Suppl. Table 1. Genes downregulated in miR-24 over-expressing cells

				miR-24 binding sites in 3'UTR (TargetScan 4.2)						
Gene	**ACCESSION #**	**Z-ratio Ctl/miR-24**	**p-value<**	**Conserved**	**Nonconserved**	**CDS**	**Seed**	**Perfect Hexamer**	**Perfect Heptamer**	**Perfect Octamer**
UBD	NM_006398.2	6.1	0.00001	0	0	225.722	No			
CNDP2	NM_018235.1	5.24	0.0004	0	3	163..1590	Yes	2198, 2029, 2110, 2290		
FLJ33814	NM_173510.1	4.68	0.00001	0	0	132..971	Yes	2930, 2066	3356	
CARD10	NM_014550.3	4.5	0.00001	0	2	4..3102	Yes		3528, 3180	
SCML1	NM_006746.3	4.49	0.00001	0	2	326..1234	Yes	2178	2347	
C22orf13	NM_031444.2	4.37	0.0017	0	3	317..1039	Yes	1343, 3571		1384
KLHDC3	NM_057161.2	4.35	0.00001	0	2	170..1318	Yes	1710, 1703	1344, 1651	
DCP2	NM_152624.4	4.23	0.0001	0	0	199..1461	Yes	3466		
CMTM4	NM_178818.2	4.17	0.0026	1	0	183..887	Yes		2786	2442
AAMP	NM_001087.2	4.08	0.00001	0	1	85..1389	Yes	1652		
TOP1	NM_003286.2	4.07	0.0419	1	1	247..2544	Yes		2707	2605
HBQ1	NM_005331.3	4.03	0.00001	0	0	152..580	No			
PDXK	NM_003681.3	3.98	0.001	0	6	199..1137	Yes	7278, 5532, 5687	6199, 4838, 5128	
PER2	NM_022817.1	3.98	0.0108	1	1	238..4005	Yes	5057, 5598, 6196		6124
KIAA1967	NM_021174.4	3.73	0.00001	0	0	420..3191	No			
KLHL23	NM_144711.3	3.6	0.0009	0	0	339..2015	No			
RALA	NM_005402.2	3.59	0.0001	1	0	301..921	Yes	2759		
NOL5A	NM_006392.2	3.58	0.00001	0	0	54..1838	No			
CCDC32	NM_052849.2	3.53	0.0128	0	2	274..858	Yes	1245	1654	
ALDH5A1	NM_001080.3	3.46	0.0004	0	4	29..1675	Yes	2564, 2875	2745, 2720	
POLR2D	NM_004805.2	3.43	0.00001	0	1	31..459	Yes	1186		
HIC2	NM_015094.1	3.3	0.00001	1	4	231..2078	Yes	3393, 3567, 2566	4048, 2900, 5045	
SLC5A6	NM_021095.1	3.26	0.016	0	1	392..2299	Yes	2760	3035	
ALS2CR2	NM_018571.4	3.23	0.00001	1	1	366..1622	Yes	1913		2130
DUS1L	NM_022156.3	3.22	0.00001	0	0	203..1624	No			
FZD4	NM_012193.2	3.21	0.0028	0	3	307..1920	Yes	4857, 3755, 6120, 6685		
MDC1	NM_014641.1	3.16	0.0179	0	0	441..6710	No			
NRIP1	NM_003489.2	3.07	0.0083	0	0	599..4075	No			
CCDC58	NM_001017928.2	3.06	0.00001	1	0	4..438	Yes		546	
KIAA0020	NM_014878.3	3.05	0.0089	0	0	97..2043	No			
MRPL27	NM_016504.2	3.03	0.00001	0	0	32..478	Yes	668		
METAP2	NM_006838.2	3.01	0.00001	0	0	135..1571	No			
PRIM1	NM_000946.2	3	0.0059	0	0	65..1327	No			
GMFB	NM_004124.2	2.99	0.0003	0	2	100..528	Yes	3614		
PTPLAD1	NM_016395.1	2.98	0.0354	0	1	149..1237	Yes	1269, 2225		2902
OXSR1	NM_005109.2	2.98	0.0042	0	1	343..1926	Yes		3569	
SLC2A3	NM_006931.1	2.96	0.0054	0	0	243..1733	No			
LSM14A	NM_015578.1	2.93	0.0052	0	1	197..1588	Yes	1976		
KIAA1970	NM_133451.1	2.92	0.00001	0	0	33-1604	Yes	3246, 3784		
BCL2L12	NM_052842.2	2.91	0.00001	0	0	683..1213	Yes		1395	
MIDN	NM_177401.4	2.91	0.019	1	0	516..1922	Yes			2810
MARCKSL1	NM_023009.4	2.91	0.00001	1	0	201..788	Yes		1153	
TNIP2	NM_024309.2	2.84	0.00001	0	0	46..1335	No			
RFWD2	NM_022457.5	2.8	0.00001	0	1	257..2452	Yes	2694		
MCM10	NM_018518.3	2.76	0.00001	0	0	102..2726	No			
KPNA6	NM_012316.3	2.76	0.00001	0	2	89..1699	Yes	6854, 6531		
ABCE1	NM_002940.1	2.75	0.0005	0	0	444..2243	No			
NEDD4L	NM_015277.2	2.74	0.00001	0	1	114..2981	Yes		4189	
CCAR1	NM_018237.2	2.73	0.00001	0	0	120..3572	No			
VHL	NM_000551.2	2.72	0.0355	0	1	214..855	Yes	1351, 2894, 2757, 2738		
UBE2C	NM_181802.1	2.71	0.041	0	0	838..1260	Yes	1403		
NETO2	NM_018092.3	2.7	0.00001	0	0	386..1963	Yes	2962		
SESN1	NM_014454.1	2.7	0.0209	1	0	12..1667	Yes		2149	
OGFR	NM_007346.2	2.7	0.0038	0	0	36..2069	No			
C9orf74	NM_030914.1	2.67	0.0209	0	0	63..368	Yes	531		
CDCA7	NM_145810.1	2.64	0.0348	0	0	132..1247	No			
SLC29A4	NM_153247.1	2.61	0.00001	0	1	162..1754	Yes		1852	
ERBB3	NM_001005915.1	2.61	0.0168	0	2	194..745	No			
CGI-115	NM_016052.2	2.59	0.0003	0	0	31..879	Yes	3568, 1747		
CDKN1B	NM_004064.2	2.57	0.0007	1	0	473..1069	Yes			2321
SLC11A2	NM_000617.1	2.57	0.00001	0	1	89..1774	Yes		3207	
GBAS	NM_001483.1	2.57	0.0187	0	1	9..869	No			
AGPAT3	NM_020132.3	2.56	0.0007	1	2	223..1353	Yes	1486, 3932		3479
CCL2	NM_002982.3	2.54	0.00001	0	0	74..373	No			
VPS35	NM_018206.3	2.53	0.0208	0	0	100..2490	No			
CCNB1	NM_031966.2	2.52	0.0002	0	0	178..1479	No			
GTF2E1	NM_005513.1	2.51	0.0103	0	0	115..1434	Yes	2953		
CMTM3	NM_144601.2	2.51	0.0015	0	2	252..542	Yes		567, 692	
TOMM34	NM_006809.4	2.5	0.00001	0	1	141..1070	Yes		1619	
NUBPL	NM_025152.1	2.48	0.00001	0	0	56..1015	Yes	2380		
KIAA0323	NM_015299.1	2.46	0.0002	0	3	203..2239	Yes	4710	4967, 5363	
LLGL1	NM_004140.3	2.45	0.002	0	2	62..3256	Yes	3874		3456
MBD6	NM_052897.3	2.44	0.0001	2	0	225..3236	Yes		3391, 3285	
MCM4	NM_005914.2	2.44	0.0426	0	1	212..2803	Yes	3234		
NFKBIA	NM_020529.1	2.44	0.00001	0	0	111..1064	No			
PAF1	NM_019088.2	2.44	0.0001	0	0	176..1771	Yes	1845		
PSTPIP2	NM_024430.3	2.43	0.0084	0	3	97..1101	Yes	2677	1684, 1443	
PRKRIR	NM_004705.2	2.43	0.0052	0	0	1..2286	No			
PSME3	NM_005789.2	2.43	0.0084	0	0	227..991	No			

PAK4	NM_001014832.1	2.41	0.0055	1	0	163..1938	Yes		2408	
USP10	NM_005153.1	2.4	0.0266	0	1	143..2539	Yes	2985		
KIAA0195	NM_014738.2	2.4	0.0001	0	1	164..4234	Yes	4929	4390	
VPS25	NM_032353.2	2.39	0.0008	0	1	41..571	Yes	826		
RRM2	NM_001034.1	2.39	0.00001	0	0	195..1364	Yes	1632		
PLAGL2	NM_002657.2	2.38	0.00001	0	1	218..1708	Yes	1895	2831	
SNTB1	NM_021021.2	2.38	0.0005	0	1	227..1843	Yes		2522	
ADPGK	NM_031284.3	2.37	0.0005	0	1	95..1585	Yes		2345	
N-PAC	NM_032569.2	2.36	0.0052	0	2	38..1699	Yes	2212, 2559		
GTF3C2	NM_001521.1	2.36	0.0009	0	0	364..3099	No			
LOC129531	NM_138798.1	2.35	0.00001	0	0	49..798	No			
S100P	NM_005980.2	2.35	0.0146	0	1	95..382	Yes		465	
SUMO3	NM_006936.2	2.35	0.00001	0	0	162..473	No			
PHOSPHO2	NM_001008489.2	2.35	0.00001	0	0	389..1114	No			
NCBP2	NM_007362.2	2.35	0.0384	0	0	91..561	No			
MYC	NM_002467.3	2.35	0.00001	0	1	525..1889	Yes	2357		
HMGB2	NM_002129.2	2.34	0.0378	0	0	194..823	No			
MGC40405	NM_152789.1	2.34	0.00001	0	0	102..845	No			
MED16	NM_005481.2	2.32	0.00001	0	0	152..2785	No			
FBXO34	NM_017943.2	2.31	0.0179	0	0	246..2381	No			
H2AFX	NM_002105.2	2.3	0.0117	2	0	74..505	Yes		593	1475
TCEA3	NM_003196.1	2.3	0.0043	0	0	136..1182	No			
BCL2L2	NM_004050.2	2.29	0.0006	0	1	189..770	Yes	1587	2118	
SLC7A2	NM_003046.2	2.28	0.0217	0	0	31..2124	Yes	5726, 5861, 6078		
MAP2K1IP1	NM_021970.2	2.28	0.0001	0	0	250..624	Yes	2289, 4130, 955		
DHCR24	NM_014762.2	2.27	0.0249	0	2	130..1680	Yes		1950, 2977	
SLC35B2	NM_178148.1	2.27	0.0076	0	1	137..1435	Yes	1955	1641	
PDPK1	NM_002613.3	2.27	0.00001	0	0	145..1815	Yes	3556, 6231, 2613		
RPL7L1	NM_198486.2	2.26	0.0003	0	1	6..746	Yes	1219		
STK35	NM_080836.2	2.25	0.0002	0	1	1..1206	Yes	3360	2643	
CYP20A1	NM_177538.1	2.24	0.0001	0	9	623..2011	Yes	8389, 6655, 10584, 4920, 9582, 3031, 9957, 3747, 8075, 3274, 6242, 5935, 9982, 8741, 4444	3964	
SLC7A1	NM_003045.3	2.24	0.00001	0	2	388..2277	Yes		3964	6504
COPS7A	NM_016319.1	2.23	0.0167	0	0	142..969	No			
RNF144A	NM_014746.2	2.23	0.039	0	1	443..1321	Yes	3350, 3189	4709	
NKD1	NM_033119.3	2.21	0.00001	0	0	225..1637	No			
NET1	NM_005863.2	2.21	0.0371	1	0	184..1812	Yes	2610		
STX16	NM_001001433.1	2.21	0.0179	0	1	736..1713	Yes	4189, 4005	3636	
C1orf106	NM_018265.1	2.2	0.00001	0	3	1..1992	Yes	3095, 2317	3919	
IQCB1	NM_001023570.1	2.19	0.0104	0	0	216..2012	No			
HSF2	NM_004506.2	2.18	0.0134	0	0	188..1798	Yes	2435		
DTL	NM_016448.1	2.18	0.00001	0	1	315..2507	Yes		3547	
MTF2	NM_007358.1	2.17	0.0048	0	0	242..2023	No			
WDR21A	NM_181340.1	2.16	0.0011	0	0	376..1563	No			
PACSIN3	NM_016223.3	2.16	0.0005	0	0	163..1437	No			
M6PRBP1	NM_005817.3	2.16	0.00001	0	3	74..1378	Yes	1827, 1915	1583, 2125	
ARHGEF7	NM_003899.2	2.14	0.00001	0	0	498..2438	No			
LSM12	NM_152344.1	2.14	0.00001	0	0	51..638	No			
GYG2	NM_003918.1	2.14	0.0001	0	0	283..1788	No			
TNFAIP3	NM_006290.2	2.14	0.0011	0	0	67..2439	No			
ATAD3A	NM_018188.2	2.14	0.0001	0	1	95..1999	Yes		2325	
MATR3	NM_018834.4	2.13	0.0178	1	0	318..2861	Yes		3284	
EXOSC8	NM_181503.1	2.12	0.0003	0	0	27..857	No			
MGC2747	NM_024104.2	2.11	0.002	0	0	48..275	Yes	1248		
E2F2	NM_004091.2	2.11	0.00001	0	0	429..1742	No			
GNPAT	NM_014236.1	2.11	0.0018	0	0	144..2186	No			
HRB	NM_004504.3	2.1	0.0273	0	0	251..1939	Yes	4296	7009	
CDC2	NM_033379.2	2.1	0.0002	0	0	26..748	No			
MED24	NM_014815.2	2.1	0.0014	0	0	314..3283	No			
BTBD3	NM_014962.2	2.09	0.00001	0	0	360..1928	No			
C19orf22	NM_138774.2	2.08	0.00001	0	0	69..875	Yes	1537		
DSC2	NM_004949.2	2.07	0.0003	0	1	455..2998	Yes	4490		
RHOT2	NM_138769.1	2.07	0.00001	0	0	68..1924	No			
MRPL40	NM_003776.2	2.07	0.0002	0	0	1..787	No			
UGDH	NM_003359.2	2.06	0.0002	0	2	317..1801	Yes	2101, 2177		
LOC130074	NM_001009993.1	2.06	0.0234	0	5	230..817	Yes	3848, 3747	3962, 5248	2572
NOTUM	NM_178493.3	2.05	0.0143	0	0	477..1769	No			
SULT2A1	NM_003167.2	2.05	0.00001	0	1	80..937	Yes	1474		
FLJ11259	NM_018370.1	2.05	0.028	0	0	464..1180	Yes	2961, 2801	2935	
C1orf135	NM_024037.1	2.03	0.0034	0	0	1..1074	No			
SLC25A15	NM_014252.1	2.03	0.00001	0	1	273..1178	Yes		1194	
DSCR3	NM_006052.1	2.02	0.0001	0	4	240..1133	Yes	2409, 2631, 1955	2607	
PSMD1	NM_002807.2	2.02	0.00001	0	0	132..2993	No			
CIRBP	NM_001280.1	2.02	0.00001	0	0	150..668	No			
C20orf44	NM_018244.3	2.01	0.0005	0	1	68..238	Yes		1959	
NEK6	NM_014397.3	2.01	0.00001	0	1	146..1087	Yes	1478	1935	
C14orf108	NM_018229.2	2.01	0.0011	0	1	407..1879	Yes			2227
MED22	NM_181491.1	2.01	0.0055	0	0	235..657	Yes		3726, 3269	
FLJ14803	NM_032842.2	2	0.0038	0	1	124..1809	Yes		1876	
FOXQ1	NM_033260.2	1.97	0.0036	0	0	266..1477	No			

AK3	NM_016282.2	1.95	0.0056	0	0	141..824	No			
FAH	NM_000137.1	1.95	0.0212	0	0	57..1316	No			
ACD	NM_022914.1	1.95	0.0241	0	0	338..1963	No			
NR0B2	NM_021969.1	1.94	0.0131	0	0	137..910	No			
AKAP7	NM_016377.2	1.93	0.00001	0	0	12..992	No			
CCDC59	NM_014167.1	1.92	0.0029	0	0	18..743	No			
C16orf9	NM_032039.1	1.91	0.0155	0	0	165..1823	Yes	2914	2497	
LOC389541	NM_001008395.1	1.91	0.00001	0	0	67..366	No			
RBM13	NM_032509.2	1.9	0.0109	0	0	41..943	No			
SDCCAG10	NM_005869.2	1.89	0.0105	0	0	220..1638	No			
ADRM1	NM_007002.2	1.89	0.0287	0	0	81..1304	No			
FEN1	NM_004111.4	1.89	0.00001	0	0	373..1515	No			
NASP	NM_002482.2	1.87	0.0053	0	0	103..2469	Yes	2906		
PCGF6	NM_032154.3	1.87	0.00001	0	0	69..896	No			
APPBP1	NM_003905.3	1.87	0.0001	0	0	78..1682	No			
TSPAN14	NM_030927.1	1.85	0.00001	1	1	108..920	Yes	4811	1518, 944	
CSTF3	NM_001033505.1	1.84	0.0013	0	0	167..478	No			
TAF15	NM_003487.2	1.84	0.0001	0	0	87..1856	No			
ARL1	NM_001177.3	1.83	0.0171	0	0	150..695	No			
TUBGCP2	NM_006659.1	1.83	0.0018	0	0	358..3066	No			
SNRPD3	NM_004175.3	1.83	0.0081	0	0	441..821	No			
PCK2	NM_001018073.1	1.82	0.0011	0	0	133..1458	No			
ARS2	NM_015908.4	1.82	0.0088	0	0	269..2899	No			
CHD8	NM_020920.1	1.81	0.0212	0	0	95..7003	No			
NCOA6	NM_014071.2	1.81	0.0007	0	0	323..6514	Yes	6688		
GGA2	NM_015044.3	1.81	0.00001	0	3	77..1918	Yes	4288, 3831, 3697	4373, 3219	
EIF2S3	NM_001415.2	1.8	0.00001	0	2	22..1440	Yes	2962, 2002		
TRIB3	NM_021158.3	1.79	0.0003	0	1	507..1583	Yes			1660
PHF16	NM_014735.2	1.79	0.00001	0	0	299..2770	No			
CTCF	NM_006565.2	1.78	0.0306	0	0	291..2474	No			
C15orf39	NM_015492.3	1.77	0.00001	0	1	231..3374	Yes	4374, 4300	3687	
ALG5	NM_013338.3	1.77	0.003	0	0	41..1015	No			
CTDSP1	NM_021198.1	1.76	0.0023	0	0	337..1122	No			
ADD3	NM_016824.3	1.75	0.00001	0	2	377..2497	Yes	4031, 4332		
SERGEF	NM_012139.2	1.75	0.00001	0	0	81..1457	No			
NARF	NM_031968.1	1.75	0.00001	0	0	41..1649	No			
TNPO3	NM_012470.2	1.75	0.0011	0	0	375..3146	No			
MMS19	NM_022362.2	1.75	0.0276	0	1	64..3219	Yes	3275		
C8orf42	NM_175075.2	1.74	0.0001	0	0	575..1132	No			
C18orf56	NM_001012716.1	1.74	0.0372	0	0	94..465	Yes	785		
C8orf33	NM_023080.1	1.74	0.0077	0	0	55..744	Yes	1985		
KIAA0690	NM_015179.2	1.73	0.0166	0	0	78..3971	No			
CHFR	NM_018223.1	1.72	0.0103	0	0	65..1936	Yes	3120		
C21orf45	NM_018944.2	1.72	0.0222	0	0	52..753	Yes	925		
ACTL6A	NM_177989.1	1.71	0.0385	0	0	156..1319	No			
EXOSC3	NM_016042.2	1.71	0.0016	0	0	25..852	No			
COMMD9	NM_014186.1	1.71	0.0043	0	1	18..614	Yes		1123	
C7orf30	NM_138446.1	1.7	0.00001	0	0	33..737	No			
ALG1	NM_019109.3	1.7	0.0196	0	0	42..1436	No			
ACACA	NM_198834.1	1.68	0.0102	0	2	514..858	Yes	8402, 2660, 8190	9278	
FNTB	NM_002028.3	1.68	0.0187	0	1	166..1479	Yes			2084
PPM1F	NM_014634.2	1.68	0.0049	0	3	115..1479	Yes	4700, 4338	4535, 3927	
UNG	NM_003362.2	1.67	0.0008	0	0	126..1040	No			
CTDSP2	NM_005730.2	1.66	0.00001	0	1	530..1345	Yes	2604	2013	
C1orf171	NM_138467.1	1.66	0.0286	0	0	90..869	No			
FLJ10847	NM_018242.2	1.66	0.00001	0	1	87..1799	Yes	2723		
GPR172A	NM_024531.3	1.66	0.00001	0	1	1..1338	No			
PA2G4	NM_006191.1	1.66	0.00001	0	0	20..1604	No			
KIAA0100	NM_014680.2	1.65	0.0334	0	0	100..6807	No			
MRPS24	NM_032014.1	1.64	0.0221	0	0	52..555	No			
CSK	NM_004383.1	1.64	0.0077	1	0	703..2055	Yes			2143
WBSCR1	NM_022170.1	1.64	0.00001	0	0	9..755	No			
TBPL1	NM_004865.2	1.64	0.0001	0	0	308..868	No			
VRK1	NM_003384.2	1.64	0.00001	0	0	107..1297	No			
ZNF317	NM_020933.2	1.63	0.0039	0	0	276..2063	No			
ZBED1	NM_004729.3	1.62	0.0275	0	2	202..2286	Yes	3482, 3457	4074	
NUP54	NM_017426.2	1.62	0.0001	0	0	129..1652	No			
PDLIM7	NM_213636.1	1.61	0.0037	0	1	86..754	Yes		873	
SNRPB2	NM_003092.3	1.59	0.0011	0	0	217..894	No			
C4orf9	NM_003703.1	1.59	0.0259	0	0	73..2646	No			
ANPEP	NM_001150.1	1.57	0.0043	0	1	293..3196	Yes	3346		
RAP2C	NM_021183.3	1.56	0.005	1	0	785..1336	Yes			1434
EIF4G3	NM_003760.2	1.55	0.0002	0	0	582..5339	No			
DDHD2	NM_015214.1	1.55	0.0307	0	0	280..2415	No			
ADD1	NM_001119.3	1.55	0.00001	0	2	189..2402	Yes		3662, 2722	
ABCB10	NM_012089.1	1.55	0.0025	0	0	44..2260	No			
MGC15416	NM_138418.2	1.55	0.0003	0	0	144..626	No			
BEX1	NM_018476.3	1.55	0.0304	0	0	241..618	No			
ARHGEF18	NM_015318.2	1.54	0.0031	0	3	207..3254	Yes	3292, 4266, 3613	4807	
ZDHHC3	NM_016598.1	1.54	0.0282	0	0	275..1258	Yes	7370, 6896, 10762, 3306, 4797, 5005, 4409	9208, 12498	
RCE1	NM_001032279.1	1.54	0.0018	0	0	353..1030	No			
MRPS22	NM_020191.2	1.53	0.00001	0	0	9..1091	No			

THOP1	NM_003249.3	1.53	0.0239	0	0	156..2225	No
C13orf23	NM_025138.2	1.52	0.0264	0	0	874..3708	No
C6orf130	NM_145063.2	1.52	0.0008	0	0	173..631	No
ZMYND19	NM_138462.2	1.52	0.0002	0	0	223..906	No
TINP1	NM_014886.2	1.52	0.0062	0	0	84..866	No
SMBP	NM_020123.2	1.51	0.0009	0	0	218..1987	No
TOMM22	NM_020243.4	1.51	0.0026	0	0	31..459	No
UBE3A	NM_130839.1	1.51	0.0077	0	0	658..3276	No

The Z-ratio is the ratio of the normalized microarray signal of the gene from total RNA obtained from control (Ctl) miRNA-transfected cells compared to the signal for the gene from miR-24 mimic-transfected cells. The p-value gives the probability that the mRNA is over-represented in the miR-24 down-regulated genes. Genes highlighted in yellow have conserved binding sites for miR-24; those in red are the transcripts that are non-conserved miR-24 targets by TargetScan 4.2. Numbers in columns G show the location of the coding region (CDS). The presence or absence of a perfect hexamer, heptamer or octamer seed for a gene is shown in Column H as a "Yes" or "No". Numbers in columns I-K correspond to the sixth, seventh or eigth nucleotide of a perfect 6-mer (Hexamer), 7-mer (Heptamer) or 8-mer (Octamer) seed. Perfect seeds have exact match for a 6-mer, 7-mer or 8-mer sequence complementary to nucleotides 2-7, 2-8 or 2-9 at the 5'-end of miR-24. Presence of a miR-24 seed was identified by using PITA (http://132.77.150.113/pubs/mir07/mir07_prediction.html). The miR-24 mature miRNA sequence was obtained from miRBase (www.mirbase.com).

Suppl. Table 2. Significantly over-represented GO processes amongst 248 genes down-regulated by miR-24.

Gene Ontology (GO) Process	# of genes in data set	# in GO process	% of genes	p-value<	Score
biopolymer metabolic process	131	5717	2.29	2.07E-08	7.68
cellular macromolecule metabolic process	140	6549	2.14	4.5E-07	6.34
macromolecule metabolic process	140	6671	2.10	1.54E-06	5.81
primary metabolic process	159	7932	2.00	2.19E-06	5.66
cellular metabolic process	162	8237	1.97	5.78E-06	5.24
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	87	3724	2.34	1.35E-05	4.87
DNA metabolic process	25	625	4.00	1.36E-05	4.87
arginine transport	3	4	75.00	1.44E-05	4.84
ornithine transport	3	4	75.00	1.44E-05	4.84
cellular biopolymer metabolic process	88	3839	2.29	2.51E-05	4.6
DNA replication	14	248	5.65	3.23E-05	4.49
RNA metabolic process	36	1148	3.14	3.72E-05	4.43
protein-DNA complex assembly	14	252	5.56	3.85E-05	4.41
transcription initiation	9	111	8.11	5.53E-05	4.26
metabolic process	167	8846	1.89	5.85E-05	4.23
DNA damage checkpoint	6	46	13.04	7.11E-05	4.15
transcription initiation from RNA polymerase II promoter	8	90	8.89	7.5E-05	4.13
cell cycle	31	962	3.22	8.27E-05	4.08
DNA unwinding during replication	4	17	23.53	0.000113	3.95
cellular macromolecule catabolic process	28	844	3.32	0.000115	3.94
basic amino acid transport	3	7	42.86	0.000121	3.92
DNA integrity checkpoint	6	51	11.76	0.000128	3.92
macromolecular complex assembly	29	901	3.22	0.000145	3.84
modification-dependent protein catabolic process	22	596	3.69	0.000146	3.84
modification-dependent macromolecule catabolic process	22	596	3.69	0.000146	3.84
ubiquitin-dependent protein catabolic process	22	596	3.69	0.000146	3.84
proteolysis involved in cellular protein catabolic process	22	604	3.64	0.000177	3.75
cellular protein catabolic process	22	607	3.62	0.00019	3.72
macromolecule catabolic process	28	878	3.19	0.000221	3.66
lysine transport	2	2	100.00	0.000237	3.63
DNA duplex unwinding	4	21	19.05	0.00027	3.57
DNA geometric change	4	21	19.05	0.00027	3.57
macromolecular complex subunit organization	29	937	3.09	0.000281	3.55
biopolymer catabolic process	25	767	3.26	0.000352	3.45
protein catabolic process	22	636	3.46	0.000362	3.44
response to DNA damage stimulus	18	473	3.81	0.000412	3.39
cellular catabolic process	35	1247	2.81	0.000412	3.39
DNA-dependent DNA replication	7	89	7.87	0.000451	3.35
anti-apoptosis	12	257	4.67	0.000669	3.17
cellular component assembly	29	989	2.93	0.000673	3.17
cytoplasmic sequestering of transcription factor	3	12	25.00	0.000721	3.14
deoxyribonucleotide biosynthetic process	3	12	25.00	0.000721	3.14
anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	6	70	8.57	0.000731	3.14
cell cycle checkpoint	7	98	7.14	0.000805	3.09
cellular response to DNA damage stimulus	16	419	3.82	0.000827	3.08
cytoplasmic sequestering of protein	3	13	23.08	0.000926	3.03
RNA elongation	6	75	8.00	0.001053	2.98
positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	6	75	8.00	0.001053	2.98
positive regulation of ubiquitin-protein ligase activity	6	76	7.89	0.001129	2.95
catabolic process	36	1373	2.62	0.001175	2.93

For each GO process, the number of genes in the data set is compared to the number of genes assigned to the GO process. The percent of genes in the data set that are also assigned to the GO process is given and used to determine the probablility that the GO process is over-represented in the data set. p-value gives the probability that a process is over-represented upon miR-24 overexpression. The Score is defined as -log[p-value].

Suppl. Table 3. Significantly over-represented GO processes amongst genes down-regulated by miR-24 that are also predicted miR-24 targets by TargetScan 4.2 (conserved or nonconserved)

Gene Ontology (GO) Process	# of genes in data set	# in GO process	% of genes	p-value<	Score
DNA damage checkpoint	4	44	9.1	1.18E-04	3.93
double-strand break repair via homologous recombination	3	17	17.65	1.19E-04	3.93
recombinational repair	3	17	17.65	1.19E-04	3.93
regulation of cell cycle	12	598	2.01	1.59E-04	3.8
DNA integrity checkpoint	4	49	8.17	1.80E-04	3.75
post-translational protein modification	22	1719	1.28	2.33E-04	3.64
protein modification process	24	2027	1.19	3.67E-04	3.44
biopolymer modification	24	2100	1.15	6.19E-04	3.21
cell cycle arrest	5	122	4.1	6.95E-04	3.16
macromolecular complex assembly	13	821	1.59	8.21E-04	3.09
cell cycle	15	1061	1.42	1.02E-03	3
negative regulation of cell cycle	7	276	2.54	1.07E-03	2.98
DNA damage response, signal transduction	4	80	5	1.17E-03	2.94
DNA recombination	5	138	3.63	1.21E-03	2.92
cell cycle checkpoint	4	91	4.4	1.88E-03	2.73
protein metabolic process	36	4026	0.9	2.12E-03	2.68
cellular component assembly	13	914	1.43	2.16E-03	2.67
response to DNA damage stimulus	8	401	2	2.18E-03	2.67
DNA metabolic process	10	605	1.66	2.49E-03	2.61
double-strand break repair	3	48	6.25	2.66E-03	2.58
NLS-bearing substrate import into nucleus	2	15	13.34	3.29E-03	2.49
interphase	5	178	2.81	3.67E-03	2.44
I-kappaB kinase/NF-kappaB cascade	5	190	2.64	4.83E-03	2.32
negative regulation of cell proliferation	7	371	1.89	5.58E-03	2.26
UDP-glucuronate biosynthetic process	1	1	100	5.77E-03	2.24
plasminogen activation	1	1	100	5.77E-03	2.24
ferrous iron transport	1	1	100	5.77E-03	2.24
biotin transport	1	1	100	5.77E-03	2.24
glucuronate biosynthetic process	1	1	100	5.77E-03	2.24
pantothenate transport	1	1	100	5.77E-03	2.24
meiosis	4	126	3.18	6.06E-03	2.22
M phase of meiotic cell cycle	4	126	3.18	6.06E-03	2.22
regulation of protein kinase activity	7	377	1.86	6.08E-03	2.22
DNA unwinding during replication	2	21	9.53	6.43E-03	2.2
meiotic cell cycle	4	129	3.11	6.58E-03	2.19
regulation of kinase activity	7	386	1.82	6.89E-03	2.17
protein complex assembly	8	491	1.63	7.36E-03	2.14
phosphorus metabolic process	14	1186	1.19	7.71E-03	2.12
phosphate metabolic process	14	1186	1.19	7.71E-03	2.12
regulation of transferase activity	7	398	1.76	8.09E-03	2.1
programmed cell death	14	1193	1.18	8.11E-03	2.1
DNA duplex unwinding	2	25	8	9.05E-03	2.05
DNA geometric change	2	25	8	9.05E-03	2.05
protein kinase cascade	9	622	1.45	9.56E-03	2.02
protein export from nucleus	2	26	7.7	9.77E-03	2.02
cell cycle phase	8	525	1.53	1.08E-02	1.97
intracellular protein transport	9	635	1.42	1.09E-02	1.97
regulation of osteoblast differentiation	2	28	7.15	1.13E-02	1.95
negative regulation of growth hormone secretion	1	2	50	1.15E-02	1.94

For each GO process, the number of genes in the data set is compared to the number of genes assigned to the GO process. The percent of genes in the data set that are also assigned to the GO process is given and used to determine the probablility that the GO process is over-represented in the data set. p-value gives the probability that a process is over-represented upon miR-24 overexpression. The Score is defined as -log[p-value].

Suppl. Table 4. Sequence of primers used for qRT-PCR

Gene	Forward Primer	Reverse Primer
GAPDH	TGCACCACCAACTGCTTAGC	GGCATGGACTGTGGTCATGAG
SDHA	TGGGAACAAGAGGGCATCTG	CCACCACTGCATCAAATTCATG
UBC	ATTTGGGTCGCGGTTCTTG	TGCCTTGACATTCTCGATGGT
c-myc	TCTTCCCCTACCCTCTCAACGA	TTCCTCATCTTCTTGTTCCTCCTCA
H2AFX	AGCAAACTCAACTCGGCAAT	ACTCCCCAATGCCTAAGGTT
UBD	GCTCAGTGGCACAAGTGAAA	CTGCCATCATCTTCCCATCT
CNDP2	GGGCTTATGAGTGACCTGGA	GTGCTTTTGGACCTTGGGTA
PER2	AAATGGATCCCCCTTGAATC	AGCACCACCTGGTGTACCTC
BCL2L12	CGCCTCCTCTTTTCCTCTTT	GGCTGTGTACTCTGGGGAAA
STX16	CCAGACTTTGAGAGGCCAAG	CCACCCGGCTAATTTTTGTA
ZNF317	GACTGGACCTCCCGTATGAA	TCACGTGACTCTCCAAGCTG
MBD6	CCTGCCAAAAACAAGAGGAG	AGGCTCAGCACTCAGCTCTC
MCM4	TTGAAGCCATTGATGTGGAA	GGCACTCATCCCCGTAGTAA
MCM10	TTGTTGTGGGAGATGGTTGA	CCTTCCACCCAATTAGAGCA
RRM2	AGCTTGGTCGACAAGGAGAA	GGCAGCTGCTTTAGTTTTCG
BRCA1	CTGAAGATGTTCCTTGGATAACA	TTGATTCAGACTCCCCATCAT
E2F1	TACCCCAACTCCCTCTACCC	GTCTCCCTCCCTCACTTTCC
E2F2	GAGCTCACTCAGACCCCAAG	AACAGGCTGAAGCCAAAAGA
E2F3	GGGTATGCGTGGGTGTATGT	AGTGTGTGTGAGGGGAGGAG
PCNA	CGGATACCTTGGCGCTAGTA	CACAGCTGTACTCCTGTTCTGG
AURKB	TCTGCTCTTAGGGCTCAAGG	TGCCACACATTGTCTTCCTC
CCNA2	CACAGCATGCACAACAGTCA	AGAAAACAAAGGCAGTCTTTCA
CHEK1	TGCAGAACCAGTTGATGTTTG	ACAGCTGTCACTGGGTTGGT
CDC2	TGAGTTTCTTTCCATGGATCTG	CAATCCCCTGTAGGATTTGG
FEN1	AACCCCGAACCAAGCTTTAG	GGGCCACATCAGCAATTAGT
TOP1	GAGATGAAAGTCCGGCAGAG	GTGTCCGCTGTTTCTCCTTC
pri-miR-24	AGGGCTTAGCTGCTTGTGAG	CAAGGCCAGAGGAGGTGAG

Suppl. Table 5. Sequence of primers and oligonucleotides used for cloning 3'UTR and MREs for miR-24 target genes

Forward primer	Sequence of Forward Primer (5' to 3')	Reverse Primer	Sequence of Reverse Primer (5' to 3')
AURKB 3'UTR FP	ATGACTCGAGTGGTCCCTGTCATTCACTCGGGTGCG	AURKB 3'UTR RP	ATGAGCGGCCGCTCATGAGTACAAAAAGCTTCAGCC
BRCA1 3'UTR FP	ATGACTCGAGCTGCAGCCAGCCACAGGTACAGAGCCACAG	BRCA1 3'UTR RP	ATGAGCGGCCGCGTGTTTGCTACCAAGTTTATTTGCAGTG
CDC2 3'UTR FP	ATGACTCGAGATATCAACAGATAGTTGTGTTTTTATTGTT	CDC2 3'UTR RP	ATGAGCGGCCGCTTAAATATACATTAGAGCCTTTTTAGATGG
CHEK1 3'UTR FP	ATGACTCGAGCTGGGGAATCCTGGTGAATA	CHEK1 3'UTR RP	ATGAGCGGCCGCCACAAGAATTATGTCTTTATTGGTTCA
CDK4 3'UTR FP	ATGACTCGAGGCAATGGAGTGGCTGCCATGGAAGGAAG	CDK4 3'UTR RP	ATGAGCGGCCGCGACCATTATTTCTTTGTTTTGTTTTTCCT
CCNA2 3'UTR FP	ATGACTCGAGCAATGAAAGACTGCCTTTGTTTTCTAAG	CCNA2 3'UTR RP	ATGAGCGGCCGCTAACAAATTTCTGGTTTATTTCAAATGT
FEN1 3UTRFP	ATGACTCGAGATGTGTTTCCCCATTATACCTC	FEN1 3UTRRP	ATGAGCGGCCGCAAAAACAGCGCATGAAAACC
E2F1 3'UTR FP	ATGACTCGAGCAGGGCTTGGAGGGACCAGGGTTTC	E2F1 3'UTR RP	ATGAGCGGCCGCACCTTTACTGGATCTGCTTTTGAGTTAGGACC
E2F2 3'UTR FP	ATGACTCGAGGTGGCCCTGCCTGCCCCCAGCAGCCTG	E2F2 3'UTR RP	ATGAGCGGCCGCCCCAGAGCTGCAGTTTAATGTTTAATG
E2F3 3'UTR FP	ATGACTCGAGTTATGCTTCGTGTGAACTCTCCT	E2F3 3'UTR RP	ATGAGCGGCCGCCTTAAAAAAAATCATTTTATTGATCCTTTA
MYC 3'UTR FP	ATGACTCGAGGGAAAAGTAAGGAAAACGATTCCTTCT	MYC 3'UTR RP	ATGAGCGGCCGCTTTGGCTCAATGATATATTTGCCAGTTA
WTCCNA2 short 3'UTR fragment FP	ATGACTCGAGGGGAAGTGAAAAGCCTTCCT	WTCCNA2 short 3'UTR fragment RP	ATGAGCGGCCGCAGCGAAAAAGTCTGGGGAAT
MT CCNA2 short 3'UTR forward oligo	5'-TCGAGGGGAAGTGAAAAGCCTTCCTCTAAAATTAAAGTAGGTTTAGGAAAACAGACCCTCAAATTCTGACATTCATTTTCCTAAGCAACTGGAACAAGGACGACTCGACTCGATAATCTAATCTAAGCATATCTGAATACAGTATTCAGAGATAGATACAGTAGAGATTCCCCAGACTTTTTCGCTGC-3'	MT CCNA2 short 3'UTR reverse oligo	5'-GGCCGCAGCGAAAAAGTCTGGGGAATCTCTACTGTATCTATCTCTGAATACTGTATTCAGATATGCTTAGATTAGATTATCGAGTCGAGTCGTCCTTGTTCCAGTTGCTTAGGAAAATGAATGTCAGAATTTGAGGGTCTGTTTTCCTAAACCTACTTTAATTTTAGAGGAAGGCTTTTCACTTCCCC-3'
WTAURKB MRE1 FP	TCGAGCGTGTGTTTGTATGTCTGTGTAGC	WTAURKB MRE1 RP	GGCCGCTACACAGACATACAAACACACGC
MTAURKB MRE1 FP	TCGAGGGACAGGGAAGAACTGACTCGTGC	MTAURKB MRE1 RP	GGCCGCACGAGTCAGTTCTTCCCTGTCCC
WTBRCA1 MRE1 FP	TCGAGTGTTCACAAAGGCAGAGAGTCAGC	WTBRCA1 MRE1 RP	GGCCGCTGACTCTCTGCCTTTGTGAACAC
WTBRCA1 MRE2 FP	TCGAGTCTCAAATGTTGGAGTGGAACAGC	WTBRCA1 MRE2 RP	GGCCGCTGTTCCACTCCAACATTTGAGAC
WTBRCA1 MRE3 FP	TCGAGGTGACAGTGAGACTGTGGCTCAGC	WTBRCA1 MRE3 RP	GGCCGCTGAGCCACAGTCTCACTGTCACC
WTBRCA1 MRE4 FP	TCGAGGCCTGAAAAGGACTTCTGGCTAGC	WTBRCA1 MRE4 RP	GGCCGCTAGCCAGAAGTCCTTTTCAGGCC
WTBRCA1 MRE5 FP	TCGAGAGGTGGAGGTTGCAGTGAGCCAGC	WTBRCA1 MRE5 RP	GGCCGCTGGCTCACTGCAACCTCCACCTC
MTBRCA1 MRE5 FP	TCGAGAGGTGGAGGTTGCAGCCTTAGCAGC	MTBRCA1 MRE5 RP	GGCCGCTGCTAAGGCTGCAACCTCCACCTC
WTCDC2 MRE1 FP	TCGAGCTTGGCTTTCGAGTCTGAGTTTGC	WTCDC2 MRE1 RP	GGCCGCAAACTCAGACTCGAAAGCCAAGC
MTCDC2 MRE1 FP	TCGAGGATGGGGATGGATTGACTCGGTGC	MTCDC2 MRE1 RP	GGCCGCACCGAGTCAATCCATCCCCATCC
WTCDC2 MRE2 FP	TCGAGGCTTATCTTGGCTTTCGAGTCTGC	WTCDC2 MRE2 RP	GGCCGCAGACTCGAAAGCCAAGATAAGCC
WTCDC2 MRE3 FP	TCGAGCATGCCAAAATTTGCTAAGTCTGC	WTCDC2 MRE3 RP	GGCCGCAGACTTAGCAAATTTTGGCATGC
WTCDK4 MRE1 FP	TCGAGCTTTGCCTTTATCTCTGAGGCTGC	WTCDK4 MRE1 RP	GGCCGCAGCCTCAGAGATAAAGGCAAAGC
MTCDK4 MRE1 FP	TCGAGGATAGGGATGATCTGACTCGGTGC	MTCDK4 MRE1 RP	GGCCGCACCGAGTCAGATCATCCCTATCC
WTCDK4 MRE2 FP	TCGAGTTCCCTTCTGGACACTGAGAGGGC	WTCDK4 MRE2 RP	GGCCGCCCTCTCAGTGTCCAGAAGGGAAC
WTCDK4 MRE3 FP	TCGAGCATTTCTCTACACTAAGGGGTAGC	WTCDK4 MRE3 RP	GGCCGCTACCCCTTAGTGTAGAGAAATGC
WTCCNA2 MRE1 FP	TCGAGATCAATTTGCTGACTTGGGCATGC	WTCCNA2 MRE1 RP	GGCCGCATGCCCAAGTCAGCAAATTGATC
WTCCNA2 MRE2 FP	TCGAGATTTTCCTAAGCAACTGGATCAGC	WTCCNA2 MRE2 RP	GGCCGCTGATCCAGTTGCTTAGGAAAATC
WTCCNA2 MRE3 FP	TCGAGAAAATGTGTCAGCTATGAGTAAGC	WTCCNA2 MRE3 RP	GGCCGCTTACTCATAGCTGACACATTTTC
WTFEN1 MRE1 FP	TCGAGCACCTGGCAATCAGCTGAGTTGGC	WTFEN1 MRE1 RP	GGCCGCCAACTCAGCTGATTGCCAGGTGC
MT FEN1 MRE1 FP	TCGAGGACCAGGCAAACTTGACTCGGTGC	MT FEN1 MRE1 RP	GGCCGCACCGAGTCAAGTTTGCCTGGTCC
WT FEN1 MRE2 FP	TCGAGTGACTGATTACTGGCTGTGTCTGC	WT FEN1 MRE2 RP	GGCCGCAGACACAGCCAGTAATCAGTCAC
WT FEN1 MRE3 FP	TCGAGGACCCACCTTGAGAGAGAGCCAGC	WT FEN1 MRE3 RP	GGCCGCTGGCTCTCTCTCAAGGTGGGTCC
WTE2F2 MRE1 FP	TCGAGGTGGGTGCTCTGGGCTGAACCAGC	WTE2F2 MRE1 RP	GGCCGCTGGTTCAGCCCAGAGCACCCACC
MTE2F2 MRE1 FP	TCGAGGACGGAGGAGACTTGACTAGGTGC	MTE2F2 MRE1 RP	GGCCGCACCTAGTCAAGTCTCCTCCGTCC
WTE2F2 MRE2 FP	TCGAGGCTCCTGTGGAAACAGGAGCCAGC	WTE2F2 MRE2 RP	GGCCGCTGGCTCCTGTTTCCACAGGAGCC
WTE2F2 MRE3 FP	TCGAGTGGCTCCTGAGCTGACTGACTGGC	WTE2F2 MRE3 RP	GGCCGCCAGTCAGTCAGCTCAGGAGCCAC
WTE2F2 MRE4 FP	TCGAGACTCCTGACCTCAAGTGATCCAGC	WTE2F2 MRE4 RP	GGCCGCTGGATCACTTGAGGTCAGGAGTC
WTE2F2 MRE5 FP	TCGAGCACATCTCCAGCTGAGCTGCCGGC	WTE2F2 MRE5 RP	GGCCGCCGGCAGCTCAGCTGGAGATGTGC
WTMYC MRE1 FP	TCGAGACTTGTTTCAAATGCATGATCAGC	WTMYC MRE1 RP	GGCCGCTGATCATGCATTTGAAACAAGTC
WTMYC MRE2 FP	TCGAGAATCACCTATGAACTTGTTTCAGC	WTMYC MRE2 RP	GGCCGCTGAAACAAGTTCATAGGTGATTC
WTMYC MRE3 FP	TCGAGTGTTTCTCTGTAAATATTGCCAGC	WTMYC MRE3 RP	GGCCGCTGGCAATATTTACAGAGAAACAC
MTMYC MRE3 FP	TCGAGTGAATGTCTGTACACATTTGGAGC	MTMYC MRE3 RP	GGCCGCTCCAAATGTGTACAGACATTCA C
WTMYC MRE4 FP	TCGAGCCTTGGCTGAGTCTTGAGACTGGC	WTMYC MRE4 RP	GGCCGCCAGTCTCAAGACTCAGCCAAGGC
WTMYC MRE5 FP	TCGAGGCCTCAAATTGGACTTTGGGCAGC	WTMYC MRE5 RP	GGCCGCTGCCCAAAGTCCAATTTGAGGCC
WTMYC MRE6 FP	TCGAGCTGGCAAATATATCATTGAGCCAGC	WTMYC MRE6 RP	GGCCGCTGGCTCAATGATATATTTGCCAGC
MTMYC MRE6 FP	TCGAGCTGGCAAATATATCCGAACAAGGC	MTMYC MRE6 RP	GGCCGCCTTGTTCGGATATATTTGCCAGC

Wild-type miR-24 MREs start with WT and mutant MREs start with MT. Details of cloning procedure are in Materials and methods.