

## Identification of a novel ceRNA network in multiple sclerosis

**Supplementary Table 2.** List of differentially expressed miRNAs

miRNA	logFC
hsa-miR-142-3p	4.2357085
hsa-miR-186	2.8655732
hsa-miR-98	2.83486
hsa-miR-130b	2.8221545
hsa-miR-7	2.4432054
hsa-miR-629	2.2825346
hsa-let-7c	2.1986221
hsa-let-7b	2.0665432
hsa-miR-619	2.0400192
hsa-let-7i	2.0122884
hsa-miR-140-5p	1.9960535
hsa-miR-34a	1.9393444
hsa-miR-892a	1.9002699
hsa-miR-615-5p	1.8999755
hsa-miR-145	1.8747742
hsa-miR-942	1.8390816
hsa-miR-148a	1.832381
hsa-miR-126	1.8322806
hsa-miR-1303	1.820051
hsa-miR-501-5p	1.814394
hsa-miR-608	1.8105159
hsa-miR-513a-3p	1.7980756
hsa-let-7e	1.7511411
hsa-miR-758	1.7443687
hsa-miR-223	1.7135023
hsa-miR-939	1.7101038
hsa-let-7g	1.6996091
hsa-miR-135a	1.5998915
hsa-miR-625	1.5803306
hsa-miR-1275	1.5745042
hsa-miR-885-5p	1.5727329
hsa-miR-658	1.5363959
hsa-miR-516b	1.5155584
hsa-miR-133a	1.5154452
hsa-miR-1207-5p	1.5098694
hsa-miR-624	1.5051318
hsa-miR-744	1.5032509
hsa-miR-451	1.4904226
hsa-miR-643	1.4800798
hsa-miR-22	1.4712502
hsa-miR-30d	1.4712471
hsa-miR-765	1.4316639
hsa-miR-1252	1.4127972
hsa-miR-365	1.3680369
hsa-miR-1911	1.3673465
hsa-miR-29b	1.35631
hsa-miR-200a	1.3394042
hsa-miR-572	1.3369357
hsa-miR-130a	1.3309718
hsa-miR-943	1.3189531
hsa-miR-199a-5p	1.3058443
hsa-miR-30e	1.2926271
hsa-miR-1287	1.2442879
hsa-miR-10b	1.2429673
hsa-miR-633	1.2279873
hsa-miR-1908	1.2208933
hsa-miR-659	1.2076403
hsa-miR-551b	-1.2224948

## Identification of a novel ceRNA network in multiple sclerosis

hsa-miR-371-5p	-1.2258024
hsa-miR-138	-1.2268572
hsa-miR-551a	-1.2494338
hsa-miR-647	-1.3045325
hsa-miR-211	-1.3164134
hsa-miR-302f	-1.3610912
hsa-miR-95	-1.3696805
hsa-miR-513a-5p	-1.3711852
hsa-miR-1910	-1.3731038
hsa-miR-654-3p	-1.3948593
hsa-miR-1270	-1.438118
hsa-miR-1256	-1.4412986
hsa-miR-548m	-1.4456289
hsa-miR-924	-1.4534229
hsa-miR-181d	-1.4737541
hsa-miR-641	-1.4997038
hsa-miR-1827	-1.5029866
hsa-miR-548l	-1.5206597
hsa-miR-10a	-1.5798142
hsa-miR-513b	-1.588105
hsa-miR-196a	-1.5955017
hsa-miR-19b	-1.5961783
hsa-miR-574-3p	-1.5991436
hsa-miR-30c	-1.6551129
hsa-miR-369-3p	-1.6664258
hsa-miR-513c	-1.6797069
hsa-miR-585	-1.6874115
hsa-miR-767-3p	-1.698606
hsa-miR-202	-1.7138339
hsa-miR-488	-1.7141297
hsa-miR-105	-1.726449
hsa-miR-99a	-1.7748024
hsa-miR-1249	-1.8006722
hsa-miR-644	-1.8014929
hsa-miR-379	-1.8200307
hsa-miR-1204	-1.8259435
hsa-miR-556-3p	-1.8261462
hsa-miR-609	-1.8485651
hsa-miR-382	-1.8701316
hsa-miR-218	-1.8763228
hsa-miR-299-3p	-1.9087321
hsa-miR-373	-1.9617412
hsa-miR-190b	-1.9789102
hsa-miR-548h	-2.0524013
hsa-miR-620	-2.0609552
hsa-miR-581	-2.114451
hsa-miR-610	-2.1596633
hsa-miR-875-5p	-2.170514
hsa-miR-651	-2.1708898
hsa-miR-125b	-2.1779881
hsa-miR-586	-2.1830611
hsa-miR-184	-2.2018869
hsa-miR-1306	-2.205356
hsa-miR-520d-3p	-2.2263496
hsa-miR-593	-2.2555876
hsa-miR-455-5p	-2.2946039
hsa-let-7a	-2.4571552
hsa-miR-1914	-2.4584416
hsa-let-7f	-2.4922172
hsa-miR-212	-2.654097
hsa-miR-512-3p	-3.3559523

---

## Identification of a novel ceRNA network in multiple sclerosis

**Supplementary Table 3.** Functional enriched analysis of the DEmRNAs

Category	ID	Term	Genes	p-value
BP	GO:0019731	antibacterial humoral response	IGHM, DEFA4, DEFA1B, B2M, CAMP, LTF	0.000458014
BP	GO:0050853	B cell receptor signaling pathway	BLK, IGHM, CD79A, CD19, IGHV3-23, IGHD	0.001183328
BP	GO:0006955	immune response	CXCL8, IGHV3-23, IFI6, SERPINB9, FCAR, TAPBP, VPREB3, ZEB1, IL7, IGHD, CEACAM8, DEFA1B, HLA-DOB, B2M, CD22, HLA-DQB1	0.001529446
BP	GO:0050830	defense response to Gram-positive bacterium	ADAM17, DEFA4, DEFA1B, LYZ, B2M, TIRAP, CAMP	0.001614498
BP	GO:0045087	innate immune response	BLK, IGHM, ANXA1, DDX3X, DEFA4, IGHV3-23, CYBB, TIRAP, LILRA5, CLEC7A, PCBP2, IGHD, DEFA1B, B2M, CAMP	0.004876241
CC	GO:0005833	hemoglobin complex	HBM, HBG2, HBB, HBA2, AHSP, HBD	4.15122E-07
CC	GO:0005654	nucleoplasm	ATF2, RBM25, RIF1, CELF1, CHD9, SPPL2B, KIAA1033, RORA, SMC3, AFF3, CLINT1, SYNE2, ACTB, NAMPT, PPP6R3, POLK, TGIF1, DDX17, SRRM2, PNISR, RBM14, ANXA1, DUSP3, SCAF11, TEX10, PPP4R3B, SAFB, SETSIP, TIRAP, FOXF1, SGO2, ZEB1, TBL1XR1, THRAP3, HNRNPH1, KAT6A, PPIG, TOP1, TP53, SF1, FKBP5, HEMGN, PRKDC, ANKRD11, BOD1L1, ANKRD12, GATA2, EXOSC6, CLEC7A, UBN1, PCBP2, USP1, FEM1C, TBL1X, SPEN, EGR1, RBM39, KDM4B, ALYREF, NONO, STAT2, DNAJC14, FOSL2, NR4A2, MLLT10, SNRNP40, ESF1, PKN2, MDM4, HSPA1B	1.72215E-06
CC	GO:0016020	membrane	CELF1, SPPL2B, PRF1, CD3G, PTPRK, CLINT1, SLC8A1, ACTB, TOMM22, ICAM1, LAMP1, CNTRL, CASP2, B2M, DDX17, EIF5A, ANXA3, APLP2, KRT1, SERPINB9, HBA2, CDKAL1, LRRC41, F5, TAPBP, ADAM17, PRKAR1A, HNRNPH1, HLA-DQB1, FKBP5, ARF6, KCNE3, CBFB, LUZP1, PRKDC, SELENBP1, APH1A, NT5E, RNF213, PCBP2, SNCA, MGEA5, SLC16A1, PLEKHA2, AMFR, ALYREF, NONO, PRRC2C, DNAJC14, TSPAN13, REEP3, GNAS, STT3A, KRAS, NAA15, CALR, CD24, CDS2	4.83176E-06
CC	GO:0005737	cytoplasm	ATF2, RIF1, SMC3, ACTB, LAMP1, CSPP1, NAMPT, NFATC2IP, NEK1, B2M, PNISR, SWAP70, LMO7, PPP4R3B, PLPP5, RAB30, ADAM17, PRKAR1A, PPIG, TP53, CDC42SE1, GGNBP2, KCNE3, UBA6, ANKRD11, ANKRD12, LPP, CD79A, RNF213, CLEC7A, PDGFC, PCBP2, STAP1, SCN3A, KLHDC10, EGR1, SYNRG, STYX, AZIN1, NR4A2, MLLT10, GLUD1, EIF2S3, GNAS, CALR, UBE2M, RBM25, DDX3X, CHD9, CELF1, CELF2, CD-CA7L, AFF3, SYNE2, OSBPL10, FCRLA, AKAP12, CA1, HINT3, CNTRL, PPP6R3, BLNK, CASP2, EPG5, EIF5A, RBM14, ANXA1, DUSP3, CNOT6L, ANXA3, ARG1, STRBP, TEX10, STRADB, CEP295, LIX1L, PAWR, SERPINB9, SETSIP, TIRAP, LRRC41, PTP4A1, ZEB1, HNRNPH1, CHI3L1, STRAP, LTF, ARPC4-TLLL3, TRAK2, FGD4, NT5E, ABLIM1, FEM1C, DEDD, SNCA, KDM4B, PLEKHA2, STAT2, HIPK3, P2RX5, SNRNP40, KRAS, PKN2, NAA15, HSPA1B	5.00075E-05
CC	GO:0072562	blood microparticle	IGHM, HBG2, KRT1, IGHV3-23, IGHD, HBB, HBA2, SLC4A1, HBD, HSPA1B, ACTB	6.68121E-05
MF	GO:0005515	protein binding	ATF2, SPPL2B, PRF1, SLC4A1, RORA, SMC3, ACTB, SLC8A1, ICAM1, CRKL, TOMM22, TCL1A, LAMP1, NAMPT, NEK1, B2M, BORCS5, DDX17, SCAF11, SWAP70, APLP2, KRT1, EBF1, CYBB, CDKAL1, FOXF1, SGO2, ADAM17, TBL1XR1, PRKAR1A, KAT6A, ADAM9, PPIG, TP53, SF1, FKBP5, BLK, RTN3, KCNE3, CBFB, EPB42, YTHDC1, UBA6, PRKDC, GATA2, LPP, APH1A, CD79A, CLEC7A, CD19, PDGFC, PCBP2, STAP1, LONRF1, NADK, KLHDC10, EGR1, SYNRG, ALYREF, NONO, STYX, ARPC4, AZIN1, FOSL2, NR4A2, MLLT10, GLUD1, EIF2S3, IL7, STT3A, GNAS, CYCS, MDM4, CALR, CD24, CD22, CD200, UBE2M, IGHM, RBM25, ALAS2, DDX3X, MS4A3, CXCL8, CELF1, ITGB3, CDCA7L, HBB, C1ORF174, PTPRK, HBD, CLINT1, SYNE2, AKAP12, CA1, CNTRL, NFKBIZ, PPP6R3, BLNK, PHACTR2, CASP2, CCR3, TGIF1, SRGN, EIF5A, FCRL2, RBM14, ANXA1, CNOT6L, KLF13, SECISBP2L, STRBP, TEX10, STRADB, ATRX, PAWR, SERPINB9, HBA2, PAX5, SAFB, FAM126B, TIRAP, F5, TAPBP, FCER2, ZEB1, HNRNPH1, THRAP3, STRAP, CEACAM8, TOP1, MS4A1, NUP58, ARF6, LTF, HEMGN, RUSC1-AS1, SDC-CAG3, HDC, IFI6, TRAK2, PCNP, SELENBP1, ABLIM1, MAT2A, UBN1, USP1, FEM1C, AHSP, TBL1X, DEDD, SNCA, LRRC25, SPEN, RBM39, CD72, PLEKHA2, AMFR, STAT2, GOS2, SNX20, SNRNP40, KRAS, PKN2, NAA15, COPG1, CLC, HSPA1B	1.10951E-10

## Identification of a novel ceRNA network in multiple sclerosis

MF	GO:0044822	poly(A) RNA binding	RBM25, DDX3X, PRKDC, CELF1, YTHDC1, CELF2, SAMS1, CRKL, EXOSC6, ALKBH5, PCBP2, EIF5A, DDX17, SRRM2, SPEN, PNISR, RBM39, RBM14, SCAF11, SECISBP2L, ALYREF, NONO, STRBP, PRRC2C, SAFB, SNRNP40, THRAP3, HNRNP1, STRAP, ESF1, PKN2, PPIG, NAA15, CALR, TOP1, SF1	4.11234E-06
MF	GO:0005344	oxygen transporter activity	HBM, HBG2, HBB, HBA2, HBD	3.01877E-05
MF	GO:0019825	oxygen binding	HBM, HBG2, HBB, HBA2, HBD	0.003784713
MF	GO:0019899	enzyme binding	LAMP1, PRKDC, ITGB3, PCBP2, TSPAN5, PAWR, CASP2, MDM4, ARPC4, TP53, HSPA1B, TRAK2	0.006107352
KEGG	hsa05416	Viral myocarditis	PRF1, CYCS, HLA-DOB, ACTB, ICAM1, HLA-DQB1	0.001825969
KEGG	hsa04662	B cell receptor signaling pathway	CD79A, CD72, CD19, BLNK, KRAS, CD22	0.004230988
KEGG	hsa05164	Influenza A	ATF2, CXCL8, STAT2, CYCS, HLA-DOB, HSPA1B, ACTB, ICAM1, HLA-DQB1	0.005537628
KEGG	hsa04612	Antigen processing and presentation	CALR, B2M, HLA-DOB, HSPA1B, TAPBP, HLA-DQB1	0.006385287
KEGG	hsa05161	Hepatitis B	ATF2, DDX3X, CXCL8, STAT2, CYCS, KRAS, TP53, TIRAP	0.007212606

**Supplementary Table 4. GO biological process terms for top 4 modules**

Mode	GO biological process	Description	Genes	adjust P-value
mode1	GO:0031640	killing of cells of other organism	FCER2/LTF/LYZ/CAMP/DEFA4/ARG1	5.85E-09
mode1	GO:0044364	disruption of cells of other organism	FCER2/LTF/LYZ/CAMP/DEFA4/ARG1	5.85E-09
mode1	GO:0001906	cell killing	FCER2/B2M/LTF/LYZ/CAMP/DEFA4/ARG1	1.85E-08
mode1	GO:0043312	neutrophil degranulation	HBB/B2M/LTF/CHI3L1/TCN1/LYZ/CAMP/DEFA4/ARG1	2.57E-08
mode1	GO:0002283	neutrophil activation involved in immune response	HBB/B2M/LTF/CHI3L1/TCN1/LYZ/CAMP/DEFA4/ARG1	2.57E-08
mode1	GO:0042119	neutrophil activation	HBB/B2M/LTF/CHI3L1/TCN1/LYZ/CAMP/DEFA4/ARG1	2.57E-08
mode1	GO:0002446	neutrophil mediated immunity	HBB/B2M/LTF/CHI3L1/TCN1/LYZ/CAMP/DEFA4/ARG1	2.57E-08
mode1	GO:0015671	oxygen transport	HBB/HBA2/HBM/HBG2	6.92E-08
mode1	GO:0015669	gas transport	HBB/HBA2/HBM/HBG2	1.74E-07
mode1	GO:0035821	modification of morphology or physiology of other organism	FCER2/LTF/LYZ/CAMP/DEFA4/ARG1	4.39E-07
mode1	GO:0006959	humoral immune response	FCER2/CD19/LTF/LYZ/CAMP/PAX5/DEFA4	1.20E-06
mode1	GO:0042744	hydrogen peroxide catabolic process	HBB/HBA2/HBM/HBG2	1.20E-06
mode1	GO:0015893	drug transport	HBB/HBA2/TCN1/HBM/HBG2/ARG1	2.01E-06
mode1	GO:0017001	antibiotic catabolic process	HBB/HBA2/HBM/HBG2	1.04E-05
mode1	GO:0042743	hydrogen peroxide metabolic process	HBB/HBA2/HBM/HBG2	1.04E-05
mode1	GO:0051187	cofactor catabolic process	HBB/HBA2/HBM/HBG2	2.00E-05
mode1	GO:0050829	defense response to Gram-negative bacterium	LTF/LYZ/CAMP/DEFA4	5.08E-05
mode1	GO:0002227	innate immune response in mucosa	LTF/CAMP/DEFA4	5.59E-05
mode1	GO:0097237	cellular response to toxic substance	HBB/HBA2/HBM/HBG2/ARG1	7.86E-05
mode1	GO:0098869	cellular oxidant detoxification	HBB/HBA2/HBM/HBG2	7.86E-05
mode1	GO:1990748	cellular detoxification	HBB/HBA2/HBM/HBG2	8.74E-05
mode1	GO:0019730	antimicrobial humoral response	LTF/LYZ/CAMP/DEFA4	0.000133
mode1	GO:0002385	mucosal immune response	LTF/CAMP/DEFA4	0.000138
mode1	GO:0050853	B cell receptor signaling pathway	CD79A/CD19/BLK/PAX5	0.000138
mode1	GO:0098754	detoxification	HBB/HBA2/HBM/HBG2	0.000138
mode1	GO:0002251	organ or tissue specific immune response	LTF/CAMP/DEFA4	0.000147
mode1	GO:0050832	defense response to fungus	LTF/DEFA4/ARG1	0.000163
mode1	GO:0051291	protein heterooligomerization	HBB/HBA2/HBM/HBG2	0.000163
mode1	GO:0042737	drug catabolic process	HBB/HBA2/HBM/HBG2	0.000199
mode1	GO:0019731	antibacterial humoral response	LTF/CAMP/DEFA4	0.000257
mode1	GO:0016999	antibiotic metabolic process	HBB/HBA2/HBM/HBG2	0.000257
mode1	GO:0009620	response to fungus	LTF/DEFA4/ARG1	0.000318
mode1	GO:0031343	positive regulation of cell killing	FCER2/B2M/ARG1	0.000612

## Identification of a novel ceRNA network in multiple sclerosis

mode1	GO:0051673	membrane disruption in other organism	LTF/DEFA4	0.000766
mode1	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	LTF/CAMP/DEFA4	0.000789
mode1	GO:0001895	retina homeostasis	B2M/LTF/LYZ	0.000833
mode1	GO:0051851	modification by host of symbiont morphology or physiology	LTF/CAMP/ARG1	0.000915
mode1	GO:0051712	positive regulation of killing of cells of other organism	FCER2/ARG1	0.000979
mode1	GO:0051873	killing by host of symbiont cells	CAMP/ARG1	0.000979
mode1	GO:0051702	interaction with symbiont	LTF/CAMP/ARG1	0.000986
mode1	GO:0031341	regulation of cell killing	FCER2/B2M/ARG1	0.001222
mode1	GO:0051709	regulation of killing of cells of other organism	FCER2/ARG1	0.001222
mode1	GO:0051852	disruption by host of symbiont cells	CAMP/ARG1	0.001222
mode1	GO:0050830	defense response to Gram-positive bacterium	LYZ/CAMP/DEFA4	0.001423
mode1	GO:0050851	antigen receptor-mediated signaling pathway	CD79A/CD19/BLK/PAX5	0.001423
mode1	GO:0051883	killing of cells in other organism involved in symbiotic interaction	CAMP/ARG1	0.001505
mode1	GO:0072593	reactive oxygen species metabolic process	HBB/HBA2/HBM/HBG2	0.001742
mode1	GO:0051818	disruption of cells of other organism involved in symbiotic interaction	CAMP/ARG1	0.001837
mode1	GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	LTF/CAMP/ARG1	0.002191
mode1	GO:0042742	defense response to bacterium	LTF/LYZ/CAMP/DEFA4	0.002855
mode1	GO:0050855	regulation of B cell receptor signaling pathway	BLK/PAX5	0.003108
mode1	GO:0002705	positive regulation of leukocyte mediated immunity	FCER2/B2M/ARG1	0.003278
mode1	GO:0002237	response to molecule of bacterial origin	B2M/LTF/DEFA4/ARG1	0.003321
mode1	GO:0002724	regulation of T cell cytokine production	B2M/ARG1	0.003726
mode1	GO:0042542	response to hydrogen peroxide	HBB/HBA2/ARG1	0.003847
mode1	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	FCER2/B2M/ARG1	0.00402
mode1	GO:0002706	regulation of lymphocyte mediated immunity	FCER2/B2M/ARG1	0.004112
mode1	GO:0043900	regulation of multi-organism process	FCER2/LTF/CAMP/ARG1	0.004374
mode1	GO:0002819	regulation of adaptive immune response	FCER2/B2M/ARG1	0.004914
mode1	GO:0002369	T cell cytokine production	B2M/ARG1	0.006292
mode1	GO:0002429	immune response-activating cell surface receptor signaling pathway	CD79A/CD19/BLK/PAX5	0.006292
mode1	GO:0002697	regulation of immune effector process	FCER2/CD19/B2M/ARG1	0.007715
mode1	GO:0002768	immune response-regulating cell surface receptor signaling pathway	CD79A/CD19/BLK/PAX5	0.007988
mode1	GO:0015701	bicarbonate transport	HBB/HBA2	0.008015
mode1	GO:0002703	regulation of leukocyte mediated immunity	FCER2/B2M/ARG1	0.008508
mode1	GO:0071222	cellular response to lipopolysaccharide	LTF/DEFA4/ARG1	0.008755
mode1	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	LTF/CAMP/ARG1	0.009136
mode1	GO:0071219	cellular response to molecule of bacterial origin	LTF/DEFA4/ARG1	0.009391
mode1	GO:0002699	positive regulation of immune effector process	FCER2/B2M/ARG1	0.00965
mode1	GO:0001894	tissue homeostasis	B2M/LTF/LYZ	0.011173
mode1	GO:0000302	response to reactive oxygen species	HBB/HBA2/ARG1	0.011452
mode1	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	B2M/ARG1	0.011635
mode1	GO:0051896	regulation of protein kinase B signaling	CD19/CHI3L1/BANK1	0.011708
mode1	GO:0071216	cellular response to biotic stimulus	LTF/DEFA4/ARG1	0.011708
mode1	GO:0050854	regulation of antigen receptor-mediated signaling pathway	BLK/PAX5	0.011991
mode1	GO:0046686	response to cadmium ion	B2M/ARG1	0.01443
mode1	GO:0043491	protein kinase B signaling	CD19/CHI3L1/BANK1	0.014971
mode1	GO:0001818	negative regulation of cytokine production	LTF/BANK1/ARG1	0.01522
mode1	GO:0002709	regulation of T cell mediated immunity	B2M/ARG1	0.01522
mode1	GO:0001910	regulation of leukocyte mediated cytotoxicity	B2M/ARG1	0.019855
mode1	GO:0002718	regulation of cytokine production involved in immune response	B2M/ARG1	0.020121
mode1	GO:0055072	iron ion homeostasis	B2M/LTF	0.023585
mode1	GO:0060333	interferon-gamma-mediated signaling pathway	B2M/ARG1	0.026678
mode1	GO:0046677	response to antibiotic	HBB/HBA2/ARG1	0.027351
mode1	GO:0032496	response to lipopolysaccharide	LTF/DEFA4/ARG1	0.027351
mode1	GO:0002367	cytokine production involved in immune response	B2M/ARG1	0.028622

## Identification of a novel ceRNA network in multiple sclerosis

mode1	GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	FCER2/B2M	0.031253
mode1	GO:0002449	lymphocyte mediated immunity	FCER2/B2M/ARG1	0.031253
mode1	GO:0006898	receptor-mediated endocytosis	HBB/B2M/HBA2	0.031407
mode1	GO:0002456	T cell mediated immunity	B2M/ARG1	0.031425
mode1	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	FCER2/B2M/ARG1	0.031838
mode1	GO:0001909	leukocyte mediated cytotoxicity	B2M/ARG1	0.031838
mode1	GO:0002708	positive regulation of lymphocyte mediated immunity	FCER2/B2M	0.031838
mode1	GO:0002821	positive regulation of adaptive immune response	FCER2/B2M	0.031838
mode1	GO:0000041	transition metal ion transport	B2M/TCN1	0.03449
mode1	GO:0002920	regulation of humoral immune response	FCER2/CD19	0.044423
mode1	GO:0002831	regulation of response to biotic stimulus	LTF/ARG1	0.046705
mode1	GO:0002700	regulation of production of molecular mediator of immune response	B2M/ARG1	0.048312
mode1	GO:0055076	transition metal ion homeostasis	B2M/LTF	0.049451
mode1	GO:0060249	anatomical structure homeostasis	B2M/LTF/LYZ	0.049451
mode1	GO:0051250	negative regulation of lymphocyte activation	BANK1/ARG1	0.049636
mode2	GO:0000209	protein polyubiquitination	RNF213/LMO7/LONRF1	0.001492
mode2	GO:0043687	post-translational protein modification	LRRC41/UBE2M/LMO7	0.002048
mode2	GO:0045116	protein neddylation	UBE2M	0.046956
mode3	GO:0042743	hydrogen peroxide metabolic process	SNCA/HBD/CYBB	0.016945
mode3	GO:0030520	intracellular estrogen receptor signaling pathway	RBM14/DDX17/SAFB	0.016945
mode3	GO:0048545	response to steroid hormone	RBM14/CYBB/DDX17/SAFB/3ARG1	0.018909
mode3	GO:0020027	hemoglobin metabolic process	ALAS2/AHSP	0.025107
mode3	GO:0008380	RNA splicing	HNRNPH1/DDX17/NONO/SNRNP40/SRRM2	0.025472
mode3	GO:0071383	cellular response to steroid hormone stimulus	RBM14/DDX17/SAFB/3ARG1	0.028159
mode3	GO:0072593	reactive oxygen species metabolic process	SNCA/HBD/CYBB/3ARG1	0.028904
mode3	GO:0034599	cellular response to oxidative stress	SNCA/CYBB/4841/CYCS	0.028904
mode3	GO:1903409	reactive oxygen species biosynthetic process	SNCA/CYBB/3ARG1	0.028904
mode3	GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	SNCA/DDX3X/CYCS	0.031828
mode3	GO:0001666	response to hypoxia	ALAS2/EGR1/CYBB/3ARG1	0.031828
mode3	GO:0036293	response to decreased oxygen levels	ALAS2/EGR1/CYBB/3ARG1	0.031828
mode3	GO:0030518	intracellular steroid hormone receptor signaling pathway	RBM14/DDX17/SAFB	0.031828
mode3	GO:2001056	positive regulation of cysteine-type endopeptidase activity	SNCA/DDX3X/CYCS	0.031828
mode3	GO:0070482	response to oxygen levels	ALAS2/EGR1/CYBB/3ARG1	0.031828
mode3	GO:0042744	hydrogen peroxide catabolic process	SNCA/HBD	0.031828
mode3	GO:0016999	antibiotic metabolic process	SNCA/HBD/CYBB	0.031828
mode3	GO:0070555	response to interleukin-1	SNCA/EGR1/3ARG1	0.031828
mode3	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	HNRNPH1/DDX17/SNRNP40/SRRM2	0.031828
mode3	GO:0000398	mRNA splicing, via spliceosome	HNRNPH1/DDX17/SNRNP40/SRRM2	0.031828
mode3	GO:0071456	cellular response to hypoxia	EGR1/CYBB/3ARG1	0.031828
mode3	GO:0000375	RNA splicing, via transesterification reactions	HNRNPH1/DDX17/SNRNP40/SRRM2	0.031828
mode3	GO:0036294	cellular response to decreased oxygen levels	EGR1/CYBB/3ARG1	0.034505
mode3	GO:0010950	positive regulation of endopeptidase activity	SNCA/DDX3X/CYCS	0.034505
mode3	GO:0015701	bicarbonate transport	SLC4A1/7S9	0.036528
mode3	GO:0046688	response to copper ion	SNCA/3ARG1	0.036528
mode3	GO:0022900	electron transport chain	SNCA/CYBB/CYCS	0.036528
mode3	GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	3ARG1/CEACAM8	0.036528
mode3	GO:0071453	cellular response to oxygen levels	EGR1/CYBB/3ARG1	0.036755
mode3	GO:0010952	positive regulation of peptidase activity	SNCA/DDX3X/CYCS	0.036755
mode3	GO:0043401	steroid hormone mediated signaling pathway	RBM14/DDX17/SAFB	0.036755
mode3	GO:0006979	response to oxidative stress	SNCA/CYBB/NONO/CYCS	0.039168

## Identification of a novel ceRNA network in multiple sclerosis

mode3	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	SNCA/DDX3X/CYCS	0.043551
mode3	GO:0032722	positive regulation of chemokine production	EGR1/DDX3X	0.043551
mode3	GO:0017001	antibiotic catabolic process	SNCA/HBD	0.047378
mode3	GO:0042108	positive regulation of cytokine biosynthetic process	EGR1/CYBB	0.047378
mode3	GO:2001234	negative regulation of apoptotic signaling pathway	3ARG1/NONO/DDX3X	0.047378
mode4	GO:0042113	B cell activation	BLNK/MS4A1/CD22	0.004031
mode4	GO:0042100	B cell proliferation	MS4A1/CD22	0.008512
mode4	GO:0002377	immunoglobulin production	VPREB3/CD22	0.021385
mode4	GO:0046651	lymphocyte proliferation	MS4A1/CD22	0.021385
mode4	GO:0032943	mononuclear cell proliferation	MS4A1/CD22	0.021385
mode4	GO:0002440	production of molecular mediator of immune response	VPREB3/CD22	0.021385
mode4	GO:0070661	leukocyte proliferation	MS4A1/CD22	0.021385
mode4	GO:0002638	negative regulation of immunoglobulin production	CD22	0.021385
mode4	GO:0006959	humoral immune response	BLNK/MS4A1	0.02702
mode4	GO:0051023	regulation of immunoglobulin secretion	CD22	0.027968
mode4	GO:0048305	immunoglobulin secretion	CD22	0.029651
mode4	GO:0050855	regulation of B cell receptor signaling pathway	CD22	0.029852
mode4	GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	CD22	0.029852
mode4	GO:0050849	negative regulation of calcium-mediated signaling	CD22	0.035143
mode4	GO:0002701	negative regulation of production of molecular mediator of immune response	CD22	0.035143

**Supplementary Table 5. KEGG enriched pathways for top 4 modules**

Mode	Pathway ID	Description	Genes	adjust <i>P</i> -value
mode1	hsa05143	African trypanosomiasis	HBB/HBA2	0.011927
mode1	hsa05340	Primary immunodeficiency	CD79A/CD19	0.011927
mode1	hsa05144	Malaria	HBB/HBA2	0.011927
mode1	hsa05169	Epstein-Barr virus infection	FCER2/CD19/B2M	0.011927
mode1	hsa04662	B cell receptor signaling pathway	CD79A/CD19	0.020777
mode1	hsa04970	Salivary secretion	LYZ/CAMP	0.020777
mode1	hsa05150	Staphylococcus aureus infection	CAMP/DEFA4	0.020777
mode1	hsa04640	Hematopoietic cell lineage	FCER2/CD19	0.020777
mode2	hsa04120	Ubiquitin mediated proteolysis	UBA6/UBE2M	0.001756
mode2	hsa04520	Adherens junction	LMO7	0.026044
mode3	hsa04933	AGE-RAGE signaling pathway in diabetic complications	EGR1/CYBB/ICAM1	0.018172
mode4	hsa04662	B cell receptor signaling pathway	CD72/BLNK/CD22	2.77E-05
mode4	hsa04640	Hematopoietic cell lineage	MS4A1/CD22	0.00305
mode4	hsa05340	Primary immunodeficiency	BLNK	0.043444