

Figure 1 Proteinuria

Graph in figure 1 is showing total protein excretion of rats at the baseline (day 0) and after induction of disease (day 3 and day 6).

Table 1 Differentially expressed genes (DEGs)

List of 234 differentially regulated genes (>1.5 fold) in PHN induced rats on day three and or day six. Genes are annotated with NCBI Gene Symbols and grouped according to biological function. Starred (*) Gene Symbols mark predicted genes.

Figure 2 Enriched biological processes

Enriched biological processes and number of differentially expressed genes are given in figure 2. Numbers in brackets depict expected gene numbers according to the background distribution of all human genes.

Table 2 List of over- and underrepresented ontology terms in the dataset

List of genes assigned to the over- or under-represented GO terms. Genes in the list are sorted according their cellular function. Significance levels are given as Bonferroni corrected p-values ($p < 0.005$) following a chi-square test.

Figure 3 Protein interaction modules

Graphical visualization of the top four network modules. Node fill colour indicates the measured fold-change, where green represents down regulated genes (light green < -1.5 , dark green < -2) and red represents upregulated genes (orange < 1.5 , red > 1.5 , dark red > 2). The node's border colour indicates the subcellular localization of the protein (yellow for membrane and blue for extra cellular). Hexagon shape of the node represents DEGs and circular shape represents direct interacting proteins.

Figure 4 SM22 levels in PHN

(A) Staining for SM22 is absent in control glomeruli, but is detected in the blood vessels. (B) SM22 staining is detected in the glomerulus at day 3 of PHN, in a podocyte distribution. (C) SM22 staining is markedly increased at day 6 of PHN in podocytes. Staining was absent when the primary antibody was omitted (not shown).

Webfigure 1 Heatmap showing expression levels of the 234 differentially expressed genes

Horizontal rows represent the expression levels of the 234 DEGs sorted by fold-change when comparing controls and treated animals. Arrays were clustered using average linkage distance and the Pearson correlation coefficient in the clustering algorithm. Gene Symbols marked with an asterisk depict predicted genes. Grey bars indicate non-significant expression changes.

	Symbol	Gene Name	Fold Change	
			Day 3	Day 6
Apoptosis				
BE112895	Pea15 *	phosphoprotein enriched in astrocytes 15		2.55
AI411997	Adamtsl4	ADAMTS-like 4		1.90
NM_012935	Cryab	crystallin, alpha B		1.75
NM_022546	Dapk3	death-associated protein kinase 3	1.51	1.54
BF282636	RGD1305457	similar to RIKEN cDNA 1700023M03		1.54
NM_017180	Phlda1	pleckstrin homology-like domain, family A, member 1		1.50
Cell Adhesion				
Z78279	Col1a1	collagen, type 1, alpha 1	7.68	14.09
AF056034	Nexn	nexilin	4.77	4.55
BI303379	Tnfrsf12	tumor necrosis factor receptor superfamily, member 12a	3.70	4.21
BF407194	Itgb1bp2 *	integrin beta 1 binding protein 2	2.14	2.09
NM_030828	Gpc1	glypican 1		2.02
NM_017022	Itgb1	integrin beta 1		1.82
NM_012811	Mfge8	milk fat globule-EGF factor 8 protein		1.79
BG379319	Tgfb1	transforming growth factor, beta induced		1.72
NM_022266	Ctgf	connective tissue growth factor		1.66
AW433888	Vcl *	vinculin		1.63
NM_133409	Ilk	integrin linked kinase	1.52	1.61
BI275904	Lims2 *	LIM and senescent cell antigen like domains 2	1.63	1.59
AI008975	LOC311772	similar to nidogen 2		1.57
NM_022523	Cd151	CD151 antigen		1.51
NM_019237	Pcolce	procollagen C-proteinase enhancer protein		1.50
AB001382	Spp1	secreted phosphoprotein 1	2.10	
NM_012774	Gpc3	glypican 3	1.87	
Cell Structure and Motility				
U22520	Cxcl10	chemokine (C-X-C motif) ligand 10		3.66
BE111697	Kif20a *	kinesin family member 20A		3.55
NM_022531	Des	desmin	1.85	3.29
NM_031005	Actn1	actinin, alpha 1	3.00	3.19

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gene expression in PHN

BI283060	Flna *	filamin, alpha	2.60	2.96
NM_019131	Tpm1	tropomyosin 1, alpha	3.33	2.90
BI279044	Myl9 *	myosin, light polypeptide 9, regulatory	5.58	2.81
AI179391	Enh	enigma homolog	2.04	2.58
NM_017148	Csrp1	cysteine and glycine-rich protein 1	1.92	2.42
X03369	Tubb2b	tubulin, beta 2b		2.34
BI274903	RGD1305887 *	similar to RIKEN cDNA 2310057H16	1.80	2.27
AA012755	MGC109519	similar to tropomyosin 1, embryonic fibroblast - rat		2.23
NM_019361	Arc	activity regulated cytoskeletal-associated protein		2.18
NM_012987	Nes	nestin		2.07
AI598442	RGD1564875 *	similar to mKIAA0613 protein		2.04
AW919109	Cap2	CAP, adenylate cyclase-associated protein, 2 (S. cerevisiae)	1.88	2.03
BI285440	Tubb5	tubulin, beta 5		1.91
AI103106	Lmnb1	lamin B1		1.86
AA892044	Tubb2	tubulin, beta, 2		1.80
NM_013194	Myh9	myosin, heavy polypeptide 9		1.76
NM_031970	Hspb1	heat shock 27kDa protein 1		1.74
BG381583	RGD1565118 *	similar to mKIAA0843 protein		1.68
X70706	Pls3	plastin 3 (T-isoform)		1.67
BM391364	LOC290704		1.60	1.67
BI296011	Cfl2 *	cofilin 2, muscle		1.65
NM_021755	Lmna	lamin A		1.63
NM_130411	Coro1a	coronin, actin binding protein 1A		1.63
BI278813	Ckap4 *	cytoskeleton-associated protein 4		1.60
BM383953	LOC367171	microtubule-associated protein 4		1.57
NM_031675	Actn4	actinin alpha 4	1.51	1.56
AA891834	Col4a5 *	collagen, type IV, alpha 5		1.56
AI407239	Myom2	myomesin 2		1.55
NM_031140	Vim	vimentin		1.54
NM_134452	Col5a1	collagen, type V, alpha 1		1.52
AI180161	Mapre1	microtubule-associated protein, RP/EB family, member 1		1.52
AW252250	Nebi *	nebulin		1.51
NM_019212	Acta1	actin, alpha 1, skeletal muscle	6.03	

Cell Cycle

BG379338	Rrm2	ribonucleotide reductase M2		6.87
BE113362	Cdkn3 *	cyclin-dependent kinase inhibitor 3		5.53
AI409259	Racgap1 *	Rac GTPase-activating protein 1		5.02
AA944180	RGD1562047 *	similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2)		5.00
NM_019296	Cdc2a	cell division cycle 2 homolog A (S. pombe)		4.40
AW253821	Ccnb2 *	cyclin B2		3.47
BI296084	Ube2c *	ubiquitin-conjugating enzyme E2C		3.15
NM_031131	Tgfb2	transforming growth factor, beta 2	2.06	3.06
NM_021989	Timp2	tissue inhibitor of metalloproteinase 2	1.58	2.44
BF417638	RGD:1359093	similar to cell division cycle associated 3		2.27
BG380355	Cdca8	cell division cycle associated 8		2.24
U05341	Cdc20	cell division cycle 20 homolog (S. cerevisiae)		2.20
BE117002	LOC362021			2.12
AI408269	Spbc25	spindle pole body component 25 homolog (S. cerevisiae)		2.06
NM_053483	Kpna2	karyopherin (importin) alpha 2		2.04
AA874827	Dlg7 *	discs, large homolog 7 (Drosophila)		1.84
AA996882	Stk6	serine/threonine kinase 6		1.82
AW920000	LOC362587	similar to microfilament and actin filament cross-linker protein isoform b		1.81
NM_022381	Pcna	proliferating cell nuclear antigen		1.78
X64589	Ccnb1	cyclin B1		1.72
AI407985	LOC686524	hypothetical protein LOC686524		1.70
AF140232	S100a6	S100 calcium binding protein A6 (calcyclin)		1.69
BM386384	Nap1l1	nucleosome assembly protein 1-like 1		1.65
NM_053819	Timp1	Tissue inhibitor of metalloproteinase 1		2.30
AA957183	Cit	citron		1.57
NM_013174	Tgfb3	transforming growth factor, beta 3		1.55

Immunity and Defense

AI233530	C1qtnf3 *	C1q and tumor necrosis factor related protein 3		2.67
BI284441	Colec12	collectin sub-family member 12		2.59
BI278802	Prnp	prion protein		2.51
BF389535	LOC299339	similar to Tumor necrosis factor, alpha-induced protein 2 (primary response gene B94)		2.14
NM_053843	Fcgr3	Fc receptor, IgG, low affinity III		2.10

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gene expression in PHN

AI176519	Ier3	immediate early response 3		2.08
L12458	Lyz	lysozyme		2.05
AW918311	C1qtnf4 *	C1q and tumor necrosis factor related protein 4		2.02
NM_012620	Serpine1	serine (or cysteine) proteinase inhibitor, clade E, member 1		1.66
AI228623	Nptx2 *	neuronal pentraxin II		1.64
NM_031971	Hspa1a	heat shock 70kD protein 1A		1.54
Transport (membrane)				
BI293600	Slc35b2	solute carrier family 35, member B2	2.08	2.64
NM_019354	Ucp2	uncoupling protein 2		1.50
Transport (intracellular)				
NM_022959	Pamci	peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor		1.57
BG381589	Stx6	syntaxin 6		1.50
Transport (other)				
AI170609	RGD1560252 *	similar to hypothetical protein MGC31967	4.02	3.10
AI407838	Ecm1	extracellular matrix protein 1		2.04
NM_022278	Glrx1	glutaredoxin 1 (thioltransferase)		1.52
BE111722	Ndufs2 *	NADH dehydrogenase (ubiquinone) Fe-S protein 2		1.52
Metabolism (lipid)				
NM_031043	Gyg1	glycogenin 1	1.59	2.64
NM_013200	Cpt1b	carnitine palmitoyltransferase 1b	1.60	2.43
AF248543	A3galt2	alpha 1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase)		1.74
NM_017235	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7		1.67
NM_012941	Cyp51	cytochrome P450, subfamily 51		1.67
NM_031840	Fdps	faresyl diphosphate synthase		1.51
Metabolism (glycogen)				
AW919180	Pygm	muscle glycogen phosphorylase	1.85	1.76
Metabolism (DNA)				
NM_022674	H2afz	H2A histone family, member Z		1.61
Metabolism (other)				
AA891760	RGD1308350 *	similar to hypothetical protein MGC13251		1.68
BG381486	Large *	like-glycosyltransferase		1.64
BM385390	Uxs1	UDP-glucuronate decarboxylase 1		1.58

BI282076	Prdx4	peroxiredoxin 4		1.52
Protein Modification				
AI236997	Dusp14 *	dual specificity phosphatase 14		2.24
NM_130403	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A		1.82
AW531714	Ube2t *	ubiquitin-conjugating enzyme E2T (putative)		1.76
BI276525	Ate1 *	arginine-tRNA-protein transferase 1		1.70
BI283703	Mapkapk2	MAP kinase-activated protein kinase 2		1.69
AF106659	Usp2	ubiquitin specific protease 2		1.68
NM_053323	Degs	degenerative spermatocyte homolog (Drosophila)		1.64
AI010241	Usp1 *	ubiquitin specific protease 1		1.63
AA799400	B3galt3 *	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3		1.59
AA849399	Ctsz	cathepsin Z		1.54
BI279788	Ube2s *	ubiquitin-conjugating enzyme E2S		1.51
NM_024135	Limk2	LIM motif-containing protein kinase 2		1.50
Protein Folding				
AI175031	Dnajb4 *	DnaJ (Hsp40) homolog, subfamily B, member 4		1.53
BG671521	Hspca	heat shock protein 1, alpha		1.54
Signal Transduction				
NM_019904	Lgals1	lectin, galactose binding, soluble 1	1.61	3.71
NM_012715	Adm	adrenomedullin	1.78	2.86
BF405151	Gpr39 *	G protein-coupled receptor 39	1.72	2.80
NM_053634	Fcnb	ficolin B	1.91	2.70
NM_033099	Ptprv	protein tyrosine phosphatase, receptor type, V		2.27
BE117002	RGD1560967 *	similar to Pins		2.12
AW253242	Magi1 *	membrane associated guanylate kinase interacting protein-like 1		1.74
X78595	Npr3	natriuretic peptide receptor 3		1.74
BG378926	S100a11	S100 calcium binding protein A11 (calizzarin)		1.73
BI276015	RGD1559882 *	similar to hypothetical protein E130310N06		1.66
BM386204	Ran	RAN, member RAS oncogene family		1.65
BI295991	Rab2l	RAB2, member RAS oncogene family-like		1.60
NM_022236	Pde10a	phosphodiesterase 10A	1.56	1.56

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gene expression in PHN

NM_012823	Anxa3	annexin A3		1.51
NM_053299	Ubd	ubiquitin D	1.72	
M35297	Mrgprf	MAS-related GPR, member F	1.79	
Transcription				
BM385445	Top2a	topoisomerase (DNA) 2 alpha		3.37
L81174	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	2.62	3.02
NM_031628	Nr4a3	nuclear receptor subfamily 4, group A, member 3		2.34
NM_017187	Hmgb2	high mobility group box 2		2.04
NM_131902	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)		2.01
NM_017365	Pdlim1	PDZ and LIM domain 1 (elfin)		2.00
AI170362	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100		1.95
U17565	Mcmd6	mini chromosome maintenance deficient 6 (S. cerevisiae)		1.88
NM_053583	Zfp423	zinc finger protein 423		1.87
BM387864	Lrrfp1	similar to FLI-LRR associated protein-1		1.76
BG664147	Ptrf *	polymerase I and transcript release factor		1.65
BG380385	Srf *	serum response factor	1.95	1.64
BF403027	Hdac5	histone deacetylase 5		1.64
AI179264	Creb3	cAMP responsive element binding protein 3		1.50
Homeostasis				
BI285437	Nxn *	nucleoredoxin		1.62
Nucleus				
BE104102	RGD1306774 *	similar to SPT3-associated factor 42		1.83
Membrane				
BM385031	Plp2	proteolipid protein 2	1.76	2.55
BM388441	RGD1311946 *	similar to RIKEN cDNA 1810055G02		1.97
NM_030847	Emp3	epithelial membrane protein 3		1.89
AW917760	RGD1564216 *	similar to Myoferlin (Fer-1 like protein 3)		1.88
AI009530	MGC72614	hypothetical LOC310540		1.86
BI296048	Myadm	myeloid-associated differentiation marker	1.55	1.77
J03867	Dia1	diaphorase 1		1.60

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BM385463	Tmem43	transmembrane protein 43		1.55
AI230273	RGD:735199	Unknown (protein for MGC:72987)		1.55
BF283798	Nipsnap3a	nipsnap homolog 3A (C. elegans)		1.53
AA850909	Pvr12 *	poliovirus receptor-related 2 (herpesvirus entry mediator B)		1.50
BI290029	RGD1562920 *	similar to Aig1 protein		1.50
AI407016	RGD1307736 *	similar to Hypothetical protein KIAA0152	1.55	
BI294974	Ldlr	low density lipoprotein receptor	1.69	
Developmental Processes				
NM_031549	Tagln	transgelin	69.77	38.66
NM_012636	Pthlh	parathyroid hormone-like peptide		3.13
NM_030584	Sost	sclerostin		3.12
AW141680	Bmp6	bone morphogenetic protein 6		2.36
NM_019242	Ifrd1	interferon-related developmental regulator 1	2.05	2.32
AW251450	Mustn1	musculoskeletal, embryonic nuclear protein 1		2.13
AI235465	Ssg1	steroid sensitive gene 1		2.07
AW435036	Smtn *	smoothelin		1.65
BI290551	Fnbp1	Formin binding protein 1		1.60
BI275485	Sema3b *	semaphorin 3B, immunoglobulin domain, secreted		1.57
AW144216	Enpep	glutamyl aminopeptidase	2.11	1.57
BG666787	Gmfg	glia maturation factor, gamma		1.56
BM384088	Socs2	suppressor of cytokine signaling 2		1.54
NM_031114	S100a10	S100 calcium binding protein A10 (calpactin)		1.51
Others				
AI229404	RGD1566097 *	similar to Anillin	2.47	8.41
BI295828			2.28	3.31
BI279587			2.12	3.01
BI283695			1.73	2.48
AW531909				2.44
BF419834			1.62	2.29
BF415061	RGD1307034 *	similar to hypothetical protein CG003		2.21
BF408518	RGD1305081 *	similar to ionized calcium binding adapter molecule 2 (Iba2)	1.98	2.16
AI712694	RGD1308747 *	similar to hypothetical protein FLJ10156		2.15

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gene expression in PHN

BI296728	RGD1564957 *	similar to RIKEN cDNA 3110007P09		2.04
AI176172				2.03
BM387112			1.71	2.03
AI071000				2.00
AA799328	RGD1560913 *	similar to expressed sequence AW413625		1.93
BE096535		transcribed locus, strongly similar to XP_574462.1 similar to hypoth. protein C230069C04		1.89
BG378155	RGD1565079 *	similar to hypothetical protein MGC17839		1.88
AA943808	RGD1307215	similar to protein phosphatase 1, inhibitory subunit 1C; thymocyte ARPP		1.82
AW143197				1.79
AW529960				1.78
AI177743	LOC498261			1.72
AI317841	Gramd3	GRAM domain containing 3		1.69
BI303106				1.64
BF561368	RGD1306959 *	similar to C11orf17 protein		1.63
AW253004		CDNA clone IMAGE:7317367		1.62
BF398756				1.62
AI009167	Zfp451 *	zinc finger protein 451		1.62
AI412389				1.61
BE111057				1.60
BI282694	RGD1565037 *	similar to selenoprotein SelM		1.60
AI231225				1.58
AA942716	Hn1	hematological and neurological expressed sequence 1		1.56
BF284519				1.55
BG671786				1.53
AW914928				1.53
AI113146	Acpl2	acid phosphatase-like 2		1.51
AI170820	RGD1310383 *	similar to T-cell activation protein phosphatase 2C		1.50
AA800892	RGD1563599 *	similar to putative SH3BGR protein	1.81	
BG380430	RGD1564105 *	similar to RIKEN cDNA B130052G07	1.54	
NM_021584	Ania4	activity and neurotransmitter-induced early gene protein 4 (ania-4)		2.53
AA997359	Serpib6	serine (or cysteine) peptidase inhibitor, clade B, member 6		1.54
NM_012618	S100a4	S100 calcium-binding protein A4		1.80
NM_022382	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)		1.70
AI112962	Rcn *	reticulocalbin		1.92

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gene expression in PHN

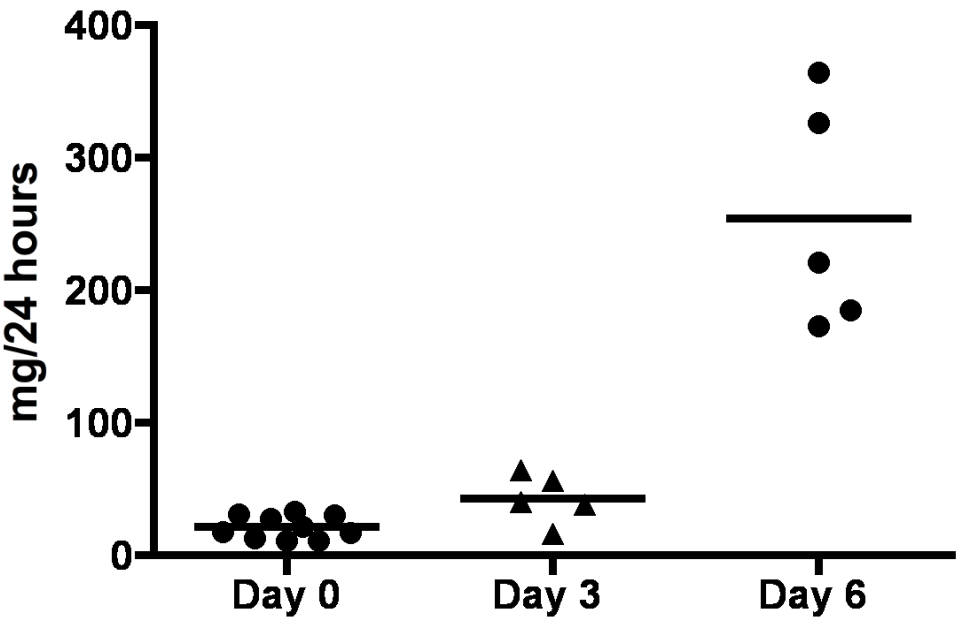
AI232065

Arhgap18 *

Rho GTPase activating protein 18

1.55

Figure 1



	day 3			day 6		
	genes	over/under	p-value	genes	over/under	p-value
Biological Processes						
Cell structure and motility	15	+	4.20E-010	35	+	1.02E-013
-Cell structure	12	+	1.33E-009	27	+	3.08E-013
-Cell motility	6	+	3.74E-005	17	+	9.07E-010
Developmental processes	11	+	1.46E-003	36	+	9.29E-007
-Mesoderm development	4	/	/	15	+	2.68E-005
Cell cycle	3	/	/	27	+	2.29E-010
-Mitosis	3	/	/	10	+	2.53E-004
-Cell cycle control	1	/	/	10	+	1.01E-003
Muscle contraction	4	+	4.29E-004	11	+	2.30E-007
Immunity and defense	2	/	/	21	+	4.34E-004
-Macrophage-mediated immunity	0	/	/	5	+	1.81E-003
-Stress response	0	/	/	8	+	1.86E-004
Tumor supressor	1	/	/	5	+	4.73E-004
Metabolism			/			
- sulfur redox	0	/	/	2	+	1.23E-002
- glycogen	2	+	3.84E-003	2	/	/
Cell adhesion	6	+	6.59E-004	9	/	/
G-protein mediated signaling	1	/	/	2	-	1.11E-002
Protein modification	2	/	/	16	+	1.14E-002
Molecular Function						
Cytoskeletal protein	15	+	4.58E-012	37	+	1.14E-019
-Actin binding cytoskeletal protein	12	+	2.10E-012	23	+	5.29E-015
-Microtubule family cytoskeletal protein	2	/	/	7	+	1.58E-003
-Intermediate filament	1	/	/	5	+	1.05E-003
Non-motor actin binding protein	4	+	2.35E-004	11	+	4.73E-008
Actin binding motor protein	1	/	/	3	+	7.30E-003
Tubulin	2	+	1.37E-003	4	+	7.37E-005
Select regulatory molecule	2	/	/	22	+	3.87E-005
-Kinase modulator	1	/	/	7	+	1.99E-004
Metalloprotease inhibitor	1	+	8.26E-003	2	+	5.35E-004

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gene expression in PHN

Miscellaneous function	5	/	/	14	+	2.49E-003
-Structural protein	2	/	/	8	+	1.01E-004
Signaling molecule	4	/	/	16	+	2.29E-004
-Growth factor	1	/	/	4	+	1.30E-002
Defense/Immunity protein	2	/	/	8	+	6.04E-003
Non-receptor serine/threonine kinase	2	/	/	7	+	8.53E-003
Select calcium binding protein	1	/	/	8	+	1.15E-003
-Calmodulin related protein	1	/	/	6	+	1.01E-003
G-protein coupled receptor	1	/	/	0	-	2.09E-003
Nucleic acid binding	2	/	/	9	-	1.16E-002

PANTHER pathways

Integrin signaling pathway	6	+	3.88E-006	10	+	8.61E-006
Cytoskeletal regulation by Rho GTPase	2	/	/	7	+	1.97E-005
Hedgehog signaling pathway	2	+	3.35E-003	4	+	4.14E-004
p53 pathway	0	/	/	5	+	2.31E-003
DNA replication	0	/	/	2	+	1.00E-002

KEGG pathways

Focal adhesion	6	9
Cell cycle	1	9
Regulation of actin cytoskeleton	3	8
MAPK signaling pathway	3	7
Cell communication	2	7
Leukocyte transendothelial migration	3	5
Gap junction	2	5
axon guidance	0	5
Tight junction	3	4
Adherens junction	2	4
p53 signaling pathway	0	4
Adipocytokine signaling pathway	2	3
ECM-receptor interaction	1	3
TGF-beta signaling pathway	1	3
Cytokine-cytokine receptor interaction	1	2

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gene expression in PHN

Cell adhesion molecules	0	2
Toll-like receptor signaling pathway	0	2

Figure 2

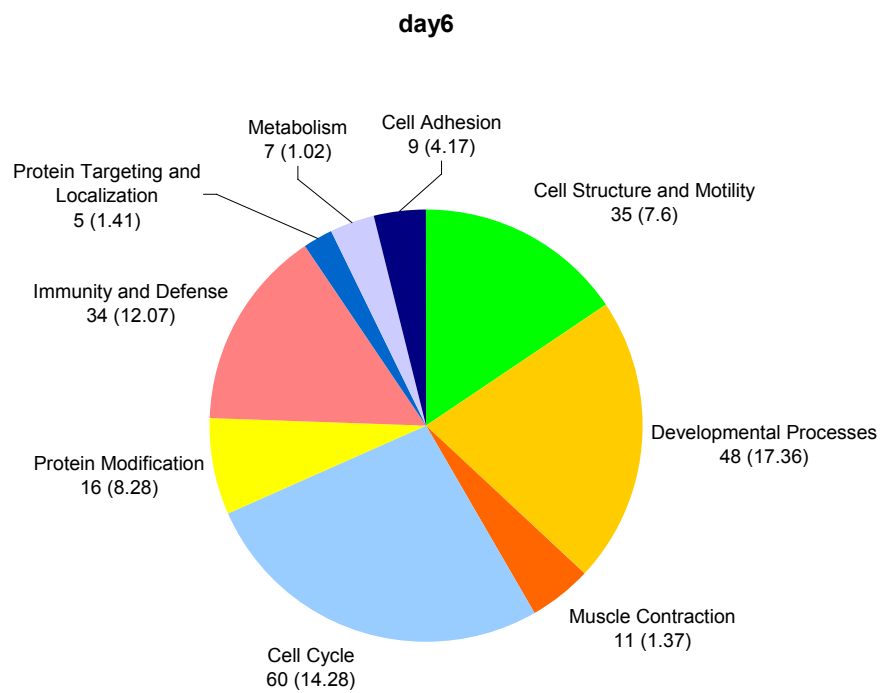
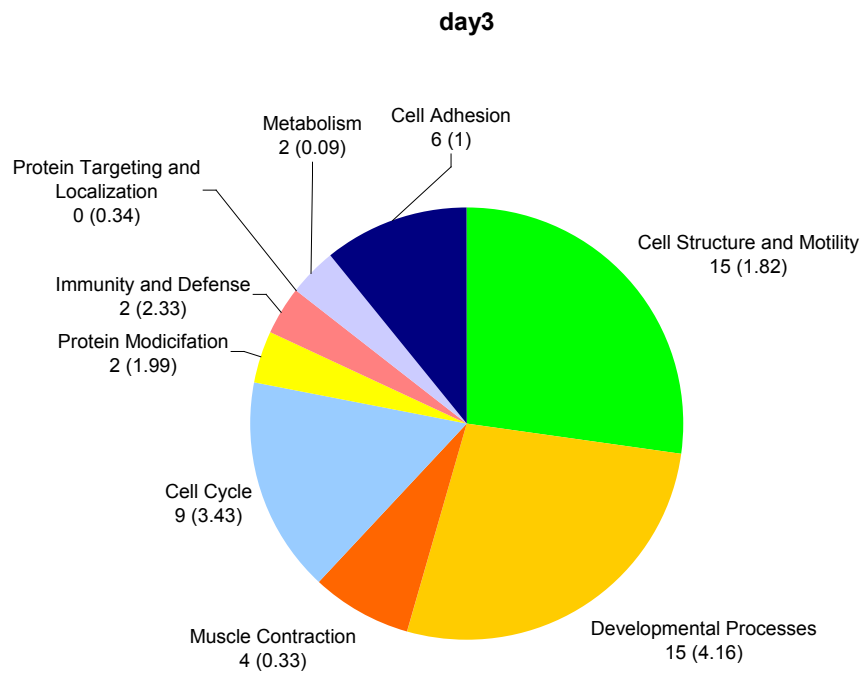


Figure 3

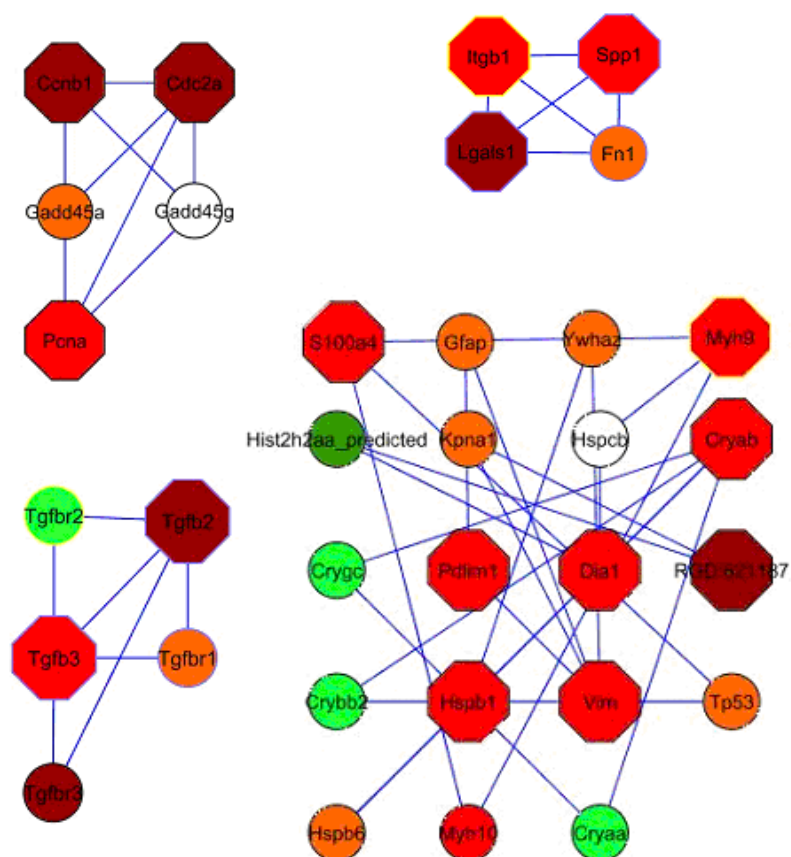
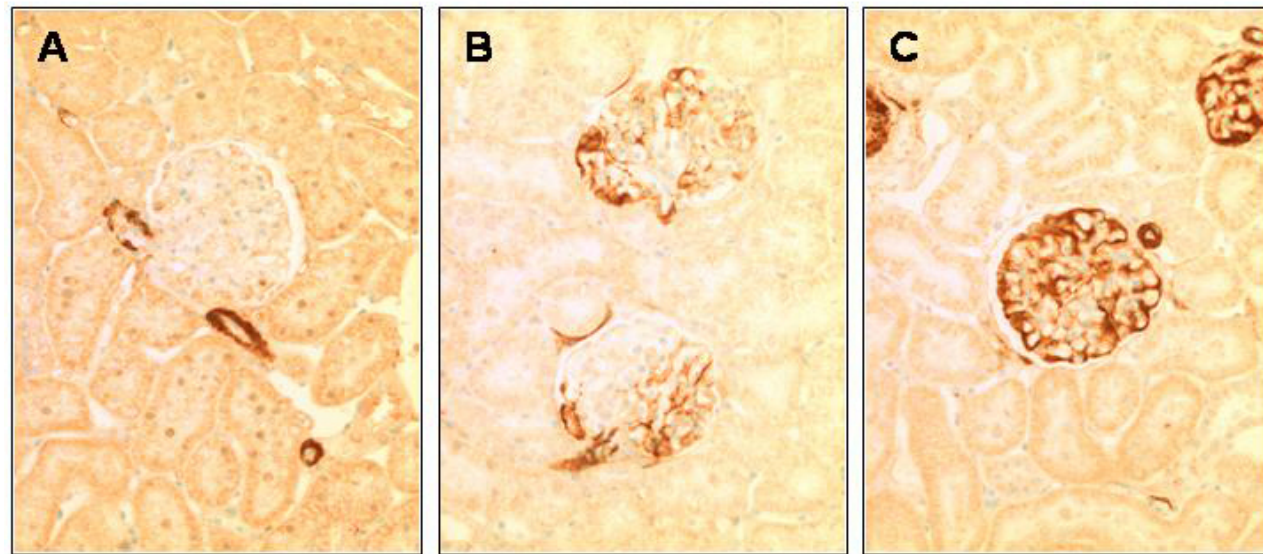


Figure 4



Webfigure 1

