AN OPTIMIZED ISOLATION OF BIOTINYLATED CELL SURFACE PROTEINS REVEALS NOVEL PLAYERS IN CANCER METASTASIS

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Metastasis Associated Proteins (excluding HLA)

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Abstract

This Moksiskaan analysis describes the known relationships between the metastasis associated proteins and the other proteins and data sets associated to them. All HLA proteins are excluded from this report. Protein-protein interactions are filtered so that the network is formed between the genes with an expression correlation in The Cancer Genome Atlas breast cancer samples. The actual article hosting this supplementary document is titled: *An optimized isolation of biotinylated cell surface proteins reveals novel players in cancer metastasis.*

This document is generated automatically by Anduril (Engine 1.2.5). Section 3 provides a detailed description of the analysis and the versions of the data sources in use.

Contents

1 Candidate report for the protein functions

1.1 Moksiskaan candidate pathway

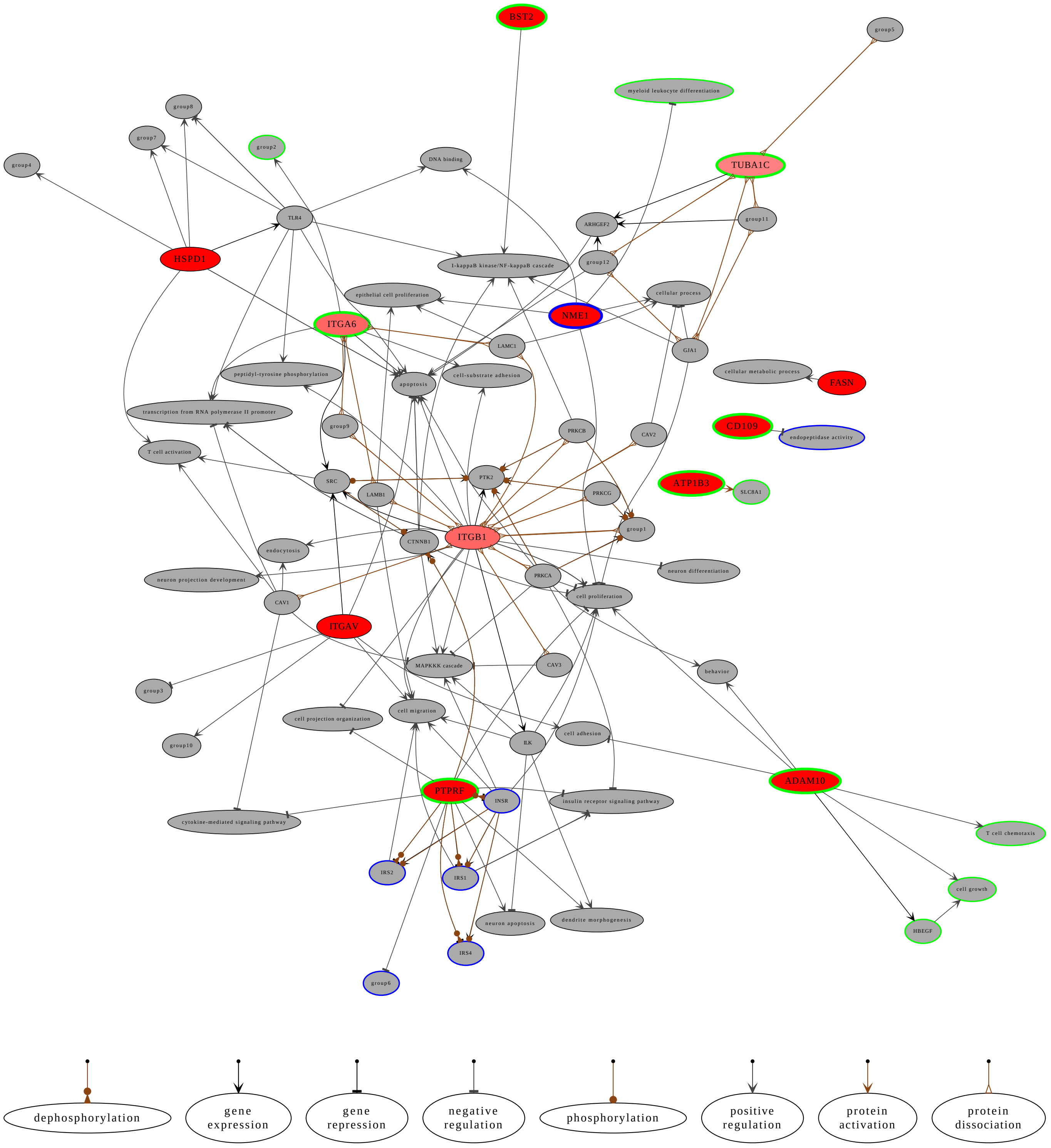

Figure 1: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The network of candidate genes is expanded by fetching genes 1 step(s) down stream. The down stream genes are shown on gray. Nodes that share all their connections and properties are combined in order to reduce the complexity of the graph. The joint nodes are labeled as *group#* and the participating entities are described in Table 1. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

You may use this Cytoscape session to browse the candidate pathway graph interactively.

Table 1: This table describes the actual genes of each set of combined nodes in Figure 1.

ID	Members
group1	ACTB, ACTG1
group2	cell-cell adhesion, phosphorylation
group3	cellular protein metabolic process, lipid storage, lipid transport, lipoprotein metabolic process, low-density lipoprotein particle receptor biosynthetic process, macrophage derived foam cell differentiation
group4	cysteine-type endopeptidase activity, interleukin-12 production, macrophage activation, T cell mediated immune response to tumor cell
group5	DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1
group6	epidermal growth factor receptor signaling pathway, nerve growth factor receptor signaling pathway
group7	innate immune response, interferon-alpha production, interleukin-10 production
group8	interferon-gamma production, interleukin-6 production
group9	LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB2, LAMB3, LAMB4, LAMC2, LAMC3
group10	osteoblast proliferation, phagocytosis
group11	RP11-631M21.2, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4, TUBB4Q, TUBB6
group12	TUBB, TUBB2C

Table 2: Descriptions of the intermediated genes between the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. This table has 49 rows.

name	description	studies
ACTB	actin, beta [Source:HGNC Symbol;Acc:132] locus=7:5566782-5603415	tcgaOvarianMethyl
ACTG1	actin, gamma 1 [Source:HGNC Symbol;Acc:144] locus=17:79476999-79479827	tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCa
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Source:HGNC Symbol;Acc:682] locus=1:155916645-155966129	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa, tscapeProstated
CAV1	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:1527] locus=7:116164839-116201233	snp3dLungC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCa
CAV2	caveolin 2 [Source:HGNC Symbol;Acc:1528] locus=7:115927434-116148595	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCa
CAV3	caveolin 3 [Source:HGNC Symbol;Acc:1529] locus=3:8775486-8883492	tcgaBreastGE, tcgaColonGE
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa [Source:HGNC Symbol;Acc:2514] locus=3:41236328-41301587	cosmicPrimary, cosmicRecurrent, snp3dCRC, snp3dLungC, snp3dMetastasis, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
DYNC1H1	dynein, cytoplasmic 1, heavy chain 1 [Source:HGNC Symbol;Acc:2961] locus=14:102430865-102517129	cosmicPrimary, tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad
DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC Symbol;Acc:2963] locus=7:95401866-95739634	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2 [Source:HGNC Symbol;Acc:2964] locus=2:172543919-172604930	
DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1 [Source:HGNC Symbol;Acc:18745] locus=3:32567463-32612366	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGNC Symbol;Acc:2966] locus=16:66754796-66785701	tcgaColonGE, tscapeOvariand
DYNC2H1	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:2962] locus=11:102980160-103350591	tcgaBreastGE
GJA1	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;Acc:4274] locus=6:121756791-121770873	fileBC2brain, tcgaBreastMethyl, tcgaColonMethyl
HBEGF	heparin-binding EGF-like growth factor [Source:HGNC Symbol;Acc:3059] locus=5:139712428-139726216	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
ILK	integrin-linked kinase [Source:HGNC Symbol;Acc:6040] locus=11:6624961-6632102	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd
INSR	insulin receptor [Source:HGNC Symbol;Acc:6091] locus=19:7112266-7294011	snp3dDiabetes, snp3dObesity, tcgaColonGE, tcgaColonMethyl
IRS1	insulin receptor substrate 1 [Source:HGNC Symbol;Acc:6125] locus=2:227599757-227664475	snp3dBC, snp3dDiabetes, snp3dObesity, tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd
IRS2	insulin receptor substrate 2 [Source:HGNC Symbol;Acc:6126] locus=13:110406184-110438915	snp3dDiabetes, snp3dObesity, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCa, tscapeNSCLCa, tscapeSCLCa
IRS4	insulin receptor substrate 4 [Source:HGNC Symbol;Acc:6128] locus=X:107975712-107979651	tcgaBreastMethyl, tcgaColonMethyl
LAMA1	laminin, alpha 1 [Source:HGNC Symbol;Acc:6481] locus=18:6941743-7117813	cosmicMetastasis, cosmicPrimary, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tscapeCRCd
LAMA2	laminin, alpha 2 [Source:HGNC Symbol;Acc:6482] locus=6:129204286-129837714	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE
LAMA3	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483] locus=18:21269562-21535030	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
LAMA4	laminin, alpha 4 [Source:HGNC Symbol;Acc:6484] locus=6:112429963-112576141	fileBC2brain, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeCRCd
LAMA5	laminin, alpha 5 [Source:HGNC Symbol;Acc:6485] locus=20:60883011-60942368	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tscapeBCa
LAMB1	laminin, beta 1 [Source:HGNC Symbol;Acc:6486] locus=7:107564244-107643700	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
LAMB2	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:6487] locus=3:49158547-49170551	tcgaGliomaGE
LAMB3	laminin, beta 3 [Source:HGNC Symbol;Acc:6490] locus=1:209788220-209825811	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
LAMB4	laminin, beta 4 [Source:HGNC Symbol;Acc:6491] locus=7:107663993-107770801	
LAMC1	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;Acc:6492] locus=1:182992597-183114727	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
LAMC2	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493] locus=1:183155373-183214035	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
LAMC3	laminin, gamma 3 [Source:HGNC Symbol;Acc:6494] locus=9:133884469-133969860	tcgaGliomaGE
PRKCA	protein kinase C, alpha [Source:HGNC Symbol;Acc:9393] locus=17:64298944-64801114	cosmicRecurrent, snp3dGlioma, snp3dLungC, snp3dProstateC, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PRKCB	protein kinase C, beta [Source:HGNC Symbol;Acc:9395] locus=16:23847322-24231932	tcgaColonGE, tcgaGliomaGE
PRKCG	protein kinase C, gamma [Source:HGNC Symbol;Acc:9402] locus=19:54382444-54410906	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tscapeBCa, tscapeNSCLCa, tscapeOvariana
PTK2	PTK2 protein tyrosine kinase 2 [Source:HGNC Symbol;Acc:9611] locus=8:141667999-142012315	snp3dBC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCa, tscapeOvariana, tscapeOvariand
RP11-631M21.2	Tubulin beta-8 chain [Source:UniProtKB/Swiss-Prot;Acc:Q3ZCM7] locus=10:92828-96053	
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:HGNC Symbol;Acc:11068] locus=2:40339286-40838193	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE

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name	description	studies
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:11283] locus=20:35973088-36034453	tcgaBreastGE
TLR4	toll-like receptor 4 [Source:HGNC Symbol;Acc:11850] locus=9:120466610-120479149	fileBC2brain, tcgaBreastGE, tcgaColonMethyl
TUBB	tubulin, beta [Source:HGNC Symbol;Acc:20778] locus=6:30687978-30693203	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl
TUBB1	tubulin, beta 1 [Source:HGNC Symbol;Acc:16257] locus=20:57594309-57601709	tcgaColonMethyl, tcgaOvarianCGHa
TUBB2A	tubulin, beta 2A [Source:HGNC Symbol;Acc:12412] locus=6:3153903-3157809	snp3dLungC, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariana, tscapeSCLCd
TUBB2B	tubulin, beta 2B [Source:HGNC Symbol;Acc:30829] locus=6:3224517-3231964	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariana, tscapeSCLCd
TUBB2C	tubulin, beta 2C [Source:HGNC Symbol;Acc:20771] locus=9:140135665-140138159	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa
TUBB3	tubulin, beta 3 [Source:HGNC Symbol;Acc:20772] locus=16:89987800-90005169	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd, tscapeProstated
TUBB4	tubulin, beta 4 [Source:HGNC Symbol;Acc:20774] locus=19:6494331-6502330	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tscapeHCCd, tscapeRCCd
TUBB4Q	tubulin, beta polypeptide 4, member Q, pseudogene [Source:HGNC Symbol;Acc:12413] locus=4:190903678-190906026	tcgaBreastGE, tscapeBCd, tscapeHCCd, tscapeMelanomad, tscapeNSCLCd, tscapeProstated, tscapeRCCd
TUBB6	tubulin, beta 6 [Source:HGNC Symbol;Acc:20776] locus=18:12308070-12326568	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE

Table 3: List of KEGG [8] pathways supporting the relationships between the genes shown in Figure 1. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Toxoplasmosis	48	ITGA6, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMB4, LAMC1, LAMC2, LAMC3, TLR4
Phagosome	32	ACTB, ACTG1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, ITGAV, ITGB1, RP11-631M21.2, TLR4, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB4Q, TUBB6
Gap junction	22	GJA1, PRKCA, PRKCB, PRKCG, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB4Q, TUBB6
Focal adhesion	21	ACTB, ACTG1, CAV1, CAV2, CAV3, CTNNB1, ILK, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMB4, LAMC1, LAMC2, LAMC3, PRKCA, PRKCB, PRKCG, PTK2, SRC
Insulin signaling pathway	14	FASN, INSR, IRS1, IRS2, IRS4, PTPRF
Vibrio cholerae infection	12	ACTB, ACTG1, PRKCA, PRKCB, PRKCG
Pathogenic Escherichia coli infection	11	ACTB, ACTG1, ARHGEF2, CTNNB1, ITGB1, PRKCA, RP11-631M21.2, TLR4, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB4Q, TUBB6
Tight junction	6	ACTB, ACTG1, CTNNB1, PRKCA, PRKCB, PRKCG, SRC
Hypertrophic cardiomyopathy (HCM)	4	ACTB, ACTG1, ITGA6, ITGAV, ITGB1, LAMA2, SLC8A1
Adherens junction	4	ACTB, ACTG1, CTNNB1, INSR, PTPRF, SRC
Aldosterone-regulated sodium reabsorption	3	ATP1B3, INSR, IRS1, IRS2, IRS4, PRKCA, PRKCB, PRKCG
Type II diabetes mellitus	3	INSR, IRS1, IRS2, IRS4
Regulation of actin cytoskeleton	3	ACTB, ACTG1, ITGA6, ITGAV, ITGB1, PTK2, SRC
Bacterial invasion of epithelial cells	2	ACTB, ACTG1, CAV1, CAV2, CAV3, CTNNB1, ILK, ITGB1, PTK2, SRC
Chemokine signaling pathway	2	PRKCB, PTK2, SRC
ErbB signaling pathway	2	HBEGF, PRKCA, PRKCB, PRKCG, PTK2, SRC
Tuberculosis	1	HSPD1, SRC, TLR4
Epithelial cell signaling in Helicobacter pylori infection	1	ADAM10, HBEGF, SRC
Endocrine and other factor-regulated calcium reabsorption	1	ATP1B3, PRKCA, PRKCB, PRKCG, SLC8A1

1.1.1 GO enrichment of the candidate pathway

Table 4: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.01$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.525	BP	cellular component assembly at cellular level	ACTB, ACTG1, CAV1, CAV2, CAV3, CTNNB1, DYNC1H1, DYNC2H1, GJA1, HSPD1, ILK, ITGA6, ITGB1, LAMA3, LAMA5, LAMB3, LAMC1, LAMC2, PRKCA, PTK2, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.750	CC	protein complex	ACTB, ACTG1, ARHGEF2, ATP1B3, CAV1, CAV2, CAV3, CTNNB1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, GJA1, HSPD1, ILK, INSR, IRS1, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMC1, LAMC2, NME1, PRKCA, RP11-631M21.2, SLC8A1, TLR4, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.424	MF	structural molecule activity	ACTB, ACTG1, CAV1, CAV3, CTNNB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMC1, LAMC3, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.233	CC	basement membrane	ITGA6, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMB4, LAMC1, LAMC2, LAMC3
0.458	BP	cellular component movement	ACTB, ACTG1, ADAM10, ATP1B3, CAV1, GJA1, HBEGF, ILK, INSR, IRS1, IRS2, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMC1, PRKCA, PTK2, SRC, TUBB, TUBB2B, TUBB2C
0.150	CC	laminin complex	LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMC1, LAMC2
0.339	BP	microtubule-based process	ARHGEF2, CAV1, CAV3, CTNNB1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC2H1, PTK2, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.300	CC	microtubule	ARHGEF2, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, RP11-631M21.2, SLC8A1, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.237	BP	microtubule-based movement	DYNC1H1, DYNC1I1, DYNC1I2, DYNC2H1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.390	BP	cell migration	ADAM10, ATP1B3, CAV1, GJA1, HBEGF, ILK, INSR, IRS1, IRS2, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMC1, PRKCA, PTK2, SRC, TUBB2B
0.271	MF	protein complex binding	ADAM10, CAV3, ILK, INSR, IRS1, IRS2, IRS4, ITGA6, ITGB1, LAMA5, LAMB1, LAMB2, LAMB3, PTPRF, SRC, TUBB
0.424	MF	receptor binding	ADAM10, CAV1, CAV2, CTNNB1, GJA1, HBEGF, ILK, INSR, IRS1, IRS2, IRS4, ITGA6, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, PRKCB, PTPRF, SRC, TUBB, TUBB2C
0.117	CC	laminin-1 complex	LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMC1
0.356	BP	protein complex assembly	CAV1, CAV2, CAV3, GJA1, HSPD1, ILK, INSR, IRS1, LAMC1, PTK2, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.678	BP	system development	ACTB, ACTG1, ARHGEF2, CAV1, CAV2, CAV3, CTNNB1, DYNC2H1, GJA1, HBEGF, HSPD1, ILK, INSR, IRS1, IRS2, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, NME1, PRKCA, PTK2, PTPRF, SLC8A1, SRC, TLR4, TUBB, TUBB2A, TUBB2B, TUBB3
0.220	BP	cell junction assembly	ACTB, ACTG1, CTNNB1, GJA1, ILK, ITGA6, ITGB1, LAMA3, LAMA5, LAMB3, LAMC1, LAMC2, SRC
0.169	BP	'de novo' protein folding	ACTB, HSPD1, TUBA1C, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.254	BP	cellular protein complex assembly	CAV1, CAV3, HSPD1, PTK2, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.203	BP	protein polymerization	CAV1, CAV3, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.254	BP	regulation of cell migration	ADAM10, HBEGF, ILK, INSR, IRS1, IRS2, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, PRKCA
0.153	BP	'de novo' posttranslational protein folding	ACTB, TUBA1C, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.356	BP	cellular component morphogenesis	ACTB, ACTG1, ARHGEF2, CAV3, CTNNB1, DYNC2H1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMA5, LAMB1, LAMB2, LAMC1, LAMC3, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.339	BP	cell morphogenesis	ACTB, ACTG1, ARHGEF2, CTNNB1, DYNC2H1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMA5, LAMB1, LAMB2, LAMC1, LAMC3, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.183	CC	membrane raft	ATP1B3, CAV1, CAV2, CAV3, GJA1, INSR, IRS1, ITGB1, PRKCA, SRC, TLR4
0.339	BP	cell adhesion	ADAM10, CTNNB1, ILK, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMB3, LAMB4, LAMC1, LAMC2, LAMC3, PTK2, PTPRF
0.288	BP	cell projection morphogenesis	ACTB, ACTG1, DYNC2H1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMA5, LAMB1, LAMB2, LAMC1, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.305	MF	nucleoside-triphosphatase activity	ATP1B3, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, HSPD1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.356	BP	neurogenesis	ACTB, ACTG1, ARHGEF2, CTNNB1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMB1, LAMB2, LAMC1, LAMC3, PRKCA, PTK2, PTPRF, SRC, TUBB, TUBB2A, TUBB2B, TUBB3
0.288	BP	cell morphogenesis involved in differentiation	ACTB, ACTG1, CTNNB1, ILK, ITGAV, ITGB1, LAMA1, LAMA5, LAMB1, LAMB2, LAMC1, LAMC3, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.186	BP	regulation of cell adhesion	ADAM10, ILK, ITGA6, ITGAV, ITGB1, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5, PTK2
0.339	BP	generation of neurons	ACTB, ACTG1, ARHGEF2, CTNNB1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMB1, LAMB2, LAMC1, PRKCA, PTK2, PTPRF, SRC, TUBB, TUBB2A, TUBB2B, TUBB3
0.136	MF	integrin binding	ADAM10, ILK, ITGA6, ITGB1, LAMA5, LAMB1, LAMB2, SRC
0.424	MF	purine ribonucleoside triphosphate binding	ACTB, ACTG1, DYNC1H1, DYNC1LI1, DYNC1LI2, DYNC2H1, HSPD1, ILK, INSR, NME1, PRKCA, PRKCB, PRKCG, PTK2, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.339	BP	regulation of cell proliferation	ADAM10, ARHGEF2, CAV1, CAV2, CTNNB1, GJA1, HBEGF, ILK, INSR, IRS1, IRS2, ITGAV, ITGB1, LAMA5, LAMB1, LAMC1, NME1, PRKCA, PTPRF, TLR4
0.271	BP	wound healing	ACTB, ACTG1, ATP1B3, CAV1, GJA1, HBEGF, ITGA6, ITGAV, ITGB1, PRKCA, PRKCB, PRKCG, PTK2, SLC8A1, SRC, TLR4
0.203	MF	kinase binding	ACTB, ACTG1, ADAM10, CAV1, CTNNB1, INSR, IRS1, IRS2, ITGB1, PRKCB, PTK2, TLR4
0.117	CC	caveola	ATP1B3, CAV1, CAV2, CAV3, INSR, IRS1, SRC
0.169	BP	positive regulation of cell migration	ADAM10, HBEGF, ILK, INSR, IRS1, IRS2, ITGAV, ITGB1, LAMB1, PRKCA
0.119	BP	regulation of embryonic development	CTNNB1, INSR, LAMA1, LAMA2, LAMA3, LAMA4, LAMA5
0.254	BP	neuron projection morphogenesis	ACTB, ACTG1, GJA1, ILK, ITGAV, ITGB1, LAMA1, LAMB1, LAMB2, LAMC1, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.085	BP	hemidesmosome assembly	ITGA6, LAMA3, LAMB3, LAMC1, LAMC2
0.100	CC	dynein complex	DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1
0.203	MF	GTP binding	INSR, NME1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.237	BP	blood coagulation	ACTB, ACTG1, ATP1B3, CAV1, ITGA6, ITGAV, ITGB1, PRKCA, PRKCB, PRKCG, PTK2, SLC8A1, SRC, TLR4
0.119	BP	integrin-mediated signaling pathway	ADAM10, ILK, ITGA6, ITGAV, ITGB1, LAMA5, PTK2
0.237	BP	cell morphogenesis involved in neuron differentiation	ACTB, ACTG1, ILK, ITGAV, ITGB1, LAMA1, LAMB1, LAMB2, LAMC1, PRKCA, PTK2, PTPRF, SRC, TUBB3
0.237	BP	positive regulation of cell proliferation	ADAM10, CTNNB1, HBEGF, ILK, INSR, IRS1, IRS2, ITGAV, ITGB1, LAMB1, LAMC1, NME1, PRKCA, TLR4
0.203	BP	muscle structure development	ACTG1, CAV1, CAV2, CAV3, CTNNB1, GJA1, HBEGF, ILK, ITGB1, LAMA2, LAMA5, LAMB2
0.169	MF	GTPase activity	RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.169	MF	protein kinase binding	ACTB, ACTG1, ADAM10, CTNNB1, INSR, IRS1, IRS2, ITGB1, PRKCB, PTK2
0.220	BP	axonogenesis	ACTB, ACTG1, ILK, ITGAV, ITGB1, LAMA1, LAMB1, LAMB2, LAMC1, PRKCA, PTK2, SRC, TUBB3
0.441	BP	organ development	CAV1, CAV2, CAV3, CTNNB1, DYNC2H1, GJA1, HBEGF, ILK, INSR, IRS1, IRS2, ITGA6, ITGB1, LAMA2, LAMA3, LAMA5, LAMB1, LAMB2, LAMB3, LAMC2, LAMC3, NME1, PRKCA, SLC8A1, SRC, TLR4
0.067	CC	cytoplasmic dynein complex	DYNC1H1, DYNC1I1, DYNC1LI1, DYNC1LI2
0.400	CC	cytosol	ACTB, ACTG1, ARHGEF2, CAV1, CAV2, CTNNB1, DYNC1H1, DYNC1I2, FASN, GJA1, HSPD1, ILK, INSR, IRS1, IRS2, NME1, PRKCA, PRKCB, PRKCG, PTK2, SRC, TUBB, TUBB2C, TUBB4
0.153	BP	microtubule cytoskeleton organization	ARHGEF2, CAV1, CAV3, CTNNB1, DYNC1H1, DYNC1LI1, PTK2, TUBB, TUBB1
0.271	BP	positive regulation of response to stimulus	ADAM10, BST2, CAV1, CAV2, CTNNB1, GJA1, HBEGF, HSPD1, ILK, INSR, IRS1, ITGB1, PRKCA, PRKCB, PRKCG, TLR4
0.271	BP	regulation of cellular component organization	ADAM10, ARHGEF2, CAV1, CAV2, CAV3, CTNNB1, DYNC1LI1, HBEGF, ILK, INSR, ITGAV, ITGB1, PRKCA, PTK2, PTPRF, SRC
0.136	BP	cell-substrate adhesion	CTNNB1, ILK, ITGA6, ITGAV, ITGB1, LAMA5, LAMB1, LAMC1
0.271	BP	cell cycle process	ARHGEF2, CAV2, CTNNB1, DYNC1H1, DYNC1I2, DYNC1LI1, ILK, INSR, ITGB1, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4
0.050	CC	laminin-10 complex	LAMA5, LAMB1, LAMC1
0.050	CC	laminin-11 complex	LAMA5, LAMB2, LAMC1
0.237	BP	intracellular protein kinase cascade	BST2, CAV1, CAV3, CTNNB1, GJA1, HBEGF, ILK, INSR, ITGAV, ITGB1, PRKCA, PRKCB, SRC, TLR4
0.220	BP	purine ribonucleoside triphosphate metabolic process	ATP1B3, HSPD1, NME1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.186	BP	regulation of intracellular protein kinase cascade	BST2, CAV1, CAV3, CTNNB1, GJA1, HBEGF, ILK, INSR, ITGB1, PRKCB, TLR4
0.117	CC	receptor complex	HSPD1, INSR, IRS1, ITGA6, ITGAV, ITGB1, TLR4

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Ratio	Type	Description	Genes
0.169	BP	axon guidance	ACTB, ACTG1, ITGAV, ITGB1, LAMA1, LAMB1, LAMC1, PTK2, SRC, TUBB3
0.068	MF	phosphatidylinositol 3-kinase binding	INSR, IRS1, IRS2, TLR4
0.119	BP	peptidyl-tyrosine phosphorylation	CAV1, INSR, ITGB1, PRKCA, PTK2, SRC, TLR4
0.203	BP	positive regulation of signal transduction	BST2, CAV1, CAV2, CTNNB1, GJA1, HBEGF, ILK, INSR, IRS1, ITGB1, PRKCB, TLR4
0.068	BP	substrate adhesion-dependent cell spreading	ILK, LAMA5, LAMB1, LAMC1
0.153	BP	muscle organ development	CAV1, CAV2, CAV3, GJA1, HBEGF, ILK, LAMA2, LAMA5, LAMB2
0.237	BP	cell cycle phase	ARHGEF2, CAV2, DYNC1H1, DYNC1I2, DYNC1LI1, INSR, ITGB1, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4
0.136	BP	leukocyte migration	ADAM10, ATP1B3, CAV1, ITGA6, ITGAV, ITGB1, PRKCA, SRC
0.237	BP	enzyme linked receptor protein signaling pathway	ADAM10, ARHGEF2, CAV1, CTNNB1, HBEGF, ILK, INSR, IRS1, IRS2, PRKCA, PRKCG, PTK2, PTPRF, SRC
0.169	BP	positive regulation of cellular component organization	CAV1, CAV3, CTNNB1, ILK, INSR, ITGAV, ITGB1, PRKCA, PTPRF, SRC
0.250	CC	cell projection	ACTB, ACTG1, ARHGEF2, CAV1, CTNNB1, DYNC2H1, ILK, ITGA6, ITGB1, PRKCA, PRKCG, PTK2, PTPRF, SLC8A1, TUBB4
0.102	BP	cellular component assembly involved in morphogenesis	ACTG1, CAV3, DYNC2H1, ILK, ITGB1, LAMA5
0.153	BP	positive regulation of intracellular protein kinase cascade	BST2, CTNNB1, GJA1, HBEGF, ILK, INSR, ITGB1, PRKCB, TLR4
0.186	BP	GTP metabolic process	NME1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.167	CC	cell surface	ADAM10, CAV1, CAV2, CAV3, HBEGF, HSPD1, ITGA6, ITGAV, ITGB1, TLR4
0.220	BP	mitotic cell cycle	ARHGEF2, CAV2, DYNC1H1, DYNC1I2, DYNC1LI1, INSR, ITGB1, TUBB, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4
0.117	CC	adherens junction	CAV1, CTNNB1, GJA1, ILK, ITGA6, ITGB1, PTK2
0.203	BP	transmembrane receptor protein tyrosine kinase signaling pathway	ADAM10, ARHGEF2, CTNNB1, HBEGF, INSR, IRS1, IRS2, PRKCA, PRKCG, PTK2, PTPRF, SRC
0.233	CC	membrane fraction	CAV1, CAV2, CAV3, CTNNB1, GJA1, INSR, IRS1, IRS2, ITGB1, LAMB2, LAMC2, PRKCA, PRKCG, PTPRF
0.220	BP	cell activation	ADAM10, BST2, CAV1, CTNNB1, HSPD1, IRS2, ITGB1, PRKCA, PRKCB, PRKCG, SLC8A1, SRC, TLR4
0.102	BP	striated muscle cell development	ACTG1, CAV2, CAV3, ILK, ITGB1, LAMB2
0.136	BP	positive regulation of phosphorylation	CAV1, ILK, INSR, IRS1, ITGA6, ITGB1, PRKCA, TLR4
0.085	BP	regulation of microtubule cytoskeleton organization	ARHGEF2, CAV1, CAV3, CTNNB1, DYNC1LI1
0.051	MF	nitric-oxide synthase binding	ACTB, CAV1, CAV3
0.068	MF	SH2 domain binding	INSR, IRS1, PTK2, SRC
0.068	MF	insulin receptor binding	IRS1, IRS2, IRS4, PTPRF
0.051	BP	membrane raft organization	CAV1, CAV2, CAV3
0.305	BP	apoptosis	ARHGEF2, CAV1, CTNNB1, GJA1, HSPD1, ILK, IRS2, ITGA6, ITGAV, ITGB1, NME1, PRKCA, PRKCB, PTK2, PTPRF, TLR4, TUBB, TUBB2C
0.102	MF	motor activity	DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1
0.186	BP	purine ribonucleoside triphosphate catabolic process	HSPD1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.305	BP	response to organic substance	ADAM10, CAV1, CTNNB1, GJA1, HSPD1, INSR, IRS1, IRS2, ITGA6, ITGB1, NME1, PRKCA, PRKCB, PTK2, PTPRF, SLC8A1, SRC, TLR4
0.186	BP	ribonucleoside triphosphate catabolic process	HSPD1, RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.102	BP	cell-matrix adhesion	CTNNB1, ILK, ITGA6, ITGAV, ITGB1, LAMA5
0.153	BP	interspecies interaction between organisms	CAV1, DYNC1I2, DYNC1LI1, HSPD1, INSR, ITGAV, ITGB1, SRC, TLR4
0.169	BP	GTP catabolic process	RP11-631M21.2, TUBA1C, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB2C, TUBB3, TUBB4, TUBB6
0.068	BP	regulation of glucose import	INSR, IRS1, IRS2, PRKCA
0.169	BP	M phase	ARHGEF2, CAV2, DYNC1H1, DYNC1LI1, INSR, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3
0.169	BP	leukocyte activation	ADAM10, BST2, CAV1, CTNNB1, HSPD1, IRS2, ITGB1, PRKCB, SRC, TLR4
0.167	CC	neuron projection	ACTB, ACTG1, ARHGEF2, CTNNB1, ILK, PRKCA, PRKCG, PTPRF, SLC8A1, TUBB4
0.051	BP	positive regulation of glycogen biosynthetic process	INSR, IRS1, IRS2
0.254	BP	regulation of apoptosis	ARHGEF2, CAV1, CTNNB1, HSPD1, ILK, IRS2, ITGA6, ITGAV, ITGB1, NME1, PRKCA, PTPRF, TLR4, TUBB, TUBB2C
0.051	MF	protein kinase C activity	PRKCA, PRKCB, PRKCG
0.153	BP	MAPKKK cascade	CAV1, CAV3, CTNNB1, ILK, INSR, ITGAV, ITGB1, PRKCA, TLR4
0.119	BP	nerve growth factor receptor signaling pathway	ARHGEF2, IRS1, IRS2, PRKCA, PRKCG, PTPRF, SRC
0.390	BP	negative regulation of cellular process	ADAM10, ARHGEF2, CAV1, CAV2, CAV3, CTNNB1, DYNC1LI1, GJA1, HBEGF, HSPD1, ILK, INSR, IRS1, IRS2, ITGA6, ITGAV, ITGB1, NME1, PRKCA, PRKCG, PTK2, PTPRF, TLR4
0.153	BP	lymphocyte activation	BST2, CAV1, CTNNB1, HSPD1, IRS2, ITGB1, PRKCB, SRC, TLR4
0.119	BP	regulation of MAPKKK cascade	CAV1, CAV3, CTNNB1, ILK, INSR, ITGB1, TLR4
0.102	BP	B cell activation	BST2, HSPD1, IRS2, ITGB1, PRKCB, TLR4
0.085	BP	fibroblast growth factor receptor signaling pathway	CTNNB1, INSR, IRS1, IRS2, SRC
0.051	BP	sarcomere organization	ACTG1, CAV3, ITGB1
0.136	BP	mitosis	ARHGEF2, CAV2, DYNC1LI1, INSR, TUBB, TUBB2A, TUBB2B, TUBB3
0.136	BP	nuclear division	ARHGEF2, CAV2, DYNC1LI1, INSR, TUBB, TUBB2A, TUBB2B, TUBB3
0.083	CC	cell-substrate adherens junction	CAV1, CTNNB1, ILK, ITGB1, PTK2
0.085	BP	cell-cell junction organization	ACTB, ACTG1, CTNNB1, GJA1, ITGB1
0.169	BP	positive regulation of apoptosis	ARHGEF2, CTNNB1, HSPD1, ITGA6, ITGB1, PRKCA, PTPRF, TLR4, TUBB, TUBB2C
0.102	BP	regulation of epithelial cell proliferation	CAV1, CAV2, CTNNB1, LAMB1, LAMC1, NME1
0.034	MF	histone kinase activity (H3-T6 specific)	PRKCA, PRKCB
0.033	CC	laminin-2 complex	LAMB1, LAMC2
0.033	CC	laminin-3 complex	LAMA1, LAMB2
0.051	BP	negative regulation of insulin receptor signaling pathway	IRS1, PRKCA, PTPRF
0.136	BP	negative regulation of cell differentiation	ARHGEF2, CAV1, CTNNB1, ITGAV, ITGB1, NME1, PTK2, TLR4
0.051	BP	regulation of glycoprotein biosynthetic process	CTNNB1, HBEGF, INSR
0.233	CC	integral to plasma membrane	ATP1B3, BST2, CAV1, CAV2, GJA1, HBEGF, INSR, IRS1, ITGA6, ITGAV, ITGB1, PTPRF, SLC8A1, TLR4
0.288	BP	system process	CAV1, CAV2, CAV3, CTNNB1, GJA1, HBEGF, ILK, LAMB2, LAMC3, PRKCA, PRKCB, PRKCG, PTK2, PTPRF, SLC8A1, SRC, TLR4
0.237	BP	tissue development	CAV1, CAV2, CTNNB1, GJA1, ILK, ITGB1, LAMA3, LAMA5, LAMB2, LAMB3, LAMC1, LAMC2, PRKCA, SRC
0.034	BP	caveola assembly	CAV1, CAV2
0.034	BP	histone H3-T6 phosphorylation	PRKCA, PRKCB
0.034	BP	membrane raft assembly	CAV1, CAV2
0.153	BP	negative regulation of cell proliferation	CAV1, CAV2, CTNNB1, GJA1, ILK, ITGB1, NME1, PRKCA, PTPRF
0.050	CC	intercalated disc	CTNNB1, GJA1, ITGB1
0.051	BP	modification by symbiont of host morphology or physiology	INSR, ITGAV, TLR4
0.136	BP	positive regulation of transport	CAV1, INSR, IRS1, IRS2, ITGAV, ITGB1, PRKCA, TLR4
0.133	CC	perinuclear region of cytoplasm	CAV1, CAV2, CTNNB1, DYNC1I1, LAMB1, LAMC2, NME1, TLR4
0.186	BP	chemical homeostasis	CAV1, CAV3, CTNNB1, ILK, INSR, IRS1, IRS2, ITGB1, PRKCA, PRKCB, SLC8A1
0.033	CC	insulin receptor complex	INSR, IRS1
0.068	BP	regulation of smooth muscle cell proliferation	CTNNB1, HBEGF, ILK, PRKCA
0.085	BP	G2/M transition of mitotic cell cycle	DYNC1H1, DYNC1I2, TUBB, TUBB2C, TUBB4
0.085	BP	positive regulation of MAPKKK cascade	CTNNB1, ILK, INSR, ITGB1, TLR4
0.085	BP	response to carbohydrate stimulus	INSR, IRS2, PRKCA, PRKCB, SLC8A1
0.068	MF	structural constituent of cytoskeleton	ACTB, ACTG1, TUBB, TUBB1
0.051	BP	positive regulation of glucose import	INSR, IRS1, IRS2
0.102	MF	peptide binding	INSR, ITGB1, TUBB, TUBB2A, TUBB2B, TUBB3
0.033	CC	lipopolysaccharide receptor complex	HSPD1, TLR4
0.068	MF	microtubule motor activity	DYNC1H1, DYNC1I1, DYNC1I2, DYNC2H1
0.050	CC	integrin complex	ITGA6, ITGAV, ITGB1
0.051	BP	negative regulation of myeloid leukocyte differentiation	CTNNB1, NME1, TLR4
0.254	MF	ATP binding	ACTB, ACTG1, DYNC1H1, DYNC1LI1, DYNC1LI2, DYNC2H1, HSPD1, ILK, INSR, NME1, PRKCA, PRKCB, PRKCG, PTK2, SRC
0.085	BP	regulation of calcium ion transport	CAV1, CAV3, CTNNB1, GJA1, SLC8A1
0.050	CC	basal plasma membrane	CAV1, ITGA6, ITGB1
0.068	MF	extracellular matrix structural constituent	LAMA1, LAMA4, LAMB1, LAMC1
0.085	BP	negative regulation of kinase activity	CAV1, CAV3, ILK, IRS2, PRKCA
0.136	BP	blood vessel development	CAV1, CTNNB1, GJA1, ITGAV, ITGB1, LAMA4, LAMA5, PTK2
0.034	MF	ion channel binding	CTNNB1, SRC
0.102	BP	regulation of MAP kinase activity	CAV1, CAV3, ILK, INSR, PRKCA, TLR4
0.085	BP	positive regulation of I-kappaB kinase/NF-kappaB cascade	BST2, CTNNB1, GJA1, PRKCB, TLR4

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Ratio	Type	Description	Genes
0.050	CC	dendritic shaft	ARHGEF2, CTNNB1, ILK
0.051	BP	cell adhesion mediated by integrin	ITGA6, ITGB1, PTK2
0.102	BP	extracellular structure organization	CTNNB1, ILK, LAMB2, LAMC1, PRKCA, PTK2
0.102	BP	striated muscle tissue development	CAV1, CAV2, GJA1, ILK, ITGB1, LAMB2
0.102	BP	muscle contraction	CAV1, CAV3, GJA1, PRKCA, SLC8A1, TLR4
0.102	BP	cellular calcium ion homeostasis	CAV1, CAV3, ITGB1, PRKCA, PRKCB, SLC8A1
0.051	BP	positive regulation of mesenchymal cell proliferation	CTNNB1, IRS1, IRS2
0.136	MF	protein tyrosine kinase activity	ILK, INSR, IRS1, PRKCA, PRKCB, PRKCG, PTK2, SRC
0.034	MF	insulin-like growth factor I binding	INSR, ITGAV
0.102	BP	platelet activation	PRKCA, PRKCB, PRKCG, SLC8A1, SRC, TLR4
0.119	BP	response to inorganic substance	ACTB, ACTG1, CAV1, CTNNB1, INSR, PRKCA, SLC8A1
0.051	BP	regulation of microtubule polymerization or depolymerization	ARHGEF2, CAV1, CAV3
0.051	BP	regulation of nitric oxide biosynthetic process	CAV1, INSR, TLR4
0.034	BP	positive regulation of fatty acid beta-oxidation	IRS1, IRS2
0.034	BP	positive regulation of interferon-alpha production	HSPD1, TLR4
0.102	BP	protein oligomerization	CAV1, CAV2, GJA1, ILK, INSR, IRS1
0.051	BP	cytoskeleton-dependent intracellular transport	DYNC1I1, TUBA1C, TUBB
0.068	BP	tissue homeostasis	CTNNB1, ITGB1, SRC, TLR4
0.051	BP	adherens junction organization	ACTB, ACTG1, CTNNB1
0.119	BP	blood vessel morphogenesis	CAV1, CTNNB1, GJA1, ITGAV, ITGB1, LAMA5, PTK2
0.068	BP	odontogenesis	CTNNB1, ITGA6, LAMA5, LAMB1
0.102	BP	regulation of lymphocyte activation	CAV1, CTNNB1, HSPD1, IRS2, SRC, TLR4
0.203	BP	cell-cell signaling	ADAM10, BST2, CAV2, CTNNB1, GJA1, IRS1, IRS2, PRKCA, PRKCB, PRKCG, PTK2, PTPRF
0.102	BP	negative regulation of cellular component organization	ARHGEF2, CAV3, DYNC1LI1, ITGB1, PTK2, PTPRF
0.102	BP	gland development	CAV1, CTNNB1, IRS1, IRS2, LAMA5, SRC
0.051	BP	response to activity	INSR, ITGB1, TLR4
0.119	BP	regulation of nervous system development	ARHGEF2, CTNNB1, ILK, ITGB1, PRKCA, PTK2, PTPRF
0.068	BP	regulation of endocytosis	CAV1, ITGAV, ITGB1, PRKCA
0.068	BP	regulation of heart contraction	CAV3, GJA1, HBEGF, PRKCA
0.067	CC	focal adhesion	CAV1, ILK, ITGB1, PTK2
0.119	BP	response to cytokine stimulus	ADAM10, CAV1, CTNNB1, INSR, PRKCA, PTPRF, SRC
0.050	CC	cell-cell adherens junction	CTNNB1, GJA1, ITGA6
0.068	BP	positive regulation of cell adhesion	ILK, ITGA6, ITGAV, ITGB1
0.051	BP	positive regulation of protein kinase B signaling cascade	HBEGF, ILK, INSR
0.051	BP	regulation of synapse structure and activity	PRKCA, PTK2, PTPRF
0.068	BP	positive regulation of epithelial cell proliferation	CTNNB1, LAMB1, LAMC1, NME1
0.034	MF	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	IRS1, IRS2
0.034	BP	positive regulation of glycoprotein biosynthetic process	CTNNB1, INSR
0.068	BP	synapse organization	CTNNB1, LAMB2, PRKCA, PTK2
0.167	CC	vesicle	ADAM10, ATP1B3, CAV1, CAV2, DYNC1I1, DYNC1I2, FASN, GJA1, HSPD1, ITGB1
0.051	BP	positive regulation of cell-substrate adhesion	ILK, ITGA6, ITGB1
0.067	CC	synaptosome	ITGB1, LAMB2, PRKCA, PRKCG
0.068	BP	epidermal growth factor receptor signaling pathway	ADAM10, HBEGF, PTPRF, SRC
0.068	BP	regulation of peptidyl-tyrosine phosphorylation	CAV1, ITGB1, PRKCA, TLR4
0.034	MF	MHC class I protein binding	TUBB, TUBB2C
0.153	BP	central nervous system development	CTNNB1, DYNC2H1, IRS2, LAMB2, LAMC3, PRKCA, PTK2, SLC8A1, SRC
0.034	BP	positive regulation of microtubule polymerization	CAV1, CAV3
0.100	CC	centrosome	CTNNB1, DYNC1H1, DYNC1I2, DYNC1LI1, DYNC1LI2, NME1
0.085	BP	positive regulation of lymphocyte activation	CAV1, HSPD1, IRS2, SRC, TLR4
0.051	BP	negative regulation of MAPKKK cascade	CAV1, CAV3, TLR4
0.034	BP	astrocyte development	LAMB2, LAMC3
0.033	CC	acrosomal membrane	CAV1, CAV2
0.033	CC	fascia adherens	CTNNB1, GJA1
0.119	BP	regulation of cell development	ARHGEF2, CAV3, CTNNB1, ILK, ITGB1, PTK2, PTPRF
0.034	BP	positive regulation of dendrite morphogenesis	ILK, PTPRF
0.117	CC	synapse	ADAM10, CAV3, CTNNB1, ILK, INSR, ITGB1, PTPRF
0.034	MF	insulin-like growth factor receptor binding	INSR, IRS1
0.034	MF	lipopolysaccharide binding	HSPD1, TLR4
0.068	BP	mammary gland development	CAV1, IRS1, IRS2, SRC
0.068	BP	response to mechanical stimulus	CAV1, ITGB1, PRKCA, TLR4
0.067	CC	myofibril	ACTG1, CAV3, CTNNB1, ILK
0.085	BP	positive regulation of protein phosphorylation	CAV1, INSR, ITGB1, PRKCA, TLR4
0.034	BP	negative regulation of osteoclast differentiation	CTNNB1, TLR4
0.068	BP	positive regulation of growth	ADAM10, HBEGF, ILK, INSR
0.085	BP	epithelial tube morphogenesis	CTNNB1, GJA1, ILK, LAMA5, SRC
0.051	BP	positive regulation of endocytosis	CAV1, ITGAV, ITGB1
0.051	BP	protein heterooligomerization	ILK, INSR, IRS1
0.051	BP	regulation of wound healing	CAV1, HBEGF, TLR4
0.051	MF	signaling adaptor activity	IRS1, IRS4, SRC
0.051	BP	B cell proliferation	HSPD1, IRS2, TLR4
0.051	BP	branching involved in ureteric bud morphogenesis	CTNNB1, ILK, LAMA5
0.051	BP	negative regulation of cell projection organization	ITGB1, PTK2, PTPRF
0.051	BP	negative regulation of protein phosphorylation	CAV1, INSR, PRKCA
0.051	BP	odontogenesis of dentine-containing tooth	CTNNB1, ITGA6, LAMA5
0.051	BP	vasculogenesis	CAV1, CTNNB1, PTK2

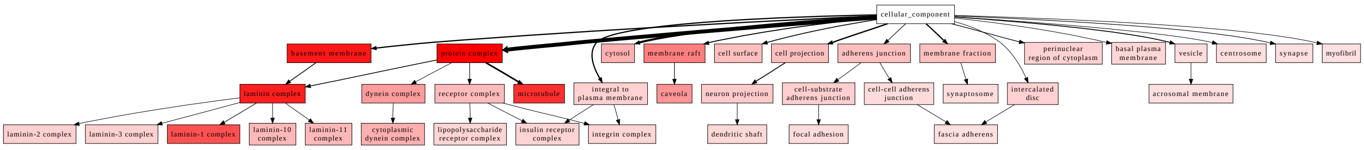


Figure 2: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 4. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

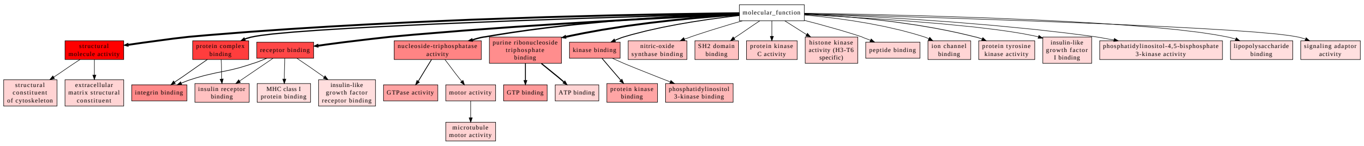


Figure 3: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 4. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

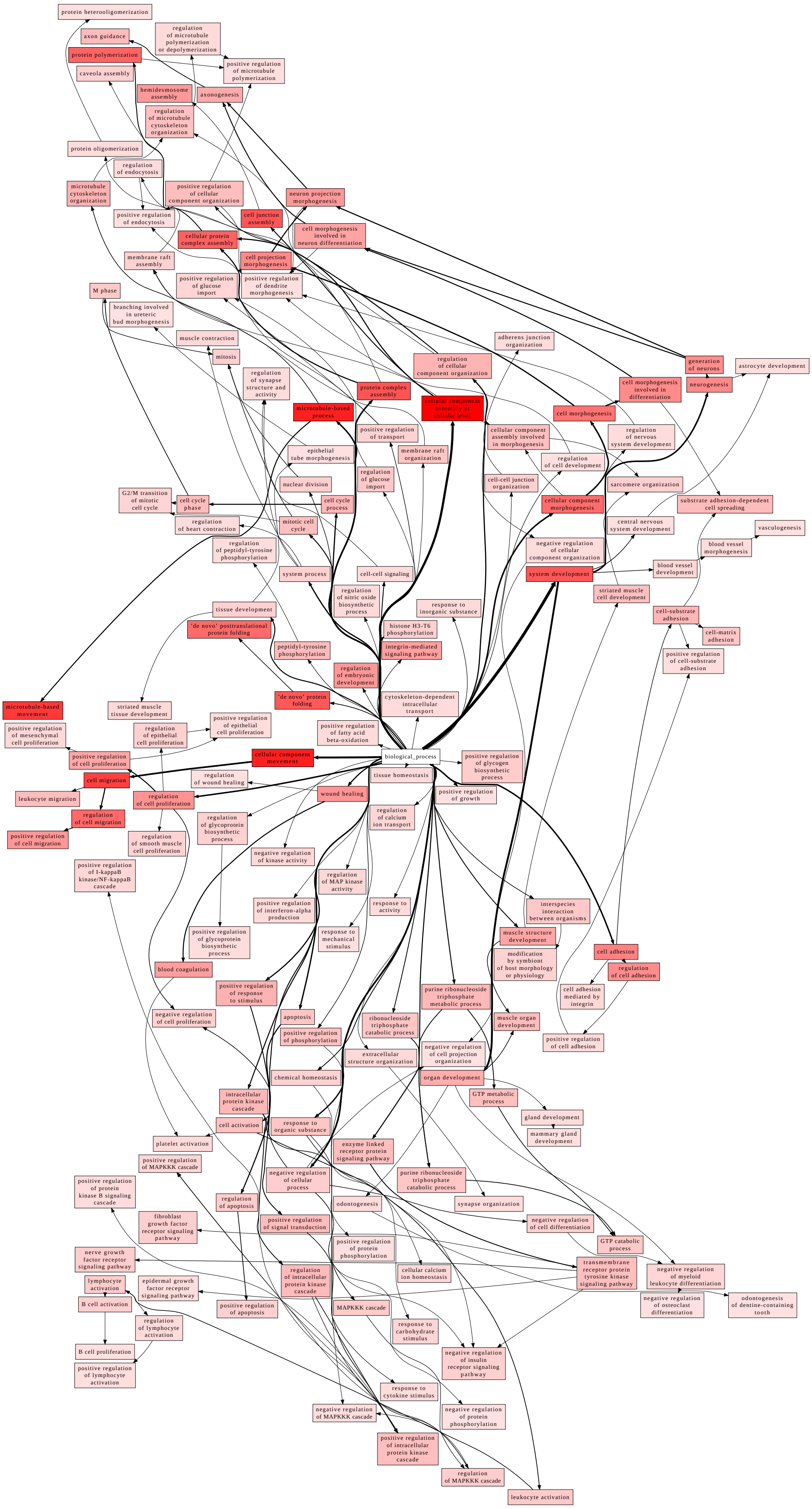


Figure 4: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 4. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

1.2 Candidate genes

Table 5: Descriptions of the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 23 rows.

S	name	locus	description	studies
u*	ADAM10	15:58887403-59042177 15q21.3	ADAM metallopeptidase domain 10 [Source:HGNC Symbol;Acc:188], type=processed_transcript,protein_coding,retained_intron, GO=[constitutive protein ectodomain proteolysis; PMA-inducible membrane protein ectodomain proteolysis; monocyte activation; T cell chemotaxis; regulation of T cell chemotaxis; positive regulation of T cell chemotaxis; Notch receptor processing; Golgi-associated vesicle; negative regulation of cell adhesion; integrin-mediated signaling pathway; response to tumor necrosis factor; integrin binding; Notch signaling pathway; positive regulation of cell growth; myeloid leukocyte activation; metalloendopeptidase activity; postsynaptic density; epidermal growth factor receptor signaling pathway; SH3 domain binding; positive regulation of cell migration; regulation of cell adhesion; leukocyte migration; protein kinase binding; in utero embryonic development; cell surface; protein homodimerization activity; chemotaxis; protein dimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCd
	ALDH7A1	5:125877533-125931110 5q23.2	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC Symbol;Acc:877], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[betaine-aldehyde dehydrogenase activity; L-aminoadipate-semialdehyde dehydrogenase activity; lysine catabolic process; lysine metabolic process; aldehyde dehydrogenase (NAD) activity; aspartate family amino acid catabolic process; cellular aldehyde metabolic process; aspartate family amino acid metabolic process; sensory perception of sound; mitochondrial matrix]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeOvariand, tscapeProstated
u	ART3	4:76932337-77033955 4q21.1	ADP-ribosyltransferase 3 [Source:HGNC Symbol;Acc:725], type=processed_transcript,protein_coding,retained_intron, GO=[NAD(P)+-protein-arginine ADP-ribosyltransferase activity; NAD+ ADP-ribosyltransferase activity; protein ADP-ribosylation; anchored to membrane]	tcgaBreastMethyl
	ATP10A	15:25922420-26110317 15q12	ATPase, class V, type 10A [Source:HGNC Symbol;Acc:13542], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[phospholipid-translocating ATPase activity; phospholipid transport; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; regulation of cell shape; ATP biosynthetic process; purine ribonucleoside triphosphate biosynthetic process; ATP metabolic process; magnesium ion binding; lipid transport; ion transmembrane transport]	tcgaBreastMethyl, tcgaColonMethyl, tscapeBCd, tscapeCRCd
u*	ATP1B3	3:141594966-141645356 3q23	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HGNC Symbol;Acc:806], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[sodium:potassium-exchanging ATPase complex; sodium:potassium-exchanging ATPase activity; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; caveola; ATP biosynthetic process; melanosome; purine ribonucleoside triphosphate biosynthetic process; ATP metabolic process; sodium ion transport; membrane raft; potassium ion transport; leukocyte migration; ion transmembrane transport; blood coagulation]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	BST2	19:17502082-17516457 19p13.11	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1119], type=processed_transcript,protein_coding,retained_intron, GO=[defense response to virus; late endosome; anchored to membrane; humoral immune response; positive regulation of I-kappaB kinase/NF-kappaB cascade; B cell activation; positive regulation of intracellular protein kinase cascade; endosome; protein homodimerization activity; protein dimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl
u*	CD109	6:74405508-74538040 6q13	CD109 molecule [Source:HGNC Symbol;Acc:21685], type=processed_transcript,protein_coding, GO=[serine-type endopeptidase inhibitor activity; anchored to membrane; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE
	CD97	19:14492213-14519531 19p13.12	CD97 molecule [Source:HGNC Symbol;Acc:1711], type=protein_coding, GO=[neuropeptide signaling pathway; inflammatory response; calcium ion binding; extracellular space; G-protein coupled receptor activity]	cosmicRecurrent, tcgaGliomaGE, tcgaOvarianCGHa
	CHL1	3:238279-451090 3p26.3	cell adhesion molecule with homology to L1CAM (close homolog of L1) [Source:HGNC Symbol;Acc:1939], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[adult locomotory behavior; neuron migration; cognition; apical part of cell; dendrite; axon guidance; cell morphogenesis involved in neuron differentiation; neuron projection morphogenesis; chemotaxis]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeNSCLCd, tscapeOvariand
*	FASN	17:80036215-80056106 17q25.3	fatty acid synthase [Source:HGNC Symbol;Acc:3594], type=protein_coding, GO=[enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity; 3-oxoacyl-[acyl-carrier-protein] reductase activity; [acyl-carrier-protein] S-acetyltransferase activity; 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity; myristoyl-[acyl-carrier-protein] hydrolase activity; [acyl-carrier-protein] S-malonyltransferase activity; palmitoyl-[acyl-carrier-protein] hydrolase activity; 3-oxoacyl-[acyl-carrier-protein] synthase activity; oleoyl-[acyl-carrier-protein] hydrolase activity; phosphopantetheine binding; acyl carrier activity; glycogen granule; pantothenate metabolic process; long-chain fatty-acyl-CoA biosynthetic process; long-chain fatty-acyl-CoA metabolic process; triglyceride biosynthetic process; melanosome; vitamin binding; fatty acid biosynthetic process; energy reserve metabolic process; cofactor binding]	tcgaGliomaGE, tscapeMelanomaa, tscapeNSCLCa, tscapeOvariana
d	GOT2	16:58741035-58768239 16q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) [Source:HGNC Symbol;Acc:4433], type=protein_coding,retained_intron, GO=[L-aspartate:2-oxoglutarate aminotransferase activity; aspartate biosynthetic process; glutamate catabolic process to aspartate; glutamate catabolic process to 2-oxoglutarate; aspartate catabolic process; oxaloacetate metabolic process; aspartate family amino acid catabolic process; aspartate family amino acid biosynthetic process; aspartate family amino acid metabolic process; pyridoxal phosphate binding; gluconeogenesis; fatty acid transport; response to ethanol; vitamin binding; lipid transport; mitochondrial matrix; cofactor binding; mitochondrial inner membrane]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u	GPR56	16:57662419-57698944 16q21	G protein-coupled receptor 56 [Source:HGNC Symbol;Acc:4512], type=protein_coding, GO=[neuropeptide signaling pathway; brain development; G-protein coupled receptor activity]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
*	HSPD1	2:198351305-198381461 2q33.1	heat shock 60kDa protein 1 (chaperonin) [Source:HGNC Symbol;Acc:5261], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[B cell cytokine production; T cell mediated immune response to tumor cell; regulation of T cell mediated immune response to tumor cell; positive regulation of T cell mediated immune response to tumor cell; lipopolysaccharide receptor complex; cyclin-dependent protein kinase activating kinase holoenzyme complex; DNA replication origin binding; positive regulation of interferon-alpha production; positive regulation of macrophage activation; isotype switching to IgG isotypes; chaperone-mediated protein complex assembly; lipopolysaccharide binding; protein refolding; positive regulation of interleukin-10 production; positive regulation of interleukin-12 production; positive regulation of interferon-gamma production; positive regulation of interleukin-6 production; p53 binding; chaperone binding; cell surface binding; coated pit; protein stabilization; 'de novo' protein folding; single-stranded DNA binding; B cell proliferation; response to unfolded protein; MyD88-dependent toll-like receptor signaling pathway; activation of caspase activity; ATP catabolic process; myeloid leukocyte activation; protein maturation; unfolded protein binding; early endosome; ATP metabolic process; positive regulation of T cell activation; B cell activation; response to protein stimulus; coated vesicle; stored secretory granule; mitochondrial matrix; mitochondrial inner membrane; cell surface; endosome; negative regulation of apoptosis; positive regulation of apoptosis; extracellular space]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	IGSF8	1:160061130-160068733 1q23.2	immunoglobulin superfamily, member 8 [Source:HGNC Symbol;Acc:17813], type=processed_transcript,protein_coding, GO=[single fertilization; skeletal muscle tissue development; striated muscle tissue development]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	ITGA6	2:173292082-173371181 2q31.1	integrin, alpha 6 [Source:HGNC Symbol;Acc:6142], type=protein_coding,retained_intron, GO=[alpha6-beta4 integrin complex; hemidesmosome assembly; laminin binding; positive regulation of cell-cell adhesion; brown fat cell differentiation; integrin complex; basal plasma membrane; cell adhesion mediated by integrin; cellular response to organic cyclic compound; cell-cell adherens junction; filopodium assembly; filopodium; positive regulation of cell-substrate adhesion; odontogenesis of dentine-containing tooth; integrin-mediated signaling pathway; integrin binding; basement membrane; positive regulation of cell adhesion; cell-matrix adhesion; external side of plasma membrane; adherens junction; regulation of cell adhesion; leukocyte migration; positive regulation of phosphorylation; cell-cell adhesion; cell surface; blood coagulation; negative regulation of apoptosis; positive regulation of apoptosis; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
*	ITGAV	2:187454790-187545628 2q32.1	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) [Source:HGNC Symbol;Acc:6150], type=processed_transcript,protein_coding,retained_intron, GO=[entry of bacterium into host cell; entry of symbiont into host cell by promotion of host phagocytosis; regulation of apoptotic cell clearance; negative regulation of low-density lipoprotein particle receptor biosynthetic process; positive regulation of osteoblast proliferation; negative regulation of lipoprotein metabolic process; opsonin binding; insulin-like growth factor I binding; transforming growth factor beta binding; negative regulation of macrophage derived foam cell differentiation; negative regulation of lipid storage; entry of virus into host cell; negative regulation of lipid transport; integrin complex; integrin-mediated signaling pathway; ERK1 and ERK2 cascade; positive regulation of cell adhesion; cell-matrix adhesion; external side of plasma membrane; positive regulation of cell migration; lipid transport; regulation of cell adhesion; leukocyte migration; negative regulation of cell differentiation; axon guidance; cell surface; blood coagulation; negative regulation of apoptosis; cell morphogenesis involved in neuron differentiation; neuron projection morphogenesis; chemotaxis]	snp3dMetastasis, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
*	ITGB1	10:33189247-33294720 10p11.22	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) [Source:HGNC Symbol;Acc:6153], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[alpha3-beta1 integrin complex; protein transport within lipid bilayer; alpha9-beta1 integrin complex; hemidesmosome; alpha-actinin binding; cell-cell adhesion mediated by integrin; cellular response to vitamin D; cell migration involved in sprouting angiogenesis; germ cell migration; sarcomere organization; intercalated disc; fibronectin binding; laminin binding; response to gonadotropin stimulus; maternal process involved in female pregnancy; response to transforming growth factor beta stimulus; cellular response to ionizing radiation; integrin complex; cleavage furrow; basal plasma membrane; myelin sheath; tight junction assembly; cell adhesion mediated by integrin; leukocyte cell-cell adhesion; neuromuscular junction; positive regulation of neuron projection development; ruffle membrane; protease binding; response to activity; collagen binding; cardiac muscle cell differentiation; positive regulation of cell-substrate adhesion; cellular response to mechanical stimulus; glycoprotein binding; negative regulation of neuron differentiation; acrosomal vesicle; negative regulation of cell projection organization; positive regulation of neuron differentiation; cellular defense response; cell fate specification; integrin-mediated signaling pathway; cellular response to protein stimulus; B cell differentiation; integrin binding; regulation of G-protein coupled receptor protein signaling pathway; sarcolemma; basement membrane; positive regulation of peptidyl-tyrosine phosphorylation; melanosome; tissue homeostasis; focal adhesion; positive regulation of cell adhesion; synaptosome; positive regulation of cell projection organization; cell-matrix adhesion; positive regulation of MAPKKK cascade; homophilic cell adhesion; adherens junction; membrane raft; B cell activation; response to protein stimulus; positive regulation of cell migration; G1/S transition of mitotic cell cycle; regulation of cell adhesion; peptide binding; leukocyte migration; stored secretory granule; striated muscle tissue development; positive regulation of phosphorylation; cellular calcium ion homeostasis; protein heterodimerization activity; protein kinase binding; in utero embryonic development; positive regulation of intracellular protein kinase cascade; actin binding; cell-cell adhesion; negative regulation of cell differentiation; response to drug; axon guidance; cell surface; negative regulation of cell proliferation; blood coagulation; cell morphogenesis involved in neuron differentiation; positive regulation of apoptosis; neuron projection morphogenesis; chemotaxis; regulation of cell cycle; protein dimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand, tscapeRCCd
	MTR	1:236958581-237067281 1q43	5-methyltetrahydrofolate-homocysteine methyltransferase [Source:HGNC Symbol;Acc:7468], type=processed_transcript,protein_coding, GO=[methionine synthase activity; homocysteine S-methyltransferase activity; homocysteine metabolic process; cobalamin binding; tetrahydrofolate metabolic process; methionine biosynthetic process; folic acid binding; aspartate family amino acid biosynthetic process; aspartate family amino acid metabolic process; protein methylation; vitamin binding; xenobiotic metabolic process; soluble fraction]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeBCd, tscapeOvariana, tscapeProstated, tscapeSCLCd
d*	NME1	17:49230897-49239789 17q21.33	non-metastatic cells 1, protein (NM23A) expressed in [Source:HGNC Symbol;Acc:7849], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[nucleoside diphosphate kinase activity; nucleoside diphosphate phosphorylation; GTP biosynthetic process; UTP biosynthetic process; CTP biosynthetic process; gamma-tubulin binding; nucleobase, nucleoside and nucleotide interconversion; negative regulation of myeloid leukocyte differentiation; deoxyribonuclease activity; response to cAMP; purine ribonucleoside triphosphate biosynthetic process; positive regulation of epithelial cell proliferation; positive regulation of DNA binding; magnesium ion binding; intermediate filament; centrosome; GTP binding; negative regulation of cell differentiation; response to drug; perinuclear region of cytoplasm; negative regulation of cell proliferation; identical protein binding]	snp3dLungC, snp3dMetastasis, tcgaBreastGE
u	PROCR	20:33758727-33765165 20q11.22	protein C receptor, endothelial [Source:HGNC Symbol;Acc:9452], type=protein_coding, GO=[MHC class I protein complex; antigen processing and presentation; centrosome; blood coagulation]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u	PTGFRN	1:117452679-117532980 1p13.1	prostaglandin F2 receptor negative regulator [Source:HGNC Symbol;Acc:9601], type=processed_transcript,protein_coding, GO=[lipid particle organization; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeNSCLCd, tscapeSCLCa, tscapeSCLCd
u*	PTPRF	1:43990858-44089343 1p34.2	protein tyrosine phosphatase, receptor type, F [Source:HGNC Symbol;Acc:9670], type=processed_transcript,protein_coding, GO=[negative regulation of nerve growth factor receptor signaling pathway; transmembrane receptor protein tyrosine phosphatase signaling pathway; phosphate binding; positive regulation of dendrite morphogenesis; excitatory synapse; transmembrane receptor protein tyrosine phosphatase activity; negative regulation of insulin receptor signaling pathway; negative regulation of cytokine-mediated signaling pathway; receptor tyrosine kinase binding; insulin receptor binding; positive regulation of neuron apoptosis; negative regulation of epidermal growth factor receptor signaling pathway; regulation of synapse structure and activity; negative regulation of cell projection organization; peptidyl-tyrosine dephosphorylation; growth cone; epidermal growth factor receptor signaling pathway; positive regulation of cell projection organization; homophilic cell adhesion; neuronal cell body; microsome; cell-cell adhesion; endosome; negative regulation of cell proliferation; cell morphogenesis involved in neuron differentiation; positive regulation of apoptosis; neuron projection morphogenesis]	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
u*	TUBA1C	12:49582519-49667116 12q13.12	tubulin, alpha 1c [Source:HGNC Symbol;Acc:20768], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cytoplasmic microtubule; cytoskeleton-dependent intracellular transport; 'de novo' posttranslational protein folding; 'de novo' protein folding; microtubule-based movement; protein polymerization; GTPase activity; GTP binding; cell division; GTP catabolic process; structural molecule activity]	tcgaBreastGE, tcgaGliomaGE

1.2.1 GO enrichment of all candidates

Table 6: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.05$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.435	CC	integral to plasma membrane	ART3, ATP1B3, BST2, CD97, GPR56, ITGA6, ITGAV, ITGB1, PROCR, PTPRF
0.182	BP	integrin-mediated signaling pathway	ADAM10, ITGA6, ITGAV, ITGB1
0.739	CC	plasma membrane	ADAM10, ART3, ATP10A, ATP1B3, BST2, CD109, CD97, CHL1, FASN, GOT2, GPR56, HSPD1, ITGA6, ITGAV, ITGB1, PROCR, PTPRF
0.130	CC	integrin complex	ITGA6, ITGAV, ITGB1
0.227	BP	leukocyte migration	ADAM10, ATP1B3, ITGA6, ITGAV, ITGB1
0.364	BP	cell adhesion	ADAM10, CD97, CHL1, GPR56, ITGA6, ITGAV, ITGB1, PTPRF
0.136	BP	aspartate family amino acid metabolic process	ALDH7A1, GOT2, MTR
0.091	BP	aspartate family amino acid catabolic process	ALDH7A1, GOT2
0.217	CC	cell surface	ADAM10, HSPD1, ITGA6, ITGAV, ITGB1
0.130	MF	integrin binding	ADAM10, ITGA6, ITGB1
0.130	CC	melanosome	ATP1B3, FASN, ITGB1
0.136	BP	purine ribonucleoside triphosphate biosynthetic process	ATP10A, ATP1B3, NME1
0.182	BP	regulation of cell adhesion	ADAM10, ITGA6, ITGAV, ITGB1
0.091	BP	aspartate family amino acid biosynthetic process	GOT2, MTR
0.136	BP	positive regulation of cell adhesion	ITGA6, ITGAV, ITGB1
0.087	MF	laminin binding	ITGA6, ITGB1
0.364	BP	cell proliferation	ADAM10, BST2, HSPD1, IGSF8, ITGAV, ITGB1, NME1, PTPRF
0.130	CC	anchored to membrane	ART3, BST2, CD109
0.227	BP	blood coagulation	ATP1B3, ITGA6, ITGAV, ITGB1, PROCR
0.136	BP	cell-matrix adhesion	ITGA6, ITGAV, ITGB1
0.087	CC	basal plasma membrane	ITGA6, ITGB1
0.130	MF	vitamin binding	FASN, GOT2, MTR
0.091	BP	cell adhesion mediated by integrin	ITGA6, ITGB1
0.136	BP	ATP metabolic process	ATP10A, ATP1B3, HSPD1
0.043	MF	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity	FASN
0.043	MF	3-oxoacyl-[acyl-carrier-protein] reductase activity	FASN
0.087	MF	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	ATP10A, ATP1B3
0.136	BP	B cell activation	BST2, HSPD1, ITGB1
0.045	BP	B cell cytokine production	HSPD1
0.043	MF	L-aminoadipate-semialdehyde dehydrogenase activity	ALDH7A1
0.045	BP	T cell mediated immune response to tumor cell	HSPD1
0.043	MF	[acyl-carrier-protein] S-acetyltransferase activity	FASN
0.043	CC	alpha3-beta1 integrin complex	ITGB1
0.043	CC	alpha6-beta4 integrin complex	ITGA6
0.043	MF	betaine-aldehyde dehydrogenase activity	ALDH7A1
0.045	BP	constitutive protein ectodomain proteolysis	ADAM10
0.043	MF	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity	FASN
0.045	BP	entry of bacterium into host cell	ITGAV
0.045	BP	entry of symbiont into host cell by promotion of host phagocytosis	ITGAV
0.261	CC	extracellular region part	CD109, CD97, CHL1, HSPD1, ITGA6, ITGB1
0.136	BP	lipid transport	ATP10A, GOT2, ITGAV
0.043	MF	methionine synthase activity	MTR
0.364	BP	nervous system development	CHL1, GPR56, IGSF8, ITGAV, ITGB1, MTR, NME1, PTPRF
0.045	BP	positive regulation of T cell mediated immune response to tumor cell	HSPD1
0.136	BP	positive regulation of cell migration	ADAM10, ITGAV, ITGB1
0.091	BP	positive regulation of cell-substrate adhesion	ITGA6, ITGB1
0.045	BP	protein transport within lipid bilayer	ITGB1
0.045	BP	regulation of T cell mediated immune response to tumor cell	HSPD1
0.455	BP	response to chemical stimulus	ADAM10, CHL1, GOT2, HSPD1, ITGA6, ITGAV, ITGB1, MTR, NME1, PTPRF
0.091	BP	'de novo' protein folding	HSPD1, TUBA1C
0.091	BP	negative regulation of cell projection organization	ITGB1, PTPRF
0.043	MF	3-oxoacyl-[acyl-carrier-protein] synthase activity	FASN
0.043	MF	L-aspartate:2-oxoglutarate aminotransferase activity	GOT2
0.043	MF	[acyl-carrier-protein] S-malonyltransferase activity	FASN
0.043	CC	alpha9-beta1 integrin complex	ITGB1
0.043	MF	myristoyl-[acyl-carrier-protein] hydrolase activity	FASN
0.043	MF	oleoyl-[acyl-carrier-protein] hydrolase activity	FASN
0.043	MF	palmitoyl-[acyl-carrier-protein] hydrolase activity	FASN
0.045	BP	aspartate biosynthetic process	GOT2
0.045	BP	glutamate catabolic process to 2-oxoglutarate	GOT2
0.045	BP	glutamate catabolic process to aspartate	GOT2
0.045	BP	regulation of apoptotic cell clearance	ITGAV
0.318	BP	response to organic substance	ADAM10, GOT2, HSPD1, ITGA6, ITGB1, NME1, PTPRF

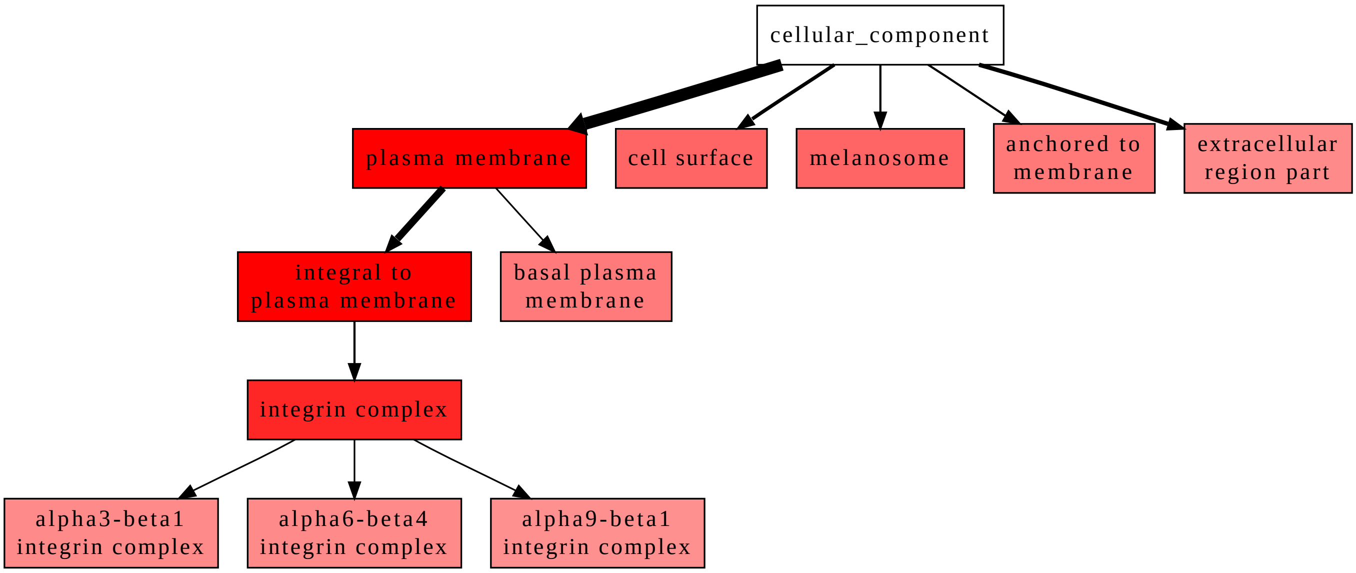


Figure 5: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 6. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

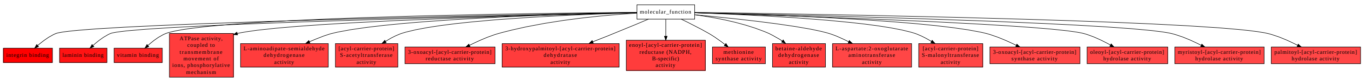


Figure 6: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 6. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

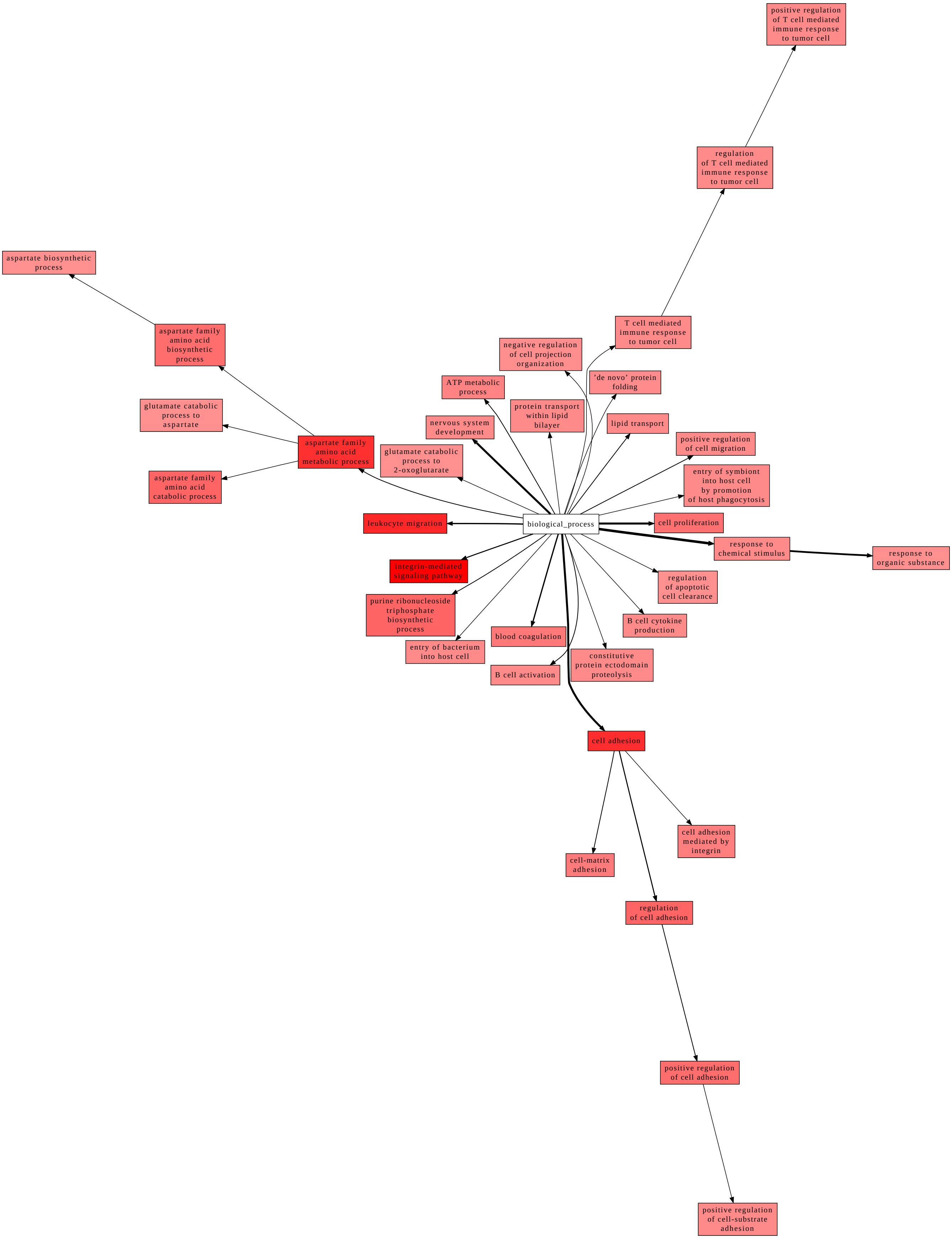
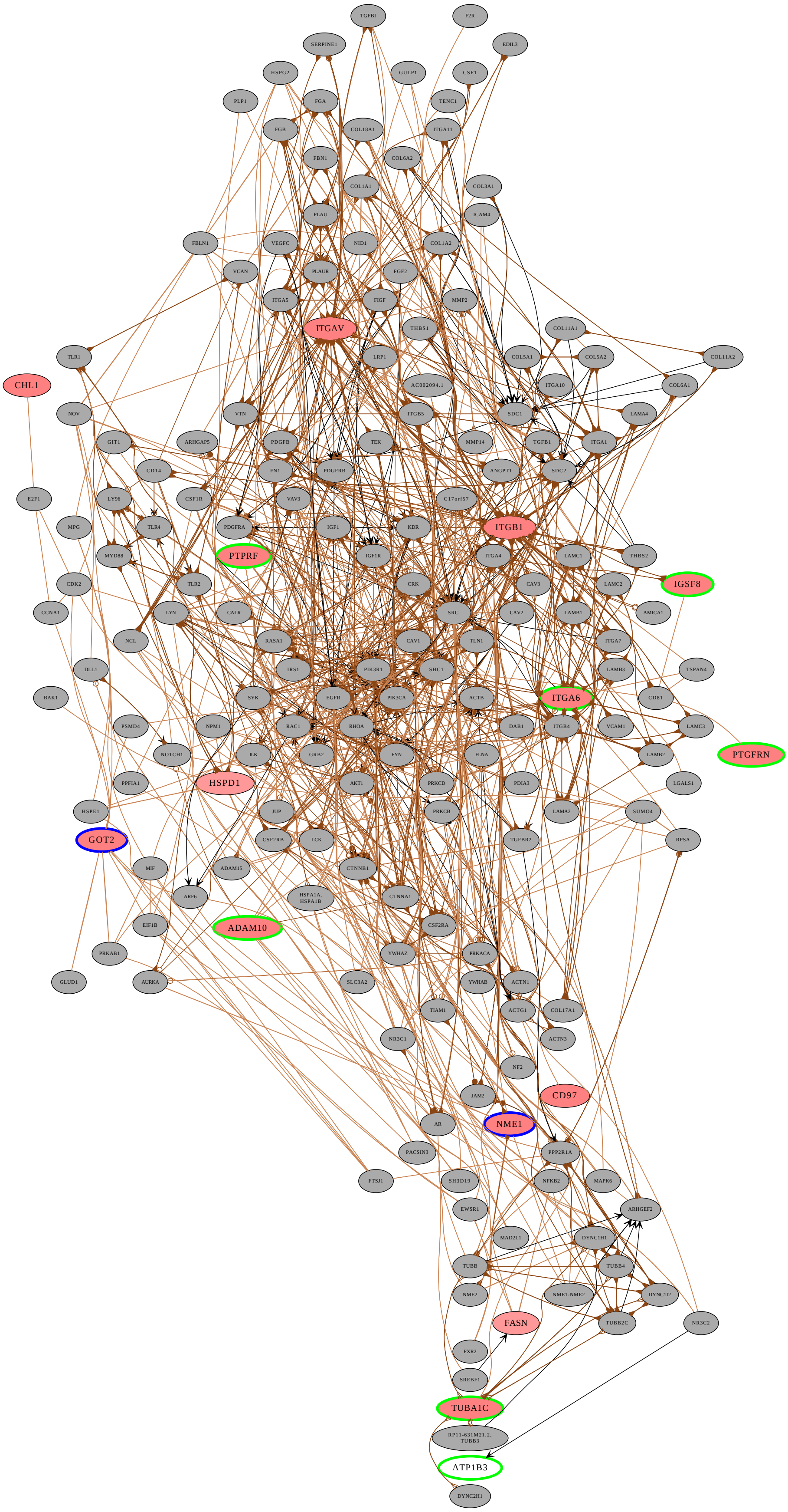


Figure 7: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 6. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

2 Candidate report for the proteins interactions

2.1 Moksiskaan candidate pathway



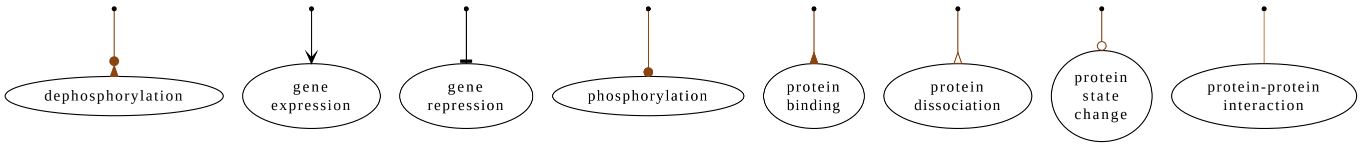


Figure 8: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The network of candidate genes is expanded by fetching related genes 1 step(s) to up and down stream. The related genes are shown on gray. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

You may use this Cytoscape session to browse the candidate pathway graph interactively.

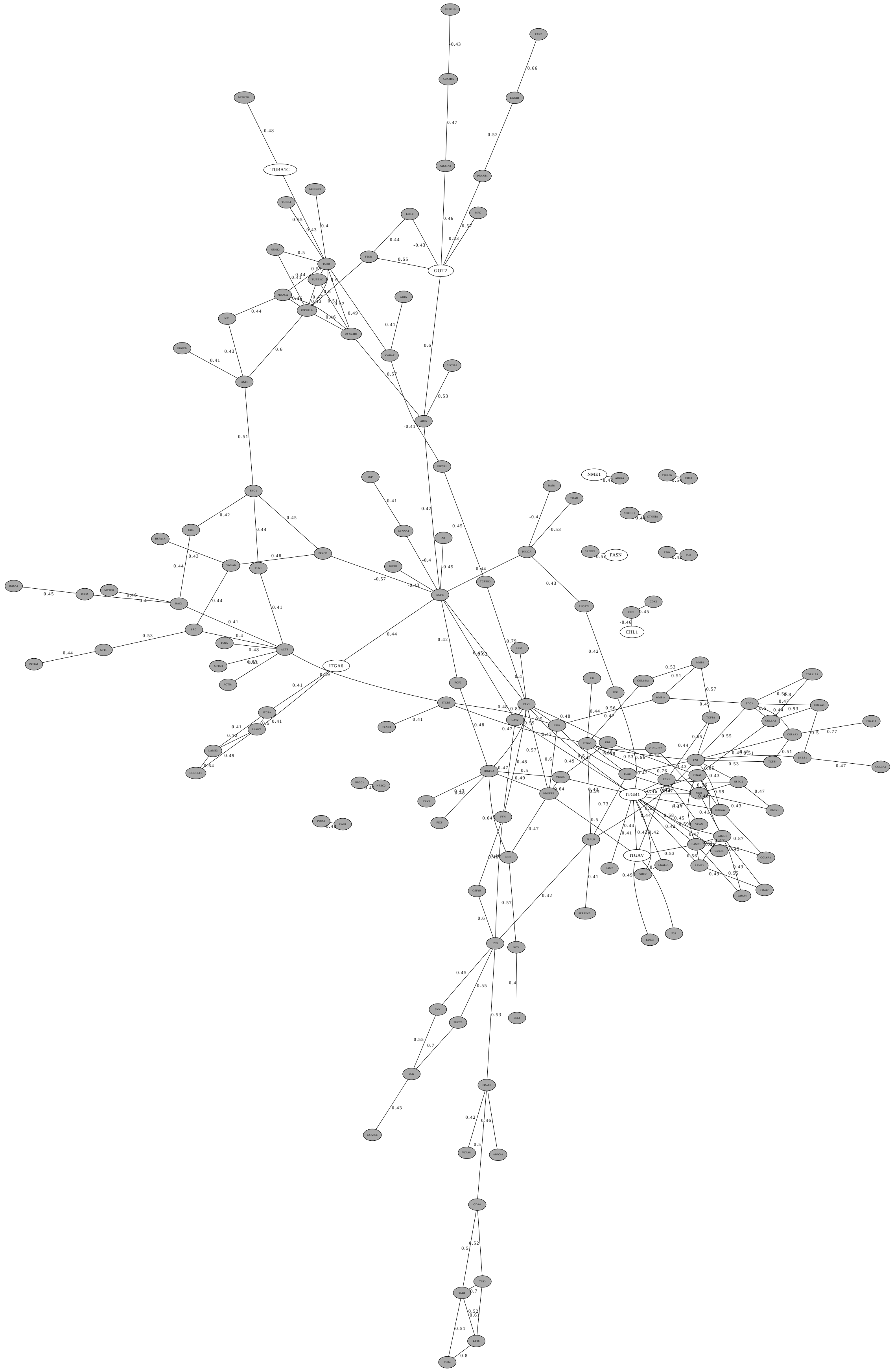


Figure 9: Observed correlations for the candidate pathway (Figure 8).

Table 7: Descriptions of the intermediated genes between the candidate genes. This table has 175 rows.

name	**description**
AC002094.1	VitronectinVitronectin V65 subunitVitronectin V10 subunitSomatomedin-B [Source:UniProtKB/Swiss-Prot;Acc:P04004] locus=17:26694297-26700110
ACTB	actin, beta [Source:HGNC Symbol;Acc:132] locus=7:5566782-5603415
ACTG1	actin, gamma 1 [Source:HGNC Symbol;Acc:144] locus=17:79476999-79479827
ACTN1	actinin, alpha 1 [Source:HGNC Symbol;Acc:163] locus=14:69340860-69446157

Continued on next page...

name	description
ACTN3	actinin, alpha 3 [Source:HGNC Symbol;Acc:165] locus=11:66313866-66330800
ADAM15	ADAM metallopeptidase domain 15 [Source:HGNC Symbol;Acc:193] locus=1:155023042-155035252
AKT1	v-akt murine thymoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:391] locus=14:105235686-105262088
AMICA1	adhesion molecule, interacts with CXADR antigen 1 [Source:HGNC Symbol;Acc:19084] locus=11:118064455-118095809
ANGPT1	angiopoietin 1 [Source:HGNC Symbol;Acc:484] locus=8:108261721-108510283
AR	androgen receptor [Source:HGNC Symbol;Acc:644] locus=X:66763874-66950461
ARF6	ADP-ribosylation factor 6 [Source:HGNC Symbol;Acc:659] locus=14:50359810-50361490
ARHGAP5	Rho GTPase activating protein 5 [Source:HGNC Symbol;Acc:675] locus=14:32545320-32628934
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Source:HGNC Symbol;Acc:682] locus=1:155916645-155966129
AURKA	aurora kinase A [Source:HGNC Symbol;Acc:11393] locus=20:54944445-54967393
BAK1	BCL2-antagonist/killer 1 [Source:HGNC Symbol;Acc:949] locus=6:33540324-33548070
C17orf57	chromosome 17 open reading frame 57 [Source:HGNC Symbol;Acc:26864] locus=17:45331208-45518678
CALR	calreticulin [Source:HGNC Symbol;Acc:1455] locus=19:13049414-13055304
CAV1	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:1527] locus=7:116164839-116201233
CAV2	caveolin 2 [Source:HGNC Symbol;Acc:1528] locus=7:115927434-116148595
CAV3	caveolin 3 [Source:HGNC Symbol;Acc:1529] locus=3:8775486-8883492
CCNA1	cyclin A1 [Source:HGNC Symbol;Acc:1577] locus=13:37005967-37017019
CD14	CD14 molecule [Source:HGNC Symbol;Acc:1628] locus=5:140011313-140013286
CD81	CD81 molecule [Source:HGNC Symbol;Acc:1701] locus=11:2397407-2418627
CDK2	cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:1771] locus=12:56360553-56366568
COL11A1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:2186] locus=1:103342023-103574052
COL11A2	collagen, type XI, alpha 2 [Source:HGNC Symbol;Acc:2187] locus=6:33130458-33160276
COL17A1	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194] locus=10:105791044-105845760
COL18A1	collagen, type XVIII, alpha 1 [Source:HGNC Symbol;Acc:2195] locus=21:46825052-46933634
COL1A1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197] locus=17:48260650-48278993
COL1A2	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198] locus=7:94023873-94060544
COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201] locus=2:189839046-189877472
COL5A1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209] locus=9:137533620-137736686
COL5A2	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210] locus=2:189896622-190044605
COL6A1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211] locus=21:47401651-47424964
COL6A2	collagen, type VI, alpha 2 [Source:HGNC Symbol;Acc:2212] locus=21:47518011-47552763
CRK	v-crk sarcoma virus CT10 oncogene homolog (avian) [Source:HGNC Symbol;Acc:2362] locus=17:1323983-1359552
CSF1	colony stimulating factor 1 (macrophage) [Source:HGNC Symbol;Acc:2432] locus=1:110452864-110473614
CSF1R	colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:2433] locus=5:149432854-149492935
CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:2435] locus=X:1387693-1429274
CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:2436] locus=22:37309670-37336491
CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa [Source:HGNC Symbol;Acc:2509] locus=5:137946656-138270723
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa [Source:HGNC Symbol;Acc:2514] locus=3:41236328-41301587
DAB1	disabled homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:2661] locus=1:57460451-59012406
DLL1	delta-like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908] locus=6:170591294-170599561
DYNC1H1	dynein, cytoplasmic 1, heavy chain 1 [Source:HGNC Symbol;Acc:2961] locus=14:102430865-102517129
DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2 [Source:HGNC Symbol;Acc:2964] locus=2:172543919-172604930
DYNC2H1	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:2962] locus=11:102980160-103350591
E2F1	E2F transcription factor 1 [Source:HGNC Symbol;Acc:3113] locus=20:32263489-32274210
EDIL3	EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol;Acc:3173] locus=5:83236373-83680611
EGFR	epidermal growth factor receptor [Source:HGNC Symbol;Acc:3236] locus=7:55086714-55324313
EIF1B	eukaryotic translation initiation factor 1B [Source:HGNC Symbol;Acc:30792] locus=3:40351175-40353915
EWSR1	Ewing sarcoma breakpoint region 1 [Source:HGNC Symbol;Acc:3508] locus=22:29663998-29696515
F2R	coagulation factor II (thrombin) receptor [Source:HGNC Symbol;Acc:3537] locus=5:76011868-76031606
FBLN1	fibulin 1 [Source:HGNC Symbol;Acc:3600] locus=22:45898118-45997015
FBN1	fibrillin 1 [Source:HGNC Symbol;Acc:3603] locus=15:48700503-48937985
FGA	fibrinogen alpha chain [Source:HGNC Symbol;Acc:3661] locus=4:155504278-155511918
FGB	fibrinogen beta chain [Source:HGNC Symbol;Acc:3662] locus=4:155484108-155492238
FGF2	fibroblast growth factor 2 (basic) [Source:HGNC Symbol;Acc:3676] locus=4:123747863-123819391
FIGF	c-fos induced growth factor (vascular endothelial growth factor D) [Source:HGNC Symbol;Acc:3708] locus=X:15363713-15402498
FLNA	filamin A, alpha [Source:HGNC Symbol;Acc:3754] locus=X:153576892-153603006
FN1	fibronectin 1 [Source:HGNC Symbol;Acc:3778] locus=2:216225163-216300895
FTSJ1	FtsJ homolog 1 (E. coli) [Source:HGNC Symbol;Acc:13254] locus=X:48334541-48344752
FXR2	fragile X mental retardation, autosomal homolog 2 [Source:HGNC Symbol;Acc:4024] locus=17:7494548-7518215
FYN	FYN oncogene related to SRC, FGR, YES [Source:HGNC Symbol;Acc:4037] locus=6:111981535-112194655
GIT1	G protein-coupled receptor kinase interacting ArfGAP 1 [Source:HGNC Symbol;Acc:4272] locus=17:27900487-27916645
GLUD1	glutamate dehydrogenase 1 [Source:HGNC Symbol;Acc:4335] locus=10:88810243-88854627
GRB2	growth factor receptor-bound protein 2 [Source:HGNC Symbol;Acc:4566] locus=17:73314157-73401790
GULP1	GULP, engulfment adaptor PTB domain containing 1 [Source:HGNC Symbol;Acc:18649] locus=2:189156396-189460653
HSPA1A	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:5232] locus=6:31783291-31785723
HSPA1B	heat shock 70kDa protein 1B [Source:HGNC Symbol;Acc:5233] locus=6:31795512-31798031
HSPE1	heat shock 10kDa protein 1 (chaperonin 10) [Source:HGNC Symbol;Acc:5269] locus=2:198364718-198368181
HSPG2	heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:5273] locus=1:22148738-22263790
ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group) [Source:HGNC Symbol;Acc:5347] locus=19:10397650-10399198
IGF1	insulin-like growth factor 1 (somatomedin C) [Source:HGNC Symbol;Acc:5464] locus=12:102789645-102874423
IGF1R	insulin-like growth factor 1 receptor [Source:HGNC Symbol;Acc:5465] locus=15:99192200-99507759
ILK	integrin-linked kinase [Source:HGNC Symbol;Acc:6040] locus=11:6624961-6632102
IRS1	insulin receptor substrate 1 [Source:HGNC Symbol;Acc:6125] locus=2:227599757-227664475
ITGA1	integrin, alpha 1 [Source:HGNC Symbol;Acc:6134] locus=5:52083730-52252327
ITGA10	integrin, alpha 10 [Source:HGNC Symbol;Acc:6135] locus=1:145524891-145543868
ITGA11	integrin, alpha 11 [Source:HGNC Symbol;Acc:6136] locus=15:68594050-68724502
ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) [Source:HGNC Symbol;Acc:6140] locus=2:182321619-182400914
ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Source:HGNC Symbol;Acc:6141] locus=12:54789045-54813244
ITGA7	integrin, alpha 7 [Source:HGNC Symbol;Acc:6143] locus=12:56078352-56109827
ITGB4	integrin, beta 4 [Source:HGNC Symbol;Acc:6158] locus=17:73713474-73753898
ITGB5	integrin, beta 5 [Source:HGNC Symbol;Acc:6160] locus=3:124480795-124606674
JAM2	junctional adhesion molecule 2 [Source:HGNC Symbol;Acc:14686] locus=21:27011584-27089874
JUP	junction plakoglobin [Source:HGNC Symbol;Acc:6207] locus=17:39775692-39943183
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase) [Source:HGNC Symbol;Acc:6307] locus=4:55944644-55991756
LAMA2	laminin, alpha 2 [Source:HGNC Symbol;Acc:6482] locus=6:129204286-129837714
LAMA4	laminin, alpha 4 [Source:HGNC Symbol;Acc:6484] locus=6:112429963-112576141
LAMB1	laminin, beta 1 [Source:HGNC Symbol;Acc:6486] locus=7:107564244-107643700
LAMB2	laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:6487] locus=3:49158547-49170551
LAMB3	laminin, beta 3 [Source:HGNC Symbol;Acc:6490] locus=1:209788220-209825811
LAMC1	laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;Acc:6492] locus=1:182992597-183114727
LAMC2	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493] locus=1:183155373-183214035
LAMC3	laminin, gamma 3 [Source:HGNC Symbol;Acc:6494] locus=9:133884469-133969860
LCK	lymphocyte-specific protein tyrosine kinase [Source:HGNC Symbol;Acc:6524] locus=1:32716840-32751766
LGALS1	lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6561] locus=22:38071615-38075813
LRP1	low density lipoprotein receptor-related protein 1 [Source:HGNC Symbol;Acc:6692] locus=12:57522276-57607134
LY96	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156] locus=8:74903587-74941322
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog [Source:HGNC Symbol;Acc:6735] locus=8:56792372-56923939
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:6763] locus=4:120980577-120988229
MAPK6	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:6879] locus=15:52311417-52358462
MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor) [Source:HGNC Symbol;Acc:7097] locus=22:24236191-24237414
MMP14	matrix metallopeptidase 14 (membrane-inserted) [Source:HGNC Symbol;Acc:7160] locus=14:23305766-23318236
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) [Source:HGNC Symbol;Acc:7166] locus=16:55512883-55540603
MPG	N-methylpurine-DNA glycosylase [Source:HGNC Symbol;Acc:7211] locus=16:127006-135852
MYD88	myeloid differentiation primary response gene (88) [Source:HGNC Symbol;Acc:7562] locus=3:38179969-38184513
NCL	nucleolin [Source:HGNC Symbol;Acc:7667] locus=2:232318242-232348352
NF2	neurofibromin 2 (merlin) [Source:HGNC Symbol;Acc:7773] locus=22:29999545-30094587
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) [Source:HGNC Symbol;Acc:7795] locus=10:104154229-104162281
NID1	nidogen 1 [Source:HGNC Symbol;Acc:7821] locus=1:236139130-236228462
NME1-NME2	NME1-NME2 readthrough [Source:HGNC Symbol;Acc:33531] locus=17:49230951-49249105
NME2	non-metastatic cells 2, protein (NM23B) expressed in [Source:HGNC Symbol;Acc:7850] locus=17:49230920-49249108
NOTCH1	notch 1 [Source:HGNC Symbol;Acc:7881] locus=9:139388896-139440314
NOV	nephroblastoma overexpressed gene [Source:HGNC Symbol;Acc:7885] locus=8:120428546-120436593
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin) [Source:HGNC Symbol;Acc:7910] locus=5:170814120-170838141
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) [Source:HGNC Symbol;Acc:7978] locus=5:142657496-142815077
NR3C2	nuclear receptor subfamily 3, group C, member 2 [Source:HGNC Symbol;Acc:7979] locus=4:148999913-149365850
PACSIN3	protein kinase C and casein kinase substrate in neurons 3 [Source:HGNC Symbol;Acc:8572] locus=11:47199076-47207994
PDGFB	platelet-derived growth factor beta polypeptide [Source:HGNC Symbol;Acc:8800] locus=22:39619364-39640756
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide [Source:HGNC Symbol;Acc:8803] locus=4:55095264-55164414
PDGFRB	platelet-derived growth factor receptor, beta polypeptide [Source:HGNC Symbol;Acc:8804] locus=5:149493400-149535423
PDIA3	protein disulfide isomerase family A, member 3 [Source:HGNC Symbol;Acc:4606] locus=15:44038590-44065477
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide [Source:HGNC Symbol;Acc:8975] locus=3:178865902-178957881
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) [Source:HGNC Symbol;Acc:8979] locus=5:67511548-67597649
PLAU	plasminogen activator, urokinase [Source:HGNC Symbol;Acc:9052] locus=10:75668935-75677255

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name	description
PLAUR	plasminogen activator, urokinase receptor [Source:HGNC Symbol;Acc:9053] locus=19:44150271-44174502
PLP1	proteolipid protein 1 [Source:HGNC Symbol;Acc:9086] locus=X:103028647-103047548
PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Source:HGNC Symbol;Acc:9245] locus=11:70116806-70230509
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha [Source:HGNC Symbol;Acc:9302] locus=19:52693274-52730687
PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit [Source:HGNC Symbol;Acc:9378] locus=12:120105558-120119435
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha [Source:HGNC Symbol;Acc:9380] locus=19:14202509-14228574
PRKCB	protein kinase C, beta [Source:HGNC Symbol;Acc:9395] locus=16:23847322-24231932
PRKCD	protein kinase C, delta [Source:HGNC Symbol;Acc:9399] locus=3:53190025-53226733
PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Source:HGNC Symbol;Acc:9561] locus=1:151227179-151239955
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) [Source:HGNC Symbol;Acc:9801] locus=7:6414154-6443608
RASA1	RAS p21 protein activator (GTPase activating protein) 1 [Source:HGNC Symbol;Acc:9871] locus=5:86563705-86688145
RHOA	ras homolog gene family, member A [Source:HGNC Symbol;Acc:667] locus=3:49396578-49450431
RP11-631M21.2	Tubulin beta-8 chain [Source:UniProtKB/Swiss-Prot;Acc:Q3ZCM7] locus=10:92828-96053
RPSA	ribosomal protein SA [Source:HGNC Symbol;Acc:6502] locus=3:39448180-39453929
SDC1	syndecan 1 [Source:HGNC Symbol;Acc:10658] locus=2:20400558-20425194
SDC2	syndecan 2 [Source:HGNC Symbol;Acc:10659] locus=8:97505579-97624000
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 [Source:HGNC Symbol;Acc:8583] locus=7:100770370-100782547
SH3D19	SH3 domain containing 19 [Source:HGNC Symbol;Acc:30418] locus=4:152041431-152149182
SHC1	SHC (Src homology 2 domain containing) transforming protein 1 [Source:HGNC Symbol;Acc:10840] locus=1:154934774-154946871
SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 [Source:HGNC Symbol;Acc:11026] locus=11:62623518-62656352
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:11283] locus=20:35973088-36034453
SREBF1	sterol regulatory element binding transcription factor 1 [Source:HGNC Symbol;Acc:11289] locus=17:17714653-17740325
SUMO4	SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae) [Source:HGNC Symbol;Acc:21181] locus=6:149721495-149722177
SYK	spleen tyrosine kinase [Source:HGNC Symbol;Acc:11491] locus=9:93564069-93660831
TEK	TEK tyrosine kinase, endothelial [Source:HGNC Symbol;Acc:11724] locus=9:27109139-27230173
TENC1	tensin like C1 domain containing phosphatase (tensin 2) [Source:HGNC Symbol;Acc:19737] locus=12:53440753-53458156
TGFB1	transforming growth factor, beta 1 [Source:HGNC Symbol;Acc:11766] locus=19:41836813-41859831
TGFBI	transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:11771] locus=5:135364584-135399507
TGFBR2	transforming growth factor, beta receptor II (70/80kDa) [Source:HGNC Symbol;Acc:11773] locus=3:30647994-30735634
THBS1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785] locus=15:39873127-39891119
THBS2	thrombospondin 2 [Source:HGNC Symbol;Acc:11786] locus=6:169615875-169654139
TIAM1	T-cell lymphoma invasion and metastasis 1 [Source:HGNC Symbol;Acc:11805] locus=21:32361860-32932290
TLN1	talin 1 [Source:HGNC Symbol;Acc:11845] locus=9:35696945-35732392
TLR1	toll-like receptor 1 [Source:HGNC Symbol;Acc:11847] locus=4:38792298-38858438
TLR2	toll-like receptor 2 [Source:HGNC Symbol;Acc:11848] locus=4:154622652-154626851
TLR4	toll-like receptor 4 [Source:HGNC Symbol;Acc:11850] locus=9:120466610-120479149
TSPAN4	tetraspanin 4 [Source:HGNC Symbol;Acc:11859] locus=11:842808-867116
TUBB	tubulin, beta [Source:HGNC Symbol;Acc:20778] locus=6:30687978-30693203
TUBB2C	tubulin, beta 2C [Source:HGNC Symbol;Acc:20771] locus=9:140135665-140138159
TUBB3	tubulin, beta 3 [Source:HGNC Symbol;Acc:20772] locus=16:89987800-90005169
TUBB4	tubulin, beta 4 [Source:HGNC Symbol;Acc:20774] locus=19:6494331-6502330
VAV3	vav 3 guanine nucleotide exchange factor [Source:HGNC Symbol;Acc:12659] locus=1:108113782-108507766
VCAM1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Acc:12663] locus=1:101185305-101204601
VCAN	versican [Source:HGNC Symbol;Acc:2464] locus=5:82767284-82878122
VEGFC	vascular endothelial growth factor C [Source:HGNC Symbol;Acc:12682] locus=4:177604689-177713881
VTN	vitronectin [Source:HGNC Symbol;Acc:12724] locus=17:26691290-26697373
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Source:HGNC Symbol;Acc:12849] locus=20:43514317-43537173
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Source:HGNC Symbol;Acc:12855] locus=8:101930804-101965616

Table 8: List of KEGG [8] pathways supporting the relationships between the genes shown in Figure 8. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Focal adhesion	93	AC002094.1, ACTB, ACTG1, ACTN1, ACTN3, AKT1, ARHGAP5, C17orf57, CAV1, CAV2, CAV3, COL11A1, COL11A2, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COL6A1, COL6A2, CRK, CTNNB1, EGFR, FIGF, FLNA, FN1, FYN, GRB2, IGF1, IGF1R, ILK, ITGA1, ITGA10, ITGA11, ITGA4, ITGA5, ITGA6, ITGA7, ITGAV, ITGB1, ITGB4, ITGB5, KDR, LAMA2, LAMA4, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1, PRKCB, RAC1, RHOA, SHC1, SRC, THBS1, THBS2, TLN1, VAV3, VEGFC
Toxoplasmosis	40	AKT1, HSPA1A, HSPA1B, ITGA6, ITGB1, LAMA2, LAMA4, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, LY96, MYD88, PIK3CA, PIK3R1, TGFB1, TLR2, TLR4
Adherens junction	37	ACTB, ACTG1, ACTN1, ACTN3, CTNNA1, CTNNB1, EGFR, FYN, IGF1R, PTPRF, RAC1, RHOA, SRC, TGFBR2
Prostate cancer	26	AKT1, AR, CDK2, CTNNB1, E2F1, EGFR, GRB2, IGF1, IGF1R, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1
ECM-receptor interaction	24	AC002094.1, C17orf57, COL11A1, COL11A2, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COL6A1, COL6A2, FN1, HSPG2, ITGA1, ITGA10, ITGA11, ITGA4, ITGA5, ITGA6, ITGA7, ITGAV, ITGB1, ITGB4, ITGB5, LAMA2, LAMA4, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, SDC1, SDC2, THBS1, THBS2
Regulation of actin cytoskeleton	23	ACTB, ACTG1, ACTN1, ACTN3, C17orf57, CD14, CRK, EGFR, F2R, FGF2, FN1, GIT1, ITGA1, ITGA10, ITGA11, ITGA4, ITGA5, ITGA6, ITGA7, ITGAV, ITGB1, ITGB4, ITGB5, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1, RAC1, RHOA, SRC, TIAM1, VAV3
Chemokine signaling pathway	21	AKT1, CRK, GRB2, LYN, PIK3CA, PIK3R1, PRKACA, PRKCB, PRKCD, RAC1, RHOA, SHC1, SRC, TIAM1, VAV3
Glioma	20	AKT1, E2F1, EGFR, GRB2, IGF1, IGF1R, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1, PRKCB, SHC1
Melanoma	18	AKT1, E2F1, EGFR, FGF2, IGF1, IGF1R, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1
VEGF signaling pathway	17	AKT1, KDR, PIK3CA, PIK3R1, PRKCB, RAC1, SRC
Phagosome	16	ACTB, ACTG1, C17orf57, CALR, CD14, DYNC1H1, DYNC1I2, DYNC2H1, ITGA5, ITGAV, ITGB1, ITGB5, RAC1, RP11-631M21.2, THBS1, THBS2, TLR2, TLR4, TUBA1C, TUBB, TUBB2C, TUBB3, TUBB4
Hypertrophic cardiomyopathy (HCM)	16	ACTB, ACTG1, C17orf57, IGF1, ITGA1, ITGA10, ITGA11, ITGA4, ITGA5, ITGA6, ITGA7, ITGAV, ITGB1, ITGB4, ITGB5, LAMA2, PRKAB1, TGFB1
Pathways in cancer	14	AKT1, AR, CCNA1, CDK2, CRK, CSF1R, CSF2RA, CTNNA1, CTNNB1, E2F1, EGFR, FGF2, FIGF, FN1, GRB2, IGF1, IGF1R, ITGA6, ITGAV, ITGB1, JUP, LAMA2, LAMA4, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, MMP2, NFKB2, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1, PRKCB, RAC1, RHOA, TGFB1, TGFBR2, VEGFC
Fc gamma R-mediated phagocytosis	14	AKT1, ARF6, CRK, LYN, PIK3CA, PIK3R1, PRKCB, PRKCD, RAC1, SYK, VAV3
HTLV-I infection	13	AKT1, CALR, CTNNB1, E2F1, LCK, MAD2L1, NFKB2, PDGFB, PDGFRA, PDGFRB, PIK3CA, PIK3R1, PRKACA, TGFB1, TGFBR2, TLN1, VCAM1
Osteoclast differentiation	11	AKT1, C17orf57, CSF1, CSF1R, FYN, GRB2, LCK, NFKB2, PIK3CA, PIK3R1, RAC1, SYK, TGFB1, TGFBR2
Fc epsilon RI signaling pathway	11	AKT1, FYN, GRB2, LYN, PIK3CA, PIK3R1, PRKCB, PRKCD, RAC1, SYK, VAV3
ErbB signaling pathway	11	AKT1, CRK, EGFR, GRB2, PIK3CA, PIK3R1, PRKCB, SHC1, SRC
Neurotrophin signaling pathway	10	AKT1, CRK, GRB2, IRS1, PIK3CA, PIK3R1, PRKCD, RAC1, RHOA, SHC1, YWHAB, YWHAZ
Tight junction	10	ACTB, ACTG1, ACTN1, ACTN3, AKT1, CTNNA1, CTNNB1, JAM2, PPP2R1A, PRKCB, PRKCD, RHOA, SRC
Leukocyte transendothelial migration	9	ACTB, ACTG1, ACTN1, ACTN3, ARHGAP5, CTNNA1, CTNNB1, ITGA4, ITGB1, JAM2, MMP2, PIK3CA, PIK3R1, PRKCB, RAC1, RHOA, VAV3, VCAM1
Gap junction	9	EGFR, GRB2, PDGFB, PDGFRA, PDGFRB, PRKACA, PRKCB, RP11-631M21.2, SRC, TUBA1C, TUBB, TUBB2C, TUBB3, TUBB4
Toll-like receptor signaling pathway	9	AKT1, CD14, LY96, MYD88, PIK3CA, PIK3R1, RAC1, TLR1, TLR2, TLR4
Endometrial cancer	9	AKT1, CTNNA1, CTNNB1, EGFR, GRB2, ILK, PIK3CA, PIK3R1
MAPK signaling pathway	9	AKT1, CD14, CRK, EGFR, FGF2, FLNA, GRB2, HSPA1A, HSPA1B, NFKB2, PDGFB, PDGFRA, PDGFRB, PRKACA, PRKCB, RAC1, RASA1, TGFB1, TGFBR2
Measles	8	AKT1, CDK2, FYN, HSPA1A, HSPA1B, MYD88, PIK3CA, PIK3R1, TLR2, TLR4
Non-small cell lung cancer	8	AKT1, E2F1, EGFR, GRB2, PIK3CA, PIK3R1, PRKCB
Pathogenic Escherichia coli infection	8	ACTB, ACTG1, ARHGEF2, CD14, CTNNB1, FYN, ITGB1, LY96, NCL, RHOA, RP11-631M21.2, TLR4, TUBA1C, TUBB, TUBB2C, TUBB3, TUBB4, YWHAZ
Insulin signaling pathway	7	AKT1, CRK, FASN, GRB2, IRS1, PIK3CA, PIK3R1, PRKAB1, PRKACA, PTPRF, SHC1, SREBF1
Natural killer cell mediated cytotoxicity	7	FYN, GRB2, LCK, PIK3CA, PIK3R1, PRKCB, RAC1, SHC1, SYK, VAV3
Cholinergic synapse	6	AKT1, FYN, PIK3CA, PIK3R1, PRKACA, PRKCB
Bacterial invasion of epithelial cells	6	ACTB, ACTG1, CAV1, CAV2, CAV3, CRK, CTNNA1, CTNNB1, FN1, ILK, ITGA5, ITGB1, PIK3CA, PIK3R1, RAC1, RHOA, SHC1, SRC
Influenza A	6	ACTB, ACTG1, AKT1, HSPA1A, HSPA1B, MYD88, PIK3CA, PIK3R1, PRKCB, TLR4
Chagas disease (American trypanosomiasis)	6	AKT1, CALR, MYD88, PIK3CA, PIK3R1, PPP2R1A, SERPINE1, TGFB1, TGFBR2, TLR2, TLR4
GnRH signaling pathway	5	EGFR, GRB2, MMP14, MMP2, PRKACA, PRKCB, PRKCD, SRC

Continued on next page...

name	edges	genes
Cytokine-cytokine receptor interaction	5	CSF1, CSF1R, CSF2RA, CSF2RB, EGFR, FIGF, KDR, PDGFB, PDGFRA, PDGFRB, TGFB1, TGFBR2, VEGFC
T cell receptor signaling pathway	5	AKT1, FYN, GRB2, LCK, PIK3CA, PIK3R1, RHOA, VAV3
Salmonella infection	4	ACTB, ACTG1, CD14, DYNC1H1, DYNC1I2, DYNC2H1, FLNA, MYD88, RAC1, TLR4
Chronic myeloid leukemia	4	AKT1, CRK, E2F1, GRB2, PIK3CA, PIK3R1, SHC1, TGFB1, TGFBR2
Type II diabetes mellitus	4	IRS1, PIK3CA, PIK3R1, PRKCD
Tuberculosis	4	AKT1, CD14, HSPD1, MYD88, RHOA, SRC, SYK, TGFB1, TLR1, TLR2, TLR4
Vibrio cholerae infection	4	ACTB, ACTG1, PRKACA, PRKCB
Legionellosis	4	CD14, HSPA1A, HSPA1B, HSPD1, MYD88, NFKB2, TLR2, TLR4
Small cell lung cancer	4	AKT1, CDK2, E2F1, FN1, ITGA6, ITGAV, ITGB1, LAMA2, LAMA4, LAMB1, LAMB2, LAMB3, LAMC1, LAMC2, LAMC3, PIK3CA, PIK3R1
Acute myeloid leukemia	4	AKT1, CCNA1, GRB2, JUP, PIK3CA, PIK3R1
Long-term depression	3	IGF1, IGF1R, LYN, PPP2R1A, PRKCB
Aldosterone-regulated sodium reabsorption	3	ATP1B3, IGF1, IRS1, NR3C2, PIK3CA, PIK3R1, PRKCB
TGF-beta signaling pathway	3	PPP2R1A, RHOA, TGFB1, TGFBR2, THBS1, THBS2
Rheumatoid arthritis	2	ANGPT1, CSF1, TEK, TGFB1, TLR2, TLR4
Colorectal cancer	2	AKT1, CTNNB1, PIK3CA, PIK3R1, RAC1, RHOA, TGFB1, TGFBR2
Hepatitis C	2	AKT1, CD81, EGFR, GRB2, PIK3CA, PIK3R1, PPP2R1A
Complement and coagulation cascades	2	F2R, FGA, FGB, PLAU, PLAUR, SERPINE1
Jak-STAT signaling pathway	2	AKT1, CSF2RA, CSF2RB, GRB2, PIK3CA, PIK3R1
Dopaminergic synapse	2	AKT1, PPP2R1A, PRKACA, PRKCB
Malaria	2	CD81, LRP1, MYD88, SDC1, SDC2, TGFB1, THBS1, THBS2, TLR2, TLR4, VCAM1
Leishmaniasis	2	ITGA4, ITGB1, MYD88, PRKCB, TGFB1, TLR2, TLR4
B cell receptor signaling pathway	2	AKT1, CD81, GRB2, LYN, PIK3CA, PIK3R1, PRKCB, RAC1, SYK, VAV3
Viral myocarditis	2	ACTB, ACTG1, CAV1, FYN, LAMA2, RAC1
Notch signaling pathway	1	DLL1, NOTCH1
Dorso-ventral axis formation	1	EGFR, GRB2, NOTCH1
Wnt signaling pathway	1	CTNNB1, PPP2R1A, PRKACA, PRKCB, RAC1, RHOA
Oocyte meiosis	1	AR, AURKA, CDK2, IGF1, IGF1R, MAD2L1, PPP2R1A, PRKACA, YWHAB, YWHAZ
Progesterone-mediated oocyte maturation	1	AKT1, CCNA1, CDK2, IGF1, IGF1R, MAD2L1, PIK3CA, PIK3R1, PRKACA
Herpes simplex infection	1	CDK2, MYD88, TLR2

2.2 Candidate genes

Table 9: Descriptions of the candidate genes. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 23 rows.

S	name	locus	description
u*	ADAM10	15:58887403-59042177 15q21.3	ADAM metallopeptidase domain 10 [Source:HGNC Symbol;Acc:188], type=processed_transcript,protein_coding,retained_intron, GO=[constitutive protein ectodomain proteolysis; PMA-inducible membrane protein ectodomain proteolysis; monocyte activation; T cell chemotaxis; regulation of T cell chemotaxis; positive regulation of T cell chemotaxis; Notch receptor processing; Golgi-associated vesicle; negative regulation of cell adhesion; integrin-mediated signaling pathway; response to tumor necrosis factor; integrin binding; Notch signaling pathway; positive regulation of cell growth; myeloid leukocyte activation; metalloendopeptidase activity; postsynaptic density; epidermal growth factor receptor signaling pathway; SH3 domain binding; positive regulation of cell migration; regulation of cell adhesion; leukocyte migration; protein kinase binding; in utero embryonic development; cell surface; protein homodimerization activity; chemotaxis; protein dimerization activity; identical protein binding]
	ALDH7A1	5:125877533-125931110 5q23.2	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC Symbol;Acc:877], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[betaine-aldehyde dehydrogenase activity; L-aminoadipate-semialdehyde dehydrogenase activity; lysine catabolic process; lysine metabolic process; aldehyde dehydrogenase (NAD) activity; aspartate family amino acid catabolic process; cellular aldehyde metabolic process; aspartate family amino acid metabolic process; sensory perception of sound; mitochondrial matrix]
u	ART3	4:76932337-77033955 4q21.1	ADP-ribosyltransferase 3 [Source:HGNC Symbol;Acc:725], type=processed_transcript,protein_coding,retained_intron, GO=[NAD(P)+-protein-arginine ADP-ribosyltransferase activity; NAD+ ADP-ribosyltransferase activity; protein ADP-ribosylation; anchored to membrane]
	ATP10A	15:25922420-26110317 15q12	ATPase, class V, type 10A [Source:HGNC Symbol;Acc:13542], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[phospholipid-translocating ATPase activity; phospholipid transport; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; regulation of cell shape; ATP biosynthetic process; purine ribonucleoside triphosphate biosynthetic process; ATP metabolic process; magnesium ion binding; lipid transport; ion transmembrane transport]
u*	ATP1B3	3:141594966-141645356 3q23	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HGNC Symbol;Acc:806], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[sodium:potassium-exchanging ATPase complex; sodium:potassium-exchanging ATPase activity; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; caveola; ATP biosynthetic process; melanosome; purine ribonucleoside triphosphate biosynthetic process; ATP metabolic process; sodium ion transport; membrane raft; potassium ion transport; leukocyte migration; ion transmembrane transport; blood coagulation]
u	BST2	19:17502082-17516457 19p13.11	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1119], type=processed_transcript,protein_coding,retained_intron, GO=[defense response to virus; late endosome; anchored to membrane; humoral immune response; positive regulation of I-kappaB kinase/NF-kappaB cascade; B cell activation; positive regulation of intracellular protein kinase cascade; endosome; protein homodimerization activity; protein dimerization activity; identical protein binding]
u	CD109	6:74405508-74538040 6q13	CD109 molecule [Source:HGNC Symbol;Acc:21685], type=processed_transcript,protein_coding, GO=[serine-type endopeptidase inhibitor activity; anchored to membrane; extracellular space]
*	CD97	19:14492213-14519531 19p13.12	CD97 molecule [Source:HGNC Symbol;Acc:1711], type=protein_coding, GO=[neuropeptide signaling pathway; inflammatory response; calcium ion binding; extracellular space; G-protein coupled receptor activity]
*	CHL1	3:238279-451090 3p26.3	cell adhesion molecule with homology to L1CAM (close homolog of L1) [Source:HGNC Symbol;Acc:1939], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[adult locomotory behavior; neuron migration; cognition; apical part of cell; dendrite; axon guidance; cell morphogenesis involved in neuron differentiation; neuron projection morphogenesis; chemotaxis]
*	FASN	17:80036215-80056106 17q25.3	fatty acid synthase [Source:HGNC Symbol;Acc:3594], type=protein_coding, GO=[enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity; 3-oxoacyl-[acyl-carrier-protein] reductase activity; [acyl-carrier-protein] S-acetyltransferase activity; 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity; myristoyl-[acyl-carrier-protein] hydrolase activity; [acyl-carrier-protein] S-malonyltransferase activity; palmitoyl-[acyl-carrier-protein] hydrolase activity; 3-oxoacyl-[acyl-carrier-protein] synthase activity; oleoyl-[acyl-carrier-protein] hydrolase activity; phosphopantetheine binding; acyl carrier activity; glycogen granule; pantothenate metabolic process; long-chain fatty-acyl-CoA biosynthetic process; long-chain fatty-acyl-CoA metabolic process; triglyceride biosynthetic process; melanosome; vitamin binding; fatty acid biosynthetic process; energy reserve metabolic process; cofactor binding]
d*	GOT2	16:58741035-58768239 16q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) [Source:HGNC Symbol;Acc:4433], type=protein_coding,retained_intron, GO=[L-aspartate:2-oxoglutarate aminotransferase activity; aspartate biosynthetic process; glutamate catabolic process to aspartate; glutamate catabolic process to 2-oxoglutarate; aspartate catabolic process; oxaloacetate metabolic process; aspartate family amino acid catabolic process; aspartate family amino acid biosynthetic process; aspartate family amino acid metabolic process; pyridoxal phosphate binding; gluconeogenesis; fatty acid transport; response to ethanol; vitamin binding; lipid transport; mitochondrial matrix; cofactor binding; mitochondrial inner membrane]
u	GPR56	16:57662419-57698944 16q21	G protein-coupled receptor 56 [Source:HGNC Symbol;Acc:4512], type=protein_coding, GO=[neuropeptide signaling pathway; brain development; G-protein coupled receptor activity]
*	HSPD1	2:198351305-198381461 2q33.1	heat shock 60kDa protein 1 (chaperonin) [Source:HGNC Symbol;Acc:5261], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[B cell cytokine production; T cell mediated immune response to tumor cell; regulation of T cell mediated immune response to tumor cell; positive regulation of T cell mediated immune response to tumor cell; lipopolysaccharide receptor complex; cyclin-dependent protein kinase activating kinase holoenzyme complex; DNA replication origin binding; positive regulation of interferon-alpha production; positive regulation of macrophage activation; isotype switching to IgG isotypes; chaperone-mediated protein complex assembly; lipopolysaccharide binding; protein refolding; positive regulation of interleukin-10 production; positive regulation of interleukin-12 production; positive regulation of interferon-gamma production; positive regulation of interleukin-6 production; p53 binding; chaperone binding; cell surface binding; coated pit; protein stabilization; 'de novo' protein folding; single-stranded DNA binding; B cell proliferation; response to unfolded protein; MyD88-dependent toll-like receptor signaling pathway; activation of caspase activity; ATP catabolic process; myeloid leukocyte activation; protein maturation; unfolded protein binding; early endosome; ATP metabolic process; positive regulation of T cell activation; B cell activation; response to protein stimulus; coated vesicle; stored secretory granule; mitochondrial matrix; mitochondrial inner membrane; cell surface; endosome; negative regulation of apoptosis; positive regulation of apoptosis; extracellular space]
u*	IGSF8	1:160061130-160068733 1q23.2	immunoglobulin superfamily, member 8 [Source:HGNC Symbol;Acc:17813], type=processed_transcript,protein_coding, GO=[single fertilization; skeletal muscle tissue development; striated muscle tissue development]
u*	ITGA6	2:173292082-173371181 2q31.1	integrin, alpha 6 [Source:HGNC Symbol;Acc:6142], type=protein_coding,retained_intron, GO=[alpha6-beta4 integrin complex; hemidesmosome assembly; laminin binding; positive regulation of cell-cell adhesion; brown fat cell differentiation; integrin complex; basal plasma membrane; cell adhesion mediated by integrin; cellular response to organic cyclic compound; cell-cell adherens junction; filopodium assembly; filopodium; positive regulation of cell-substrate adhesion; odontogenesis of dentine-containing tooth; integrin-mediated signaling pathway; integrin binding; basement membrane; positive regulation of cell adhesion; cell-matrix adhesion; external side of plasma membrane; adherens junction; regulation of cell adhesion; leukocyte migration; positive regulation of phosphorylation; cell-cell adhesion; cell surface; blood coagulation; negative regulation of apoptosis; positive regulation of apoptosis; positive regulation of transcription from RNA polymerase II promoter]
*	ITGAV	2:187454790-187545628 2q32.1	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) [Source:HGNC Symbol;Acc:6150], type=processed_transcript,protein_coding,retained_intron, GO=[entry of bacterium into host cell; entry of symbiont into host cell by promotion of host phagocytosis; regulation of apoptotic cell clearance; negative regulation of low-density lipoprotein particle receptor biosynthetic process; positive regulation of osteoblast proliferation; negative regulation of lipoprotein metabolic process; opsonin binding; insulin-like growth factor I binding; transforming growth factor beta binding; negative regulation of macrophage derived foam cell differentiation; negative regulation of lipid storage; entry of virus into host cell; negative regulation of lipid transport; integrin complex; integrin-mediated signaling pathway; ERK1 and ERK2 cascade; positive regulation of cell adhesion; cell-matrix adhesion; external side of plasma membrane; positive regulation of cell migration; lipid transport; regulation of cell adhesion; leukocyte migration; negative regulation of cell differentiation; axon guidance; cell surface; blood coagulation; negative regulation of apoptosis; cell morphogenesis involved in neuron differentiation; neuron projection morphogenesis; chemotaxis]
*	ITGB1	10:33189247-33294720 10p11.22	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) [Source:HGNC Symbol;Acc:6153], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[alpha3-beta1 integrin complex; protein transport within lipid bilayer; alpha9-beta1 integrin complex; hemidesmosome; alpha-actinin binding; cell-cell adhesion mediated by integrin; cellular response to vitamin D; cell migration involved in sprouting angiogenesis; germ cell migration; sarcomere organization; intercalated disc; fibronectin binding; laminin binding; response to gonadotropin stimulus; maternal process involved in female pregnancy; response to transforming growth factor beta stimulus; cellular response to ionizing radiation; integrin complex; cleavage furrow; basal plasma membrane; myelin sheath; tight junction assembly; cell adhesion mediated by integrin; leukocyte cell-cell adhesion; neuromuscular junction; positive regulation of neuron projection development; ruffle membrane; protease binding; response to activity; collagen binding; cardiac muscle cell differentiation; positive regulation of cell-substrate adhesion; cellular response to mechanical stimulus; glycoprotein binding; negative regulation of neuron differentiation; acrosomal vesicle; negative regulation of cell projection organization; positive regulation of neuron differentiation; cellular defense response; cell fate specification; integrin-mediated signaling pathway; cellular response to protein stimulus; B cell differentiation; integrin binding; regulation of G-protein coupled receptor protein signaling pathway; sarcolemma; basement membrane; positive regulation of peptidyl-tyrosine phosphorylation; melanosome; tissue homeostasis; focal adhesion; positive regulation of cell adhesion; synaptosome; positive regulation of cell projection organization; cell-matrix adhesion; positive regulation of MAPKKK cascade; homophilic cell adhesion; adherens junction; membrane raft; B cell activation; response to protein stimulus; positive regulation of cell migration; G1/S transition of mitotic cell cycle; regulation of cell adhesion; peptide binding; leukocyte migration; stored secretory granule; striated muscle tissue development; positive regulation of phosphorylation; cellular calcium ion homeostasis; protein heterodimerization activity; protein kinase binding; in utero embryonic development; positive regulation of intracellular protein kinase cascade; actin binding; cell-cell adhesion; negative regulation of cell differentiation; response to drug; axon guidance; cell surface; negative regulation of cell proliferation; blood coagulation; cell morphogenesis involved in neuron differentiation; positive regulation of apoptosis; neuron projection morphogenesis; chemotaxis; regulation of cell cycle; protein dimerization activity; identical protein binding]

Continued on next page...

S	name	locus	description
	MTR	1:236958581-237067281 1q43	5-methyltetrahydrofolate-homocysteine methyltransferase [Source:HGNC Symbol;Acc:7468], type=processed_transcript,protein_coding, GO=[methionine synthase activity; homocysteine S-methyltransferase activity; homocysteine metabolic process; cobalamin binding; tetrahydrofolate metabolic process; methionine biosynthetic process; folic acid binding; aspartate family amino acid biosynthetic process; aspartate family amino acid metabolic process; protein methylation; vitamin binding; xenobiotic metabolic process; soluble fraction]
d*	NME1	17:49230897-49239789 17q21.33	non-metastatic cells 1, protein (NM23A) expressed in [Source:HGNC Symbol;Acc:7849], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[nucleoside diphosphate kinase activity; nucleoside diphosphate phosphorylation; GTP biosynthetic process; UTP biosynthetic process; CTP biosynthetic process; gamma-tubulin binding; nucleobase, nucleoside and nucleotide interconversion; negative regulation of myeloid leukocyte differentiation; deoxyribonuclease activity; response to cAMP; purine ribonucleoside triphosphate biosynthetic process; positive regulation of epithelial cell proliferation; positive regulation of DNA binding; magnesium ion binding; intermediate filament; centrosome; GTP binding; negative regulation of cell differentiation; response to drug; perinuclear region of cytoplasm; negative regulation of cell proliferation; identical protein binding]
u	PROCR	20:33758727-33765165 20q11.22	protein C receptor, endothelial [Source:HGNC Symbol;Acc:9452], type=protein_coding, GO=[MHC class I protein complex; antigen processing and presentation; centrosome; blood coagulation]
u*	PTGFRN	1:117452679-117532980 1p13.1	prostaglandin F2 receptor negative regulator [Source:HGNC Symbol;Acc:9601], type=processed_transcript,protein_coding, GO=[lipid particle organization; endoplasmic reticulum membrane]
u*	PTPRF	1:43990858-44089343 1p34.2	protein tyrosine phosphatase, receptor type, F [Source:HGNC Symbol;Acc:9670], type=processed_transcript,protein_coding, GO=[negative regulation of nerve growth factor receptor signaling pathway; transmembrane receptor protein tyrosine phosphatase signaling pathway; phosphate binding; positive regulation of dendrite morphogenesis; excitatory synapse; transmembrane receptor protein tyrosine phosphatase activity; negative regulation of insulin receptor signaling pathway; negative regulation of cytokine-mediated signaling pathway; receptor tyrosine kinase binding; insulin receptor binding; positive regulation of neuron apoptosis; negative regulation of epidermal growth factor receptor signaling pathway; regulation of synapse structure and activity; negative regulation of cell projection organization; peptidyl-tyrosine dephosphorylation; growth cone; epidermal growth factor receptor signaling pathway; positive regulation of cell projection organization; homophilic cell adhesion; neuronal cell body; microsome; cell-cell adhesion; endosome; negative regulation of cell proliferation; cell morphogenesis involved in neuron differentiation; positive regulation of apoptosis; neuron projection morphogenesis]
u*	TUBA1C	12:49582519-49667116 12q13.12	tubulin, alpha 1c [Source:HGNC Symbol;Acc:20768], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cytoplasmic microtubule; cytoskeleton-dependent intracellular transport; 'de novo' posttranslational protein folding; 'de novo' protein folding; microtubule-based movement; protein polymerization; GTPase activity; GTP binding; cell division; GTP catabolic process; structural molecule activity]

Table 10: Descriptions of the study identifiers. The numbers of results reported and their units are reported in *hits* and *score type* columns, respectively.

name	description	ref	id	hits	score type
cosmicMetastasis	Consists of frequent somatic mutations in metastasis tumours as reported in COSMIC database.	[6]	20500	370	Proportion
cosmicPrimary	Consists of frequent somatic mutations in primary tumours as reported in COSMIC database.	[6]	20501	140	Proportion
cosmicRecurrent	Consists of frequent somatic mutations in recurrent tumours as reported in COSMIC database.	[6]	20502	230	Proportion
fileAmpOver	Amplified and overexpressed genes in human cancer.	[14]	21008	77	Ascending rank
fileBC2brain	Set of differentially expressed genes related to brain metastases of the breast cancer tumor.	[3]	21000	26	Fold change
fileCIN70	Set of genes associated with chromosomal instability.	[4]	21005	70	Ascending rank
snp3dBC	Genes associated to 'BREAST CANCER' in PUBMED abstracts.	[17]	20001	43	Descending rank
snp3dCRC	Genes associated to 'COLORECTAL CANCER' in PUBMED abstracts.	[17]	20002	29	Descending rank
snp3dDementia	Genes associated to 'DEMENTIA' in PUBMED abstracts.	[17]	20007	47	Descending rank
snp3dDiabetes	Genes associated to 'DIABETES MELLITUS' in PUBMED abstracts.	[17]	20003	63	Descending rank
snp3dGlioma	Genes associated to 'GLIOMA' in PUBMED abstracts.	[17]	20006	80	Descending rank
snp3dLungC	Genes associated to 'LUNG CANCER' in PUBMED abstracts.	[17]	20005	80	Descending rank
snp3dMetastasis	Genes associated to 'METASTASIS' in PUBMED abstracts.	[17]	20009	73	Descending rank
snp3dObesity	Genes associated to 'OBESITY' in PUBMED abstracts.	[17]	20008	49	Descending rank
snp3dProstateC	Genes associated to 'PROSTATE CANCER' in PUBMED abstracts.	[17]	20004	58	Descending rank
tcgaBreastCGHa	CGH gains in TCGA Breast samples	[13]	22043	172	Proportion
tcgaBreastCGHd	CGH losses in TCGA Breast samples	[13]	22044	70	Proportion
tcgaBreastGE	Differentially expressed genes in TCGA Breast samples	[13]	22040	9546	Fold change
tcgaBreastGESurv	Genes with survival associated expressions in TCGA Breast samples	[13]	22041	185	Probability
tcgaBreastMethyl	Differentially methylated genes in TCGA Breast samples	[13]	22042	6527	Fold change
tcgaColonCGHa	CGH gains in TCGA Colon samples	[13]	22063	41	Proportion
tcgaColonCGHd	CGH losses in TCGA Colon samples	[13]	22064	78	Proportion
tcgaColonGE	Differentially expressed genes in TCGA Colon samples	[13]	22060	8434	Fold change
tcgaColonGESurv	Genes with survival associated expressions in TCGA Colon samples	[13]	22061	11	Probability
tcgaColonMethyl	Differentially methylated genes in TCGA Colon samples	[13]	22062	7282	Fold change
tcgaGliomaCGHa	CGH gains in TCGA Glioma samples	[13, 12]	22023	25	Proportion
tcgaGliomaCGHd	CGH losses in TCGA Glioma samples	[13, 12]	22024	469	Proportion
tcgaGliomaGE	Differentially expressed genes in TCGA Glioma samples	[13, 12]	22020	6593	Fold change
tcgaGliomaGESurv	Genes with survival associated expressions in TCGA Glioma samples	[13, 12]	22021	130	Probability
tcgaOvarianCGHa	CGH gains in TCGA Ovarian samples	[11]	22003	535	Proportion
tcgaOvarianCGHd	CGH losses in TCGA Ovarian samples	[11]	22004	148	Proportion
tcgaOvarianGE	Differentially expressed genes in TCGA Ovarian samples	[11]	22000	625	Fold change
tcgaOvarianGESurv	Genes with survival associated expressions in TCGA Ovarian samples	[11]	22001	28	Probability
tcgaOvarianMethyl	Differentially methylated genes in TCGA Ovarian samples	[11]	22002	7056	Fold change
tscapeBCa	Frequent chromosomal amplifications in Breast tumours	[2]	20600	1095	Proportion
tscapeBCd	Frequent chromosomal deletions in Breast tumours	[2]	20601	2326	Proportion
tscapeCRCa	Frequent chromosomal amplifications in Colorectal tumours	[2]	20602	386	Proportion
tscapeCRCd	Frequent chromosomal deletions in Colorectal tumours	[2]	20603	1094	Proportion
tscapeGliomaa	Frequent chromosomal amplifications in Glioma tumours	[2]	20604	25	Proportion
tscapeGliomad	Frequent chromosomal deletions in Glioma tumours	[2]	20605	253	Proportion
tscapeHCCa	Frequent chromosomal amplifications in Hepatocellular tumours	[2]	20616	444	Proportion
tscapeHCCd	Frequent chromosomal deletions in Hepatocellular tumours	[2]	20617	941	Proportion
tscapeMelanomaa	Frequent chromosomal amplifications in Melanoma tumours	[2]	20610	555	Proportion
tscapeMelanomad	Frequent chromosomal deletions in Melanoma tumours	[2]	20611	685	Proportion
tscapeNSCLCa	Frequent chromosomal amplifications in Lung NSC tumours	[2]	20606	1340	Proportion
tscapeNSCLCd	Frequent chromosomal deletions in Lung NSC tumours	[2]	20607	2211	Proportion
tscapeOvariana	Frequent chromosomal amplifications in Ovarian tumours	[2]	20612	1188	Proportion
tscapeOvariand	Frequent chromosomal deletions in Ovarian tumours	[2]	20613	2111	Proportion
tscapeProstatea	Frequent chromosomal amplifications in Prostate tumours	[2]	20614	171	Proportion
tscapeProstated	Frequent chromosomal deletions in Prostate tumours	[2]	20615	1181	Proportion
tscapeRCCa	Frequent chromosomal amplifications in Renal tumours	[2]	20618	392	Proportion
tscapeRCCd	Frequent chromosomal deletions in Renal tumours	[2]	20619	945	Proportion
tscapeSCLCa	Frequent chromosomal amplifications in Lung SC tumours	[2]	20608	331	Proportion
tscapeSCLCd	Frequent chromosomal deletions in Lung SC tumours	[2]	20609	573	Proportion

3 System configuration

Pipeline configuration

3.1 System configurations

The following table shows the properties of **ensembl** component.

property	value
`database.driver`	com.mysql.jdbc.Driver
`database.recycle`	true
`database.timeout`	20
`database.url`	jdbc:mysql://deebee.giu.fi:3306/homo_sapiens_core_64_37
`database.user`	anonymous

The following table shows the properties of **moksiskaanInit-init** component.

property	value
`database.driver`	org.postgresql.Driver
`database.recycle`	true
`database.timeout`	20
`database.url`	jdbc:postgresql:moksiskaan
`database.user`	moksiskaan

This analysis is based on Moksiskaan [10] (version 1.08) that is running on top of Hibernate with *org.hibernate.dialect.PostgreSQLDialect* to access the native database.

Database history:
`[2011-04-08]` EnsemblImport: *jdbc:mysql://deebee.giu.fi:3306/mus_musculus_core_61_37n (29136 genes, 15661 proteins)* See also [7].
`[2011-04-08]` EnsemblImport: *jdbc:mysql://deebee.giu.fi:3306/homo_sapiens_core_61_37f (33615 genes, 18881 proteins)* See also [7].
`[2011-04-09]` Keggonen: *KEGG pathway import from {SOAP/KEGG}KEGG: http://soap.genome.jp/keggapi/request_v6.2.cgi produced 230 Homo sapiens pathways.* See also [8].
`[2011-04-09]` Keggonen: *KEGG pathway import from {SOAP/KEGG}KEGG: http://soap.genome.jp/keggapi/request_v6.2.cgi produced 226 Mus musculus pathways.* See also [8].
`[2011-04-09]` Narggari: *Drug target import from the KEGG DRUG database.* See also [8].
`[2011-04-09]` DrugBankImport: *Total of 1619 drugs identified from http://www.drugbank.ca/system/downloads/current/drugbank.xml.zip.* See also [9, 15].
`[2011-04-09]` PINAImport: *Total of 4496 protein-protein interactions obtained from http://csbi.ltdk.helsinki.fi/pina/download/Mus%20musculus.txt.* See also [16].
`[2011-04-09]` PINAImport: *Total of 52462 protein-protein interactions obtained from http://csbi.ltdk.helsinki.fi/pina/download/Homo%20sapiens.txt.* See also [16].
`[2011-04-09]` PathwayCommonsImport: *Total of 35 new links obtained from http://www.pathwaycommons.org/pc-snapshot/current-release/tab_delim_network/by_species/mus-musculus-10090-edge-attributes.txt.zip.* See also [5].
`[2011-04-09]` PathwayCommonsImport: *Total of 59555 new links obtained from http://www.pathwaycommons.org/pc-snapshot/current-release/tab_delim_network/by_species/homo-sapiens-9606-edge-attributes.txt.zip.* See also [5].

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