein	418	0	4	1.77E-02
Ion channel	343	8	3	1.88E-02
Non-motor actin binding protein	166	5	2	2.29E-02
Other transfer/carrier protein	111	4	1	2.29E-02

Acyltransferase	113	4	1	2.43E-02
Oxygenase	115	4	1	2.57E-02
Transcription factor	1868	26	18	3.74E-02
Acetyltransferase	76	3	1	3.75E-02
Kinase inhibitor	33	2	0	4.06E-02
Hydrolase	707	12	7	4.20E-02
Voltage-gated ion channel	135	4	1	4.22E-02
Carbohydrate transporter	34	2	0	4.28E-02
DNA strand-pairing protein	5	1	0	4.68E-02
Dehydratase	36	2	0	4.74E-02
Phosphodiesterase	36	2	0	4.74E-02
Cytoskeletal protein	802	13	8	4.76E-02
By pathway				
Notch signaling pathway	50	3	0	1.28E-02
Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	161	5	2	2.04E-02
JAK/STAT signaling pathway	24	2	0	2.27E-02
Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway	195	5	2	4.11E-02
Interferon-gamma signaling pathway	35	2	0	4.51E-02
Inflammation mediated by chemokine and cytokine signaling pathway	345	7	3	5.04E-02
