

Supplementary table 1 - Results of GO annotation analysis for differentially expressed genes between E18.5 transgenic (Nkx2.1-Cre) and E18.5 control lungs

For the description of the statistical analysis see in the materials and methods section

Upregulated in transgene

GO term	P-value	Matches
regulation of cell communication	8.91E-10	145
regulation of signaling	3.40E-09	144
tissue development	3.88E-08	96
regulation of signal transduction	2.88E-07	121
negative regulation of cellular process	3.6861E-06	173
developmental process	1.08229E-05	212
negative regulation of nitrogen compound metabolic process	3.35843E-05	99
animal organ development	4.13292E-05	135
multicellular organism development	5.65948E-05	186
anatomical structure development	0.00010333	198
negative regulation of cellular metabolic process	0.000204992	102
response to organic substance	0.000229543	120
negative regulation of macromolecule metabolic process	0.000238732	106
system development	0.000245075	167
regulation of molecular function	0.000257879	103
negative regulation of biological process	0.000274753	182
regulation of response to stimulus	0.000285001	142
cell proliferation	0.000308887	88
negative regulation of metabolic process	0.00075341	112
transmembrane receptor protein tyrosine kinase signaling pathway	0.000789796	36
regulation of multicellular organismal process	0.001879232	122
regulation of primary metabolic process	0.002244979	177
positive regulation of biological process	0.00246477	200
regulation of cell proliferation	0.002791757	74
regulation of catalytic activity	0.002794698	79
intracellular signal transduction	0.003790052	103
multicellular organismal process	0.004184216	252
regulation of cellular protein metabolic process	0.005121921	99
response to chemical	0.005180724	145
regulation of cellular metabolic process	0.005721308	179
epithelial cell proliferation	0.006884314	29
positive regulation of cellular process	0.006979719	180
regulation of signaling receptor activity	0.009438949	15

Downregulated in transgene

GO term	P-value	Matches
regulation of developmental process	0.000736	80
regulation of multicellular organismal process	0.002	89

regulation of protein serine/threonine kinase activity	0.009730279	29
negative regulation of cell communication	0.010275246	62
negative regulation of signaling	0.011379519	62
negative regulation of response to stimulus	0.012514824	70
regulation of MAP kinase activity	0.016653123	23
regulation of kinase activity	0.019677377	40
cellular response to organic substance	0.021363535	94
regulation of MAPK cascade	0.023280416	41
MAPK cascade	0.024161615	43
cell surface receptor signaling pathway	0.026495941	97
regulation of localization	0.02724886	105
regulation of epithelial cell proliferation	0.032002253	25
regulation of nitrogen compound metabolic process	0.032675792	168
regulation of protein kinase activity	0.033796028	37
regulation of cell death	0.036706664	72
signal transduction by protein phosphorylation	0.042708876	43
multicellular organismal homeostasis	0.042776122	30
negative regulation of cellular protein metabolic process	0.042814354	49
regulation of protein metabolic process	0.046964038	101
regulation of intracellular signal transduction	0.048322866	72
response to stress	0.048614391	126
negative regulation of protein metabolic process	0.048688384	51
positive regulation of cell communication	0.049514705	76