

SUPPLEMENTARY TABLES

Supplementary Table 1. The 86 genes in the green module of the WGCNA analysis

ENSMUSG0000000776	Polr3d
ENSMUSG0000001774	Chordc1
ENSMUSG0000002981	Clptm1
ENSMUSG0000005483	Dnajib1
ENSMUSG0000007617	Homer1
ENSMUSG0000007721	Ccdc124
ENSMUSG0000007777	0610009B22Rik
ENSMUSG0000007877	Tcap
ENSMUSG0000008668	Rps18
ENSMUSG00000013878	Rnf170
ENSMUSG00000014226	Cacybp
ENSMUSG00000014294	Ndufa2
ENSMUSG00000018906	P4ha2
ENSMUSG00000020092	Pald1
ENSMUSG00000020482	Ccdc117
ENSMUSG00000020827	Mink1
ENSMUSG00000021361	Tmem14c
ENSMUSG00000022237	Ankrd33b
ENSMUSG00000022426	Josd1
ENSMUSG00000022433	Csnk1e
ENSMUSG00000024219	Anks1
ENSMUSG00000024247	Pkdcc
ENSMUSG00000024900	Cpt1a
ENSMUSG00000024966	Stip1
ENSMUSG00000024978	Gpam
ENSMUSG00000025261	Huwe1
ENSMUSG00000025558	Dock9
ENSMUSG00000025907	Rb1cc1
ENSMUSG00000026500	Cox20
ENSMUSG00000026977	07-Mar
ENSMUSG00000027255	Arfgap2
ENSMUSG00000028034	Fubp1
ENSMUSG00000028271	Gtf2b
ENSMUSG00000028318	Polr1e
ENSMUSG00000028427	Aqp7
ENSMUSG00000030653	Gm45837
ENSMUSG00000031068	Glrx3
ENSMUSG00000031167	Rbm3
ENSMUSG00000031309	Rps6ka3
ENSMUSG00000031667	Aktip
ENSMUSG00000032295	Man2c1
ENSMUSG00000032942	Ucp3

ENSMUSG00000033020	Polr2f
ENSMUSG00000033191	Tie1
ENSMUSG00000035242	Oaz1
ENSMUSG00000035849	Krt222
ENSMUSG00000036585	Fgf1
ENSMUSG00000037266	Rsrp1
ENSMUSG00000037805	Rpl10a
ENSMUSG00000038550	Ciart
ENSMUSG00000038880	Mrps34
ENSMUSG00000040026	Saa3
ENSMUSG00000040269	Mrps28
ENSMUSG00000040459	Arglu1
ENSMUSG00000046691	Chtf8
ENSMUSG00000048007	Timm8a1
ENSMUSG00000052305	Hbb-bs
ENSMUSG00000054364	Rhob
ENSMUSG00000055116	Arntl
ENSMUSG00000056749	Nfil3
ENSMUSG00000057580	Gm10012
ENSMUSG00000058135	Gstm1
ENSMUSG00000059824	Dbp
ENSMUSG00000060147	Serpib6a
ENSMUSG00000060152	Pop5
ENSMUSG00000063077	Kif1b
ENSMUSG00000064326	Siva1
ENSMUSG00000064791	Snord14e
ENSMUSG00000064796	Terc
ENSMUSG00000067547	Gm7666
ENSMUSG00000067847	Romo1
ENSMUSG00000069917	Hba-a2
ENSMUSG00000069919	Hba-a1
ENSMUSG00000070803	Cited4
ENSMUSG00000071347	C1qtnf9
ENSMUSG00000071540	3425401B19Rik
ENSMUSG00000072772	Grccl0
ENSMUSG00000073940	Hbb-bt
ENSMUSG00000076128	Mir686
ENSMUSG00000078915	Hsp25-ps1
ENSMUSG00000091562	Crybg3
ENSMUSG00000097656	Gm26712
ENSMUSG00000098462	Gm27694
ENSMUSG00000106362	AL672049.1
ENSMUSG00000107283	Mpv17
ENSMUSG00000107478	Gm45234

Supplementary Table 2. GSEA report for upregulated pathways

NAME	SIZE	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	LEADING EDGE
PANTHER_MM_INTEGRIN_SIG NALLING_PATHWAY	54	0.605	2.231	0.000	0.000	0.000	tags=59%, list=22%, signal=75%
INOH_MM_INTEGRIN	35	0.665	2.190	0.000	0.000	0.000	tags=69%, list=23%, signal=88%
WIKIPATHWAYS_MM_FOCAL_ ADHESION-WP306	54	0.592	2.162	0.000	0.000	0.000	tags=57%, list=22%, signal=72%
PANTHER_MM_CYTOSKELET AL_REGULATION_BY_RHO_G TPASE	26	0.636	1.983	0.000	0.002	0.011	tags=73%, list=27%, signal=100%
NETPATH_MM_EGFR1_SIGNA LING_PATHWAY	136	0.426	1.826	0.000	0.019	0.108	tags=46%, list=27%, signal=61%
WIKIPATHWAYS_MM_REGUL ATION_OF_ACTIN_CYTOSKEL ETON-WP51	37	0.533	1.776	0.001	0.028	0.182	tags=62%, list=27%, signal=84%
NETPATH_MM_WNT_SIGNALI NG_PATHWAY	21	0.570	1.681	0.018	0.066	0.421	tags=48%, list=21%, signal=60%
PANTHER_MM_HUNTINGTON_ DISEASE	43	0.472	1.653	0.006	0.078	0.529	tags=77%, list=40%, signal=126%
PANTHER_MM_ALZHEIMER_D ISEASE- PRESENILIN_PATHWAY	16	0.611	1.651	0.014	0.071	0.534	tags=44%, list=8%, signal=47%

Supplementary Table 3. GSEA report for downregulated pathways

NAME	SIZE	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val	LEADING EDGE
WIKIPATHWAYS_MM_ELECTR ON_TRANSPORT_CHAIN-WP111	64.000	-0.751	-3.185	0.000	0.000	0.000	tags=86%, list=20%, signal=105%
WIKIPATHWAYS_MM_OXIDATI VE_PHOSPHORYLATION-WP623	36.000	-0.764	-2.854	0.000	0.000	0.000	tags=81%, list=14%, signal=93%
INOH_MM_CITRATE_CYCLE	21.000	-0.716	-2.302	0.000	0.000	0.000	tags=76%, list=20%, signal=94%
WIKIPATHWAYS_MM_FATTY_ ACID_BETA_OXIDATION-WP143	21.000	-0.706	-2.243	0.000	0.000	0.000	tags=67%, list=19%, signal=82%
WIKIPATHWAYS_MM_TCA_CY CLE-WP78	29.000	-0.627	-2.184	0.000	0.000	0.001	tags=69%, list=20%, signal=85%
WIKIPATHWAYS_MM_GLYCOL YSIS_AND_GLUCONEOGENESIS -WP534	27.000	-0.617	-2.156	0.000	0.000	0.002	tags=63%, list=21%, signal=79%

Supplementary Table 4. Gene alteration in WNT signaling pathway

PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES
SFRP2	26	1.233115	0.151679
LRP1	188	0.748588	0.200758
KREMEN1	258	0.660285	0.265666
CTNNB1	266	0.650148	0.347624
YWHAB	400	0.535507	0.377453
CCND1	469	0.498205	0.42171
RHOA	494	0.479338	0.476556
ILK	519	0.463446	0.529349
AKT1	686	0.395137	0.531264
RAC1	724	0.381176	0.569574
CSNK1A1	1033	0.273293	0.513692
CDH2	1216	0.211877	0.487182
PPP2CA	1388	0.158804	0.457071
MAPK1	1410	0.15206	0.470506
RYK	1478	0.129619	0.467419
JUP	1635	0.085088	0.432221
CTBP1	1651	0.08129	0.438286
PRKACA	2156	-0.07241	0.2984
PPP1CA	2285	-0.10943	0.27464
JUN	2440	-0.15866	0.249543
RAF1	2683	-0.25956	0.21143

Supplementary Table 5. Gene alterations in integrin signaling pathway

PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES
COL8A1	24	1.250044	0.041699
ITGBL1	34	1.204578	0.086106
COL4A2	46	1.108793	0.126169
ITGB5	51	1.086318	0.167447
COL5A2	128	0.846045	0.1778
COL4A1	129	0.839928	0.21064
COL6A2	131	0.83876	0.243136
COL6A1	132	0.838017	0.275902
ACTN4	141	0.824349	0.305741
RHOB	157	0.788537	0.332087
FN1	159	0.787086	0.362562
COL3A1	190	0.747269	0.382808
RHOC	213	0.717562	0.404286
LAMC1	314	0.605321	0.398049
FLNA	321	0.59947	0.419694
CAV1	363	0.55932	0.429302
RAP1B	389	0.540683	0.442966
ITGB1	425	0.525241	0.453036
ARPC1A	441	0.514583	0.46867
COL1A2	453	0.507689	0.485231

CDC42	459	0.505299	0.503493
RHOA	494	0.479338	0.512067
ILK	519	0.463446	0.52301
TLN1	521	0.462268	0.540786
LAMA4	542	0.455688	0.552622
ARPC1B	594	0.432813	0.554293
ARPC5	623	0.421344	0.562394
ARF6	631	0.418681	0.576671
LAMB2	669	0.401626	0.58131
RRAS	681	0.396598	0.593527
RAC1	724	0.381176	0.595871
ACTB	742	0.376136	0.605494
ARPC3	871	0.327444	0.580019
MAP3K3	883	0.324298	0.58941
ARPC2	934	0.305842	0.586416
VCL	1071	0.260906	0.555947
ARL1	1082	0.256929	0.563002
ARF1	1207	0.213645	0.534274
MAP2K1	1262	0.198721	0.525896
CRK	1363	0.166898	0.502517
MAPK1	1410	0.15206	0.494707
ACTG1	1494	0.125848	0.474807
ACTN2	1513	0.122105	0.474198
LIMS1	1678	0.071031	0.427932
RAP1A	1680	0.0706	0.430394
LAMB1	1707	0.063852	0.425115
MAP2K2	2045	-0.0357	0.325733
LIMS2	2364	-0.13732	0.236007
ITGA7	2570	-0.21246	0.18301
RAF1	2683	-0.25956	0.159666
ARHGAP10	2686	-0.26164	0.169298
ARAF	2689	-0.26324	0.178992
PIK3R1	2831	-0.32677	0.149604
GRB2	3099	-0.49504	0.089115

Supplementary Table 6. Gene alterations in fatty acid beta oxidation pathway

PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES
HADH	1575	0.105087	-0.45296
TPI1	2110	-0.05695	-0.60381
PNPLA2	2190	-0.0827	-0.61663
CHKB	2217	-0.09075	-0.61273
ACAT1	2221	-0.0911	-0.60197
ACSL1	2484	-0.17422	-0.65729
CPT1B	2599	-0.22258	-0.66259
DLD	2746	-0.29057	-0.66868
ACADL	2764	-0.29748	-0.63569
LPL	2801	-0.31471	-0.60612

ACADS	2830	-0.32602	-0.57274
CPT2	2932	-0.38384	-0.55359
ACADM	3000	-0.4278	-0.51874
GCDH	3038	-0.45053	-0.47211
DECRI	3070	-0.4718	-0.42098
HADHA	3173	-0.55233	-0.38058
SLC25A20	3197	-0.57364	-0.31407
CRAT	3199	-0.58078	-0.24013
ECHS1	3263	-0.67054	-0.17307
ACADVL	3276	-0.68272	-0.08935
ECI1	3351	-0.97703	0.013621

Supplementary Table 7. Gene alterations in glycolysis and gluconeogenesis pathway

PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES
PFKP	744	0.375565	-0.17815
HK1	842	0.339539	-0.16844
PFKL	1186	0.221405	-0.2451
GPI1	1476	0.130336	-0.31606
PGK1	1863	0.017227	-0.42862
TPI1	2110	-0.05695	-0.49514
PGAM1	2240	-0.09476	-0.52267
PKM	2281	-0.10786	-0.52231
PDHX	2291	-0.11455	-0.512
DLAT	2333	-0.12668	-0.5098
PFKM	2696	-0.26618	-0.58703
PGAM2	2704	-0.27234	-0.55824
HK2	2712	-0.27505	-0.52915
LDHA	2719	-0.27801	-0.49942
MDH2	2744	-0.29021	-0.47365
DLD	2746	-0.29057	-0.44102
PDHA1	2846	-0.3355	-0.43237
MDH1	2868	-0.35118	-0.3988
GOT2	3013	-0.4349	-0.39223
SLC2A4	3030	-0.4472	-0.3463
PDHB	3051	-0.45979	-0.30013
ALDOA	3116	-0.50893	-0.26144
ENO3	3147	-0.53595	-0.20961
LDHB	3201	-0.58166	-0.15941
ATP5G1	3220	-0.60351	-0.09636
GM10039	3224	-0.60566	-0.02861
GOT1	3286	-0.70273	0.032928

Supplementary Table 8. Gene alterations in TCA cycle pathway

PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES
PDK4	431	0.518681	-0.07767
PDP1	899	0.318727	-0.1854
OGDH	1073	0.260313	-0.21152
IDH2	1230	0.209108	-0.23756
SUCLG2	2185	-0.08099	-0.51288
DLST	2266	-0.1051	-0.52644
PDK1	2288	-0.11027	-0.52199
PDHX	2291	-0.11455	-0.51148
DLAT	2333	-0.12668	-0.51138
SDHD	2725	-0.28036	-0.60027
MDH2	2744	-0.29021	-0.57748
DLD	2746	-0.29057	-0.54962
IDH3G	2754	-0.29351	-0.52326
PDHA1	2846	-0.3355	-0.51776
MDH1	2868	-0.35118	-0.48996
ACO2	2907	-0.37008	-0.46537
SDHC	2914	-0.37358	-0.43095
IDH3A	2931	-0.38174	-0.3987
SDHB	3022	-0.44	-0.38278
SUCLA2	3023	-0.44078	-0.34006
CS	3027	-0.4455	-0.29778
IDH3B	3028	-0.44555	-0.2546
PDK2	3041	-0.45338	-0.21423
PDHB	3051	-0.45979	-0.17234
FH1	3081	-0.47873	-0.13456
SDHA	3150	-0.53694	-0.10271
SUCLG1	3214	-0.59806	-0.06345
ATP5G1	3220	-0.60351	-0.00645
GM10039	3224	-0.60566	0.05135

Supplementary Table 9. Ninety five genes simultaneously differentially regulated at both 1 and 8 months after MI

gene	baseMean	baseMean	log2FC_1m	log2FC_8m	padj_1m	padj_8m
9330159F19Rik	72.38382	263.2386	1.338094853	0.772947365	0.017056744	0.013809142
Abca12	469.6926	907.8357	-1.58722346	-1.243272159	3.36E-10	0.000107469
AC022682.2	61.96831	80.27954	-1.994359763	-1.33919269	2.14E-05	0.039376723
AC157516.1	69.37918	179.0611	-2.157162233	-1.636440248	9.17E-06	0.002207262
Adamts20	33.94426	91.08125	1.77092724	1.660193472	0.00091548	3.46E-06
Adamts11	165.3911	496.4326	1.451609157	0.537405511	1.54E-07	0.022820712
Adcy8	27.36026	51.14039	-1.622768953	-1.993648065	0.007910621	3.46E-06
Add2	32.75743	39.58893	2.425409933	1.206885392	0.000488474	0.001304079
AL591207.3	17.84717	28.20068	3.507431259	1.499062707	0.000266199	0.02008895
Aldh1l2	338.0175	670.2361	-1.325518758	-0.744502034	8.32E-07	0.028921143
Ankrd63	33.96433	107.6297	-2.036353914	-1.157061168	6.31E-05	0.028436322
Aqp2	20.00909	44.6289	1.914123072	1.709417141	0.015780422	0.004250746
Atp8b4	89.5417	406.8387	1.814641735	-0.657079691	2.93E-08	0.049443001
Azin2	89.13142	209.8742	0.984562372	0.935053131	0.006373882	2.94E-07
B4galnt3	31.85274	75.94876	8.307744623	2.056435946	2.89E-08	1.54E-07
Btla	61.95872	128.2981	0.900534149	1.446972316	0.01685731	6.03E-06
Carmil3	84.0663	146.8175	-1.237885337	-0.736173573	0.004326839	0.007285041
Ccdc88b	102.5025	347.5408	0.963590651	-0.587584473	0.017493028	0.042258024
Ccnj	300.905	602.3457	-0.686261923	-0.381715554	0.000265836	0.022820712
Cd22	24.32314	59.99578	2.062886595	2.350666596	0.002042038	8.27E-07
Cdh3	19.31972	73.22186	7.587282833	1.05376394	3.70E-07	0.011799969
Cenpe	100.7449	246.5119	1.235381018	-0.838841904	0.00786079	0.008075965
Clec18a	42.49937	64.59779	-2.194397745	-1.259674449	0.000188506	0.009800352
Col11a1	150.3847	192.7107	5.530428761	1.319914559	1.78E-09	0.046809408
Col27a1	355.7013	443.4263	0.940474882	0.430679306	0.000897193	0.023879553
Crb1	47.02913	83.74538	-2.044517118	-1.229102818	0.000852805	0.012802213
Csf2rb2	57.18061	179.2012	2.032208005	1.050353439	1.25E-05	0.020314203
Dchs2	190.7537	267.483	3.014351889	1.556945263	9.63E-22	1.12E-06
Ereg	42.28248	116.9084	5.215061922	1.724405437	1.09E-09	1.41E-05
Esr1	75.94608	297.3961	1.41602485	0.764006532	0.003032061	0.047435928
Exoc3l2	59.00953	252.4834	1.083413536	0.730190962	0.008056726	0.008757768
Eya4	88.7854	157.3741	2.052361136	1.067523645	3.76E-06	0.008094616
Faim2	15.37698	87.69929	4.430092583	2.564079235	0.000253018	4.64E-08
Fam171b	119.2217	269.3606	1.146632937	0.709317266	0.004534949	0.000717559
Flt3	16.80729	54.71801	4.447239656	1.473136516	0.000609507	0.002537139
Fmn1	116.176	268.8948	1.599808852	1.346818513	1.48E-05	0.002798257
Gabrb3	21.80811	49.84956	2.087083127	1.684009619	0.002830015	0.002798257
Gabbr2	45.87044	68.02024	-1.866615384	-1.519079251	0.00026071	0.001018617
Gent4	45.7202	57.86883	2.894881795	1.358232514	5.21E-09	0.047670774
Gli2	85.43764	131.6428	1.820966739	0.679523708	1.43E-05	0.002270175
Gng8	43.2071	59.78843	3.703775196	2.125041857	6.28E-08	1.47E-05
Gprin3	79.06171	177.0166	0.982998678	1.286644524	0.026854629	0.002537139
Greb1	57.37384	57.11321	1.588753271	0.953314325	0.0055535	0.011017089
Gria3	193.0349	250.5424	1.905922134	0.805614693	1.30E-10	0.013596458
H2-Ob	46.0266	106.5466	1.145888193	1.039805101	0.01422812	0.009800352
Hebp2	48.05972	139.9614	2.209293862	0.740453665	4.19E-07	0.001097243
Heph1l1	16.70996	48.75719	4.986008608	2.555201241	0.000360475	0.002237368
Hgf	95.50513	333.1287	1.023382578	0.613775256	0.014562949	1.76E-05

Il1rl2	173.3036	310.0596	0.738374965	0.762135194	0.025622396	0.032075891
Il6	24.57122	44.46563	3.580218916	2.015820222	1.59E-05	0.022246819
Kcna6	58.95865	148.0705	-1.690368067	-1.033712286	0.000326346	0.021063736
Kcnj14	49.22876	78.13598	1.106644663	1.423185549	0.0416764	0.000191724
Kif2c	16.6513	76.90939	2.289965649	-0.883948709	0.017160253	0.047670774
Kif6	109.24	196.2545	-1.022273418	-0.670650265	0.004250182	0.009567669
Klhl29	97.04787	144.4202	2.319237182	1.323077437	1.10E-12	8.27E-07
Lgi3	108.5846	196.035	-1.168515181	-1.149833657	0.001143076	0.000839157
Lrp8	52.63052	68.47234	2.17990467	1.688064528	2.89E-05	0.000705942
Mgat5b	21.88977	74.99011	3.284347677	1.681484684	0.000217058	0.014531136
Mmp12	29.26492	186.795	1.442865736	1.614741137	0.009105975	0.004494978
Mylk2	19.4292	23.98107	7.597182009	1.356109249	7.64E-07	0.01630661
Osgin1	70.18034	163.4612	-0.848248138	-0.766289406	0.045968856	0.038826495
P2ry10	25.68545	109.2988	1.507248036	1.3779083	0.02045988	0.000839157
P4ha3	26.37245	35.69365	8.037336988	2.220418479	2.24E-08	0.006814691
Padi4	28.44141	62.34945	1.469349664	1.206210285	0.027370478	0.008492938
Pak3	81.95312	166.8805	2.832568299	2.024932516	3.36E-10	7.13E-06
Pira2	17.9124	217.0514	3.275330959	-1.325123732	0.010418457	3.91E-05
Pitpnm3	122.0296	145.7451	-1.213835066	-0.642499843	6.31E-05	0.022820712
Rab17	50.76643	89.00408	-1.245182676	-1.058803418	0.00547896	0.007285041
Rasgef1a	37.1663	150.3048	1.412350672	1.577620716	0.004241616	1.36E-05
Rassf10	116.5135	245.6662	-0.585507308	0.525495859	0.043312449	0.049865687
Ret	212.9693	506.869	-1.404154551	-1.082278928	9.69E-10	3.10E-05
RMST_1	92.13399	161.2933	-1.081845815	-0.913073663	0.01617561	0.00097616
Scg2	33.79235	56.83588	8.395686327	4.52288006	3.61E-09	2.83E-13
Sec16b	270.5756	403.384	1.297867542	0.647384726	1.94E-10	0.001215566
Slc6a7	51.69015	41.8191	5.803694687	2.310969091	1.71E-12	0.001225144
Slit2	636.5364	1174.787	0.895635384	0.534440627	2.22E-05	1.71E-06
Sntg2	40.96716	119.7424	8.672300191	2.121286353	4.42E-10	5.02E-09
Specc1	290.5399	501.3615	0.598185465	0.459398396	0.011156035	0.000839157
Sphk1	59.47501	191.2715	1.368656126	0.89744868	0.002773203	0.001185865
Srgap3	131.9378	175.2212	2.65425815	0.822610595	3.61E-09	0.004971559
St14	35.53093	88.13187	3.92784732	1.01547955	7.49E-10	0.009497068
Steap2	119.16	258.9819	1.726286203	0.888052602	2.57E-08	0.001723239
Tbx15	49.93634	140.4692	1.104645046	1.524652685	0.015516497	0.000139045
Tc2n	46.51239	133.5308	2.431350799	0.823009946	2.12E-06	0.009369206
Tmem56	147.233	562.4513	-1.209475891	-1.009392798	0.000664798	3.46E-06
Tmprss13	39.14196	149.0266	-1.575697533	-1.033357272	0.00147481	0.044786353
Tnni2	28.0641	68.64875	-1.14286515	-0.915060635	0.03912346	0.004258662
Trpm6	47.30285	99.68346	2.001789475	1.131149033	3.13E-05	0.000705942
Wscd2	40.32155	83.34609	3.789955949	1.548127677	4.50E-07	0.002942176
Xylt1	244.5109	426.3965	1.122938768	0.540895006	2.19E-06	0.001160318
Zfp30	425.8207	634.8073	-0.752838829	-0.53850983	9.80E-06	0.008757768
Zfp354c	275.2212	512.1063	0.888658091	0.638990311	1.48E-06	0.001798011
Zfp423	154.85	365.9361	1.532558639	0.547260101	7.06E-08	0.001086937
Zfp783	80.43104	135.5416	1.066661879	0.809561367	0.002956994	0.002038413
Zfp995	85.12412	168.2397	0.868114571	0.684070644	0.041180192	0.002653893