

Compute Overlaps for Selected Genes

Converted 106 submitted identifiers into 101 entrez genes. [click here for details](#).

Collections	# Overlaps Shown	# Gene Sets in Collections	# Genes in Comparison (n)	# Genes in Universe (N)
BP, CP, CP:BIOCARTA, CP:KEGG, CP:REACTOME	99	2145	101	45956

Click the gene set name to see the gene set page. Click the number of genes [in brackets] to download the list of genes.

Color bar shading from light green to black, where lighter colors indicate more significant FDR q-values (< 0.05) and black indicates less significant FDR q-values (≥ 0.05).

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Gene Set Name [# Genes (K)]	Description	# Genes in Overlap (k)	k/K	p-value ?	FDR q-value ?
KEGG_GLYCOLYSIS_GLUONEOGENESIS [62]	Glycolysis / Gluconeogenesis	10		1.63×10^{-16}	3.49×10^{-13}
REACTOME_GLUPOSE_METABOLISM [69]	Genes involved in Glucose metabolism	10		5.08×10^{-16}	5.45×10^{-13}
REACTOME_GLUONEOGENESIS [34]	Genes involved in Gluconeogenesis	8		7.1×10^{-15}	5.08×10^{-12}
REACTOME_GLYCOLYSIS [29]	Genes involved in Glycolysis	7		3.01×10^{-13}	1.61×10^{-10}
BIOCARTA_GLYCOLYSIS_PATHWAY [10]	Glycolysis Pathway	5		1.16×10^{-11}	4.97×10^{-9}
REACTOME_METABOLISM_OF_CARBOHYDRATES [247]	Genes involved in Metabolism of carbohydrates	10		2.1×10^{-10}	7.5×10^{-8}
KEGG_PENTOSE_PHOSPHATE_PATHWAY [27]	Pentose phosphate pathway	5		3.6×10^{-9}	1.1×10^{-6}
PID_HIF1_TFPATHWAY [66]	HIF-1-alpha transcription factor network	6		7.92×10^{-9}	2.12×10^{-6}
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS [478]	Genes involved in Metabolism of lipids and lipoproteins	11		9.42×10^{-9}	2.23×10^{-6}
KEGG_PPAR_SIGNALING_PATHWAY [69]	PPAR signaling pathway	6		1.04×10^{-8}	2.23×10^{-6}
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION [208]	Genes involved in Platelet activation, signaling and aggregation	8		2.17×10^{-8}	4.23×10^{-6}
CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS [126]	Genes annotated by the GO term GO:0044262. The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the	6		3.86×10^{-7}	6.26×10^{-5}

	general formula $Cx(H_2O)_y$, as carried out by individual cells.				
REGULATION_OF_BIOLOGICAL_QUALITY [419]	Genes annotated by the GO term GO:0065008. Any process that modulates the frequency, rate or extent of a biological quality. A biological quality is a measurable attribute of an organism or part of an organism, such as size, mass, shape, color, etc.	9		3.98×10^{-7}	6.26×10^{-5}
HOMEOSTATIC_PROCESS [207]	Genes annotated by the GO term GO:0042592. The biological processes involved in the maintenance of an internal equilibrium.	7		4.08×10^{-7}	6.26×10^{-5}
SYSTEM_PROCESS [563]	Genes annotated by the GO term GO:0003008. A biological process, occurring at the level of an organ system pertinent to the function of the organism. An organ system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process.	10		4.98×10^{-7}	6.48×10^{-5}
APOPTOSIS_GO [431]	Genes annotated by the GO term GO:0006915. A form of programmed cell death induced by external or internal signals that trigger the activity of proteolytic caspases, whose actions dismantle the cell and result in cell death. Apoptosis begins internally with condensation and subsequent fragmentation of the cell nucleus (blebbing) while the plasma membrane remains intact. Other characteristics of apoptosis include DNA fragmentation and the exposure of phosphatidyl serine on the cell surface.	9		5.04×10^{-7}	6.48×10^{-5}
PROGRAMMED_CELL_DEATH [432]	Genes annotated by the GO term GO:0012501. Cell death resulting from activation of endogenous cellular processes.	9		5.14×10^{-7}	6.48×10^{-5}
CELL_DEVELOPMENT [577]	Genes annotated by the GO term GO:0048468. The process whose specific outcome is the progression of the cell over time, from its formation to the mature structure. Cell development does not include the steps involved in committing a	10		6.22×10^{-7}	7.42×10^{-5}

	cell to a specific fate.				
REACTOME_COMPLEMENT_CASCADE [32]	Genes involved in Complement cascade	4		7.54 e ⁻⁷	8.51 e ⁻⁵
REGULATION_OF_APOPTOSIS [341]	Genes annotated by the GO term GO:0042981. Any process that modulates the occurrence or rate of cell death by apoptosis.	8		9.4 e ⁻⁷	9.03 e ⁻⁵
REGULATION_OF_PROGRAMMED_CELL_DEATH [342]	Genes annotated by the GO term GO:0043067. Any process that modulates the frequency, rate or extent of programmed cell death, cell death resulting from activation of endogenous cellular processes.	8		9.6 e ⁻⁷	9.03 e ⁻⁵
REACTOME_HEMOSTASIS [466]	Genes involved in Hemostasis	9		9.61 e ⁻⁷	9.03 e ⁻⁵
KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM [34]	Fructose and mannose metabolism	4		9.69 e ⁻⁷	9.03 e ⁻⁵
REACTOME_IMMUNE_SYSTEM [933]	Genes involved in Immune System	12		1.04 e ⁻⁶	9.31 e ⁻⁵
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_LET_CYTOSOLIC_CA2+ [89]	Genes involved in Response to elevated platelet cytosolic Ca2+	5		1.66 e ⁻⁶	1.43 e ⁻⁴
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL [91]	Genes involved in Cell surface interactions at the vascular wall	5		1.86 e ⁻⁶	1.53 e ⁻⁴
REACTOME_PLATELET_ADHESION_TO_EXPOSED_ED_COLLAGEN [12]	Genes involved in Platelet Adhesion to exposed collagen	3		2.23 e ⁻⁶	1.77 e ⁻⁴
ANATOMICAL_STRUCTURE_DEVELOPMENT [1013]	Genes annotated by the GO term GO:0048856. The biological process whose specific outcome is the progression of an anatomical structure from an initial condition to its mature state. This process begins with the formation of the structure and ends with the mature structure, whatever form that may be including its natural destruction. An anatomical structure is any biological entity that occupies space and is distinguished from its surroundings. Anatomical structures can be macroscopic such as a carpel, or microscopic such as an acrosome.	12		2.43 e ⁻⁶	1.86 e ⁻⁴
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_AR_METABOLISM [44]	Amino sugar and nucleotide sugar metabolism	4		2.79 e ⁻⁶	2.06 e ⁻⁴
REACTOME_INNATE_IMMUNE_SYSTEM [279]	Genes involved in Innate Immune System	7		2.98 e ⁻⁶	2.13 e ⁻⁴
CARBOHYDRATE_METABOLIC_PROCESS [180]	Genes annotated by the GO term GO:0005975. The chemical reactions and pathways involving carbohydrates, any of a	6		3.09 e ⁻⁶	2.14 e ⁻⁴

	group of organic compounds based of the general formula $C_x(H_2O)_y$.				
SYSTEM_DEVELOPMENT [861]	Genes annotated by the GO term GO:0048731. The process whose specific outcome is the progression of an organismal system over time, from its formation to the mature structure. A system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process.	11		3.22×10^{-6}	2.16×10^{-4}
REACTOME_LIPID_DIGESTION_MOBILIZATION_ON_AND_TRANSPORT [46]	Genes involved in Lipid digestion, mobilization, and transport	4		3.34×10^{-6}	2.17×10^{-4}
MULTICELLULAR_ORGANISMAL_DEVELOPMENT [1049]	Genes annotated by the GO term GO:0007275. The biological process whose specific outcome is the progression of an organism over time from an initial condition (e.g. a zygote or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	12		3.48×10^{-6}	2.19×10^{-4}
BIOCARTA_CLASSIC_PATHWAY [14]	Classical Complement Pathway	3		3.68×10^{-6}	2.26×10^{-4}
KEGG_GLUTATHIONE_METABOLISM [50]	Glutathione metabolism	4		4.68×10^{-6}	2.79×10^{-4}
REGULATION_OF_DEVELOPMENTAL_PROCESS [440]	Genes annotated by the GO term GO:0050793. Any process that modulates the frequency, rate or extent of development, the biological process whose specific outcome is the progression of a multicellular organism over time from an initial condition (e.g. a zygote, or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	8		6.16×10^{-6}	3.57×10^{-4}
BIOCARTA_COMP_PATHWAY [19]	Complement Pathway	3		9.73×10^{-6}	5.49×10^{-4}
PID_IL4_2PATHWAY [65]	IL4-mediated signaling events	4		1.34×10^{-5}	7.38×10^{-4}
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES [69]	Complement and coagulation cascades	4		1.7×10^{-5}	9.13×10^{-4}
CELLULAR_HOMEOSTASIS [147]	Genes annotated by the GO term GO:0019725. The processes involved in the maintenance of an internal equilibrium at the level of the cell.	5		1.93×10^{-5}	1.01×10^{-3}
PID_LYMPHANGIOGENESIS_PATHWAY [25]	VEGFR3 signaling in lymphatic endothelium	3		2.29×10^{-5}	1.17×10^{-3}
PID_MYC_ACTIVPATHWAY [79]	Validated targets of C-MYC transcriptional activation	4		2.91×10^{-5}	1.45×10^{-3}
GLUCOSE_METABOLIC_PROCESS [28]	Genes annotated by the	3		3.24×10^{-5}	1.55×10^{-3}

	GO term GO:0006006. The chemical reactions and pathways involving glucose, the aldohexose gluco-hexose. D-glucose is dextrorotatory and is sometimes known as dextrose; it is an important source of energy for living organisms and is found free as well as combined in homo- and hetero-oligosaccharides and polysaccharides.				
REACTOME_LIPOPROTEIN_METABOLISM [28]	Genes involved in Lipoprotein metabolism	3		3.24 e ⁻⁵	1.55 e ⁻³
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM [168]	Genes involved in Fatty acid, triacylglycerol, and ketone body metabolism	5		3.67 e ⁻⁵	1.69 e ⁻³
PID_CMYB_PATHWAY [84]	C-MYB transcription factor network	4		3.7 e ⁻⁵	1.69 e ⁻³
ORGAN_DEVELOPMENT [571]	Genes annotated by the GO term GO:0048513. Development of a tissue or tissues that work together to perform a specific function or functions. Development pertains to the process whose specific outcome is the progression of a structure over time, from its formation to the mature structure. Organs are commonly observed as visibly distinct structures, but may also exist as loosely associated clusters of cells that work together to perform a specific function or functions.	8		3.97 e ⁻⁵	1.78 e ⁻³
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE [31]	Genes involved in GPVI-mediated activation cascade	3		4.43 e ⁻⁵	1.91 e ⁻³
ALCOHOL_METABOLIC_PROCESS [88]	Genes annotated by the GO term GO:0006066. The chemical reactions and pathways involving alcohols, any of a class of alkyl compounds containing a hydroxyl group.	4		4.45 e ⁻⁵	1.91 e ⁻³
KEGG_PRION_DISEASES [35]	Prion diseases	3		6.41 e ⁻⁵	2.69 e ⁻³
PID_P38ALPHABETADOWNSTREAMPATHWAY [38]	Signaling mediated by p38-alpha and p38-beta	3		8.22 e ⁻⁵	3.39 e ⁻³
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS [646]	Genes annotated by the GO term GO:0048523. Any process that stops, prevents or reduces the frequency, rate or extent of cellular processes, those that are carried out at the cellular level, but are not necessarily restricted to a single cell. For example, cell communication occurs among more than one cell,	8		9.37 e ⁻⁵	3.79 e ⁻³

	but occurs at the cellular level.				
IMMUNE_SYSTEM_PROCESS [332]	Genes annotated by the GO term GO:0002376. Any process involved in the development or functioning of the immune system, an organismal system for calibrated responses to potential internal or invasive threats.	6		9.68 e ⁻⁵	3.84 e ⁻³
PID_INTEGRIN3_PATHWAY [43]	Beta3 integrin cell surface interactions	3		1.19 e ⁻⁴	4.65 e ⁻³
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS [677]	Genes annotated by the GO term GO:0048519. Any process that stops, prevents or reduces the frequency, rate or extent of a biological process. Biological processes are regulated by many means; examples include the control of gene expression, protein modification or interaction with a protein or substrate molecule.	8		1.29 e ⁻⁴	4.95 e ⁻³
PID_HNF3BPATHWAY [45]	FOXA2 and FOXA3 transcription factor networks	3		1.37 e ⁻⁴	5.14 e ⁻³
BIOCARTA_FEEDER_PATHWAY [9]	Feeder Pathways for Glycolysis	2		1.7 e ⁻⁴	6.3 e ⁻³
KEGG_STARCH_AND_SUCROSE_METABOLISM [52]	Starch and sucrose metabolism	3		2.11 e ⁻⁴	7.36 e ⁻³
BIOCARTA_SARS_PATHWAY [10]	The SARS-coronavirus Life Cycle	2		2.13 e ⁻⁴	7.36 e ⁻³
REACTOME_PECAM1_INTERACTIONS [10]	Genes involved in PECAM1 interactions	2		2.13 e ⁻⁴	7.36 e ⁻³
TRIACYLGLYCEROL_METABOLIC_PROCESS [10]	Genes annotated by the GO term GO:0006641. The chemical reactions and pathways involving triacylglycerol, any triester of glycerol. The three fatty acid residues may all be the same or differ in any permutation. Triacylglycerols are important components of plant oils, animal fats and animal plasma lipoproteins.	2		2.13 e ⁻⁴	7.36 e ⁻³
MACROMOLECULE_CATABOLIC_PROCESS [137]	Genes annotated by the GO term GO:0009057. The chemical reactions and pathways resulting in the breakdown of a macromolecule, any large molecule including proteins, nucleic acids and carbohydrates.	4		2.47 e ⁻⁴	8.4 e ⁻³
REACTOME_DEVELOPMENTAL_BIOLOGY [396]	Genes involved in Developmental Biology	6		2.51 e ⁻⁴	8.41 e ⁻³
GLUCOSE_CATABOLIC_PROCESS [11]	Genes annotated by the GO term GO:0006007. The	2		2.6 e ⁻⁴	8.57 e ⁻³

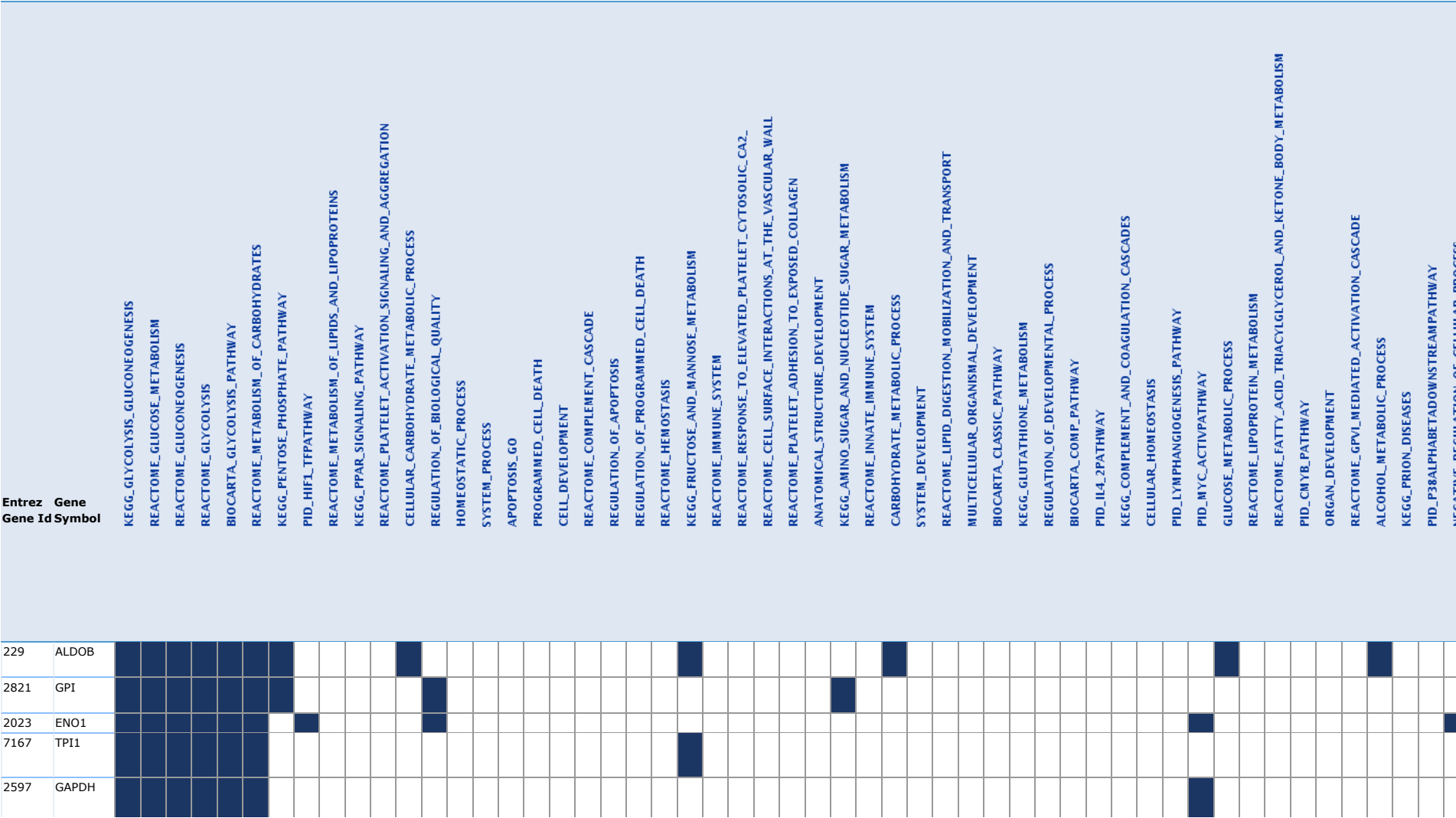
	chemical reactions and pathways resulting in the breakdown of glucose, the aldohexose gluco-hexose.				
BIOCARTA_LECTIN_PATHWAY [12]	Lectin Induced Complement Pathway	2		3.11 e ⁻⁴	1.01 e ⁻²
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_NE_SYSTEM [270]	Genes involved in Cytokine Signaling in Immune system	5		3.37 e ⁻⁴	1.08 e ⁻²
NEGATIVE_REGULATION_OF_APOPTOSIS [150]	Genes annotated by the GO term GO:0043066. Any process that stops, prevents or reduces the frequency, rate or extent of cell death by apoptosis.	4		3.48 e ⁻⁴	1.1 e ⁻²
NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH [151]	Genes annotated by the GO term GO:0043069. Any process that stops, prevents or reduces the frequency, rate or extent of programmed cell death, cell death resulting from activation of endogenous cellular processes.	4		3.57 e ⁻⁴	1.11 e ⁻²
REACTOME_INTERFERON_GAMMA_SIGNALING [63]	Genes involved in Interferon gamma signaling	3		3.72 e ⁻⁴	1.14 e ⁻²
CHEMICAL_HOMEOSTASIS [155]	Genes annotated by the GO term GO:0048878. The biological processes involved in the maintenance of an internal equilibrium of a chemical.	4		3.94 e ⁻⁴	1.19 e ⁻²
PID_INTEGRIN1_PATHWAY [66]	Beta1 integrin cell surface interactions	3		4.26 e ⁻⁴	1.26 e ⁻²
STRIATED_MUSCLE_CONTRACTION_GO_0006941 [14]	Genes annotated by the GO term GO:0006941. A process whereby force is generated within striated muscle tissue, resulting in a change in muscle geometry. Force generation involves a chemo-mechanical energy conversion step. The chemo-mechanical energy conversion step is carried out by the actin/myosin complex activity, which generates force through ATP hydrolysis. Striated muscle is a type of muscle in which the repeating units (sarcomeres) of the contractile myofibrils are arranged in registry throughout the cell, resulting in transverse or oblique striations observable at the level of the light microscope.	2		4.28 e ⁻⁴	1.26 e ⁻²
REACTOME_INTERFERON_SIGNALING [159]	Genes involved in Interferon Signaling	4		4.34 e ⁻⁴	1.26 e ⁻²

REACTOME_HDL_MEDIATED_LIPID_TRANSPORT [15]	Genes involved in HDL-mediated lipid transport	2		4.93 e ⁻⁴	1.41 e ⁻²
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_OF_WHITE_ADIPOCYTE_DIFFERENTIATION [72]	Genes involved in Transcriptional Regulation of White Adipocyte Differentiation	3		5.5 e ⁻⁴	1.55 e ⁻²
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT [16]	Genes involved in Chylomicron-mediated lipid transport	2		5.62 e ⁻⁴	1.57 e ⁻²
PID_AVB3_INTEGRIN_PATHWAY [75]	Integrins in angiogenesis	3		6.2 e ⁻⁴	1.71 e ⁻²
BIOCARTA_LAIR_PATHWAY [17]	Cells and Molecules involved in local acute inflammatory response	2		6.37 e ⁻⁴	1.71 e ⁻²
REACTOME_REGULATION_OF_KIT_SIGNALING [17]	Genes involved in Regulation of KIT signaling	2		6.37 e ⁻⁴	1.71 e ⁻²
RESPONSE_TO_CHEMICAL_STIMULUS [314]	Genes annotated by the GO term GO:0042221. A change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a chemical stimulus.	5		6.69 e ⁻⁴	1.77 e ⁻²
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS [79]	Genes involved in Integrin cell surface interactions	3		7.22 e ⁻⁴	1.89 e ⁻²
BIOCARTA_MTA3_PATHWAY [19]	Downregulated of MTA-3 in ER-negative Breast Tumors	2		7.98 e ⁻⁴	2.06 e ⁻²
KEGG_ECM_RECEPTOR_INTERACTION [84]	ECM-receptor interaction	3		8.63 e ⁻⁴	2.2 e ⁻²
NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS [197]	Genes annotated by the GO term GO:0051093. Any process that stops, prevents or reduces the rate or extent of development, the biological process whose specific outcome is the progression of an organism over time from an initial condition (e.g. a zygote, or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	4		9.67 e ⁻⁴	2.44 e ⁻²
KEGG_FOCAL_ADHESION [201]	Focal adhesion	4		1.04 e ⁻³	2.6 e ⁻²
CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS [23]	Genes annotated by the GO term GO:0044275. The chemical reactions and pathways resulting in the breakdown of carbohydrates, any of a group of organic compounds based on the general formula C _x (H ₂ O) _y , as carried out by individual cells.	2		1.17 e ⁻³	2.89 e ⁻²
CELLULAR_CATABOLIC_PROCESS [212]	Genes annotated by the GO term GO:0044248. The chemical reactions and pathways resulting in the breakdown of substances, carried out by individual cells.	4		1.27 e ⁻³	3.01 e ⁻²

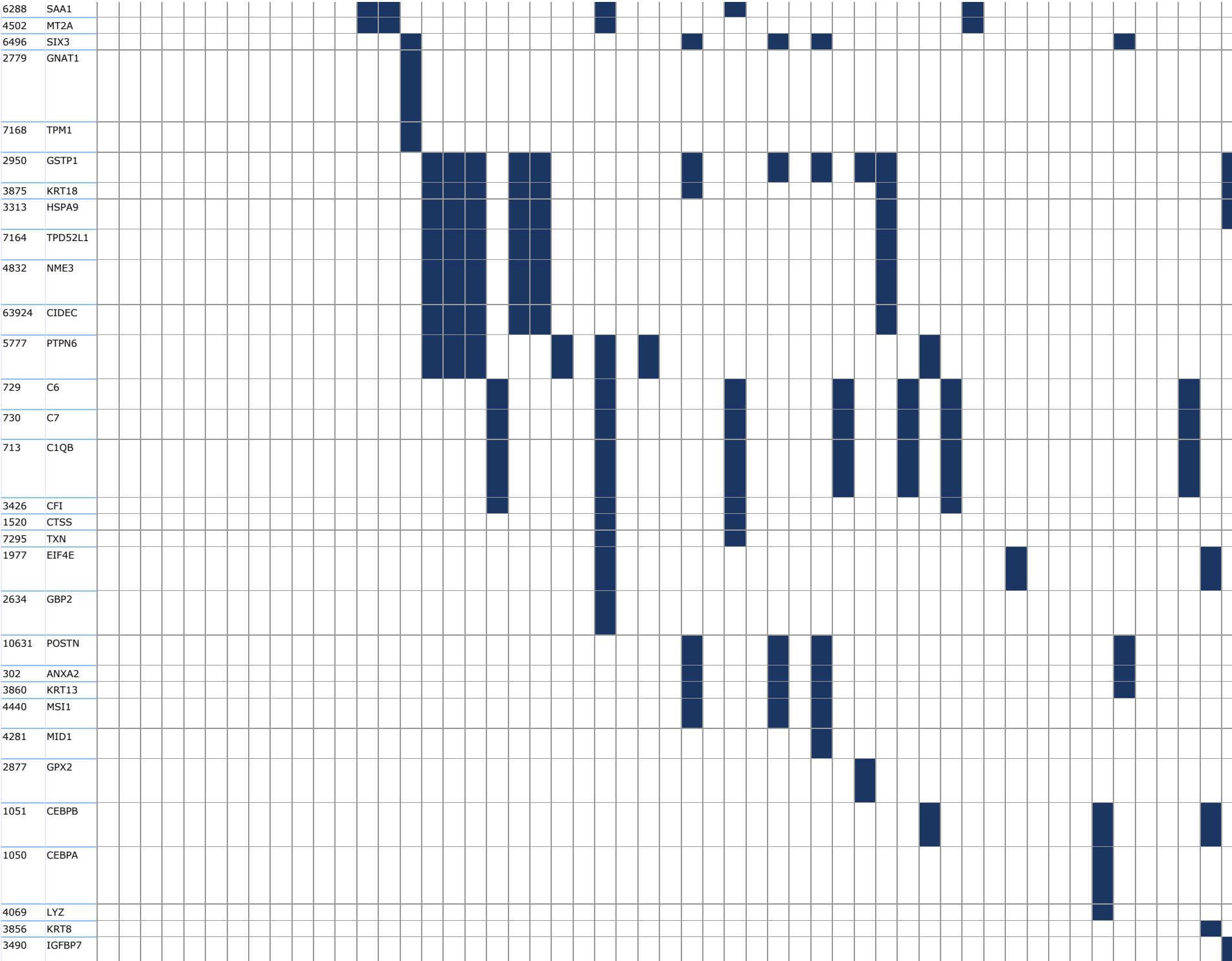
CARBOHYDRATE_CATABOLIC_PROCESS [24]	Genes annotated by the GO term GO:0016052. The chemical reactions and pathways resulting in the breakdown of carbohydrates, any of a group of organic compounds based of the general formula C _x (H ₂ O) _y .	2		1.28 e ⁻³	3.01 e ⁻²
PID_RHODOPSIN_PATHWAY [24]	Visual signal transduction: Rods	2		1.28 e ⁻³	3.01 e ⁻²
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING [24]	Genes involved in Growth hormone receptor signaling	2		1.28 e ⁻³	3.01 e ⁻²
POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS [218]	Genes annotated by the GO term GO:0051094. Any process that activates or increases the rate or extent of development, the biological process whose specific outcome is the progression of an organism over time from an initial condition (e.g. a zygote, or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	4		1.4 e ⁻³	3.27 e ⁻²
KEGG_GALACTOSE_METABOLISM [26]	Galactose metabolism	2		1.5 e ⁻³	3.46 e ⁻²
NEUROLOGICAL_SYSTEM_PROCESS [379]	Genes annotated by the GO term GO:0050877. The processes pertaining to the functions of the nervous system of an organism.	5		1.54 e ⁻³	3.51 e ⁻²
SKELETAL_DEVELOPMENT [103]	Genes annotated by the GO term GO:0001501. The process whose specific outcome is the progression of the skeleton over time, from its formation to the mature structure. The skeleton is the bony framework of the body in vertebrates (endoskeleton) or the hard outer envelope of insects (exoskeleton or dermoskeleton).	3		1.55 e ⁻³	3.51 e ⁻²
CATABOLIC_PROCESS [225]	Genes annotated by the GO term GO:0009056. The chemical reactions and pathways resulting in the breakdown of substances, including the breakdown of carbon compounds with the liberation of energy for use by the cell or organism.	4		1.58 e ⁻³	3.52 e ⁻²
CELLULAR_MACROMOLECULE_CATABOLIC_PROCESS [104]	Genes annotated by the GO term GO:0044265. The chemical reactions and pathways resulting in the breakdown of a macromolecule, any large molecule including proteins, nucleic acids and carbohydrates, as carried	3		1.6 e ⁻³	3.53 e ⁻²

	out by individual cells.				
IMMUNE_RESPONSE [235]	Genes annotated by the GO term GO:0006955. Any immune system process that functions in the calibrated response of an organism to a potential internal or invasive threat.	4		1.85 e ⁻³	4.04 e ⁻²
ANTI_APOPTOSIS [118]	Genes annotated by the GO term GO:0006916. A process which directly inhibits any of the steps required for cell death by apoptosis.	3		2.29 e ⁻³	4.96 e ⁻²

Gene/geneset overlap matrix







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MSigDB database v4.0 updated May 31, 2013
GSEA/MSigDB web site v4.05 released June 8, 2014