UBERON:0002048 lung

(Unique DEGs among top-100 found by the distance-based method, 48 genes)
2 genes are specifically directly related to lung
11 additional genes are related to lung

rps27rt: ribosomal protein S27, retrogene.

hepacam2: HEPACAM family member 2:

Required during prometaphase for centrosome maturation. Following poly-ADP-ribosylation (PARsylation) by TNKS, translocates from the Golgi apparatus to mitotic centrosomes and **plays a key role in the formation of robust microtubules for prompt movement of chromosomes- anchors** AKAP9/CG-NAP, a scaffold protein of the gamma-tubulin ring complex and promotes centrosome maturation.

dock9: dedicator of cytokinesis 9:

Guanine nucleotide-exchange factor (GEF) that activates CDC42 by exchanging bound GDP for free GTP. Overexpression induces filopodia formation.

nr3c2: nuclear receptor subfamily 3, group C, member 2:

Receptor for both mineralocorticoids (MC) such as aldosterone and glucocorticoids (GC) such as corticosterone or cortisol. Binds to mineralocorticoid response elements (MRE) and transactivates target genes. The **effect of MC is to increase ion and water transport** and thus raise extracellular fluid volume and blood pressure and lower potassium levels.

acta2: actin, alpha 2, smooth muscle, aorta:

The protein encoded by this gene belongs to the **actin family of proteins**, which are highly conserved proteins that play a role in cell motility, structure and integrity. Alpha, beta and gamma actin isoforms have been identified, with alpha actins being **a major constituent of the contractile apparatus**, while beta and gamma actins are involved in the regulation of cell motility. This actin is an alpha actin that is found in skeletal muscle.
Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.

bmp5: bone morphogenetic protein 5:

This gene encodes a secreted ligand of the TGF-beta (transforming growth factor-beta) superfamily of proteins. Ligands of this family bind various TGF-beta receptors leading to recruitment and activation of SMAD family transcription factors that regulate gene expression. The encoded preproprotein is proteolytically processed to generate each subunit of the disulfide-linked homodimer, which **plays a role in bone and cartilage development**. Mice with null mutations in this gene exhibit a short ear phenotype, which is characterized by reduced size of the external ear, altered size and shape of the sternum, and other skeletal and soft-tissue abnormalities.
Induces cartilage and bone formation.

calb1: calbindin 1:

Buffers cytosolic calcium. May stimulate a membrane Ca(2+)-ATPase and a 3',5'-cyclic nucleotide phosphodiesterase.

ccne1: cyclin E1:

Essential for the control of the cell cycle at the G1/S (start) transition.

chga: chromogranin A:

This gene encodes a member of the granin family of acidic secretory glycoproteins that are expressed in endocrine cells and neurons. The encoded preproprotein undergoes proteolytic processing to generate multiple functions peptides including pancreastatin, catestatin and serpinin. The encoded protein plays important roles in the neuroendocrine system including regulated secretion of peptide hormones and neurotransmitters.
Pancreastatin- Strongly inhibits glucose induced insulin release from the pancreas.

clu: clusterin:

The protein encoded by this gene is a secreted chaperone that can, under some stress conditions, also be found in the cell cytosol. It has been suggested to be involved in several basic biological events such as **cell death, tumor progression, and neurodegenerative disorders**. The encoded preproprotein undergoes proteolytic processing to generate a disulfide-linked heterodimeric mature protein comprised of alpha and beta subunits. Mice lacking the encoded protein exhibit increased severity of autoimmune myocarditis, faster progression of the acute inflammation to myocardial scarring and decreased brain injury following neonatal hypoxic-ischemic injury.
Functions as extracellular chaperone that prevents aggregation of nonnative proteins. Prevents stress-induced aggregation of blood plasma proteins. Inhibits formation of amyloid fibrils by APP, APOC2, B2M, CALCA, CSN3, SNCA and aggregation-prone LYZ variants (in vitro). Does not require ATP. Maintains partially unfolded proteins in a state appropriate for subsequent refolding by other chaperones, such as HSPA8/HSC70. Does not refold proteins by itself. Binding to cell surface receptors triggers internalization of the chaperone-client complex and subsequent lysosomal.

cnr1: cannabinoid receptor 1 (brain):

Involved in cannabinoid-induced CNS effects. Acts by inhibiting adenylate cyclase. Could be a receptor for anandamide. Inhibits L-type Ca(2+) channel current.

col1a2: collagen, type I, alpha 2:

This gene encodes the alpha-**2 subunit of the fibril-forming type I collagen, the most abundant protein of bone, skin and tendon extracellular matrices**. The encoded protein, in association with alpha-1 subunit, forms heterotrimeric type I procollagen that undergoes proteolytic processing during fibril formation. Mice harboring certain mutations in the encoded gene exhibit symptoms of moderate to severe forms of osteogenesis imperfecta. Type I collagen is a member of group I collagen (fibrillar forming collagen).

ctla2b: cytotoxic T **lymphocyte**-associated protein 2 beta:

Expressed in activated T-cell.

g6pc2: glucose-6-phosphatase, catalytic, 2:

This gene encodes an enzyme that belongs to the glucose-6-phosphatase catalytic subunit family. Members of this family catalyze the hydrolysis of glucose-6-phosphate, the terminal step in gluconeogenic and glycogenolytic pathways, to **release glucose into the bloodstream**. The family member encoded by this gene is **found specifically in pancreatic islets** but has not been shown to have phosphotransferase or phosphatase activity exhibited by a similar liver enzyme. The non-obese diabetic (NOD) mouse is a model for human type 1 diabetes, an autoimmune disease in which T lymphocytes attack and destroy insulin-producing pancreatic beta cells. In NOD mice, the protein encoded by this gene is a major target of cell-mediated autoimmunity. Variations in the human and mouse genes are associated with lower fasting plasma glucose levels.
May hydrolyze glucose-6-phosphate to glucose in the endoplasmic reticulum. May be responsible for glucose production through glycogenolysis and gluconeogenesis.

gcg: glucagons:

This gene encodes glucagon**, a pancreatic hormone that counteracts the action of insulin in the bloodstream**. The encoded protein is processed to generate glucagon and two other glucagon-like peptides, GLP1 and GLP2. Glucagon stimulates gluconeogenesis, glycogenolysis and lipolysis. GLP1 induces secretion of insulin, suppresses glucagon secretion and inhibits feeding. GLP2 induces intestinal absorption of glucose by stimulating the growth of intestinal cells and preventing apoptosis..
Glicentin may **modulate gastric acid secretion** and gastro-pyloro-duodenal activity.

gsta3: glutathione S-transferase, alpha 3:

Conjugation of reduced **glutathione** to a wide number of exogenous and endogenous hydrophobic electrophiles. This GST has a high catalytic activity for aflatoxin B1-8,9 epoxide.

gsta4: glutathione S-transferase, alpha 4:

Conjugation of reduced **glutathione** to a wide number of exogenous and endogenous hydrophobic electrophiles.

gstm1: glutathione S-transferase, mu 1:

Conjugation of reduced **glutathione** to a wide number of exogenous and endogenous hydrophobic electrophiles.

gstm2: glutathione S-transferase, mu 2:

Conjugation of reduced **glutathione** to a wide number of exogenous and endogenous hydrophobic electrophiles.

gstt1: glutathione S-transferase, theta 1:

Conjugation of reduced **glutathione** to a wide number of exogenous and endogenous hydrophobic electrophiles. Also binds steroids, bilirubin, carcinogens and numerous organic anions. Has dichloromethane dehalogenase activity.

gsto1: glutathione S-transferase omega 1:

This gene encodes **a member of the omega class of glutathione** S-transferase (GST) proteins. **GSTs are involved in the metabolism of xenobiotics and carcinogens**. There is evidence that the encoded protein is involved in the biotransformation of arsenic. Exhibits glutathione-dependent thiol transferase and dehydroascorbate reductase activities. Has S-(phenacyl)glutathione reductase activity. Has also glutathione S-transferase activity. Participates in the biotransformation of inorganic arsenic and reduces monomethylarsonic acid (MMA) and dimethylarsonic acid.

hdc: histidine decarboxylase:

Catalyzes the biosynthesis of histamine from histidine.

hes1: hes family bHLH transcription factor 1:

Transcriptional repressor of genes that require a bHLH protein for their transcription. May act as a negative regulator of myogenesis by inhibiting the functions of MYOD1 and ASH1 (By similarity). Binds DNA on N-box motifs- 5'-CACNAG-3' with high affinity and on E-box motifs- 5'-CANNTG-3' with low affinity. May **play a role in a functional FA core complex response to DNA cross- link damage**, being required for the stability and nuclear localization of FA core complex proteins, as well as for FANCD2 monoubiquitination in response to DNA damage.

hp: haptoglobin:

This gene encodes a plasma glycoprotein called haptoglobin that binds free hemoglobin. The encoded preproprotein undergoes proteolytic processing to generate alpha and beta subunits that form a disulfide-linked tetrameric protein that **plays an important role in the sequestration and clearance of extracorpuscular hemoglobin**. Mice lacking the encoded protein exhibit stunted development of lymphoid organs associated with lower counts of mature T and B cells in the blood and secondary lymphoid compartments.
As a result of hemolysis, hemoglobin is found to accumulate in the kidney and is secreted in the urine. Haptoglobin captures, and combines with free plasma hemoglobin to allow hepatic recycling of heme iron and to prevent kidney damage. **Haptoglobin also acts as an antioxidant**, has antibacterial activity and plays a role in modulating many aspects of the acute phase response. Hemoglobin/haptoglobin complexes are rapidely cleared by the macrophage CD163 scavenger receptor expressed on the surface of liver Kupfer cells through an endocytic lysosomal degradation pathway.

elavl2: ELAV like RNA binding protein 1

Binds RNA. Seems to recognize a GAAA motif. Can bind to its own 3'-UTR, the FOS 3'-UTR and the ID 3'-UTR.

iapp: islet amyloid polypeptide:

Selectively **inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle**, while not affecting adipocyte glucose metabolism.

idh1: isocitrate dehydrogenase 1 (NADP+), soluble:

ins1: insulin I:

This gene **encodes insulin**, a peptide hormone that plays a vital role in the regulation of carbohydrate and lipid metabolism. The encoded precursor protein undergoes proteolytic cleavage to produce a disulfide-linked heterodimeric functional protein that is stored in secretory granules. An increase in blood glucose levels, among others, induces the release of insulin from the secretory granules. Mice deficient in the functional hormone encoded by this gene develop diabetes mellitus.
Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

ins2: insulin II:

This gene **encodes insulin**, a peptide hormone that plays a vital role in the regulation of carbohydrate and lipid metabolism. The encoded precursor protein undergoes proteolytic cleavage to produce a disulfide-linked heterodimeric functional protein that is stored in secretory granules. An increase in blood glucose levels, among others, induces the release of insulin from the secretory granules. Mice deficient in the functional hormone encoded by this gene develop diabetes mellitus.
Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

isl1: ISL1 transcription factor, LIM/homeodomain:

Binds and **regulates the promoters of the insulin, glucagon and somatostatin genes**. Involved in the specificarion of motor neurons in cooperation with LHX3 and LDB1.

napsa: napsin A aspartic peptidase:

May be involved in **processing of pneumocyte** surfactant precursors.

lamb1: laminin B1:

Binding to cells via a high affinity receptor, laminin is thought to **mediate the attachment, migration and organization of cells into tissues during embryonic development** by interacting with other extracellular matrix components. Involved in the organization of the laminar architecture of the cerebral cortex (By similarity). It is probably required for the integrity of the basement membrane/glia limitans that serves as an anchor point for the endfeet of radial glial cells and **as a physical barrier to migrating neurons**.

lcn2: lipocalin 2:

Iron-trafficking protein involved in multiple **processes such as apoptosis, innate immunity and renal development**. Binds iron through association with 2,5-dihydroxybenzoic acid (2,5- DHBA), a siderophore that shares structural similarities with bacterial enterobactin, and delivers or removes iron from the cell, depending on the context. Iron-bound form (holo-24p3) is internalized following binding to the SLC22A17 (24p3R) receptor, leading to release of iron and subsequent increase of intracellular iron concentration.

ldhb: lactate dehydrogenase B:

This gene encodes the B subunit of **lactate dehydrogenase enzyme**, which **catalyzes the interconversion of pyruvate and lactate** with concomitant interconversion of NADH and NAD+ in a post-glycolysis process. Alternatively spliced transcript variants have also been found for this gene. Recent studies have shown that a C-terminally extended isoform is produced by use of an alternative in-frame translation termination codon via a stop codon readthrough mechanism, and that this isoform is localized in the peroxisomes. Pseudogenes have been identified on chromosomes 1 and 19.

cnmd: chondromodulin.

lgals1: lectin, galactose binding, soluble 1:

Lectin that binds beta-galactoside and a wide array of complex carbohydrates. **Plays a role in regulating apoptosis, cell proliferation and cell differentiation**. Inhibits CD45 protein phosphatase activity and therefore the dephosphorylation of Lyn kinase. Strong inducer of T-cell apoptosis.

lox: lysyl oxidase:

This gene encodes a precursor protein that belongs to the lysyl oxidase family of proteins. The secreted proprotein is proteolytically processed to an active mature peptide and a propeptide. This propeptide is thought to function in tumor suppression by inhibiting the Ras signaling pathway. The active enzyme **plays a role in cross-linking of collagen and elastin** and **is essential for development of cardiovascular and respiratory systems**, and development of skin and connective tissue.

Responsible for the post-translational oxidative deamination of peptidyl lysine residues in precursors to fibrous collagen and elastin.

lrrn1: leucine rich repeat protein 1, neuronal:

lsp1: **lymphocyte** specific 1:

May play a role in mediating neutrophil activation and chemotaxis.

ltf: lactotransferrin:

Transferrins are iron binding transport proteins which can **bind two Fe(3+) ions in association with the binding of an anion, usually bicarbonate**.

ly6e: **lymphocyte** antigen 6 complex, locus E:

Involved in T-cell development.

lyz2: lysozyme 2:

Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte- macrophage system and **enhance the activity of immunoagents.** Lyz2 is **active against a range of Gram-positive and Gram-negative bacteria**. More effective than Lyz1 in killing Gram-negative bacteria. Lyz1 and Lyz2 are equally effective in killing Gram- positive bacteria.

mfap2: microfibrillar-associated protein 2:

Component of the elastin-associated microfibrils.

nme7: NME/NM23 family member 7:
Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.

matk: megakaryocyte-associated tyrosine kinase:
Could play a significant role in the signal transduction of hematopoietic cells. May regulate tyrosine kinase activity of SRC-family members in brain by specifically phosphorylating their C-terminal regulatory tyrosine residue which acts as a negative regulatory site. It may play an inhibitory role in the control of T-cell proliferation.

met: met proto-oncogene:
Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by **binding to hepatocyte growth factor**/HGF ligand. **Regulates many physiological processes including proliferation, scattering, morphogenesis and survival**. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1.

mmp2: matrix metallopeptidase 2:
This gene encodes a member of the matrix metalloproteinase family of extracellular matrix-degrading enzymes that are **involved in tissue remodeling, wound repair, progression of atherosclerosis and tumor invasion**. The encoded preproprotein undergoes proteolytic processing to generate a mature, zinc-dependent endopeptidase enzyme that hydrolyzes collagens, gelatins, laminin, fibronectin and elastin. Mice lacking the encoded protein exhibit suppressed angiogenesis and attenuated features of human multicentric osteolysis with arthritis including abnormal skeletal and craniofacial development.