

# Appendix E

## Innate immune response modules

Table E.1 GO term enrichment in IFN- $\beta$  response gene modules

GO term ID	GO term name	Enrichment p-value
<b>Canonical Type I IFN</b>		
GO:0051607	defense response to virus	2.36e-44
GO:0060337	type I interferon signaling pathway	8.34e-38
GO:0032479	regulation of type I interferon production	3.18e-13
GO:0070647	protein modification by small protein conjugation or removal	2.4e-05
GO:0044248	cellular catabolic process	0.000405
GO:0006508	proteolysis	0.00116
GO:0071360	cellular response to exogenous dsRNA	0.0016
GO:0032020	ISG15-protein conjugation	0.00591
GO:0006471	protein ADP-ribosylation	0.00613
GO:0003373	dynamain family protein polymerization involved in membrane fission	0.00769
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleaseolytic	0.0103
GO:2001034	positive regulation of double-strand break repair via nonhomologous end joining	0.0114
GO:1904469	positive regulation of tumor necrosis factor secretion	0.0114
GO:0052548	regulation of endopeptidase activity	0.0114

GO term ID	GO term name	Enrichment p-value
GO:0000266	mitochondrial fission	0.0115
GO:0034058	endosomal vesicle fusion	0.0136
GO:0019985	translesion synthesis	0.0138
GO:0070206	protein trimerization	0.0185
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	0.0213
GO:0035563	positive regulation of chromatin binding	0.0213
GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway	0.0268
GO:0009200	deoxyribonucleoside triphosphate metabolic process	0.0299
GO:0051248	negative regulation of protein metabolic process	0.0299
GO:0034162	toll-like receptor 9 signaling pathway	0.033
GO:0061025	membrane fusion	0.0403
GO:0002737	negative regulation of plasmacytoid dendritic cell cytokine production	0.0411
GO:0072308	negative regulation of metanephric nephron tubule epithelial cell differentiation	0.0411
GO:1905795	cellular response to puromycin	0.0411
GO:0090616	mitochondrial mRNA 3'-end processing	0.0411
GO:0031324	negative regulation of cellular metabolic process	0.0448
GO:0051100	negative regulation of binding	0.0498
GO:0048661	positive regulation of smooth muscle cell proliferation	0.0498

#### Regulator/signal transduction

GO:0006952	defense response	8.86e-17
GO:0060333	interferon-gamma-mediated signaling pathway	1.09e-08
GO:0008219	cell death	5.81e-06
GO:0010952	positive regulation of peptidase activity	1.79e-05
GO:0001817	regulation of cytokine production	1.84e-05
GO:0032940	secretion by cell	0.000203
GO:0002274	myeloid leukocyte activation	0.00033
GO:0045055	regulated exocytosis	0.00102
GO:0043687	post-translational protein modification	0.00147

GO term ID	GO term name	Enrichment p-value
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.0016
GO:0016485	protein processing	0.00245
GO:0061180	mammary gland epithelium development	0.00426
GO:1902728	positive regulation of growth factor dependent skeletal muscle satellite cell proliferation	0.00482
GO:0048872	homeostasis of number of cells	0.00933
GO:0006775	fat-soluble vitamin metabolic process	0.0117
GO:0010957	negative regulation of vitamin D biosynthetic process	0.0186
GO:1903903	regulation of establishment of T cell polarity	0.0186
GO:0071360	cellular response to exogenous dsRNA	0.0199
GO:1901224	positive regulation of NIK/NF-kappaB signaling	0.0219
GO:0042325	regulation of phosphorylation	0.0223
GO:0046902	regulation of mitochondrial membrane permeability	0.0286
GO:1903599	positive regulation of autophagy of mitochondrion	0.0299
GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	0.0338
GO:0032020	ISG15-protein conjugation	0.0368
GO:0048050	post-embryonic eye morphogenesis	0.0368
GO:0070647	protein modification by small protein conjugation or removal	0.0374
GO:0001503	ossification	0.0405
GO:0001885	endothelial cell development	0.0463
GO:0002291	T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	0.0468
GO:0003382	epithelial cell morphogenesis	0.0497
<b>Effector</b>		
GO:0051707	response to other organism	0.00596
GO:0034097	response to cytokine	0.00596

GO term ID	GO term name	Enrichment p-value
GO:0006955	immune response	0.00596
GO:0019079	viral genome replication	0.00596
GO:0045069	regulation of viral genome replication	0.0112
GO:0010529	negative regulation of transposition	0.0143
GO:0006952	defense response	0.0143
GO:0010528	regulation of transposition	0.0143
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	0.0188
GO:0051172	negative regulation of nitrogen compound metabolic process	0.0315
GO:0045944	positive regulation of transcription by RNA polymerase II	0.0317
GO:0051254	positive regulation of RNA metabolic process	0.0317
GO:0010557	positive regulation of macromolecule biosynthetic process	0.0423
GO:0048705	skeletal system morphogenesis	0.0453
GO:0010463	mesenchymal cell proliferation	0.0467
GO:0043374	CD8-positive, alpha-beta T cell differentiation	0.0467
GO:0065007	biological regulation	0.0467
GO:0001816	cytokine production	0.0468
GO:0060324	face development	0.0471
GO:0097152	mesenchymal cell apoptotic process	0.0483
GO:0010628	positive regulation of gene expression	0.0483

#### Cell cycle

GO:0007049	cell cycle	1.42e-58
GO:0006259	DNA metabolic process	6.06e-26
GO:0006974	cellular response to DNA damage stimulus	7.19e-13
GO:0051310	metaphase plate congression	3.75e-08
GO:0031145	anaphase-promoting complex-dependent catabolic process	6.72e-08
GO:0051169	nuclear transport	3.11e-06
GO:0034502	protein localization to chromosome	8.81e-06
GO:0000723	telomere maintenance	6e-05
GO:0007019	microtubule depolymerization	0.000169
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.000367

GO term ID	GO term name	Enrichment p-value
GO:0009263	deoxyribonucleotide biosynthetic process	0.000591
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	0.000611
GO:0006403	RNA localization	0.000798
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.00111
GO:0006606	protein import into nucleus	0.00166
GO:0016572	histone phosphorylation	0.00234
GO:0085020	protein K6-linked ubiquitination	0.0025
GO:0009411	response to UV	0.00308
GO:0006405	RNA export from nucleus	0.00342
GO:0002200	somatic diversification of immune receptors	0.004
GO:0001556	oocyte maturation	0.00416
GO:0045814	negative regulation of gene expression, epigenetic	0.00416
GO:0051347	positive regulation of transferase activity	0.00583
GO:0031100	animal organ regeneration	0.00639
GO:0031291	Ran protein signal transduction	0.00754
GO:1905448	positive regulation of mitochondrial ATP synthesis coupled electron transport	0.0139
GO:0006235	dTTP biosynthetic process	0.0139
GO:0046075	dTTP metabolic process	0.0139
GO:0009123	nucleoside monophosphate metabolic process	0.0207
GO:0035519	protein K29-linked ubiquitination	0.0215
GO:0044314	protein K27-linked ubiquitination	0.0215
GO:0006189	'de novo' IMP biosynthetic process	0.0294
GO:0031503	protein-containing complex localization	0.0297
GO:0009314	response to radiation	0.0322
GO:0072383	plus-end-directed vesicle transport along microtubule	0.0381
GO:0000056	ribosomal small subunit export from nucleus	0.0381
GO:1904666	regulation of ubiquitin protein ligase activity	0.0423
GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	0.0483
GO:0055015	ventricular cardiac muscle cell development	0.0483
GO:0000055	ribosomal large subunit export from nucleus	0.0483

GO term ID	GO term name	Enrichment p-value
GO:0075713	establishment of integrated proviral latency	0.0483

**Chromatin organisation**

GO:0051171	regulation of nitrogen compound metabolic process	1.42e-06
GO:0016070	RNA metabolic process	2.46e-06
GO:0006325	chromatin organization	5.81e-06
GO:0018394	peptidyl-lysine acetylation	2.75e-05
GO:0010605	negative regulation of macromolecule metabolic process	3.4e-05
GO:0006403	RNA localization	0.000411
GO:0050657	nucleic acid transport	0.000854
GO:0048511	rhythmic process	0.00139
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	0.00189
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	0.00189
GO:0010604	positive regulation of macromolecule metabolic process	0.00217
GO:0071426	ribonucleoprotein complex export from nucleus	0.00218
GO:0030330	DNA damage response, signal transduction by p53 class mediator	0.00241
GO:0016575	histone deacetylation	0.00308
GO:0006337	nucleosome disassembly	0.00361
GO:2000773	negative regulation of cellular senescence	0.00361
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	0.00412
GO:0080182	histone H3-K4 trimethylation	0.0044
GO:0016447	somatic recombination of immunoglobulin gene segments	0.00476
GO:0032233	positive regulation of actin filament bundle assembly	0.00793
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.00842
GO:0050872	white fat cell differentiation	0.01

GO term ID	GO term name	Enrichment p-value
GO:0045023	G0 to G1 transition	0.0167
GO:0060338	regulation of type I interferon-mediated signaling pathway	0.0182
GO:0090500	endocardial cushion to mesenchymal transition	0.0194
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	0.0212
GO:0010948	negative regulation of cell cycle process	0.0346
GO:0072655	establishment of protein localization to mitochondrion	0.0361
GO:0031647	regulation of protein stability	0.0396
GO:1902177	positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.0469
GO:0070345	negative regulation of fat cell proliferation	0.0469

Table E.2 GO term enrichment poly(I:C) response gene modules

GO term ID	GO term name	Enrichment p-value
<b>Canonical Type I IFN</b>		
GO:0045087	innate immune response	4.73e-41
GO:0051607	defense response to virus	5.82e-33
GO:0019221	cytokine-mediated signaling pathway	8.24e-27
GO:0032479	regulation of type I interferon production	6.38e-17
GO:0012501	programmed cell death	1.1e-12
GO:0051092	positive regulation of NF-kappaB transcription factor activity	8.8e-11
GO:0042127	regulation of cell proliferation	6.1e-05
GO:1903463	regulation of mitotic cell cycle DNA replication	0.000226
GO:0042270	protection from natural killer cell mediated cytotoxicity	0.000226
GO:0070383	DNA cytosine deamination	0.00155
	negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	0.00274
GO:0031087	deadenylation-independent decapping of nuclear-transcribed mRNA	0.00274

GO term ID	GO term name	Enrichment p-value
GO:0001568	blood vessel development	0.0035
GO:0061180	mammary gland epithelium development	0.00398
GO:0001525	angiogenesis	0.00479
GO:0016553	base conversion or substitution editing	0.00888
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	0.00947
GO:0007569	cell aging	0.00965
GO:0030218	erythrocyte differentiation	0.0101
GO:0097343	riposome assembly	0.0144
GO:2000045	regulation of G1/S transition of mitotic cell cycle	0.0179
GO:0007159	leukocyte cell-cell adhesion	0.0201
GO:0010594	regulation of endothelial cell migration	0.0201
GO:0046208	spermine catabolic process	0.0243
GO:1904798	positive regulation of core promoter binding	0.0243
GO:0035282	segmentation	0.0253
GO:0010528	regulation of transposition	0.0258
GO:0032088	negative regulation of NF-kappaB transcription factor activity	0.0294
GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway	0.03
GO:0032495	response to muramyl dipeptide	0.0349
GO:0014732	skeletal muscle atrophy	0.0349
GO:0042359	vitamin D metabolic process	0.0349
GO:0140052	cellular response to oxidised low-density lipoprotein particle stimulus	0.0349
GO:0002730	regulation of dendritic cell cytokine production	0.0349
GO:0048289	isotype switching to IgE isotypes	0.0349
GO:0010667	negative regulation of cardiac muscle cell apoptotic process	0.0397
GO:0046135	pyrimidine nucleoside catabolic process	0.0397
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.0417
GO:0022612	gland morphogenesis	0.0466
GO:0010966	regulation of phosphate transport	0.0467

GO term ID	GO term name	Enrichment p-value
GO:1990668	vesicle fusion with endoplasmic reticulum-Golgi intermediate compartment (ERGIC) membrane	0.0467
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0482

### Mitochondrial

GO:0006119	oxidative phosphorylation	3.38e-15
GO:0022904	respiratory electron transport chain	2.84e-14
GO:0032981	mitochondrial respiratory chain complex I assembly	1.06e-08
GO:1902600	proton transmembrane transport	5.77e-07
GO:0046597	negative regulation of viral entry into host cell	0.00232
GO:0006979	response to oxidative stress	0.00263
GO:0055093	response to hyperoxia	0.0029
GO:0000028	ribosomal small subunit assembly	0.00348
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	0.00348
GO:0035455	response to interferon-alpha	0.00348
GO:0035456	response to interferon-beta	0.00494
GO:0046688	response to copper ion	0.0054
GO:0046677	response to antibiotic	0.00578
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.00578
GO:0042493	response to drug	0.00694
GO:0042407	cristae formation	0.00727
GO:0035094	response to nicotine	0.00761
GO:0045071	negative regulation of viral genome replication	0.0134
GO:0010729	positive regulation of hydrogen peroxide biosynthetic process	0.0168
GO:0006413	translational initiation	0.0181
GO:0071357	cellular response to type I interferon	0.0261
GO:0010035	response to inorganic substance	0.0261
GO:0072513	positive regulation of secondary heart field cardioblast proliferation	0.0283
GO:0021549	cerebellum development	0.0306
GO:0007568	aging	0.0316

GO term ID	GO term name	Enrichment p-value
GO:0002181	cytoplasmic translation	0.0377
GO:0042538	hyperosmotic salinity response	0.0388
GO:0010940	positive regulation of necrotic cell death	0.0388
GO:0048318	axial mesoderm development	0.0439
GO:0046689	response to mercury ion	0.0439

### Signal transduction

<i>No significant gene sets</i>		
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### Organelle localisation

GO:0006996	organelle organization	7.97e-06
GO:0051649	establishment of localization in cell	3.28e-05
GO:0090066	regulation of anatomical structure size	0.00111
GO:0007165	signal transduction	0.00111
GO:0006464	cellular protein modification process	0.00111
GO:0042060	wound healing	0.00111
GO:0036211	protein modification process	0.00111
GO:0016032	viral process	0.00123
GO:0016477	cell migration	0.00123
GO:0009057	macromolecule catabolic process	0.00615
GO:0070936	protein K48-linked ubiquitination	0.00664
GO:0006793	phosphorus metabolic process	0.0076
GO:0070534	protein K63-linked ubiquitination	0.0145
GO:1901660	calcium ion export	0.0146
GO:0044265	cellular macromolecule catabolic process	0.0146
GO:0007167	enzyme linked receptor protein signaling pathway	0.0147
GO:0007049	cell cycle	0.0175
GO:1902309	negative regulation of peptidyl-serine dephosphorylation	0.0185
GO:0090435	protein localization to nuclear envelope	0.0186
GO:1990314	cellular response to insulin-like growth factor stimulus	0.0186
GO:0031329	regulation of cellular catabolic process	0.0238
GO:0010769	regulation of cell morphogenesis involved in differentiation	0.026
GO:0061037	negative regulation of cartilage development	0.0262
GO:0030900	forebrain development	0.0262

GO term ID	GO term name	Enrichment p-value
GO:0007599	hemostasis	0.0291
GO:1903984	positive regulation of TRAIL-activated apoptotic signaling pathway	0.0363
GO:0060978	angiogenesis involved in coronary vascular morphogenesis	0.0363
GO:0097350	neutrophil clearance	0.0363
GO:0001655	urogenital system development	0.0369
GO:0051301	cell division	0.0374
GO:0043010	camera-type eye development	0.0381
GO:0044794	positive regulation by host of viral process	0.0423
GO:0048609	multicellular organismal reproductive process	0.0443
GO:0021543	pallium development	0.046
GO:0050765	negative regulation of phagocytosis	0.0488

#### Metabolic processes

GO:0006810	transport	9.37e-13
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	3.09e-08
GO:0006518	peptide metabolic process	2.12e-06
GO:0006735	NADH regeneration	2.87e-05
GO:0061621	canonical glycolysis	2.87e-05
GO:0021762	substantia nigra development	3e-05
GO:1901844	regulation of cell communication by electrical coupling involved in cardiac conduction	0.000644
GO:0034976	response to endoplasmic reticulum stress	0.00124
GO:0036500	ATF6-mediated unfolded protein response	0.00124
GO:0075206	positive regulation by host of symbiont cAMP-mediated signal transduction	0.00321
GO:0010524	positive regulation of calcium ion transport into cytosol	0.00383
GO:0006094	gluconeogenesis	0.00473
GO:0048013	ephrin receptor signaling pathway	0.00473
GO:0006936	muscle contraction	0.00532
GO:0051343	positive regulation of cyclic-nucleotide phosphodiesterase activity	0.00562
GO:0051186	cofactor metabolic process	0.00666

GO term ID	GO term name	Enrichment p-value
GO:0097066	response to thyroid hormone	0.00852
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	0.00955
GO:0001568	blood vessel development	0.00965
GO:0044092	negative regulation of molecular function	0.0148
GO:0050790	regulation of catalytic activity	0.017
GO:0001893	maternal placenta development	0.018
GO:0097064	ncRNA export from nucleus	0.0183
GO:2001235	positive regulation of apoptotic signaling pathway	0.0194
GO:0045792	negative regulation of cell size	0.0223
GO:0001765	membrane raft assembly	0.0223
GO:0038093	Fc receptor signaling pathway	0.0223
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	0.0225
GO:0002478	antigen processing and presentation of exogenous peptide antigen	0.0228
GO:0033631	cell-cell adhesion mediated by integrin	0.0262
GO:0045214	sarcomere organization	0.0269
GO:0050999	regulation of nitric-oxide synthase activity	0.0269
GO:0018279	protein N-linked glycosylation via asparagine	0.0269
GO:0031623	receptor internalization	0.0274
GO:0042060	wound healing	0.0288
GO:0035304	regulation of protein dephosphorylation	0.0301
GO:0000910	cytokinesis	0.0306
GO:0022898	regulation of transmembrane transporter activity	0.0334
GO:0001667	ameboidal-type cell migration	0.036
GO:0031952	regulation of protein autophosphorylation	0.0383
GO:0019511	peptidyl-proline hydroxylation	0.0393
GO:0042744	hydrogen peroxide catabolic process	0.0433
GO:0022604	regulation of cell morphogenesis	0.0446
GO:0007596	blood coagulation	0.0463
GO:0034381	plasma lipoprotein particle clearance	0.0469
GO:0031639	plasminogen activation	0.0469

GO term ID	GO term name	Enrichment p-value
GO:0032516	positive regulation of phosphoprotein phosphatase activity	0.0469
GO:0007166	cell surface receptor signaling pathway	0.047
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	0.0486
GO:0043687	post-translational protein modification	0.0489
GO:0044147	negative regulation of development of symbiont involved in interaction with host	0.0491
GO:1905581	positive regulation of low-density lipoprotein particle clearance	0.0491
GO:1903673	mitotic cleavage furrow formation	0.0491
GO:1904313	response to methamphetamine hydrochloride	0.0491
GO:1903609	negative regulation of inward rectifier potassium channel activity	0.0491
GO:0002842	positive regulation of T cell mediated immune response to tumor cell	0.0491
GO:1905152	positive regulation of voltage-gated sodium channel activity	0.0491
GO:1904695	positive regulation of vascular smooth muscle contraction	0.0491
GO:0071528	tRNA re-export from nucleus	0.0491
GO:1904401	cellular response to Thyroid stimulating hormone	0.0491
GO:0050832	defense response to fungus	0.0491
GO:2000811	negative regulation of anoikis	0.0491
GO:0035606	peptidyl-cysteine S-trans-nitrosylation	0.0491
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	0.0491
GO:0051621	regulation of norepinephrine uptake	0.0491
GO:0002368	B cell cytokine production	0.0491
GO:0060051	negative regulation of protein glycosylation	0.0491
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	0.0491
GO:0034238	macrophage fusion	0.0491

GO term ID	GO term name	Enrichment p-value
GO:2000147	positive regulation of cell motility	0.0491
GO:1905597	positive regulation of low-density lipoprotein particle receptor binding	0.0491
GO:0001998	angiotensin-mediated vasoconstriction involved in regulation of systemic arterial blood pressure	0.0491
GO:1900085	negative regulation of peptidyl-tyrosine autophosphorylation	0.0491

### Protein regulation

GO:0070972	protein localization to endoplasmic reticulum	5.21e-13
GO:0006413	translational initiation	4.39e-08
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	8.04e-08
GO:0044403	symbiont process	5.71e-05
GO:0070887	cellular response to chemical stimulus	0.000588
GO:0043687	post-translational protein modification	0.00139
GO:0097435	supramolecular fiber organization	0.00208
GO:0050821	protein stabilization	0.0028
GO:0002376	immune system process	0.00356
GO:0001666	response to hypoxia	0.00753
GO:0051897	positive regulation of protein kinase B signaling	0.00803
GO:0034309	primary alcohol biosynthetic process	0.0114
GO:0048251	elastic fiber assembly	0.017
GO:0043312	neutrophil degranulation	0.0193
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	0.0196
GO:2000121	regulation of removal of superoxide radicals	0.0198
GO:0006089	lactate metabolic process	0.0303
GO:0048678	response to axon injury	0.0336
GO:0044409	entry into host	0.0346
GO:0018208	peptidyl-proline modification	0.0346
GO:0010608	posttranscriptional regulation of gene expression	0.0363
GO:0031333	negative regulation of protein complex assembly	0.0363
GO:1903206	negative regulation of hydrogen peroxide-induced cell death	0.0477

GO term ID	GO term name	Enrichment p-value
GO:0009651	response to salt stress	0.0477
GO:1901388	regulation of transforming growth factor beta activation	0.0479
GO:1903189	glyoxal metabolic process	0.0479
GO:0048693	regulation of collateral sprouting of injured axon	0.0479
GO:1903200	positive regulation of L-dopa decarboxylase ac- tivity	0.0479
GO:1903072	regulation of death-inducing signaling complex assembly	0.0479
GO:0034120	positive regulation of erythrocyte aggregation	0.0479
GO:1901194	negative regulation of formation of translation preinitiation complex	0.0479
GO:0045454	cell redox homeostasis	0.0479
GO:0036531	glutathione deglycation	0.0479
GO:1990478	response to ultrasound	0.0479
GO:1903195	regulation of L-dopa biosynthetic process	0.0479
GO:1902546	positive regulation of DNA N-glycosylase activ- ity	0.0479
GO:0036529	protein deglycation, glyoxal removal	0.0479
GO:0140041	cellular detoxification of methylglyoxal	0.0479
GO:1903197	positive regulation of L-dopa biosynthetic pro- cess	0.0479
GO:2001272	positive regulation of cysteine-type endopep- tidase activity involved in execution phase of apoptosis	0.0479
GO:0048689	formation of growth cone in injured axon	0.0479
GO:0018323	enzyme active site formation via L-cysteine sulfenic acid	0.0479
GO:0018032	protein amidation	0.0479
GO:1903168	positive regulation of pyrroline-5-carboxylate reductase activity	0.0479
GO:2000277	positive regulation of oxidative phosphorylation	0.0479
GO:0106046	uncoupler activity	0.0479
GO:0106046	guanine deglycation, glyoxal removal	0.0479

GO term ID	GO term name	Enrichment p-value
GO:0015872	dopamine transport	0.0479
GO:2001023	regulation of response to drug	0.0479
GO:1990262	anti-Mullerian hormone signaling pathway	0.0479
GO:1905578	regulation of ERBB3 signaling pathway	0.0479
GO:1903122	negative regulation of TRAIL-activated apoptotic signaling pathway	0.0479
GO:0032535	regulation of cellular component size	0.0479
GO:1903659	regulation of complement-dependent cytotoxicity	0.0479
GO:1903176	regulation of tyrosine 3-monooxygenase activity	0.0479
GO:1905572	ganglioside GM1 transport to membrane	0.0479

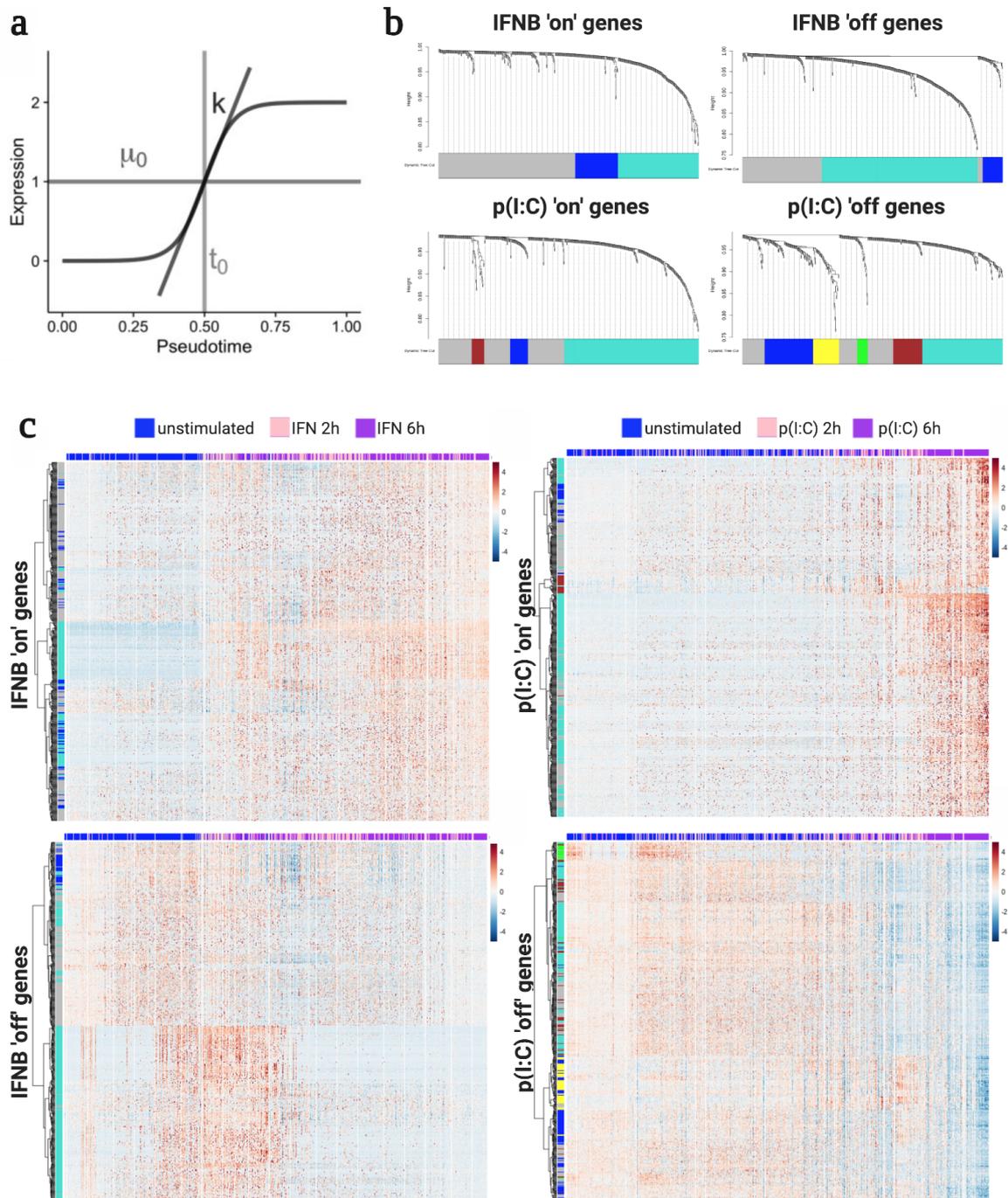


Fig. E.1 Modules of co-expressed innate immune response genes using WGCNA. a) The SwitchDE package [97] was used to infer a dynamic model of expression for each gene. b) WGCNA was applied to detect modules of co-expressed genes. The 500 most significant up- and down-regulated genes in each response pathway were used; dendrogram and inferred clusters are shown. Dynamic tree cutting approach was used to determine the optimum number of gene clusters. c) The expression of these genes over 'IFN pathway', left, and 'poly(I:C) pathway', right, are shown. Expression values are scaled within each row, and WGCNA cluster assignment is shown in the left-side colour bar.

