

Supplementary Figures and Tables

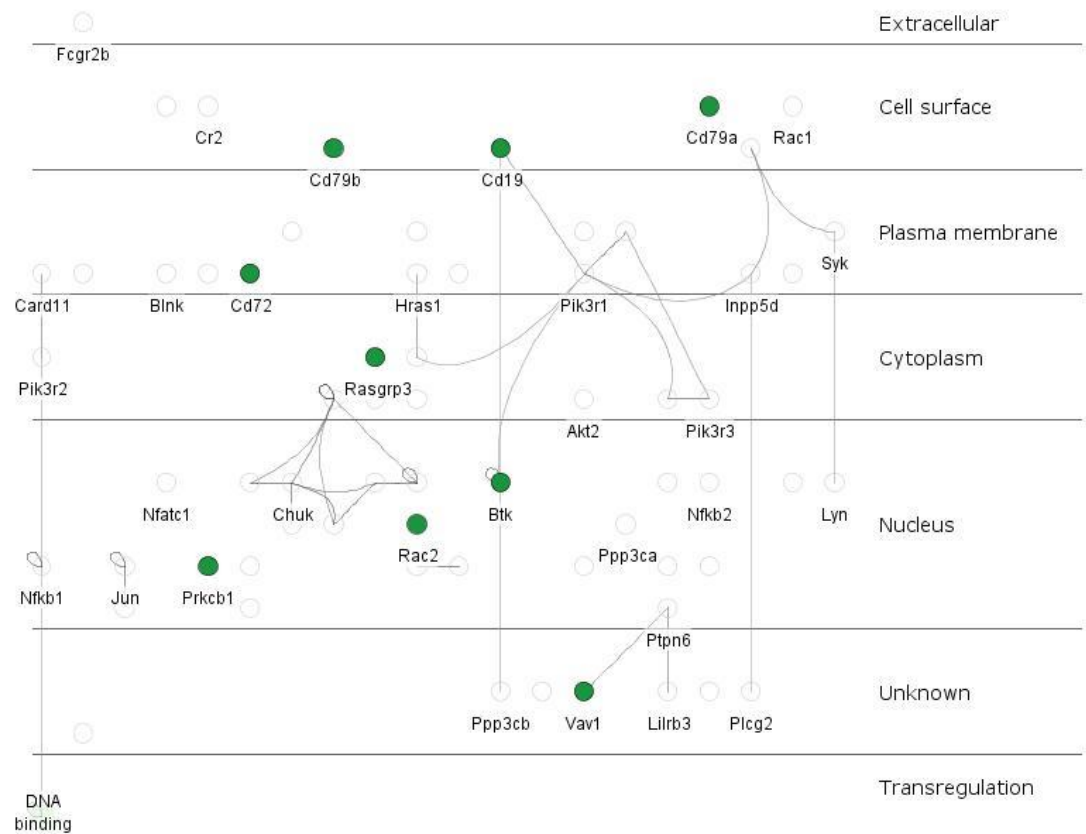
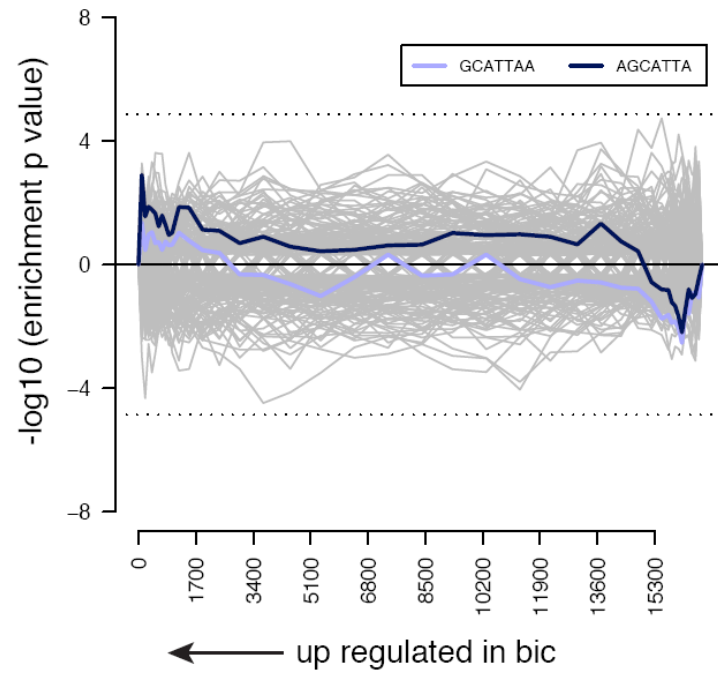


Figure S 1. The B cell Receptor signalling pathway is downregulated in the caecal patch of miR-155-deficient mice on day 4 pi

InnateDB analysis of mRNAs down-regulated in miR-155-deficient vs wild-type caecal patch 4 days pi identified that there was an over-representation of genes involved in the B cell receptor signalling pathway. Figure shows genes involved in B cell receptor signalling and those identified as being significantly down-regulated (green nodes).

Colon bic vs wt



Cecal patch bic vs wt

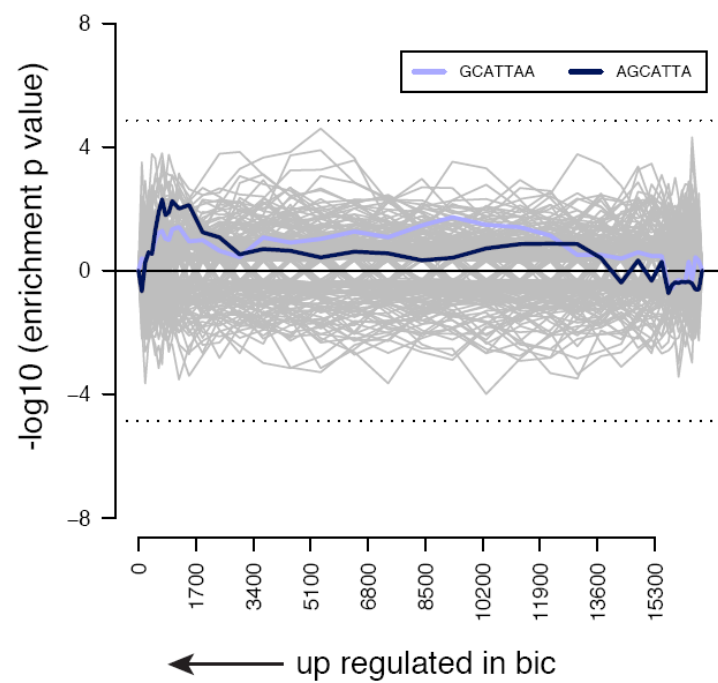


Figure S 2. Sylamer analysis

Sylamer analysis of mRNAs extracted from colon (colon, bic (miR-155-deficient) vs wt (wild-type)) and caecal patch (caecal patch, bic (miR-155-deficient) vs wt (wild-type)). The x-axis represents all the genes with an annotated 3'UTR sequence, sorted starting from the most up-regulated in the miR-155-deficient samples. The y-axis represents the $-\log_{10}$ transformed hyper-geometric P-values, with positive values denoting enrichment and negative values depletion. Each gray line represents a single 7-nucleotide seed-matching word and those corresponding to miR-155 are highlighted. Dotted lines represent Bonferroni-corrected P-value significance thresholds of 0.01.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
00980	8.5e-08	9.4	1.75	12	57	Metabolism of xenobiotics by cytochrome P450	Metabolism of xenobiotics by cytochrome P450
00071	1.4e-06	10.6	1.17	9	38	Fatty acid metabolism	Fatty acid metabolism
00150	1.5e-04	7.3	1.20	7	39	Androgen and estrogen metabolism	Androgen and estrogen metabolism
00280	9.1e-04	6.2	1.17	6	38	Valine, leucine and isoleucine degradation	Valine, leucine and isoleucine degradation
00040	1.5e-03	10.0	0.52	4	17	Pentose and glucuronate interconversions	Pentose and glucuronate interconversions
00010	2.5e-03	5.0	1.42	6	46	Glycolysis / Gluconeogenesis	Glycolysis / Gluconeogenesis
00410	2.8e-03	8.2	0.62	4	20	beta-Alanine metabolism	beta-Alanine metabolism
00360	3.4e-03	7.7	0.65	4	21	Phenylalanine metabolism	Phenylalanine metabolism
00220	4.8e-03	6.9	0.71	4	23	Urea cycle and metabolism of amino groups	Urea cycle and metabolism of amino groups
00640	6.5e-03	6.2	0.77	4	25	Propanoate metabolism	Propanoate metabolism
00350	8.6e-03	4.4	1.29	5	42	Tyrosine metabolism	Tyrosine metabolism
00650	9.5e-03	4.3	1.32	5	43	Butanoate metabolism	Butanoate metabolism
00120	1.3e-02	5.0	0.92	4	30	Bile acid biosynthesis	Bile acid biosynthesis
00860	1.4e-02	4.8	0.95	4	31	Porphyrin and chlorophyll metabolism	Porphyrin and chlorophyll metabolism
00340	1.7e-02	4.5	1.02	4	33	Histidine metabolism	Histidine metabolism
00680	1.8e-02	12.8	0.22	2	7	Methane metabolism	Methane metabolism
00590	1.9e-02	3.5	1.57	5	51	Arachidonic acid metabolism	Arachidonic acid metabolism
00480	2.1e-02	4.2	1.08	4	35	Glutathione metabolism	Glutathione metabolism
00140	2.3e-02	10.7	0.25	2	8	C21-Steroid hormone metabolism	C21-Steroid hormone metabolism
00920	2.3e-02	10.7	0.25	2	8	Sulfur metabolism	Sulfur metabolism
00641	2.9e-02	9.2	0.28	2	9	3-Chloroacrylic acid degradation	3-Chloroacrylic acid degradation
03320	3.4e-02	3.0	1.82	5	59	PPAR signaling pathway	PPAR signaling pathway
00720	4.3e-02	7.1	0.34	2	11	Reductive carboxylate cycle (CO2 fixation)	Reductive carboxylate cycle (CO2 fixation)

Table S 5. Gene to KEGG test for over-representation within upregulated mRNAs in miR-155-deficient caecal patch on day 4 pi

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
04662	1.0e-06	8.0	1.81	11	57	B cell receptor signaling pathway	B cell receptor signaling pathway
04514	1.6e-05	4.5	3.77	14	119	Cell adhesion molecules (CAMs)	Cell adhesion molecules (CAMs)
04940	5.8e-04	5.7	1.49	7	47	Type I diabetes mellitus	Type I diabetes mellitus
04650	7.7e-04	3.8	3.04	10	96	Natural killer cell mediated cytotoxicity	Natural killer cell mediated cytotoxicity
04670	2.6e-03	3.4	2.98	9	94	Leukocyte transendothelial migration	Leukocyte transendothelial migration
04612	6.6e-03	3.5	2.25	7	71	Antigen processing and presentation	Antigen processing and presentation
04060	7.8e-03	2.3	6.18	13	195	Cytokine-cytokine receptor interaction	Cytokine-cytokine receptor interaction
04640	1.7e-02	3.2	2.09	6	66	Hematopoietic cell lineage	Hematopoietic cell lineage
00601	2.5e-02	10.4	0.25	2	8	Glycosphingolipid biosynthesis - lactoseries	Glycosphingolipid biosynthesis - lactoseries
00240	2.8e-02	2.8	2.35	6	74	Pyrimidine metabolism	Pyrimidine metabolism
04664	4.5e-02	2.8	1.96	5	62	Fc epsilon RI signaling pathway	Fc epsilon RI signaling pathway

Table S 6. Gene to KEGG test for over-representation within downregulated mRNAs in miR-155-deficient caecal patch on day 4 pi

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006631	9.7e-07	5.3	3.30	15	133	fatty acid metabolic process
GO:0019752	3.8e-05	2.9	8.45	22	342	carboxylic acid metabolic process
GO:0044255	6.1e-05	3.2	6.31	18	270	cellular lipid metabolic process
GO:0006816	2.5e-04	4.8	2.11	9	85	calcium ion transport
GO:0006812	3.1e-04	2.5	9.10	21	367	cation transport
GO:0050801	5.9e-04	3.3	3.94	12	159	ion homeostasis
GO:0055082	1.2e-03	3.2	3.70	11	149	cellular chemical homeostasis
GO:0008272	1.6e-03	17.0	0.25	3	10	sulfate transport
GO:0001523	2.1e-03	14.9	0.27	3	11	retinoid metabolic process
GO:0006694	2.5e-03	4.8	1.38	6	56	steroid biosynthetic process
GO:0030003	3.6e-03	3.8	1.98	7	80	cellular cation homeostasis
GO:0042445	4.2e-03	4.3	1.54	6	62	hormone metabolic process
GO:0006766	7.1e-03	4.5	1.22	5	49	vitamin metabolic process
GO:0051234	8.9e-03	1.4	47.55	63	1917	establishment of localization
GO:0006829	1.3e-02	7.0	0.50	3	20	zinc ion transport
GO:0042493	1.3e-02	7.0	0.50	3	20	response to drug
GO:0055066	1.3e-02	3.3	1.93	6	78	di-, tri-valent inorganic cation homeostasis
GO:0030155	1.3e-02	4.8	0.92	4	37	regulation of cell adhesion
GO:0006732	1.7e-02	2.8	2.65	7	107	coenzyme metabolic process
GO:0006639	1.9e-02	6.0	0.57	3	23	acylglycerol metabolic process
GO:0006814	1.9e-02	3.0	2.11	6	85	sodium ion transport
GO:0008366	2.1e-02	5.7	0.60	3	24	axon ensheathment
GO:0008015	2.1e-02	3.0	2.16	6	87	blood circulation
GO:0006790	2.3e-02	4.0	1.09	4	44	sulfur metabolic process
GO:0006941	2.3e-02	5.4	0.62	3	25	striated muscle contraction
GO:0019228	2.3e-02	5.4	0.62	3	25	regulation of action potential in neuron
GO:0006721	2.4e-02	9.9	0.25	2	10	terpenoid metabolic process
GO:0007431	2.4e-02	9.9	0.25	2	10	salivary gland development
GO:0030865	2.4e-02	9.9	0.25	2	10	cortical cytoskeleton organization and biogenesis
GO:0006811	2.6e-02	2.2	4.22	9	179	ion transport
GO:0042592	3.1e-02	1.8	8.04	14	324	homeostatic process
GO:0002009	3.3e-02	2.6	2.41	6	97	morphogenesis of an epithelium
GO:0002026	3.4e-02	7.9	0.30	2	12	regulation of the force of heart contraction
GO:0009069	3.4e-02	7.9	0.30	2	12	serine family amino acid metabolic process
GO:0042364	3.4e-02	7.9	0.30	2	12	water-soluble vitamin biosynthetic process
GO:0006081	4.0e-02	7.2	0.32	2	13	aldehyde metabolic process
GO:0008152	4.1e-02	1.3	133.96	148	5400	metabolic process
GO:0001501	4.3e-02	2.1	3.92	8	158	skeletal development
GO:0044242	4.3e-02	4.1	0.79	3	32	cellular lipid catabolic process
GO:0006776	4.6e-02	6.6	0.35	2	14	vitamin A metabolic process
GO:0007339	4.6e-02	6.6	0.35	2	14	binding of sperm to zona pellucida
GO:0043506	4.6e-02	6.6	0.35	2	14	regulation of JNK activity

Table S 7. Gene to GO-BP conditional test for over-representation within mRNAs upregulated in miR-155-deficient caecal patch on day 4 pi

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006334	2.3e-19	15.8	2.37	25	85	nucleosome assembly
GO:0006323	2.0e-17	11.0	3.37	27	121	DNA packaging
GO:0006333	5.7e-17	11.1	3.21	26	115	chromatin assembly or disassembly
GO:0065003	3.8e-11	4.8	7.78	31	279	macromolecular complex assembly
GO:0051276	7.6e-10	4.4	7.75	29	278	chromosome organization and biogenesis
GO:0006955	3.0e-08	4.3	6.49	24	239	immune response
GO:0002504	1.8e-06	23.7	0.42	6	15	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0048534	7.6e-06	3.6	5.94	19	213	hemopoietic or lymphoid organ development
GO:0019886	2.6e-05	19.7	0.39	5	14	antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0046649	6.0e-05	3.6	4.63	15	166	lymphocyte activation
GO:0001775	1.2e-04	3.2	5.49	16	197	cell activation
GO:0019884	2.3e-04	11.1	0.59	5	21	antigen processing and presentation of exogenous antigen
GO:0030217	2.7e-04	5.4	1.70	8	61	T cell differentiation
GO:0050863	3.0e-04	5.3	1.73	8	62	regulation of T cell activation
GO:0007067	4.4e-04	3.5	3.82	12	137	mitosis
GO:0042100	5.5e-04	8.9	0.70	5	25	B cell proliferation
GO:0002521	5.5e-04	3.6	3.37	11	121	leukocyte differentiation
GO:0032943	5.7e-04	4.8	1.90	8	68	mononuclear cell proliferation
GO:0048002	6.6e-04	8.4	0.72	5	26	antigen processing and presentation of peptide antigen
GO:0051301	6.8e-04	2.8	5.77	15	207	cell division
GO:0002684	7.7e-04	3.4	3.51	11	126	positive regulation of immune system process
GO:0002694	1.3e-03	4.7	1.66	7	60	regulation of leukocyte activation
GO:0002429	1.3e-03	7.1	0.84	5	30	immune response-activating cell surface receptor signaling pathway
GO:0045619	1.5e-03	6.8	0.86	5	31	regulation of lymphocyte differentiation
GO:0051251	1.6e-03	4.5	1.73	7	62	positive regulation of lymphocyte activation
GO:0050670	1.8e-03	5.2	1.31	6	47	regulation of lymphocyte proliferation
GO:0050867	1.9e-03	4.4	1.78	7	64	positive regulation of cell activation
GO:0006954	2.0e-03	2.8	4.54	12	163	inflammatory response
GO:0002376	2.3e-03	2.8	4.61	12	183	immune system process
GO:0000278	2.3e-03	2.7	5.24	13	188	mitotic cell cycle
GO:0050776	2.6e-03	3.7	2.38	8	86	regulation of immune response
GO:0006935	3.1e-03	3.6	2.45	8	88	chemotaxis
GO:0030574	5.0e-03	10.6	0.36	3	13	collagen catabolic process
GO:0044243	5.0e-03	10.6	0.36	3	13	multicellular organismal catabolic process
GO:0044256	5.0e-03	10.6	0.36	3	13	protein digestion
GO:0044266	5.0e-03	10.6	0.36	3	13	multicellular organismal macromolecule catabolic process
GO:0044268	5.0e-03	10.6	0.36	3	13	multicellular organismal protein metabolic process

GO:0009605	5.6e-03	2.0	10.01	19	359	response to external stimulus
GO:0000279	5.9e-03	2.5	5.19	12	186	M phase
GO:0030890	6.2e-03	9.6	0.39	3	14	positive regulation of B cell proliferation
GO:0006260	6.3e-03	2.9	3.35	9	120	DNA replication
GO:0022402	6.4e-03	2.2	7.28	15	261	cell cycle process
GO:0006220	1.3e-02	7.0	0.50	3	18	pyrimidine nucleotide metabolic process
GO:0032946	1.4e-02	4.7	0.95	4	34	positive regulation of mononuclear cell proliferation
GO:0045582	1.5e-02	6.6	0.53	3	19	positive regulation of T cell differentiation
GO:0051239	1.9e-02	2.0	6.78	13	245	regulation of multicellular organismal process
GO:0048584	2.0e-02	2.7	2.76	7	99	positive regulation of response to stimulus
GO:0007265	2.6e-02	2.2	4.24	9	152	Ras protein signal transduction
GO:0051130	2.7e-02	3.8	1.14	4	41	positive regulation of cellular component organization and biogenesis
GO:0030155	2.8e-02	5.1	0.67	3	24	regulation of cell adhesion
GO:0002253	2.9e-02	3.1	1.73	5	62	activation of immune response
GO:0019882	2.9e-02	8.9	0.27	2	10	antigen processing and presentation
GO:0009220	3.0e-02	8.8	0.28	2	10	pyrimidine ribonucleotide biosynthetic process
GO:0051056	3.1e-02	2.3	3.68	8	132	regulation of small GTPase mediated signal transduction
GO:0002695	3.1e-02	4.8	0.70	3	25	negative regulation of leukocyte activation
GO:0030099	3.6e-02	2.6	2.45	6	88	myeloid cell differentiation
GO:0006911	3.6e-02	7.8	0.31	2	11	phagocytosis, engulfment
GO:0007051	3.6e-02	7.8	0.31	2	11	spindle organization and biogenesis
GO:0007159	3.6e-02	7.8	0.31	2	11	leukocyte adhesion
GO:0043331	3.6e-02	7.8	0.31	2	11	response to dsRNA
GO:0045191	3.6e-02	7.8	0.31	2	11	regulation of isotype switching
GO:0050869	3.6e-02	7.8	0.31	2	11	negative regulation of B cell activation
GO:0001776	3.8e-02	4.4	0.75	3	27	leukocyte homeostasis
GO:0006270	4.3e-02	7.0	0.33	2	12	DNA replication initiation
GO:0006541	4.3e-02	7.0	0.33	2	12	glutamine metabolic process
GO:0050766	4.3e-02	7.0	0.33	2	12	positive regulation of phagocytosis
GO:0050798	4.3e-02	7.0	0.33	2	12	activated T cell proliferation
GO:0051085	4.3e-02	7.0	0.33	2	12	chaperone cofactor-dependent protein folding
GO:0009617	4.3e-02	2.8	1.92	5	69	response to bacterium
GO:0022610	4.4e-02	1.6	12.44	19	446	biological adhesion
GO:0001817	4.6e-02	4.1	0.81	3	29	regulation of cytokine production
GO:0032615	4.9e-02	6.4	0.36	2	13	interleukin-12 production
GO:0045785	4.9e-02	6.4	0.36	2	13	positive regulation of cell adhesion
GO:0050777	4.9e-02	6.4	0.36	2	13	negative regulation of immune response
GO:0009607	5.0e-02	2.1	4.04	8	145	response to biotic stimulus

Table S 8. Gene to GO-BP conditional test for over-representation within mRNAs downregulated in miR-155-deficient caecal patch on day 4 pi

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
00150	0.025	9.3	0.247	2	39	Androgen and estrogen metabolism	Androgen and estrogen metabolism
04115	0.048	6.3	0.355	2	56	p53 signaling pathway	p53 signaling pathway
00140	0.050	23.5	0.051	1	8	C21-Steroid hormone metabolism	C21-Steroid hormone metabolism
00920	0.050	23.5	0.051	1	8	Sulfur metabolism	Sulfur metabolism

Table S 14. Gene to KEGG test for over-representation within mRNAs upregulated in miR-155-deficient caecal patch on day 14 pi

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
00601	0.036	34	0.036	1	8	Glycosphingolipid biosynthesis - lactoseries	Glycosphingolipid biosynthesis - lactoseries

Table S 15. Gene to KEGG test for over-representation within mRNAs downregulated in miR-155-deficient caecal patch on day14 pi

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006953	0.00026	28.9	0.13	3	20	acute-phase response
GO:0007050	0.00204	13.3	0.25	3	40	cell cycle arrest
GO:0008202	0.00604	5.9	0.73	4	115	steroid metabolic process
GO:0045859	0.00642	5.8	0.74	4	117	regulation of protein kinase activity
GO:0051338	0.00808	5.5	0.79	4	125	regulation of transferase activity
GO:0006986	0.01258	12.9	0.17	2	27	response to unfolded protein
GO:0033673	0.01955	10.1	0.22	2	34	negative regulation of kinase activity
GO:0043086	0.04001	6.7	0.32	2	50	negative regulation of catalytic activity
GO:0006066	0.04479	3.2	1.34	4	211	alcohol metabolic process
GO:0051726	0.04544	3.1	1.35	4	212	regulation of cell cycle
GO:0008643	0.04754	6.1	0.35	2	55	carbohydrate transport

Table S 16. Gene to GO-BP conditional test for over-representation within mRNAs upregulated in miR-155-deficient caecal patch on day14 pi

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006935	0.00005	23.7	0.210	4	88	chemotaxis
GO:0002437	0.00030	101.5	0.026	2	11	inflammatory response to antigenic stimulus
GO:0050766	0.00035	91.3	0.029	2	12	positive regulation of phagocytosis
GO:0007626	0.00047	12.9	0.374	4	157	locomotory behavior
GO:0002824	0.00064	65.2	0.038	2	16	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002708	0.00101	50.7	0.048	2	20	positive regulation of lymphocyte mediated immunity
GO:0002819	0.00101	50.7	0.048	2	20	regulation of adaptive immune response
GO:0032103	0.00101	50.7	0.048	2	20	positive regulation of response to external stimulus
GO:0006690	0.00111	48.0	0.050	2	21	icosanoid metabolic process
GO:0002703	0.00145	41.5	0.057	2	24	regulation of leukocyte mediated immunity
GO:0050727	0.00158	39.6	0.060	2	25	regulation of inflammatory response
GO:0031349	0.00171	38.0	0.062	2	26	positive regulation of defense response
GO:0030100	0.00184	36.5	0.064	2	27	regulation of endocytosis
GO:0050900	0.00198	35.1	0.067	2	28	leukocyte migration
GO:0002768	0.00242	31.4	0.074	2	31	immune response-regulating cell surface receptor signaling pathway
GO:0001525	0.00265	12.3	0.281	3	118	angiogenesis
GO:0002757	0.00291	28.5	0.081	2	34	immune response-activating signal transduction
GO:0048583	0.00387	10.7	0.321	3	135	regulation of response to stimulus
GO:0051130	0.00421	23.3	0.098	2	41	positive regulation of cellular component organization and biogenesis
GO:0007599	0.00442	22.8	0.100	2	42	hemostasis
GO:0050817	0.00462	22.2	0.102	2	43	coagulation
GO:0009611	0.00520	9.7	0.358	3	163	response to wounding
GO:0051240	0.00530	9.6	0.360	3	151	positive regulation of multicellular organismal process
GO:0006952	0.00541	6.5	0.726	4	305	defense response
GO:0002526	0.00801	16.5	0.136	2	57	acute inflammatory response
GO:0001568	0.00887	7.9	0.433	3	182	blood vessel development
GO:0042060	0.01094	14.0	0.160	2	67	wound healing
GO:0002449	0.01357	12.4	0.179	2	75	lymphocyte mediated immunity
GO:0002460	0.01357	12.4	0.179	2	75	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0051239	0.01941	10.3	0.216	2	102	regulation of multicellular organismal process
GO:0007155	0.01990	4.3	1.062	4	446	cell adhesion
GO:0000272	0.02357	48.5	0.024	1	10	polysaccharide catabolic process
GO:0019370	0.02357	48.5	0.024	1	10	leukotriene biosynthetic process
GO:0050854	0.02357	48.5	0.024	1	10	regulation of antigen receptor-mediated signaling pathway
GO:0006928	0.02491	5.3	0.638	3	268	cell motility
GO:0009605	0.02517	9.0	0.249	2	129	response to external stimulus
GO:0006693	0.02590	43.7	0.026	1	11	prostaglandin metabolic process
GO:0006911	0.02590	43.7	0.026	1	11	phagocytosis, engulfment
GO:0043449	0.02590	43.7	0.026	1	11	alkene metabolic process
GO:0045055	0.02590	43.7	0.026	1	11	regulated secretory pathway
GO:0048286	0.02590	43.7	0.026	1	11	alveolus development
GO:0002252	0.02740	8.5	0.260	2	109	immune effector process
GO:0030199	0.03054	36.4	0.031	1	13	collagen fibril organization
GO:0042461	0.03054	36.4	0.031	1	13	photoreceptor cell development
GO:0006044	0.03285	33.6	0.033	1	14	N-acetylglucosamine metabolic process
GO:0019886	0.03285	33.6	0.033	1	14	antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0030335	0.03285	33.6	0.033	1	14	positive regulation of cell migration
GO:0032635	0.03285	33.6	0.033	1	14	interleukin-6 production
GO:0002504	0.03516	31.2	0.036	1	15	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0032640	0.03516	31.2	0.036	1	15	tumor necrosis factor production
GO:0048519	0.03660	3.1	1.896	5	796	negative regulation of biological process
GO:0000902	0.03738	4.5	0.748	3	314	cell morphogenesis
GO:0040017	0.03746	29.1	0.038	1	16	positive regulation of locomotion
GO:0002682	0.03911	6.9	0.315	2	138	regulation of immune system process
GO:0050852	0.03975	27.3	0.040	1	17	T cell receptor signaling pathway
GO:0006040	0.04433	24.2	0.045	1	19	amino sugar metabolic process
GO:0048593	0.04433	24.2	0.045	1	19	camera-type eye morphogenesis
GO:0002699	0.04472	24.0	0.046	1	20	positive regulation of immune effector process
GO:0006958	0.04661	23.0	0.048	1	20	complement activation, classical pathway
GO:0019884	0.04888	21.8	0.050	1	21	antigen processing and presentation of exogenous antigen
GO:0006909	0.04913	21.7	0.050	1	22	phagocytosis

Table S 17. Gene to GO-BP conditional test for over-representation within downregulated mRNAs in miR-155-deficient caecal patch on day 14 pi

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
04620	0.012	16	0.177	2	84	Toll-like receptor signaling pathway	Toll-like receptor signaling pathway
00100	0.046	26	0.046	1	22	Biosynthesis of steroids	Biosynthesis of steroids

Table S 23. Gene to KEGG test for over-representation within mRNAs upregulated in miR-155-deficient colon on day4 pi

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
00910	0.043	28	0.043	1	18	Nitrogen metabolism	Nitrogen metabolism

Table S 24. Gene to KEGG test for over-representation within mRNAs downregulated in miR-155-deficient colon on day4 pi

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006954	0.00082	20.6	0.194	3	163	inflammatory response
GO:0009605	0.00776	9.1	0.427	3	359	response to external stimulus
GO:0009607	0.01235	13.9	0.173	2	145	response to biotic stimulus
GO:0051704	0.01368	13.1	0.182	2	153	multi-organism process
GO:0009161	0.01420	83.1	0.014	1	12	ribonucleoside monophosphate metabolic process
GO:0009124	0.01538	76.2	0.015	1	13	nucleoside monophosphate biosynthetic process
GO:0006629	0.01809	6.6	0.583	3	490	lipid metabolic process
GO:0006749	0.02124	53.7	0.021	1	18	glutathione metabolic process
GO:0007157	0.02124	53.7	0.021	1	18	heterophilic cell adhesion
GO:0006953	0.02357	48.1	0.024	1	20	acute-phase response
GO:0030258	0.02357	48.1	0.024	1	20	lipid modification
GO:0009615	0.02912	38.6	0.029	1	27	response to virus
GO:0016126	0.03170	35.1	0.032	1	27	sterol biosynthetic process
GO:0006950	0.03234	5.2	0.728	3	611	response to stress
GO:0050900	0.03285	33.8	0.033	1	28	leukocyte migration
GO:0048015	0.03976	27.6	0.040	1	34	phosphoinositide-mediated signaling

Table S 25. Gene to GO-BP conditional test for over-representation within mRNAs upregulated in miR-155-deficient colon on day4 pi

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006631	0.018	10.8	0.211	2	133	fatty acid metabolic process
GO:0006635	0.020	55.8	0.021	1	13	fatty acid beta-oxidation
GO:0016525	0.020	55.8	0.021	1	13	negative regulation of angiogenesis
GO:0030574	0.020	55.8	0.021	1	13	collagen catabolic process
GO:0044243	0.020	55.8	0.021	1	13	multicellular organismal catabolic process
GO:0044256	0.020	55.8	0.021	1	13	protein digestion
GO:0044266	0.020	55.8	0.021	1	13	multicellular organismal macromolecule catabolic process
GO:0044268	0.020	55.8	0.021	1	13	multicellular organismal protein metabolic process
GO:0006094	0.022	51.5	0.022	1	14	gluconeogenesis
GO:0046395	0.030	37.2	0.030	1	19	carboxylic acid catabolic process
GO:0051260	0.030	37.2	0.030	1	19	protein homooligomerization
GO:0019216	0.031	35.2	0.032	1	20	regulation of lipid metabolic process
GO:0046364	0.033	33.5	0.033	1	21	monosaccharide biosynthetic process
GO:0001944	0.034	7.7	0.294	2	185	vasculature development
GO:0010033	0.041	26.8	0.041	1	26	response to organic substance
GO:0032502	0.042	2.8	3.502	7	2206	developmental process
GO:0008645	0.042	25.7	0.043	1	27	hexose transport
GO:0042593	0.042	25.7	0.043	1	27	glucose homeostasis
GO:0050770	0.042	25.7	0.043	1	27	regulation of axonogenesis
GO:0000187	0.045	23.9	0.046	1	29	activation of MAPK activity
GO:0002429	0.047	23.1	0.048	1	30	immune response-activating cell surface receptor signaling pathway
GO:0048731	0.047	3.0	2.086	5	1314	system development
GO:0007249	0.050	21.6	0.051	1	32	I-kappaB kinase/NF-kappaB cascade

Table S 26. Gene to GO-BP conditional test for over-representation within mRNAs downregulated in miR-155-deficient colon on day 4 pi

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
00150	0.0036	11.3	0.32	3	39	Androgen and estrogen metabolism	Androgen and estrogen metabolism
00361	0.0081	17.4	0.14	2	17	gamma-Hexachlorocyclohexane degradation	gamma-Hexachlorocyclohexane degradation
00910	0.0090	16.4	0.15	2	18	Nitrogen metabolism	Nitrogen metabolism
00980	0.0105	7.5	0.46	3	57	Metabolism of xenobiotics by cytochrome P450	Metabolism of xenobiotics by cytochrome P450
00340	0.0289	8.4	0.27	2	33	Histidine metabolism	Histidine metabolism
00480	0.0323	7.9	0.29	2	35	Glutathione metabolism	Glutathione metabolism

Table S 32. Gene to KEGG test for over-representation within mRNAs upregulated in miR-155-deficient colon on day14 pi

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	Description
04514	0.0085	4.5	1.29	5	119	Cell adhesion molecules (CAMs)	Cell adhesion molecules (CAMs)
04660	0.0099	5.3	0.86	4	79	T cell receptor signaling pathway	T cell receptor signaling pathway
04650	0.0192	4.3	1.04	4	96	Natural killer cell mediated cytotoxicity	Natural killer cell mediated cytotoxicity
04640	0.0338	4.6	0.72	3	66	Hematopoietic cell lineage	Hematopoietic cell lineage
04512	0.0392	4.4	0.76	3	70	ECM-receptor interaction	ECM-receptor interaction

Table S 33. Gene to KEGG test for over-representation within mRNAs downregulated in miR-155-deficient colon on day14 pi

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006508	0.0020	3.1	3.98	11	472	proteolysis
GO:0006629	0.0026	3.0	4.13	11	490	lipid metabolic process
GO:0008202	0.0028	5.6	0.97	5	115	steroid metabolic process
GO:0006953	0.0121	13.4	0.17	2	20	acute-phase response
GO:0006323	0.0190	4.2	1.02	4	121	DNA packaging
GO:0003012	0.0262	5.0	0.64	3	76	muscle system process
GO:0006937	0.0262	8.6	0.25	2	30	regulation of muscle contraction
GO:0006334	0.0349	4.4	0.72	3	85	nucleosome assembly

Table S 34. Gene to GO-BP conditional test for over-representation within mRNAs upregulated in miR-155-deficient colon on day14 pi

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0050900	1.3e-06	32.9	0.197	5	28	leukocyte migration
GO:0006935	3.4e-05	11.2	0.620	6	88	chemotaxis
GO:0007155	5.8e-05	4.5	3.142	12	446	cell adhesion
GO:0009605	5.9e-05	5.3	2.193	10	319	response to external stimulus
GO:0050766	7.0e-05	49.0	0.085	3	12	positive regulation of phagocytosis
GO:0002696	8.3e-05	12.8	0.451	5	64	positive regulation of leukocyte activation
GO:0006954	1.2e-04	7.1	1.125	7	162	inflammatory response
GO:0050865	3.2e-04	9.4	0.599	5	85	regulation of cell activation
GO:0019884	4.1e-04	24.5	0.148	3	21	antigen processing and presentation of exogenous antigen
GO:0051240	6.6e-04	6.3	1.064	6	151	positive regulation of multicellular organismal process
GO:0048002	7.8e-04	19.2	0.183	3	26	antigen processing and presentation of peptide antigen
GO:0007626	8.1e-04	6.0	1.106	6	157	locomotory behavior
GO:0030106	8.7e-04	18.4	0.190	3	27	regulation of endocytosis
GO:0045321	1.8e-03	5.1	1.296	6	184	leukocyte activation
GO:0002764	1.9e-03	13.8	0.247	3	35	immune response-regulating signal transduction
GO:0000272	2.1e-03	36.2	0.070	2	10	polysaccharide catabolic process
GO:0002861	2.6e-03	32.2	0.077	2	11	regulation of inflammatory response to antigenic stimulus
GO:0006911	2.6e-03	32.2	0.077	2	11	phagocytosis, engulfment
GO:0050729	2.6e-03	32.2	0.077	2	11	positive regulation of inflammatory response
GO:0051249	2.6e-03	7.6	0.578	4	82	regulation of lymphocyte activation
GO:0006955	2.7e-03	4.7	1.406	6	212	immune response
GO:0051130	2.9e-03	11.6	0.289	3	41	positive regulation of cellular component organization and biogenesis
GO:0006950	3.4e-03	2.9	4.305	11	611	response to stress
GO:0006044	4.2e-03	24.1	0.099	2	14	N-acetylglucosamine metabolic process
GO:0019886	4.2e-03	24.1	0.099	2	14	antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0032635	4.2e-03	24.1	0.099	2	14	interleukin-6 production
GO:0050870	4.4e-03	10.0	0.331	3	47	positive regulation of T cell activation
GO:0002504	4.8e-03	22.3	0.106	2	15	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0048584	5.1e-03	6.2	0.697	4	99	positive regulation of response to stimulus
GO:0002821	5.5e-03	20.7	0.113	2	16	positive regulation of adaptive immune response
GO:0050852	6.2e-03	19.3	0.120	2	17	T cell receptor signaling pathway
GO:0006040	7.7e-03	17.0	0.134	2	19	amino sugar metabolic process
GO:0016054	7.7e-03	17.0	0.134	2	19	organic acid catabolic process
GO:0019724	7.8e-03	8.0	0.409	3	58	B cell mediated immunity
GO:0002705	8.6e-03	16.1	0.141	2	20	positive regulation of leukocyte mediated immunity
GO:0002822	8.6e-03	16.1	0.141	2	20	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0046634	8.6e-03	16.1	0.141	2	20	regulation of alpha-beta T cell activation
GO:0002253	9.4e-03	7.4	0.437	3	62	activation of immune response
GO:0006690	9.4e-03	15.2	0.148	2	21	icosanoid metabolic process
GO:0042398	9.4e-03	15.2	0.148	2	21	amino acid derivative biosynthetic process
GO:0045621	9.4e-03	15.2	0.148	2	21	positive regulation of lymphocyte differentiation
GO:0048872	1.0e-02	7.2	0.451	3	64	homeostasis of number of cells
GO:0006928	1.1e-02	3.4	1.888	6	268	cell motility
GO:0002706	1.2e-02	13.2	0.169	2	24	regulation of lymphocyte mediated immunity
GO:0032270	1.5e-02	6.3	0.514	3	73	positive regulation of cellular protein metabolic process

GO:0001558	1.6e-02	6.1	0.528	3	75	regulation of cell growth
GO:0002250	1.6e-02	6.1	0.528	3	75	adaptive immune response
GO:0051050	1.6e-02	11.3	0.195	2	28	positive regulation of transport
GO:0002429	1.7e-02	10.9	0.201	2	29	immune response-activating cell surface receptor signaling pathway
GO:0002443	1.9e-02	5.7	0.564	3	80	leukocyte mediated immunity
GO:0050776	2.2e-02	5.3	0.603	3	88	regulation of immune response
GO:0002520	2.2e-02	3.3	1.613	5	229	immune system development
GO:0030098	2.3e-02	5.3	0.606	3	86	lymphocyte differentiation
GO:0051094	2.6e-02	3.2	1.684	5	239	positive regulation of developmental process
GO:0002440	2.6e-02	8.5	0.254	2	36	production of molecular mediator of immune response
GO:0051258	2.9e-02	8.0	0.268	2	38	protein polymerization
GO:0044264	3.1e-02	7.8	0.275	2	39	cellular polysaccharide metabolic process
GO:0032101	3.2e-02	7.6	0.282	2	40	regulation of response to external stimulus
GO:0008361	3.3e-02	4.6	0.697	3	99	regulation of cell size
GO:0042742	3.4e-02	7.4	0.289	2	41	defense response to bacterium
GO:0031347	3.7e-02	7.0	0.303	2	43	regulation of defense response
GO:0032787	3.9e-02	3.3	1.282	4	182	monocarboxylic acid metabolic process
GO:0042035	4.0e-02	6.7	0.317	2	45	regulation of cytokine biosynthetic process
GO:0051707	4.0e-02	4.2	0.761	3	108	response to other organism
GO:0031328	4.3e-02	6.4	0.331	2	47	positive regulation of cellular biosynthetic process
GO:0042110	4.3e-02	4.0	0.782	3	111	T cell activation
GO:0009309	4.7e-02	6.1	0.345	2	49	amine biosynthetic process
GO:0030097	4.7e-02	3.1	1.360	4	193	hemopoiesis
GO:0018108	4.8e-02	6.0	0.352	2	50	peptidyl-tyrosine phosphorylation

Table S 35. Gene to GO-BP conditional test for over-representation within mRNAs downregulated in miR-155-deficient colon on day14 pi

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

List of Supplementary Figures and Tables

Figure S1. B cell Receptor signalling pathway downregulated Caecal patch Day 4

InnateDB analysis of mRNAs down-regulated in miR-155-deficient vs wild-type caecal patch 4 days pi identified that there was an over-representation of genes involved in the B cell receptor signalling pathway. Figure shows genes involved in B cell receptor signalling identified as being down-regulated (green nodes).

Figure S2. Sylamer analysis

Sylamer analysis of mRNAs extracted from colon (colon, bic (miR-155-deficient) vs wt (wild-type)) and caecal patch (caecal patch, bic (miR-155-deficient) vs wt (wild-type)). The x-axis represents all the genes with an annotated 3'UTR sequence, sorted starting from the most up-regulated in the miR-155-deficient samples. The y-axis represents the $-\log_{10}$ transformed hyper-geometric P-values, with positive values denoting enrichment and negative values depletion. Each gray line represents a single 7-nucleotide seed-matching word and those corresponding to miR-155 are highlighted. Dotted lines represent Bonferroni-corrected P-value significance thresholds of 0.01.

Table S1. Upregulated mRNAs in caecal patch Day 4

Up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S2. Upregulated mRNAs in miR-155-deficient vs wild-type Caecal patch Day 4

Up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S3. Downregulated mRNAs in Caecal patch Day 4

Down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S4. Downregulated mRNAs in miR-155-deficient vs wild-type Caecal patch Day 4

Down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S5. Gene to KEGG test over-representation Upregulated Caecal patch Day 4

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S6. Gene to KEGG test over-representation Downregulated Caecal patch Day 4

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S7. Gene to GO-BP conditional test over-representation Upreg Caecal patch Day 4

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S8. Gene to GO-BP conditional test over-representation Downreg Caecal patch Day 4

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S9. InnateDB Pathways Caecal patch Day 4

InnateDB analysis of mRNAs up- and down-regulated in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S10. Upregulated mRNAs in Caecal patch Day 14

Up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S11. Upregulated mRNAs in miR-155-deficient vs wild-type Caecal patch Day 14

Up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S12. Downreg mRNAs in Caecal patch Day 14

Down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S13. Downregulated mRNAs in miR-155-deficient vs wild-type Caecal patch Day 14

Down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi. Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S14. Gene to KEGG test over-representation Upregulated Caecal patch Day 14

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

Table S15. Gene to KEGG test over-representation Downregulated Caecal patch Day 14

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

Table S16. Gene to GO-BP conditional test over-representation Upreg Caecal patch Day 14

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

Table S17. Gene to GO-BP conditional test over-representation Downreg Caecal patch Day 14

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type caecal patch 14 days pi.

Table S18. InnateDB Pathways Caecal patch Day 14

InnateDB analysis of mRNAs up- and down-regulated in miR-155-deficient vs wild-type caecal patch 4 days pi.

Table S19. Upregulated mRNAs in Colon Day 4

Up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S20. Upregulated mRNAs in miR-155-deficient vs wild-type Colon Day 4

Up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S21. Downregulated mRNAs in Colon Day 4

Down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S22. Downregulated mRNAs in miR-155-deficient vs wild-type Colon Day 4

Down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S23. Gene to KEGG test over-representation Upregulated Colon Day 4

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

Table S24. Gene to KEGG test over-representation Downregulated Colon Day 4

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

Table S25. Gene to GO-BP conditional test over-representation Upreg mRNAs Colon Day 4

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

Table S26. Gene to GO-BP conditional test over-representation Downreg mRNAs Colon Day 4

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

Table S27. InnateDB Pathways Colon Day 4

InnateDB analysis of mRNAs up- and down-regulated in miR-155-deficient vs wild-type colon 4 days pi.

Table S28. Upregulated mRNAs in Colon Day 14

Up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S29. Upregulated mRNAs in miR-155-deficient vs wild-type Colon Day 14

Up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S30. Downregulated mRNAs in Colon Day 14

Down-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S31. Downregulated mRNAs in miR-155-deficient vs wild-type Colon Day 14

Down-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.
Differentially expressed genes were only considered significant if they altered by at least 1.5 fold and had adjusted P-value of less than 0.05.

Table S32. Gene to KEGG test over-representation Upregulated Colon Day 14

Gene to KEGG test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

Table S33. Gene to KEGG test over-representation Downregulated Colon Day 14

Gene to KEGG test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 4 days pi.

Table S34. Gene to GO-BP conditional test over-representation Upreg Colon Day 14

Gene to GO-biological process terms test for over-representation within up-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

Table S35. Gene to GO-BP conditional test over-representation Downreg
Colon Day 14

Gene to GO-biological process terms test for over-representation within down-regulated mRNAs in miR-155-deficient vs wild-type colon 14 days pi.

Table S36. InnateDB Pathways Colon Day 14

InnateDB analysis of mRNAs up- and down-regulated in miR-155-deficient vs wild-type colon 14 days pi.