Supplemental Information

Hedgehog signaling strength is orchestrated by the *mir-310* cluster of microRNAs in response to diet

Ibrahim Ömer Çiçek[1], Samir Karaca[2], Marko Brankatschk[3], Suzanne Eaton[3], Henning Urlaub[2], and Halyna R. Shcherbata[1]*

[1] Max Planck Research Group of Gene Expression and Signaling, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077, Göttingen, Germany

[2] Bioanalytical Mass Spectrometry Research Group, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077, Göttingen, Germany

[3] Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 01307, Dresden, Germany

*corresponding author: halyna.shcherbata@mpibpc.mpg.de

Running title: upon diet, miRNAs modulate Hh signaling

Keywords: *Drosophila*; oogenesis; follicle stem cell; Hedgehog signaling; miRNA; the *mir-310s*; *Rab23*; dietary restriction; metabolic stress; Hh ligand

Supplemental Figures

Figure S1

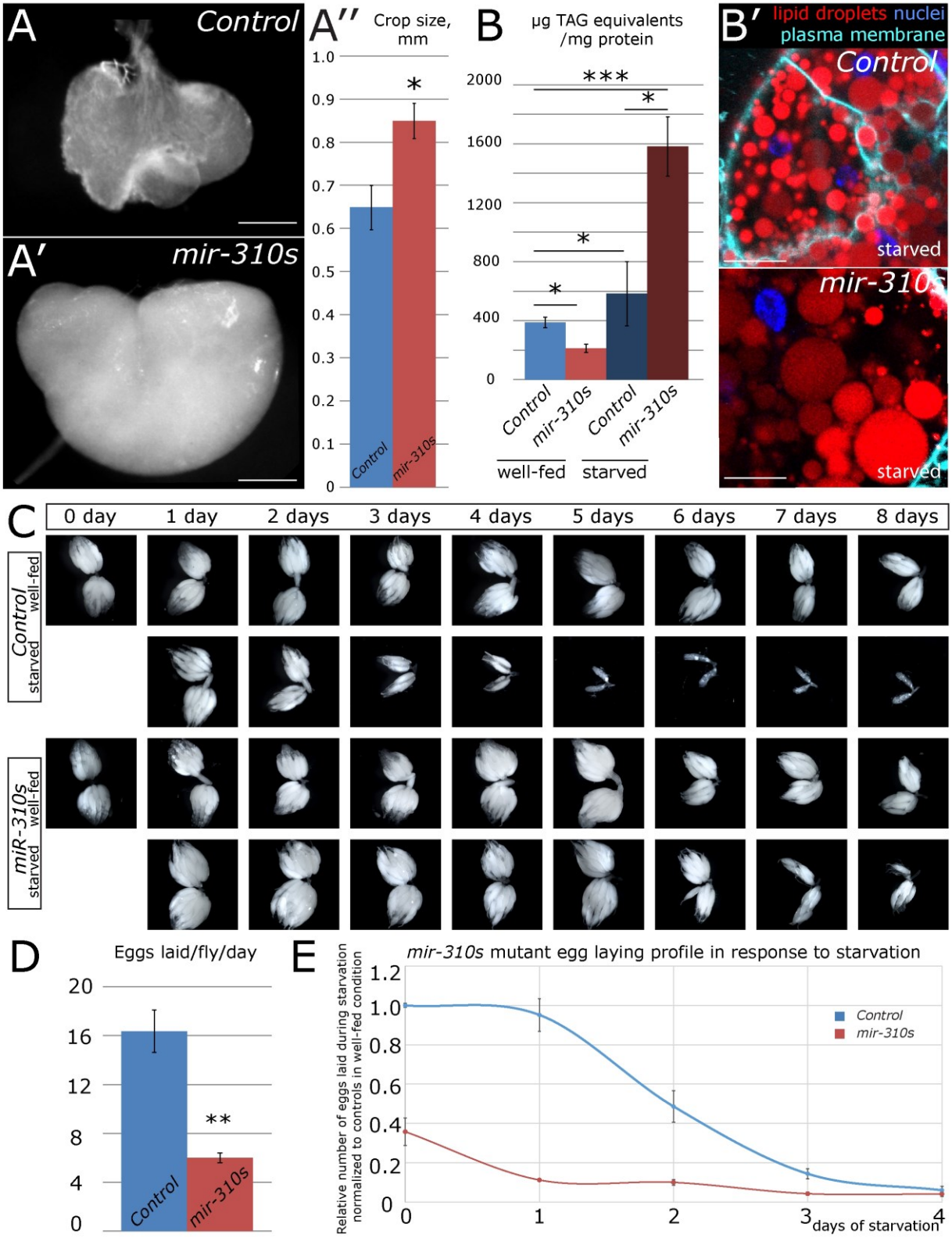

Figure S1. The *mir-310s* mutant female ovaries respond to protein starvation abnormally

(A, A`) Bright field images of control (w^{1118}) and *mir-310s* mutant (*KT40/KT40*) crops dissected from comparably sized females kept under normal conditions. Note the enlarged crop size of *mir-310s* mutant females (A``) (Table S3).

(B) *mir-310s* mutant females have abnormal energy metabolism as measured by the total body fat. However, upon nutritional restriction for 10 days, *mir-310s* mutants accumulate ~2.5-fold more lipids and larger lipid droplets than controls (B`) (Table S3).

(C) In response to nutritional restriction, control females cease egg production after day 4. *mir-310s* mutant ovaries contain substantial amounts of late egg chambers even after 7-8 days of nutritional restriction (Table S3). *mir-310s* loss-of-function mutants, similarly to *hh* (*tub-Gal80^{ts}/+; bab1-Gal4/UAS-hh* at 29°C) and *Rab23* (*bab1-Gal4/UAS-Rab23*) overexpression (data not shown), demonstrate a delayed cessation of egg chamber production after stage 6 in response to starvation.

(D) Note that even under well-fed condition, *mir-310s* mutant females lay significantly fewer eggs than controls (Table S3).

(E) Egg laying profiles for control and *mir-310s* mutant females (Table S3).

In (A``), (B), (D), and (E) the data points indicate AVE±SEM (Table S3). Significances were calculated using two-tailed Student's t-test. *$p<0.05$, **$p<0.005$, ***$p<0.0005$. Scale bar represents 250µm in (A, A`) and 20µm in B`.

Supplemental Tables

Table S1, related to Figure 1. Proteins significantly deregulated in *mir-310s* mutants

CG number	Gene name
Energy metabolism	
CG10924	CG10924
CG11594	CG11594
CG17530	GstE6
CG2827	Tal
CG30360	**Mal-A6**
CG31692	fbp
CG33138	CG33138
CG3763	Fbp2
CG4178	Lsp1beta
CG5177	CG5177
CG6806	Lsp2
CG8036	CG8036
CG8094	Hex-C
CG8696	**LvpH**
CG9092	Gal
CG9232	Galt
Lipid metabolism	
CG10622	Sucb
CG10932	CG10932
CG11064	Rfabg
CG11129	Yp3
CG11198	ACC
CG15828	Apoltp
CG1648	CG1648
CG1742	Mgstl
CG18212	**alt**
CG2979	Yp2
CG2985	Yp1
CG3050	**Cyp6d5**
CG31150	crossveinless d
CG3481	Adh
CG3523	CG3523
CG3524	v(2)k05816
CG3699	EG:BACR7A4.14
CG3752	Aldh
CG4581	Thiolase
CG4729	CG4729
CG5170	**Dp1**
CG5590	CG5590
CG5885	CG5885
CG5958	CG5958
CG7400	**Fatp**
CG8256	Gpo-1
CG8628	CG8628
CG8778	CG8778
CG9035	Tapdelta
CG9412	**rin**
CG9577	**CG9577**
CG9914	CG9914
Protein homeostasis	
CG10236	LanA
CG10302	bsf
CG10686	tral
CG11512	GstD4
CG11899	CG11899
CG12163	CG12163
CG13393	lethal (2) k12914
CG14715	CG14715
CG15261	UK114
CG15369	CG15369
CG2852	CG2852
CG3011	CG3011
CG31198	CG31198
CG31343	CG5839
CG33103	Ppn
CG3926	Spat
CG3949	hoip
CG3999	CG3999
CG4067	pug
CG4181	GstD2
CG4463	Hsp23
CG4659	Srp54k
CG4916	me31B
CG4954	eIF3-S8
CG5064	Srp68
CG5330	Nap1
CG5394	Aats-glupro
CG5474	SsRbeta
CG5839	CG31233
CG6287	CG6287
CG6370	CG6370
CG6512	CG6512
CG6781	se
CG6950	CG6950
CG7014	RpS5b
CG7637	CG7637
CG8396	Ssb-c31a
CG8431	Aats-cys
CG8858	CG8858
CG8938	GstS1
CG9012	Chc
CG9423	**Kap-alpha3**
CG9539	**Sec61alpha**
CG9805	eIF3-S10
CG9842	**Pp2B-14D**
CG9897	CG9897
Mitochondria	
CG3902	CG3902
CG10340	CG10340
CG12203	CG12203
CG12079	CG12079
CG12151	Pdp
CG14757	CG14757
CG16944	sesB
CG2286	ND75
CG32531	mRpS14
CG3283	SdhB
CG34073	mt:ATPase6
CG3566	CG3566
CG4169	CG4169
CG4769	CG4769
CG5670	**Atpalpha**
CG5889	Men-b
CG6022	Cchl
CG6455	CG6455
CG6612	Adk3
CG6647	**porin**

CG6666	SdhC
CG6782	**sea**
CG6878	**CG6878**
CG7580	CG7580
CG7610	ATPsyn-gamma
CG8479	opa1-like
CG8790	Dic1
CG8844	Pdsw
CG9090	CG9090
Nucleotide synthesis	
CG11089	CG11089
CG16758	CG16758
CG18572	r
CG2194	su(r)
CG31628	ade3
CG3989	ade5
CG4584	dUTPase
CG7917	Nlp
CG8132	CG8132
CG9127	ade2
CG9193	mus209
CG9242	bur
CG9674	CG9674
Muscle	
CG10067	Act57B
CG1106	Gel
CG11949	cora
CG12408	TpnC4
CG15792	zip
CG17927	Mhc
CG17927	MHC isoforms
CG18290	Act87E
CG2184	Mlc2
CG2981	**TpnC41C**
CG4183	Hsp26
CG4466	Hsp27
CG4843	Tm2
CG4898	**Tm1**
CG5125	ninaC
CG5178	Act88F
CG5596	Mlc1
CG7107	up
CG7178	wupA
CG7445	**fln**
CG7478	Act79B

CG7930	TpnC73F
CG9138	**uif**
CG9432	l(2)01289
CG9480	Glycogenin
Neural	
CG11797	Obp56a
CG12202	Nat1
CG12908	Ndg
CG15457	Obp19c
CG1618	comt
CG1634	Nrg
CG17029	CG17029
CG1744	chp
CG17870	**14-3-3zeta**
CG18102	shi
CG18111	Obp99a
CG1873	Ef1alpha100E
CG1977	alpha-Spec
CG2028	CkIalpha
CG2297	Obp44a
CG30021	metro
CG32234	axo
CG33950	trol
CG3620	norpA
CG3725	Ca-P60A, CG3725
CG3747	Eaat1
CG43079	nrm
CG4609	fax
CG5119	pAbp
CG5711	Arr1
CG5779	proPO-A1
CG5779	proPo
CG5870	beta-Spec
CG7088	bnb
CG7576	Rab3
CG7592	Obp99b
CG8462	**Obp56e**
CG8663	nrv3
CG9206	Gl
CG9261	Nrv2
Cuticle	
CG10112	Cpr51A
CG10287	Gasp
CG12045	Cpr100A
CG17052	obst-A

CG1919	Cpr62Bc
CG3244	Clect27
CG4475	CG4475
CG4784	Cpr72Ec
CG7532	l(2)34Fc
CG8505	Cpr49Ae
CG8511	Cpr49Ag
CG9079	Cpr47Ea
Histone	
CG10638	CG10638
CG11765	Prx2540-2
CG12171	CG12171
CG12405	Prx2540-1
CG12896	CG12896
CG18547	CG18547
CG1982	Sodh-1
CG3609	CG3609
CG3835	EG:87B1.3
CG6084	CG6084
CG6776	GStO3
CG6776	CG6776
CG7322	CG7322
CG8503	CG8503
CG9119	CG9119
CG9331	CG9331
His2B	His2B
His4	His4
No association	
CG12008	kst
CG10031	CG10031
CG10527	CG10527
CG10691	l(2)37Cc
CG10978	jagn
CG11785	bai
CG11920	CG11920
CG11999	CG11999
CG12403	Vha68-1
CG14168	Zasp67
CG1444	CG1444
CG1462	Aph-4
CG14661	CG14661
CG15081	l(2)03709
CG15881	**CG15881**
CG16884	BG:DS00180.3
CG16985	CG16985
CG18591	SmE

CG1885	CG1885
CG2082	CG2082
CG2216	Fer1HCH
CG2233	**CG2233**
CG2310	CG2310
CG2943	CG2943
CG30222	**CG30222**
CG3082	l(2)k09913
CG31195	CG31195
CG34026	CG34026
CG34215	CG34215
CG42314	PMCA
CG4239	CG4239
CG5945	CG5945
CG6214	MRP
CG6544	fau
CG6702	Cbp53E
CG6815	bor
CG6851	Mtch
CG6917	Est-6
CG6950	CG6950
CG7646	CG7646
CG8108	CG8108
CG8790	CG8790
CG9297	CG9297
Putative *mir-310s* target	

Table S2, related to Figure 1. Relative mRNA expression levels of the starvation-sensitive genes upon *mir-310s* deficit and/or nutritional stress

Genotype/ Condition	Target Gene	C_T AVE±SEM[b]	Δ C_T AVE±SEM[b]	ΔΔ C_T AVE±SEM[b]	Relative mRNA level[a,c] AVE± SEM[b]	*log₁₀* Relative mRNA level AVE± SEM[b]
Plate 1						
Control (w^{1118}) well-fed	*Act88F*	2.76E+01 ±5.57E-02	9.47 ±6.27E-02	3.18E-07 ±5.57E-02	1.00 ±3.80E-02	-9.57E-08 ±1.68E-02
Control (w^{1118}) starved		2.16E+01 ±1.79E-02	3.58 ±2.69E-02	-5.88 ±1.79E-02	5.90E+01 ±7.30E-01 $p^{Control\ well\text{-}fed}$=1.52E-07	1.77 ±5.38E-03
mir-310s (*KT40/KT40*) well-fed		2.50E+01 ±3.11E-02	6.45 ±4.29E-02	-3.02 ±3.11E-02	8.09 ±1.73E-01 $p^{Control\ well\text{-}fed}$=2.30E-06	9.08E-01 ±9.37E-03
mir-310s (*KT40/KT40*) starved		2.40E+01 ±9.20E-03	5.79 ±1.19E-02	-3.68 ±9.20E-03	1.28E+01 ±8.18E-02 $p^{Control\ well\text{-}fed}$=2.05E-08	1.11 ±2.77E-03
Control (w^{1118}) well-fed	*ade2*	2.29E+01 ±3.16E-02	4.70 ±4.28E-02	1.59E-07 ±3.16E-02	1.00 ±2.18E-02	-4.78E-08 ±9.52E-03
Control (w^{1118}) starved		2.32E+01 ±4.70E-02	5.17 ±5.12E-02	4.65E-01 ±4.70E-02	7.25E-01 ±2.35E-02 $p^{Control\ well\text{-}fed}$=1.01E-03	-1.40E-01 ±1.42E-02
mir-310s (*KT40/KT40*) well-fed		2.19E+01 ±2.31E-02	3.32 ±3.75E-02	-1.38 ±2.31E-02	2.61 ±4.15E-02 $p^{Control\ well\text{-}fed}$=4.30E-06	4.16E-01 ±6.95E-03
mir-310s (*KT40/KT40*) starved		2.25E+01 ±1.49E-02	4.36 ±1.67E-02	-3.45E-01 ±1.49E-02	1.27 ±1.32E-02 $p^{Control\ well\text{-}fed}$=4.48E-04	1.04E-01 ±4.49E-03
Control (w^{1118}) well-fed	*ade3*	2.34E+01 ±1.77E-02	5.21 ±3.38E-02	-1.59E-07 ±1.77E-02	1.00 ±1.22E-02	4.78E-08 ±5.33E-03
Control (w^{1118}) starved		2.49E+01 ±2.39E-02	6.91 ±3.13E-02	1.70 ±2.39E-02	3.09E-01 ±5.09E-03 $p^{Control\ well\text{-}fed}$=8.01E-07	-5.11E-01 ±7.19E-03
mir-310s (*KT40/KT40*) well-fed		2.27E+01 ±1.78E-02	4.15 ±3.45E-02	-1.06 ±1.78E-02	2.08 ±2.56E-02 $p^{Control\ well\text{-}fed}$=2.82E-06	3.18E-01 ±5.36E-03
mir-310s (*KT40/KT40*) starved		2.39E+01 ±2.81E-02	5.73 ±2.91E-02	5.16E-01 ±2.81E-02	6.99E-01 ±1.37E-02 $p^{Control\ well\text{-}fed}$=8.16E-05	-1.55E-01 ±8.46E-03
Control (w^{1118}) well-fed	*Arr1*	2.30E+01 ±9.35E-03	4.80 ±3.03E-02	0.00 ±9.35E-03	1.00 ±6.49E-03	0.00 ±2.82E-03
Control (w^{1118}) starved		2.03E+01 ±4.21E-02	2.27 ±4.67E-02	-1.83 ±7.03E-01	3.56 ±1.49 $p^{Control\ well\text{-}fed}$=4.02E-05	5.52E-01 ±1.27E-02
mir-310s (*KT40/KT40*) well-fed		2.28E+01 ±1.09E-01	4.27 ±1.13E-01	-9.41E-01 ±5.17E-01	1.92 ±8.63E-01 $p^{Control\ well\text{-}fed}$=2.35E-01	2.83E-01 ±1.56E-01
mir-310s (*KT40/KT40*) starved		2.14E+01 ±3.34E-02	3.19 ±3.43E-02	-8.18E-01 ±8.12E-01	1.76 ±8.43E-01 $p^{Control\ well\text{-}fed}$=2.11E-01	2.46E-01 ±2.44E-01
Control (w^{1118}) well-fed	*CG3699*	2.39E+01 ±5.05E-02	5.72 ±5.81E-02	-1.59E-07 ±5.05E-02	1.00 ±3.55E-02	4.78E-08 ±1.52E-02
Control (w^{1118}) starved		2.53E+01 ±2.82E-02	7.28 ±3.47E-02	1.56 ±2.82E-02	3.38E-01 ±6.55E-03 $p^{Control\ well\text{-}fed}$=5.16E-05	-4.71E-01 ±8.49E-03

mir-310s (KT40/KT40) well-fed		2.50E+01 ±7.56E-03	6.43 ±3.05E-02	7.14E-01 ±7.56E-03	6.09E-01 ±3.19E-03 $p^{Control\ well\text{-}fed}$=3.88E-04	-2.15E-01 ±2.28E-03
mir-310s (KT40/KT40) starved		2.52E+01 ±7.45E-03	7.03 ±1.06E-02	1.31 ±7.45E-03	4.03E-01 ±2.08E-03 $p^{Control\ well\text{-}fed}$=7.28E-05	-3.95E-01 ±2.24E-03
Control (w^{1118}) well-fed	*CG3902*	2.29E+01 ±1.99E-03	4.78 ±2.89E-02	1.59E-07 ±1.99E-03	1.00 ±1.38E-03	-4.78E-08 ±5.99E-04
Control (w^{1118}) starved		2.43E+01 ±2.56E-02	6.32 ±3.26E-02	1.54 ±2.56E-02	3.44E-01 ±6.17E-03 $p^{Control\ well\text{-}fed}$=5.18E-08	-4.63E-01 ±7.72E-03
mir-310s (KT40/KT40) well-fed		2.26E+01 ±1.72E-02	4.04 ±3.41E-02	-7.34E-01 ±1.72E-02	1.66 ±1.98E-02 $p^{Control\ well\text{-}fed}$=4.79E-06	2.21E-01 ±5.16E-03
mir-310s (KT40/KT40) starved		2.33E+01 ±1.23E-02	5.18 ±1.45E-02	3.97E-01 ±1.23E-02	7.60E-01 ±6.46E-03 $p^{Control\ well\text{-}fed}$=3.42E-06	-1.19E-01 ±3.71E-03
Control (w^{1118}) well-fed	*Rpl32*	1.82E+01 ±2.88E-02	0.00 ±2.88E-02			
Control (w^{1118}) starved		1.80E+01 ±2.02E-02	6.36E-07 ±2.02E-02			
mir-310s (KT40/KT40) well-fed		1.86E+01 ±2.95E-02	1.91E-06 ±2.95E-02			
mir-310s (KT40/KT40) starved		1.82E+01 ±7.58E-03	6.36E-07 ±7.58E-03			
No Reverse Transcriptase						
Control (w^{1118}) well-fed	*Rpl32*	3.34E+01 ±2.44E-01	1.53E+01 ±2.44E-01	1.53E+01 ±2.44E-01	2.53E-05 ±4.68E-06	-4.60 ±7.35E-02
Control (w^{1118}) starved		3.30E+01 ±2.87E-01	1.50E+01 ±2.87E-01	1.50E+01 ±2.87E-01	3.06E-05 ±5.89E-06	-4.51 ±8.65E-02
mir-310s (KT40/KT40) well-fed		3.28E+01 ±1.09E-01	1.43E+01 ±1.09E-01	1.43E+01 ±1.09E-01	5.06E-05 ±3.98E-06	-4.30 ±3.29E-02
mir-310s (KT40/KT40) starved		3.37E+01 ±1.36E-01	1.56E+01 ±1.36E-01	1.56E+01 ±1.36E-01	2.08E-05 ±1.95E-06	-4.68 4.10E-02
Plate 2						
Control (w^{1118}) well-fed	*CG3999*	2.69E+01 ±1.07E-02	9.08 ±2.33E-02	-6.36E-07 ±1.07E-02	1.00 ±7.44E-03	1.91E-07 ±3.22E-03
Control (w^{1118}) starved		2.85E+01 ±2.78E-02	1.08E+01 ±2.98E-02	1.72 ±2.78E-02	3.04E-01 ±5.90E-03 $p^{Control\ well\text{-}fed}$=2.08E-07	-5.17E-01 ±8.36E-03
mir-310s (KT40/KT40) well-fed		2.68E+01 ±3.90E-02	8.55 ±4.82E-02	-5.30E-01 ±3.90E-02	1.44 ±3.95E-02 $p^{Control\ well\text{-}fed}$=3.79E-04	1.60E-01 ±1.17E-02
mir-310s (KT40/KT40) starved		2.76E+01 ±4.55E-02	9.69 ±4.81E-02	6.09E-01 ±4.55E-02	6.56E-01 ±2.10E-02 $p^{Control\ well\text{-}fed}$=1.03E-04	-1.83E-01 ±1.37E-02
Control (w^{1118}) well-fed	*CG9914*	3.08E+01 ±4.14E-02	1.30E+01 ±4.63E-02	-9.54E-07 ±4.14E-02	1.00 ±2.83E-02	2.87E-07 ±1.25E-02
Control (w^{1118}) starved		3.19E+01 ±2.46E-02	1.42E+01 ±2.69E-02	1.20 ±2.46E-02	4.34E-01 ±7.41E-03 $p^{Control\ well\text{-}fed}$=4.19E-05	-3.62E-01 ±7.42E-03

mir-310s (KT40/KT40) well-fed		3.08E+01 ±2.57E-02	1.25E+01 ±3.83E-02	-4.46E-01 ±2.57E-02	1.36 ±2.44E-02 $p^{Control\ well\text{-}fed}$=6.35E-04	1.34E-01 ±7.74E-03
mir-310s (KT40/KT40) starved		3.06E+01 ±5.07E-02	1.27E+01 ±5.30E-02	-2.91E-01 ±5.07E-02	1.22 ±4.31E-02 $p^{Control\ well\text{-}fed}$=1.22E-02	8.76E-02 ±1.53E-02
Control (w^{1118}) well-fed	*CG11089*	2.22E+01 ±2.57E-02	4.41 ±3.30E-02	-7.95E-07 ±2.57E-02	1.00 ±1.80E-02	2.39E-07 ±7.73E-03
Control (w^{1118}) starved		2.30E+01 ±1.08E-02	5.33 ±1.54E-02	9.29E-01 ±1.08E-02	5.25E-01 ±3.96E-03 $p^{Control\ well\text{-}fed}$=1.33E-05	-2.80E-01 ±3.27E-03
mir-310s (KT40/KT40) well-fed		2.15E+01 ±9.71E-03	3.30 ±3.00E-02	-1.10 ±9.71E-03	2.15 ±1.44E-02 $p^{Control\ well\text{-}fed}$=9.64E-07	3.32E-01 ±2.92E-03
mir-310s (KT40/KT40) starved		2.30E+01 ±1.41E-02	5.10 ±2.10E-02	6.99E-01 ±1.41E-02	6.16E-01 ±6.07E-03 $p^{Control\ well\text{-}fed}$=3.49E-05	-2.10E-01 ±4.26E-03
Control (w^{1118}) well-fed	*CG15369*	3.29E+01 ±8.65E-03	1.51E+01 ±2.24E-02	-3.18E-07 ±8.65E-03	1.00 ±5.97E-03	9.57E-08 ±2.60E-03
Control (w^{1118}) starved		3.17E+01 ±1.71E-01	1.40E+01 ±1.72E-01	-1.12 ±1.71E-01	2.18 ±2.56E-01 $p^{Control\ well\text{-}fed}$=9.14E-03	3.38E-01 ±5.15E-02
mir-310s (KT40/KT40) well-fed		3.29E+01 ±8.31E-02	1.47E+01 ±8.78E-02	-4.16E-01 ±8.31E-02	1.33 ±7.67E-02 $p^{Control\ well\text{-}fed}$=1.17E-02	1.25E-01 ±2.50E-02
mir-310s (KT40/KT40) starved		3.11E+01 ±8.40E-02	1.32E+01 ±8.54E-02	-1.86 ±8.40E-02	3.64 ±2.06E-01 $p^{Control\ well\text{-}fed}$=2.12E-04	5.61E-01 ±2.53E-02
Control (w^{1118}) well-fed	*CG16884*	3.60E+01 ±1.55E-01	1.82E+01 ±1.57E-01	0.00 ±1.55E-01	1.00 ±1.03E-01	0.00 ±4.68E-02
Control (w^{1118}) starved		3.48E+01 ±6.19E-02	1.70E+01 ±6.29E-02	-1.13 ±6.19E-02	2.20 ±9.23E-02 $p^{Control\ well\text{-}fed}$=1.02E-03	3.41E-01 ±1.86E-02
mir-310s (KT40/KT40) well-fed		3.63E+01 ±5.23E-02	1.81E+01 ±5.95E-02	-8.92E-02 ±5.23E-02	1.06 ±3.80E-02 $p^{Control\ well\text{-}fed}$=6.50E-01	2.69E-02 ±1.57E-02
mir-310s (KT40/KT40) starved		3.49E+01 ±1.49E-01	1.71E+01 ±1.50E-01	-1.13 ±1.49E-01	2.18 ±2.27E-01 $p^{Control\ well\text{-}fed}$=8.67E-03	3.39E-01 ±4.48E-02
Control (w^{1118}) well-fed	*CG30360*	2.19E+01 ±1.06E-02	4.11 ±2.32E-02	-7.95E-07 ±1.06E-02	1.00 ±7.30E-03	2.39E-07 ±3.18E-03
Control (w^{1118}) starved		2.30E+01 ±1.63E-02	5.32 ±1.96E-02	1.22 ±1.63E-02	4.30E-01 ±4.86E-03 $p^{Control\ well\text{-}fed}$=3.35E-07	-3.67E-01 ±4.91E-03
mir-310s (KT40/KT40) well-fed		2.27E+01 ±1.47E-02	4.50 ±3.19E-02	3.92E-01 ±1.47E-02	7.62E-01 ±7.78E-03 $p^{Control\ well\text{-}fed}$=2.40E-05	-1.18E-01 ±4.41E-03
mir-310s (KT40/KT40) starved		2.34E+01 ±2.02E-02	5.52 ±2.55E-02	1.41 ±2.02E-02	3.76E-01 ±5.23E-03 $p^{Control\ well\text{-}fed}$=2.58E-07	-4.24E-01 ±6.08E-03
Control (w^{1118}) well-fed	*Rpl32*	1.78E+01 ±2.07E-02	-6.36E-07 ±2.07E-02			
Control (w^{1118}) starved		1.77E+01 ±1.09E-02	0.00 ±1.09E-02			
mir-310s (KT40/KT40) well-fed		1.82E+01 ±2.84E-02	-1.27E-06 ±2.84E-02			

mir-310s (KT40/KT40) starved		1.79E+01 ±1.55E-02	6.36E-07 ±1.55E-02			
No Reverse Transcriptase						
Control (w^{1118}) well-fed	*Rpl32*	3.28E+01 ±1.19E-01	1.50E+01 ±1.19E-01	1.50E+01 ±1.19E-01	3.07E-05 ±2.64E-06	-4.51 ±3.59E-02
Control (w^{1118}) starved		3.28E+01 ±1.03E-01	1.51E+01 ±1.03E-01	1.51E+01 ±1.03E-01	2.92E-05 ±2.16E-06	-4.53 ±3.10E-02
mir-310s (KT40/KT40) well-fed		3.22E+01 ±9.10E-02	1.40E+01 ±9.10E-02	1.40E+01 ±9.10E-02	6.13E-05 ±3.82E-06	-4.21 ±2.74E-02
mir-310s (KT40/KT40) starved		3.27E+01 ±2.33E-01	1.49E+01 ±2.33E-01	1.49E+01 ±2.33E-01	3.37E-05 ±5.94E-06	-4.47 ±7.00E-02
Plate 3						
Control (w^{1118}) well-fed	*CG31233*	2.54E+01 ±1.38E-02	7.51 ±2.92E-02	0.00 ±1.38E-02	1.00 ±9.53E-03	0.00 ±4.14E-03
Control (w^{1118}) starved		2.36E+01 ±1.64E-03	5.80 ±9.31E-03	-1.72 ±1.64E-03	3.29 ±3.73E-03 $p^{Control\ well\text{-}fed}$=2.41E-09	5.17E-01 ±4.93E-04
mir-310s (KT40/KT40) well-fed		2.59E+01 ±3.60E-02	7.76 ±1.04E-01	2.41E-01 ±3.60E-02	8.46E-01 ±2.13E-02 $p^{Control\ well\text{-}fed}$=2.79E-03	-7.25E-02 ±1.09E-02
mir-310s (KT40/KT40) starved		2.43E+01 ±1.91E-02	6.43 ±2.24E-02	-1.08 ±1.91E-02	2.12 ±2.82E-02 $p^{Control\ well\text{-}fed}$=2.96E-06	3.26E-01 ±5.74E-03
Control (w^{1118}) well-fed	*Cpr62Bc*	3.45E+01 ±7.64E-02	1.66E+01 ±8.06E-02	6.36E-07 ±7.64E-02	1.00 ±5.16E-02	-1.91E-07 ±2.30E-02
Control (w^{1118}) starved		3.15E+01 ±3.45E-02	1.37E+01 ±3.57E-02	-2.93 ±3.45E-02	7.64 ±1.84E-01 $p^{Control\ well\text{-}fed}$=4.10E-06	8.83E-01 ±1.04E-02
mir-310s (KT40/KT40) well-fed		3.20E+01 ±5.19E-02	1.38E+01 ±1.11E-01	-2.79 ±5.19E-02	6.90 ±2.46E-01 $p^{Control\ well\text{-}fed}$=1.94E-05	8.39E-01 ±1.56E-02
mir-310s (KT40/KT40) starved		3.01E+01 ±1.61E-02	1.23E+01 ±2.00E-02	-4.31 ±1.61E-02	1.98E+01 ±2.22E-01 $p^{Control\ well\text{-}fed}$=1.29E-07	1.30 ±4.84E-03
Control (w^{1118}) well-fed	*Cpr72Ec*	3.25E+01 ±8.92E-02	1.46E+01 ±9.28E-02	-3.18E-07 ±8.92E-02	1.00 ±6.37E-02	9.57E-08 ±2.68E-02
Control (w^{1118}) starved		3.29E+01 ±1.73E-02	1.51E+01 ±1.96E-02	5.13E-01 ±1.73E-02	7.01E-01 ±8.41E-03 $p^{Control\ well\text{-}fed}$=9.22E-03	-1.54E-01 ±5.22E-03
mir-310s (KT40/KT40) well-fed		2.80E+01 ±9.14E-03	9.84 ±9.80E-02	-4.76 ±9.14E-03	2.70E+01 ±1.71E-01 $p^{Control\ well\text{-}fed}$=1.46E-08	1.43 ±2.75E-03
mir-310s (KT40/KT40) starved		2.62E+01 ±3.01E-02	8.39 ±3.24E-02	-6.21 ±3.01E-02	7.40E+01 ±1.54 $p^{Control\ well\text{-}fed}$=1.19E-06	1.87 ±9.07E-03
Control (w^{1118}) well-fed	*Cpr100A*	3.18E+01 ±1.13E-01	1.39E+01 ±1.16E-01	0.00 ±1.13E-01	1.00 ±8.06E-02	0.00 ±3.41E-02
Control (w^{1118}) starved		2.79E+01 ±1.96E-02	1.01E+01 ±2.17E-02	-3.78 ±1.96E-02	1.38E+01 ±1.89E-01 $p^{Control\ well\text{-}fed}$=4.00E-07	1.14 ±5.91E-03
mir-310s (KT40/KT40) well-fed		2.78E+01 ±4.13E-02	9.63 ±1.06E-01	-4.27 ±4.13E-02	1.93E+01 ±5.45E-01 $p^{Control\ well\text{-}fed}$=4.90E-06	1.29 ±1.24E-02

mir-310s (KT40/KT40) starved		2.84E+01 ±3.03E-02	1.06E+01 ±3.25E-02	-3.31 ±3.03E-02	9.93 ±2.10E-01 $p^{Control\ well\text{-}fed}$=2.43E-06	9.97E-01 ±9.11E-03
Control (w^{1118}) well-fed	*Gal*	2.76E+01 ±6.26E-02	9.77 ±6.77E-02	-3.18E-07 ±6.26E-02	1.00 ±4.26E-02	9.57E-08 ±1.89E-02
Control (w^{1118}) starved		2.79E+01 ±4.60E-02	1.01E+01 ±4.69E-02	3.15E-01 ±4.60E-02	8.04E-01 ±2.55E-02 $p^{Control\ well\text{-}fed}$=1.65E-02	-9.50E-02 ±1.38E-02
mir-310s (KT40/KT40) well-fed		2.86E+01 ±1.76E-02	1.04E+01 ±9.91E-02	6.79E-01 ±1.76E-02	6.25E-01 ±7.62E-03 $p^{Control\ well\text{-}fed}$=9.55E-04	-2.04E-01 ±5.31E-03
mir-310s (KT40/KT40) starved		2.80E+01 ±1.89E-02	1.01E+01 ±2.23E-02	3.70E-01 ±1.89E-02	7.74E-01 ±1.02E-02 $p^{Control\ well\text{-}fed}$=6.50E-03	-1.11E-01 ±5.68E-03
Control (w^{1118}) well-fed	*Gasp*	2.99E+01 ±4.09E-02	1.20E+01 ±4.83E-02	3.18E-07 ±4.09E-02	1.00 ±2.79E-02	-9.57E-08 ±1.23E-02
Control (w^{1118}) starved		2.61E+01 ±1.95E-02	8.34 ±2.16E-02	-3.67 ±1.95E-02	1.27E+01 ±1.73E-01 $p^{Control\ well\text{-}fed}$=2.97E-07	1.10 ±5.88E-03
mir-310s (KT40/KT40) well-fed		2.90E+01 ±2.72E-02	1.08E+01 ±1.01E-01	-1.16 ±2.72E-02	2.23 ±4.20E-02 $p^{Control\ well\text{-}fed}$=1.66E-05	3.49E-01 ±8.20E-03
mir-310s (KT40/KT40) starved		2.76E+01 ±1.90E-02	9.77 ±2.24E-02	-2.24 ±1.90E-02	4.72 ±6.19E-02 $p^{Control\ well\text{-}fed}$=6.65E-07	6.74E-01 ±5.72E-03
Control (w^{1118}) well-fed	*Rpl32*	1.79E+01 ±2.57E-02	0.00 ±2.57E-02			
Control (w^{1118}) starved		1.78E+01 ±9.16E-03	6.36E-07 ±9.16E-03			
mir-310s (KT40/KT40) well-fed		1.81E+01 ±9.76E-02	0.00 ±9.76E-02			
mir-310s (KT40/KT40) starved		1.78E+01 ±1.18E-02	0.00 ±1.18E-02			
No Reverse Transcriptase						
Control (w^{1118}) well-fed	*Rpl32*	3.30E+01 ±6.88E-02	1.51E+01 ±6.88E-02	1.51E+01 ±6.88E-02	2.81E-05 ±1.34E-06	-4.55 2.07E-02
Control (w^{1118}) starved		3.29E+01 ±1.01E-01	1.51E+01 ±1.01E-01	1.51E+01 ±1.01E-01	2.90E-05 ±2.03E-06	-4.54 3.04E-02
mir-310s (KT40/KT40) well-fed		3.23E+01 ±2.68E-01	1.42E+01 ±2.68E-01	1.42E+01 ±2.68E-01	5.32E-05 ±9.93E-06	-4.27 8.06E-02
mir-310s (KT40/KT40) starved		3.30E+01 ±9.89E-03	1.52E+01 ±9.89E-03	1.52E+01 ±9.89E-03	2.67E-05 ±1.83E-07	-4.57 2.98E-03
Plate 4						
Control (w^{1118}) well-fed	*GstD4*	2.55E+01 ±3.46E-02	8.26 ±3.85E-02	-3.18E-07 ±3.46E-02	1.00 ±2.42E-02	9.57E-08 ±1.04E-02
Control (w^{1118}) starved		2.56E+01 ±2.51E-02	8.55 ±2.63E-02	2.91E-01 ±2.51E-02	8.17E-01 ±1.43E-02 $p^{Control\ well\text{-}fed}$=2.85E-03	-8.77E-02 ±7.57E-03
mir-310s (KT40/KT40) well-fed		2.54E+01 ±1.23E-02	7.72 ±3.97E-02	-5.38E-01 ±1.23E-02	1.45 ±1.24E-02 $p^{Control\ well\text{-}fed}$=7.65E-05	1.62E-01 ±3.71E-03

mir-310s (KT40/KT40) starved		2.59E+01 ±1.08E-02	8.72 ±1.58E-02	4.55E-01 ±1.08E-02	7.30E-01 ±5.46E-03 $p^{Control\ well\text{-}fed}$=3.97E-04	-1.37E-01 ±3.26E-03
Control (w^{1118}) well-fed	*Lsp1beta*	2.69E+01 ±3.96E-02	9.65 ±4.31E-02	-6.36E-07 ±3.96E-02	1.00 ±2.73E-02	1.91E-07 ±1.19E-02
Control (w^{1118}) starved		3.17E+01 ±9.43E-03	1.47E+01 ±1.23E-02	5.08 ±9.43E-03	2.95E-02 ±1.93E-04 $p^{Control\ well\text{-}fed}$=3.72E-06	-1.53 ±2.84E-03
mir-310s (KT40/KT40) well-fed		2.39E+01 ±2.93E-02	6.26 ±4.78E-02	-3.39 ±2.93E-02	1.05E+01 ±2.12E-01 $p^{Control\ well\text{-}fed}$=1.54E-06	1.02 ±8.82E-03
mir-310s (KT40/KT40) starved		2.40E+01 ±2.88E-02	6.85 ±3.11E-02	-2.80 ±2.88E-02	6.98 ±1.38E-01 $p^{Control\ well\text{-}fed}$=1.83E-06	8.44E-01 ±8.67E-03
Control (w^{1118}) well-fed	*Lsp2*	1.98E+01 ±1.86E-02	2.57 ±2.52E-02	-6.36E-07 ±1.86E-02	1.00 ±1.28E-02	1.91E-07 ±5.61E-03
Control (w^{1118}) starved		2.87E+01 ±4.05E-02	1.17E+01 ±4.12E-02	9.17 ±4.05E-02	1.74E-03 ±4.95E-05 $p^{Control\ well\text{-}fed}$=1.64E-07	-2.76 ±1.22E-02
mir-310s (KT40/KT40) well-fed		2.19E+01 ±2.81E-03	4.30 ±3.78E-02	1.72 ±2.81E-03	3.03E-01 ±5.89E-04 $p^{Control\ well\text{-}fed}$=6.91E-07	-5.19E-01 ±8.45E-04
mir-310s (KT40/KT40) starved		2.34E+01 ±2.49E-02	6.17 ±2.74E-02	3.59 ±2.49E-02	8.28E-02 ±1.44E-03 $p^{Control\ well\text{-}fed}$=2.36E-07	-1.08 ±7.49E-03
Control (w^{1118}) well-fed	*LvpH*	2.17E+01 ±4.82E-02	4.53 ±5.10E-02	-4.77E-07 ±4.82E-02	1.00 ±3.29E-02	1.44E-07 ±1.45E-02
Control (w^{1118}) starved		2.18E+01 ±2.57E-02	4.76 ±2.69E-02	2.35E-01 ±2.57E-02	8.50E-01 ±1.52E-02 $p^{Control\ well\text{-}fed}$=1.41E-02	-7.06E-02 ±7.74E-03
mir-310s (KT40/KT40) well-fed		2.23E+01 ±2.06E-02	4.63 ±4.30E-02	1.01E-01 ±2.06E-02	9.32E-01 ±1.34E-02 $p^{Control\ well\text{-}fed}$=1.26E-01	-3.04E-02 ±6.21E-03
mir-310s (KT40/KT40) starved		2.29E+01 ±2.60E-03	5.74 ±1.19E-02	1.21 ±2.60E-03	4.32E-01 ±7.80E-04 $p^{Control\ well\text{-}fed}$=6.58E-05	-3.64E-01 ±7.84E-04
Control (w^{1118}) well-fed	*Mgstl*	2.29E+01 ±1.60E-02	5.71 ±2.33E-02	-4.77E-07 ±1.60E-02	1.00 ±1.11E-02	1.44E-07 ±4.82E-03
Control (w^{1118}) starved		2.34E+01 ±1.61E-02	6.38 ±1.79E-02	6.76E-01 ±1.61E-02	6.26E-01 ±6.96E-03 $p^{Control\ well\text{-}fed}$=8.94E-06	-2.04E-01 ±4.83E-03
mir-310s (KT40/KT40) well-fed		2.24E+01 ±5.28E-03	4.78 ±3.81E-02	-9.32E-01 ±5.28E-03	1.91 ±6.99E-03 $p^{Control\ well\text{-}fed}$=2.62E-07	2.80E-01 ±1.59E-03
mir-310s (KT40/KT40) starved		2.24E+01 ±1.72E-01	5.22 ±1.72E-01	-4.89E-01 ±1.72E-01	1.40 ±1.76E-01 $p^{Control\ well\text{-}fed}$=7.43E-02	1.47E-01 ±5.17E-02
Control (w^{1118}) well-fed	*mus209*	2.19E+01 ±1.36E-02	4.70 ±2.17E-02	-6.36E-07 ±1.36E-02	1.00 ±9.37E-03	1.91E-07 ±4.08E-03
Control (w^{1118}) starved		2.44E+01 ±9.25E-03	7.39 ±1.21E-02	2.69 ±9.25E-03	1.55E-01 ±9.93E-04 $p^{Control\ well\text{-}fed}$=9.25E-08	-8.10E-01 ±2.78E-03
mir-310s (KT40/KT40) well-fed		2.19E+01 ±5.19E-03	4.24 ±3.81E-02	-4.61E-01 ±5.19E-03	1.38 ±4.96E-03 $p^{Control\ well\text{-}fed}$=3.74E-06	1.39E-01 ±1.56E-03
mir-310s (KT40/KT40) starved		2.34E+01 ±3.90E-03	6.20 ±1.22E-02	1.51 ±3.90E-03	3.52E-01 ±9.51E-04 $p^{Control\ well\text{-}fed}$=2.67E-07	-4.54E-01 ±1.18E-03

Control (w^{1118}) well-fed	*Rpl32*	1.72E+01 ±1.69E-02	-6.36E-07 ±1.69E-02			
Control (w^{1118}) starved		1.70E+01 ±7.88E-03	6.36E-07 ±7.88E-03			
mir-310s (*KT40/KT40*) well-fed		1.76E+01 ±3.77E-02	0.00 ±3.77E-02			
mir-310s (*KT40/KT40*) starved		1.72E+01 ±1.16E-02	1.27E-06 ±1.16E-02			
No Reverse Transcriptase						
Control (w^{1118}) well-fed	*Rpl32*	3.19+E01	1.47E+01	1.47E+01	3.70E-05	-4.43
Control (w^{1118}) starved		3.30E+01	1.33E+01	1.33E+01	9.94E-05	-4.00
mir-310s (*KT40/KT40*) well-fed		3.03E+01	1.27E+01	1.27E+01	1.50E-04	-3.82
mir-310s (*KT40/KT40*) starved		3.05E+01	1.33E+01	1.33E+01	9.94E-05	-4.00
Plate 5						
Control (w^{1118}) well-fed	*Obp44a*	2.69E+01 ±3.37E-02	8.55 ±3.55E-02	-3.18E-07 ±3.37E-02	1.00 ±2.36E-02	9.57E-08 ±1.01E-02
Control (w^{1118}) starved		2.67E+01 ±1.68E-02	8.41 ±5.16E-02	-1.33E-01 ±1.68E-02	1.10 ±1.29E-02 $p^{Control\ well\text{-}fed}$=2.30E-02	4.01E-02 ±5.07E-03
mir-310s (*KT40/KT40*) well-fed		2.68E+01 ±3.72E-02	7.95 ±5.92E-02	-6.01E-01 ±3.72E-02	1.52 ±3.89E-02 $p^{Control\ well\text{-}fed}$=3.42E-04	1.81E-01 ±1.12E-02
mir-310s (*KT40/KT40*) starved		2.66E+01 ±1.28E-02	8.12 ±3.78E-02	-4.28E-01 ±1.28E-02	1.35 ±1.19E-02 $p^{Control\ well\text{-}fed}$=1.98E-04	1.29E-01 ±3.84E-03
Control (w^{1118}) well-fed	*Obp56a*	2.57E+01 ±2.06E-02	7.32 ±2.34E-02	-1.59E-07 ±2.06E-02	1.00 ±1.43E-02	4.78E-08 ±6.20E-03
Control (w^{1118}) starved		2.49E+01 ±7.92E-03	6.70 ±4.94E-02	-6.17E-01 ±7.92E-03	1.53 ±8.39E-03 $p^{Control\ well\text{-}fed}$=5.50E-06	1.86E-01 ±2.38E-03
mir-310s (*KT40/KT40*) well-fed		2.79E+01 ±2.00E-02	9.05 ±5.02E-02	1.73 ±2.00E-02	3.02E-01 ±4.16E-03 $p^{Control\ well\text{-}fed}$=1.22E-06	-5.21E-01 ±6.01E-03
mir-310s (*KT40/KT40*) starved		2.75E+01 ±5.34E-02	9.00 ±6.41E-02	1.68 ±5.34E-02	3.11E-01 ±1.17E-02 $p^{Control\ well\text{-}fed}$=3.07E-06	-5.07E-01 ±1.61E-02
Control (w^{1118}) well-fed	*Obp56e*	2.46E+01 ±3.45E-02	6.25 ±3.63E-02	0.00 ±3.45E-02	1.00 ±2.41E-02	0.00 ±1.04E-02
Control (w^{1118}) starved		2.56E+01 ±1.69E-02	7.36 ±5.16E-02	1.11 ±1.69E-02	4.64E-01 ±5.41E-03 $p^{Control\ well\text{-}fed}$=2.63E-05	-3.34E-01 ±5.10E-03
mir-310s (*KT40/KT40*) well-fed		2.76E+01 ±1.19E-02	8.76 ±4.76E-02	2.51 ±1.19E-02	1.76E-01 ±1.45E-03 $p^{Control\ well\text{-}fed}$=4.35E-06	-7.55E-01 ±3.59E-03
mir-310s (*KT40/KT40*) starved		2.69E+01 ±2.14E-02	8.36 ±4.15E-02	2.11 ±2.14E-02	2.32E-01 ±3.47E-03 $p^{Control\ well\text{-}fed}$=5.96E-06	-6.35E-01 ±6.45E-03

Control (w^{1118}) well-fed	*Obp99b*	2.56E+01 ±2.63E-02	7.30 ±2.85E-02	1.59E-07 ±2.63E-02	1.00 ±1.83E-02	-4.78E-08 ±7.90E-03
Control (w^{1118}) starved		2.93E+01 ±5.85E-02	1.10E+01 ±7.62E-02	3.75 ±5.85E-02	7.44E-02 ±3.05E-03 $p^{Control\ well\text{-}fed}$=9.65E-07	-1.13 ±1.76E-02
mir-310s (*KT40/KT40*) well-fed		2.17E+01 ±5.31E-03	2.88 ±4.64E-02	-4.42 ±5.31E-03	2.14E+01 ±7.86E-02 $p^{Control\ well\text{-}fed}$=1.48E-09	1.33 ±1.60E-03
mir-310s (*KT40/KT40*) starved		2.39E+01 ±6.43E-03	5.36 ±3.61E-02	-1.94 ±6.43E-03	3.83 ±1.71E-02 $p^{Control\ well\text{-}fed}$=3.68E-08	5.83E-01 ±1.94E-03
Control (w^{1118}) well-fed	*Obst-A*	2.99E+01 ±3.09E-02	1.15E+01 ±3.29E-02	-3.18E-07 ±3.09E-02	1.00 ±2.16E-02	9.57E-08 ±9.31E-03
Control (w^{1118}) starved		2.86E+01 ±5.96E-02	1.04E+01 ±7.70E-02	-1.15 ±5.96E-02	2.21 ±8.97E-02 $p^{Control\ well\text{-}fed}$=1.92E-04	3.45E-01 ±1.79E-02
mir-310s (*KT40/KT40*) well-fed		2.88E+01 ±4.78E-02	9.92 ±6.64E-02	-1.62 ±4.78E-02	3.07 ±1.04E-01 $p^{Control\ well\text{-}fed}$=3.97E-05	4.88E-01 ±1.44E-02
mir-310s (*KT40/KT40*) starved		2.80E+01 ±2.56E-02	9.46 ±4.38E-02	-2.07 ±2.56E-02	4.20 ±7.39E-02 $p^{Control\ well\text{-}fed}$=2.00E-06	6.24E-01 ±7.71E-03
Control (w^{1118}) well-fed	*pro-PO-A1*	2.67E+01 ±3.29E-02	8.33 ±3.47E-02	3.18E-07 ±3.29E-02	1.00 ±2.26E-02	-9.57E-08 ±9.89E-03
Control (w^{1118}) starved		2.67E+01 ±4.36E-02	8.46 ±6.54E-02	1.27E-01 ±4.36E-02	9.16E-01 ±2.75E-02 $p^{Control\ well\text{-}fed}$=7.73E-02	-3.83E-02 ±1.31E-02
mir-310s (*KT40/KT40*) well-fed		3.62E+01 ±2.55E-01	1.73E+01 ±2.59E-01	8.99 ±2.55E-01	1.96E-03 ±3.78E-04 $p^{Control\ well\text{-}fed}$=1.56E-06	-2.71 ±7.68E-02
mir-310s (*KT40/KT40*) starved		3.62E+01 ±5.30E-01	1.77E+01 ±5.31E-01	9.39 ±5.30E-01	1.50E-03 ±6.56E-04 $p^{Control\ well\text{-}fed}$=1.56E-06	-2.83 ±1.59E-01
Control (w^{1118}) well-fed	*Rpl32*	1.83E+01 ±1.11E-02	0.00 ±1.11E-02			
Control (w^{1118}) starved		1.82E+01 ±4.88E-02	0.00 ±4.88E-02			
mir-310s (*KT40/KT40*) well-fed		1.89E+01 ±4.61E-02	-6.36E-07 ±4.61E-02			
mir-310s (*KT40/KT40*) starved		1.85E+01 ±3.56E-02	0.00 ±3.56E-02			
No Reverse Transcriptase						
Control (w^{1118}) well-fed -RT	*Rpl32*	3.06E+01 ±1.02E-01	1.22E+01 ±1.02E-01	1.22E+01 ±1.02E-01	9.15E-05	-4.04
Control (w^{1118}) starved -RT		3.08E+01 ±1.01E-01	1.27E+01 ±1.01E-01	1.27E+01 ±1.01E-01	1.05E-04	-3.98
mir-310s (*KT40/KT40*) well-fed -RT		3.06E+01 ±1.08E-01	1.20E+01 ±1.08E-01	1.20E+01 ±1.08E-01	1.39E-04	-3.86
mir-310s (*KT40/KT40*) starved -RT		2.99E+01 ±7.07E-01	1.17E+01 ±7.07E-01	1.17E+01 ±7.07E-01	9.03E-05	-4.04
Plate 6						

Control (w^{1118}) well-fed	*Sucb*	2.38E+01 ±3.20E-02	5.40 ±4.19E-02	1.11E-06 ±3.20E-02	1.00 ±2.20E-02	-3.35E-07 ±9.62E-03
Control (w^{1118}) starved		2.43E+01 ±2.38E-02	6.23 ±5.19E-02	8.30E-01 ±2.38E-02	5.62E-01 ±9.29E-03 $p^{Control\ well\text{-}fed}$=5.23E-05	-2.50E-01 ±7.16E-03
mir-310s (*KT40/KT40*) well-fed		2.39E+01 ±3.60E-02	5.24 ±6.33E-02	-1.59E-01 ±3.60E-02	1.12 ±2.80E-02 $p^{Control\ well\text{-}fed}$=3.08E-02	4.78E-02 ±1.08E-02
mir-310s (*KT40/KT40*) starved		2.43E+01 ±1.63E-02	5.99 ±4.23E-02	5.95E-01 ±1.63E-02	6.62E-01 ±7.46E-03 $p^{Control\ well\text{-}fed}$=1.30E-04	-1.79E-01 ±4.90E-03
Control (w^{1118}) well-fed	*Rpl32*	1.84E+01 ±2.71E-02	1.27E-06 ±2.71E-02			
Control (w^{1118}) starved		1.81E+01 ±4.62E-02	-6.36E-07 ±4.62E-02			
mir-310s (*KT40/KT40*) well-fed		1.86E+01 ±5.21E-02	6.36E-07 ±5.21E-02			
mir-310s (*KT40/KT40*) starved		1.83E+01 ±3.91E-02	-6.36E-07 ±3.91E-02			
No Reverse Transcriptase						
Control (w^{1118}) well-fed	*Rpl32*	3.06E+01 ±1.02E-01	1.22E+01 ±1.02E-01	1.22E+01 ±1.02E-01	2.11E-05 ±1.45E-05	-3.68 3.08E-02
Control (w^{1118}) starved		3.08E+01 ±1.01E-01	1.27E+01 ±1.01E-01	1.27E+01 ±1.01E-01	1.51E-05 ±1.03E-05	-3.82 3.05E-02
mir-310s (*KT40/KT40*) well-fed		3.06E+01 ±1.08E-01	1.20E+01 ±1.08E-01	1.20E+01 ±1.08E-01	2.45E-05 ±1.81E-05	-3.61 3.24E-02
mir-310s (*KT40/KT40*) starved		2.99E+01 ±7.07E-01	1.17E+01 ±7.07E-01	1.17E+01 ±7.07E-01	3.05E-04 ±1.43E-04	-3.52 2.13E-01

[a] The relative mRNA levels were calculated by $2^{-\Delta\Delta CT}$.

[b] Average (AVE) and standard error of the mean (SEM) values were calculated based on three replicates for each genotype/condition/gene value.

[c] Significance was calculated using two-tailed non-paired Student's t-test.

Flies were fed with nutritionally rich or poor medium for 10 days before analysis.

Table S3, related to Figure S1. *mir-310s* mutants exhibit global defects associated with nutritional stress

Genotype/Condition / Phenotype	*Control* (w^{1118}) well-fed[a]	*mir-310s* (*KT40/KT40*) well-fed[a]	*Control* (w^{1118}) starved[a]	*mir-310s* (*KT40/KT40*) starved[a]
Crop diameter[b]: (in mm) (AVE±SEM) n=number of crops analyzed	0.65±0.05 n=12	0.85±0.04 n=10 $p^{Control\ well\text{-}fed}$=0.007	0.44±0.05 n=10	0.44±0.04 n=10 $p^{Control\ starved}$=1,00
Lipid Accumulation: µg TAG equivalents per mg protein (AVE±SEM) n=number of females analyzed	(3 days) 386.77±35.68 n=30	(3 days) 210.67±28.57 n=20 $p^{Control\ well\text{-}fed}$=0.008	(10 days) 582.07±217.43 n = 30 $p^{Control\ well\text{-}fed}$=0.04	(10 days) 1581.0±202.03 n=30 $p^{Control\ well\text{-}fed}$=0.0002 $p^{Control\ starved}$=0.006
Fecundity: Eggs laid per fly per day (AVE±SEM) n=number of females analyzed	16.48±1.76 n=49	6.03±0.4 n=50 $p^{Control}$=0.004		

Relative egg laying efficiency under starvation	well-fed	1 day starved	2 day starved	3 day starved	4 day starved
Control (w^{1118}) n=50	1±0.01	0.95±0.08	0.49±0.08	0.14±0.03	0.06±0.02
mir-310s (*KT40/KT40*) n=50	1±0.19 $p^{Control\ well\text{-}fed}$= 7.82E-04	0.31±0.01 $p^{Control\ 1\ day}$ = 5.48E-04	0.28±0.04 $p^{Control\ 2\ day}$ = 8.9E-03	0.12±0.03 $p^{Control\ 3\ day}$ = 2.22E-02	0.11±0.04 $p^{Control\ 4\ day}$ = 4.5E-01

[a] Flies were fed with nutritionally rich and starvation medium for 10 days prior to analysis.

[b] Maximum crop diameters were measured from bright field images using Adobe Photoshop software.

Three biological replicates were analyzed for each genotype/condition.

Significance was tested using two-tailed non-paired Student's t-test.

Table S4, related to Figure 3. The *mir-310s* target *Rab23, DHR96,* and *ttk in vitro*

3'UTR Reporter	Control *3'UTR* without *mir-310s* binding site	*Rab23 3`UTR*	*DHR96 3`UTR*	*ttk 3`UTR*	negative control short *Dg 3'UTR* without *mir-310s* binding site[a]	positive control long *Dg 3'UTR* with *mir*-310s binding site[b]
Luciferase Signal (*Renilla/Firefly*) AVE±SEM	7.76E-02 ±3.62E-03	2.41E-02 ±3.96E-03	3.75E-02 ±2.10E-03	3.60E-02 ±3.18E-03	9.16E-02 ±1.96E-03	2.09E-02 ±8.29E-04
Relative Luciferase Signal AVE±SEM	1.00 ±4.67E-02	3.11E-01 ±5.10E-02 p=2.09E-04	4.83E-01 ±2.71E-02 p=1.54E-04	4.63E-01 ±4.10E-02 p=3.48E-04	1.18 ±2.52E-02 p=1.14E-02	2.69E-01 ±1.07E-02 p=1.03E-05

Luciferase reporter assays were performed in three biological replicates for each gene.

Significance was tested using two-tailed non-paired Student's t-test.

The short ([a]) and long ([b]) *3`UTR*s of a confirmed *mir-310s* target gene, *Dystroglycan* (*Dg*)

(YATSENKO *et al.* 2014), were used as negative and positive controls, respectively.

Table S5, related to Figure 2 and 3. Relative mRNA and miRNA expression levels

qRT-PCR					
Genotype/ Condition	C_T^{Rab23} AVE±SEM[b]	C_T^{Rpl32} AVE±SEM[b]	Δ C_T AVE±SEM[b]	ΔΔ C_T AVE±SEM[b]	Relative ***Rab23*** mRNA level[a,c] AVE± SEM[b]
Control (w^{1118}) well-fed	2.42E+01 ±2.7E-01	1.85E+01 ±1.97E-01	5.71 ±8.18E-02	0.00 ±8.18E-02	1.00 ±5.18E-02
mir-310s (*KT40/KT40*) well-fed	2.41E+01 ±1.04E-01	1.9E+01 ±5.34E-02	5.06 ±6.22E-02	-6.48E-01 ±7.23E-02	1.57 ±7.08E-02 $p^{Control\ well\text{-}fed}$ =2.9E-03
Control (w^{1118}) starved	2.8E+01 ±3.1E-01	1.86E+01 ±1.21E-01	9.32 ±1.79E-01	3.61 ±2.67E-01	8.17E-02 ±1.4E-02 $p^{Control\ well\text{-}fed}$ =1.04E-05
mir-310s (*KT40/KT40*) starved	2.59E+01 ±1.98E-01	1.87E+01 ±9.29E-02	7.2 ±1.15E-01	1.49 ±1.52E-01	3.56E-01 ±3.47E-02 $p^{Control\ starved}$ =5.64E-04
	C_T^{DHR96} AVE±SEM	C_T^{Rpl32} AVE±SEM	Δ C_T AVE±SEM	ΔΔ C_T AVE±SEM	Relative ***DHR96*** mRNA level AVE± SEM
Control (w^{1118}) well-fed	2.66E+01 ±1.87E-01	1.83E+01 ±1.34E-01	8.24 ±1.21E-01	0.00 ±6.43E-02	1.00 ±3.23E-02
mir-310s (*KT40/KT40*) well-fed	2.66E+01 ±1.52E-01	1.90E+01 ±5.72E-02	7.61 ±8.62E-02	-6.35E-01 ±1.11E-01	1.55 ±9.1E-02 $p^{Control\ well\text{-}fed}$ =5.52E-03
Control (w^{1118}) starved	2.85E+01 ±1.14E+01	1.86E+01 ±1.14E-01	9.93 ±9.17E-02	1.69 ±9.36E-02	3.12E-01 ±1.43E-02 $p^{Control\ well\text{-}fed}$ =7.99E-06
mir-310s (*KT40/KT40*) starved	2.75E+01 ±1.1E-01	1.86E+01 ±5.7E-02	8.87 ±5.79E-02	6.28E-01 ±6.06E-02	6.47E-01 ±1.53E-02 $p^{Control\ starved}$ =1.3E-04
	C_T^{ttk} AVE±SEM	C_T^{Rpl32} AVE±SEM	Δ C_T AVE±SEM	ΔΔ C_T AVE±SEM	Relative ***ttk*** mRNA level AVE± SEM
Control (w^{1118}) well-fed	2.56E+01 ±2.48E-01	1.89E+01 ±2.06E-01	6.67 ±1.72E-01	0.00 ±5.53E-02	1.00 ±4.04E-02
mir-310s (*KT40/KT40*) well-fed	2.64E+01 ±9.0E-02	1.97E+01 ±2.12E-01	6.66 ±1.61E-01	-4.0E-03 ±1.22E-01	1.002 ±8.94E-02 $p^{Control\ well\text{-}fed}$=9.54E-01
Control (w^{1118}) starved	2.69E+01 ±1.18E-01	1.91E+01 ±1.08E-01	7.82 ±1.03E-01	1.16 ±3.42E-01	0.45 ±4.2E-02 $p^{Control\ well\text{-}fed}$ =5.63E-05
mir-310s (*KT40/KT40*) starved	2.64E+01 ±1.13E-01	1.93E+01 ±1.53E-01	7.17 ±1.61E-01	5.06E-01 ±1.39E-01	0.70 ±9.93E-02 $p^{Control\ starved}$=2.14E-02
TaqMan MicroRNA Assay					
	$C_T^{mir\text{-}310}$ AVE±SEM	$C_T^{2S\ rRNA}$ AVE±SEM	Δ C_T AVE±SEM	ΔΔ C_T AVE±SEM	Relative ***mir-310*** level AVE± SEM
Control (w^{1118}/*Oregon-R-C*) well-fed	2.54E+01 ±2.26E+00	1.05E+01 ±2.26E+00	1.49E+01 ±4.45E-02	0.00 ±5.86E-02	1.00 ±4.07E-02
Control (w^{1118}/*Oregon-R-C*) starved	2.42E+01 ±2.01E+00	9.83E+00 ±2.01E+00	1.43E+01 ±6.58+E-02	-6.14E-01 ±1.03E-01	1.54 ±1.12E-01 $p^{Control\ well\text{-}fed}$ =1.07E-02
	$C_T^{mir\text{-}312}$ AVE±SEM	$C_T^{2S\ rRNA}$ AVE±SEM	Δ C_T AVE±SEM	ΔΔ C_T AVE±SEM	Relative ***mir-312*** level AVE± SEM
Control (w^{1118}/*Oregon-R-C*) well-fed	2.55E+01 ±2.26E+00	9.48E+00 ±1.60E+00	1.60E+01 ±6.67E-01	0.00 ±1.03E-01	1.00 ±6.62E-02
Control (w^{1118}/*Oregon-R-C*) starved	2.86E+01 ±2.23E+00	1.13E+01 ±1.31E+00	1.54E+01 ±1.00E+00	-5.27E-01 ±2.54E-01	1.49 ±2.53E-01 $p^{Control\ well\text{-}fed}$ = 2.94E-02

[a] The relative mRNA levels were calculated by $2^{-\Delta\Delta CT}$.

[b] Average (AVE) and standard error of the mean (SEM) values were calculated using at least three biological replicates for each genotype and condition.

[c] Significance was tested using two-tailed non-paired Student's t-test.

Flies were fed with nutritionally rich and poor medium for 10 days prior analysis.

Table S6, related to Figure 4. Rab23 is upregulated at the germarial niche upon *mir-310s* loss

Genotype/ Condition	Rab23-expressing CpC percentage AVE±SEM[a]		
	negative	positive	
		low	high
w^{1118}; Rab23::YFP::4xmyc well-fed n=6	17.75±2.41%	36.33±5.34%	45.92±6.19%
mir-310s; Rab23::YFP::4xmyc well-fed n=6	4.46±3.1% $p^{w1118;\ Rab23::YFP::4xmyc}_{well\text{-}fed}$ =0.0035	51.19±9.4%	44.35±10.95%
w^{1118}; Rab23::YFP::4xmyc starved n=6	6.94±3.47%	72.22±4.36%	20.83±4.08%
mir-310s; Rab23::YFP::4xmyc starved n=6	7.54±3.71%	35.19±3.09%	57.28±4.7% $p^{w1118;\ Rab23::YFP::4xmyc}_{starved}$ =0.00082

[a] Averages and the standard errors of the means were calculated using five replicates.

Significances between the percentages of the cap cells (CpCs) that differentially express Rab23 protein: Rab23 negative CpCs under well-fed condition and the CpCs that have high Rab23 expression under starvation condition were calculated using a two tailed Student's t-test.

In order to analyze the significance between the frequencies of CpCs that differentially express Rab23 protein [negative or positive (high or low)] in control and *mir-310s* mutant germaria under well-fed and starved conditions, two-way tables and chi-squared test with 6 degrees of freedom were used. Chi-square value is 11.311 and p value is 0.079227.

Table S7, related to Figure 4. Upon *mir-310s* loss or Rab23 overexpression, the number of Hh-positive speckles in the germarium increases

Genotype	number Hh speckles AVE±SEM	
	well-fed	starved
Control (w^{1118}/*Oregon-R-C*)	92.67±3.66 n=9	55.11±8.62 n=9 $p^{Control\ well\text{-}fed}$ =1.04E-02
mir-310s (*KT40/KT40*)	198.67±17.53 n=9 $p^{Control\ well\text{-}fed}$ =7.25E-05	169.33±6.09 n=9 $p^{Control\ starved}$ =9.04E-09 $p^{mir\text{-}310s\ well\text{-}fed}$ =1.33E-01
bab1>Rab23 (*bab1-Gal4/UAS-Rab23*)	260.0±26.86 n=9 $p^{Control\ well\text{-}fed}$ =2.41E-05	198.89±11.96 n=9 $p^{Control\ starved}$ =3.89E-08 $p^{bab1>Rab23\ well\text{-}fed}$ =5.41E-02

Confocal images were analyzed using the particle analyzer tool from ImageJ software to quantify Hedgehog (Hh) speckle numbers.

p-values were calculated using two-tailed non-paired Student's t-test.

Table S8, related to Figure 4. Rab23 co-immunoprecipitated proteins

CG number	Gene name
CG2108	Rab23
CG7920	CG7920
CG2152	Pcmt
CG4916	me31B
CG7445	fln
CG30395	CG30395
CG6821	Lsp1gamma
CG6803	Mf
CG8867	Jon25Bi
CG9769	eIF3-S5-1
CG5887	desat1
CG5654	yps
CG7113	scu
CG4153	eIF-2beta
CG4466	Hsp27
CG1742	Mgstl
CG16765	ps
CG7178	wupA
CG11844	vig2;fdy
CG5330	Nap1
CG2229	Jon99Fii
CG4769	CG4769
CG10306	CG10306
CG3800	CG3800
CG4533	l(2)efl
CG4183	Hsp26
CG18811	Capr
CG8308	alphaTub67C
CG1633	Jafrac1
CG9641	CG9641
CG45077	fau
CG34069	mt:CoII
CG5422	Rox8
CG8871	Jon25Biii
CG5885	BEST:CK01296
CG13425	bl
CG5258	NHP2
CG10922	La
CG10578	DnaJ-1
CG10849	Sc2
CG6543	CG6543
CG4302	BEST:GH09393

CG5641	CG5641
CG8053	eIF-1A
CG6341	Ef1beta
CG4008	und
CG4170	vig
CG4666	CG4666
CG10279	Rm62
CG1469	Fer2LCH
CG13849	Nop56
CG6987	SF2
CG8189	ATPsyn-b
CG4193	dhd
CG4912	eEF1delta
CG6258	RfC38
CG8427	SmD3
CG10851	B52
CG3972	Cyp4g1
CG14999	RfC4
CG6617	CG6617
CG4003	pont
CG17136	Rbp1
CG31362	Jon99Cii
CG14813	deltaCOP
CG10206	nop5
CG5313	RfC3
CG5352	SmB
CG32701	l(1)G0320
CG8231	Tcp-1zeta
CG4376	Actn
CG8142	CG8142
CG4978	Mcm7
CG4611	CG4611
CG13240	l(2)35Di
CG11835	CG11835
CG45076	fau
CG7172	CG7172
CG7436	Nmt
CG6693	CG6693
CG9306	CG9306
CG7917	Nlp
CG15092	Jabba
CG8977	Cctgamma
CG13887	CG13887
CG7637	CG7637

CG18067	CG18067
CG8844	Pdsw
CG17686	DIP1
CG5289	Pros26.4
CG5047	mTerf3
CG4799	Pen
CG11107	CG11107
CG5374	T-cp1
CG4422	Gdi
CG18591	SmE
CG8715	lig
CG4082	Mcm5
CG2216	Fer1HCH
CG12203	CG12203
CG10628	CG10628
CG3029	or
CG5167	CG5167
CG12306	polo
CG4729	CG4729
CG6519	Cp15
CG30185	Gr59f
CG7182	CG7182
CG17566	gammaTub37C
CG11999	CG11999
CG16725	Smn
CG17280	levy
CG3446	CG3446
CG12400	CG12400
CG4553	CG4553
CG8322	ATPCL
CG3039	ogre
CG6094	CG6094
CG10097	CG10097
CG1489	Pros45
CG14207	HspB8
CG17611	eIF6
CG3333	Nop60B
CG7409	CG7409
CG3944	ND23
CG30008	CG12138
CG5371	RnrL
CG3267	l(2)04524
CG4824	BicC
CG5903	CG5903

CG15481	Ski6
CG14476	BcDNA.GH04962
CG3436	CG3436
CG31249	CG7477
CG6746	CG6746
CG7581	Bub3
CG7378	CG7378
CG8905	Sod2
CG6013	CG6013
CG1616	dpa
CG1938	Dlic
CG4634	Nurf-38
CG7911	CG7911
CG3747	Eaat1
CG4164	CG4164
CG6202	Surf4
CG4619	CG4619
CG13126	CG13126
CG5703	CG5703
CG31523	CG9798
CG9155	Myo61F
CG8258	CG8258
CG30176	wibg
CG8947	26-29-p
CG3710	TfIIS
CG3606	caz
CG1249	SmD2
CG13163	CG13163
CG3683	CG3683
CG12984	CG12984
CG8547	CG8547
CG8542	Hsc70-5
CG7033	CG7033
CG4206	Mcm3
CG12163	CG12163
CG3564	CHOp24
CG10833	Cyp28d1
CG5826	Prx3
CG8190	eIF2B-gamma
CG5183	KdelR
CG7006	CG7006
CG12357	Cbp20
CG4274	fzy
CG7830	Ostgamma

CG16912	CG16912
CG5508	BcDNA
CG3416	Mov34
CG7483	eIF4AIII
CG17437	wds
CG4020	CG4020
CG9548	CG9548
CG18444	alphaTry
CG1101	Ref1
CG10297	Acp65Aa
CG5000	msps
CG3420	CG3420
CG14309	CG14309
CG9987	CG9987
CG7123	LanB1
CG1751	Spase25
CG8680	CG8680
CG6137	aub
CG3422	Pros28.1
CG10469	CG10469
CG7619	Pros54
CG1828	dre4
CG34026	CG34026
CG3359	mfas
CG7361	RFeSP
CG9054	Ddx1
CG8351	Tcp-1eta
CG16904	CG16904
CG11804	ced-6
CG9302	CG9302
CG7697	CstF-64
CG9172	CG9172
CG9383	asf1
CG10045	GstD1
CG7488	CG7488
CG4760	bol
CG1453	Klp10A
CG6782	sea
CG7008	Tudor-SN
CG11876	CG11876
CG4463	Hsp23
CG4279	LSm1
CG11989	vnc
CG5864	AP-1sigma
CG44255	CG13644
CG10212	SMC2
CG10470	CG10470

CG2910	nito
CG15735	CG15735
CG1877	lin19
CG8749	snRNP-U1-70K
CG5548	CG5548
CG8711	Cul-4
CG16983	skpA
CG18559	Cyp309a2
CG7946	CG7946
CG3845	NAT1
CG13298	CG13298
CG33104	eca;p24-2
CG2014	CG2014
CG5555	CG5555
CG9741	Dhod
CG3424	path
CG10687	Aats-asn
CG2621	sgg
CG13091	CG13091
CG42807	CG6183
CG3917	Grip84
CG3909	CG3909
CG3664	Rab5
CG3059	NTPase
CG15877	CG15877
CG32441	CG32441
CG6416	Zasp66
CG1548	cathD
CG8409	Su(var)205
CG13277	LSm7
CG10203	x16
CG4115	CG4115
CG13570	spag
CG12908	Ndg
CG11785	bai
CG15531	CG15531
CG6249	Csl4
CG8827	Ance
CG3200	Reg-2
CG1703	CG1703
CG4447	CG4447
CG11837	CG11837
CG7359	Sec22
CG5670	Atpalpha
CG10360	ref(2)P
CG2604	CG2604
CG5252	Ranbp9

CG30149	rig
CG6235	tws
CG3678	CG17556
CG10210	tst
CG8548	Kap-alpha1
CG3068	aur
CG2175	CG2175
CG6375	pit
CG3295	CG3295
CG9018	CG9018
CG3959	pelo
CG9799	CG9799
CG14224	Ubqn
CG11092	Nup93-1
CG6866	loqs
CG1119	Gnf1
CG8625	Iswi
CG9128	Sac1
CG3815	CG3815
CG4051	egl
CG34074	mt:CoIII
CG1091	CG1091
CG13935	Cpr62Bb
CG3299	Vinc
CG8397	CG8397
CG2867	Prat
CG11015	CoVb
CG9889	yellow-d
CG2071	Ser6
CG3582	U2af38
CG3561	Dbp21E2
CG8648	Fen1
CG7833	Orc5
CG33141	sns
CG7288	CG7288
CG2031	Hpr1
CG1307	CG1307
CG9749	Abi
CG5272	gnu
CG10159	BEAF-32
CG31368	CG31368
CG11137	CG11137
CG3071	EG:25E8.3
CG14788	ns3
CG4088	lat
CG7109	mts
CG3056	ssx

CG9159	Kr-h2
CG31717	CG31717
CG18347	CG18347
CG4038	CG4038
CG10498	cdc2c
CG13472	CG13472
CG6841	CG6841
CG9350	CG9350
CG10472	CG10472
CG6948	Clc
CG12000	Prosbeta7
CG1179	LysB;LysD;LysA;LysE
CG11777	CG11777
CG1685	pen
CG33129	CG6089
CG33503	Cyp12d1-d
CG4039	Mcm6
CG9547	CG9547
CG10333	CG10333
CG9441	Pu
CG3157	gammaTub23C
CG5001	CG5001
CG5193	TfIIB
CG18124	mTTF
CG7929	ocn
CG12128	CG12128
CG3320	Rab1
CG1401	Cul-5
CG3412	slmb
CG15433	Elp3
CG4152	l(2)35Df
CG3501	CG3501
CG11397	glu
CG9253	CG9253
CG4365	CG4365
CG17454	CG17454
CG7970	CG7970
CG1406	U2A
CG5099	msi
CG3625	CG3625
CG5358	Art4
CG8571	smid
CG11583	CG11583
CG10326	CG10326
CG17018	CG17018
CG8553	SelD

CG9267	CG9267
CG3262	CG3262
CG5205	CG5205
CG12325	CG12325
CG9191	Klp61F
CG4609	fax
CG7375	CG7375
CG5726	CG5726
CG4097	Pros26
CG11984	CG11984
CG10327	TBPH
CG9829	poly
CG11007	CG11007
CG6601	Rab6;Rab39
CG17608	fu12
CG12170	CG12170
CG6450	lva
CG17285	Fbp1
CG3509	CG3509
CG5655	Rsf1
CG2034	anon-i1
CG9246	CG9246
CG12333	CG12333
CG3605	CG3605
CG4086	Su(P)
CG1963	Pcd
CG12352	san
CG10673	CG10673
CG31137	twin
CG14100	CG14100
CG3224	CG3224
CG11077	CG11077
CG12343	Syf2
CG9802	Cap
CG2875	CG2875
CG9621	Adgf-D
CG8323	CG8323
CG33214	Glg1
CG5913	CG5913
CG4241	att-ORFA
CG5495	Txl
CG6907	CG6907
CG6796	CG6796
CG5553	DNApol-alpha60
CG2076	CG2076
CG11416	uri
CG11875	Nup37

CG11241	CG11241
CG4857	tyf
CG7910	CG7910
CG5442	SC35
CG2917	Orc4
CG5266	Pros25
CG5923	DNApol-alpha73
CG8385	Arf79F
CG4303	Bap60
CG1081	Rheb
CG8453	Cyp6g1
CG7382	CG7382
CG5677	Spase22-23
CG5581	Ote
CG1512	Cul-2
CG10850	ida
CG3265	Eb1
CG14542	vps2
CG7626	Spt5
CG10535	Elp1
CG7175	mTerf5
CG11943	Nup205
CG8454	Vps16A
CG14802	MED18
CG6311	Edc3
CG6339	rad50
CG7704	Taf5
CG5949	DNApol-delta
CG1768	dia
CG8360	CG8360
CG18125	Send2
CG10254	CG10254
CG18543	mtrm
CG9143	CG9143
CG33523	CG33523
CG12702	CG12702
CG8306	CG8306
CG3431	Uch-L5
CG9446	CG9446
CG9890	CG9890
CG1956	R
CG34325	CG34325
CG14995	CG14995
CG4798	l(2)k01209
CG32638	CG32638
CG10988	l(1)dd4
CG3808	CG3808

CG1634	Nrg
CG2161	Rga
CG6851	Mtch
CG14213	Rcd-1
CG2925	noi
CG2789	CG2789
CG12323	Prosbeta5
CG2051	CG2051
CG5942	brm
CG4901	CG4901
CG17255	nocte
CG9300	CG9300
CG9399	CG9399
CG2358	twr
CG12473	stnB
CG14472	poe
CG12320	CG12320
CG18259	CG18259
CG6113	Lip4
CG18190	CG18190
CG6768	DNApol-epsilon
CG6998	ctp;Cdlc2
CG4461	CG4461
CG3312	Rnp4F
CG6582	Aac11
CG8705	pnut
CG44248	Snp
CG45076	CG45076
CG10415	TflIEalpha
CG1057	MED31
CG12363	Dlc90F
CG4254	tsr
CG5198	CG5198
CG6717	Spn28B
CG3697	mei-9
CG5222	IntS9
CG9742	SmG
CG7595	ck
CG4665	Dhpr
CG6958	Nup133
CG4118	nxf2
CG5989	CG5989
CG4215	spel1
CG31671	tho2
CG11887	Elp2
CG5208	Patr-1
CG3291	pcm

CG7238	sip1
CG3151	Rbp9
CG6197	CG6197
CG10622	Sucb
CG17492	mib2
CG12878	btz
CG9050	psd
CG12050	CG12050
CG31322	Aats-met
CG10189	CG10189
CG17337	CG17337
CG8156	Arf51F
CG32549	CG32549
CG4091	CG4091
CG18076	shot
CG9250	Mpp6
CG34387	futsch
CG2684	lds
CG12752	Nxt1
CG12031	MED14
CG12298	sub
CG6967	CG6967
CG1490	Usp7
CG4268	Pitslre
CG14257	CG14257
CG12217	PpV
CG32732	CG12542
CG6354	Rb97D
CG10153	CG10153
CG33113	Rtnl1
CG1750	CG1750
CG18273	CG18273
CG1216	mri
CG11981	Prosbeta3
CG6995	Saf-B
CG7351	PCID2
CG8545	CG8545
CG6805	CG6805
CG9323	CG9323
CG17259	CG17259
CG32075	CG6316
CG32211	Taf6
CG18069	CaMKII
CG9774	rok
CG9791	CG9791
CG17947	alpha-Cat
CG8778	CG8778

CG12272	CG12272
CG8602	CG8602
CG7433	CG7433
CG6349	DNApol-alpha180
CG5714	ecd
CG30021	metro
CG34033	CG34033
CG5819	CG5819
CG4780	membrin
CG12113	IntS4
CG1318	Hexo1
CG6233	Ufd1-like
CG1372	yl
CG7899	Acph-1
CG10418	CG10418
CG33217	CG33217
CG6363	MRG15
CG34407	Not1
CG6418	CG6418
CG11414	CG11414
CG18176	defl
CG32721	NELF-B
CG8725	CSN4
CG10215	Ercc1
CG7670	WRNexo
CG10990	Pdcd4
CG3460	Nmd3
CG11909	tobi
CG1669	kappaB-Ras
CG10545	Gbeta13F
CG4165	CG4165
CG8590	Klp3A
CG33505	U3-55K
CG4845	psidin
CG10630	blanks
CG3642	Clp
CG18600	CG18600
CG1276	TfIIEbeta
CG12391	CG12391
CG10572	Cdk8
CG42468	Sfp24F
CG10938	Prosalpha5
CG3093	dor
CG4572	CG4572
CG2699	Pi3K21B
CG5884	par-6
CG1597	CG1597

CG7831	ncd
CG7108	DNApol-alpha50
CG31852	Tap42
CG8448	mrj
CG3173	IntS1
CG5465	MED16
CG16892	CG16892
CG7718	CG7718
CG14444	APC7
CG8729	rnh1
CG40300	AGO3
CG4379	Pka-C1
CG3423	SA
CG31390	MED7
CG34034	CG34034
CG1440	CG1440
CG9104	CG9104
CG4764	CG4764
CG6769	CG6769
CG12372	spt4
CG7338	CG7338
CG18332	CSN3
CG8211	IntS2
CG32438	Smc5
CG11132	DMAP1
CG5168	CG5168
CG10261	aPKC
CG2146	didum
CG12018	CG12018
CG2941	CG2941
CG7003	Msh6
CG3699	EG:BACR7A4.14
CG34424	CG34424
CG18729	zwilch
CG5643	wdb
CG9630	CG9630
CG9623	if
CG31716	Cnot4
CG6603	Hsc70Cb
CG8392	Prosbeta1
CG1009	Psa
CG30488	CG30488
CG7843	Ars2
CG11334	CG11334
CG2072	Mad1
CG32498	dnc

CG1911	CAP-D2
CG7839	CG7839
CG31048	spg
CG14286	CG14286
CG15701	CG15701
CG6176	Grip75
CG8440	Lis-1
CG9916	Cyp1
CG1709	Vha100-1
CG4749	CG4749
CG18780	MED20
CG4261	Hel89B
CG2158	Nup50
CG6875	asp
CG9841	EfSec
CG33122	cutlet
CG9591	omd
CG5008	GNBP3
CG7741	CG7741
CG4364	CG4364
CG1666	Hlc
CG7764	mrn
CG4291	CG4291
CG9248	CG9248
CG12785	Mat89Ba
CG1945	faf
CG17665	IntS3
CG9755	pum
CG2206	l(1)G0193
CG5800	CG5800
CG11990	hyx
CG13957	CG13957
CG7999	MED24
CG8019	hay
CG9925	CG9925
CG11710	CG11710
CG2124	CG2124
CG16865	CG16865
CG17912	CG17912
CG12819	sle;CG12592
CG9953	CG9953
CG9067	CG9067
CG9297	CG9297
CG16812	CG16812
CG9997	CG9997
CG4633	Aats-ala-m
CG17242	CG17242

CG2244	MTA1-like
CG2078	Myd88
CG13492	CG13492
CG1725	dlg1
CG14215	CG14215
CG11722	CG11722
CG9601	CG9601
CG12267	CG12267
CG31418	CG31418
CG33106	mask
CG7261	CG7261
CG10347	CG10347
CG11821	Cyp12a5
CG10923	Klp67A
CG6364	CG6364
CG5116	CG5116
CG6673	GstO2
CG10092	CG10092
CG12896	Prx2540-2
CG15645	cerv
CG33180	Ranbp16
CG11061	GM130
CG14299	CG14299
CG8426	l(2)NC136
CG31278	CG31278
CG2669	hd
CG10582	Sin
CG8610	Cdc27
CG7180	CG7180
CG8815	Sin3A
CG33056	CG10517
CG7825	Rad17
CG4700	Sema-2a
CG42600	clos
CG8367	cg
CG11330	cort
CG4561	Aats-tyr
CG6814	Asun
CG30463	pgant9
CG1258	pav
CG42574	ctrip
CG3975	Pol32
CG8771	CG8771
CG11143	Inos
CG11799	fd68A
CG6760	Pex1
CG1664	sbr

CG34408	CG34408
CG9198	shtd
CG7989	wcd
CG33139	Ranbp11
CG32473	CG32473
CG9088	lid
CG10726	barr
CG8915	CG8915
CG8318	Nf1
CG10542	Bre1
CG11486	CG11486
CG33484	zormin
CG6677	ash2
CG15811	Rop
CG4589	Letm1
CG6170	HDAC6
CG2701	crm
CG31045	Mhcl
CG13142	CG13142
CG18140	Cht3
CG3999	CG3999
CG3329	Prosbeta2

CG4790	fs(1)M3
CG1569	rod
CG17704	Nipped-B
CG6379	CG6379
CG2049	Pkn
CG6415	CG6415
CG9911	CG9911
CG1345	Gfat2
CG4069	CG4069
CG3228	kz
CG9594	Chd3
CG2864	Parg
CG11120	CG11120
CG7235	Hsp60C
CG7162	MED1
CG4792	Dcr-1
CG12052	lola
CG6511	CG6511
CG6606	Rip11
CG17209	CG17209
CG1643	Atg5
CG3510	CycB

CG15737	wisp
CG31793	CG17338
CG10042	MBD-R2
CG7660	Pxt
CG1031	alpha-Est1
CG6623	SIDL
CG10837	eIF-4B
CG1782	Uba1
CG32562	xmas-2
CG12010	CG12010
CG11411	fs(1)N
CG1433	Atu
CG4453	Nup153
CG42250	lqfR
CG3041	Orc2
CG43078	CG43078
CG4554	CG4554
CG7487	RecQ4
CG12153	Hira
CG32604	l(1)G0007
CG12090	CG12090
CG12499	CG12499

CG2707	fs(1)Ya
CG8153	mus210
CG1915	sls
CG5859	IntS8
CG12196	egg
CG13397	ESTS:172F5T
CG6206	LM408
CG3520	CG3520
CG12005	Mms19
CG33554	Nipped-A
CG6535	tefu
CG31445	CG11955
CG5874	Nelf-A
CG6539	Gem3
CG7337	CG7337
CG44162	Strn-Mlck
CG2520	lap
CG14796	Mur2B
CG2747	CG2747

Co-immunoprecipitated protein hits were filtered for 5-fold enrichment in the tagged Rab23 sample (w^{1118}; *Rab23::YFP::4xmyc*) compared to control (w^{1118}), resulting in 821 unique proteins.

COPI-associated proteins are highlighted.

Table S9, related to Figures 5 and 6. The frequencies of the analyzed ovarian phenotypes

Genotype \ Phenotype	Disorganized germarium architecture at region 2A/B	Abnormal egg chamber encapsulation	Multilayered stalk	Persisting FasIII expression	Multilayered follicular epithelium	
Control (*w^{1118}/Oregon-R-C*)	26.7% n=30	0% n=20	5% n=20	0% n=35	well-fed[a] 15% n=20	starved[a] 0% n=20 $p^{well\text{-}fed}$=0.072
mir-310s (*KT40/KT40*)	86.7% n=30 $p^{Control}$<0.0001	35% n=20 $p^{Control}$=0.004	75% n=20 $p^{Control}$<0.0001	44.4% n=35 $p^{Control}$<0.0001	well-fed[a] 45% n=20	starved[a] 5% n=20 $p^{well\text{-}fed}$=0.003
mir-310s (*w[*]; Df(2R)mir-310-311-312-313 FRT42D*)	66.7% n=30 $p^{Control}$=0.002	5% n=20 $p^{Control}$=0.311	65% n=20 $p^{Control}$<0.0001	54.2% n=35 $p^{Control}$<0.0001	50% n=20 $p^{Control}$=0.018	
mir-310s/ Df6070 (*w[1118]; KT40/Df(2R)Exel6070, P{w[+mC]=XP-U}Exel6070*)	80% n=30 $p^{Control}$<0.0001	40% n=20 $p^{Control}$=0.002	70% n=20 $p^{Control}$<0.0001	59.1% n=35 $p^{Control}$<0.0001	70% n=20 $p^{Control}$<0.0001	
bab1>hh (*tub-Gal80^{ts}/+; bab1-Gal4/UAS-hh*)	100% n=30 $p^{Control}$<0.0001	95% n=20 $p^{Control}$<0.0001	100% n=20 $p^{Control}$<0.0001	48% n=35 $p^{Control}$<0.0001	well-fed[b] 100% n=20	starved[b] 50% n=20 $p^{well\text{-}fed}$<0.0001
bab1>Rab23 (*bab1-Gal4/UAS-Rab23*)	76.7% n=30 $p^{Control}$<0.0001	35% n=20 $p^{Control}$=0.004	70% n=20 $p^{Control}$<0.0001	52.2% n=35 $p^{Control}$<0.0001	35% n=20 $p^{Control}$=0.144	
Rescue *mir-310s* (*KT40/KT40; attB2 mir-310s res long 2 /+*)	33.3% n=30 $p^{KT40/Df6070}$<0.0001	5% n=20 $p^{KT40/Df6070}$=0.008	30% n=20 $p^{KT40/Df6070}$=0.011	16% n=35 $p^{KT40/Df6070}$=0.002	35% n=20 $p^{KT40/Df6070}$=0.027	
mir-310s; bab1>hh RNAi (*KT40/KT40; bab1-Gal4/ UAS-hh-RNAi*)	50% n=30 $p^{KT40/Df6070}$=0.015	12% n=20 $p^{KT40/Df6070}$=0.077	20% n=20 $p^{KT40/Df6070}$=0.001	28.6% n=35 $p^{KT40/Df6070}$=0.03	15% n=20 $p^{KT40/Df6070}$<0.0001	
mir-310s; bab1>Rab23 RNAi (*KT40/KT40; bab1-Gal4/ UAS-Rab23-RNAi*)	46.7% n=30 $p^{KT40/Df6070}$=0.007	20% n=20 $p^{KT40/Df6070}$=0.168	20% n=20 $p^{KT40/Df6070}$=0.001	25% n=35 $p^{KT40/Df6070}$=0.015	40% n=20 $p^{KT40/Df6070}$=0.057	

[a] Flies were kept on nutritionally rich or poor medium for 7 days prior to analysis.

[b] *tub-Gal80^{ts}/+; bab1-Gal4/UAS-hh* flies were kept for 3 days at restrictive temperature (29°C).

Occurrences of the listed phenotypes per ovariole are indicated as percentages.

Significance was tested using Pearson's chi-Square test and IBM SPSS Statistics software.

Table S10, related to Figure 6. The high mitotic activity in *mir-310s* mutant egg chambers is rescued by downregulating Rab23 or Hh levels

Genotype	Number of $PH3^+$ follicle cells (AVE±SEM) n=number of stage 2 egg chambers analyzed	
	well-fed (7 days)	Starved (7 days)
Control (*w^{1118}/Oregon-R-C*)	4.17±0.25 n=30	0.20±0.09 n=30
bab1>hh RNAi[a] (*tub-Gal80^{ts}/+; bab1-Gal4/ UAS-hh-RNAi*)	2.00±0.34 n=30 $p^{Control}$=1.6E-05	0.27±0.12 n=15 $p^{Control}$=0.378
bab1>Rab23 RNAi[a] (*tub-Gal80^{ts}/+; bab1-Gal4/ UAS-Rab23-RNAi*)	2.4±0.33 n=30 $p^{Control}$=1.04E-04	0.20±0.11 n=15 $p^{Control}$=0.50
bab1>hh (*tub-Gal80^{ts}/+; bab1-Gal4/UAS-hh*)	8.4±0.68[b] n=30 $p^{Control}$<0.00001	1.07±0.23[a] n=15 $p^{Control}$=0.006
bab1>Rab23 (*tub-Gal80^{ts}/+; bab1-Gal4/UAS-Rab23*)	6.37±0.68 n=30 $p^{Control}$=0.0036	1.13±0.29 n=15 $p^{Control}$=0.007
mir-310s/ Df6070 (*w[1118]; KT40/Df(2R)Exel6070, P{w[+mC]=XP-U}Exel6070*)	5.3±0.38 n=30 $p^{Control}$=0.0233	0.70±0.16 n=30 $p^{Control}$=0.011
mir-310s (*KT40/KT40*)	5.63±0.51 n=30 $p^{Control}$=0.0222	0.8±0.19 n=30 $p^{Control}$=0.015
Rescue *mir-310s* (*KT40/KT40; attB2 mir-310s res long 2 /+*)	4.23±0.27 n=30 $p^{KT40/Df6070}$=0.0367	0.13±0.29 n=15 $p^{KT40/Df6070}$=0.0197
mir-310s; bab1>hh RNAi (*KT40/KT40; bab1-Gal4/ UAS-hh-RNAi*)	4.03±0.26 n=30 $p^{KT40/Df6070}$=0.011	0.4±0.13 n=15 $p^{KT40/Df6070}$=0.1075
mir-310s; bab1>Rab23 RNAi (*KT40/KT40; bab1-Gal4/ UAS-Rab23-RNAi*)	4.2±0.27 n=30 $p^{KT40/Df6070}$=0.0367	0.33±0.13 n=15 $p^{KT40/Df6070}$=0.0735

Significance was tested using Mann-Whitney U test and z statistic.

[a] Flies were kept at restrictive temperature (29°C) for 7 days.

[b] Flies were kept at restrictive temperature (29°C) for 3 days.

Table S11, related to Figures 1 and 3. Primers used in this study

3`UTR Luciferase reporter cloning[a]	*Rab23*	*NotI*	Forward	GCAAGCGGCCGCTTTTTGCATAGAATGCGAGCAGC
		XhoI	Reverse	GCAACTCGAGCCAAGCCCAGATCACAGGTCC
	ttk	*XhoI*	Forward	GCAACTCGAGAAGCGCAATCAAATAATAAACAAG
		NotI	Reverse	GCAAGCGGCCGCGCGAGAAAATTGCTGAAGGTT
	DHR96	*XhoI*	Forward	GCAACTCGAGTGTCTGTTTTATCTTGTCGCTTGT
		NotI	Reverse	GCAAGCGGCCGCTCCTTTTTGCACAGAACCCAC
qRT-PCR	*Rab23*		Forward	AGCTGGCCATTAAAGTGGTCATT
			Reverse	GATCTCGATCTGTCGCTCTAGGA
	DHR96		Forward	CCTCAGCGCCCTGATGATGG
			Reverse	CAGCTGCAATAGCTTTGGGTTGTG
	ttk		Forward	CGAAACGATCAAAGAACTCCAAGG
			Reverse	CGCCTGCTCGTTGAGGTGACTAC
	Rpl32		Forward	AAGATGACCATCCGCCCAGC
			Reverse	GTCGATACCCTTGGGCTTGC
	Act88F		Forward	GCGCCACCCGAGAGGAAGTA
			Reverse	TGGAAGGTGGACAGCGAGGC
	ade2		Forward	TTCCGTCGGTTTGCCTACATCA
			Reverse	TCCGCGACGAGAAGCTCATTAG
	ade3		Forward	GCCCAAACCCAAAGCCAAGG
			Reverse	CATCCAGCTGGTGGAGAAGTGC
	Arr1		Forward	CAGTCAGGATGCGAGGGATGC
			Reverse	CCCAGGGCTCCCAAGAAAAG
	CG3699		Forward	TCTGCCTGCGTGCCCTTCA
			Reverse	CCGCCATCGCCCAAGTTCT
	CG3902		Forward	CACGGTGGCGATCTGATGCT
			Reverse	GCGCAAGCAGTTCGGTGATG
	CG3999		Forward	CCATCGACAATGGGCGTGTTC
			Reverse	CTGGGCATTCATGTTGGCTCC
	CG9914		Forward	GGGACCCAGGAAGGCGTAGC
			Reverse	GCCGGCATCCTGAATGTCAAG
	CG11089		Forward	CCCGCAGGATCCACCAATGA
			Reverse	GGGCCATGATGATACCGTGCTC
	CG15369		Forward	CGGTGCACCAAAAGTCCTCG
			Reverse	GTCCTTCGCCAGCAGCCAAT
	CG16884		Forward	GCGATCGCGGGACCACTGT
			Reverse	GGCCACGGAAGCTACGGACAT
	CG30360		Forward	CGATCAGCGGAGAGTGGGTAGT
			Reverse	ACGCCGGGCAGGAACATCT
	CG31233		Forward	CCAGCACGCAGACCAACATAGC
			Reverse	GCCACCAGATCACCAAACCACA
	Cpr62Bc		Forward	CGTCTCCGGTGTGAGAGTCAGC
			Reverse	GGTCACCACGACGAGGGAATC
	Cpr72Ec		Forward	CGCATCCTCATCGGTCAGACTC
			Reverse	GCGTGAGGAGGCGGACAGA
	Cpr100A		Forward	TCCAGCCAGCACTATCACCAGG
			Reverse	AGCTCCGAACTTTCCATCTCCG

	Gal	Forward	CCAGACGCTTAGCGGGATTCA
		Reverse	CCGGTGGCGTCACCACTAAGTA
	Gasp	Forward	CTCGCCGTTCCAGCAGTTCC
		Reverse	CTCGCCTGTACGGCATCTTCC
	GstD4	Forward	TCCCCAGCACACCATTCCC
		Reverse	CCTTGCCGTACTTTTCCACCAG
	Lsp1beta	Forward	CCCGCCCACGAGCAGTTCT
		Reverse	CGCACGGTCGAAGGGATAGC
	Lsp2	Forward	TGCCCAACCGAATGATGCTG
		Reverse	CGGGCTGGTGGTACGGGTAG
	LvpH	Forward	CGACTTGAATATGGGCGACAGC
		Reverse	ACGGCATTGGCGACCTGAAC
	Mgstl	Forward	GATGTCCCCCAAGCTGAAGGTC
		Reverse	GGCGAAGAAGGGCAGGATGTT
	mus209	Forward	ACATCGACAGCTGCACTTGGGT
		Reverse	GCCGGTGACGCTGACATTTG
	Obp44a	Forward	TGCTCGCTCGGAGGAAACTGT
		Reverse	TGCGACATACCCACATTGAGCG
	Obp56a	Forward	CGCCTCCAAGTTGTACGATTGC
		Reverse	CCGAATCACAATTTGCCAAGCA
	Obp56e	Forward	CCGCCCTTGCAGCTCTATCTTT
		Reverse	TTGCCTCAGCCTTTTGGGAATC
	Obp99b	Forward	CTCCTCGCTGGCGTGAACCT
		Reverse	TCACCATCACCATCACCACGAC
	obst-A	Forward	CATCCCACCGACTGCCAGAAG
		Reverse	ATCGTTGTAGACCTCGCCCAGC
	pro-PO-A1	Forward	GGCGGTCCACGTCCCTCAG
		Reverse	CCAGCACGAATAACCGCACCTA
	Sucb	Forward	TTGGCTGATCTGCGGTGGTAAC
		Reverse	CGGCGATTTTCGGTTGTGTTT

[a] For cloning, cutting sites for indicated restriction enzymes were added to 5`end of the designed primers.

All primers were designed using Lasergene Software.

File S1. Supplemental Experimental Procedures

SILAC labeling and MS/MS Analysis

Heavy amino acid-labeled (Lys-8, Lys-13C615N2, Cambridge Isotope Laboratories, Inc.) yeast and flies were cultivated as published (SURY *et al.* 2010). Lysine auxotrophic *S. cerevisiae* strain SUB62 (kindly provided by Matthias Selbach) was precultured 1:1000 for 24 hours and then inoculated for 1:100 and incubated for another 24 hours in defined, labeling medium before harvesting. Prior to feeding of *Drosophila*, incorporation of Lys-8 to yeast cells was measured by mass spectrometry and almost complete incorporation (>95%) was achieved. We used w^{1118} stock as the control strain. Control flies were grown with light-labeled (Lys-0, Lys-12C614N2, Sigma) and *mir-310s* mutant (*KT40/KT40*) flies with heavy-labeled yeast (Lys-8). In parallel, as a replicate experiment the reverse labeling was done, where control flies were fed with heavy and *mir-310s* mutant flies were fed with light-labeled yeast. Hatched flies were kept on the same medium with labeled yeast pellet for 3 days before harvesting. For sample preparation, 10 female flies were snap frozen in liquid nitrogen and homogenized in 100µl RIPA buffer (SURY *et al.* 2010) supplemented with 1X Protease inhibitor cocktail (Thermo). Total protein amounts were quantified using Bradford Reagent (Sigma). Samples containing 25µg of total protein from each labeling-genotype experiment were used for the analysis.

Proteins were separated by one-dimensional SDS-PAGE (4%–12% NuPAGE Bis-Tris Gel, Invitrogen) and stained with Coomassie Blue G-250 (Fluka). The complete gel lanes were cut into 23 equally sized slices. Proteins were digested as described previously (SHEVCHENKO *et al.* 2006). Briefly, proteins were reduced with 10 mM DTT for 50 min at 50°C, afterwards alkylated with 55

mM iodoacetamide for 20 min at 26°C. In-gel digestion was performed with Lys-C (Roche Applied Science) overnight. Extracted peptides from gel slices were loaded onto the in-house packed C18 trap column (ReproSil-Pur 120 C18-AQ, 5 µm, Dr. Maisch GmbH; 20 x 0.100 mm) at a flow rate of 5 µl/min loading buffer (2% acetonitrile, 0.1% formic acid). Peptides were separated on the analytical column (ReproSil-Pur 120 C18-AQ, 3 µm, Dr. Maisch GmbH; 200 x 0.050 mm, packed in-house into a PF360-75-15-N picofrit capillary, New Objective) with a 90 min linear gradient from 5% to 40% acetonitrile containing 0.1% formic acid at a flow rate of 300 nl/min using nanoflow liquid chromatography system (EASY n-LC 1000, Thermo Scientific) coupled to hybrid quadrupole-Orbitrap (Q Exactive, Thermo Scientific). The mass spectrometer was operated in data-dependent acquisition mode where survey scans acquired from m/z 350-1600 in the Orbitrap at resolution settings of 70,000 FWHM at m/z 200 at a target value of 1 x 10E6. Up to 15 most abundant precursor ions with charge states 2+ or more were sequentially isolated and fragmented with higher collision-induced dissociation (HCD) with normalized collision energy of 28. Dynamic exclusion was set to 18 s to avoid repeating the sequencing of the peptides.

The generated raw Mass Spectrometry files were analyzed with MaxQuant software (version 1.3.0.5, using Andromeda search engine) (COX AND MANN 2008) against UniProtKB *D. melanogaster* database containing 18826 entries (downloaded in April 2013) and Flybase *D. melanogaster* database (release 6.02) supplemented with common contaminants and concatenated with the reverse sequences of all entries. The following Andromeda search parameters were set: carbamidomethylation of cysteines as a fixed modification, oxidation of methionine and N-terminal

acetylation as a variable modification; and Lys-C specificity with no proline restriction and up to two missed cleavages. The MS survey scan mass tolerance was 7 ppm and for MS/MS 20 ppm. For protein identification minimum of five amino acids per identified peptide and at least one peptide per protein group were required. The false discovery rate was set to 1% at both peptide and protein levels. "Re-quantify" was enabled, and "keep low scoring versions of identified peptides" was disabled. Statistical analysis was performed with Perseus bioinformatics platform which is part of MaxQuant (COX AND MANN 2008).

qRT-PCR

Total RNA was extracted using Trizol (Ambion) followed by isolation using Direct-Zol RNA Miniprep (Zymo Research) following the manufacturers' protocols.

Relative transcript levels were measured using total RNA extracts from 10 females of control (w^{1118}) and *mir-310s* mutant (*KT40/KT40*) genotypes kept under well-fed or starved condition for 10 days using 3 biological replicates. To synthesize total cDNA, High-Capacity reverse transcription kit (Applied Biosystems) and random primers were used. Quantitative PCR (qPCR) was performed using SYBR green master mix (Applied Biosystems) using a StepOne Plus thermocycler (Applied Biosystems) according to manufacturer's instructions. The gene *Rpl32* was used as an endogenous control. Primers for qPCR for each gene were designed using Lasergene software (Table S11). The amplicons were selected to be intron spanning. If that was not possible, additional DNAse (Zymo Research) treatment of the RNA samples was performed and reverse transcriptase negative controls were included.

Relative miRNA levels were measured using RNA extracts from 5 ovaries from 7 day well-fed or starved control (w^{1118}/*Oregon-R-C*) females in at least 3 biological replicates. TaqMan microRNA assays (Applied Biosystems) and High-Capacity reverse transcription kit were used to synthesize cDNA specific to *mir-310, mir-312,* and *2S rRNA* as an endogenous control. qPCR was performed using the Taqman qPCR master mix (Applied Biosystems) using a StepOne Plus thermocycler.

For the relative quantitative analysis, average C_T values of technical replicates were first normalized by subtraction of the housekeeping gene expression (*Rpl32* for transcript expression and *2S rRNA* for miRNA expression) and then of the gene of interest expression in the well-fed controls. Relative expression levels were obtained with these calculated $\Delta\Delta C_T$ values using the formula $2^{-\Delta\Delta CT}$. Statistical analysis was done using non-paired two-tailed Student's t-test.

Immunohistochemistry

Adult ovaries were dissected in cold 1X PBS and fixed for 10-15 minutes in 4% formaldehyde (Polysciences Inc.) at room temperature. The subsequent staining procedure was performed as described (KONIG AND SHCHERBATA 2013). The following antibodies were used with the indicated dilutions: mouse monoclonal anti-Adducin (1:50), anti-LaminC (1:20), anti-Fasciclin III (1:50), and anti-β-Gal (1:25), rat monoclonal anti-DE-Cadherin (1:25) (Developmental Studies Hybridoma Bank); chicken polyclonal anti-GFP (1:5000, Abcam); guinea pig polyclonal anti-Hh (1:100, gift from Acaimo González-Reyes); rabbit polyclonal anti-PH3 (1:5000, Upstate Biotechnology); goat secondary antibodies Alexa 568 anti-mouse, Alexa 488 anti-rat, Alexa 488 anti-rabbit, Alexa 488 anti-chicken, and Alexa 568 anti-guinea pig (1:500, Invitrogen). To stain cell nuclei, DAPI dye

(Sigma) was used. All samples were mounted on glass slides in 1X PBS with 70% glycerol and 3% n-propyl gallate. Fluorescence images of the stained tissues were taken with confocal laser-scanning microscope (Zeiss LSM 700) and processed with Adobe Photoshop software.

Luciferase Assay

The reporter constructs with a short *3`UTR* fragment of each gene containing the *mir-310s* binding site was cloned downstream of *Renilla* luciferase gene (Table S11). The same vector contained an unmodified *Firefly* luciferase gene, activity of which served as an internal transfection control for each experiment and for the normalization of *Renilla* luciferase signal. *Drosophila* S2 cells were kept in Schneider's *Drosophila* medium (Gibco) supplemented with 10% heat inactivated fetal bovine serum (GE healthcare), 100 units/ml penicillin, and 100 µg/ml streptomycin (Gibco). The cells were split 1:6 the day before transfection and seeded into 96 well plates. All wells were transfected with 5ng actin Gal4, 20ng of *UAS-mir-310s* (gifts from Eric Lai), and 10ng psiCHECK™-2 vectors (Promega) with or without the *3`UTR* fragment of the respective gene using Effectene® Transfection Reagent (Qiagen). Experiments were done in triplicates. *Firefly* and *Renilla* luciferase activities were measured 72h after transfection using Dual-Glo® Luciferase Assay System (Promega) by Wallac 1420 luminometer (PerkinElmer). For analysis, the *Renilla* luciferase signal was divided by *Firefly* luciferase signal to normalize the data to the amount of cells transfected in each well. Next, this ratio was normalized to the control, unmodified *Renilla* luciferase signals, for each respective miRNA overexpression experiment.

Coupled Colorimetric Assay (CCA)

Total body fat content of the flies was measured by CCA as described (GALIKOVA *et al.* 2015). Five female flies were homogenized in 1000µl 0.05% TWEEN® 20 (Sigma) and incubated at 70°C for 5 minutes. Samples were cleared by centrifuging at 3000g for 3 minutes and the supernatant was used for subsequent colorimetric analyses. To measure the triglyceride (TAG) equivalent amounts, we used 200µl of prewarmed (37°C) Triglycerides Reagent (Thermo Scientific™) with 50µl of the well-fed and 75µl of the starved samples measuring the absorbance at 540nm after incubation at 37°C for 30 minutes. Absolute TAG equivalent amounts were calculated with help of serial dilutions of Thermo Trace Triglyceride standard (Thermo Scientific™) and calculated standard curve. For normalization, we measured total protein content of the samples using BCA Protein Assay Reagent (Thermo Scientific Pierce), where we used 50µl of the samples with 200µl BCA-mix and measured absorbance at 570nm after an incubation for 30 minutes at 37°C. Absolute protein contents of the samples were calculated with the help of a standard curve obtained using measurements of serial dilutions of bovine serum albumin standard. Both absorbance measurements were done in 96 well microtest plates (Sarstedt) using a Benchmark Microplate Reader (Biorad).

Fat bodies were visualized from non-fixed dorsal carcass preparations using Bodipy493/503 (38 µM; Invitrogen) to label lipid droplets, CellMaskTM Deep Red (5 µg/mL; Invitrogen) to label plasma membrane, and DAPI (3,6 µM; Invitrogen) to label nuclei (GALIKOVA *et al.* 2015).

Co-immunoprecipitation

Whole lysates were prepared from approximately 1-week-old male and female flies, which were kept on nutrient rich food for 2-3 days and harvested by snap freezing in liquid nitrogen. Three biological

replicates of 750mg of both control (w^{1118}) and *Rab23::YFP::4xmyc* flies were homogenized by grinding in 2ml buffer with 20mM Tris (pH 7.4), 150mM NaCl, 5% glycerol, 5mM EDTA, 0.1% Triton™ X-100 (Sigma) and 2X protease inhibitor cocktail (Roche) in a mortar with pestle using liquid nitrogen. Lysates were cleared by three centrifuging steps once for 10 minutes at 15000g and twice at 21000g at 4°C. Next, control and *Rab23::YFP::4xmyc* lysates were diluted with buffer to 5ml and were added 50µl agarose beads coupled with anti-myc antibodies (Sigma) in 15ml tubes and incubated rotating at 4°C for 100 minutes. To collect the beads, lysates were centrifuged at 100g for 2 minutes at 4°C. The beads were washed 10 times with 700µl buffer at 100g for 30 seconds at 4°C and finally eluted with 50µl warm 2X sample buffer (NuPAGE® LDS Sample Buffer, Novex®). The eluates were analyzed by mass spectrometry with the same workflow used in SILAC analysis described above with the exception for trypsin used for in-gel digestion.

Supplemental References

Cox, J., and M. Mann, 2008 MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. Nat Biotechnol 26**:** 1367-1372.

Galikova, M., M. Diesner, P. Klepsatel, P. Hehlert, Y. Xu *et al.*, 2015 Energy Homeostasis Control in Drosophila Adipokinetic Hormone Mutants. Genetics 201**:** 665-683.

Konig, A., and H. R. Shcherbata, 2013 Visualization of adult stem cells within their niches using the Drosophila germline as a model system. Methods Mol Biol 1035**:** 25-33.

Shevchenko, A., H. Tomas, J. Havlis, J. V. Olsen and M. Mann, 2006 In-gel digestion for mass spectrometric characterization of proteins and proteomes. Nat Protoc 1**:** 2856-2860.

Sury, M. D., J. X. Chen and M. Selbach, 2010 The SILAC fly allows for accurate protein quantification in vivo. Mol Cell Proteomics 9**:** 2173-2183.

Yatsenko, A. S., A. K. Marrone and H. R. Shcherbata, 2014 miRNA-based buffering of the cobblestone-lissencephaly-associated extracellular matrix receptor dystroglycan via its alternative 3'-UTR. Nat Commun 5**:** 4906.