Material for online supplementary information

Supplementary tables

Supplementary Table 1. *List of investigated human miRNAs that were detectable with the Applied Biosystems miRNA Early Access Kit.*

miRNA	mature miRNA sequence
hsa-miR-9	ucuuugguuaucuagcuguauga
hsa-miR-9*	uaaagcuagauaaccgaaagu
hsa-miR-10a	uacccuguagauccgaauuugug
hsa-miR-15a	uagcagcacauaaugguuugug
hsa-miR-15b	uagcagcacaucaugguuuaca
hsa-miR-16	uagcagcacguaaauauuggcg
hsa-miR-17*	acugcagugaaggcacuugu
hsa-miR-17	caaagugcuuacagugcagguagu
hsa-miR-19a	ugugcaaaucuaugcaaaacuga
hsa-miR-20	uaaagugcuuauagugcaggua
hsa-miR-21	uagcuuaucagacugauguuga
hsa-miR-23a	aucacauugccagggauuucc
hsa-miR-23b	aucacauugccagggauuaccac
hsa-miR-25	cauugcacuugucucggucuga
hsa-miR-26a	uucaaguaauccaggauaggcu
hsa-miR-26b	uucaaguaauucaggauaggu
hsa-miR-27a	uucacaguggcuaaguuccgcc
hsa-miR-27b	uucacaguggcuaaguucug
hsa-miR-28	aaggagcucacagucuauugag
hsa-miR-29a	cuagcaccaucugaaaucgguu
hsa-miR-29b	uagcaccauuugaaaucagu
hsa-miR-29c	uagcaccauuugaaaucgguua
hsa-miR-30a*	cuuucagucggauguuugcagc
hsa-miR-30b	uguaaacauccuacacucagc
hsa-miR-30c	uguaaacauccuacacucucagc
hsa-miR-30d	uguaaacauccccgacuggaag
hsa-miR-30e	uguaaacauccuugacugga
hsa-miR-31	ggcaagaugcuggcauagcug
hsa-miR-34a	uggcagugucuuagcugguugu
hsa-miR-34b	aggcagugucauuagcugauug
hsa-miR-34c	aggcaguguaguuagcugauug
hsa-miR-92	uauugcacuugucccggccugu
hsa-miR-95	uucaacggguauuuauugagca
hsa-miR-96	uuuggcacuagcacauuuuugc
hsa-miR-98	ugagguaguaaguuguauuguu
hsa-miR-99a	aacccguagauccgaucuugug
hsa-miR-100	aacccguagauccgaacuugug
hsa-miR-103	agcagcauuguacagggcuauga
hsa-miR-104	ucaacaucagucugauaagcua
hsa-miR-105	ucaaaugcucagacuccugu
hsa-miR-106a	aaaagugcuuacagugcagguagc
hsa-miR-107	agcagcauuguacagggcuauca
hsa-miR-122a	uggagugugacaaugguguuugu
hsa-miR-124a	uuaaggcacgcggugaaugcca
hsa-miR-124b	uuaaggcacgcggugaaugc
hsa-miR-125a	ucccugagacccuuuaaccugug
hsa-miR-125b	ucccugagacccuaacuuguga
hsa-miR-126	ucguaccgugaguaauaaugc
hsa-miR-127	ucggauccgucugagcuuggcu
hsa-miR-128a	ucacagugaaccggucucuuuu
hsa-miR-128b	ucacagugaaccggucucuuuc
hsa-miR-129	cuuuuugcggucugggcuugc
hsa-miR-130a	cagugcaauguuaaaagggc

miRNA	mature miRNA sequence
hsa-miR-130b	cagugcaaugaugaaagggcau
hsa-miR-132	uaacagucuacagccauggucg
hsa-miR-133a	uugguccccuucaaccagcugu
hsa-miR-133b	uugguccccuucaaccagcua
hsa-miR-134	ugugacugguugaccagaggg
hsa-miR-135a	uauggcuuuuuauuccuauguga
hsa-miR-135b	uauggcuuuucauuccuaugug
hsa-miR-137	uauugcuuaagaauacgcguag
hsa-miR-138	agcugguguugugaauc
hsa-miR-139	ucuacagugcacgugucu
hsa-miR-140	agugguuuuacccuaugguag
hsa-miR-141	aacacugucugguaaagaugg
hsa-miR-142-3p	uguaguguuuccuacuuuaugga
hsa-miR-142-5p	cauaaaguagaaagcacuac
hsa-miR-144	uacaguauagaugauguacuag
hsa-miR-145	guccaguuuucccaggaaucccuu
hsa-miR-146	ugagaacugaauuccaugggu
hsa-miR-147	guguguggaaaugcuucugc
hsa-miR-148a	ucagugcacuacagaacuuugu
hsa-miR-149	ucuggcuccgugucuucacucc
hsa-miR-150	ucucccaacccuuguaccagug
hsa-miR-151	acuagacugaagcuccuugagg
hsa-miR-152	ucagugcaugacagaacuugg
hsa-miR-154	uagguuauccguguugccuucg
hsa-miR-154*	aaucauacacgguugaccuauu
hsa-miR-155	uuaaugcuaaucgugauagggg
hsa-miR-181a	aacauucaacgcugucggugagu
hsa-miR-181b	aacauucauugcugucgguggguu
hsa-miR-181c	aacauucaaccugucggugagu
hsa-miR-182	uuuggcaaugguagaacucaca
hsa-miR-182*	ugguucuagacuugccaacua
hsa-miR-183	uauggcacugguagaauucacug
hsa-miR-184	uggacggagaacugauaagggu
hsa-miR-185	uggagagaaaggcaguuc
hsa-miR-186	caaagaauucuccuuuugggcuu
hsa-miR-187	ucgugucuuguguugcagccg
hsa-miR-189	gugccuacugagcugauaucagu
hsa-miR-190	ugauauguuugauauauuaggu
hsa-miR-191	caacggaaucccaaaagcagcu
hsa-miR-193	aacuggccuacaaagucccag
hsa-miR-194	uguaacagcaacuccaugugga
hsa-miR-195	uagcagcacagaaauauuggc
hsa-miR-197	uucaccaccuucuccacccagc
hsa-miR-198	gguccagaggggagauagg
hsa-miR-199a-5p	cccaguguucagacuaccuguuc
hsa-miR-199a-3p	uacaguagucugcacauugguu
hsa-miR-199b	cccaguguuuagacuaucuguuc
hsa-miR-199-s	cccaguguucagacuaccuguu
hsa-miR-200a	uaacacugucugguaacgaugu
hsa-miR-200b	cucuaauacugccugguaaugaug
hsa-miR-200c	aauacugccggguaaugaugga
hsa-miR-203	gugaaauguuuaggaccacuag
hsa-miR-204	uucccuuugucauccuaugccu

miRNA	mature miRNA sequence
hsa-miR-205	uccuucauuccaccggagucug
hsa-miR-210	cugugcgugugacagcggcug
hsa-miR-211	uucccuuugucauccuucgccu
hsa-miR-213	accaucgaccguugauuguacc
hsa-miR-214	acagcaggcacagacaggcag
hsa-miR-215	augaccuaugaauugacagac
hsa-miR-216	uaaucucagcuggcaacugug
hsa-miR-218	uugugcuugaucuaaccaugu
hsa-miR-219	ugauuguccaaacgcaauucu
hsa-miR-220	ccacaccguaucugacacuuu
hsa-miR-221	agcuacauugucugcuggguuuc
hsa-miR-222	agcuacaucuggcuacugggucuc
hsa-miR-223	ugucaguuugucaaauacccc
hsa-miR-224	caagucacuagugguuccguuua
hsa-miR-296	agggcccccccucaauccugu
hsa-miR-299	ugguuuaccgucccacauacau
hsa-miR-301	cagugcaauaguauugucaaagc
hsa-miR-302a	uaagugcuuccauguuuugguga
hsa-miR-302b	uaagugcuuccauguuuuaguag
hsa-miR-302b*	acuuuaacauggaagugcuuucu
hsa-miR-302c	uaagugcuuccauguuucagugg
hsa-miR-302c*	uuuaacauggggguaccugcug
hsa-miR-302d	uaagugcuuccauguuugagugu
hsa-miR-320	aaaagcugggguugagagggcgaa
hsa-miR-323	gcacauuacacggucgaccucu
hsa-miR-324-5p	cgcauccccuagggcauuggugu
hsa-miR-325	ccuaguagguguccaguaagu
hsa-miR-326	ccucugggcccuuccuccag
hsa-miR-328	cuggcccucucugcccuuccgu
hsa-miR-330	gcaaagcacacggccugcagaga
hsa-miR-331	gccccugggccuauccuagaa
hsa-miR-335	ucaagagcaauaacgaaaaaugu
hsa-miR-337	uccagcuccuauaugaugccuuu
hsa-miR-338	uccagcaucagugauuuuguuga
hsa-miR-339	ucccuguccuccaggagcuca
hsa-miR-340	uccgucucaguuacuuuauagcc
hsa-miR-342	ucucacacagaaaucgcacccguc
hsa-miR-367	aauugcacuuuagcaauggugа
hsa-miR-368	acauagaggaaauuccacguuu
hsa-miR-370	gccugcugggguggaaccugg
hsa-miR-371	gugccgccaucuuuugagugu
hsa-miR-372	aaagugcugcgacauuugagcgu
hsa-miR-373	gaagugcuucgauuuuggggugu
hsa-miR-373*	acucaaaaugggggcgcuuucc
hsa-miR-374	uuauaauacaaccugauaagug
hsa-let-7a	ugagguaguagguuguauaguu
hsa-let-7b	ugagguaguagguugugugguu
hsa-let-7d	agagguaguagguugcauagu
hsa-let-7e	ugagguaggagguuguauagu
hsa-let-7g	ugagguaguaguuuguacagu
hsa-let-7i	ugagguaguaguuugugcu

Supplementary Table 2. *Primer sequences used for duplex-PCR analysis of miRNA loci and expression analyses of putative miRNA targets.*

	Primer sequences		**Amplicon size**
	forward	**reverse**	
miR-17	5’-tcaaagtgcttacagtgcaggt-3	5’-aaaagcactcaacatcagcag-3’	134
miR-184	5’-tcctgcaaagcttcatcaaa-3’	5’-cggaggctgtgagtgtcaat-3’	132
APRT	5’-cctggtgaagatcacggaat-3’	5’-gcagtgttgtggctccag-3’	185
WI-3306	5’-gtaatgcaggtttggccatt-3’	5’-tgctctgttctcaggcagac-3’	213
AKRIC3	5’-gatcctcaacaagccaggac-3’	5’-tctcgttgagatcccagagc-3’	147
AKT2	5’-aacacaaggaaagggaacca-3’	5’-acctagctcgggacagctc-3’	146
CDC25A	5’-ctctggacagctcctctcgt-3’	5’-gctggagctacacagggaag-3’	87
CENTG1	5’-gcagctgagttcccttcg-3’	5’-tagctgcagcgtttcatgtc-3’	110
CTBP1	5’-catcatcgtccggattgg-3’	5’-ccggtacaggttcaggatgt-3’	145
MAZ	5’-actgtggcaagagcttctcc-3’	5’-cctcgtgtcgtactgtgtgc-3’	147
NRN1	5’-acgaacatcaagaccgtgtg-3’	5’-tcgaataagctgccttggat-3’	149
S100A16	5’-ctggagaggaggcagactga-3’	5’-ccttctccagctccgtgtag-3’	85
SH3GL1	5’-ggaccaagctggatgatgac-3’	5’-tggacaccgtgttgagcat-3’	150

Supplementary Table 3. ***Potential target genes of miR-184 identified by expression profiling using Affymetrix Human Genome U133 plus 2.0 arrays.*** The mRNA expression profiles of glioma cells with miR-184 over-expression (pre-184) and glioma cells transfected with negative controls (pre-NC) were compared. The list contains targets of miR-184 as predicted by the mirBase target database with signal log ratios (pre-184/pre-NC) < -1 and change p-values < 0.05 in both investigated glioma cell lines (A172 and T98G).

Gene Symbol	**Affy-No.**	**signal log ratio (pre-184/pre-NC)**	
		A172	**T98G**
CDC25A	1555772_a_at	-1.5	-1.2
CDC25A	204695_at	-1.6	-1.1
CENTG1	1555907_at	-1.0	-1.3
LITAF	200704_at	-1.9	-1.3
ARHGDIA	201167_x_at	-2.1	-1.6
ARHGDIA	211716_x_at	-2.7	-1.3
ARHGDIA	213606_s_at	-2.8	-1.8
SH3GL1	201851_at	-2.5	-1.3
CTBP1	203392_s_at	-2.1	-1.5
CTBP1	212863_x_at	-1.9	-1.3
CTBP1	213980_s_at	-2.2	-1.5
DAG1	205417_s_at	-1.8	-1.0
AKR1C3	209160_at	-2.6	-2.1
PPAP2B	209355_s_at	-1.4	-2.2
PPAP2B	212226_s_at	-1.5	-1.5
MAZ	212064_x_at	-1.1	-1.0
NRN1	218625_at	-1.7	-2.1
KLC2	218906_x_at	-2.2	-1.3
LRRC8A	224624_at	-1.7	-1.6
LRRC8A	233487_s_at	-2.2	-1.1
NSMCE1	224666_at	-2.3	-1.7
AKT2	225471_s_at	-1.7	-1.1
TMEM142A	226531_at	-2.3	-1.8
S100A16	227998_at	-2.6	-1.4

Supplementary Table 4. *Differential protein expression caused by miR-184 overexpression.* A172 and T98G cells were transfected with miR-184 precursors (pre-184) or negative controls (pre-NC). 2D-DIGE analyses were performed to identify differentially expressed proteins. Note that Npm1 is a predicted target of miR-184.

Spot-No.	Accession-No.	Protein	Gene Symbol	Av. Ratio	p-Value	Seq. pI	Seq. MW	Seq. Coverage	Mascot Score
Up-regulated in A172 cells transfected with pre-184 as compared to pre-NC									
1	IPI00514561.1	Heterogeneous nuclear ribonucleoprotein K	HNRPK	1.4	0.028	5.3	47.5	60.3	253.0
2	IPI00216746.1	Heterogeneous nuclear ribonucleoprotein K	HNRPK	1.4	0.033	5.0	51.0	44.2	177.0
3	IPI00024175.3	Proteasome subunit alpha type-7	PSMA7	1.3	0.049	9.3	27.9	70.6	202.0
4	IPI00472102.3	61 kDa protein	HSPD1	1.3	0.043	5.6	61.2	40.9	87.0
5	IPI00383296.5	Heterogeneous nuclear ribonucleoprotein M	HNRPM	1.3	0.034	9.6	73.6	51.1	86.2
6	IPI00514561.1	Heterogeneous nuclear ribonucleoprotein K	HNRPK	1.3	0.011	5.3	47.5	44.4	148.0
7	IPI00219018.7	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	1.2	0.048	9.3	36.0	60.0	189.0
8	IPI00383296.5	Heterogeneous nuclear ribonucleoprotein M	HNRPM	1.2	0.023	9.6	73.6	57.5	284.0
9	IPI00013881.6	Heterogeneous nuclear ribonucleoprotein H	HNRPH1	1.2	0.049	5.9	49.2	63.9	230.0
10	IPI00220271.3	Alcohol dehydrogenase	AKR1A1	1.2	0.012	6.4	36.5	26.8	71.6
11	IPI00847536.1	heat shock 70kDa protein 1B	HSPA1B; HSPA1A	1.2	0.050	5.4	70.0	56.2	268.0
12	IPI00013894.1	Stress-induced-phosphoprotein 1	STIP1	1.2	0.015	6.4	62.6	47.1	216.0
Down-regulated in A172 cells transfected with pre-184 as compared to pre-NC									
13	IPI00418169.3	annexin A2	ANXA2	-6.6	0.044	9.2	40.4	45.1	114.0
14	IPI00295081.1	Tubulin gamma-1 chain	TUBG1	-2.3	0.002	5.7	51.1	22.8	121.0
15	IPI00018206.3	Aspartate amino-transferase, mitochondrial precursor	GOT2	-1.8	0.005	9.8	47.4	49.5	127.0
16	IPI00021828.1	Cystatin-B	CSTB	-1.6	0.049	7.9	11.1	61.2	91.3
17	IPI00293167.4	Stromal cell-derived factor 2 precursor	SDF2	-1.6	0.033	7.0	23.0	50.7	103.0
18	IPI00024540.3	Endophilin-B2	SH3GLB2	-1.4	0.043	5.6	43.9	26.1	72.4
19	IPI00025796.3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	NDUFS3	-1.4	0.045	7.8	30.2	56.8	196.0
20	IPI00027341.1	Macrophage-capping protein	CAPG	-1.4	0.032	5.9	38.5	30.7	85.2
21	IPI00793199.1	annexin IV	ANXA4	-1.4	0.044	5.8	36.1	63.2	152.0
22	IPI00008530.1	60S acidic ribosomal protein P0	RPLP0	-1.3	0.025	5.6	34.3	46.4	103.0
23	IPI00012011.6	Cofilin-1	CFL1	-1.3	0.039	9.1	18.5	77.7	149.0
24	IPI00012011.6	Cofilin-1	CFL1	-1.2	0.047	9.1	18.5	45.8	65.9

Up-regulated in T98G cells transfected with pre-184 as compared to pre-NC									
1	IPI00216308.5	Voltage-dependent anion-selective channel protein 1	VDAC1	2.8	0.012	9.2	30.8	61.1	190.0
2	IPI00021439.1	Actin, cytoplasmic 1	ACTB	2.2	0.045	5.2	41.7	33.1	94.7
3	IPI00021439.1	Actin, cytoplasmic 1	ACTB	2.2	0.044	5.2	41.7	34.1	95.4
4	IPI00025491.1	Eukaryotic initiation factor 4A-I	EIF4A1	2.1	0.040	5.2	46.1	35.2	80.6
5	IPI00026260.1	Nucleoside diphosphate kinase B	NME1; NME2	2.0	0.045	9.4	17.3	59.9	90.5
6	IPI00607693.2	carboxylesterase 1 isoform c precursor	CES1	1.9	0.009	6.2	62.4	18.0	69.2
7	IPI00465439.5	Fructose-bisphosphate aldolase A	ALDOA	1.8	0.016	9.2	39.4	32.7	82.2
8	IPI00021439.1	Actin, cytoplasmic 1	ACTB Actin,	1.8	0.010	5.2	41.7	78.4	209.0
9	IPI00843748.1	89 kDa protein	VCP	1.8	0.036	5.0	89.3	30.5	142.0
10	IPI00026260.1	Nucleoside diphosphate kinase B	NME1; NME2	1.8	0.010	9.4	17.3	59.9	90.5
11	IPI00022082.7	Septin-8	SEPT8	1.7	0.020	5.7	49.8	46.2	150.0
12	IPI00021439.1	Actin, cytoplasmic 1	ACTB	1.7	0.019	5.2	41.7	32.3	74.4
13	IPI00021439.1	Actin, cytoplasmic 1	ACTB	1.7	0.016	5.2	41.7	40.5	150.0
14	IPI00021440.1	Actin, cytoplasmic 2	PSPHL; ACTG1	1.7	0.035	5.2	41.8	25.9	77.8
15	IPI00021440.1	Actin, cytoplasmic 2	PSPHL; ACTG1	1.7	0.031	5.2	41.8	62.7	164.0
16	IPI00003881.5	Heterogeneous nuclear ribonucleoprotein F	HNRPF	1.7	0.012	5.3	45.6	48.9	144.0
17	IPI00003362.2	HSPA5 protein	HSPA5	1.6	0.048	4.9	72.4	52.5	351.0
18	IPI00017855.1	Aconitate hydratase, mitochondrial precursor	ACO2	1.6	0.019	7.9	85.4	51.3	292.0
19	IPI00171903.2	Heterogeneous nuclear ribonucleoprotein M	HNRPM	1.6	0.039	9.6	77.5	19.6	68.8
20	IPI00011229.1	Cathepsin D precursor	CTSD	1.5	0.024	6.1	44.5	31.3	125.0
21	IPI00387144.4	Tubulin alpha-1B chain	TUBA1B	1.5	0.015	4.8	50.1	49.9	127.0
22	IPI00744692.1	Transaldolase	TALDO1	1.5	0.008	6.4	37.5	44.8	165.0
23	IPI00291419.5	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	1.5	0.020	6.5	41.3	42.6	140.0
24	IPI00465439.5	Fructose-bisphosphate aldolase A	ALDOA	1.5	0.048	9.2	39.4	72.5	234.0
25	IPI00396378.3	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNP A2B1	1.4	0.026	9.3	37.4	34.6	88.4
26	IPI00002966.1	Heat shock 70 kDa protein 4	HSPA4	1.4	0.008	5.0	94.2	23.6	101.0
27	IPI00021439.1	Actin, cytoplasmic 1	ACTB	1.4	0.019	5.2	41.7	44.5	125.0
28	IPI00216746.1	Heterogeneous nuclear ribonucleoprotein K	HNRPK	1.4	0.018	5.0	51.0	40.5	150.0
29	IPI00021439.1	Actin, cytoplasmic 1	ACTB	1.4	0.030	5.2	41.7	58.4	170.0
30	IPI00418471.6	Vimentin	VIM	1.3	0.049	4.9	53.6	53.0	153.0
31	IPI00455315.4	Annexin A2	ANXA2	1.3	0.010	8.5	38.6	63.7	171.0
32	IPI00334190.4	Stomatin-like protein 2	STOML2	1.3	0.007	7.7	38.5	45.2	94.2
33	IPI00783586.1	43 kDa protein	NDRG1	1.3	0.018	5.4	42.8	29.2	66.0
34	IPI00297477.3	U2 small nuclear ribonucleoprotein A'	SNRPA1	1.3	0.030	9.4	28.4	29.4	120.0

35	IPI00305383.1	Cytochrome b-c1 complex subunit 2, mitochondrial precursor	UQCRC2	1.3	0.039	9.3	48.4	39.7	132.0
36	IPI00179964.5	Polypyrimidine tract-binding protein 1	PTBP1	1.2	0.001	9.8	57.2	25.2	73.3
37	IPI00002966.1	Heat shock 70 kDa protein 4	HSPA4	1.1	0.005	5.0	94.2	57.0	303.0
Down-regulated in T98G cells transfected with pre-184 as compared to pre-NC									
38	IPI00549248.4	Nucleophosmin	NPM1	-1.6	0.026	4.5	32.6	34.4	95.1
39	IPI00017855.1	Aconitate hydratase, mitochondrial precursor	ACO2	-1.6	0.050	7.9	85.4	46.0	225.0
40	IPI00015833.1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3	CHCHD3	-1.5	0.043	9.3	26.1	52.4	197.0
41	IPI00017855.1	Aconitate hydratase, mitochondrial precursor	ACO2	-1.5	0.023	7.9	85.4	48.2	214.0
42	IPI00005087.1	Tropomodulin-3	TMOD3	-1.4	0.041	4.9	39.6	53.1	225.0
43	IPI00411706.1	S-formylglutathione hydrolase	ESD	-1.4	0.018	6.6	31.4	60.3	114.0
44	IPI00010779.4	Tropomyosin alpha-4 chain	TPM4	-1.4	0.005	4.5	28.5	44.8	178.0
45	IPI00021440.1	Actin, cytoplasmic 2	PSPHL; ACTG1	-1.4	0.001	5.2	41.8	35.5	115.0
46	IPI00029744.1	Single-stranded DNA-binding protein, mitochondrial precursor	SSBP1	-1.4	0.046	9.9	17.2	41.2	88.6
47	IPI00021439.1	Actin, cytoplasmatic 1	ACTB	-1,3	0,033	5,2	41,7	42,7	98,2
48	IPI00641950.3	Lung cancer oncogene 7	GNB2L1	-1.3	0.012	9.6	37.9	70.6	198.0
49	IPI00549885.4	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	PDHB	-1.3	0.033	5.6	37.2	26.7	72.2
50	IPI00218918.5	Annexin A1	ANXA1	-1.3	0.029	6.7	38.7	35.3	95.7
51	IPI00015018.1	Inorganic pyrophosphatase	PPA1	-1.3	0.029	5.5	32.6	74.0	212.0
52	IPI00289800.7	Glucose-6-phosphate 1-dehydrogenase	G6PD	-1.2	0.037	6.4	59.2	48.0	92.3
53	IPI00759575.1	Glutathione reductase, mitochondrial precursor	GSR I	-1.2	0.005	8.6	51.7	58.9	193.0
54	IPI00289800.7	Glucose-6-phosphate 1-dehydrogenase	G6PD	-1.2	0.007	6.4	59.2	77.5	375.0

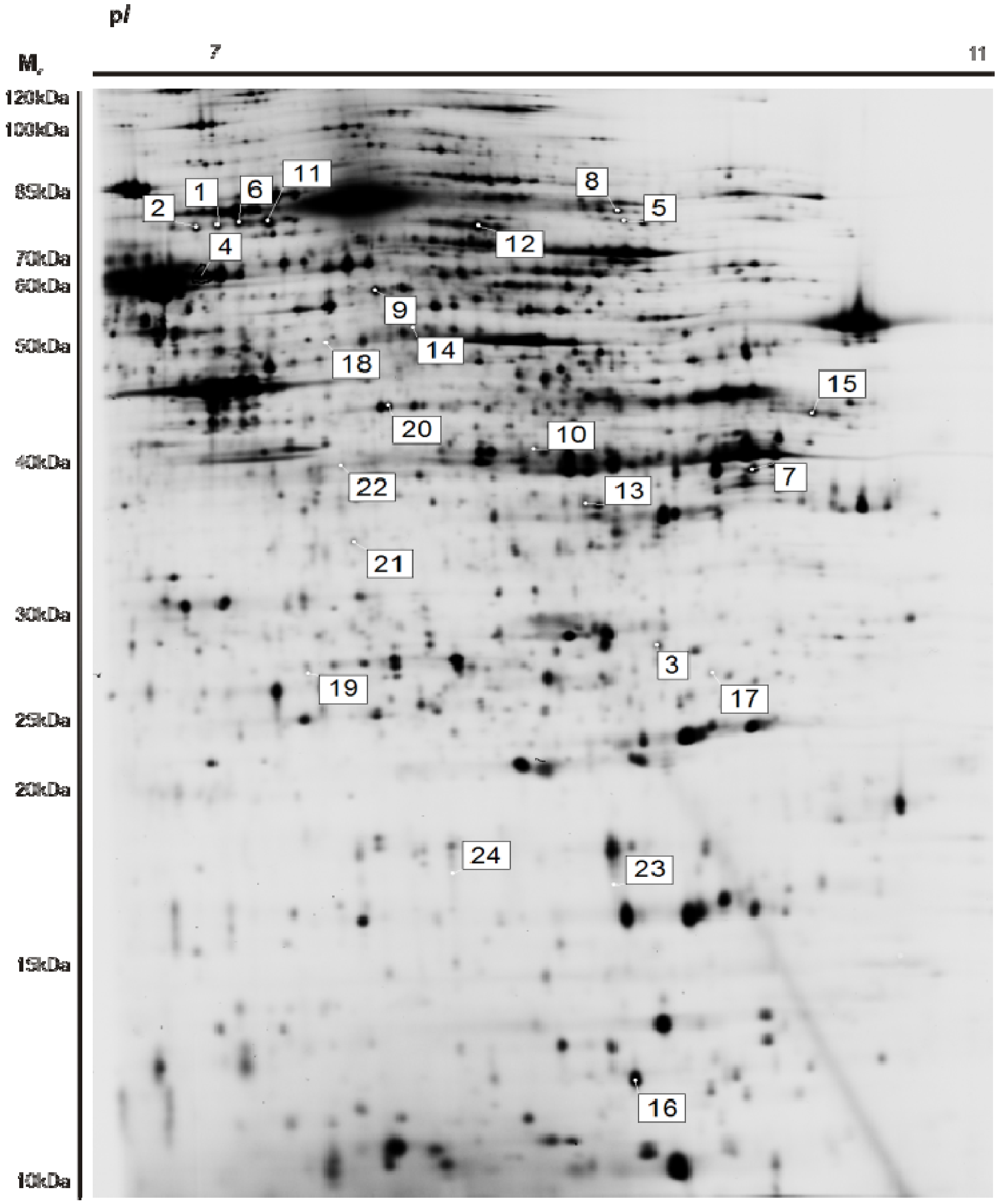
Supplementary Table 5. ***Differential protein expression caused by inhibition of miR-17.*** A172 and T98G cells were transfected with miR-17 inhibitors (anti-17) or negative controls (anti-NC). 2D-DIGE analyses were performed to identify differentially expressed proteins. Note that Pold2 is a predicted target of miR-17.

Spot-No.	Accession	Protein	Gene Symbol	Av. Ratio	p-Value	Seq. pI	Seq. MW	Seq. Coverage	Mascot Score
Up-regulated in A172 cells transfected with anti-17 as compared to anti-NC									
1	IPI00003362.2	HSPA5 protein	HSPA5	1.4	0.023	4.9	72.4	42.4	214.0
2	IPI00216746.1	Heterogeneous nuclear ribonucleoprotein K	HNRPK	1.3	0.026	5.0	51.0	41.8	197.0
3	IPI00845339.1	heat shock 70kDa protein 1A	HSPA1B; HSPA1A	1.3	0.025	5.4	70.0	51.0	193.0
4	IPI00003865.1	Heat shock cognate 71 kDa protein	HSPA8	1.2	0.022	5.2	70.9	51.7	220.0
5	IPI00219757.13	Glutathione S-transferase P	GSTP1	1.2	0.013	5.3	23.3	57.6	109.0
6	IPI00021440.1	Actin, cytoplasmic 2	PSPHL; ACTG1	1.2	0.026	5.2	41.8	25.3	76.5
7	IPI00396485.3	Elongation factor 1-alpha 1	EEF1A1	1.2	0.047	9.7	50.1	37.0	107.0
8	IPI00007765.5	Stress-70 protein, mitochondrial precursor	HSPA9	1.2	0.050	5.8	73.6	56.4	331.0
9	IPI00843975.1	Ezrin	VIL2	1.2	0.022	5.9	69.4	57.8	224.0
10	IPI00304925.5	Heat shock 70 kDa protein 1	HSPA1B; HSPA1A	1.2	0.001	5.4	70.0	43.2	147.0
11	IPI00479209.1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	1.2	0.033	7.7	45.9	34.4	121.0
12	IPI00219219.3	Galectin-1	LGALS1	1.2	0.007	5.2	14.7	60.0	126.0
13	IPI00465248.5	Alpha-enolase	ENO1	1.2	0.012	7.7	47.1	52.1	177.0
14	IPI00010720.1	T-complex protein 1 subunit epsilon	CCT5	1.1	0.010	5.3	59.6	67.5	240.0
15	IPI00000105.4	Major vault protein	MVP	1.1	0.010	5.2	99.3	20.2	86.9
16	IPI00007765.5	Stress-70 protein, mitochondrial precursor	HSPA9	1.1	0.003	5.8	73.6	49.9	216.0
17	IPI00465248.5	Alpha-enolase	ENO1	1.1	0.049	7.7	47.1	55.8	189.0
18	IPI00009771.6	Lamin-B2	LMNB2	1.1	0.016	5.4	69.9	31.8	163.0
19	IPI00414696.1	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	1.1	0.019	9.1	36.0	57.8	187.0
20	IPI00000105.4	Major vault protein	MVP	1.1	0.033	5.2	99.3	35.1	183.0
Down-regulated in A172 cells transfected with anti-17 as compared to anti-NC									
21	IPI00016832.1	Proteasome subunit alpha type-1	PSMA1	-1.6	0.042	6.2	29.5	54.4	101.0
22	IPI00396485.3	Elongation factor 1-alpha 1	EEF1A1	-1.3	0.049	9.7	50.1	45.2	127.0
23	IPI00479186.5	Pyruvate kinase isozymes M1/M2	PKM2	-1.3	0.043	9.0	57.9	75.3	350.0
Up-regulated in T98G cells transfected with anti-17 as compared to anti-NC									
1	IPI00002922.5	F-box-like/WD repeat-containing protein TBL1XR1	TBL1XR1	1.5	0.032	5.2	55.6	33.5	88.9
2	IPI00168554.1	Sulfiredoxin-1	SRXN1; SCRT2	1.4	0.016	9.1	14.3	65.0	84.0

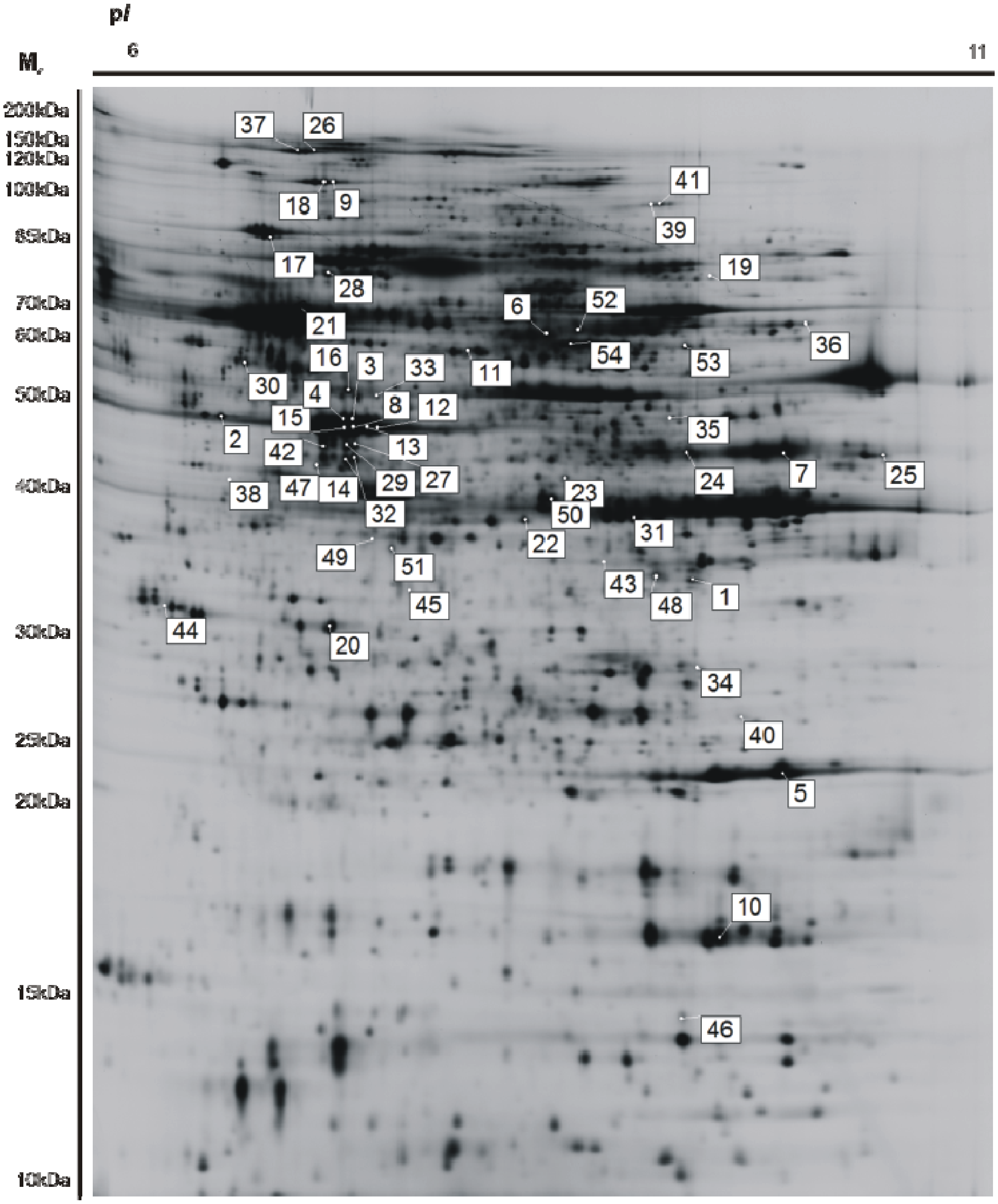
3	IPI00465248.5	Alpha-enolase	ENO1	1.4	0.015	7.7	47.1	56.5	195.0
4	IPI00017855.1	Aconitate hydratase, mitochondrial precursor	ACO2	1.3	0.039	7.9	85.4	36.4	172.0
5	IPI00657680.1	Uncharacterized protein PDIA3	PDIA3	1.3	0.001	6.4	54.9	50.5	228.0
6	IPI00297779.7	T-complex protein 1 subunit beta	CCT2	1.3	0.029	6.0	57.5	43.0	97.1
7	IPI00025616.1	DNA polymerase subunit delta-2	POLD2	1.3	0.033	5.2	51.3	29.2	68.9
8	IPI00025512.2	Heat shock protein beta-1	HSPB1	1.3	0.037	6.0	22.8	33.7	72.0
9	IPI00182728.2	Vacuolar protein sorting-associating protein 4B	VPS4B	1.3	0.039	6.9	49.3	30.4	76.7
10	IPI00218342.10	C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	1.3	0.036	7.0	101.5	57.6	405.0
11	IPI00032826.1	Hsc70-interacting protein	ST13	1.3	0.013	5.0	41.3	32.8	69.6
12	IPI00011126.6	26S protease regulatory subunit 4	PSMC1	1.2	0.010	5.8	49.2	39.8	140.0
13	IPI00025252.1	Protein disulfide-isomerase A3 precursor	PDIA3	1.2	0.009	5.9	56.7	46.9	204.0
14	IPI00784104.1	Sequestosome-1	SQSTM1	1.2	0.004	5.2	38.6	54.8	134.0
15	IPI00444704.2	G-rich sequence factor 1	GRSF1	1.2	0.038	5.4	48.0	32.5	88.7
16	IPI00643920.2	Transketolase	TKT	1.2	0.016	8.5	67.8	56.7	177.0
17	IPI00010720.1	T-complex protein 1 subunit epsilon	CCT5	1.2	0.002	5.3	59.6	46.6	90.8
18	IPI00783357.1	Sequestosome-1	SQSTM1	1.2	0.012	5.0	47.7	48.6	148.0
19	IPI00289800.7	Glucose-6-phosphate 1-dehydrogenase	G6PD	1.2	0.010	6.4	59.2	63.7	295.0
20	IPI00304925.5	Heat shock 70 kDa protein 1	HSPA1B; HSPA1A	1.2	0.046	5.4	70.0	54.4	224.0
21	IPI00219018.7	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	1.2	0.016	9.3	36.0	57.9	123.0
22	IPI00303476.1	ATP synthase subunit beta, mitochondrial precursor	ATP5B	1.2	0.028	5.1	56.5	63.9	224.0
23	IPI00018452.1	Copine-1	CPNE1	1.2	0.044	5.4	59.0	25.1	90.6
24	IPI00550689.3	UPF0027 protein C22orf28	C22orf28	1.2	0.028	6.9	55.2	60.4	224.0
25	IPI00008475.1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	1.1	0.014	5.1	57.3	44.4	180.0
26	IPI00012795.3	Eukaryotic translation initiation factor 3 subunit 2	EIF3I	1.1	0.006	5.3	36.5	42.2	126.0
27	IPI00031420.3	UDP-glucose 6-dehydrogenase	UGDH	1.1	0.011	6.9	55.0	79.6	166.0
28	IPI00150961.2	membrane component chromosome 11 surface marker 1 isoform 1	CAPRIN1	1.1	0.032	5.0	78.3	22.0	81.6
29	IPI00021405.3	Lamin-A/C	LMNA	1.1	0.012	6.6	74.1	47.7	235.0
30	IPI00746165.2	WD repeat-containing protein 1	WDR1	1.1	0.038	6.2	66.2	59.6	271.0
31	IPI00395646.1	Thioredoxin domain containing 5	TXNDC5; MUTED	1.1	0.045	5.7	43.6	42.7	118.0
32	IPI00465439.5	Fructose-bisphosphate aldolase A	ALDOA	1.1	0.045	9.2	39.4	34.6	101.0
33	IPI00029079.5	GMP synthase	GMPS	1.1	0.004	6.4	76.7	37.5	172.0
34	IPI00440493.2	ATP synthase subunit alpha, mitochondrial precursor	ATP5A1	1.1	0.028	9.6	59.7	37.4	126.0
35	IPI00306369.3	tRNA	NSUN2	1.1	0.031	6.3	86.4	46.9	186.0

36	IPI00788802.1	Transketolase variant (Fragment)	TKT	1.1	0.003	8.8	67.9	46.1	206.0
Down-regulated in T98G cells transfected with anti-17 as compared to anti-NC									
37	IPI00012011.6	Cofilin-1	CFL1	-1.7	0.007	9.1	18.5	59.0	125.0
38	IPI00171199.5	Proteasome subunit alpha type-3	PSMA3	-1.5	0.005	5.1	27.6	33.9	99.4
39	IPI00216691.5	Profilin-1	PFN1	-1.3	0.027	9.4	15.0	60.7	81.2
40	IPI000015842.1	Reticulocalbin-1 precursor	RCN1	-1.2	0.011	4.7	38.9	44.4	149.0
41	IPI00096066.2	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor	SUCLG2	-1.2	0.006	6.1	46.5	23.6	70.8
42	IPI00021440.1	Actin, cytoplasmic 2	PSPHL; ACTG1	-1.2	0.004	5.2	41.8	70.7	213.0
43	IPI00334175.3	Polypyrimidine tract-binding protein 1	PTBP1	-1.1	0.040	9.7	59.0	29.1	89.5
44	IPI00014537.3	Calumenin precursor	CALU	-1.1	0.010	4.3	37.1	52.4	142.0
45	IPI00011107.2	Isocitrate dehydrogenase [NADP], mitochondrial precursor	IDH2	-1.1	0.015	9.6	50.9	19.5	72.4
46	IPI00290416.3	Obg-like ATPase 1	OLA1	-1.1	0.000	8.6	44.7	73.2	258.0
47	IPI00386114.1	Splicing factor 1	SF1	-1.1	0.042	9.7	68.3	18.6	74.0
48	IPI00465028.7	Triosephosphate isomerase	TPI1	-1.1	0.045	5.6	30.8	50.3	133.0

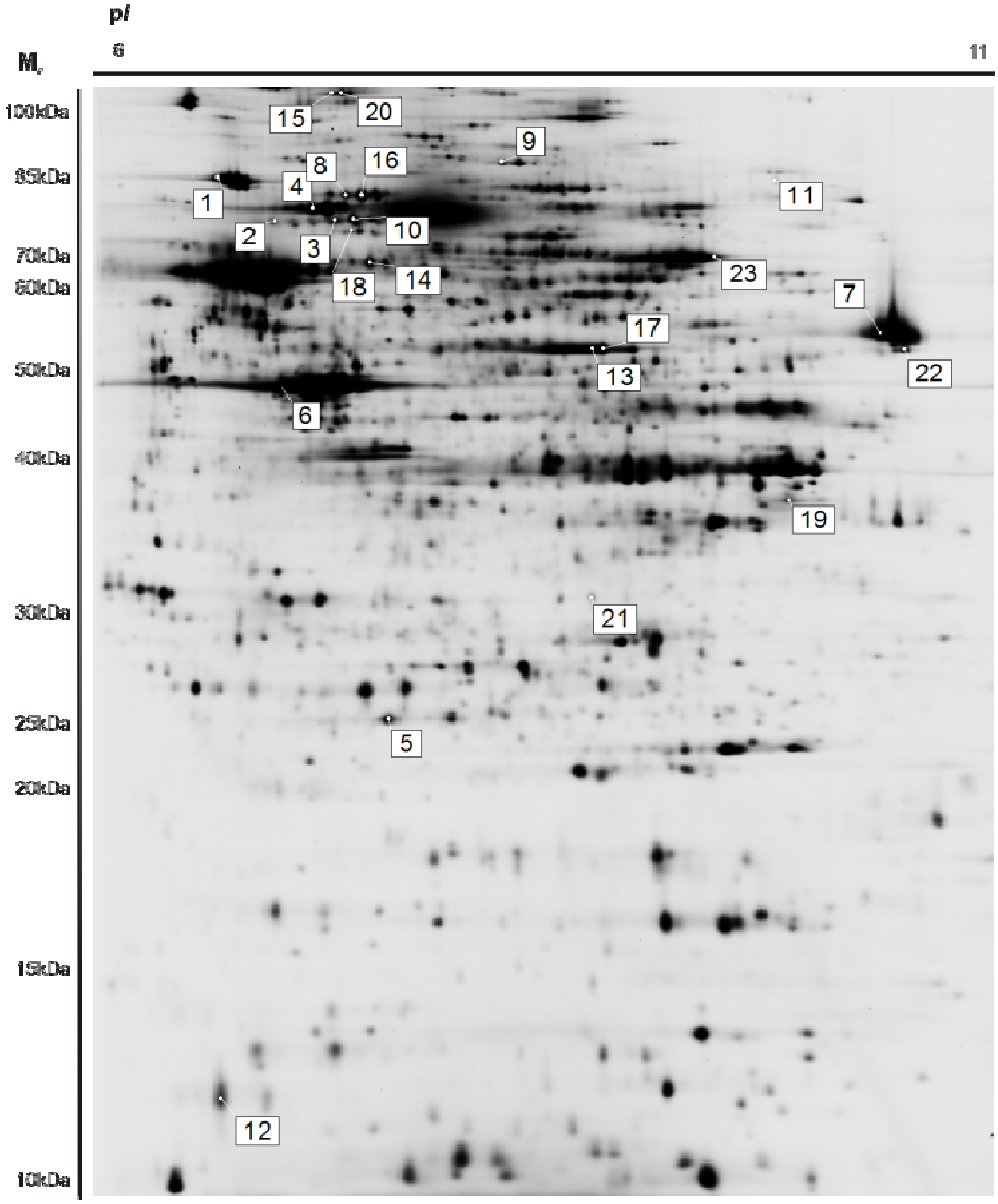
Supplementary figures



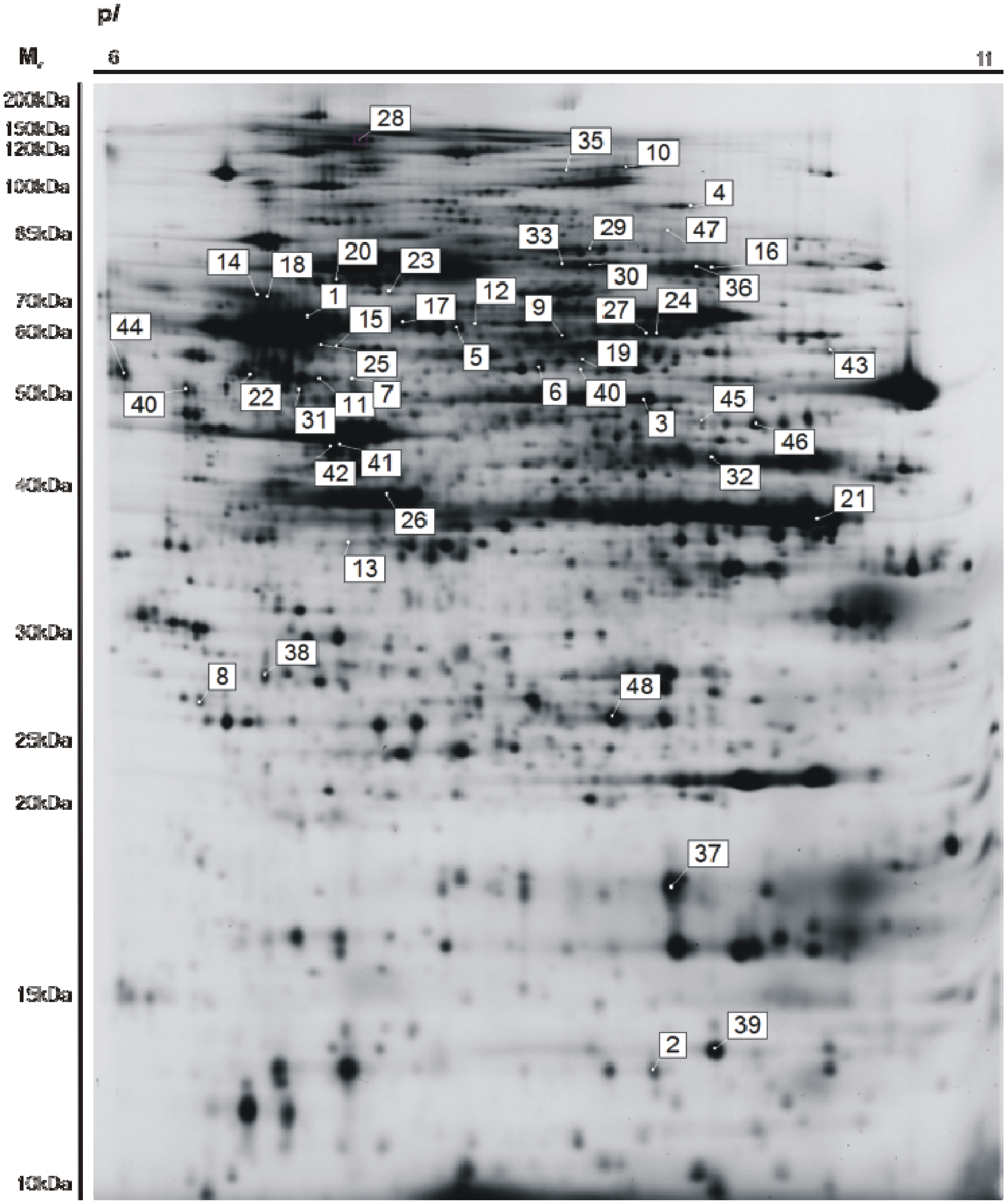
Supplementary Figure 1. Representative proteome pattern of A172 cells transfected with miR-184 precursors revealed by 2D-DIGE. Image analysis and subsequent MS-analyses led to the identification of 24 significantly regulated proteins.



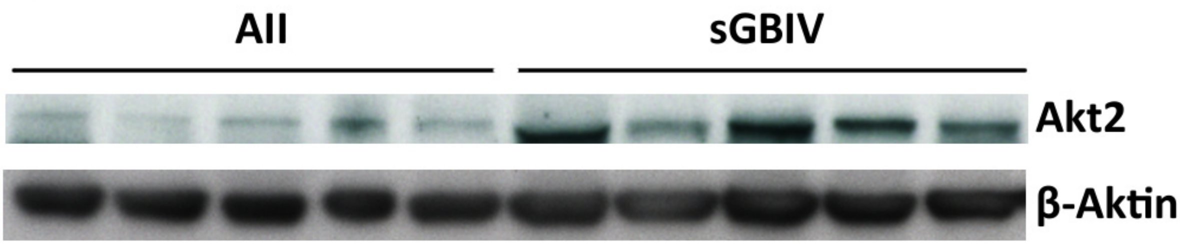
Supplementary Figure 2. Representative proteome pattern of T98G cells transfected with miR-184 precursors revealed by 2D-DIGE. Image analysis and subsequent MS-analyses led to the identification of 54 significantly regulated proteins.



Supplementary Figure 3. Representative proteome pattern of A172 cells transfected with miR-17 inhibitors revealed by 2D-DIGE. Image analysis and subsequent MS-analyses led to the identification of 23 significantly regulated proteins.



Supplementary Figure 4. Representative proteome pattern of T98G cells transfected with miR-17 inhibitors revealed by 2D-DIGE. Image analysis and subsequent MS-analyses led to the identification of 48 significantly regulated proteins.



Supplementary Figure 5. Expression of Akt2 protein in diffuse astrocytomas as compared to secondary glioblastomas. Western blots containing protein extracts from five diffuse astrocytomas (AII) and five secondary glioblastomas (sGBIV) were probed with antibodies against Akt2 and beta-actin as a loading control. Note increased Akt2 protein levels in secondary glioblastomas as compared to the low-grade diffuse astrocytomas.