Supplemental Tables
Subasic et al. (2015)

Supplementary Table 1. Differential protein and mRNA expression of TargetScan predicted, MIRZA predicted and ALG-1 bound targets (from Grosswendt et al. 2014) in *mir-58.1*, *mir-80; mir-58.1* and *mir-80; mir-58.1; mir-81-82* mutants relative to wild-type. Protein and mRNA abundance data are normalized to a group of 518 non-targets identified in three replicates of unfractionated SILAC experiment for which mRNA abundance was obtained. Top scoring (i) and alternative (ii) MIRZA predicted miRNA:mRNA hybrids for non-canonical miR-58 family targets are shown.

TargetScan targets	log2 fold change protein (*mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1; mir-81-82* / WT)	Protein quantification method	log2 fold change mRNA (*mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1; mir-81-82* / WT)
B0336.3	NA	0.27	NA	SILAC fractionated	0.17	0.49	0.62
C30B5.7	-1.24	0.76	5.38	SRM	0.86	0.34	0.78
C32E8.3	0.54	0.42	0.74	SILAC fractionated	0.25	0.52	1.24
C37H5.13	0.37	1.12	1.44	SILAC fractionated	0.30	1.03	1.27
C56G2.1	0.13	0.18	1.90	SRM	0.16	0.38	0.43
cah-5	0.27	0.47	0.82	SILAC fractionated	0.33	0.51	0.44
cgh-1	0.09	0.28	0.33	SILAC unfractionated	-0.17	0.98	0.97
cids-1	0.10	0.03	1.32	SRM	0.04	0.59	0.94
cra-1	0.14	-0.03	0.29	SILAC fractionated	0.44	0.57	0.43
daf-21	0.13	0.26	0.39	SILAC unfractionated	0.19	0.60	1.03
dnj-20	0.47	0.73	0.62	SILAC fractionated	0.71	1.18	1.12
dpy-28	0.49	1.17	1.23	SRM	0.58	1.32	1.53
elo-3	0.77	0.19	0.32	SILAC fractionated	0.26	0.52	0.74
F08G12.2	0.12	1.18	0.78	SILAC fractionated	0.04	0.27	0.59
F13D12.6*	0.30	0.66	-0.22	SRM	-0.01	0.40	0.42
F26B1.2	0.07	0.27	0.23	SILAC fractionated	-0.03	0.36	0.42
F27C1.2	1.19	1.68	1.14	SRM	0.48	0.86	1.32
F40F8.5*	1.33	1.32	4.03	SRM	0.17	0.48	0.79
F47B7.2	-0.54	-0.58	-1.13	SRM	0.04	0.16	0.16
F56D3.1	0.42	0.71	0.19	SRM	0.29	0.68	0.75
F58E10.3	-1.13	-0.93	-0.99	SILAC unfractionated	0.08	0.32	0.50
F59A3.3	0.51	0.65	0.23	SILAC fractionated	0.17	0.52	0.44
fkb-6	-0.52	-0.21	0.74	SILAC unfractionated	-0.31	0.59	1.19
flh-2	-0.91	1.46	-0.64	SRM	0.55	1.30	1.74

TargetScan targets	log2 fold change protein (*mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1; mir-81-82* / WT)	Protein quantification method	log2 fold change mRNA (*mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1; mir-81-82* / WT)
gfl-1	NA	1.14	NA	SRM	0.09	0.61	1.00
gpb-1	0.52	0.51	0.52	SILAC unfractionated	0.38	0.38	0.37
his-72	0.41	NA	NA	SILAC fractionated	0.39	0.96	1.37
hmg-1.1	0.32	0.26	NA	SILAC unfractionated	-0.01	0.55	0.97
hsp-1	0.08	0.17	0.22	SILAC unfractionated	-0.09	0.11	0.04
htz-1	0.34	0.54	0.69	SILAC fractionated	0.16	0.43	0.61
ife-3	0.24	0.65	0.65	SRM	0.09	0.61	0.66
isw-1	0.47	1.07	0.95	SRM	0.44	1.12	1.38
ivd-1	0.16	0.37	0.45	SILAC unfractionated	0.13	0.48	0.36
K08F4.2	-0.27	0.13	0.17	SILAC unfractionated	-0.08	0.46	0.58
lys-1	0.63	0.95	1.33	SILAC unfractionated	0.61	1.67	2.21
lys-2	0.44	0.74	0.31	SILAC fractionated	1.40	2.65	1.99
M28.8	0.51	-1.52	-0.33	SRM	0.03	-0.05	-0.07
mcm-3	0.08	-0.10	0.50	SILAC fractionated	0.30	0.80	0.93
mcm-7	0.41	-0.15	0.20	SILAC fractionated	0.12	0.42	0.84
mep-1	0.40	0.65	0.33	SILAC fractionated	0.25	0.73	0.97
osm-11	0.60	0.70	1.05	SILAC fractionated	0.24	0.15	0.99
pcn-1	0.18	1.07	0.98	SILAC fractionated	0.21	0.81	1.15
pgp-9	-0.11	0.98	1.10	SILAC fractionated	0.44	0.93	1.01
pqn-70	NA	0.48	NA	SILAC fractionated	-0.20	0.55	1.00
R09B3.3	-0.23	-0.41	-0.09	SILAC unfractionated	-0.08	0.41	0.51
R11A8.5	0.20	0.43	0.54	SRM	0.26	0.58	0.51
rnr-2	0.33	0.33	0.25	SILAC fractionated	0.71	0.96	1.16
rpa-1	0.52	1.28	1.56	SRM	0.45	0.89	1.04
rsp-1	0.24	0.41	0.50	SILAC fractionated	-0.05	0.29	0.32
snr-1	NA	0.45	0.45	SILAC fractionated	0.00	0.12	0.18
snr-3	0.24	0.78	0.50	SILAC unfractionated	-0.05	0.21	0.27
snr-6	0.32	0.72	1.06	SILAC unfractionated	-0.09	0.24	0.24
tag-170	0.25	0.58	0.47	SILAC fractionated	0.12	0.32	0.57
tag-297	-0.39	0.03	0.36	SILAC fractionated	-0.01	0.08	0.42
tag-342*	0.84	NA	1.92	SRM	-0.28	0.55	1.37
tag-72	0.65	0.39	0.51	SILAC fractionated	0.11	0.51	0.83
top-2	0.50	0.64	0.95	SILAC fractionated	0.12	0.93	1.15
ubq-1	0.16	0.16	0.32	SILAC unfractionated	0.29	0.60	0.77
unc-130	NA	NA	3.10	SRM	0.39	0.35	1.30
unc-45*	0.46	0.63	0.50	SRM	0.00	0.02	-0.03
vbh-1	-0.31	0.01	-0.37	SILAC fractionated	0.13	0.60	0.56
ZK418.9	0.79	1.55	0.76	SRM	0.20	0.57	0.69
ZK616.4	0.55	1.20	1.38	SRM	0.39	0.92	1.29

MIRZA non-canonical targets	MIRZA score non-canonical sites	miRNA	log2 fold change protein (*mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1; mir-81-82* / WT)	Protein quantification method	log2 fold change mRNA (*mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1; mir-81-82* /
hmg-3	55.04	cel-miR-82	0.45	0.27	0.52	SILAC unfractionated	-0.50	0.65	0.72
alg-1	51.56	cel-miR-80	0.25	0.27	0.33	SILAC unfractionated	0.33	0.31	0.47
his-41	46.32	cel-miR-80	0.17	0.46	0.68	SILAC fractionated	0.65	1.42	2.13
K07H8.3	40.83	cel-miR-80	-0.26	-0.07	-0.20	SILAC unfractionated	-0.08	-0.05	-0.12
mlc-3	38.28	cel-miR-80	0.22	-0.02	-0.10	SILAC fractionated	0.03	-0.20	-0.40
C15C7.5	31.81	cel-miR-80	-0.41	-0.76	-0.46	SILAC unfractionated	-0.35	-0.66	-0.48
C56G2.7	30.93	cel-miR-80	-0.01	0.42	-0.03	SILAC unfractionated	-0.05	-0.13	-0.06
mec-7	29.23	cel-miR-82	0.51	0.30	0.47	SILAC unfractionated	0.45	0.27	0.27
F48E3.3	28.45	cel-miR-80	-0.06	-0.15	-0.14	SILAC unfractionated	0.18	-0.12	-0.28
lin-53	28.05	cel-miR-81	0.26	0.31	0.42	SILAC unfractionated	0.28	0.42	0.50
mrg-1	26.92	cel-miR-80	0.34	0.61	0.57	SILAC unfractionated	0.23	0.63	0.76
dcap-1	26.33	cel-miR-80	0.43	0.27	0.44	SILAC unfractionated	0.01	0.24	0.41
lst-3	26.14	cel-miR-80	0.62	0.85	1.15	SILAC unfractionated	-0.02	0.45	0.51
cyn-7	25.13	cel-miR-80	-0.29	0.14	0.15	SILAC fractionated	-0.21	-0.05	-0.09
mcm-2	23.38	cel-miR-82	-0.20	0.12	0.40	SILAC unfractionated	0.32	0.78	0.74
K10D3.4	23.02	cel-miR-82	-0.05	-0.21	-0.13	SILAC unfractionated	0.59	0.70	0.60
dnj-11	22.42	cel-miR-80	-0.31	-0.07	-0.20	SILAC unfractionated	0.00	0.22	0.12
cpf-2	22.12	cel-miR-80	0.35	0.39	0.77	SILAC unfractionated	-0.07	0.30	0.50
nas-37	21.41	cel-miR-82	-0.05	-0.05	-0.13	SILAC unfractionated	0.69	0.76	0.51
icd-1	21.39	cel-miR-80	0.25	0.48	0.12	SILAC fractionated	0.07	0.02	0.35
F13C5.2	20.48	cel-miR-80	1.07	0.61	1.17	SILAC unfractionated	0.10	0.12	0.40
F58B3.6	20.08	cel-miR-80	0.66	0.63	0.50	SILAC unfractionated	0.42	0.45	0.77
lpr-4	19.11	cel-miR-58	0.44	0.10	-0.30	SILAC unfractionated	0.69	1.13	1.21
hmg-4	18.76	cel-miR-80	0.45	0.27	0.52	SILAC unfractionated	0.46	0.89	1.11
C25A1.4	18.14	cel-miR-80	-0.43	-0.03	-0.15	SILAC unfractionated	-0.02	0.24	0.28
emb-5	17.59	cel-miR-80	-0.35	-0.08	0.23	SILAC unfractionated	0.50	0.73	0.80
lam-2	17.42	cel-miR-58	0.36	0.26	0.51	SILAC unfractionated	0.52	0.69	0.56
his-24	17.29	cel-miR-80	0.83	0.30	1.00	SILAC unfractionated	0.01	1.16	1.27
C05G5.4	17.21	cel-miR-80	-0.04	0.13	0.22	SILAC fractionated	0.05	-0.09	-0.21
B0495.7	17.12	cel-miR-80	-0.24	-0.12	-0.24	SILAC fractionated	-0.06	-0.25	-0.28
math-33	16.49	cel-miR-82	0.30	0.35	0.23	SILAC unfractionated	0.30	0.69	0.74
myo-2	15.64	cel-miR-80	0.24	0.03	0.06	SILAC fractionated	0.19	0.27	0.10
H34C03.2	15.33	cel-miR-58	-0.21	-0.25	-0.31	SILAC unfractionated	0.23	0.47	0.38
mbf-1	14.99	cel-miR-82	-0.42	-0.17	-0.05	SILAC unfractionated	-0.28	-0.34	-0.23
abcf-2	14.95	cel-miR-58	-0.20	-0.09	-0.33	SILAC unfractionated	0.23	0.38	0.67
csn-4	14.43	cel-miR-80	-0.10	0.49	0.42	SILAC unfractionated	0.05	0.16	0.17
ile-2	14.43	cel-miR-82	0.03	-0.28	-0.26	SILAC unfractionated	-0.11	-0.27	-0.27
nex-2	13.60	cel-miR-80	0.24	0.44	0.51	SILAC unfractionated	0.35	0.81	1.32
F37C4.5	13.45	cel-miR-80	0.17	0.23	0.29	SILAC fractionated	-0.24	-0.04	0.16
F09G2.9	13.09	cel-miR-80	0.13	0.43	0.06	SILAC unfractionated	-0.27	0.16	0.26
H13N06.4	12.99	cel-miR-58	0.21	0.71	0.90	SILAC unfractionated	0.23	0.44	0.49
elb-1	12.97	cel-miR-80	0.08	-0.12	-0.20	SILAC unfractionated	-0.01	-0.04	0.04

MIRZA non-canonical targets	MIRZA score non-canonical sites	miRNA	log2 fold change protein (*mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1; mir-81-82* / WT)	Protein quantification method	log2 fold change mRNA (*mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1; mir-81-82* /
F33D11.10	12.65	cel-miR-80	0.05	0.15	0.29	SILAC unfractionated	0.38	0.59	0.74
H17B01.4	12.14	cel-miR-82	0.66	0.15	0.50	SILAC unfractionated	0.12	0.27	0.22
C18B2.5	12.13	cel-miR-80	0.32	-0.28	-0.13	SILAC unfractionated	0.10	-0.43	-0.37
F30H5.3	12.00	cel-miR-80	-0.14	-0.55	-0.40	SILAC unfractionated	0.50	0.59	0.60
K12H4.3	11.93	cel-miR-82	-0.24	-0.37	-0.40	SILAC unfractionated	0.12	-0.03	-0.02
eif-6	11.82	cel-miR-80	-0.11	-0.01	-0.18	SILAC fractionated	-0.17	-0.18	-0.17
emb-4	11.51	cel-miR-80	0.32	0.16	0.41	SILAC unfractionated	0.36	0.57	0.41
mpk-1	11.27	cel-miR-58	1.15	1.03	0.71	SILAC unfractionated	0.26	0.61	0.72
haf-9	11.09	cel-miR-82	0.09	-0.03	0.18	SILAC unfractionated	0.19	-0.36	-0.43
ftt-2	10.94	cel-miR-80	0.42	0.36	0.49	SILAC fractionated	0.23	0.19	0.34
grd-14	10.94	cel-miR-80	-0.38	-0.23	0.66	SILAC unfractionated	-0.50	-0.87	-1.22
gst-1	10.90	cel-miR-81	0.07	0.00	0.22	SILAC unfractionated	0.16	0.12	0.18
nmt-1	10.73	cel-miR-82	0.32	0.34	0.11	SILAC fractionated	-0.02	0.04	0.02
hum-4	10.38	cel-miR-80	-0.21	-0.02	-0.12	SILAC unfractionated	0.59	0.26	0.03
ifd-1	10.19	cel-miR-58	0.35	-0.06	0.20	SILAC unfractionated	0.37	-0.67	-0.67
F58G11.2	10.06	cel-miR-80	0.02	0.29	0.52	SILAC unfractionated	0.25	0.71	1.00

ALG-1 bound targets	Sequence read number miRNA:mRNA chimeras	log2 fold change protein (*mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1* / WT)	log2 fold change protein (*mir-80; mir-58.1; mir-81-82* / WT)	Protein quantification method	log2 fold change mRNA (*mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1* / WT)	log2 fold change mRNA (*mir-80; mir-58.1; mir-81-82* / WT)
alg-1	10	0.25	0.27	0.33	SILAC unfractionated	0.33	0.31	0.47
cts-1	6	0.15	0.27	0.26	SILAC fractionated	0.11	0.10	-0.04
dnj-20	6	0.47	0.73	0.62	SILAC unfractionated	0.71	1.18	1.12
eef-1A.2	17	-0.03	0.16	0.13	SILAC fractionated	NA	NA	NA
F44E5.4	48	-0.05	0.06	0.16	SILAC fractionated	NA	NA	NA
F57B10.3	8	-0.20	-0.26	0.02	SILAC fractionated	0.33	0.02	-0.05
gei-7	6	0.05	-0.33	-0.72	SILAC fractionated	0.32	0.51	0.58
gpd-2	44	0.29	0.42	0.33	SILAC fractionated	0.36	0.46	0.48
gpd-3	7	0.29	0.42	0.33	SILAC fractionated	0.20	-0.04	-0.20
gst-1	14	0.01	0.24	0.39	SILAC fractionated	0.16	0.12	0.18
his-24	6	0.83	0.30	1.00	SILAC unfractionated	0.01	1.16	1.27
hmg-1.1	9	0.23	0.58	0.88	SILAC unfractionated	-0.01	0.55	0.97
inf-1	6	0.08	0.06	0.20	SILAC unfractionated	-0.01	-0.15	-0.30
R05G6.7	6	0.14	0.21	0.31	SILAC fractionated	-0.05	-0.21	-0.30
T21C9.3	7	0.26	0.25	0.74	SILAC unfractionated	0.21	0.31	0.16
ubq-1	8	0.16	0.16	0.32	SILAC fractionated	0.29	0.60	0.77
clec-1	62	NA	NA	NA	NA	0.25	1.10	2.52
B0361.9	11	NA	NA	NA	NA	0.48	0.73	2.14
nhr-19	6	NA	NA	NA	NA	0.62	0.81	1.39
lin-1	6	NA	NA	NA	NA	0.47	1.00	1.34
K02D7.5	7	NA	NA	NA	NA	0.17	0.90	1.27
mnk-1	11	NA	NA	NA	NA	0.50	0.97	1.21
nipi-3	9	NA	NA	NA	NA	0.58	0.57	1.13
C39E9.8	7	NA	NA	NA	NA	0.01	0.18	1.09
cki-2	6	NA	NA	NA	NA	-0.10	0.69	1.02
F46G10.2	6	NA	NA	NA	NA	0.33	0.65	1.01
C06G8.1	6	NA	NA	NA	NA	0.61	1.57	0.98
lgg-1	7	NA	NA	NA	NA	0.14	0.41	0.91
C50B8.1	10	NA	NA	NA	NA	0.03	0.59	0.88
ZK470.2	25	NA	NA	NA	NA	0.23	0.61	0.88
W09D10.4	6	NA	NA	NA	NA	0.45	0.66	0.67
epc-1	7	NA	NA	NA	NA	0.32	0.54	0.60
F55H12.2	20	NA	NA	NA	NA	-0.40	0.20	0.59
F57G12.1	12	NA	NA	NA	NA	0.57	0.38	0.53
mdl-1	7	NA	NA	NA	NA	0.26	0.30	0.50
F18E3.11	39	NA	NA	NA	NA	-0.26	0.56	0.38
col-98	12	NA	NA	NA	NA	0.08	0.51	0.36
ZK822.5	7	NA	NA	NA	NA	0.23	0.34	0.21
F18E3.12	48	NA	NA	NA	NA	-0.80	0.35	0.21
F18E3.13	97	NA	NA	NA	NA	-0.16	0.38	-0.11
B0410.3	8	NA	NA	NA	NA	-0.41	-0.69	-1.24

i) Top scoring MIRZA predicted miRNA:mRNA hybrids for non-canonical miR-58 family targets (MIRZA score> 10)

MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid	MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid
hmg-3	cel-miR-82	55.044	UGAGAUCAUCGUGAAAGCCAG #||||||OOO^^||||OOOO| tctctagata--ctttcattc	B0495.7	cel-miR-80	17.1218	UGAGA-UCAUUAGUUGAAAGCC |||||v|||O^^^^^^||||## actcttagtg------tttctt
alg-1	cel-miR-80	51.5597	UGA--GAUCAUU------AGUUGAAAGCC |||vv|||||OOvvvvvv||||||^||## actgtctagttcgggcattcaact-tctt	math-33	cel-miR-82	16.4945	UGAGA-----UCAUCGUG-AAAGCCAG |||||vvvvv|||OOOOOv|||||### actctttgttagtatattgtttcgtca
his-41	cel-miR-80	46.3171	UGAGAUCAUUAGUUGAAAGCC #|||||||^^^^^||||||### tctctag-----aacttttat	myo-2	cel-miR-80	15.6359	UGAG---------AUCAUUAGUUGAAAGCC ||||vvvvvvvvv||||O^^||||^||## actcttcacagcttagtt---aact-tcgt
K07H8.3	cel-miR-80	40.8287	UGAGAUCAUUAGUUGAAAGCC #||||||OOOO^^||||||## tctctaggagg--actttccc	H34C03.2	cel-miR-58.1	15.3293	UGAGA-UCGUUCAGUACGGCAA #||||v|||OOOOO|||OOO^| cctcttagcaaaggatgggc-t
mlc-3	cel-miR-80	38.2805	UGAGAUCAUUAGUUGAA--AGCC |||||||OOOOOOOOOOvv||## actctaggttataaatgaatctg	mbf-1	cel-miR-82	14.9852	UGAGAU---CAUCGUGAAAGCCAG #|||||vvv||O^^^||||OOOO| tctctatgggtt---cttttgtcc
C15C7.5	cel-miR-80	31.808	UGA--GAUCAUUAGUUGAAAGCC #||vv|||||OOOO||||||### gcttgctagtttcgaacttttct	abcf-2	cel-miR-58.1	14.9544	UGAGAUCGUUCAGUACGGCAA #|||||OOOOOOOOOOOOOO| cctttatccttattcttttgt
C56G2.7	cel-miR-80	30.9346	UGAGAUCAUUAGUUGAA----AGCC |||||||OO^^^^|||Ovvvv||## actctaggt----actcgagctcaa	csn-4	cel-miR-80	14.4302	UGAGA--UCAUUAGUUGAAAGCC |||||vv|||OOO^^^||||### actctaaagtgtt---ctttttt
mec-7	cel-miR-82	29.2335	UGAGAUCAUCGUGAAAGCCA--G |||||||OOOOO||||OOOOvv| actttaggggtactttttttttc	ile-2	cel-miR-82	14.4301	UGAG----AUCAUCGUGAAAGCCAG ||||vvvv||||O^^^^|||OO||# actcattttagtt----ttttagtg
F48E3.3	cel-miR-80	28.4489	UGAGA-UCAUUAGUUGAAAGCC |||||v|||OOOOOOOO^||## actctcagtagtaaaag-tctt	nex-2	cel-miR-80	13.5975	UGAGAU--CAUUAG----UUGAAAGCC ||||||vv||OOOOvvvv||||||### actctaacgtacaacaataatttttac
lin-53	cel-miR-81	28.0462	UGAGAU-CAUCGUGAAAGCUAG ||||||v||^^^^^|||O^||# actctacgt-----ttta-att	F37C4.5	cel-miR-80	13.4549	UGAGAUCAUUAGUUGAAAGCC ##||||||OOOO^^^||||## tgtctagttcaa---tttcgc
mrg-1	cel-miR-80	26.9247	UGAGA-UCAUUAGUUGAAAGCC |||||v|||OOOOOOOO^||## actcttagtataagtaa-tctt	F09G2.9	cel-miR-80	13.0886	UGAGAUCAUUAGUUGAAAGCC ||||||OOOOOOOOOO||||## actctaactaaatcttttctg

MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid	MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid

dcap-1	cel-miR-80	26.3301	`UGAG--AUCAUUAGUUGAAAGCC`
			`||||vv||||OOOOOOOOO||##`
			`actctatagtagttatccctctg`
				H13N06.4	cel-miR-58.1	12.9886	`UGAGAUCGUUCAGUACGGCAA`
							`#||||||OOO^^^^||||###`
							`gctctagact----tgcctta`

lst-3	cel-miR-80	26.1385	`UGAGAUCAUUAGUUGAAAGCC`
			`##|||||||||O|||O^||##`
			`tatctagtaattaaca-tctc`
				elb-1	cel-miR-80	12.9747	`UGAGAUCAUUAGUUGAA-AGCC`
							`#||||||OOOOO|||OOv||##`
							`tctctagatgagaacacctcgg`

cyn-7	cel-miR-80	25.1288	`UGA-GAUCAUUAGUUGAAAGCC`
			`|||v|||||OOO^^|||||###`
			`actactagttct--actttttc`
				F33D11.10	cel-miR-80	12.6517	`UGAGAUCAUUAGUUGAAAGCC`
							`#|||||||O^^^^|||O^||##`
							`cctctaga----aaca-tcct`

mcm-2	cel-miR-82	23.3802	`UGAG-AUCAUC------GUGAAAGCCAG`
			`||||v||||OOvvvvv||||||OOOO|`
			`actcatagtcttcgtgccacttttagcc`
				H17B01.4	cel-miR-82	12.1383	`UGAGAUCAUCGUGAAAGCCAG`
							`||||||OOOO^^^|||OOO^|`
							`actctaaaag---tttacc-c`

K10D3.4	cel-miR-82	23.015	`UGAGAUCAUCGUGAAAGCCAG`
			`||||||OOO^^^||||OO^^|`
			`actctaccg---cttttt--c`
				C18B2.5	cel-miR-80	12.1282	`UGAGAUCAUUAGUUGAAAGCC`
							`#|||||OOOO^^|||||||###`
							`cctctaattt--aactttgg-`

dnj-11	cel-miR-80	22.4172	`UGAGAUCAUUAGUUGAAAGCC`
			`#|||||OO^^^^|||||||###`
			`gctctatg----aactttgct`
				F30H5.3	cel-miR-80	12.004	`UGAGAU----------------CAUUAGUUGAAAGCC`
							`#|||||vvvvvvvvvvvvvvvv||OOOO|||||||##`
							`tctctacgtttttgtccagtagtgtaacaaactttctt`

cpf-2	cel-miR-80	22.1156	`UGAGAUCAUUAG----UUGAAAGCC`
			`#||||||OOOOOvvvv||||^^^^|`
			`gctctaggtataaatgaact----g`
				K12H4.3	cel-miR-82	11.9265	`UGAGAUCAUCGUGAAAGCCAG`
							`||||||OO^^^^^|||OO||#`
							`actctatt-----ttttagtt`

nas-37	cel-miR-82	21.4144	`UGAG----AUCAUCGUGAAAGCCAG`
			`||||vvvv||||OOOOOOOOOOO^|`
			`actcgttatagtttgcacacccc-c`
				eif-6	cel-miR-80	11.8163	`UG--AGAUCAUUAGUUGAAAGCC`
							`||vv||||||OOOOOOO^^||##`
							`accatctagtttttttta--tcac`

icd-1	cel-miR-80	21.3939	`UGAGA-UCAUUAGUUGAAAGCC`
			`#||||v|||^^^^|||||||###`
			`tctctaagt----aactttag-`
				emb-4	cel-miR-80	11.508	`UGAGAUCAUUAGUUGAA-AGCC`
							`##|||||||OOOO||||Ov||##`
							`--tctagtattaaactactctc`

F13C5.2	cel-miR-80	20.4756	`UGAGA-UCAUUAGUUG-AAAGCC`
			`|||||v|||OOOOOOOv||||##`
			`actctaagtattatgttttttc--`
				mpk-1	cel-miR-58.1	11.2676	`UGAGAUCGUUCAGUACGGCAA`
							`#||||||OOOOOOOOOOOO|`
							`cctctagggtgtatcctactt`

MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid	MIRZA non-canonical target	miRNA	MIRZA score non-canonical sites	miRNA:mRNA hybrid

F58B3.6	cel-miR-80	20.0799	`UGAGAUCAUUAG----------UUGAAAGCC`
			`##|||||||OOOOvvvvvvvvvv|||||||##`
			`aatctagtcgttatattagtattaactttctc`
				haf-9	cel-miR-82	11.0937	`UGAGAUCAUCGUGAAAGCCAG`
							`##|||||||O^^^||||^^||#`
							`tatctagtt---cttt--gta`

lpr-4	cel-miR-58.1	19.1121	`UGAGAUCGUUCA-GUACGGCAA`
			`#||||||OOOOOOv||||||||##`
			`gctctactgtcagcatgccgcg`
				ftt-2	cel-miR-80	10.9392	`UGAGAUCAUUAGUUGAAAGCC`
							`#||||||^^^^^^|||||||##`
							`gctcta------aactttccc`

hmg-4	cel-miR-80	18.7634	`UGAGA---UCAUUAG--UUGAAAGCC`
			`|||||vvv|||OOOOvv||||OOOO|`
			`actctataagtctgttgaactctatg`
				grd-14	cel-miR-80	10.9377	`UGAGAUCAUUAGUUGAAAGCC`
							`#|||||||OOO^^||||||###`
							`tttctagaac--aacttttca`

C25A1.4	cel-miR-80	18.1354	`UGAGAUCAUUAGUUGAA-AGCC`
			`||||||OOOO^^||||Ov||##`
			`actctaaggc--aactgttcct`
				gst-1	cel-miR-81	10.8979	`UGAGA-UCAUCGUGAAAGCUAG`
							`#||||v|||OOOO^^|||||##`
							`tctctaagtaacc--ttcgaaa`

emb-5	cel-miR-80	17.5873	`UGAGAUCAUUAGUUGAAAGCC`
			`##|||||||OOO^||||O||##`
			`aatctagtagc-aactatctg`
				nmt-1	cel-miR-82	10.7266	`UGAGAU----CAUCGU-GAAAGCCAG`
							`#|||||vvvv||OOOOv||||^^^^|`
							`cctctatatagtttttgcttt----c`

lam-2	cel-miR-58.1	17.4233	`UGAGA--UCGUUCAGUACGGCAA`
			`|||||vv|||OOOOOOOOOO^^|`
			`actctaaagcctattgtttt--t`
				hum-4	cel-miR-80	10.3795	`UGAGAUCAU----------UAGUUGAAAGCC`
							`||||||OOOvvvvvvvvvv||||||||||##`
							`actctacttcaatacttatatcaattttcga`

his-24	cel-miR-80	17.292	`UGAGAUCAUUAGUUGAAAGCC`
			`#||||||OOOOOOOOOO^||##`
			`cctctaggctattcaa-tcta`
				ifd-1	cel-miR-58.1	10.1916	`UGAG-AUCGUUCAGUACGGCAA`
							`#|||v||||O^^^|||OOOO^|`
							`gctcgtagcg---cattgtt-t`

C05G5.4	cel-miR-80	17.2105	`UGAGA--UCAUUAG----UUGAAAGCC`
			`#||||vv|||OOOOvvvv||||||###`
			`tctcttcagtatctttataactttaat`
				F58G11.2	cel-miR-80	10.0617	`UGA--GAUCAUUAG----UUGAAAGCC`
							`|||vv|||||OOOOvvvv||||O|###`
							`actaactagtacggtcttaactattaa`

ii) Alternative MIRZA predicted miRNA:mRNA hybrids for non-canonical miR-58 family targets (when applicable)

MIRZA non-canonical target	MIRZA score non-canonical sites	miRNA	Top scoring miRNA:mRNA hybrid (MIRZA score > 10)	Alternative miRNA:mRNA hybrid with the highest MIRZA score	Target / miRNA / MIRZA score	MIRZA non-canonical target	Alternative miRNA:mRNA hybrid with the highest MIRZA score	Target / miRNA / MIRZA score	Alternative miRNA:mRNA hybrid with the highest MIRZA score	Target / miRNA / MIRZA score
mec-7	29.2335	cel-miR-82	UGAGAUCAUCGUGAAAGCCA--G ||||||||OOOOO||||OOOOvv| actttaggggtactttttttttc	UGA------GAUCGUUCAGUACGGCAA |||vvvvvv|||||OOOOOO^^^^^| actatattgttagctagttta------t	mec-7 cel-miR-58.1 0.16822	mec-7				
lin-53	28.0462	cel-miR-81	UGAGAU-CAUCGUGAAAGCUAG ||||||v||^^^^|||O^||# actctacgt-----ttta-att	UGAGAU---CAUUAG-UUGAAAGCC ||||||vvv||OOOv||||##### attctacttgttaaacaact-----	lin-53 cel-miR-80 0.341033	lin-53				
dcap-1	26.3301	cel-miR-80	UGAG--AUCAUUAGUUGAAAGCC ||||vv||||OOOOOOOOO||## actctatagtagttatccctctg	UGAGAUCAUCGUGAAAGCUAG #|||||OO^^^^||||O^||# tttttacc----cttta-att	dcap-1 cel-miR-81 1.60599	dcap-1	UGAGAUCGUUCAGUACGGCAA #|||||OOOOOOOOO^^||## cttttaaaaacctcc--cgcc	dcap-1 cel-miR-58.1 1.41632	UGAGAUCAUCGUGAAAGCCAG #||||OOOOO^||||OOOO| tttttatctcc-cttttaccc	dcap-1 cel-miR-82 1.28703
lst-3	26.1385	cel-miR-80	UGAGAUCAUUAGUUGAAAGCC ##||||||||O|||O^||## tatctagtaattaaca-tctc	UGAGAUCGUUCAG-------UACGGCAA ##|||OOOOOOOvvvvvvv||||### aatctatataataccaataaatgccctg	lst-3 cel-miR-58.1 0.0257718	lst-3				
mcm-2	23.3802	cel-miR-82	UGAG-AUCAUC------GUGAAAGCCAG ||||v||||OOvvvvvv||||||OOOO| actcatagtcttcgtgccactttttagcc	UGAGAUCAUUAGUUGAAAGCCAG #|||||OO^^^|||O^^^| cttttagag---aactt---g	mcm-2 cel-miR-80 0.363683	mcm-2				
F13C5.2	20.4756	cel-miR-80	UGAGA-UCAUUAGUUG--AAAGCC |||||v||OOOOOOOv||||## actctaagtattatgtttttc--	UGAGAU-CAUUAGUUGAA---AGCC #|||||v||OOOO|||OOvvv||## tctctacgtatgtaaccaggttcaa	F13C5.2 cel-miR-58.1 3.1463	F13C5.2	UGAGAU------CAUCGUGAAAGCUAG #||||vvvvv||O^^^||||### cttttaacaaatgtt----tttcgccg	F13C5.2 cel-miR-81 1.22755		
F58B3.6	20.0799	cel-miR-80	UGAGAUCAUUAG-----------UUGAAAGCC ##||||||OOOOvvvvvvvvvvvv||||||## aatctagtcgttatattagtattaactttctc	UGA----GAU---CAUCGUGAAAGCUAG #||vvvv|||vvv||OO^^||||OOO^| gctttcactgattgtta--cttttt-c	F58B3.6 cel-miR-81 0.878157	F58B3.6				
hmg-4	18.7634	cel-miR-80	UGAGA---UCAUUAG--UUGAAAGCC |||||vvv|||OOOOvv||||OOOO| actctataagtctgttgaactctatg	UGAG----AUCAUCGUGAAAGCUAG #|||vvvv|||O^^^|||OO||# tttcacgttagtt----ttttaatt	hmg-4 cel-miR-81 0.705916	hmg-4	UGAGAUCAUCGUGAAAGCCAG ##|||||^^^^^^^^^^|||# agtctag----------gta	hmg-4 cel-miR-82 0.191638		
lam-2	17.4233	cel-miR-58.1	UGAGA--UCGUUCAGUACGGCAA |||||vv||OOOOOOOOO^||| actctaaagcctattgtttt--t	UGA---GAUCAUCGUGAAAGCUAG #||vvv|||^^^^||||^^^^^|||| tcttaattagt-----ttt-gatt	lam-2 cel-miR-81 1.67266	lam-2	UGA----------GAUCAUUAGUUGAAAGCC ||||vvvvvvvvv||||^^^^^^^^^||||## actcggttgttaactagt---------tcag	lam-2 cel-miR-80 0.83327	UGAGAUCAUCGUGAAAGCCAG #||||OOOOO^||||OOOO| gttttattatc-cttttctt-c	lam-2 cel-miR-82 0.175276
his-24	17.292	cel-miR-80	UGAGAUCAUUAGUUGAAAGCC #|||||OOOOOOOOOv|||# ccctctaggctattcaa-tcta	UGAGAUCGUUCAG--UACG-GCAA ||||||OOOOOOO|||Ov|||# actctatttattaatatggtcgta	his-24 cel-miR-58.1 4.81441	his-24	UGAGAUCAUCGUGAAAGCCAG #|||||OO^^^^|||||# tctttaac----cttt--gtt	his-24 cel-miR-82 0.523238	UGAGA---------UCAUCGUG--AAAGCUAG #||||vvvvvvvvv|||OOOOOvv|||OOO^| cttctgcaacttgcagtttaatagtttaaa-c	his-24 cel-miR-81 0.140715
H13N06.4	12.9886	cel-miR-58.1	UGAGAUCGUUCAGUACGGCAA #|||||OOOO^^^|||OOO^^| gctctagact----tgcctta	UGAGAUCAUCGUG-AAAGCUAG ||||||OOOOOOv|||OO^^| actctattctcctatttaa--c	H13N06.4 cel-miR-81 3.85628	H13N06.4	UGA-------GAUCAUCGUG-GAAAGCCAG ||||vvvvvvvv|||||OOOOOv|||OOO^^| actgcaaggcctagtaacctcttacg--c	H13N06.4 cel-miR-82 2.58301	UGAGAUCAUUAGUUGAAAGCC #|||||O^^^^|||||### cttctagg----aacttaaaa	H13N06.4 cel-miR-80 1.54697
H17B01.4	12.1383	cel-miR-82	UGAGAUCAUCGUGAAAGCCAG ||||||OOOO^^^||||OOO^| actctaaaag---tttacc-c	UGAGAUCAUCGUGAAAGCCAG #|||||OOOO^^^||||O^||# tctctatata---ttta-ata	H17B01.4 cel-miR-81 1.35559	H17B01.4	UGAG----------AUCAUUAGU-----UGAAAGCC ||||vvvvvvvvvv||||OOOOOvvvvv||||### acttgagcgttaaatagtgaaaaaccttacttttg	H17B01.4 cel-miR-80 0.228888		
ftt-2	10.9392	cel-miR-80	UGAGAUCAUCGUGAAAGCC #|||||^^^^^^||||||## gctccta------aacttccc	UGAGAUCAUCGUGAAAGCCAG #||||OOO^^^|||^^^||# tttttgtgg---ctt--att	ftt-2 cel-miR-81 1.53322	ftt-2	UGA--GAUCGUUCAGUACGGCAA |||vv||||OOO^^^^^^^^^^| actgtctagaaa----------t	ftt-2 cel-miR-58.1 1.18347	UGAGAUCAUCGUG-AAAGCCAG ##||||||OOOOOv|||OO^| tatttagtatactgtttat--c	ftt-2 cel-miR-82 1.12156
csn-4	14.4302	cel-miR-80	UGAGA---UCAUUAGUUGAAAGCC |||||vv|||OOO^^^||||### actctaaagtgtt---ctttttt	UGAGA----UCAUCGU----GAAAGCUAG #||||vvv||OOOOOvvvv||||##### gctcttaaagcttaaaaagctttttttt	csn-4 cel-miR-81 1.94029	csn-4	UGAGAUCGUUCAGUACGGCAA #|||||OOOOOOOOOO^^^| cttttaggccaaaaatt---t	csn-4 cel-miR-58.1 1.60575		
emb-4	11.508	cel-miR-80	UGAGAUCAUUAGUUGAAA-AGCC ##||||||OOOO||||Ov||## --tctagtattaaactactctc	UGAGAUCAUCGUGAAAGCUAG #||||||OOOO^||||OO||## tttttagcatc-cttttaagt	emb-4 cel-miR-81 1.43055	emb-4	UGAGAU--CAUCGUGAAAGCCAG #|||||vv||^^^^||||OOOO| cttttaacgt----cttttttagc	emb-4 cel-miR-82 1.19488		
grd-14	10.9377	cel-miR-80	UGAGAUCAUUAGUUGAAAGCC #|||||OOO^^||||||### tttctagaac--aacttttca	UGA--GAUCGUUCAGUACGGCAA #||vv|||OOOOOOOOOO^|||| cctcactacttgtcaaaa-cgtt	grd-14 cel-miR-58.1 1.13811	grd-14				

Supplementary Table 2. Categorization of TargetScan predicted targets in seven groups based on differential mRNA abundance in *mir-58.1*, *mir-80; mir-58.1* and *mir-80; mir-58.1; mir-81-82* mutants relative to wild-type

Target category	Target number
Additively upregulated targets	93
Synergistically upregulated targets	19
Shared miR-58.1, miR-80 targets	34
Shared miR-58.1, miR-81, miR-82 targets	47
Shared miR-80, miR-81, miR-82 targets	79
miR-58.1 specific targets	24
miR-80 specific targets	17
miR-81, miR-82 targets	12
Total targets > 1.3 fold upregulated in *mir-80; mir-58.1; mir-81-82*	325
Non-responsive predicted targets < 1.3 fold upregulated in *mir-80; mir-58.1; mir-81-82*	270

Full table can be accessed in the supplementary online material.

Supplementary Table 3. Comparison of differential protein and mRNA expression of 63 TargetScan predicted targets identified by unfractionated SILAC, fractionated SILAC, SRM and transcriptome profiling in *mir-58.1*, *mir-80; mir-58.1* and *mir-80; mir-58.1; mir-81-82* mutants relative to wild-type.

Targets are grouped based on the response of protein and RNA levels in the respective mutants to those that are regulated at the level of translational inhibition and mRNA degradation. Protein and mRNA abundance data are normalized to a group of 518 non-targets identified in three replicates of unfractionated SILAC experiment for which mRNA abundance was obtained.

Category	Differential expression boundaries	Target number in *mir-58.1*	Target number in *mir-80; mir-58.1*	Target number in *mir-80; mir-58.1; mir-81-82*
1	log2 fold change protein > 0.05, log2 fold change mRNA < 0.05	10	1	2
2	log2 fold change protein (P) > log2 fold change mRNA (R); P, R > 0	18	20	15
3	log2 fold change protein = log2 fold change mRNA (0.1 fold tolerance)	14	12	10
4	log2 fold change mRNA > log2 fold change protein	11	26	30
5	log2 fold change protein, log2 fold change mRNA < 0.05	5	1	1
6	NA	5	3	5

Differential expression boundaries	Target response in *mir-58.1* (%)	Target response in *mir-80; mir-58.1* (%)	Target response in *mir-80; mir-58.1; mir-81-82* (%)
log2 fold change protein (P) > log2 fold change mRNA (R)	48.28	35.00	29.31
Translational Inhibition (P > 0.05, R < 0.05)	17.24	1.67	3.45
Concordant protein and mRNA (P=R)	24.14	20.00	17.24
log2 fold change protein (P) < log2 fold change mRNA (R)	18.97	43.33	51.72

Full table can be accessed in the supplementary online material.

Supplementary Table 4. Differential expression comparing 1) abundances of all quantified proteins in unfractionated SILAC, fractionated SILAC and SRM, 2) abundances of all transcripts quantified in transcriptome profiling experiment and qRT-PCR and 3) abundances of all small RNAs quantified in small RNA profiling experiment, between miR-58 family mutants and wild-type

Full table can be accessed in the supplementary online material.

Supplementary Table 5. Primers used for miR-58 family target and *egl-1* induction qRT-PCR and miRNA qRT-PCR experiments

Gene public name	Gene sequence name	Group	Primer_forward	Sequence Forward	Primer_reverse	Sequence Reverse
bcs-1	F54C9.6	Random	F54C9.6_F	gaaaggacacttgatgatgacaga	F54C9.6_R	tgtcctccaggatcacaaca
R12E2.11	R12E2.11	Random	R12E2.11_F	tgccaatctcgcagaagata	R12E2.11_R	tcggtcatctcgttttttcgt
F28A12.4	F28A12.4	Random	F28A12.4_F	gggacattgggaattgacac	F28A12.4_R	tcttttgggctccatttgaa
pmt-2	F54D11.1	Random	F54D11.1_F	cgagaagctttctcaagaatctataa	F54D11.1_R	ccatacattgtgatgagcacct
F32D1.5	F32D1.5	Random	F32D1.5_F	cttcgctggacacgatca	F32D1.5_R	ctcattccgtagaacaatttgaac
rps-10	D1007.6	Random	D1007.6_F	gctcttccagctgagatcgt	D1007.6_R	tctcccttctcgccttgag
C48B4.8	C48B4.8	Random	C48B4.8_F	gatgatggacgatttgtaattgtt	C48B4.8_R	ggattatggacagaatgacgtg
F45H10.2	F45H10.2	Random	F45H10.2_F	cctacgtctgggatcagtgg	F45H10.2_R	ggctggattctttcggttg
F13G3.10	F13G3.10	Random	F13G3.10_F	aaacaacaggtggacaaacaca	F13G3.10_R	catctttctcttctctagtgtcggata
Y69E1A.2	Y69E1A.2	Random	Y69E1A.2_F	gagaacctgtcatgggtcgt	Y69E1A.2_R	ttcgttattgaaccacgagaag
smg-4	F46B6.3a	Random	F46B6.3a_F	ccgaagtcagctccaatga	F46B6.3a_R	gccgtgtatcggtttcctta
F39H2.3	F39H2.3	Random	F39H2.3_F	aaaaatatgaaaatttgcgacga	F39H2.3_R	tgagcagatcaccgtttgc
crn-1	Y47G6A.8	Random	Y47G6A.8_F	cgattcttgagaatatcgatcaaa	Y47G6A.8_R	tcacgagcacgcttgtatg
ran-1	K01G5.4	Random	K01G5.4_F	ttgactggagagttcgagaaga	K01G5.4_R	tgtggaagacaagtgggtga
F17C8.3	F17C8.3	Random	F17C8.3_F	gtcgtttggagagtgaactgg	F17C8.3_R	cttttccatttcttgcttgagaa
Y66H1A.4	Y66H1A.4	Random	Y66H1A.4_F	ccaccagaggaagttgtgct	Y66H1A.4_R	gcaaacaatatcatcttggcact
F35G12.2	F35G12.2	Random	F35G12.2_F	ctcatattcggcgactttctg	F35G12.2_R	acgttgctcgacatcttgttt
elo-1	F56H11.4	Random	F56H11.4_F	aaccattgccaacaaaggaa	F56H11.4_R	tggtgtcaacaagttcgaaaag
cey-1	F33A8.3	Random	F33A8.3_F	aatggccgagaaaaacgac	F33A8.3_R	tttgtagccttcactggcttg
dad-1	F57B10.10	Random	F57B10.10_F	ctcgtcggtacattcccatt	F57B10.10_R	acttgcatcctgagacacga
C32E8.3	C32E8.3	Random	C32E8.3_F	ctggaaagaacttcgacaagtg	C32E8.3_R	gtcgaaagtggccttcttttt
col-167	T10E10.2	Random	T10E10.2_F	aggaggttgcgaccactg	T10E10.2_R	aagacaggcaacgcaaaaa
rpa-1	F18A1.5	TargetScan	F18A1.5_F	ccacaatcaccgagaatcttt	F18A1.5_R	cgtagtcgtgtccagtattgttg
isw-1	F37A4.8	TargetScan	F37A4.8_F	ttatcattatcgcaagacaatcg	F37A4.8_R	ctttcggtggaacatccttc
tag-342	B0464.8	TargetScan	B0464.8_F	gctcaagttttctcgcatttc	B0464.8_R	ccttctgcgggattcattt
F40F8.5	F40F8.5	TargetScan	F40F8.5_F	agacgtaggagagatcaggatga	F40F8.5_R	agatctacgacgacgatgattg
unc-130	C47G2.2	TargetScan	C47G2.2_F	atgaagacggcgttccagt	C47G2.2_R	tttcggtgaccagacattga
C30B5.7	C30B5.7	TargetScan	C30B5.7_F	ttgtactctactgcaattcgaacc	C30B5.7_R	cccatccagaatgttgagact
ife-3	B0348.6a	TargetScan	B0348.6a_F	ggttgttgtcgataagcaaaga	B0348.6a_R	tcgtcgaattgctctccaa
F13D12.6	F13D12.6	TargetScan	F13D12.6_F	actgacaagctcggtcttacg	F13D12.6_R	ccgatttgacccttcacagt
unc-45	F30H5.1	TargetScan	F30H5.1_F	cgatgatttctttccctggac	F30H5.1_R	agttggcttttccttcaacg
F27C1.2	F27C1.2a	TargetScan	F27C1.2a_F	acaaatcatgcgtggagaca	F27C1.2a_R	tgttgctctgtgagtgggtaa
R11A8.5	R11A8.5	TargetScan	R11A8.5_F	cgatcagtcactcgaccaga	R11A8.5_R	agaatttgttagggtagttgagaactg
C56G2.1	C56G2.1a	TargetScan	C56G2.1a_F	tgaggatgagaagacgcaga	C56G2.1a_R	tttgtcgatcgatggttttc
ZK616.4	ZK616.4	TargetScan	ZK616.4_F	ggttttgttttctgaaagctcgt	ZK616.4_R	tggaattttcgaacatgatctc
cids-1	C02F5.4	TargetScan	C02F5.4_F	tggtccaaaatgaagaagctc	C02F5.4_R	cgcgttcatttgtctcgtt

Gene public name	Gene sequence name	Group	Primer_forward	Sequence Forward	Primer_reverse	Sequence Reverse
hmg-1.1	Y48B6A.14	TargetScan	Y48B6A.14_F	gtcgaatggggaaaactcac	Y48B6A.14_R	tcgacttcgtatctcttcttatcg
F47B7.2	F47B7.2a	TargetScan	F47B7.2a_F	accgcatgaacgaaaaagag	F47B7.2a_R	ccaagatgaatagcataaacactcc
dpy-28	Y39A1B.3	TargetScan	Y39A1B.3_F	gaaccattggtcactttgatga	Y39A1B.3_R	cacgtttcgaaggggttg
F56D3.1	F56D3.1	TargetScan	F56D3.1_F	ggatcggtttcccagaaag	F56D3.1_R	cccagcatgaaagctattaagagta
gfl-1	M04B2.3	TargetScan	M04B2.3_F	aacaggcatttttgaatgatattg	M04B2.3_R	tcacggaggtcttctatttcg
ZK418.9	ZK418.9a	TargetScan	ZK418.9a_F	ggccacttgattcggaaata	ZK418.9a_R	tcgccgacttctgatgattt
M28.8	M28.8	TargetScan	M28.8_F	gatgatttggcaatgtataactacaga	M28.8_R	attggtgttgcccacaattc
F59F5.7	F59F5.7	TargetScan	F59F5.7_F	ccaaagcaaatgacttttatttatg	F59F5.7_R	gaacaattgctactggtcgaga
flh-2	C26E6.2	TargetScan	C26E6.2_F	ccgaagaacttgcattttatga	C26E6.2_R	ttgcatgtaggatcggttga
pgk-1	T03F1.3	Normalization control	T03F1.3_F	gcgatatttatgtcaatgatgctttc	T03F1.3_R	tgagtgctcgactccaacca
cdc-42	R07G3.1	Normalization control	R07G3.1_F	ctgctggacaggaagattacg	R07G3.1_R	ctcggacattctcgaatgaag
Y45F10D.4	Y45F10D.4	Normalization control	Y45F10D.4_F	gtcgcttcaaatcagttcagc	Y45F10D.4_R	gttcttgtcaagtgatccgaca
mpk-1	F43C1.2	Normalization control	F43C1.2_F	tgctcagtaatcggccattg	F43C1.2_R	tccaacaactgccaaaatcaaa
tbp-1	T20B12.2	Normalization control	T20B12.2_F	ttggatttgaagaagattgcattg	T20B12.2_R	aatgactgctgcgaaacgttt

cDNA stem loop RT primers	Sequence	qRT-PCR primers	Sequence
miR-58.1	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGATTGCCGT	miR-58.1_F	ACACTCCAGCTGGGTGAGATCGTTCAGTAC
miR-80	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGTCGGCTTT	miR-80_F	ACACTCCAGCTGGGTGAGATCATTAGTTGAA
miR-81	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGACTAGCTT	miR-81_F	ACACTCCAGCTGGGTGAGATCATCGTGAAA
miR-82	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGACTGGCTT	miR-82_F	ACACTCCAGCTGGGTGAGATCATCGTGAAA
miR-52	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGGCTACCCT	miR-52_F	ACACTCCAGCTGGGCACGTTACAATGAAAG
miR-250	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGGCCAACAG	miR-250_F	ACACTCCAGCTGGGAATCACAGTCAACT
		Universal reverse	CTCAAGTGTCGTGGAGTCGGCAA

Gene public name	Gene sequence name	Group	Primer_forward	Sequence Forward	Primer_reverse	Sequence Reverse
pgk-1	T03F1.3	Normalization control	T03F1.3_F	gcgatatttatgtcaatgatgctttc	T03F1.3_R	tgagtgctcgactccaacca
cdc-42	R07G3.1	Normalization control	R07G3.1_F	ctgctggacaggaagattacg	R07G3.1_R	ctcggacattctcgaatgaag
Y45F10D.4	Y45F10D.4	Normalization control	Y45F10D.4_F	gtcgcttcaaatcagttcagc	Y45F10D.4_R	gttcttgtcaagtgatccgaca
egl-1	F23B12.9	CEP-1 activation assay	F23B12.9_F	ttctcaatttgccgacgact	F23B12.9_R	ggagccgatctcgtagcc

Supplementary Table 6. List of all transitions used for selected reaction monitoring of target and random group in various miR-58 family mutants and wild-type

Full table can be accessed in the supplementary online material.

Supplementary Table 7: Sequences of wild-type and mutated 3'UTRs used in dual luciferase reporters.

Gene ID	Gene name	# of sites	Sequence (WT)	Sequence (MUT)	TargetScan predicted specificity
C30B5.7	*C30B5.7*	1	TTCTCAAAATACAACCTTTACCTTCAGTTTTTAGTGCTCATTTGATATAGTTTTTAATTTATTAATTTTCTTTCCAAAATCGAAATCGATCTCTTCTGACCTGTATTTTAGTTCAAAGTGTACATTACACTGGTCTCATTGCTTGTGATTCATCATCTGTATTTTCATCCTGTTGTTGTCAAAATCCGTCACAAATAAAATATTTATATGAGG	TTCTCAAAATACAACCTTTACCTTCAGTTTTTAGTGCTCATTTGATATAGTTTTTAATTTATTAATTTTCTTTCCAAAATCGAAATCTTCTGACCTGTATTTTAGTTCAAAGTGTACATTACACTGGTCTCATTGCTTGTGATTCATCATCTGTATTTTCATCCTGTTGTTGTCAAAATCCGTCACAAATAAAATATTTATATGAGG	miR-58.1/80/81/82
C37H5.13	*C37H5.13*	1	TAGTAATAATGAAACTTGGAATCTTCATTTATTTATTGTACATCTTTTTTTTTGAAACTTCGATCAAAAATATAAACGGACATTCGTGTAGTGTTAAGTGTAGTTTTAAGTTTTTCTTTTGAATGATCTCTTTCTTTTTTAAAAAAAAAAAGTTTTTTTAGTT	TAGTAATAATGAAACTTGGAATCTTCATTTATTTATTGTACATCTTTTTTTTTGAAACTTCGATCAAAAATATAAACGGACATTCGTGTAGTGTTAAGTGTAGTTTTAAGTTTTTCTTTTGAATTTTCTTTTTTAAAAAAAAAAAGTTTTTTTAGTT	miR-58.1/80/81/82
C07H6.5	cgh-1	2	ACACTAGTTCTCTATATCCCCAAACCTCCAAAACACACTGGTCGCCTACGTTTTTTTTTTCCATTCTAGTGATCTCGTCCAGATTGTGTATGTTCTCTATTTTCCTTTAAATGCACAGTTTGTGCTAAATTTAATATTGTTCAAGCATAAGCATCTTTCCTTCCTGTTTTCTCAAATCCCCGCACATTATTTGTATCCCATCCACCTTCCCGGACCCCATCAACCCGTTCCACTTATATGCGGTGTAAAATTCTAATTTTTCTTTTTCATTAGTTTCCCCATACCCTCCAACTTGCAGTCATGGACTGTAACTCATTCAAGTCGTTGTGTTTTACATAGTCATTTAAGTTGGTCTTTATGCTCCCAAAGTAAATTGTTTCGACATTAATGTGTCGTTGCAAAATATATTTGGGAGTGTAAGGACATTGTTCATACACATCGGGTTCTTTTTGACGTGTATCATACTGGGTAGCCGGCTCTGTAGTTATTCTGTTGAGCCGCACCACATTGATCAATCTTGTAATTTCCTATCTCATTTCCCACAATTCTCCCTTCATGCCCCATACCAATGCATCCAAAATTTAAAACCACCATCCTTGCGGTTTTCCCTTGCCCATCGTGTAGGGTTTTATTCCGCTCTTGTGCTCATTCCAGTTCAACTTGTCCATCTCCTAATCTGATAGATATTTATTGCAACTATTATCATGTCAAATGGCTCAAAGACTATAATGTCTTGGAAGGCTTCCGGCTGGCCATGTGTCTCGCTTACAGCTCTTCCCCCATCCCCATTCCAAAACCATTTGTTCTCTCCCGCCTCCTCCCTCTTGTTTATTGTATAATTTGTAGAAGTTGACACCAAAAATTTGCACAATTTTTCGATTCACAAAGGATGTGCAAGCTTCCTTCTGGATGATTGCCATCTTTAACAATAAAAGACCGAATCGAAACATCGTCTTCTGTTATTTCTTTTCAGAGTTTCATATGAAGAGG	ACACTAGTTCTCTATATCCCCAAACCTCCAAAACACACTGGTCGCCTACGTTTTTTTTTTCCATTCTAGTGTCCAGATTGTGTATGTTCTCTATTTTCCTTTAAATGCACAGTTTGTGCTAAATTTAATATTGTTCAAGCATAAGCATCTTTCCTTCCTGTTTTCTCAAATCCCCGCACATTATTTGTATCCCATCCACCTTCCCGGACCCCATCAACCCGTTCCACTTATATGCGGTGTAAAATTCTAATTTTTCTTTTTCATTAGTTTCCCCATACCCTCCAACTTGCAGTCATGGACTGTAACTCATTCAAGTCGTTGTGTTTTACATAGTCATTTAAGTTGGTCTTTATGCTCCCAAAGTAAATTGTTTCGACATTAATGTGTCGTTGCAAAATATATTTGGGAGTGTAAGGACATTGTTCATACACATCGGGTTCTTTTTGACGTGTATCATACTGGGTAGCCGGCTCTGTAGTTATTCTGTTGAGCCGCACCACATTGATCAATCTTGTAATTTCCTATTTCCCACAATTCTCCCTTCATGCCCCATACCAATGCATCCAAAATTTAAAACCACCATCCTTGCGGTTTTCCCTTGCCCATCGTGTAGGGTTTTATTCCGCTCTTGTGCTCATTCCAGTTCAACTTGTCCATCTCCTAATCTGATAGATATTTATTGCAACTATTATCATGTCAAATGGCTCAAAGACTATAATGTCTTGGAAGGCTTCCGGCTGGCCATGTGTCTCGCTTACAGCTCTTCCCCCATCCCCATTCCAAAACCATTTGTTCTCTCCCGCCTCCTCCCTCTTGTTTATTGTATAATTTGTAGAAGTTGACACCAAAAATTTGCACAATTTTTCGATTCACAAAGGATGTGCAAGCTTCCTTCTGGATGATTGCCATCTTTAACAATAAAAGACCGAATCGAAACATCGTCTTCTGTTATTTCTTTTCAGAGTTTCATATGAAGAGG	miR-58.1/80/81/82
C09D1.2	isw-1	2	TTACATTCATATATTCTTTTTATCTCCTTCTCCATTCATTGCTTGATTAATGTCGATCTCTATCCTCCCCTTTGATTACTGCTAAATCATCTCATCTCTCATCTTATCTCCTCATTTCTATTTGAGTATTTCTAAGCACACCTACCTATGCTATTTATTCACCGTATCTTCTTTTTATATCTTATTAATGATTGTAAATTACTCAAATAAACTCGGAGTCTTG	TTACATTCATATATTCTTTTTATCTCCTTCTCCATTCATTGCTTGATTAATGTCTATCCTCCCCTTTGATTACTGCTAAATCATCTCTCATCTTATCTCCTCATTTCTATTTGAGTATTTCTAAGCACACCTACCTATGCTATTTATTCACCGTATCTTCTTTTTATATCTTATTAATGATTGTAAATTACTCAAATAAACTCGGAGTCTTG	miR-58.1/80/81/82
Y22F5A.4	lys-1	1	AATATTTATGTTGTGATCTCTTACCTATTTGTATTATTTCAATAAACAATCCTAGCTTTATTAAAATTTTATTTTAAAAAAATACTGAAATATACCCATATAACATACCAGATATATACCAGAAATTAAAATGAATGATCAGT	AATATTTATGTTGTTTACCTATTTGTATTATTTCAATAAACAATCCTAGCTTTATTAAAATTTTATTTTAAAAAAATACTGAAATATACCCATATAACATACCAGATATATACCAGAAATTAAAATGAATGATCAGT	miR-80/81/82
C09D1.2	clec-89	2	TATTTCCCTAATTGATTTGTTTAGTTAATTTCCTAGTCATTGCTCATTCACTTTCTTGTTTTTCCCGCTGTTCCATTCCAATCAACCCAAGAATCTCATTTCAATACCGATCTCTGAATAAACTGTGTTTTCAT	TATTTCCCTAATTGATTTGTTTAGTTAATTTCCTAGTCATTGCTCATTCACTTTCTTGTTTTTCCCGCTGTTCCATTCCAATCAACCCAAGAATTTCAATACCTGAATAAACTGTGTTTTCAT	miR-58.1/80/81/82
K06A4.1	nas-3	1	TAATTAATTGATCAAGTTCATAATTATTATTTTTCAATTTTTCCCCATCATCTCTTTCCTTTGCTCTTATTTGTATCCGATCTTTGTGCTTCAACACGTGCTTCGCTTACGATTCTTGACGATCTCAAACGTTTTTTGTTTTTATGTATGGATTAATATTTATTTAATATAATAAATAAATTGGTAAATTAAT	TAATTAATTGATCAAGTTCATAATTATTATTTTTCAATTTTTCCCCATCATCTCTTTCCTTTGCTCTTATTTGTATCCGATCTTTGTGCTTCAACACGTGCTTCGCTTACGATTCTTGACAAACGTTTTTTGTTTTTATGTATGGATTAATATTTATTTAATATAATAAATTGGTAAATTAAT	miR-58.1/80/81/82