

Bone & Joint Research

Supplementary Material

10.1302/2046-3758.132.BJR-2023-0074.R1

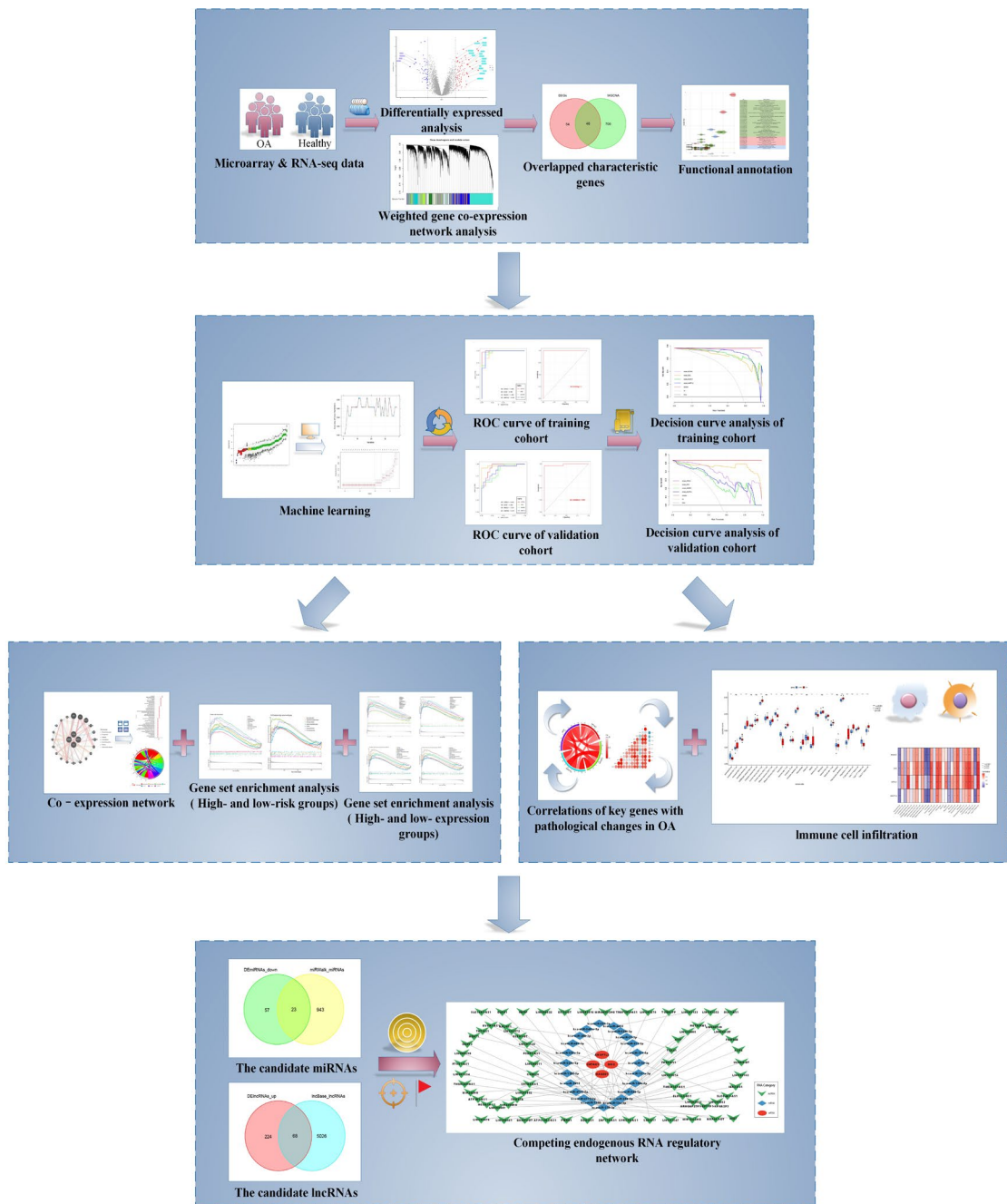


Fig a. The primary flow chart in the study.

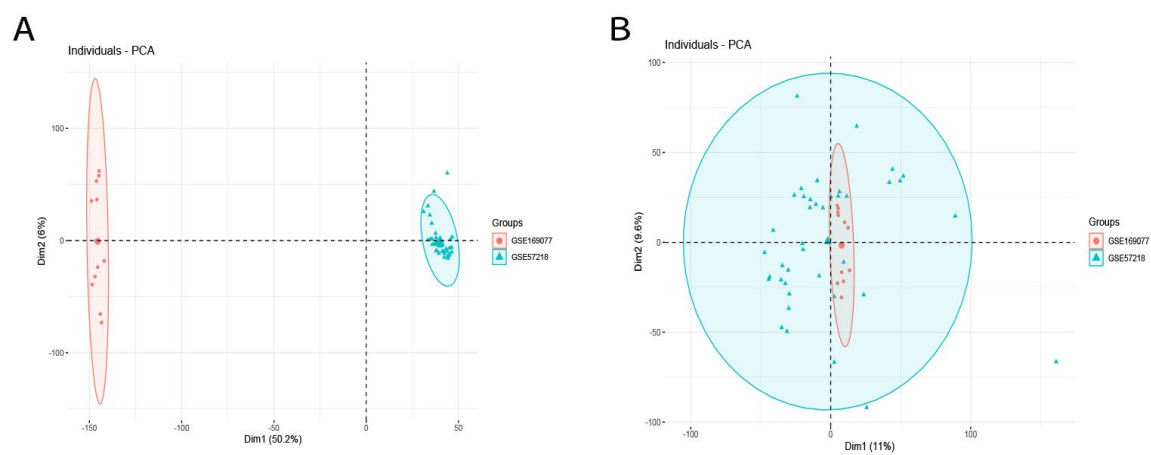


Fig b. Principal component analysis between datasets a) before and b) after debatching.

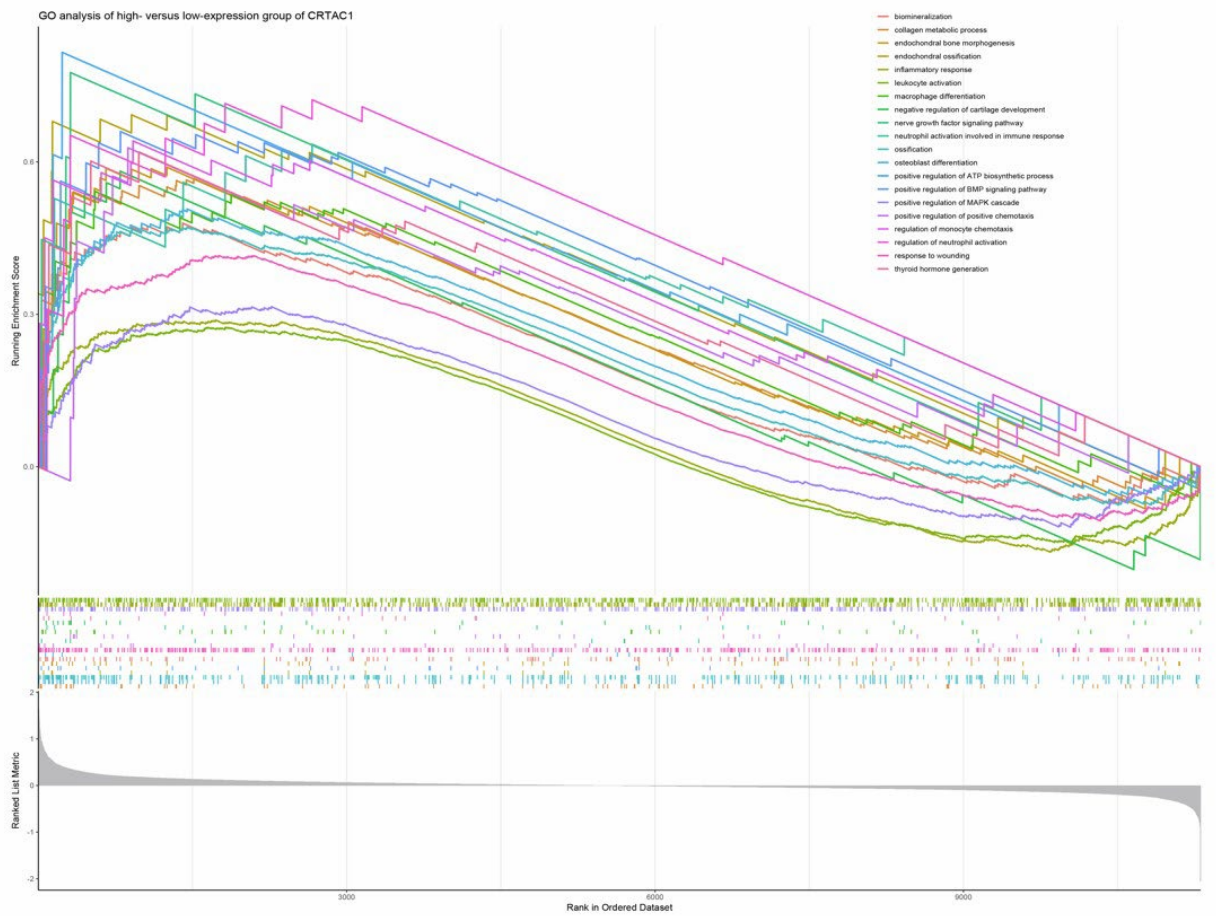


Fig c. Gene set enrichment analysis conducted for four key genes. Specific Gene Ontology (GO) biological processes in the high- versus low-expression group of CRTAC1.

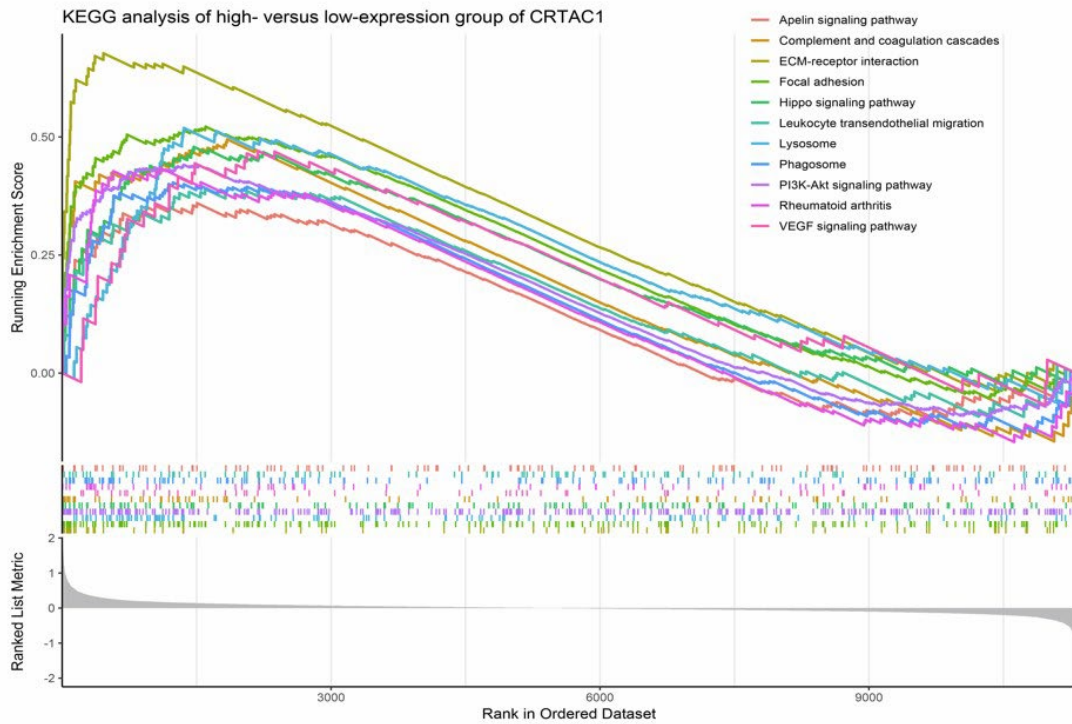


Fig d. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in the high-expression group of CRTAC1.

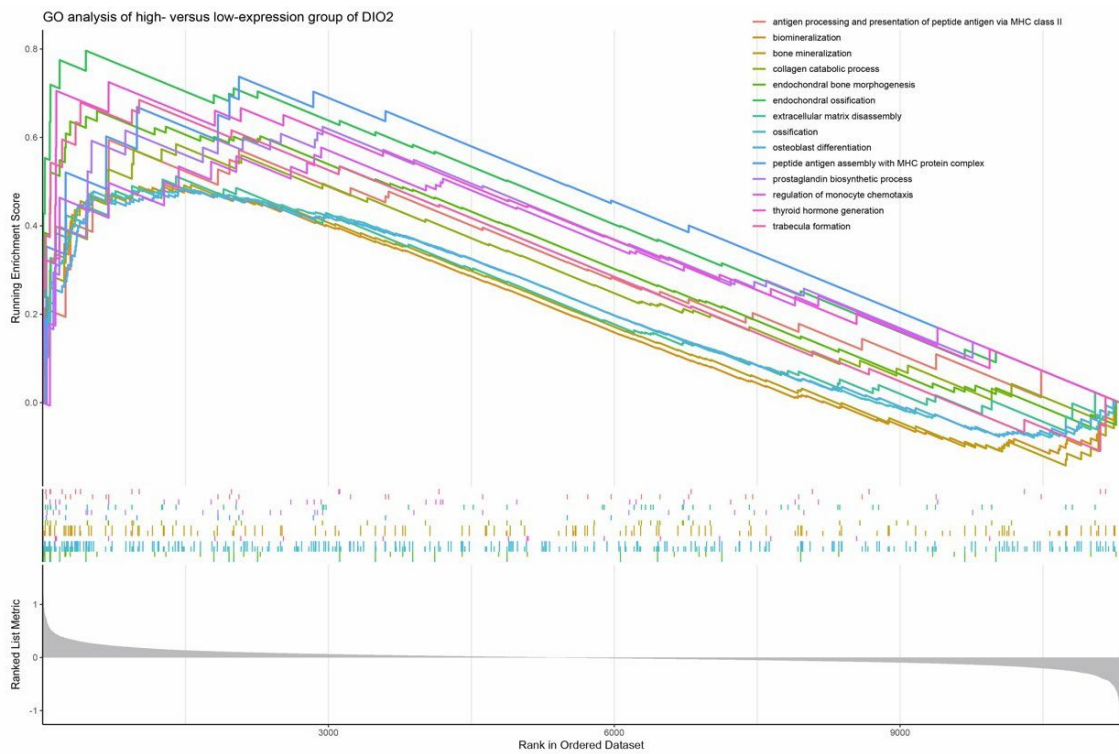


Fig e. Gene ontology (GO) biological processes in the high-expression group of DIO2.

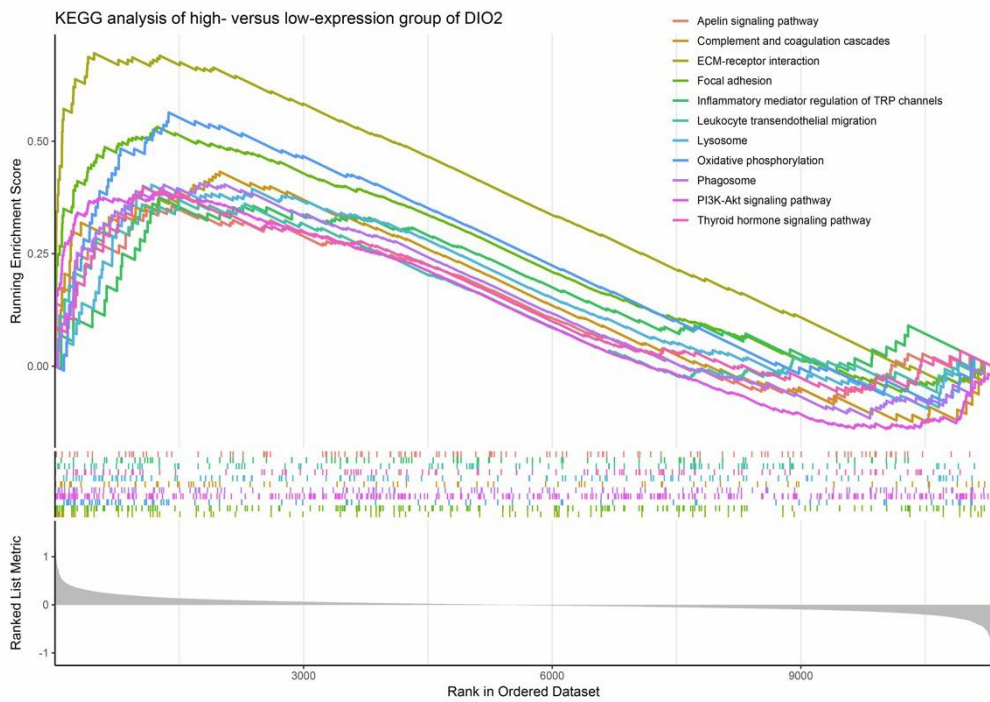


Fig f. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in the high-expression group of DIO2.

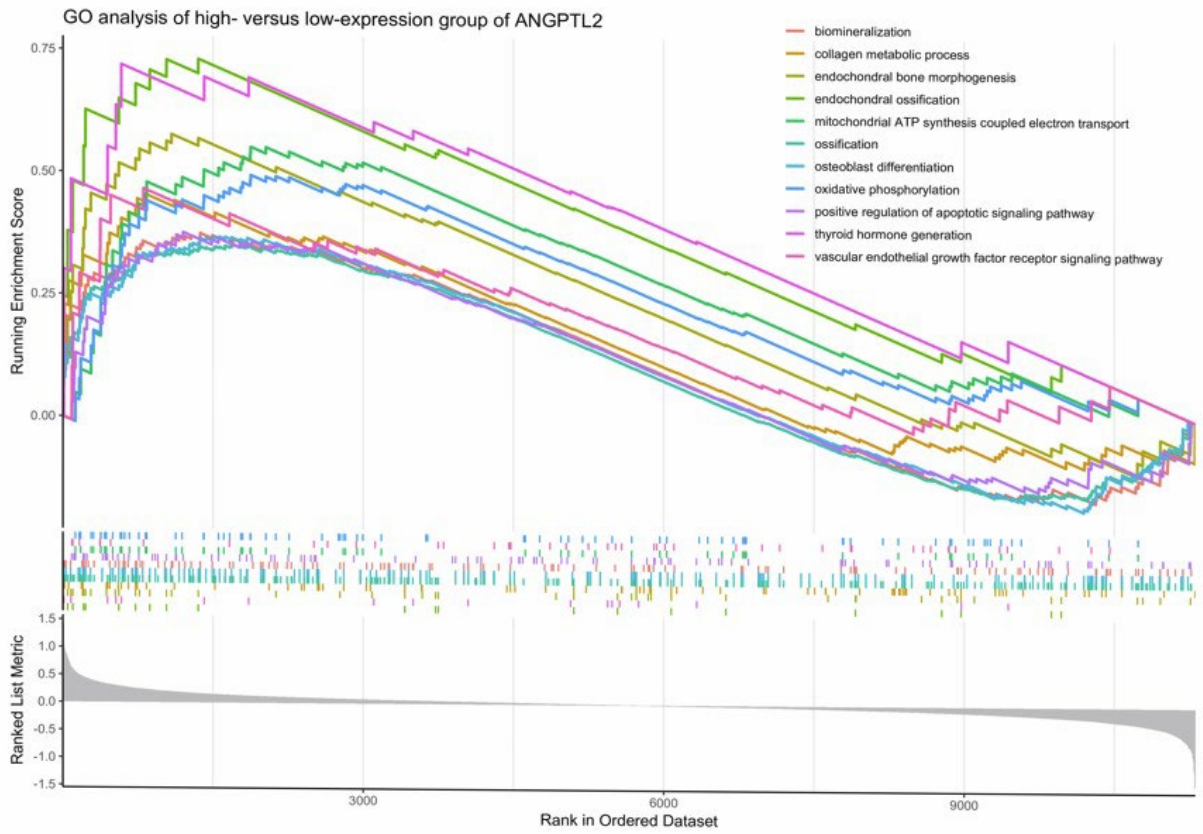


Fig g. Gene ontology (GO) biological processes in the high-expression group of ANGPTL2.

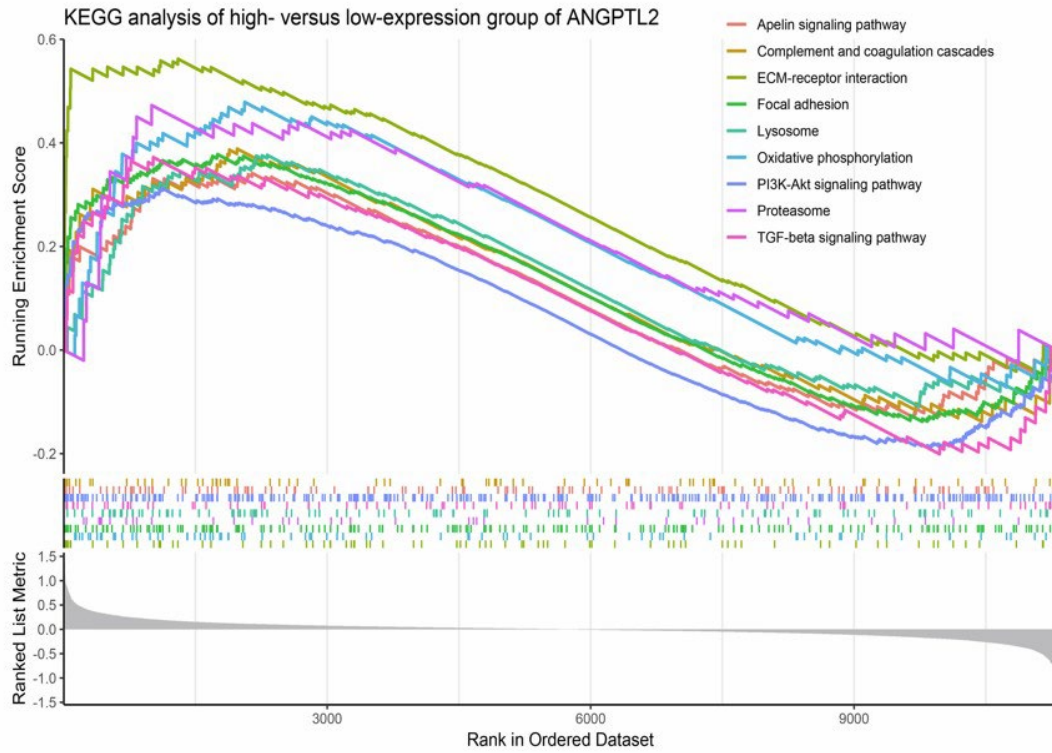


Fig h. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in the high-expression group of ANGPTL2.

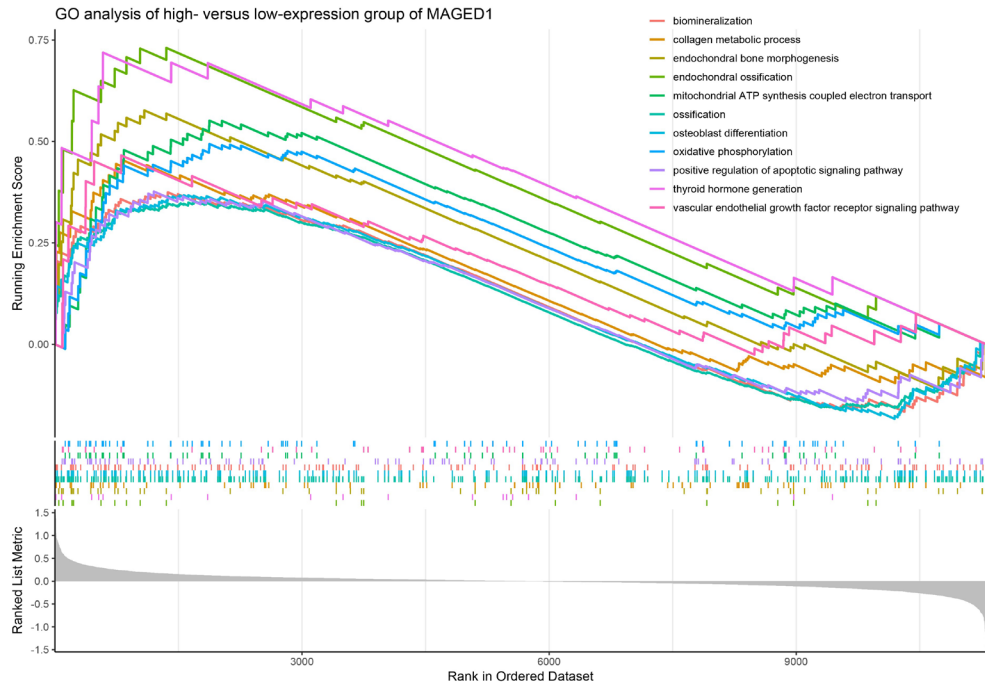


Fig i. Gene ontology (GO) biological processes in the high-expression group of MAGED1.

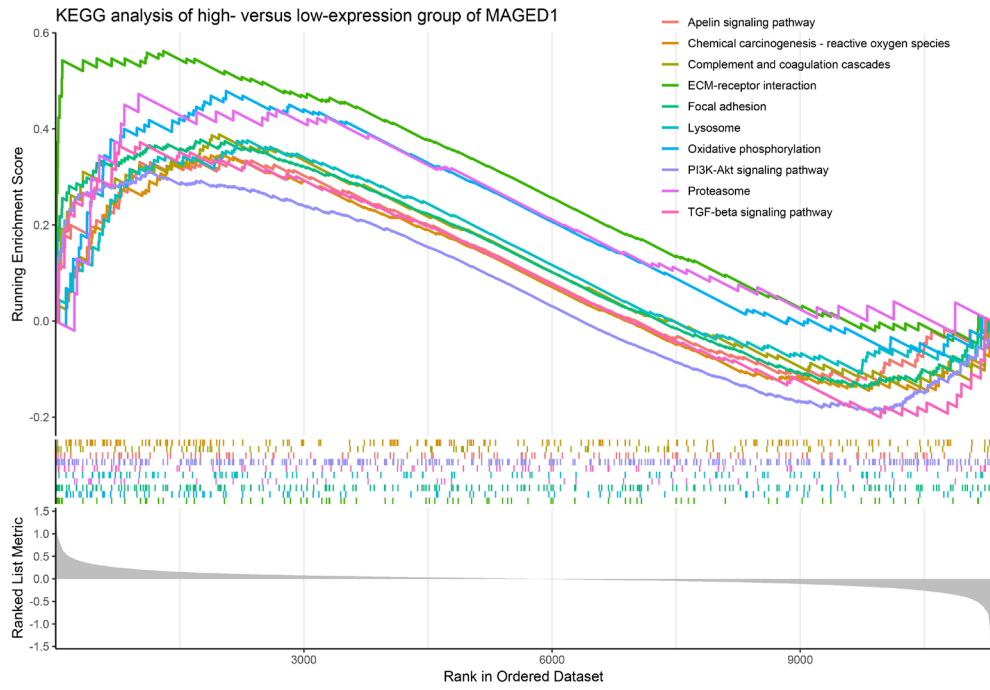
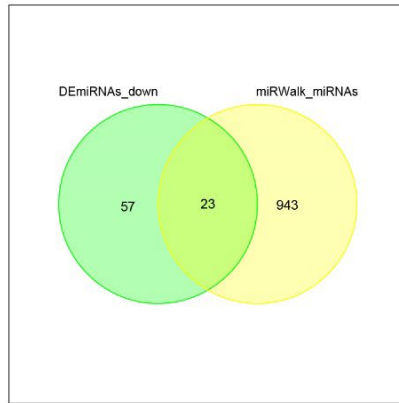
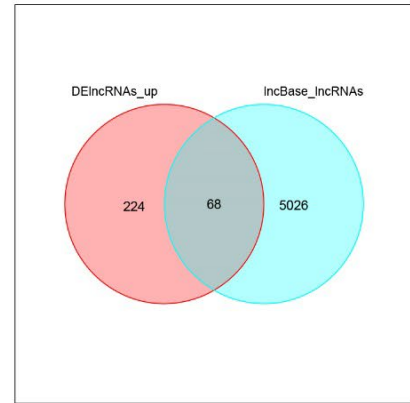


Fig j. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways in the high-expression group of MAGED1.

A



B



C

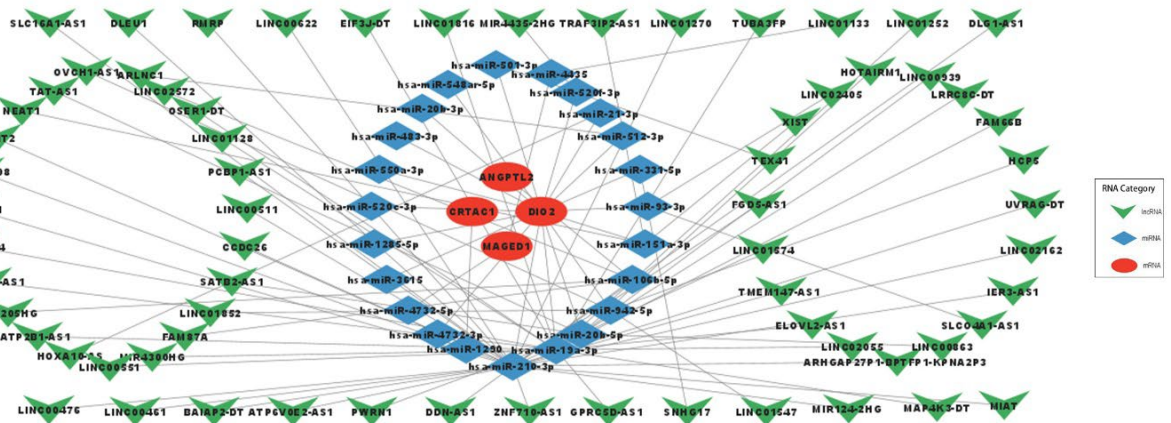


Fig k. Construction of the competing endogenous RNA regulatory network. a) Venn diagram of the candidate microRNAs (miRNAs) intersected by downregulated differentially expressed miRNAs and miRNAs predicted by miRWalk. b) Venn diagram of the candidate long noncoding RNAs (lncRNAs) intersected by upregulated differentially expressed lncRNAs and lncRNAs predicted by LncBase. c) Competing endogenous RNA (ceRNA) regulatory networks of four key genes.

Table i. Datasets of gene expression profiles.

Parameters	Type	Samples			Species	Country
		Osteoarthritis	Normal	Total		
GSE169077	Microarray	6	5	11	Homo sapiens	USA
GSE57218	Microarray	33	7	40	Homo sapiens	Netherlands
GSE174049	Microarray	3	3	6	Homo sapiens	China
GSE114007	RNA-seq	18	20	38	Homo sapiens	USA
GSE168505	RNA-seq	4	3	7	Homo sapiens	USA
GSE143514	RNA-seq	5	3	8	Homo sapiens	China

RNA-seq, RNA sequencing.

Table ii. The final decision list of Boruta algorithm.

Symbol	Mean imputation	Median imputation	Min imputation	Max imputation	NormHits	Decision
ANGPTL2	6.349285648	6.35248686	4.802938049	7.882949288	1	Confirmed
APP	2.552314295	2.584897728	0.042717767	4.327672824	0.832832833	Confirmed
BAALC	4.240624152	4.243343588	2.593122157	5.993603792	1	Confirmed
CA9	1.8673948	1.941620974	-1.735469601	3.336367049	0.534534535	Confirmed
CD55	0.961678767	1.221298668	-0.199733025	2.164129167	0.002002002	Rejected
CLIC3	2.303165879	2.322578746	-0.961882985	4.067966591	0.748748749	Confirmed
COL2A1	2.000885786	2.066143129	-1.001001503	3.441409392	0.596596597	Confirmed
CRLF1	1.909543853	2.014205831	-1.181114047	3.508575928	0.563563564	Confirmed
CRTAC1	7.493332408	7.494920051	5.742407838	9.145125451	1	Confirmed
DIO2	4.370335975	4.385656097	2.377808439	5.815807992	0.998998999	Confirmed
DYSF	2.701720228	2.711723505	0.84136644	4.260287986	0.885885886	Confirmed
FN1	0.924669573	1.001001503	0	1.987929072	0.001001001	Rejected
GAS1	2.882226124	2.891031121	0.698946385	4.469037233	0.930930931	Confirmed
GFRA2	3.477806854	3.49522971	0.691640954	5.197326168	0.983983984	Confirmed
GLIPR1	6.271070017	6.272097941	4.484496404	7.851487433	1	Confirmed
GREM1	1.962735978	2.020788423	-1.001001503	3.516262913	0.587587588	Confirmed
HAPLN1	3.099902862	3.120778895	1.108570808	4.712534499	0.967967968	Confirmed

ID2	1.008708375	1.001001503	- 0.91731028 4	2.17875671 3	0.004004 004	Rejecte d
IGFBP3	2.060256491	2.135752859	- 0.81486946 3	4.04249031 7	0.650650 651	Confir med
IGFBP4	1.712768705	1.794285906	- 1.35270019 7	3.20138507	0.463463 463	Confir med
IGFBP7	6.367773999	6.370738826	4.67471647 9	8.02189018 6	1	Confir med
IL11	1.612016916	1.727251441	- 1.41544016 7	3.14050904 2	0.150150 15	Rejecte d
ITM2A	1.862261967	1.92111076	- 0.39566070 3	3.12082248 2	0.527527 528	Confir med
KDELR3	5.22447954	5.225270187	3.56592805 9	6.75121356 8	1	Confir med
LECT1	3.021879614	3.031189634	1.26228462 5	4.38211405 2	0.955955 956	Confir med
MAGED 1	4.482308083	4.482607163	2.91111665 7	6.02746479 4	1	Confir med
MATN3	3.148936305	3.150517458	0.99833853 8	4.57848169 7	0.969969 97	Confir med
NGF	1.85413806	1.944205871	- 1.41508404 8	3.39961002 5	0.533533 534	Confir med
PAPSS2	1.559778446	1.667702481	- 1.15517520 2	3.12508344 3	0.094094 094	Rejecte d
PPIC	3.832159147	3.850504311	2.21854624	5.49428311	0.998998 999	Confir med
PTGES	1.987066945	2.062031142	- 1.87221654 1	3.67008666 5	0.580580 581	Confir med
RARRES 1	3.188242684	3.227166197	0.25768415 6	4.66631080 4	0.954954 955	Confir med
SBSPON	2.970164956	2.982340416	0.76745167 3	4.62436577 1	0.946946 947	Confir med
SERPIN A5	5.906177494	5.891739276	4.18306523 2	8.01613357 6	1	Confir med

SERPINE1	1.468952421	1.62194725	- 1.71671644 2	2.62315743 7	0.056056 056	Rejected
SERPINE2	3.37357209	3.382294678	1.57141096 7	4.71999504	0.984984 985	Confirmed
SLC16A10	1.363876717	1.480266141	- 1.00100150 3	2.39791906 1	0.005005 005	Rejected
SPOCK1	2.972948665	2.98696226	1.10408959 6	4.83348381 5	0.944944 945	Confirmed
SPP1	2.424423143	2.446237201	- 0.36212007 7	4.10399664 8	0.815815 816	Confirmed
SRPX2	4.875082275	4.876978169	3.26859490 3	6.24791129 1	1	Confirmed
SYT11	5.011366936	5.015284683	3.47282025 8	6.73107290 4	1	Confirmed
TF	3.107184674	3.158042439	0.80149625 2	5.05192552 7	0.948948 949	Confirmed
TNFAIP6	2.238938697	2.285605851	- 0.26061115 1	3.63285339 4	0.727727 728	Confirmed
TNFRSF11B	0.731548694	1.001001503	- 0.93679782 9	2.12319776 4	0.002002 002	Rejected
TNNT3	3.710374033	3.725395489	1.60225314 5	5.82690323 5	0.992992 993	Confirmed
TSPAN2	4.435817207	4.435889228	2.91745479 2	5.78321507 7	1	Confirmed

Table iii. List of competing endogenous RNA regulatory networks.

lncRNAs	miRNAs	mRNAs
NEAT1	hsa-miR-151a-3p	DIO2
TRAF3IP2-AS1	hsa-miR-151a-3p	DIO2
XIST	hsa-miR-151a-3p	DIO2
ARHGAP27P1-BPTFP1-KPNA2P3	hsa-miR-210-3p	DIO2
ATP6V0E2-AS1	hsa-miR-210-3p	DIO2
BAIAP2-DT	hsa-miR-210-3p	DIO2
CCDC26	hsa-miR-210-3p	DIO2
DANT2	hsa-miR-210-3p	DIO2
DLEU1	hsa-miR-210-3p	DIO2
DLG1-AS1	hsa-miR-210-3p	DIO2
FGD5-AS1	hsa-miR-210-3p	DIO2
IER3-AS1	hsa-miR-210-3p	DIO2
LINC00461	hsa-miR-210-3p	DIO2
LINC00476	hsa-miR-210-3p	DIO2
LINC00511	hsa-miR-210-3p	DIO2
LINC00598	hsa-miR-210-3p	DIO2
LINC00622	hsa-miR-210-3p	DIO2
LINC01270	hsa-miR-210-3p	DIO2
LINC01574	hsa-miR-210-3p	DIO2
LINC02162	hsa-miR-210-3p	DIO2
MIAT	hsa-miR-210-3p	DIO2
MIR124-2HG	hsa-miR-210-3p	DIO2
PCBP1-AS1	hsa-miR-210-3p	DIO2
PTOV1-AS1	hsa-miR-210-3p	DIO2
RMRP	hsa-miR-210-3p	DIO2
SLC16A1-AS1	hsa-miR-210-3p	DIO2
TMEM147-AS1	hsa-miR-210-3p	DIO2
UVRAG-DT	hsa-miR-210-3p	DIO2
ZNF710-AS1	hsa-miR-210-3p	DIO2
SNHG17	hsa-miR-331-5p	DIO2
ARLNC1	hsa-miR-512-3p	DIO2
MIR4435-2HG	hsa-miR-520f-3p	DIO2
TEX41	hsa-miR-501-3p	DIO2
HCP5	hsa-miR-942-5p	DIO2
LINC01547	hsa-miR-942-5p	DIO2
LINC01852	hsa-miR-942-5p	DIO2
OVCH1-AS1	hsa-miR-942-5p	DIO2
ATP2B1-AS1	hsa-miR-19a-3p	DIO2
EIF3J-DT	hsa-miR-19a-3p	DIO2
ELOVL2-AS1	hsa-miR-19a-3p	DIO2

FAM66B	hsa-miR-19a-3p	DIO2
GPRC5D-AS1	hsa-miR-19a-3p	DIO2
LINC00551	hsa-miR-19a-3p	DIO2
LINC01128	hsa-miR-19a-3p	DIO2
LINC01234	hsa-miR-19a-3p	DIO2
LINC01252	hsa-miR-19a-3p	DIO2
LINC01816	hsa-miR-19a-3p	DIO2
LINC02055	hsa-miR-19a-3p	DIO2
LRRC8C-DT	hsa-miR-19a-3p	DIO2
MAP4K3-DT	hsa-miR-19a-3p	DIO2
MIR4300HG	hsa-miR-19a-3p	DIO2
OSER1-DT	hsa-miR-19a-3p	DIO2
TMEM220-AS1	hsa-miR-19a-3p	DIO2
TUBA3FP	hsa-miR-19a-3p	DIO2
HOTAIRM1	hsa-miR-20b-5p	DIO2
LINC00863	hsa-miR-20b-5p	DIO2
LINC00939	hsa-miR-20b-5p	DIO2
PWRN1	hsa-miR-20b-5p	DIO2
SATB2-AS1	hsa-miR-20b-5p	DIO2
TAT-AS1	hsa-miR-20b-5p	DIO2
HOXA10-AS	hsa-miR-21-3p	DIO2
LINC02405	hsa-miR-93-3p	DIO2
SLCO4A1-AS1	hsa-miR-93-3p	DIO2
DDN-AS1	hsa-miR-106b-5p	ANGPTL2
FAM87A	hsa-miR-106b-5p	ANGPTL2
LINC02572	hsa-miR-106b-5p	ANGPTL2
MIR205HG	hsa-miR-106b-5p	ANGPTL2
LINC01133	hsa-miR-4435	MAGED1
N/A	hsa-miR-4732-5p	MAGED1
N/A	hsa-miR-1290	CRTAC1

mRNA, messenger RNA. N/A, not available.