SUPPLEMENTAL MATERIAL.

Supplemental Methods.

rtPCR

Total RNA was isolated from adult female flies using a Qiagen RNeasy Mini kit (Qiagen, Manchester, UK) according to the manufacturer's instructions. cDNA was prepared from 1 µg of total DNase-treated RNA by incubating the RNA with Oligo-dT primers at 65ºC for 10 min and then placing the reaction on ice for 5 min. Second strand synthesis was performed using Roche Expand RT (Roche Products Limited, Welwyn Garden City, UK). Quantitative PCR was then performed using 10 µL reaction volumes in 384-well format in a Roche LightCycler 480 Intron-spanning primers were used to determine the relative concentration of *Drosophila SPARC* (left, CGACATCGATGAGAACGAAG; right, TCGCGCTCAATATCCTTGAT), using *Actin5C* as a reference control. Quantified data are presented at the mean (+/-SEM) of six independent samples from wild type and *SPARC*-mutant flies.

Imaging the adult heart

Adults (2-3 week old unless stated otherwise) were anaesthetised with Flynap (Carolina Biological Supply Company, Burlington, NC, USA), dissected and hearts stained as described previously[1, 2]. For some experiments, vital dyes were used to identify functional nephrocytes or test their endocytic function (wheat germ agglutinin at 1µg / mL for 15 minutes or 50 µg / mL 10 kDa fluorescently labelled dextran for 0-30 minutes). Semi-intact preparations were then washed three times, fixed for 20 minutes with 1% formaldehyde and co-stained with antibodies (and then the relevant secondary antibodies) or Hoechst to visualise DNA and then imaged.

Epifluorescence microscopy of adult fly tissues

Semi-intact preparations were washed three times, fixed for 20 minutes with 1% formaldehyde, permeabilised with 0.1% TritonX-100 in phosphate buffered saline and co-stained with phalloidin (to visualise the actin cytoskeleton of the heart) and antibodies to the nephrocyte endocytosis protein Amnionless. To identify the

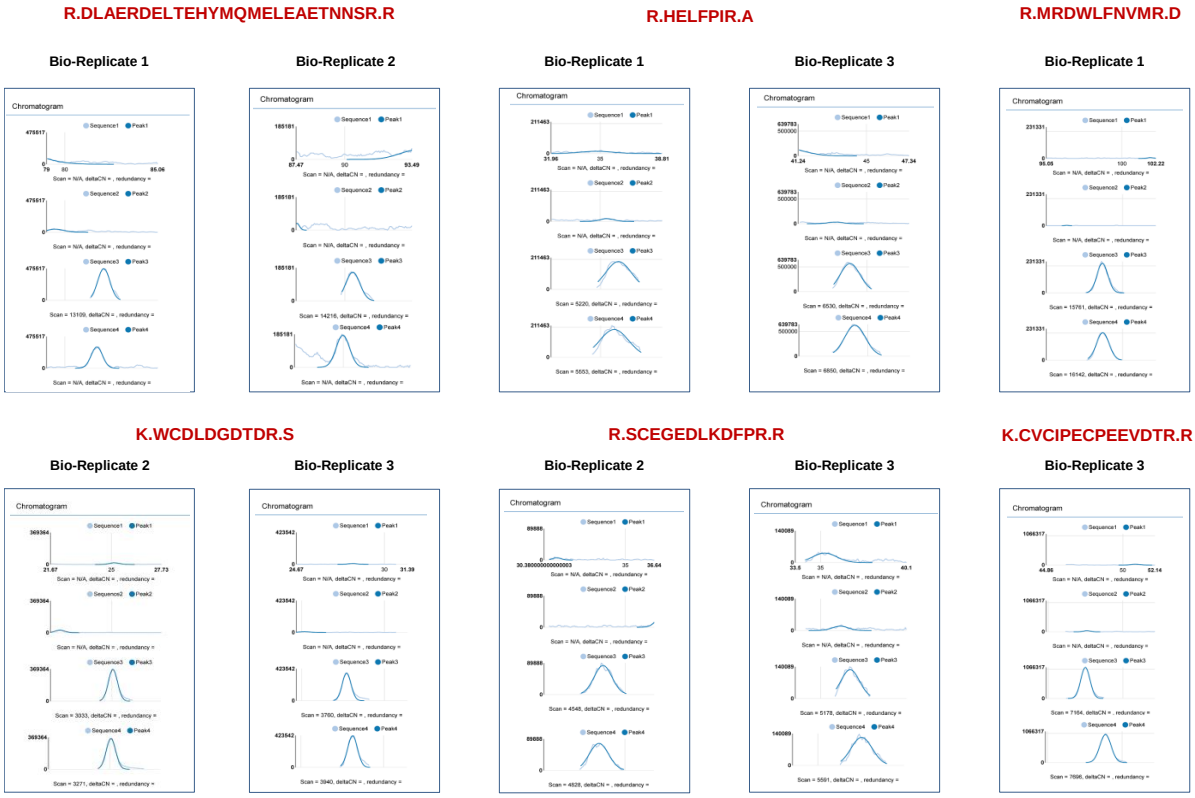
garland cells Hoechst 33342 was used to visualise DNA (garland cells having a binucleate nuclear morphology and distinct anatomical location at the interface between the oesophagus and paraventriculus). Fluoresce microscopy of flies was performed using a Zeiss LSM780 coupled to Zen image analysis software (Carl Zeiss, Welwyn Garden City, UK). Phase images were captured on a Zeiss Axiolab and images captured with an ORCA-ER CCD camera (Hamamatsu Photonics KK, Japan; Welwyn Garden City, UK) coupled to Openlab 4.1 (Improvision, Coventry, UK). Images were coloured, contrast enhanced and overlaid using Photoshop CS3. All micrographs were collected using the same microscope settings and image alterations, which were limited to contrast and brightness enhancement.

References.

1. Catterson JH, Heck MM, Hartley PS. Fermitins, the orthologs of mammalian kindlins, regulate the development of a functional cardiac syncytium in drosophila melanogaster. *PLoS One*. 2013;8:e62958.
2. Park SK, Venable JD, Xu T, Yates JR. A quantitative analysis software tool for mass spectrometry-based proteomics. *Nature Methods*. 2008;5:319-322.

Supplemental Figure S1.

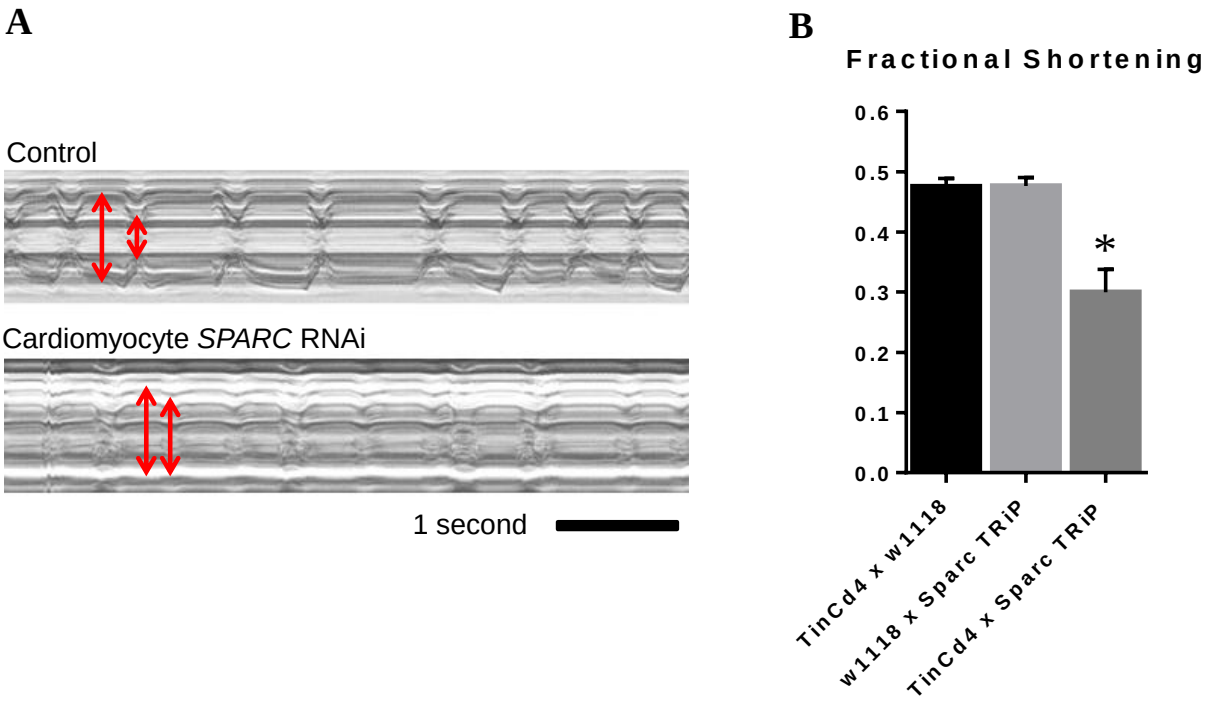
SPARC peptide peak areas. Chromatograms for identified SPARC peptides are shown. In each panel the upper two chromatograms show peptide peaks from two technical replicates of a sample from the wild type (w^{1118}) hemolymph and the lower two chromatograms correspond to two technical replicates from a sample of the mutant ($dKlf15^{NN}$) hemolymph. In each case the peptide is detected in the mutant but not the wild type hemolymph.



Supplemental Figure S2.

Effect of *SPARC* knock-down on heart function.

The function of the adult heart was analysed by high frame rate videomicroscopy (as described in the methods section of the main document). (A) The M-modes show the distance moved by the wall of the heart during a contraction (Fractional Shortening, red arrows). The control heart shows robust contraction between diastole to systole, whereas there is significantly less contraction when *SPARC* is silenced in the cardiomyocytes. (B) The graph shows the relative distance moved by the heart walls during diastole and systole (Fractional Shortening). The knock-down of *SPARC* in cardiomyocytes using the *TinCΔ4* driver (TinCd4 x Sparc TRiP) had a significant impact on fractional shortening that was not seen in either of the control genotypes (TinCd4 x w1118 and w1118 x Sparc TRiP). *n* = 19 to 29 flies per genotype. *P<0.001.



Supplemental Table. Proteomics Data

Group 1: Present in *dKlf15 ^{NN}* mutant but undetected in *w ^{1118}* control
(a mean of two spectral counts or lower was regarded as undetected)

	Uniprot ID	Annotation	w1118				dKlf15NN				w1118			dKlf15NN			
			#1	#2	#3		#1	#2	#3		Mean	SEM		Mean	SEM	t-Test	B-H Correction
tr|O97365|O97365_DROME	O97365	BM-40-SPARC	0	0	0		38	87	126		0	0		83	26	0.031	0.160
sp|Q24298|CADE_DROME	Q24298	shg	0	0	0		37	49	62		0	0		49	7	0.002	0.093
tr|Q7JR49|Q7JR49_DROME	Q7JR49	VhaAC45	0	1	0		22	16	40		0	0		26	7	0.023	0.143
sp|P10981|ACT5_DROME	P10981	Act87E	0	0	0		0	0	72		0	0		24	24	0.374	0.386
tr|A8JUV8|A8JUV8_DROME	A8JUV8	trol	0	0	0		6	16	48		0	0		23	13	0.135	0.266
sp|O01404|PHM_DROME	O01404	Phm	0	0	0		11	25	32		0	0		23	6	0.020	0.143
sp|P33438|GLT_DROME	P33438	Glt	0	0	0		6	32	26		0	0		21	8	0.057	0.216
tr|Q9VRS4|Q9VRS4_DROME	Q9VRS4	yip7	0	1	0		14	21	26		0	0		20	4	0.005	0.093
sp|Q9I7U4-1|TITIN_DROME	Q9I7U4	sls	0	0	0		14	0	38		0	0		17	11	0.197	0.327
tr|Q9VKG4|Q9VKG4_DROME	Q9VKG4	BcDNA.GH07269	0	0	0		3	20	28		0	0		17	7	0.080	0.266
tr|Q9VZQ7|Q9VZQ7_DROME	Q9VZQ7	CG14961	0	5	0		18	12	16		2	2		15	2	0.006	0.093
tr|Q9VB76|Q9VB76_DROME	Q9VB76	CG6074	0	0	0		3	12	30		0	0		15	8	0.129	0.266
tr|A1ZAP4|A1ZAP4_DROME	A1ZAP4	fat-spondin	0	0	0		6	15	24		0	0		15	5	0.042	0.178
tr|Q9VHG4|Q9VHG4_DROME	Q9VHG4	VhaM8.9	0	0	0		9	8	28		0	0		15	7	0.084	0.266
sp|P04814|TRYA_DROME	P04814	alphaTry	0	0	0		13	21	10		0	0		15	3	0.012	0.140
sp|P10987|ACT1_DROME	P10987	Act5C	0	0	0		43	0	0		0	0		14	14	0.374	0.386
tr|A1ZB62|A1ZB62_DROME	A1ZB62	CG16836	0	0	0		0	16	24		0	0		13	7	0.132	0.266
tr|Q8I0D4|Q8I0D4_DROME	Q8I0D4	CG9297	0	0	0		17	7	16		0	0		13	3	0.016	0.143
sp|Q24114|DALY_DROME	Q24114	dally	0	0	0		9	9	20		0	0		13	4	0.025	0.145
sp|P42787-1|CBPD_DROME	P42787	svr	0	0	0		3	12	22		0	0		12	5	0.084	0.266
tr|Q7JX94|Q7JX94_DROME	Q7JX94	CG30503	0	0	0		4	16	16		0	0		12	4	0.040	0.177
sp|Q9W1V6|PRPD3_DROME	Q9W1V6	Dox-A3	0	0	0		0	17	18		0	0		12	6	0.116	0.266
tr|A1Z9I0|A1Z9I0_DROME	A1Z9I0	CG6357	0	0	0		5	12	18		0	0		12	4	0.038	0.177
sp|P10674-1|FAS1_DROME	P10674	Fas1	1	0	0		6	17	10		0	0		11	3	0.027	0.148
tr|Q8IMH5|Q8IMH5_DROME	Q8IMH5	Npc2h	0	0	0		0	15	18		0	0		11	6	0.120	0.266
sp|P29413|CALR_DROME	P29413	Crc	0	0	0		6	11	16		0	0		11	3	0.023	0.143
tr|Q8IQB8|Q8IQB8_DROME	Q8IQB8	Tequila	0	0	0		5	19	8		0	0		10	4	0.067	0.240
tr|Q9VRS7|Q9VRS7_DROME	Q9VRS7	Jon65Aiii	0	0	0		6	11	14		0	0		10	2	0.014	0.143
sp|Q9V498|CSTN1_DROME	Q9V498	cals	0	0	0		5	9	16		0	0		10	3	0.037	0.177
sp|Q9VN93-1|CPR1_DROME	Q9VN93	CG12163	0	0	0		2	13	14		0	0		10	4	0.058	0.216
tr|Q9VMJ5|Q9VMJ5_DROME	Q9VMJ5	Gal	0	0	0		10	5	12		0	0		9	2	0.010	0.133
sp|O77150|IM02_DROME	O77150	IM2	0	0	0		0	0	26		0	0		9	9	0.374	0.386
tr|Q8MKJ5|Q8MKJ5_DROME	Q8MKJ5	CG30197	0	0	0		0	7	18		0	0		8	5	0.193	0.326
tr|Q8ING0|Q8ING0_DROME	Q8ING0	CG31326	0	4	0		6	19	0		1	1		8	6	0.301	0.386
tr|Q9VIQ5|Q9VIQ5_DROME	Q9VIQ5	CG10680	0	0	0		3	7	12		0	0		7	3	0.046	0.186
tr|Q7JYV3|Q7JYV3_DROME	Q7JYV3	CG12374	0	0	0		0	9	12		0	0		7	4	0.122	0.266
tr|Q8IRD6|Q8IRD6_DROME	Q8IRD6	Drsl4	0	0	2		0	5	16		1	1		7	5	0.246	0.369
sp|P13709-1|FSH_DROME	P13709	fs(1)h	0	0	0		21	0	0		0	0		7	7	0.374	0.386
tr|B7Z0T0|B7Z0T0_DROME	B7Z0T0	MP1	0	4	0		0	7	14		1	1		7	4	0.262	0.381
tr|Q9VJU6|Q9VJU6_DROME	Q9VJU6	NimB5	0	0	0		0	3	18		0	0		7	6	0.287	0.386
tr|Q9VN71|Q9VN71_DROME	Q9VN71	CG14661	0	0	0		5	7	8		0	0		6	1	0.002	0.093
tr|Q8SYQ4|Q8SYQ4_DROME	Q8SYQ4	CG31997	0	3	0		6	1	12		1	1		6	3	0.168	0.298
tr|Q9VZ66|Q9VZ66_DROME	Q9VZ66	CG15209	0	0	0		0	11	8		0	0		6	3	0.124	0.266
tr|A1Z7M8|A1Z7M8_DROME	A1Z7M8	Ance-4	0	0	0		6	8	4		0	0		6	1	0.006	0.093
sp|Q95029-1|CATL_DROME	Q95029	Cp1	0	0	0		0	7	10		0	0		6	3	0.132	0.266
tr|Q9VGK3|Q9VGK3_DROME	Q9VGK3	CG14715	0	0	0		3	5	8		0	0		6	1	0.017	0.143
tr|Q9VRT2|Q9VRT2_DROME	Q9VRT2	CG10472	0	0	0		0	4	12		0	0		5	4	0.205	0.334
sp|Q9VB11|UNC80_DROME	Q9VB11	CG18437	0	0	0		0	0	16		0	0		5	5	0.374	0.386
sp|Q9VW71|FAT2_DROME	Q9VW71	kug	0	0	0		0	0	16		0	0		5	5	0.374	0.386
tr|Q9VEP8|Q9VEP8_DROME	Q9VEP8	Irc	0	0	0		2	4	10		0	0		5	2	0.106	0.266
tr|Q86P15|Q86P15_DROME	Q86P15	ltl	0	0	0		5	11	0		0	0		5	3	0.170	0.298
tr|Q7JY07|Q7JY07_DROME	Q7JY07	CG9010	0	0	0		14	0	0		0	0		5	5	0.374	0.386
tr|Q9VAQ4|Q9VAQ4_DROME	Q9VAQ4	CG11841	0	5	0		1	5	8		2	2		5	2	0.347	0.386
tr|Q24485|Q24485_DROME	Q24485	RNaseX25	0	0	0		0	4	10		0	0		5	3	0.184	0.317
sp|Q9NB71|HIW_DROME	Q9NB71	hiw	0	0	0		0	0	14		0	0		5	5	0.374	0.386
tr|Q9VAY0|Q9VAY0_DROME	Q9VAY0	CG5527	0	3	0		3	3	8		1	1		5	2	0.123	0.266
tr|A8DY49|A8DY49_DROME	A8DY49	CG34215	0	0	0		0	3	10		0	0		4	3	0.231	0.358
tr|Q7JV39|Q7JV39_DROME	Q7JV39	CG11400	0	0	0		2	3	8		0	0		4	2	0.108	0.266
tr|Q9VQT6|Q9VQT6_DROME	Q9VQT6	CG3513	4	0	0		0	4	8		1	1		4	2	0.353	0.386
tr|Q7KTA1|Q7KTA1_DROME	Q7KTA1	NimB2	0	0	0		0	0	12		0	0		4	4	0.374	0.386
tr|Q9Y136|Q9Y136_DROME	Q9Y136	CG14526	0	4	0		2	9	0		1	1		4	3	0.452	0.457
tr|Q9W2F1|Q9W2F1_DROME	Q9W2F1	CG15674	0	0	0		6	4	2		0	0		4	1	0.021	0.143
tr|Q9VGE7|Q9VGE7_DROME	Q9VGE7	Ect3	0	0	0		6	0	6		0	0		4	2	0.117	0.266
tr|A1Z876|A1Z876_DROME	A1Z876	Ndg	0	0	0		5	7	0		0	0		4	2	0.127	0.266
tr|Q5BI82|Q5BI82_DROME	Q5BI82	CG13023	0	0	0		5	0	6		0	0		4	2	0.121	0.266
tr|Q9VIQ4|Q9VIQ4_DROME	Q9VIQ4	Hf	0	4	0		5	0	6		1	1		4	2	0.374	0.386
tr|Q8IHA8|Q8IHA8_DROME	Q8IHA8	CG8273	0	0	0		4	7	0		0	0		4	2	0.140	0.266
tr|Q9VFN7|Q9VFN7_DROME	Q9VFN7	Npc2b	0	0	0		2	4	4		0	0		3	1	0.003	0.093
tr|A1Z6H6|A1Z6H6_DROME	A1Z6H6	CG7791	0	0	0		0	0	10		0	0		3	3	0.374	0.386
tr|Q8MMD2|Q8MMD2_DROME	Q8MMD2	Eps-15	0	0	0		0	0	10		0	0		3	3	0.374	0.386
tr|Q9W1H6|Q9W1H6_DROME	Q9W1H6	CG5597	0	4	0		0	4	6		1	1		3	2	0.417	0.426
tr|Q7K088|Q7K088_DROME	Q7K088	Obp56e	0	3	0		10	0	0		1	1		3	3	0.525	0.525
tr|Q23995|Q23995_DROME	Q23995	tok	0	0	0		0	1	8		0	0		3	2	0.277	0.386
sp|P33450|FAT_DROME	P33450	ft	0	0	0		0	9	0		0	0		3	3	0.374	0.386
tr|A8JR58|A8JR58_DROME	A8JR58	CG5630	0	0	0		0	9	0		0	0		3	3	0.374	0.386
sp|Q9VEG6|PERC_DROME	Q9VEG6	Pxt	0	0	0		4	5	0		0	0		3	2	0.124	0.266
tr|Q95RA9|Q95RA9_DROME	Q95RA9	CG9796	0	0	0		3	0	6		0	0		3	2	0.152	0.283
tr|Q9W314|Q9W314_DROME	Q9W314	Ser7	0	0	0		2	7	0		0	0		3	2	0.242	0.369
tr|Q0E8P5|Q0E8P5_DROME	Q0E8P5	CG5758-RC	0	0	0		4	4	0		0	0		3	1	0.116	0.266
tr|Q9VV46|Q9VV46_DROME	Q9VV46	Cpr72Ec	0	0	0		0	4	4		0	0		3	1	0.116	0.266
tr|Q95SC0|Q95SC0_DROME	Q95SC0	CG9917-RA	0	0	0		0	8	0		0	0		3	3	0.374	0.386
tr|Q9VQ27|Q9VQ27_DROME	Q9VQ27	CG14352	0	0	0		0	8	0		0	0		3	3	0.374	0.386
tr|E1JI59|E1JI59_DROME	E1JI59	siz	0	0	0		0	0	8		0	0		3	3	0.374	0.386
tr|O77273|O77273_DROME	O77273	EG:66A1.2	0	0	0		0	0	8		0	0		3	3	0.374	0.386
tr|Q9VED8|Q9VED8_DROME	Q9VED8	DNaseII	0	0	0		0	0	8		0	0		3	3	0.374	0.386
tr|Q9VWT7|Q9VWT7_DROME	Q9VWT7	CG15043	0	0	0		2	5	0		0	0		3	2	0.170	0.298
sp|Q0KHY3-1|Y1004_DROME	Q0KHY3-1	mesh	0	0	0		0	1	6		0	0		2	2	0.250	0.369
tr|Q23984|Q23984_DROME	Q9VMD9	tig	0	0	0		2	5	0		0	0		2	2	0.217	0.342
tr|Q95SI9|Q95SI9_DROME	Q95SI9	CG3868	0	0	0		2	5	0		0	0		2	2	0.217	0.342
tr|Q9XZ34|Q9XZ34_DROME	Q9XZ34	Rif1	0	0	0		0	7	0		0	0		2	2	0.374	0.386
tr|Q8T4A8|Q8T4A8_DROME	Q8T4A8	CG7542	0	0	0		0	3	4		0	0		2	1	0.132	0.266
sp|Q70PY2|PGSB1_DROME	Q70PY2	PGRP-SB1	0	0	0		2	4	0		0	0		2	1	0.140	0.266
tr|A1Z8Q2|A1Z8Q2_DROME	A1Z8Q2	CG13185	0	0	0		6	0	0		0	0		2	2	0.374	0.386

Group 2: In both *w ^{1118}* and mutant but > 2-fold greater in *dKlf15 ^{NN}* mutant

	Uniprot ID	Annotation	w1118	dKlf15NN	w1118	dKlf15NN

			#1	#2	#3	#1	#2	#3	Mean	SEM	Mean	SEM	Fold chang	t-Test	B-H Correction
tr|A1ZBU8|A1ZBU8_DROME	A1ZBU8	CG18067	0	9	0	66	101	72	3	3	80	11	25.6	0.003	0.159
tr|Q8SXG0|Q8SXG0_DROME	Q8SXG0	CG5162	3	16	0	27	44	132	6	5	68	32	10.7	0.135	0.247
tr|Q9V3Y7|Q9V3Y7_DROME	Q9V3Y7	CG15293	0	12	0	22	49	42	4	4	38	8	9.5	0.019	0.172
sp|P54192|PBP2_DROME	P54192	Pbprp2	2	12	8	22	71	86	7	3	59	19	8.0	0.057	0.183
tr|Q7JYZ0|Q7JYZ0_DROME	Q7JYZ0	CG6426	0	7	0	8	17	26	2	2	17	5	7.7	0.058	0.183
tr|Q7KMM4|Q7KMM4_DROME	Q7KMM4	BcDNA.GH04962	0	8	0	12	17	24	3	3	18	3	6.7	0.026	0.172
sp|Q9V3Y3|DFP_DROME	Q9V3Y3	l(2)34Fc	0	9	0	18	15	26	3	3	20	3	6.3	0.022	0.172
tr|Q9W227|Q9W227_DROME	Q9W227	CG2852	5	17	10	39	52	106	11	4	66	20	6.1	0.057	0.183
sp|Q07171-1|GELS_DROME	Q07171	Gel	2	45	24	80	155	154	24	12	130	25	5.4	0.019	0.172
tr|Q8SYB5|Q8SYB5_DROME	Q8SYB5	Jon65Aiv	0	0	10	11	16	24	3	3	17	4	5.1	0.052	0.183
tr|Q7K533|Q7K533_DROME	Q7K533	CG11395	3	23	0	22	60	46	9	7	43	11	5.0	0.063	0.183
tr|Q9VH37|Q9VH37_DROME	Q9VH37	CG12811	1	5	0	4	7	20	2	2	10	5	4.5	0.201	0.266
tr|Q0KI00|Q0KI00_DROME	Q0KI00	SP1029	6	5	0	9	32	8	4	2	16	8	4.3	0.197	0.266
tr|Q7K084|Q7K084_DROME	Q7K084	Obp44a	5	12	6	23	31	46	8	2	33	7	4.3	0.022	0.172
tr|Q9W0J9|Q9W0J9_DROME	Q9W0J9	CG9119	1	8	0	5	13	20	3	2	13	4	4.0	0.131	0.247
sp|P29746|BNB_DROME	P29746	bnb	9	16	22	30	64	90	16	4	61	17	3.9	0.064	0.183
tr|Q9VCJ8|Q9VCJ8_DROME	Q9VCJ8	SPE	0	11	0	5	19	18	4	4	14	5	3.9	0.149	0.255
sp|Q9W1C9|PEB3_DROME	Q9W1C9	PebIII	2	13	18	22	45	62	11	5	43	12	3.8	0.065	0.183
tr|Q8INW9|Q8INW9_DROME	Q8INW9	fon	5	21	8	32	27	68	12	5	42	13	3.7	0.092	0.212
sp|Q8ML70-1|IM10_DROME	Q8ML70-1	IM10	3	33	16	44	77	68	17	9	63	10	3.6	0.026	0.172
sp|Q9V8F5|IM23_DROME	Q9V8F5	IM23	4	17	6	26	40	32	9	4	33	4	3.5	0.014	0.172
sp|Q06521|VTU3_DROME	Q06521	Vm34Ca	0	8	0	6	8	12	3	3	9	2	3.2	0.146	0.255
tr|Q8MYW6|Q8MYW6_DROME	Q8MYW6	CG17109	0	11	0	5	13	16	4	4	11	3	3.2	0.186	0.266
tr|Q9NF33|Q9NF33_DROME	Q9NF33	EG:103E12.2	7	36	6	33	60	50	16	10	48	8	2.9	0.069	0.183
tr|O97355|O97355_DROME	O97355	Tsf1	82	372	88	328	605	642	181	96	525	99	2.9	0.067	0.183
tr|Q7JWX3|Q7JWX3_DROME	Q7JWX3	nec	6	27	0	30	48	16	11	8	31	9	2.9	0.169	0.259
tr|Q8SY60|Q8SY60_DROME	Q8SY60	CG9928	6	31	24	38	53	82	20	7	58	13	2.9	0.063	0.183
tr|Q86BI9|Q86BI9_DROME	Q86BI9	CG18135	2	39	0	23	47	42	14	13	37	7	2.7	0.177	0.261
tr|Q9NFV5|Q9NFV5_DROME	Q9NFV5	Tep4	9	63	28	54	112	102	33	16	89	18	2.7	0.079	0.199
tr|Q9W306|Q9W306_DROME	Q9W306	CG9691	0	8	0	4	9	8	3	3	7	2	2.7	0.226	0.289
tr|A1ZAU4|A1ZAU4_DROME	A1ZAU4	CG4847-RD	0	11	0	3	15	10	4	4	9	3	2.6	0.304	0.330
tr|Q8IN51|Q8IN51_DROME	Q8IN51	CG31205-RB	10	35	26	30	61	88	24	7	60	17	2.5	0.116	0.246
sp|Q10714|ACE_DROME	Q10714	Ance	0	13	0	9	19	6	4	4	11	4	2.5	0.317	0.336
tr|Q8SZN1|Q8SZN1_DROME	Q8SZN1	CG31313	1	17	0	11	16	20	6	6	16	3	2.5	0.196	0.266
tr|A1Z7H7|A1Z7H7_DROME	A1Z7H7	CG8586-RA	0	16	0	10	17	12	5	5	13	2	2.5	0.240	0.289
sp|P06607|VIT3_DROME	P06607	Yp3	122	479	380	510	719	1184	327	106	804	199	2.5	0.102	0.225
sp|Q8MLZ7|IDGF3_DROME	Q8MLZ7	Idgf3	1	29	0	16	36	22	10	10	25	6	2.5	0.266	0.313
tr|Q7K127|Q7K127_DROME	Q7K127	CG7997	4	24	0	11	35	24	9	7	23	7	2.5	0.240	0.289
sp|Q9VU58|NPLP2_DROME	Q9VU58	Nplp2	65	328	148	226	405	694	180	78	442	136	2.5	0.171	0.259
tr|A1ZB61|A1ZB61_DROME	A1ZB61	CG15067	14	21	22	28	56	56	19	3	47	9	2.4	0.047	0.183
tr|Q9Y141|Q9Y141_DROME	Q9Y141	BcDNA.GH05741	1	13	0	4	16	16	5	4	12	4	2.4	0.291	0.330
tr|Q9VA42|Q9VA42_DROME	Q9VA42	Npc2g	10	41	28	30	83	78	27	9	63	17	2.4	0.127	0.247
tr|Q8IPH4|Q8IPH4_DROME	Q8IPH4	Tep2	7	39	4	28	37	52	17	11	39	7	2.3	0.161	0.259
sp|Q868Z9-1|PPN_DROME	Q868Z9	Ppn	4	65	28	30	60	138	33	18	76	32	2.3	0.301	0.330
tr|Q9VKR8|Q9VKR8_DROME	Q9VKR8	CG17108	16	13	14	50	7	44	14	1	33	13	2.3	0.230	0.289
tr|Q9VJQ3|Q9VJQ3_DROME	Q9VJQ3	yellow-c	2	9	12	11	21	20	8	3	18	3	2.2	0.089	0.212
tr|Q8IPB7|Q8IPB7_DROME	Q8IPB7	LM408	13	96	50	76	117	152	53	24	115	22	2.2	0.129	0.247
tr|A1ZBU5|A1ZBU5_DROME	A1ZBU5	CG13422	1	5	0	2	11	0	2	2	4	3	2.1	0.557	0.568
tr|Q9VI09|Q9VI09_DROME	Q9VI09	CG17919	0	24	4	10	23	26	9	7	20	5	2.1	0.305	0.330
tr|Q9VAI9|Q9VAI9_DROME	Q9VAI9	Obp99c	31	84	36	82	115	116	50	17	104	11	2.1	0.055	0.183
sp|Q9VLJ6|ACER_DROME	Q9VLJ6	Acer	4	73	12	26	72	84	30	22	61	18	2.0	0.332	0.345
tr|Q0E9C3|Q0E9C3_DROME	Q0E9C3	Sod3	0	11	0	0	5	16	4	4	7	5	2.0	0.579	0.579
tr|Q9VD48|Q9VD48_DROME	Q9VD48	CG5791	0	9	6	8	11	12	5	3	10	1	2.0	0.161	0.259

Group 3: In both w^{1118} and mutant and within >0.8 and <2-fold difference

	Uniprot ID	Annotation	w1118			dKlf15NN			w1118		dKlf15NN				
			#1	#2	#3	#1	#2	#3	Mean	SEM	Mean	SEM	Fold chang	t-Test	B-H Correction
sp|Q9VAI6|OB99B_DROME	Q9VAI6	Obp99b	10	24	36	31	16	90	23	7	46	23	1.9	0.402	1.000
sp|P02844|VIT2_DROME	P02844	Yp2	128	565	274	385	601	876	322	129	621	142	1.9	0.195	1.000
tr|Q9VKV2|Q9VKV2_DROME	Q9VKV2	CG5322	2	13	0	10	11	8	5	4	10	1	1.9	0.345	1.000
sp|P02843|VIT1_DROME	P02843	Yp1	143	775	316	578	784	886	411	188	749	91	1.8	0.181	1.000
tr|Q9VG08|Q9VG08_DROME	Q9VG08	yellow-f2	4	21	0	12	17	16	8	7	15	2	1.8	0.375	1.000
tr|Q9VME1|Q9VME1_DROME	Q9VME1	CG42369	2	16	0	3	9	20	6	5	11	5	1.8	0.534	1.000
tr|Q8SY86|Q8SY86_DROME	Q8SY86	CG16704	0	11	10	2	15	20	7	3	12	5	1.8	0.466	1.000
tr|Q7JQR3|Q7JQR3_DROME	Q7JQR3	CG4670	0	12	0	5	8	8	4	4	7	1	1.7	0.518	1.000
tr|Q86PE8|Q86PE8_DROME	Q86PE8	CG5390	7	25	8	15	25	30	14	6	24	4	1.7	0.247	1.000
tr|Q9VZ24|Q9VZ24_DROME	Q9VZ24	CG15201	0	3	6	2	5	8	3	2	5	2	1.7	0.457	1.000
tr|Q94881|Q94881_DROME	Q94881	Lectin-galC1	7	24	18	17	29	36	16	5	27	6	1.7	0.215	1.000
tr|A1Z6V5|A1Z6V5_DROME	A1Z6V5	Spn43Ab	4	40	26	19	51	44	23	11	38	10	1.6	0.360	1.000
sp|Q8IN44|TOTA_DROME	Q8IN44	TotA	4	77	16	36	55	62	32	23	51	8	1.6	0.484	1.000
sp|Q9V8Y2|OB56A_DROME	Q9V8Y2	Obp56a	2	29	8	14	19	28	13	8	20	4	1.5	0.478	1.000
sp|P08144|AMYA_DROME	P08144	Amy-p	0	53	20	11	43	54	24	16	36	13	1.5	0.598	1.000
tr|Q27598|Q27598_DROME	Q27598	1	46	109	92	70	132	160	82	19	121	27	1.5	0.309	1.000
sp|Q9V521|PRPA3_DROME	Q9V521	proPo-A3	50	185	102	82	173	232	112	39	162	44	1.4	0.445	1.000
sp|P23779|CYTL_DROME	P23779	Cys	27	103	102	70	107	154	77	25	110	24	1.4	0.401	1.000
tr|Q0E8C8|Q0E8C8_DROME	Q0E8C8	Spn77Ba	5	20	0	22	8	6	8	6	12	5	1.4	0.678	1.000
tr|Q7K3E2|Q7K3E2_DROME	Q7K3E2	CG5080	22	111	18	58	72	82	50	30	71	7	1.4	0.547	1.000
sp|P08171|EST6_DROME	P08171	Est-6	24	173	72	56	151	172	90	44	126	36	1.4	0.555	1.000
tr|Q2QBM1|Q2QBM1_DROME	Q2QBM1	Men	7	27	14	19	23	18	16	6	20	1	1.3	0.526	1.000
sp|P41572|6PGD_DROME	P41572	Pgd	4	0	6	2	7	4	3	2	4	1	1.2	0.713	1.000
sp|P82705|IM04_DROME	P82705	IM4	19	45	22	27	47	32	29	8	35	6	1.2	0.553	1.000
sp|Q8IN43|TOTC_DROME	Q8IN43	TotC	0	47	16	12	33	30	21	14	25	7	1.2	0.795	1.000
tr|Q9VTC3|Q9VTC3_DROME	Q9VTC3	CG6409	17	128	100	29	105	156	82	33	97	37	1.2	0.778	1.000
sp|Q9VAJ4|OB99A_DROME	Q9VAJ4	Obp99a	0	21	0	3	8	14	7	7	8	3	1.2	0.876	1.000
tr|A5XCL5|A5XCL5_DROME	A5XCL5	UGP	0	0	86	39	36	26	29	29	34	4	1.2	0.870	1.000
tr|Q76NR6|Q76NR6_DROME	Q76NR6	regucalcin	44	56	58	49	60	76	53	4	62	8	1.2	0.378	1.000
tr|Q9VBJ6|Q9VBJ6_DROME	Q9VBJ6	CG14540	0	0	12	0	0	14	4	4	5	5	1.2	0.919	1.000
sp|Q9V3D4|IDGF2_DROME	Q9V3D4	Idgf2	3	57	22	14	36	46	27	16	32	10	1.2	0.823	1.000
sp|Q8SY61|OB56D_DROME	Q8SY61	Obp56d	18	105	36	37	81	62	53	27	60	13	1.1	0.826	1.000
sp|Q23997|CH47_DROME	Q23997	CG5210	48	243	88	93	164	164	126	59	140	24	1.1	0.836	1.000
tr|Q9VQT8|Q9VQT8_DROME	Q9VQT8	CG16712	49	156	98	68	97	170	101	31	112	30	1.1	0.813	1.000
tr|Q0E9F9|Q0E9F9_DROME	Q0E9F9	CG2915-RB	4	21	10	5	17	16	12	5	13	4	1.1	0.883	1.000
tr|Q7KTG2|Q7KTG2_DROME	Q7KTG2	Apoltp	0	25	0	5	11	12	8	8	9	2	1.1	0.939	1.000
tr|Q9VVP9|Q9VVP9_DROME	Q9VVP9	CG4306	0	7	0	3	4	0	2	2	2	1	1.1	0.947	1.000
tr|Q7JYH0|Q7JYH0_DROME	Q7JYH0	CG6503	17	96	40	15	29	116	51	23	54	32	1.0	0.953	1.000
tr|B7YZV3|B7YZV3_DROME	B7YZV3	Pde1c	3	23	8	3	12	20	11	6	12	5	1.0	0.949	1.000
sp|P11449|VTU1_DROME	P11449	Vm26Aa	4	19	12	11	7	18	12	4	12	3	1.0	0.966	1.000
tr|Q9VJN0|Q9VJN0_DROME	Q9VJN0	CG31821	0	15	0	1	8	6	5	5	5	2	1.0	0.994	1.000
tr|Q9VHK7|Q9VHK7_DROME	Q9VHK7	CG8369	0	17	10	0	13	14	9	5	9	5	1.0	1.000	1.000

tr|Q8MT58|Q8MT58_DROME	Q8MT58	CG17337	1	15	30		3	12	30		15	8		15	8		1.0	0.995	1.000
tr|Q9VUC1|Q9VUC1_DROME	Q9VUC1	Hsc70Cb	4	7	12		6	4	12		7	2		7	2		1.0	0.942	1.000
sp|P48375|FKB12_DROME	P48375	FK506-bp2	12	13	26		8	19	22		17	4		16	4		0.9	0.894	1.000
tr|O97102|O97102_DROME	O97102	smt3	3	3	4		2	3	4		3	0		3	0		0.9	0.775	1.000
tr|Q7KRU8|Q7KRU8_DROME	Q7KRU8	Fer1HCH	28	156	214		26	108	236		133	55		123	61		0.9	0.917	1.000
sp|Q9V496|APLP_DROME	Q9V496	Rfabg	829	3533	2418		1111	2095	3086		2260	785		2097	570		0.9	0.875	1.000
tr|Q8INK2|Q8INK2_DROME	Q8INK2	fabp	11	11	16		11	5	18		13	2		12	4		0.9	0.797	1.000
tr|Q9V3U6|Q9V3U6_DROME	Q9V3U6	26-29-p	4	3	8		2	5	6		5	2		4	1		0.9	0.830	1.000
tr|Q9I7Q5|Q9I7Q5_DROME	Q9I7Q5	Cpr65Au	7	17	0		4	9	8		8	5		7	2		0.9	0.873	1.000
sp|Q9W303|IDGF4_DROME	Q9W303	Idgf4	31	185	54		54	96	88		90	48		79	13		0.9	0.839	1.000
tr|Q9VZR2|Q9VZR2_DROME	Q9VZR2	Drsl5	0	5	20		0	0	22		8	6		7	7		0.9	0.912	1.000

Group 4: In both w^{1118} and mutant but <0.8 lower in $dKlf15^{NN}$ mutant

	Uniprot ID	Annotation	w1118				dKlf15NN				w1118			dKlf15NN				
			#1	#2	#3		#1	#2	#3		Mean	SEM		Mean	SEM		Fold chang	t-Test	B-H Correction
sp|Q05825|ATPB_DROME	Q05825	ATPsyn-beta	62	15	46		6	0	0		41	14		2	2		0.1	0.051	0.164
sp|P05661-17|MYSA_DROME	P05661-17	Mhc	264	47	158		42	0	0		156	63		14	14		0.1	0.092	0.193
sp|P18432|MLR_DROME	P18432	Mlc2	39	12	8		8	0	0		20	10		3	3		0.1	0.167	0.295
tr|Q960M4|Q960M4_DROME	Q960M4	Prx5	19	20	8		5	3	0		16	4		2	1		0.2	0.033	0.130
tr|O76935|O76935_DROME	O76935	Irp-1B	12	33	22		6	5	0		22	6		4	2		0.2	0.043	0.156
sp|P08736|EF1A1_DROME	P08736	Ef1alpha48D	26	29	152		9	25	0		69	41		11	7		0.2	0.242	0.396
sp|P13060-1|EF2_DROME	P13060	Ef2b	32	23	44		5	7	6		33	6		6	1		0.2	0.012	0.091
tr|Q9W330|Q9W330_DROME	Q9W330	Hex-A	100	92	30		33	7	0		74	22		13	10		0.2	0.066	0.180
sp|Q9W401-1|CISY_DROME	Q9W401	kdn	81	44	84		18	13	8		70	13		13	3		0.2	0.013	0.091
sp|P31409|VATB_DROME	P31409	Vha55	13	5	18		5	3	0		12	4		2	1		0.2	0.072	0.180
tr|Q24349|Q24349_DROME	Q24349	Gdi	6	9	14		6	0	0		10	2		2	2		0.2	0.073	0.180
sp|P13706-2|GPDA_DROME	P13706-2	Gpdh	683	1108	776		268	309	0		856	129		192	97		0.2	0.015	0.091
sp|Q24560|TBB1_DROME	Q24560	betaTub56D	36	36	22		10	12	0		31	5		7	4		0.2	0.015	0.091
sp|Q9VWH4-1|IDH3A_DROME	Q9VWH4	l(1)G0156	25	16	38		7	5	6		26	6		6	1		0.2	0.034	0.130
sp|Q9Y0Y2|PURA_DROME	Q9Y0Y2	CG17273	19	12	16		7	4	0		16	2		4	2		0.2	0.014	0.091
tr|Q8IQW5|Q8IQW5_DROME	Q8IQW5	HspB8	13	23	14		6	3	4		16	3		4	1		0.2	0.019	0.109
sp|P20478-1|GLNA2_DROME	P20478	Gs2	34	29	28		10	9	4		30	2		8	2		0.3	0.001	0.034
sp|P06603|TBA1_DROME	P06603	alphaTub84B	30	25	62		13	17	0		39	12		10	5		0.3	0.084	0.193
sp|P92177-1|1433E_DROME	P92177-1	14-3-3epsilon	10	27	28		0	11	6		21	6		6	3		0.3	0.075	0.180
tr|Q9VLS4|Q9VLS4_DROME	Q9VLS4	CG8498	15	9	0		6	0	0		8	4		2	2		0.3	0.287	0.428
tr|Q9VQB4|Q9VQB4_DROME	Q9VQB4	CG3609	8	16	6		0	4	4		10	3		3	1		0.3	0.089	0.193
tr|Q8IPA2|Q8IPA2_DROME	Q8IPA2	Mal-B2	6	27	2		0	9	0		12	8		3	3		0.3	0.365	0.482
sp|P42281|ACBP_DROME	P42281	Dbi	0	15	28		0	12	0		14	8		4	4		0.3	0.320	0.458
tr|B7Z001|B7Z001_DROME	B7Z001	CG3523	91	208	174		39	47	48		158	35		45	3		0.3	0.032	0.130
tr|Q9VU38|Q9VU38_DROME	Q9VU38	AdenoK	6	13	8		2	5	0		9	2		3	2		0.3	0.072	0.180
sp|P41043|GST1_DROME	P41043	GstS1	60	60	64		27	20	6		61	1		18	6		0.3	0.002	0.039
sp|P84029|CYC2_DROME	P84029	Cyt-c-p	12	67	12		2	20	4		30	18		9	6		0.3	0.325	0.459
tr|A8DZ21|A8DZ21_DROME	A8DZ21	Acon	72	31	96		18	15	26		66	19		20	3		0.3	0.074	0.180
sp|Q7KN62-1|TERA_DROME	Q7KN62	TER94	10	7	16		7	3	0		11	3		3	2		0.3	0.087	0.193
tr|Q9VKI8|Q9VKI8_DROME	Q9VKI8	CG6287	15	23	26		6	7	6		21	3		6	0		0.3	0.011	0.091
sp|P29310-2|1433Z_DROME	P29310-2	14-3-3zeta	0	107	78		0	20	36		62	32		19	10		0.3	0.270	0.414
sp|P52034-1|K6PF_DROME	P52034	Pfk	111	80	68		50	27	4		86	13		27	13		0.3	0.033	0.130
sp|P11147|HSP7D_DROME	P11147	Hsc70-4	20	49	86		17	15	18		52	19		16	1		0.3	0.138	0.258
tr|Q8IQ18|Q8IQ18_DROME	Q8IQ18	Dp	14	23	0		12	0	0		12	7		4	4		0.3	0.344	0.472
sp|P07764-1|ALF_DROME	P07764	Ald	728	1353	674		292	281	332		919	218		302	15		0.3	0.048	0.159
sp|P52029|G6PI_DROME	P52029	Pgi	119	212	122		50	48	52		151	30		50	1		0.3	0.030	0.130
sp|Q9VUY9|PGM_DROME	Q9VUY9	Pgm	27	69	38		16	21	8		45	13		15	4		0.3	0.090	0.193
sp|Q9VFC8-1|GYS_DROME	Q9VFC8	CG6904	74	64	66		24	28	20		68	3		24	2		0.4	0.000	0.000
tr|Q8IQF8|Q8IQF8_DROME	Q8IQF8	CG6084	12	24	34		8	17	0		23	6		8	5		0.4	0.141	0.259
sp|P29310-1|1433Z_DROME	P29310	14-3-3zeta	94	109	86		42	27	36		96	7		35	5		0.4	0.002	0.039
tr|Q9Y119|Q9Y119_DROME	Q9Y119	Tps1	34	51	68		22	31	4		51	10		19	8		0.4	0.063	0.180
tr|Q9VEB1|Q9VEB1_DROME	Q9VEB1	Mdh2	44	37	64		17	12	26		48	8		18	4		0.4	0.028	0.130
sp|P91938-1|TRXR1_DROME	P91938	Trxr-1	8	25	26		3	12	8		20	6		8	3		0.4	0.129	0.246
tr|Q9Y112|Q9Y112_DROME	Q9Y112	BcDNA.GH10614	4	12	26		2	11	4		14	6		5	3		0.4	0.295	0.434
tr|E1JGQ5|E1JGQ5_DROME	E1JGQ5	CG9485	0	76	0		10	9	10		25	25		10	0		0.4	0.576	0.674
sp|P83967|ACT6_DROME	P83967	Act88F	117	93	128		67	65	0		113	10		44	22		0.4	0.048	0.159
sp|P48602|VATA1_DROME	P48602	Vha68-1	10	15	0		7	3	0		8	4		3	2		0.4	0.353	0.472
sp|Q9XTL9|PYG_DROME	Q9XTL9	GlyP	423	597	520		184	221	202		513	50		202	11		0.4	0.004	0.046
sp|P29613-1|TPIS_DROME	P29613-1	Tpi	172	233	202		90	76	78		203	18		81	4		0.4	0.003	0.039
sp|O62619-1|KPYK_DROME	O62619	PyK	375	492	382		170	161	172		416	38		168	3		0.4	0.003	0.039
tr|Q8IQG9|Q8IQG9_DROME	Q8IQG9	Adk1	14	23	18		9	9	4		18	2		7	2		0.4	0.022	0.119
tr|Q9VGB6|Q9VGB6_DROME	Q9VGB6	Pglym87	20	20	38		10	8	14		26	6		11	2		0.4	0.070	0.180
sp|Q01604|PGK_DROME	Q01604	Pgk	245	244	280		125	93	102		256	12		107	9		0.4	0.001	0.034
tr|A1Z7Z4|A1Z7Z4_DROME	A1Z7Z4	CG1648	3	4	12		0	8	0		6	3		3	3		0.4	0.401	0.511
tr|Q7KSU6|Q7KSU6_DROME	Q7KSU6	CG8036	12	20	72		15	11	18		35	19		15	2		0.4	0.350	0.472
tr|Q961N7|Q961N7_DROME	Q961N7	CG5355	9	12	4		4	3	4		8	2		4	0		0.4	0.115	0.230
sp|P17336|CATA_DROME	P17336	Cat	10	45	42		8	20	14		32	11		14	3		0.4	0.197	0.338
tr|Q9VK60|Q9VK60_DROME	Q9VK60	CG6180	10	24	24		10	8	8		19	5		9	1		0.4	0.089	0.193
sp|Q9I7S8|PUR6_DROME	Q9I7S8	ade5	7	23	10		3	15	0		13	5		6	4		0.4	0.316	0.458
sp|P15007-1|ENO_DROME	P15007	Eno	760	1099	624		402	359	346		827	141		369	17		0.4	0.032	0.130
sp|P07486|G3P1_DROME	P07486	Gapdh1	785	935	592		391	300	348		771	99		346	26		0.4	0.014	0.091
sp|P02828|HSP83_DROME	P02828	Hsp83	31	43	74		21	24	26		49	13		24	2		0.5	0.116	0.230
tr|Q9VF24|Q9VF24_DROME	Q9VF24	cv-d	3	56	14		10	13	12		24	16		12	1		0.5	0.477	0.591
tr|Q95RT1|Q95RT1_DROME	Q95RT1	CG11089	5	12	10		4	9	0		9	2		4	3		0.5	0.241	0.396
sp|P48610-1|KARG_DROME	P48610	Argk	465	588	532		246	243	296		528	36		261	17		0.5	0.003	0.039
sp|P07487|G3P2_DROME	P07487	Gapdh2	724	864	598		404	356	334		729	77		365	21		0.5	0.010	0.091
tr|B7Z0E0|B7Z0E0_DROME	B7Z0E0	Idh	22	27	28		13	20	6		26	2		13	4		0.5	0.044	0.156
tr|Q8MSI2|Q8MSI2_DROME	Q8MSI2	Scp1	27	235	426		14	124	208		229	115		115	56		0.5	0.425	0.534
sp|P45594|CADF_DROME	P45594	tsr	22	24	22		7	11	18		23	1		12	3		0.5	0.032	0.130
sp|P00334|ADH_DROME	P00334	Adh	303	572	472		201	251	266		449	79		239	20		0.5	0.061	0.180
sp|P02572|ACT2_DROME	P02572	Act42A	64	67	126		0	60	78		86	20		46	24		0.5	0.271	0.414
sp|P08879|NDKA_DROME	P08879	awd	0	53	126		1	15	84		60	37		33	26		0.6	0.583	0.675
sp|Q9VGS2|TCTP_DROME	Q9VGS2	Tctp	8	11	12		3	8	6		10	1		6	1		0.6	0.063	0.180
tr|Q8MQS7|Q8MQS7_DROME	Q8MQS7	Mdh1	28	48	24		18	33	4		33	7		19	8		0.6	0.265	0.414
sp|Q9V3P0|PRDX1_DROME	Q9V3P0	Jafrac1	21	40	30		10	21	20		30	6		17	3		0.6	0.115	0.230
sp|Q9VAN0|SERC_DROME	Q9VAN0	CG11899	4	11	8		3	4	6		8	2		4	1		0.6	0.169	0.295
tr|Q7KT11|Q7KT11_DROME	Q7KT11	CG9331	5	15	32		10	12	8		17	8		10	1		0.6	0.402	0.511
sp|Q9VZ49|ENDOU_DROME	Q9VZ49	CG2145	1	17	0		8	3	0		6	6		4	2		0.6	0.707	0.751
tr|Q9VM18|Q9VM18_DROME	Q9VM18	CG5177	13	11	22		7	12	8		15	3		9	1		0.6	0.166	0.295
tr|Q24450|Q24450_DROME	Q24450	Pglym78	18	19	36		12	9	22		24	6		14	4		0.6	0.239	0.396
sp|O77460|IPYR_DROME	O77460	Nurf-38	24	44	46		20	29	20		38	7		23	3		0.6	0.127	0.246
tr|Q9U1I4|Q9U1I4_DROME	Q9U1I4	Spn88Ea	0	27	18		2	0	26		15	8		9	8		0.6	0.647	0.717
sp|Q8IR95|Q8IR95_DROME	Q8IR95	CG32667	0	23	8		0	9	10		10	7		6	3		0.6	0.636	0.715
tr|Q7JVX3|Q7JVX3_DROME	Q7JVX3	CG4408	7	49	24		11	11	30		27	12		17	6		0.6	0.521	0.617
sp|P46415|ADHX_DROME	P46415	Fdh	7	4	20		6	11	4		10	5		7	2		0.6	0.517	0.617
tr|Q7KT33|Q7KT33_DROME	Q7KT33	fbp	9	17	12		6	13	6		13	2		8	3		0.7	0.273	0.414
sp|Q24388|LSP2_DROME	Q24388	Lsp2	22	65	20		0	3	68		36	15		24	22		0.7	0.674	0.737

sp|P61851|SODC_DROME	P61851	Sod	35	45	76		20	31	54		52	12		35	10		0.7	0.338	0.470
sp|P20432|GSTT1_DROME	P20432	GstD1	13	31	56		10	19	38		33	13		22	8		0.7	0.513	0.617
tr|Q9VGA0|Q9VGA0_DROME	Q9VGA0	GstD9	12	11	0		6	8	2		8	4		5	2		0.7	0.605	0.692
sp|P25007|PPIA_DROME	P25007	Cyp1	26	37	54		19	28	34		39	8		27	4		0.7	0.258	0.414
sp|P0CG69|UBIQP_DROME	P0CG69	Ubi-p63E	3	4	24		2	4	16		10	7		7	4		0.7	0.741	0.763
sp|Q9V429-1|THIO2_DROME	Q9V429	Trx-2	6	5	6		3	5	4		6	0		4	1		0.7	0.073	0.180
tr|Q9VHA1|Q9VHA1_DROME	Q9VHA1	SpdS	3	7	0		2	3	2		3	2		2	0		0.7	0.680	0.737
sp|P36951|HYI_DROME	P36951	Gip	4	17	6		3	11	6		9	4		7	2		0.7	0.639	0.715
sp|P02574|ACT4_DROME	P02574	Act79B	89	77	0		55	68	0		55	28		41	21		0.7	0.702	0.751
sp|Q02748|IF4A_DROME	Q02748	eIF-4a	14	17	18		5	11	22		17	1		12	5		0.8	0.482	0.591
tr|Q9W370|Q9W370_DROME	Q9W370	CG15369	14	21	12		14	7	16		16	3		12	3		0.8	0.399	0.511
tr|Q9U4U2|Q9U4U2_DROME	Q9U4U2	Fer2LCH	25	231	270		29	136	250		175	76		138	64		0.8	0.730	0.763
sp|P05303|EF1A2_DROME	P05303	Ef1alpha100E	34	27	0		10	23	16		20	10		16	4		0.8	0.736	0.763
tr|Q8SXA6|Q8SXA6_DROME	Q8SXA6	CG6045	7	36	6		9	19	12		16	10		13	3		0.8	0.780	0.795
tr|Q961T9|Q961T9_DROME	Q961T9	BG:DS00941.11	0	11	0		0	3	6		4	4		3	2		0.8	0.874	0.874
tr|Q8SXB9|Q8SXB9_DROME	Q8SXB9	CG10433	4	28	18		5	9	28		17	7		14	7		0.8	0.813	0.821

Group 5:

Present in w^{1118} control but undetected in $dKlf15^{NN}$ mutant
(a mean of two spectral counts or lower was regarded as undetected)

	Uniprot ID	Annotation	w1118				dKlf15NN				w1118			dKlf15NN				
			#1	#2	#3		#1	#2	#3		Mean	SEM		Mean	SEM		t-Test	B-H Correction
tr|E1JI91|E1JI91_DROME	E1JI91	UGP	90	105	0		0	0	0		65	33		0	0		0.118	0.407
sp|P53501|ACT3_DROME	P53501	Act57B	0	0	106		0	0	0		35	35		0	0		0.374	0.407
tr|Q7KVP4|Q7KVP4_DROME	Q7KVP4	CG9485	48	0	44		0	0	0		31	15		0	0		0.117	0.407
tr|A1ZA66|A1ZA66_DROME	A1ZA66	Strn-Mlck	45	0	28		0	0	0		24	13		0	0		0.137	0.407
sp|P35381|ATPA_DROME	P35381	blw	37	9	16		5	0	0		21	8		2	2		0.085	0.407
sp|P19889|RLA0_DROME	P19889	RpLP0	11	3	32		0	0	0		15	9		0	0		0.154	0.407
tr|A1Z992|A1Z992_DROME	A1Z992	AGBE	6	29	10		0	0	0		15	7		0	0		0.104	0.407
tr|A8JNU6|A8JNU6_DROME	A8JNU6	Nc73EF	34	9	0		0	0	0		15	10		0	0		0.229	0.407
sp|P08570|RLA1_DROME	P08570	RpLP1	7	7	26		2	0	0		13	6		1	1		0.130	0.407
sp|Q27331|VATA2_DROME	Q27331	Vha68-2	13	11	16		0	0	0		13	2		0	0		0.001	0.075
tr|A8JRB8|A8JRB8_DROME	A8JRB8	CG5028-RC	13	9	16		4	0	0		13	2		1	1		0.008	0.224
sp|P11996|LSP1B_DROME	P11996	Lsp1beta	10	28	0		2	0	0		13	8		1	1		0.227	0.407
sp|O96827|EF1B_DROME	O96827	Ef1beta	6	4	26		3	0	0		12	7		1	1		0.199	0.407
tr|Q9VGQ1|Q9VGQ1_DROME	Q9VGQ1	CG5214	15	8	12		0	0	0		12	2		0	0		0.004	0.149
tr|Q8T447|Q8T447_DROME	Q8T447	CG9961	0	0	34		0	0	0		11	11		0	0		0.374	0.407
tr|E2QCF1|E2QCF1_DROME	E2QCF1	ATPCL	4	16	12		3	0	0		11	3		1	1		0.051	0.407
tr|Q9VJZ6|Q9VJZ6_DROME	Q9VJZ6	CG6523	10	15	8		6	0	0		11	2		2	2		0.031	0.407
sp|P05389|RLA2_DROME	P05389	RpLP2	4	5	22		2	0	0		11	6		1	1		0.154	0.407
sp|P55830-1|RS3A_DROME	P55830	RpS3A	4	5	20		0	0	0		10	5		0	0		0.120	0.407
tr|B7Z0V3|B7Z0V3_DROME	B7Z0V3	CG2767	5	16	8		2	0	0		10	3		1	1		0.055	0.407
sp|Q06559|RS3_DROME	Q06559	RpS3	5	0	24		0	0	0		10	7		0	0		0.252	0.407
tr|C0PUZ9|C0PUZ9_DROME	C0PUZ9	Glycogenin-RB	0	17	10		0	0	0		9	5		0	0		0.144	0.407
tr|Q95U38|Q95U38_DROME	Q95U38	skap	15	4	8		0	0	0		9	3		0	0		0.048	0.407
sp|Q9VU68-1|WDR1_DROME	Q9VU68	flr	10	7	10		2	0	0		9	1		1	1		0.004	0.149
tr|Q8MST5|Q8MST5_DROME	Q8MST5	betaTub97EF	13	13	0		0	0	0		9	4		0	0		0.116	0.407
tr|O16043|O16043_DROME	O16043	Df31	0	0	26		0	0	0		9	9		0	0		0.374	0.407
tr|Q5U0Z2|Q5U0Z2_DROME	Q5U0Z2	CG10576	0	0	26		0	0	0		9	9		0	0		0.374	0.407
sp|P53777|MLP1_DROME	P53777	Mlp60A	10	3	12		2	0	0		8	3		1	1		0.065	0.407
tr|Q9VSU6|Q9VSU6_DROME	Q9VSU6	Dhpr	7	17	0		5	0	0		8	5		2	2		0.275	0.407
sp|P38979-1|RSSA_DROME	P38979	sta	5	1	18		0	0	0		8	5		0	0		0.179	0.407
sp|P25843|PROF_DROME	P25843	chic	11	13	0		2	1	0		8	4		1	1		0.174	0.407
sp|Q8MLY8|RS8_DROME	Q8MLY8	RpS8	6	4	14		0	0	0		8	3		0	0		0.059	0.407
tr|Q9VI04|Q9VI04_DROME	Q9VI04	pyd3	9	15	0		2	0	0		8	4		1	1		0.179	0.407
tr|Q7K860|Q7K860_DROME	Q7K860	TpnC4	7	7	10		6	0	0		8	1		2	2		0.052	0.407
tr|Q8MLU2|Q8MLU2_DROME	Q8MLU2	CG11474	7	9	6		2	0	0		8	1		1	1		0.003	0.149
sp|Q9VNA5|PSB4_DROME	Q9VNA5	Prosbeta7	3	9	10		0	0	0		7	2		0	0		0.029	0.407
sp|Q9NJH0|EF1G_DROME	Q9NJH0	Ef1gamma	2	4	16		3	0	0		7	4		1	1		0.227	0.407
sp|P02825|HSP71_DROME	P02825	Hsp70Ab	0	0	22		0	0	0		7	7		0	0		0.374	0.407
sp|P14318|MP20_DROME	P14318	Mp20	5	3	14		0	0	0		7	3		0	0		0.101	0.407
tr|Q7JYW9|Q7JYW9_DROME	Q7JYW9	Hex-C	4	17	0		2	1	0		7	5		1	1		0.314	0.407
tr|O46111|O46111_DROME	O46111	Uba1	13	8	0		6	0	0		7	4		2	2		0.289	0.407
tr|Q9VPZ5|Q9VPZ5_DROME	Q9VPZ5	CG5397	0	21	0		4	0	0		7	7		1	1		0.469	0.491
sp|P14130|RS14_DROME	P14130	RpS14a	4	0	16		3	0	0		7	5		1	1		0.304	0.407
sp|P55828|RS20_DROME	P55828	RpS20	0	0	20		0	0	0		7	7		0	0		0.374	0.407
tr|Q8MS44|Q8MS44_DROME	Q8MS44	CG9468	0	0	20		0	0	0		7	7		0	0		0.374	0.407
tr|Q0KIE6|Q0KIE6_DROME	Q0KIE6	CG12582	0	20	0		3	0	0		7	7		1	1		0.453	0.481
sp|O16797-1|RL3_DROME	O16797	RpL3	5	3	12		3	0	0		7	3		1	1		0.135	0.407
tr|Q9XYZ9|Q9XYZ9_DROME	Q9XYZ9	GstE12	5	3	12		4	0	0		7	3		1	1		0.161	0.407
sp|Q94529|GS1_DROME	Q94529	Gs1l	5	15	0		0	0	0		7	4		0	0		0.197	0.407
tr|Q9W1B9|Q9W1B9_DROME	Q9W1B9	RpL12	4	0	16		0	0	0		7	5		0	0		0.245	0.407
sp|P22769|PSA71_DROME	P22769	Pros28.1	3	11	6		0	0	0		7	2		0	0		0.043	0.407
tr|Q8MT28|Q8MT28_DROME	Q8MT28	CG10467	0	13	6		0	0	0		6	4		0	0		0.170	0.407
sp|P12881|PSA1_DROME	P12881	Pros35	5	8	6		0	0	0		6	1		0	0		0.001	0.075
sp|P46222|RL11_DROME	P46222	RpL11	3	4	12		0	0	0		6	3		0	0		0.091	0.407
sp|Q6AWN0|MTND_DROME	Q6AWN0	CG32068	3	4	12		2	0	0		6	3		1	1		0.116	0.407
sp|P35554|FTN_DROME	P35554	fln	7	0	12		0	0	0		6	3		0	0		0.147	0.407
tr|Q76NQ9|Q76NQ9_DROME	Q76NQ9	AMPdeam	8	4	6		2	0	0		6	1		1	1		0.022	0.407
tr|Q7K3J0|Q7K3J0_DROME	Q7K3J0	CG8258	7	3	8		0	0	0		6	2		0	0		0.023	0.407
tr|Q9VQF7|Q9VQF7_DROME	Q9VQF7	Bacc	0	4	14		0	3	0		6	4		1	1		0.296	0.407
tr|Q6WSQ9|Q6WSQ9_DROME	Q6WSQ9	Mitf	0	0	18		0	0	0		6	6		0	0		0.374	0.407
tr|Q95SI7|Q95SI7_DROME	Q95SI7	CG6028	6	8	4		1	0	0		6	1		0	0		0.008	0.224
sp|P18091-1|ACTN_DROME	P18091	Actn	18	0	0		0	0	0		6	6		0	0		0.374	0.407
tr|Q9VA37|Q9VA37_DROME	Q9VA37	dj-1beta	3	11	4		0	0	2		6	2		1	1		0.105	0.407
sp|P41042|RS4_DROME	P41042	RpS4	1	0	16		0	0	0		6	5		0	0		0.317	0.407
tr|Q8MYS9|Q8MYS9_DROME	Q8MYS9	CG7203	7	11	0		2	0	0		6	3		1	1		0.195	0.407
sp|P35122|UCHL_DROME	P35122	Uch	0	9	8		0	0	0		6	3		0	0		0.118	0.407
sp|P32100|RL7_DROME	P32100	RpL7	3	0	14		0	0	0		6	4		0	0		0.254	0.407
sp|P48159|RL23_DROME	P48159	RpL23	3	0	14		0	0	0		6	4		0	0		0.254	0.407
tr|Q9VV75|Q9VV75_DROME	Q9VV75	CG4169	9	0	8		0	0	0		6	3		0	0		0.117	0.407
tr|Q8IRQ5|Q8IRQ5_DROME	Q8IRQ5	l(1)G0255	7	9	0		0	0	0		6	3		0	0		0.121	0.407
tr|Q9W3L4|Q9W3L4_DROME	Q9W3L4	CG2233	0	11	6		0	0	0		6	3		0	0		0.146	0.407
tr|Q9VD58|Q9VD58_DROME	Q9VD58	CG6439	10	0	6		0	0	0		5	3		0	0		0.144	0.407
tr|Q7K5K3|Q7K5K3_DROME	Q7K5K3	CG11876	9	1	6		0	0	0		5	2		0	0		0.071	0.407
sp|Q94518|NACA_DROME	Q94518	Nacalpha	2	0	14		2	0	0		5	4		1	1		0.327	0.407
sp|P09180|RL4_DROME	P09180	RpL4	8	0	8		0	0	0		5	3		0	0		0.116	0.407
tr|Q9VTZ0|Q9VTZ0_DROME	Q9VTZ0	tral	0	0	16		0	0	0		5	5		0	0		0.374	0.407
sp|P29327-1|RS6_DROME	P29327	RpS6	6	0	10		0	0	0		5	3		0	0		0.141	0.407
tr|Q9GQV2|Q9GQV2_DROME	Q9GQV2	cher	16	0	0		0	0	0		5	5		0	0		0.374	0.407
tr|Q9VN21|Q9VN21_DROME	Q9VN21	lost	1	0	14		0	0	0		5	4		0	0		0.309	0.407
sp|O18640|GBLP_DROME	O18640	Rack1	0	1	14		0	0	0		5	4		0	0		0.316	0.407
tr|Q9VW19|Q9VW19_DROME	Q9VW19	CG9372	0	13	2		0	4	0		5	4		1	1		0.435	0.466
sp|A1ZA47-1|ZASP_DROME	A1ZA47	Zasp52	6	5	4		0	0	0		5	1		0	0		0.001	0.075

sp|P06742-1|MLC1_DROME	P06742	Mlc1	11	0	4		0	0	0		5	3		0	0		0.197	0.407
tr|Q9VB64|Q9VB64_DROME	Q9VB64	CG31063	0	7	8		0	1	4		5	2		2	1		0.320	0.407
tr|Q961R8|Q961R8_DROME	Q961R8	Aats-gly	5	9	0		0	0	0		5	3		0	0		0.147	0.407
tr|Q9I7R0|Q9I7R0_DROME	Q9I7R0	CG18815	2	4	8		0	0	0		5	2		0	0		0.050	0.407
sp|Q26365-2|ADT_DROME	Q26365-2	sesB	14	0	0		0	0	0		5	5		0	0		0.374	0.407
sp|P29844|HSP7C_DROME	P29844	Hsc70-3	0	0	14		0	0	0		5	5		0	0		0.374	0.407
sp|P50882|RL9_DROME	P50882	RpL9	0	0	14		0	0	0		5	5		0	0		0.374	0.407
tr|Q86BQ4|Q86BQ4_DROME	Q86BQ4	CG2862	6	8	0		4	0	0		5	2		1	1		0.293	0.407
sp|Q9W0P5|GALE_DROME	Q9W0P5	Gale	4	9	0		0	0	0		5	3		0	0		0.163	0.407
tr|A8JUT4|A8JUT4_DROME	A8JUT4	Ntf-2	4	9	0		0	0	0		5	3		0	0		0.163	0.407
sp|P49630|RL36_DROME	P49630	RpL36	1	0	12		0	0	0		4	4		0	0		0.299	0.407
tr|Q7JX87|Q7JX87_DROME	Q7JX87	Prx2540-2	1	12	0		4	0	0		4	4		1	1		0.474	0.494
tr|Q7KTK9|Q7KTK9_DROME	Q7KTK9	CG5261	13	0	0		0	0	0		4	4		0	0		0.374	0.407
sp|Q27415-1|NLP_DROME	Q27415	Nlp	2	0	10		0	0	0		4	3		0	0		0.249	0.407
sp|P48149|RS15A_DROME	P48149	RpS15Aa	2	0	10		3	0	0		4	3		1	1		0.401	0.434
sp|P06754-1|TPM1_DROME	P06754-1	Tm1	1	3	8		0	0	0		4	2		0	0		0.113	0.407
sp|Q9W5R8|RL5_DROME	Q9W5R8	RpL5	0	0	12		0	0	0		4	4		0	0		0.374	0.407
tr|Q8MT23|Q8MT23_DROME	Q8MT23	RpL30	0	0	12		0	0	0		4	4		0	0		0.374	0.407
tr|Q8INP8|Q8INP8_DROME	Q8INP8	CG11980	5	7	0		0	0	0		4	2		0	0		0.122	0.407
sp|Q27580|SAHH_DROME	Q27580	Ahcy13	4	8	0		0	0	0		4	2		0	0		0.166	0.407
tr|Q9VXQ5|Q9VXQ5_DROME	Q9VXQ5	Tcp-1zeta	4	0	8		0	0	0		4	2		0	0		0.166	0.407
sp|Q9GU68|IF5A_DROME	Q9GU68	eIF-5A	4	0	8		5	0	0		4	2		2	2		0.457	0.483
sp|P55841|RL14_DROME	P55841	RpL14	1	0	10		0	0	0		4	3		0	0		0.286	0.407
sp|P20241-1|NRG_DROME	P20241	Nrg	1	7	4		0	1	0		4	2		0	0		0.130	0.407
tr|Q9VSL2|Q9VSL2_DROME	Q9VSL2	GstO3	0	5	6		0	0	0		4	2		0	0		0.117	0.407
sp|Q9VA91|RS7_DROME	Q9VA91	RpS7	3	0	8		0	0	0		4	2		0	0		0.192	0.407
sp|Q9V9X4|MTNA_DROME	Q9V9X4	CG11334	1	1	8		0	0	0		4	2		0	0		0.176	0.407
sp|Q8IRH0|Q8IRH0_DROME	Q8IRH0	Psa	7	4	0		3	0	0		4	2		1	1		0.323	0.407
tr|Q9W2M4|Q9W2M4_DROME	Q9W2M4	CG10527	0	7	4		0	3	0		4	2		1	1		0.279	0.407
sp|Q9VMR8|TOTM_DROME	Q9VMR8	TotM	0	11	0		0	1	0		4	4		0	0		0.434	0.466
tr|Q8SXV8|Q8SXV8_DROME	Q8SXV8	CG3246	0	11	0		0	5	0		4	4		2	2		0.678	0.690
sp|P29843|HSP7A_DROME	P29843	Hsc70-1	5	5	0		0	0	0		4	2		0	0		0.116	0.407
sp|Q94522|SUCA_DROME	Q94522	Scsalpha	2	0	8		1	0	0		3	2		0	0		0.260	0.407
sp|P02518|HSP27_DROME	P02518	Hsp27	0	0	10		0	0	0		3	3		0	0		0.374	0.407
sp|P55935|RS9_DROME	P55935	RpS9	0	0	10		0	0	0		3	3		0	0		0.374	0.407
tr|Q0E9I6|Q0E9I6_DROME	Q0E9I6	Dscam1	0	0	10		0	0	0		3	3		0	0		0.374	0.407
tr|Q7JW48|Q7JW48_DROME	Q7JW48	CG10911	0	0	10		0	0	0		3	3		0	0		0.374	0.407
tr|Q9VBR8|Q9VBR8_DROME	Q9VBR8	CG11902	0	0	10		0	0	0		3	3		0	0		0.374	0.407
sp|P22464-1|ANXB9_DROME	P22464	AnnIX	4	1	4		0	0	0		3	1		0	0		0.029	0.407
sp|P09491-1|TPM2_DROME	P09491	Tm2	4	5	0		0	0	0		3	2		0	0		0.119	0.407
tr|Q9VPX6|Q9VPX6_DROME	Q9VPX6	capt	4	5	0		0	0	0		3	2		0	0		0.119	0.407
sp|Q24407|ATP5J_DROME	Q24407	ATPsyn-Cf6	4	0	6		0	0	0		3	2		0	0		0.137	0.407
tr|Q7KVX1|Q7KVX1_DROME	Q7KVX1	l(1)G0334	7	0	2		0	0	0		3	2		0	0		0.230	0.407
tr|Q9V3W0|Q9V3W0_DROME	Q9V3W0	UK114	0	1	8		0	0	0		3	2		0	0		0.277	0.407
sp|Q00174|LAMA_DROME	Q00174	LanA	0	9	0		0	0	0		3	3		0	0		0.374	0.407
tr|Q9VNK6|Q9VNK6_DROME	Q9VNK6	CG11459	0	9	0		0	0	0		3	3		0	0		0.374	0.407
tr|O96299|O96299_DROME	O96299	Sodh-2	2	7	0		0	0	0		3	2		0	0		0.204	0.407
tr|Q9VM19|Q9VM19_DROME	Q9VM19	CG5171	2	7	0		1	0	0		3	2		0	0		0.243	0.407
sp|P54385-1|DHE3_DROME	P54385	Gdh	4	0	4		0	0	0		3	1		0	0		0.117	0.407
sp|P17704|RS17_DROME	P17704	RpS17	2	0	6		0	0	0		3	2		0	0		0.192	0.407
sp|P41044|CAB32_DROME	P41044	Cbp53E	8	0	0		0	0	0		3	3		0	0		0.374	0.407
sp|O61231|RL10_DROME	O61231	RpL10	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|O76454|PHS_DROME	O76454	Pcd	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|P02517|HSP26_DROME	P02517	Hsp26	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|P23128-1|DDX6_DROME	P23128	me31B	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|P49847|TAF6_DROME	P49847	Taf6	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|Q9V3S0|CP4G1_DROME	Q9V3S0	Cyp4g1	0	0	8		0	0	0		3	3		0	0		0.374	0.407
sp|Q9V597|RL31_DROME	Q9V597	RpL31	0	0	8		0	0	0		3	3		0	0		0.374	0.407
tr|A1Z892|A1Z892_DROME	A1Z892	Prx2540-1	0	0	8		0	0	0		3	3		0	0		0.374	0.407
tr|Q24150|Q24150_DROME	Q24150	Nap1	0	0	8		0	0	0		3	3		0	0		0.374	0.407
tr|Q9VTM9|Q9VTM9_DROME	Q9VTM9	CG32088	0	0	8		0	0	0		3	3		0	0		0.374	0.407
tr|A1ZAA5|A1ZAA5_DROME	A1ZAA5	Got1	5	3	0		0	0	0		3	2		0	0		0.156	0.407
sp|Q00637|SODM_DROME	Q00637	Sod2	4	0	4		0	0	0		3	1		0	0		0.117	0.407
tr|A1Z6X6|A1Z6X6_DROME	A1Z6X6	CG1707	2	5	0		0	0	0		3	2		0	0		0.178	0.407
sp|Q8T3U2|RS23_DROME	Q8T3U2	RpS23	1	0	6		0	0	0		2	2		0	0		0.238	0.407
sp|O02649|CH60_DROME	O02649	Hsp60	1	0	6		0	3	0		2	2		1	1		0.468	0.491
tr|Q9VJ31|Q9VJ31_DROME	Q9VJ31	CG10623	4	3	0		0	0	0		2	1		0	0		0.141	0.407
tr|Q9W3B3|Q9W3B3_DROME	Q9W3B3	CG1885	3	4	0		1	0	0		2	1		0	0		0.169	0.407
sp|Q9VLM8|SYAC_DROME	Q9VLM8	Aats-ala	7	0	0		0	0	0		2	2		0	0		0.374	0.407
sp|P15278-1|FAS3_DROME	P15278	Fas3	0	7	0		0	0	0		2	2		0	0		0.374	0.407
tr|A4V464|A4V464_DROME	A4V464	Acon	0	3	4		0	0	0		2	1		0	0		0.132	0.407
tr|Q8ST39|Q8ST39_DROME	Q8ST39	CG9336	0	3	4		0	1	0		2	1		0	0		0.230	0.407
tr|Q7KV27|Q7KV27_DROME	Q7KV27	CG1640	4	3	0		0	0	0		2	1		0	0		0.127	0.407
tr|Q8IP97|Q8IP97_DROME	Q8IP97	Pex19	4	3	0		2	0	0		2	1		1	1		0.264	0.407
tr|O76902|O76902_DROME	O76902	rush	2	0	4		0	0	0		2	1		0	0		0.147	0.407
tr|Q8SYA6|Q8SYA6_DROME	Q8SYA6	CG7322	2	4	0		1	0	0		2	1		0	0		0.202	0.407
sp|O18405|SURF4_DROME	O18405	Surf4	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|P29742|CLH_DROME	P29742	Chc	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|P46150-1|MOEH_DROME	P46150	Moe	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|P46223|RL7A_DROME	P46223	RpL7A	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|P48598-1|IF4E_DROME	P48598	eIF-4E	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|P62152|CALM_DROME	P62152	Cam	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|Q9VG97|GSTT3_DROME	Q9VG97	GstD3	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|Q9VWG3|RS10B_DROME	Q9VWG3	RpS10b	0	0	6		0	0	0		2	2		0	0		0.374	0.407
tr|A8DZ02|A8DZ02_DROME	A8DZ02	kuz	0	0	6		0	0	0		2	2		0	0		0.374	0.407
tr|Q8MR43|Q8MR43_DROME	Q8MR43	CG1622	0	0	6		0	0	0		2	2		0	0		0.374	0.407
tr|Q9V9W2|Q9V9W2_DROME	Q9V9W2	RpL6	0	0	6		0	0	0		2	2		0	0		0.374	0.407
sp|Q26365-1|ADT_DROME	Q26365	sesB	0	0	6		2	0	0		2	2		1	1		0.607	0.621
sp|A1ZA47-4|ZASP_DROME	A1ZA47-4	Zasp52	6	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|D1YSG0|D1YSG0_DROME	D1YSG0	bt	6	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q8IPC2|Q8IPC2_DROME	Q8IPC2	CG13138	6	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q9W2X6|Q9W2X6_DROME	Q9W2X6	l(1)G0230	6	0	0		1	0	0		2	2		0	0		0.439	0.468
sp|O01666|ATPG_DROME	O01666	ATPsyn-gamma	4	0	2		1	0	0		2	1		0	0		0.213	0.407
tr|Q7KTW5|Q7KTW5_DROME	Q7KTW5	CG9391	3	3	0		0	0	0		2	1		0	0		0.117	0.407
sp|O97477|INO1_DROME	O97477	Inos	3	3	0		3	0	0		2	1		1	1		0.597	0.613
sp|P13238|VTU2_DROME	P13238	Vm26Ab	0	5	0		0	0	0		2	2		0	0		0.374	0.407
sp|Q9VMP9|GNPI_DROME	Q9VMP9	Gnpda1	0	5	0		0	0	0		2	2		0	0		0.374	0.407
tr|O97121|O97121_DROME	O97121	Eip55E	0	5	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q2MGK5|Q2MGK5_DROME	Q2MGK5	CG4970	0	5	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q8SXR1|Q8SXR1_DROME	Q8SXR1	NLaz	0	5	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q8SYA4|Q8SYA4_DROME	Q8SYA4	CG18107	0	5	0		0	0	2		2	2		1	1		0.590	0.609
sp|P04359|RL32_DROME	P04359	RpL32	5	0	0		0	0	0		2	2		0	0		0.374	0.407
sp|Q9VRJ9|OTU1_DROME	Q9VRJ9	CG4603	5	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|E1JJG7|E1JJG7_DROME	E1JJG7	CG32770	5	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q0E9E2|Q0E9E2_DROME	Q0E9E2	CG1516	5	0	0		0	0	0		2	2		0	0		0.374	0.407

tr|Q4TWT4|Q4TWT4_DROME	Q4TWT4	su(r)	5	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q9VSL4|Q9VSL4_DROME	Q9VSL4	GstO2	5	0	0		0	0	0		2	2		0	0		0.374	0.407
tr|Q7KUQ2|Q7KUQ2_DROME	Q7KUQ2	CG9674-RB	4	1	0		0	0	0		2	1		0	0		0.197	0.407
tr|O97428|O97428_DROME	O97428	cib	2	3	0		2	4	0		2	1		2	1		0.879	0.883
sp|Q02645-1|HTS_DROME	Q02645	hts	1	4	0		0	0	0		2	1		0	0		0.267	0.407
sp|Q9VNT5|TRXR2_DROME	Q9VNT5	Trxr-2	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|A1Z8U4|A1Z8U4_DROME	A1Z8U4	Cct5	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|A8DYP0|A8DYP0_DROME	A8DYP0	Unc-89	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q24062|Q24062_DROME	Q24062	b	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VFF0|Q9VFF0_DROME	Q9VFF0	CG3731	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VH01|Q9VH01_DROME	Q9VH01	Bruce	4	0	0		4	0	0		1	1		1	1		0.940	0.940
tr|Q7JVI6|Q7JVI6_DROME	Q7JVI6	GstE13	3	1	0		0	0	0		1	1		0	0		0.171	0.407
sp|Q95083|PSA5_DROME	Q95083	Prosalpha5	1	3	0		0	0	0		1	1		0	0		0.147	0.407
sp|Q9XZJ4|PSA6_DROME	Q9XZJ4	Prosalpha1	1	3	0		0	0	0		1	1		0	0		0.147	0.407
tr|Q967S0|Q967S0_DROME	Q967S0	Prat2	1	3	0		0	0	0		1	1		0	0		0.147	0.407
tr|Q7KSB5|Q7KSB5_DROME	Q7KSB5	CG4390	1	3	0		0	3	0		1	1		1	1		0.694	0.703
sp|Q6NN85-1|SSH_DROME	Q6NN85	ssh	0	4	0		0	0	0		1	1		0	0		0.374	0.407
sp|Q9V813|MTAP_DROME	Q9V813	CG4802	0	4	0		0	0	0		1	1		0	0		0.374	0.407
sp|Q9VXX8|RL371_DROME	Q9VXX8	RpL37a	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|A1Z8G7|A1Z8G7_DROME	A1Z8G7	Listericin	0	4	0		0	0	0		1	1		0	0		0.374	0.407
tr|A8QI34|A8QI34_DROME	A8QI34	CG40625	0	4	0		0	0	0		1	1		0	0		0.374	0.407
tr|B7YZX6|B7YZX6_DROME	B7YZX6	CG10600	0	4	0		0	0	0		1	1		0	0		0.374	0.407
tr|B7Z076|B7Z076_DROME	B7Z076	CG6852	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|O97479|O97479_DROME	O97479	Sodh-1	0	4	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q8INQ3|Q8INQ3_DROME	Q8INQ3	CG11760-RB	0	4	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q9U9B0|Q9U9B0_DROME	Q9U9B0	gig	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VPI8|Q9VPI8_DROME	Q9VPI8	net	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VWS5|Q9VWS5_DROME	Q9VWS5	CG15040	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|Q9W137|Q9W137_DROME	Q9W137	CG4707	0	0	4		0	0	0		1	1		0	0		0.374	0.407
tr|Q0E8H9|Q0E8H9_DROME	Q0E8H9	Hexo1	0	4	0		0	3	0		1	1		1	1		0.795	0.802
sp|Q9NIV1|E2AK3_DROME	Q9NIV1	PEK	4	0	0		0	0	0		1	1		0	0		0.374	0.407
sp|Q9V3J1-1|VATH_DROME	Q9V3J1	VhaSFD	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VIQ8|Q9VIQ8_DROME	Q9VIQ8	CoIV	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|Q9VKM3|Q9VKM3_DROME	Q9VKM3	l(2)06225	4	0	0		0	0	0		1	1		0	0		0.374	0.407
tr|A1Z784|A1Z784_DROME	A1Z784	ACC	2	1	0		0	0	0		1	1		0	0		0.141	0.407
tr|Q0E993|Q0E993_DROME	Q0E993	Aats-val	2	1	0		0	0	0		1	1		0	0		0.141	0.407
tr|Q1RL06|Q1RL06_DROME	Q1RL06	GS	1	0	2		2	0	0		1	1		1	1		0.476	0.494