Supplementary Table 1

Sample size and statistics

Figure 1b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; +/+; UAS-Kir2.1,tub-Gal80ts/+	M	Fed	22	5	33
w-; +/+; UAS-Kir2.1,tub-Gal80ts/+	M	Fed	30	4	30
w-; +/+; CN-Gal4/+	M	Fed	22	6	34
w-; +/+; CN-Gal4/+	M	Fed	30	6	32
w-; +/+; CN-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Fed	22	4	31
w-; +/+; CN-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Fed	30	6	35
w-; +/+; UAS-Kir2.1,tub-Gal80ts/+	M	Starved	22	5	35
w-; +/+; UAS-Kir2.1,tub-Gal80ts/+	M	Starved	30	5	46
w-; +/+; CN-Gal4/+	M	Starved	22	5	35
w-; +/+; CN-Gal4/+	M	Starved	30	6	34
w-; +/+; CN-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Starved	22	6	30
w-; +/+; CN-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Starved	30	6	30

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, 22 °C, *CN-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-Kir2.1,tub-Gal80ts/+ vs. CN-Gal4/+	-2.684	-27.74 to 22.38	No	ns	0.9562
UAS-Kir2.1,tub-Gal80ts/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	-6.975	-34.74 to 20.79	No	ns	0.7847
CN-Gal4/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	-4.291	-31.00 to 22.42	No	ns	0.9045

Group 2 (Fed, 30 °C, *CN-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-Kir2.1,tub-Gal80ts/+ vs. CN-Gal4/+	-13.53	-29.36 to 2.305	No	ns	0.0986
UAS-Kir2.1,tub-Gal80ts/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	-10.61	-26.44 to 5.220	No	ns	0.2179
CN-Gal4/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	2.915	-11.25 to 17.08	No	ns	0.8515

Group 3 (Starved, 22 °C, *CN-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-Kir2.1,tub-Gal80ts/+ vs. CN-Gal4/+	-7.155	-35.94 to 21.63	No	ns	0.7887
UAS-Kir2.1,tub-Gal80ts/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	3.006	-25.78 to 31.80	No	ns	0.9583
CN-Gal4/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	10.16	-18.63 to 38.95	No	ns	0.6256

Group 4 (Starved, 30 °C, *CN-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-Kir2.1,tub-Gal80ts/+ vs. CN-Gal4/+	-19.00	-41.00 to 3.004	No	ns	0.0954
UAS-Kir2.1,tub-Gal80ts/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	85.92	63.92 to 107.9	Yes	***	<0.0001
CN-Gal4/+ vs. UAS-Kir2.1,tub-Gal80ts/CN-Gal4	104.9	83.94 to 125.9	Yes	***	<0.0001

Figure 1e

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; R20F11-LexA/+; CN-Gal4/+	M	Fed	23	5	37
w-; UAS-FRT-stop-FRT-TNT/+; LexAop-FLP/+	M	Fed	23	5	30
w-; R20F11-LexA/ UAS-FRT-stop-FRT-TNT; CN-Gal4/ LexAop-FLP	M	Fed	23	5	34
w-; R20F11-LexA/+; CN-Gal4/+	M	Starved	23	5	43
w-; UAS-FRT-stop-FRT-TNT/+; LexAop-FLP/+	M	Starved	23	6	44
w-; R20F11-LexA/ UAS-FRT-stop-FRT-TNT; CN-Gal4/ LexAop-FLP	M	Starved	23	6	31

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *R20F11-LexA, CN-Gal4 X LexAop-FLP, UAS-FRT-stop-FRT-TNT*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
R20F11,CN vs. FLP,UAS-stop-TNT	2.414	-7.574 to 12.40	No	ns	0.7987
R20F11,CN vs. R20F11,CN/FLP,UAS-stop-TNT	4.804	-5.184 to 14.79	No	ns	0.4306
FLP,UAS-stop-TNT vs. R20F11,CN/FLP,UAS-stop-TNT	2.390	-7.598 to 12.38	No	ns	0.8023

Group 2 (Starved, *R20F11-LexA, CN-Gal4 X LexAop-FLP, UAS-FRT-stop-FRT-TNT*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
R20F11,CN vs. FLP,UAS-stop-TNT	-12.77	-36.95 to 11.41	No	ns	0.3719
R20F11,CN vs. R20F11,CN/FLP,UAS-stop-TNT	73.35	48.09 to 98.60	Yes	***	<0.0001
FLP,UAS-stop-TNT vs. R20F11,CN/FLP,UAS-stop-TNT	86.12	61.94 to 110.3	Yes	***	<0.0001

Figure 2c

Sample size

Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	1 mM D-glucose	7	7
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-glucose	8	8
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-fructose	6	6
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-trehalose	7	7
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	100 μM Glibenclamide	6	6

Statistics - One-way ANOVA with Tukey post hoc test

Peak amplitude

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1mM D-glucose vs. 20mM D-glucose	-106.0	-324.1 to 112.1	No	ns	0.6245
1mM D-glucose vs. 20mM D-fructose	-51.70	-286.1 to 182.7	No	ns	0.9669
1mM D-glucose vs. 20mM D-trehalose	-17.22	-242.4 to 208.0	No	ns	0.9994
1mM D-glucose vs. 100M D-Glibenclamide	-69.33	-303.7 to 165.1	No	ns	0.9091
20mM D-glucose vs. 20mM D-fructose	54.30	-173.2 to 281.8	No	ns	0.9562
20mM D-glucose vs. 20mM D-trehalose	88.78	-129.3 to 306.8	No	ns	0.7605
20mM D-glucose vs. 100M D-Glibenclamide	36.67	-190.9 to 264.2	No	ns	0.9896
20mM D-fructose vs. 20mM D-trehalose	34.48	-199.9 to 268.9	No	ns	0.9926
20mM D-fructose vs. 100M D-Glibenclamide	-17.64	-260.9 to 225.6	No	ns	0.9995
20mM D-trehalose vs. 100M D-Glibenclamide	-52.11	-286.5 to 182.3	No	ns	0.9660

Oscillation number

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1mM D-glucose vs. 20mM D-glucose	2.661	-6.740 to 12.06	No	ns	0.9214
1mM D-glucose vs. 20mM D-fructose	2.119	-7.986 to 12.22	No	ns	0.9724
1mM D-glucose vs. 20mM D-trehalose	5.429	-4.280 to 15.14	No	ns	0.4940
1mM D-glucose vs. 100μM D-Glibenclamide	6.952	-3.153 to 17.06	No	ns	0.2913
20mM D-glucose vs. 20mM D-fructose	-0.5417	-10.35 to 9.268	No	ns	0.9998
20mM D-glucose vs. 20mM D-trehalose	2.768	-6.633 to 12.17	No	ns	0.9105
20mM D-glucose vs. 100μM D-Glibenclamide	4.292	-5.518 to 14.10	No	ns	0.7100
20mM D-fructose vs. 20mM D-trehalose	3.310	-6.796 to 13.41	No	ns	0.8739
20mM D-fructose vs. 100μM D-Glibenclamide	4.833	-5.653 to 15.32	No	ns	0.6694
20mM D-trehalose vs. 100μM D-Glibenclamide	1.524	-8.582 to 11.63	No	ns	0.9919

Duration

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1mM D-glucose vs. 20mM D-glucose	-160.4	-824.8 to 503.9	No	ns	0.9544
1mM D-glucose vs. 20mM D-fructose	94.76	-619.4 to 808.9	No	ns	0.9950
1mM D-glucose vs. 20mM D-trehalose	432.9	-253.3 to 1119	No	ns	0.3745
1mM D-glucose vs. 100µM D-Glibenclamide	0.5952	-713.6 to 714.8	No	ns	>0.9999
20mM D-glucose vs. 20mM D-fructose	255.2	-438.1 to 948.5	No	ns	0.8201
20mM D-glucose vs. 20mM D-trehalose	593.3	-71.06 to 1258	No	ns	0.0975
20mM D-glucose vs. 100µM D-Glibenclamide	161.0	-532.2 to 854.3	No	ns	0.9602
20mM D-fructose vs. 20mM D-trehalose	338.1	-376.1 to 1052	No	ns	0.6472
20mM D-fructose vs. 100µM D-Glibenclamide	-94.17	-835.3 to 647.0	No	ns	0.9958
20mM D-trehalose vs. 100µM D-Glibenclamide	-432.3	-1146 to 281.9	No	ns	0.4155

Figure 2d

Sample size

Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-glucose	8	8
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM L-glucose	6	6
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-glucose + 20 mM 2-D-deoxy-glucose	9	9
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-glucose + 1 mM phlorizin	4	4
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM D-glucose + 5 µM nimodipine	4	4

Statistics - One-way ANOVA with Tukey post hoc test

Peak amplitude

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20mM D-glucose vs. 20mM L-glucose	521.8	410.8 to 632.9	Yes	***	<0.0001
20mM D-glucose vs. 20mM D-glucose+D2G	543.8	443.9 to 643.7	Yes	***	<0.0001
20mM D-glucose vs. 20mM D-glucose+phl	517.8	391.9 to 643.6	Yes	***	<0.0001
20mM D-glucose vs. 20mM D-glucose+Nimo	506.8	380.9 to 632.6	Yes	***	<0.0001
20mM L-glucose vs. 20mM D-glucose+D2G	21.97	-86.38 to 130.3	No	ns	0.9748
20mM L-glucose vs. 20mM D-glucose+phl	-4.083	-136.8 to 128.6	No	ns	>0.9999
20mM L-glucose vs. 20mM D-glucose+Nimo	-15.08	-147.8 to 117.6	No	ns	0.9972
20mM D-glucose+D2G vs. 20mM D-glucose+phl	-26.05	-149.6 to 97.49	No	ns	0.9710
20mM D-glucose+D2G vs. 20mM D-glucose+Nimo	-37.04	-160.6 to 86.49	No	ns	0.9023
20mM D-glucose+phl vs. 20mM D-glucose+Nimo	-10.99	-156.4 to 134.4	No	ns	0.9994

Oscillation number

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20mM D-glucose vs. 20mM L-glucose	7.292	0.8083 to 13.78	Yes	*	0.0219
20mM D-glucose vs. 20mM D-glucose+D2G	8.069	2.236 to 13.90	Yes	**	0.0034
20mM D-glucose vs. 20mM D-glucose+phl	7.875	0.5235 to 15.23	Yes	*	0.0314
20mM D-glucose vs. 20mM D-glucose+Nimo	7.375	0.02355 to 14.73	Yes	*	0.0490
20mM L-glucose vs. 20mM D-glucose+D2G	0.7778	-5.549 to 7.105	No	ns	0.9962
20mM L-glucose vs. 20mM D-glucose+phl	0.5833	-7.166 to 8.332	No	ns	0.9994
20mM L-glucose vs. 20mM D-glucose+Nimo	0.08333	-7.666 to 7.832	No	ns	>0.9999
20mM D-glucose+D2G vs. 20mM D-glucose+phl	-0.1944	-7.408 to 7.020	No	ns	>0.9999
20mM D-glucose+D2G vs. 20mM D-glucose+Nimo	-0.6944	-7.908 to 6.520	No	ns	0.9985
20mM D-glucose+phl vs. 20mM D-glucose+Nimo	-0.5000	-8.989 to 7.989	No	ns	0.9998

Duration

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20mM D-glucose vs. 20mM L-glucose	1111	467.3 to 1755	Yes	***	0.0003
20mM D-glucose vs. 20mM D-glucose+2DG	1289	709.3 to 1868	Yes	***	<0.0001
20mM D-glucose vs. 20mM D-glucose+phl	1267	536.9 to 1997	Yes	***	0.0002
20mM D-glucose vs. 20mM D-glucose+Nimo	1319	589.4 to 2049	Yes	***	0.0001
20mM L-glucose vs. 20mM D-glucose+2DG	177.5	-450.7 to 805.7	No	ns	0.9197
20mM L-glucose vs. 20mM D-glucose+phl	155.8	-613.6 to 925.3	No	ns	0.9749
20mM L-glucose vs. 20mM D-glucose+Nimo	208.3	-561.1 to 977.8	No	ns	0.9304
20mM D-glucose+2DG vs. 20mM D-glucose+phl	-21.67	-738.0 to 694.6	No	ns	>0.9999
20mM D-glucose+2DG vs. 20mM D-glucose+Nimo	30.83	-685.5 to 747.1	No	ns	>0.9999
20mM D-glucose+phl vs. 20mM D-glucose+Nimo	52.50	-790.4 to 895.4	No	ns	0.9997

Figure 2f

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ Crz-Gal4	M	Fed	23	6	9
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ Crz-Gal4	M	Starved	23	7	9
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ Crz-Gal4	M	Refed	23	6	10

Statistics - One-way ANOVA with Tukey post hoc test

Relative GFP intensity - Cell body: Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	0.5386	0.05890 to 1.018	Yes	*	0.0256
Fed vs. Refed	-0.1220	-0.5896 to 0.3455	No	ns	0.7940
Starved vs. Refed	-0.6607	-1.128 to -0.1931	Yes	**	0.0046

Figure 2g

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Fed	23	6	10
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Starved	23	7	9
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Refed	23	6	11

Statistics - One-way ANOVA with Tukey post hoc test

Relative GFP intensity - Neurites to IPCs: Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	0.6110	-0.02839 to 1.250	No	ns	0.0632
Fed vs. Refed	0.03432	-0.5737 to 0.6424	No	ns	0.9893
Starved vs. Refed	-0.5767	-1.202 to 0.04879	No	ns	0.0750

Figure 3b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	10	10
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Number of Syt^+ puncta - Neurites to IPCs: Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	29.80	19.33 to 40.27	Yes	***	<0.0001
Fed vs. Refed	5.891	-3.391 to 15.17	No	ns	0.2723
Starved vs. Refed	-23.91	-34.18 to -13.64	Yes	***	<0.0001

Figure 3d

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control -Fed	*w-; dilp2-LexA/ LexAop-GCaMP6s; UAS-P2X$_2$/+*	M	Fed	2.5 mM ATP	8	50
Experimental - Fed	*w-; dilp2-LexA/ LexAop-GCaMP6s; CN-Gal4/ UAS-P2X$_2$*	M	Fed	2.5 mM ATP	10	63
Experimental - Starved	*w-; dilp2-LexA/ LexAop-GCaMP6s; CN-Gal4/ UAS-P2X$_2$*	M	Starved	2.5 mM ATP	8	47

Statistics - One-way ANOVA with Tukey post hoc test

Max ΔF/F (%): Control-Fed vs. Experimental-Fed vs. Experimental-Starved

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Control vs. Fed	-259.5	-330.6 to -188.4	Yes	***	<0.0001
Control vs. Starved	-71.59	-147.9 to 4.668	No	ns	0.0707
Fed vs. Starved	187.9	115.5 to 260.2	Yes	***	<0.0001

Figure 3e

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; +/+; UAS-Kir2.1/+	M	Starved	23	11	66
w-; +/+; UAS-Kir2.1/+	M	Refed	23	7	70
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Starved	23	8	61
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Refed	23	6	48

Statistics - Unpaired two-tailed t test

UAS-Kir2.1/+: Starved vs. Refed

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=12.02, df=134
Mean of column starved	1.000
Mean of column refed	0.4716
Difference between means ± SEM	-0.5284 ± 0.04394
95% confidence interval	-0.6153 to -0.4414
R squared (eta squared)	0.5190

UAS-Kir2.1/CN-Gal4: Starved vs. Refed

Unpaired t test	
P value	0.8343
P value summary	ns
Significantly different (P < 0.05)?	No
One- or two-tailed P value?	Two-tailed
t, df	t=0.2097, df=107
Mean of column starved	0.8646
Mean of column refed	0.8556
Difference between means ± SEM	-0.009011 ± 0.04296
95% confidence interval	-0.09418 to 0.07616
R squared (eta squared)	0.0004110

Figure 3f

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-;+/+; UAS-Kir2.1/+	M	Fed	23	5	500
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Fed	23	5	500

Statistics - Unpaired two-tailed t test

UAS-Kir2.1/CN-Gal4 **vs.** ***UAS-Kir2.1/+***

Unpaired t test	
P value	0.0012
P value summary	**
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=4.917, df=8
Mean of column A	2.679
Mean of column B	1.000
Difference between means (B - A) ± SEM	-1.679 ± 0.3415
95% confidence interval	-2.466 to -0.8917
R squared (eta squared)	0.7514

Figure 3g

Sample size

Experiments	Genotype	Gender	Feeding status	treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control	*w-; R20F11-LexA/ dilp2-Ga4, UAS-GCaMP6s; +/ +*	M	Fed	20 mM D-glucose	8	30
Experimental	*w-; R20F11-LexA/ dilp2-Gal4, UAS-GCaMP6s; LexAop-TNT/+*	M	Fed	20 mM D-glucose	12	31

Statistics - Unpaired two-tailed t test

Max ΔF/F (%): Control vs. Experimental

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=8.582, df=59
Mean of column A	115.1
Mean of column B	24.49
Difference between means (B - A) ± SEM	-90.62 ± 10.56
95% confidence interval	-111.7 to -69.49
R squared (eta squared)	0.5552

Figure 4b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of animals)	Sample size (n) (# of cells)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	8	8
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	7	7

Statistics - One-way ANOVA with Tukey post hoc test

Number of Syt$^+$ puncta - Neurites to CC: Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	87.93	62.90 to 113.0	Yes	***	<0.0001
Fed vs. Refed	19.79	-5.243 to 44.81	No	ns	0.1374
Starved vs. Refed	-68.14	-93.99 to -42.29	Yes	***	<0.0001

Figure 4d

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
GCaMP-Control	*w-; R20F11-LexA/ UAS-GCaMP6s; AKH-Gal4/ +*	M	Fed	2.5 mM ATP	6	12
GCaMP-Experimental	*w-; R20F11-LexA/ UAS-GCaMP6s; AKH-Gal4/ LexAop-P2X$_2$*	M	Fed	2.5 mM ATP	6	17

Statistics - Unpaired two-tailed t test

Min ΔF/F (%): GCaMP-control vs. GCaMP Experimental

Unpaired t test	
P value	0.0258
P value summary	*
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=2.359, df=27
Mean of column A	-35.59
Mean of column B	-51.42
Difference between means (B - A) ± SEM	-15.83 ± 6.711
95% confidence interval	-29.60 to -2.060
R squared (eta squared)	0.1709

Figure 4e

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
Arclight-Control-Fed	*w-; UAS-Arclight/+; AKH-Gal4/ LexAop-P2X$_2$*	M	Fed	2.5 mM ATP	11	11
Arclight-Exp - Fed	*w-; R20F11-LexA /UAS-Arclight; AKH-Gal4/ LexAop-P2X$_2$*	M	Fed	2.5 mM ATP	11	11
Arclight-Exp - Starved	*w-; R20F11-LexA /UAS-Arclight; AKH-Gal4/ LexAop-P2X$_2$*	M	Starved	2.5 mM ATP	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Max ΔF/F (%): Arclight-control vs. Arclight Exp-Fed vs. Arclight Exp-Starved

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Control vs. Fed	-19.72	-33.30 to -6.129	Yes	**	0.0033
Control vs. Starved	-1.826	-15.41 to 11.76	No	ns	0.9414
Fed vs. Starved	17.89	4.303 to 31.48	Yes	**	0.0079

Figure 4f

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; +/+; CN-Gal4/+	M	Fed	23	10	10
w-; +/+; UAS-Kir2.1/+	M	Fed	23	13	13
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Fed	23	12	12

Statistics - One-way ANOVA with Tukey post hoc test

CN-Gal4/+* vs. *UAS-Kir2.1/+* vs. *UAS-Kir2.1/CN-Gal4

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	0.1563	-0.2332 to 0.5459	No	ns	0.5908
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	0.6334	0.2368 to 1.030	Yes	**	0.0012
UAS-Kir2.1/+ vs. UAS- Kir2.1/CN-Gal4	0.4770	0.1063 to 0.8478	Yes	**	0.0093

Figure 4g

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-;+/+; UAS-Kir2.1/+	M	Fed	23	5	500
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Fed	23	5	500

Statistics - Unpaired two-tailed t test

UAS-Kir2.1/ CN-Gal4* vs. *UAS-Kir2.1/+

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=7.488, df=8
Mean of column A	1.000
Mean of column B	2.192
Difference between means (B - A) ± SEM	1.192 ± 0.1592
95% confidence interval	0.8252 to 1.560
R squared (eta squared)	0.8751

Figure 5a

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; Crz-Gal4/+; +/+	M	Fed	23	13	32
w-; UAS-sNPF-RNAi(2)/+; +/+	M	Fed	23	7	37
w-; Crz-Gal4/ UAS-sNPF-RNAi(2); +/+	M	Fed	23	5	41
w-; +/+; UAS-sNPF-RNAi(3)/+	M	Fed	23	4	31
w-; Crz-Gal4/+; UAS-sNPF-RNAi(3)/+	M	Fed	23	4	39
w-; Crz-Gal4/+; +/+	M	Starved	23	13	30
w-; UAS-sNPF-RNAi(2)/+; +/+	M	Starved	23	8	31
w-; +/+; UAS-sNPF-RNAi(3)/+	M	Starved	23	6	39
w-; Crz-Gal4/ UAS-sNPF-RNAi(2); +/+	M	Starved	23	5	33
w-; Crz-Gal4/+; UAS-sNPF-RNAi(3)/+	M	Starved	23	4	36

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *Crz-Gal4 X UAS-sNPF-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. sNPF-RNAi(2)/+	-10.31	-31.18 to 10.55	No	ns	0.4422
Crz-Gal4/+ vs. sNPF-RNAi(2)/Crz-Gal4	1.714	-21.71 to 25.14	No	ns	0.9816
sNPF-RNAi(2)/+ vs. sNPF-RNAi(2)/Crz-Gal4	12.03	-14.04 to 38.09	No	ns	0.4892

Group 2 (Starved, *Crz-Gal4 X UAS-sNPF-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. sNPF-RNAi(2)/+	5.408	-11.31 to 22.12	No	ns	0.7006
Crz-Gal4/+ vs. sNPF-RNAi(2)/Crz-Gal4	49.37	29.80 to 68.95	Yes	***	<0.0001
sNPF-RNAi(2)/+ vs. sNPF-RNAi(2)/Crz-Gal4	43.97	22.76 to 65.17	Yes	***	<0.0001

Group 3 (Fed, *Crz-Gal4 X UAS-sNPF-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. sNPF-RNAi(3)/+	-13.20	-32.89 to 6.494	No	ns	0.2285
Crz-Gal4/+ vs. sNPF-RNAi(3)/Crz-Gal4	-11.79	-31.49 to 7.898	No	ns	0.3016
sNPF-RNAi(3)/+ vs. sNPF-RNAi(3)/Crz-Gal4	1.405	-22.95 to 25.76	No	ns	0.9881

Group 4 (Starved, *Crz-Gal4 X UAS-sNPF-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. sNPF-RNAi(3)/+	-3.819	-25.71 to 18.07	No	ns	0.8979
Crz-Gal4/+ vs. sNPF-RNAi(3)/Crz-Gal4	51.74	27.96 to 75.52	Yes	***	<0.0001
sNPF-RNAi(3)/+ vs. sNPF-RNAi(3)/Crz-Gal4	55.56	27.66 to 83.46	Yes	***	0.0002

Figure 5b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; dilp2-Gal4/+; +/+	M	Fed	23	4	30
w-,UAS-sNPFR-DN/ Y; +/+; +/+	M	Fed	23	6	33
w-,UAS-sNPFR-DN/ Y; dilp2-Gal4/+; +/+	M	Fed	23	4	31
w-; dilp2-Gal4/+; +/+	M	Fed	23	5	34
w-,UAS-sNPFR-DN/ Y; +/+; +/+	M	Fed	23	8	37
w-,UAS-sNPFR-DN/ Y; dilp2-Gal4/+; +/+	M	Starved	23	6	31

***** The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *dilp2-Gal4 X UAS-sNPFR-DN*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
dilp2-Gal4/+ vs. UAS-sNPFR-DN/+	2.084	-9.923 to 14.09	No	ns	0.8871
dilp2-Gal4/+ vs. dilp2-Gal4/UAS-sNPFR-DN	3.243	-9.910 to 16.40	No	ns	0.7875
UAS-sNPFR-DN/+ vs. dilp2-Gal4/UAS-sNPFR-DN	1.159	-10.85 to 13.17	No	ns	0.9634

Group 2 (Starved, *dilp2-Gal4 X UAS-sNPFR-DN*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
dilp2-Gal4/+ vs. UAS-sNPFR-DN/+	-15.67	-38.13 to 6.786	No	ns	0.2010
dilp2-Gal4/+ vs. dilp2-Gal4/UAS-sNPFR-DN	74.68	50.82 to 98.54	Yes	***	<0.0001
UAS-sNPFR-DN/+ vs. dilp2-Gal4/UAS-sNPFR-DN	90.35	69.08 to 111.6	Yes	***	<0.0001

Figure 5c

Sample size

Genotype	Gender	Feeding status	30 min incubation	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM sucrose	5	5
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM D-glucose	11	11
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM D-glucose + 0.5 μM TTX	6	6
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM L-glucose	6	6

Statistics - One-way ANOVA with Tukey post hoc test

Relative sNPF intensity: AHL vs. D-Glc vs. D-Glc/TTX vs. L-Glc

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
AHL vs. D-Glc	0.4514	0.1160 to 0.7868	Yes	**	0.0056
AHL vs. D-Glc/TTX	0.5499	0.1733 to 0.9264	Yes	**	0.0026
AHL vs. L-Glc	0.1845	-0.1921 to 0.5611	No	ns	0.5405
D-Glc vs. D-Glc/TTX	0.09847	-0.2172 to 0.4141	No	ns	0.8248
D-Glc vs. L-Glc	-0.2669	-0.5825 to 0.04877	No	ns	0.1186
D-Glc/TTX vs. L-Glc	-0.3653	-0.7244 to -0.006270	Yes	*	0.0451

Figure 5d

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control	*w-; dilp2-Gal4, UAS-GCaMP6s/+; +/+*	M	Fed	20 mM D-glucose	5	37
Experimental	*w-,UAS-sNPFR-DN/ Y; dilp2-Gal4/ UAS-GCaMP6s; +/+*	M	Fed	20 mM D-glucose	7	33

Statistics - Unpaired two-tailed t test

Max ΔF/F (%): Control vs. Experimental

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=7.323, df=68
Mean of column A	400.9
Mean of column B	32.74
Difference between means (B - A) ± SEM	-368.2 ± 50.28
95% confidence interval	-468.5 to -267.9
R squared (eta squared)	0.4409

Figure 5e

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; +/+; AKH-Gal4/+	M	Fed	23	8	8
w-,UAS-sNPFR-DN/ Y; +/+; +/+	M	Fed	23	10	10
w-,UAS-sNPFR-DN/ Y; +/+; AKH-Gal4/+	M	Fed	23	9	9

Statistics - One-way ANOVA with Tukey post hoc test

Relative AKH intensity: *AKH-Gal4 X UAS-sNPFR-DN*

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
AKH-Gal4/+ vs. UAS-sNPFR-DN/+	0.1187	-0.3060 to 0.5434	No	ns	0.7668
AKH-Gal4/+ vs. UAS-sNPFR-DN/AKH-Gal4	0.7158	0.2807 to 1.151	Yes	**	0.0011
UAS-sNPFR-DN/+ vs. UAS-sNPFR-DN/AKH-Gal4	0.5970	0.1857 to 1.008	Yes	**	0.0037

Figure 5f

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
Control	*w-; UAS-Arclight/+; AKH-Gal4/+*	M	Fed	DMSO only	8	8
80 μM sNPF	*w-; UAS-Arclight/+; AKH-Gal4/+*	M	Fed	80 μM sNPF	11	11
Gi inhibitor	*w-; UAS-Arclight/+; AKH-Gal4/+*	M	Fed	80 μM sNPF + 1 ng/μL pertussis toxin	8	8
Gq inhibitor	*w-; UAS-Arclight/+; AKH-Gal4/+*	M	Fed	80 μM sNPF + 1 μM U73122	10	10

Statistics - One-way ANOVA with Tukey post hoc test

Max ΔF/F (%): Control vs. sNPF vs. Gi vs. Gq

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Control vs. sNPF	-24.30	-47.01 to -1.584	Yes	*	0.0323
Control vs. Gi	1.029	-23.41 to 25.47	No	ns	0.9995
Control vs. Gq	-25.43	-48.61 to -2.244	Yes	*	0.0271
sNPF vs. Gi	25.32	2.613 to 48.04	Yes	*	0.0241
sNPF vs. Gq	-1.133	-22.49 to 20.22	No	ns	0.9989
Gi vs. Gq	-26.46	-49.64 to -3.273	Yes	*	0.0203

Figure 5g

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control	*w-; dilp2-Gal4/ UAS-GCaMP6s; +/+*	M	Fed	20 mM D-glucose + 1 μM U73343	5	36
Gq inhibitor	*w-; dilp2-Gal4/ UAS-GCaMP6s; +/+*	M	Fed	20 mM D-glucose + 1 μM U73122	8	56
Gi inhibitor	*w-; dilp2-Gal4/ UAS-GCaMP6s; +/+*	M	Fed	20 mM D-glucose + 1 ng/μL pertussis toxin	4	21

Statistics - One-way ANOVA with Tukey post hoc test

Max ΔF/F (%): Control vs. sNPF vs. Gi vs. Gq

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Control vs. Gq	456.1	350.9 to 561.3	Yes	***	<0.0001
Control vs. Gi	-121.0	-256.2 to 14.21	No	ns	0.0892
Gq vs. Gi	-577.1	-703.1 to -451.1	Yes	***	<0.0001

Figure 5h

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-; +/+; CN-Gal4/+	M	Fed	23	11	30
w-; +/+; UAS-Kir2.1/+	M	Fed	23	12	30
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Fed	23	11	30
w-; +/+; CN-Gal4/+	M	Starved	23	8	30
w-; +/+; UAS-Kir2.1/+	M	Starved	23	11	30
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Starved	23	13	30

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *CN-Gal4 X UAS-Kir2.1*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	0.3929	-0.9501 to 1.736	No	ns	0.7536
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	-2.027	-3.399 to -0.6554	Yes	**	0.0028
UAS-Kir2.1/+ vs. UAS-Kir2.1/CN-Gal4	-2.420	-3.763 to -1.077	Yes	***	0.0003

Group 2 (Starved, *CN-Gal4 X UAS-Kir2.1*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	0.1620	-1.335 to 1.659	No	ns	0.9615
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	-2.502	-3.950 to -1.054	Yes	***	0.0006
UAS-Kir2.1/+ vs. UAS-Kir2.1/CN-Gal4	-2.664	-3.984 to -1.343	Yes	***	<0.0001

Extended Data Figure 1d

Sample size

Two-choice assay screening: *Vienna Tiles (VT)-Gal4* > *UAS-Kir2.1, tub-Gal80*^{ts} (95 lines tested)

Genotype	# of trials	Genotype	# of trials	Genotype	# of trials
VT60740	2	VT12601	3	VT60202	3
VT8136	2	VT26397	2	VT31393	2
VT0618	2	VT33054	2	VT49137	1
VT12761	2	VT19352	1	VT22113	2
VT30332	2	VT55380	2	VT7166	2
VT43400	2	VT45641	2	VT12309	2
VT45583	2	VT43134	1	VT13500	5
VT60740	2	VT23818	2	VT23753	4
VT40029	1	VT39625	2	VT61724	3
VT45632	1	VT36267	2	VT1208	2
VT49136	1	VT60736	2	VT30322	5
VT24602	2	VT9837	1	VT65288	3
VT12761	2	VT1207	2	VT22112	2
VT50661	2	VT16127	1	VT18469	2
VT65288	2	VT43070	2	VT49186	2
VT50183	2	VT17928	2	VT60736	1
VT37865	2	VT25972	2	VT27955	2
VT39562	2	VT63305	1	VT9840	2
VT26647	2	VT50225	2	VT43925	2
VT49902	2	VT22113	2	VT19059	2
VT32408	2	VT43925	2	VT20739	1
VT49136	2	VT40592	2	VT44330	4
VT43132	2	VT48029	3	VT61919	1
+/ UAS-Kir2.1, tub-Gal80^{ts}	37	VT15988	2	VT30597	1
VT22017	2	VT44331	1	VT55827	2
VT5879	2	VT63729	2	VT43147	2
VT5058	1	VT58963	2	VT58471	1
VT61918	5	VT1979	2	VT28326	3
VT19774	3	VT42831	1	VT43145	2
VT30297	2	VT31494	4	VT6394	2
VT20124	4	VT49355	2	VT6395	1
VT8975	2	VT49355	2	VT0465	2

Extended Data Figure 1d

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; +/+; UAS-Kir2.1,tub-Gal80ts/+	M	Starved	23	30	37
w-; +/+; VT58471-Gal4/+	M	Starved	23	8	38
w-; +/+; VT58471-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Starved	23	7	32
w-; +/+; VT43147-Gal4/+	M	Starved	23	10	39
w-; +/+; VT43147-Gal4/ UAS-Kir2.1,tub-Gal80ts	M	Starved	23	7	37
w-; Crz-Gal4/+; +/+	M	Starved	23	10	34
w-; Crz-Gal4/+; UAS-Kir2.1,tub-Gal80ts/+	M	Starved	23	24	36

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Starved, *VT58471-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-kir2.1ts / + vs. VT58471-Gal4 / +	-41.21	-60.19 to -22.23	Yes	***	<0.0001
UAS-kir2.1ts / + vs. VT58471-Gal4/UAS-kir2.1ts	44.37	24.35 to 64.40	Yes	***	<0.0001
VT58471-Gal4 / + vs. VT58471-Gal4/UAS-kir2.1ts	85.58	60.90 to 110.3	Yes	***	<0.0001

Group 2 (Starved, *VT43147-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-kir2.1ts / + vs. VT43147-Gal4 / +	-35.62	-54.10 to -17.14	Yes	***	<0.0001
UAS-kir2.1ts / + vs. VT43147-Gal4/UAS-kir2.1ts	90.97	69.73 to 112.2	Yes	***	<0.0001
VT43147-Gal4 / + vs. VT43147-Gal4/UAS-kir2.1ts	126.6	101.7 to 151.5	Yes	***	<0.0001

Group 3 (Starved, *Crz-Gal4 X UAS-Kir2.1,tub-Gal80ts*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
UAS-kir2.1ts / + vs. Crz-Gal4 / +	16.90	-1.421 to 35.23	No	ns	0.0765
UAS-kir2.1ts / + vs. Crz-Gal4 / UAS-kir2.1ts	87.71	73.96 to 101.5	Yes	***	<0.0001
Crz-Gal4 / + vs. Crz-Gal4 / UAS-kir2.1ts	70.80	51.91 to 89.69	Yes	***	<0.0001

Extended Data Figure 2c

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; R20F11-LexA/+; +/+	M	Fed	23	8	40
w-; +/+; LexAop-TNT/+	M	Fed	23	11	30
w-; R20F11-LexA/+; LexAop-TNT/+	M	Fed	23	8	34
w-; R20F11-LexA/+; +/+	M	Starved	23	14	31
w-; +/+; LexAop-TNT/+	M	Starved	23	10	31
w-; R20F11-LexA/+; LexAop-TNT/+	M	Starved	23	11	32

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *R20F11-LexA X LexAop-TNT*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
R20F11-LexA/+ vs. LexAop-TNT/+	7.436	-5.800 to 20.67	No	ns	0.3553
R20F11-LexA/+ vs. R20F11-LexA/ LexAop-TNT	12.99	-1.253 to 27.23	No	ns	0.0785
LexAop-TNT/+ vs. R20F11-LexA/ LexAop-TNT	5.554	-7.683 to 18.79	No	ns	0.5548

Group 2 (Starved, *R20F11-LexA X LexAop-TNT*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
R20F11-LexA/+ vs. LexAop-TNT/+	-6.985	-20.94 to 6.967	No	ns	0.4444
R20F11-LexA/+ vs. R20F11-LexA/ LexAop-TNT	75.83	62.25 to 89.40	Yes	***	<0.0001
LexAop-TNT/+ vs. R20F11-LexA/ LexAop-TNT	82.81	68.09 to 97.53	Yes	***	<0.0001

Extended Data Figure 3b-e

Sample size

Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	1 mM D-glucose	7	7
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	2 mM D-glucose	9	9
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	5 mM D-glucose	9	9
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	10 mM D-glucose	6	6
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	15 mM D-glucose	6	6
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	15 mM D-glucose	8	8

Statistics - One-way ANOVA with Tukey post hoc test

Extended Data Figure 3b - Peak amplitude

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1 mM vs. 2 mM	-37.64	-227.7 to 152.5	No	ns	0.9909
1 mM vs. 5 mM	-47.78	-237.9 to 142.3	No	ns	0.9736
1 mM vs. 10 mM	-80.50	-290.4 to 129.4	No	ns	0.8575
1 mM vs. 15 mM	-93.42	-303.3 to 116.4	No	ns	0.7648
1 mM vs. 20 mM	-106.0	-301.2 to 89.23	No	ns	0.5865
2 mM vs. 5 mM	-10.14	-188.0 to 167.7	No	ns	>0.9999
2 mM vs. 10 mM	-42.86	-241.7 to 156.0	No	ns	0.9866
2 mM vs. 15 mM	-55.78	-254.6 to 143.0	No	ns	0.9579
2 mM vs. 20 mM	-68.36	-251.7 to 114.9	No	ns	0.8712
5 mM vs. 10 mM	-32.72	-231.5 to 166.1	No	ns	0.9961
5 mM vs. 15 mM	-45.64	-244.5 to 153.2	No	ns	0.9823
5 mM vs. 20 mM	-58.22	-241.5 to 125.1	No	ns	0.9301
10 mM vs. 15 mM	-12.92	-230.7 to 204.9	No	ns	>0.9999
10 mM vs. 20 mM	-25.50	-229.2 to 178.2	No	ns	0.9990
15 mM vs. 20 mM	-12.58	-216.3 to 191.1	No	ns	>0.9999

Extended Data Figure 3c - Oscillation number

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1 mM vs. 2 mM	-0.4921	-11.92 to 10.94	No	ns	>0.9999
1 mM vs. 5 mM	-2.270	-13.70 to 9.161	No	ns	0.9908
1 mM vs. 10 mM	0.7857	-11.83 to 13.40	No	ns	>0.9999
1 mM vs. 15 mM	1.452	-11.17 to 14.07	No	ns	0.9993
1 mM vs. 20 mM	2.661	-9.078 to 14.40	No	ns	0.9833
2 mM vs. 5 mM	-1.778	-12.47 to 8.915	No	ns	0.9960
2 mM vs. 10 mM	1.278	-10.68 to 13.23	No	ns	0.9995
2 mM vs. 15 mM	1.944	-10.01 to 13.90	No	ns	0.9964
2 mM vs. 20 mM	3.153	-7.869 to 14.17	No	ns	0.9543
5 mM vs. 10 mM	3.056	-8.899 to 15.01	No	ns	0.9717
5 mM vs. 15 mM	3.722	-8.232 to 15.68	No	ns	0.9355
5 mM vs. 20 mM	4.931	-6.091 to 15.95	No	ns	0.7611
10 mM vs. 15 mM	0.6667	-12.43 to 13.76	No	ns	>0.9999
10 mM vs. 20 mM	1.875	-10.37 to 14.12	No	ns	0.9973
15 mM vs. 20 mM	1.208	-11.04 to 13.46	No	ns	0.9997

Extended Data Figure 4d- Duration

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1 mM vs. 2 mM	102.0	-529.8 to 733.8	No	ns	0.9965
1 mM vs. 5 mM	58.65	-573.2 to 690.5	No	ns	0.9998
1 mM vs. 10 mM	-57.74	-755.3 to 639.8	No	ns	0.9999
1 mM vs. 15 mM	-102.7	-800.3 to 594.8	No	ns	0.9977
1 mM vs. 20 mM	-160.4	-809.3 to 488.4	No	ns	0.9754
2 mM vs. 5 mM	-43.33	-634.4 to 547.7	No	ns	>0.9999
2 mM vs. 10 mM	-159.7	-820.5 to 501.1	No	ns	0.9778
2 mM vs. 15 mM	-204.7	-865.5 to 456.1	No	ns	0.9368
2 mM vs. 20 mM	-262.4	-871.6 to 346.8	No	ns	0.7883
5 mM vs. 10 mM	-116.4	-777.2 to 544.4	No	ns	0.9947
5 mM vs. 15 mM	-161.4	-822.2 to 499.4	No	ns	0.9767
5 mM vs. 20 mM	-219.1	-828.3 to 390.1	No	ns	0.8873
10 mM vs. 15 mM	-45.00	-768.9 to 678.9	No	ns	>0.9999
10 mM vs. 20 mM	-102.7	-779.8 to 574.4	No	ns	0.9974
15 mM vs. 20 mM	-57.71	-734.8 to 619.4	No	ns	0.9998

Extended Data Figure 4e - Oscillation frequency

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
1 mM vs. 2 mM	-0.002154	-0.01167 to 0.007359	No	ns	0.9833
1 mM vs. 5 mM	-0.002278	-0.01179 to 0.007235	No	ns	0.9786
1 mM vs. 10 mM	0.001098	-0.009405 to 0.01160	No	ns	0.9996
1 mM vs. 15 mM	0.002351	-0.008152 to 0.01285	No	ns	0.9842
1 mM vs. 20 mM	0.002790	-0.006980 to 0.01256	No	ns	0.9547
2 mM vs. 5 mM	-0.0001241	-0.009023 to 0.008775	No	ns	>0.9999
2 mM vs. 10 mM	0.003252	-0.006697 to 0.01320	No	ns	0.9218
2 mM vs. 15 mM	0.004505	-0.005444 to 0.01446	No	ns	0.7518
2 mM vs. 20 mM	0.004944	-0.004229 to 0.01412	No	ns	0.5940
5 mM vs. 10 mM	0.003377	-0.006573 to 0.01333	No	ns	0.9095
5 mM vs. 15 mM	0.004630	-0.005320 to 0.01458	No	ns	0.7303
5 mM vs. 20 mM	0.005069	-0.004105 to 0.01424	No	ns	0.5683
10 mM vs. 15 mM	0.001253	-0.009646 to 0.01215	No	ns	0.9993
10 mM vs. 20 mM	0.001692	-0.008503 to 0.01189	No	ns	0.9960
15 mM vs. 20 mM	0.0004390	-0.009756 to 0.01063	No	ns	>0.9999

Extended Data Figure 3g-j

Sample size

Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM sucrose	4	4
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	20 mM pyruvate	4	4
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	1X L-(10)EAAs	3	3

Statistics - One-way ANOVA with Tukey post hoc test

Extended Data Figure 3g- Peak amplitude

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20 mM sucrose vs. 20 mM pyruvate	-364.3	-648.9 to -79.58	Yes	*	0.0158
20 mM sucrose vs. 1 X L-(10)EAAs	-20.50	-328.0 to 287.0	No	ns	0.9802
20 mM pyruvate vs. 1 X L-(10)EAAs	343.8	36.27 to 651.2	Yes	*	0.0305

Extended Data Figure 3h - Oscillation number

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20 mM sucrose vs. 20 mM pyruvate	-6.500	-11.07 to -1.926	Yes	**	0.0090
20 mM sucrose vs. 1 X L-(10)EAAs	0.000	-4.941 to 4.941	No	ns	>0.9999
20 mM pyruvate vs. 1 X L-(10)EAAs	6.500	1.559 to 11.44	Yes	*	0.0137

Extended Data Figure 3i - Duration

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20 mM sucrose vs. 20 mM pyruvate	-968.8	-1597 to -340.7	Yes	**	0.0057
20 mM sucrose vs. 1 X L-(10)EAAs	0.000	-678.4 to 678.4	No	ns	>0.9999
20 mM pyruvate vs. 1 X L-(10)EAAs	968.8	290.3 to 1647	Yes	**	0.0088

Extended Data Figure 3j - Oscillation frequency

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
20 mM sucrose vs. 20 mM pyruvate	-0.009318	-0.01811 to -0.0005286	Yes	*	0.0389
20 mM sucrose vs. 1 X L-(10)EAAs	0.000	-0.009494 to 0.009494	No	ns	>0.9999
20 mM pyruvate vs. 1 X L-(10)EAAs	0.009318	-0.0001757 to 0.01881	No	ns	0.0540

Extended Data Figure 4a

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; +/+; CN-Gal4/+	M	Fed	23	8	32
w-; +/+; UAS-Glut1-RNAi/+	M	Fed	23	7	32
w-; +/+; CN-Gal4/UAS-Glut1-RNAi	M	Fed	23	4	33
w-; +/+; UAS-Glut4EF-RNAi/+	M	Fed	23	5	32
w-; +/+; CN-Gal4/UAS-Glut4EF-RNAi	M	Fed	23	5	32
w-; UAS-Sut1-RNAi/+; +/+	M	Fed	23	5	30
w-; UAS-Sut1-RNAi /+; CN-Gal4/+	M	Fed	23	3	31
w-; UAS-Sut2-RNAi/+; +/+	M	Fed	23	4	36
w-; UAS-Sut2-RNAi /+; CN-Gal4/+	M	Fed	23	4	40
w-; UAS-Slv-RNAi/+; +/+	M	Fed	23	5	44
w-; UAS-Slv-RNAi /+; CN-Gal4/+	M	Fed	23	4	28
w-; +/+; UAS-Smvt-RNAi/+	M	Fed	23	5	31
w-; +/+; CN-Gal4/UAS-Smvt-RNAi	M	Fed	23	5	32
w-; +/+; CN-Gal4/+	M	Starved	23	8	31
w-; +/+; UAS-Glut1-RNAi/+	M	Starved	23	8	32
w-; +/+; CN-Gal4/UAS-Glut1-RNAi	M	Starved	23	5	33
w-; +/+; UAS-Glut4EF-RNAi/+	M	Starved	23	5	35
w-; +/+; CN-Gal4/UAS-Glut4EF-RNAi	M	Starved	23	5	32
w-; UAS-Sut1-RNAi/+; +/+	M	Starved	23	3	33
w-; UAS-Sut1-RNAi /+; CN-Gal4/+	M	Starved	23	3	31
w-; UAS-Sut2-RNAi/+; +/+	M	Starved	23	4	32
w-; UAS-Sut2-RNAi /+; CN-Gal4/+	M	Starved	23	4	34
w-; UAS-Slv-RNAi/+; +/+	M	Starved	23	5	34
w-; UAS-Slv-RNAi /+; CN-Gal4/+	M	Starved	23	5	37
w-; +/+; UAS-Smvt-RNAi/+	M	Starved	23	4	31
w-; +/+; CN-Gal4/UAS-Smvt-RNAi	M	Starved	23	6	32

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *CN-Gal4 X UAS-Glut1-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Glut1-RNAi(3)/+	-2.843	-20.21 to 14.53	No	ns	0.9069
CN-Gal4/+ vs. Glut1-RNAi(3)/CN-Gal4	5.661	-14.89 to 26.21	No	ns	0.7607
Glut1-RNAi(3)/+ vs. Glut1-RNAi(3)/CN-Gal4	8.504	-12.53 to 29.54	No	ns	0.5615

Group 2 (Starved, *CN-Gal4 X UAS-Glut1-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Glut1-RNAi(3)/+	5.306	-16.05 to 26.66	No	ns	0.8034
CN-Gal4/+ vs. Glut1-RNAi(3)/CN-Gal4	137.8	113.5 to 162.2	Yes	***	<0.0001
Glut1-RNAi(3)/+ vs. Glut1-RNAi(3)/CN-Gal4	132.5	108.2 to 156.9	Yes	***	<0.0001

Group 3 (Fed, *CN-Gal4 X UAS-Glut4EF-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Glut4EF-RNAi(3)/+	3.417	-19.42 to 26.26	No	ns	0.9194
CN-Gal4/+ vs. Glut4EF-RNAi(3)/CN-Gal4	6.345	-14.92 to 27.61	No	ns	0.7203
Glut4EF-RNAi(3)/+ vs. Glut4EF-RNAi(3)/CN-Gal4	2.928	-22.09 to 27.95	No	ns	0.9498

Group 4 (Starved, *CN-Gal4 X UAS-Glut4EF-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Glut4EF-RNAi(3)/+	5.999	-17.41 to 29.41	No	ns	0.7865
CN-Gal4/+ vs. Glut4EF-RNAi(3)/CN-Gal4	17.70	-5.707 to 41.12	No	ns	0.1555
Glut4EF-RNAi(3)/+ vs. Glut4EF-RNAi(3)/CN-Gal4	11.70	-14.27 to 37.68	No	ns	0.4878

Group 5 (Fed, *CN-Gal4 X UAS-Sut1-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Sut1-RNAi(2)/+	-6.778	-29.94 to 16.38	No	ns	0.7214
CN-Gal4/+ vs. Sut1-RNAi(2)/CN-Gal4	-4.748	-30.35 to 20.86	No	ns	0.8752
Sut1-RNAi(2)/+ vs. Sut1-RNAi(2)/CN-Gal4	2.030	-26.86 to 30.92	No	ns	0.9808

Group 6 (Starved, *CN-Gal4 X UAS-Sut1-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Sut1-RNAi(2)/+	-0.7974	-24.96 to 23.37	No	ns	0.9956
CN-Gal4/+ vs. Sut1-RNAi(2)/CN-Gal4	-7.382	-31.55 to 16.78	No	ns	0.6960
Sut1-RNAi(2)/+ vs. Sut1-RNAi(2)/CN-Gal4	-6.584	-35.73 to 22.56	No	ns	0.8176

Group 7 (Fed, *CN-Gal4 X UAS-Sut2-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Sut2-RNAi(2)/+	-13.29	-35.83 to 9.253	No	ns	0.2983
CN-Gal4/+ vs. Sut2-RNAi(2)/CN-Gal4	-2.886	-25.42 to 19.65	No	ns	0.9392
Sut2-RNAi(2)/+ vs. Sut2-RNAi(2)/CN-Gal4	10.40	-15.62 to 36.43	No	ns	0.5570

Group 8 (Starved, *CN-Gal4 X UAS-Sut2-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Sut2-RNAi(2)/+	-7.556	-32.01 to 16.90	No	ns	0.7002
CN-Gal4/+ vs. Sut2-RNAi(2)/CN-Gal4	12.43	-12.02 to 36.89	No	ns	0.3981
Sut2-RNAi(2)/+ vs. Sut2-RNAi(2)/CN-Gal4	19.99	-8.252 to 48.23	No	ns	0.1869

Group 9 (Fed, *CN-Gal4 X UAS-slv-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Slv-RNAi(3)/+	-2.936	-24.80 to 18.93	No	ns	0.9345
CN-Gal4/+ vs. Slv-RNAi(3)/CN-Gal4	-5.131	-28.62 to 18.36	No	ns	0.8371
Slv-RNAi(3)/+ vs. Slv-RNAi(3)/CN-Gal4	-2.195	-27.93 to 23.54	No	ns	0.9729

Group 10 (Starved, *CN-Gal4 X UAS-slv-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Slv-RNAi(3)/+	-7.514	-26.56 to 11.53	No	ns	0.5733
CN-Gal4/+ vs. Slv-RNAi(3)/CN-Gal4	1.977	-17.07 to 21.02	No	ns	0.9608
Slv-RNAi(3)/+ vs. Slv-RNAi(3)/CN-Gal4	9.491	-11.64 to 30.62	No	ns	0.4901

Group 11 (Fed, *CN-Gal4 X UAS-smvt-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Smvt-RNAi(2)/+	-17.49	-40.96 to 5.994	No	ns	0.1634
CN-Gal4/+ vs. Smvt-RNAi(2)/CN-Gal4	-13.24	-36.72 to 10.24	No	ns	0.3351
Smvt-RNAi(2)/+ vs. Smvt-RNAi(2)/CN-Gal4	4.249	-21.80 to 30.30	No	ns	0.9064

Group 12 (Starved, *CN-Gal4 X UAS-smvt-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Smvt-RNAi(2)/+	6.094	-17.21 to 29.40	No	ns	0.7789
CN-Gal4/+ vs. Smvt-RNAi(2)/CN-Gal4	6.761	-13.79 to 27.31	No	ns	0.6760
Smvt-RNAi(2)/+ vs. Smvt-RNAi(2)/CN-Gal4	0.6675	-23.90 to 25.23	No	ns	0.9973

Extended Data Figure 4b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; +/+; CN-Gal4/+	M	Fed	23	8	32
w-; +/+; UAS-HexC-RNAi/+	M	Fed	23	6	34
w-; +/+; CN-Gal4/UAS-HexC-RNAi	M	Fed	23	4	28
w-; +/+; UAS-HexT2-RNAi/+	M	Fed	23	6	33
w-; +/+; CN-Gal4/UAS-HexT2-RNAi	M	Fed	23	7	32
w-; +/+; UAS-HexA-RNAi/+	M	Fed	23	4	30
w-; +/+; CN-Gal4/UAS-HexA-RNAi	M	Fed	23	5	36
w-; +/+; CN-Gal4/+	M	Starved	23	8	31
w-; +/+; UAS-HexC-RNAi/+	M	Starved	23	4	34
w-; +/+; CN-Gal4/UAS-HexC-RNAi	M	Starved	23	7	35
w-; +/+; UAS-HexT2-RNAi/+	M	Starved	23	6	35
w-; +/+; CN-Gal4/UAS-HexT2-RNAi	M	Starved	23	7	33
w-; +/+; UAS-HexA-RNAi/+	M	Starved	23	7	30
w-; +/+; CN-Gal4/UAS-HexA-RNAi	M	Starved	23	7	34

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *CN-Gal4 X UAS-HexC-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexC-RNAi(3)/+	7.446	-9.881 to 24.77	No	ns	0.5192
CN-Gal4/+ vs. HexC/-RNAi(3)/CN-Gal4	11.93	-7.713 to 31.58	No	ns	0.2851
HexC-RNAi(3)/+ vs. HexC/-RNAi(3)/CN-Gal4	4.489	-16.22 to 25.20	No	ns	0.8415

Group 2 (Starved, *CN-Gal4 X UAS-HexC-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexC-RNAi(3)/+	6.129	-18.97 to 31.23	No	ns	0.8060
CN-Gal4/+ vs. HexC-RNAi(3)/CN-Gal4	121.6	100.4 to 142.8	Yes	***	<0.0001
HexC-RNAi(3)/+ vs. HexC-RNAi(3)/CN-Gal4	115.5	89.77 to 141.1	Yes	***	<0.0001

Group 3 (Fed, *CN-Gal4 X UAS-HexT2-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexT2-RNAi(3)/+	12.57	-4.849 to 29.99	No	ns	0.1846
CN-Gal4/+ vs. HexT2-RNAi(3)/CN-Gal4	7.948	-8.746 to 24.64	No	ns	0.4598
HexT2-RNAi(3)/+ vs. HexT2-RNAi(3)/CN-Gal4	-4.623	-22.57 to 13.32	No	ns	0.7906

Group 4 (Starved, *CN-Gal4 X UAS-HexT2-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexT2-RNAi(3)/+	5.754	-10.44 to 21.94	No	ns	0.6429
CN-Gal4/+ vs. HexT2-RNAi(3)/CN-Gal4	14.99	-0.5211 to 30.51	No	ns	0.0592
HexT2-RNAi(3)/+ vs. HexT2-RNAi(3)/CN-Gal4	9.241	-7.438 to 25.92	No	ns	0.3549

Group 5 (Fed, *CN-Gal4 X UAS-HexA-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexA-RNAi(3)/+	-3.806	-23.69 to 16.08	No	ns	0.8720
CN-Gal4/+ vs. HexA-RNAi(3)/CN-Gal4	1.448	-17.07 to 19.96	No	ns	0.9772
HexA-RNAi(3)/+ vs. HexA-RNAi(3)/CN-Gal4	5.254	-16.53 to 27.04	No	ns	0.8057

Group 6 (Starved, *CN-Gal4 X UAS-HexA-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. HexA-RNAi(3)/+	5.851	-8.950 to 20.65	No	ns	0.5832
CN-Gal4/+ vs. HexA-RNAi(3)/CN-Gal4	8.338	-6.463 to 23.14	No	ns	0.3455
HexA-RNAi(3)/+ vs. HexA-RNAi(3)/CN-Gal4	2.487	-12.80 to 17.77	No	ns	0.9106

Extended Data Figure 4c

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; +/+; CN-Gal4/+	M	Fed	23	8	32
w-; UAS-SUR1-RNAi/+; +/+	M	Fed	23	3	37
w-; UAS-SUR1-RNAi /+; CN-Gal4	M	Fed	23	5	38
w-; +/+; UAS-SUR1-RNAi/+	M	Fed	23	4	33
w-; +/+; CN-Gal4/UAS-SUR1-RNAi	M	Fed	23	5	35
w-; +/+; UAS-Ca-α1D-RNAi/+	M	Fed	23	3	38
w-; +/+; CN-Gal4/ UAS-Ca-α1D-RNAi	M	Fed	23	4	35
w-; +/+; CN-Gal4/+	M	Starved	23	8	31
w-; UAS-SUR1-RNAi/+; +/+	M	Starved	23	5	34
w-; UAS-SUR1-RNAi /+; CN-Gal4	M	Starved	23	5	43
w-; +/+; UAS-SUR1-RNAi/+	M	Starved	23	6	35
w-; +/+; CN-Gal4/UAS-SUR1-RNAi	M	Starved	23	6	36
w-; +/+; UAS-Ca-α1D-RNAi/+	M	Starved	23	5	37
w-; +/+; CN-Gal4/ UAS-Ca-α1D-RNAi	M	Starved	23	4	28

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *CN-Gal4 X UAS-SUR1-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. SUR-RNAi(2)/+	-16.31	-41.71 to 9.098	No	ns	0.2440
CN-Gal4/+ vs. SUR-RNAi(2)/CN-Gal4	4.598	-16.79 to 25.99	No	ns	0.8394
SUR-RNAi(2)/+ vs. SUR-RNAi(2)/CN-Gal4	20.90	-6.499 to 48.31	No	ns	0.1480

Group 2 (Starved, *CN-Gal4 X UAS-SUR1-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. SUR-RNAi(2)/+	-4.787	-24.24 to 14.67	No	ns	0.8012
CN-Gal4/+ vs. SUR-RNAi(2)/CN-Gal4	117.7	98.23 to 137.1	Yes	***	<0.0001
SUR-RNAi(2)/+ vs. SUR-RNAi(2)/CN-Gal4	122.5	100.9 to 144.1	Yes	***	<0.0001

Group 3 (Fed, *CN-Gal4 X UAS-SUR1-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. SUR-RNAi(3)/+	11.15	-8.236 to 30.55	No	ns	0.3182
CN-Gal4/+ vs. SUR-RNAi(3)/CN-Gal4	-7.257	-25.31 to 10.79	No	ns	0.5577
SUR-RNAi(3)/+ vs. SUR-RNAi(3)/CN-Gal4	-18.41	-39.65 to 2.829	No	ns	0.0939

Group 4 (Stared, *CN-Gal4 X UAS-SUR1-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. SUR-RNAi(3)/+	1.790	-20.51 to 24.09	No	ns	0.9769
CN-Gal4/+ vs. SUR-RNAi(3)/CN-Gal4	128.7	106.4 to 151.0	Yes	***	<0.0001
SUR-RNAi(3)/+ vs. SUR-RNAi(3)/CN-Gal4	126.9	103.0 to 150.7	Yes	***	<0.0001

Group 5 (Fed, *CN-Gal4 X UAS-Ca-1αD-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Ca-RNAi/+	4.619	-18.06 to 27.30	No	ns	0.8518
CN-Gal4/+ vs. Ca-RNAi/CN-Gal4	-1.364	-21.88 to 19.15	No	ns	0.9828
Ca-RNAi/+ vs. Ca-RNAi/CN-Gal4	-5.983	-31.57 to 19.61	No	ns	0.8101

Group 6 (Starved, *CN-Gal4 X UAS-Ca-1αD-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. Ca-RNAi/+	0.6117	-20.79 to 22.02	No	ns	0.9969
CN-Gal4/+ vs. Ca-RNAi/CN-Gal4	112.4	89.43 to 135.4	Yes	***	<0.0001
Ca-RNAi/+ vs. Ca-RNAi/CN-Gal4	111.8	86.63 to 137.0	Yes	***	<0.0001

Extended Data Figure 4e-h

Sample size

Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; UAS-GCaMP6s/+; CN-Gal4/+	M	Fed	1 mM D-glucose	6	6
w-; UAS-GCaMP6s/+; *CN-Gal4/ UAS-Glut1-RNAi*	M	Fed	1 mM D-glucose	5	5
w-; UAS-GCaMP6s/+; *CN-Gal4/ UAS-SUR1-RNAi*	M	Fed	1 mM D-glucose	4	4
w-; UAS-GCaMP6s/+; *CN-Gal4/UAS-Ca-α1D-RNAi*	M	Fed	1 mM D-glucose	4	4

Statistics - One-way ANOVA with Tukey post hoc test

Extended Data Figure 4e - Peak amplitude

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Cont vs. Glut1	456.2	310.7 to 601.6	Yes	***	<0.0001
Cont vs. SUR1	460.5	305.4 to 615.5	Yes	***	<0.0001
Cont vs. Caα1D	460.0	305.0 to 615.1	Yes	***	<0.0001
Glut1 vs. SUR1	4.293	-156.8 to 165.4	No	ns	0.9998
Glut1 vs. Caα1D	3.858	-157.3 to 165.0	No	ns	0.9999
SUR1 vs. Caα1D	-0.4350	-170.3 to 169.4	No	ns	>0.9999

Extended Data Figure 4f- Oscillation number

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Cont vs. Glut1	6.033	1.743 to 10.32	Yes	**	0.0051
Cont vs. SUR1	5.833	1.260 to 10.41	Yes	*	0.0108
Cont vs. Caα1D	6.333	1.760 to 10.91	Yes	**	0.0058
Glut1 vs. SUR1	-0.2000	-4.952 to 4.552	No	ns	0.9993
Glut1 vs. Caα1D	0.3000	-4.452 to 5.052	No	ns	0.9978
SUR1 vs. Caα1D	0.5000	-4.510 to 5.510	No	ns	0.9914

Extended Data Figure 4g - Duration

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Cont vs. Glut1	864.0	428.9 to 1299	Yes	***	0.0002
Cont vs. SUR1	822.5	358.7 to 1286	Yes	***	0.0007
Cont vs. Caα1D	772.5	308.7 to 1236	Yes	**	0.0012
Glut1 vs. SUR1	-41.50	-523.5 to 440.5	No	ns	0.9944
Glut1 vs. Caα1D	-91.50	-573.5 to 390.5	No	ns	0.9459
SUR1 vs. Caα1D	-50.00	-558.0 to 458.0	No	ns	0.9917

Extended Data Figure 4h - Oscillation frequency

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Cont vs. Glut1	-0.006513	-0.02848 to 0.01545	No	ns	0.8276
Cont vs. SUR1	0.002529	-0.02088 to 0.02594	No	ns	0.9891
Cont vs. Caα1D	0.0002994	-0.02311 to 0.02371	No	ns	>0.9999
Glut1 vs. SUR1	0.009043	-0.01529 to 0.03337	No	ns	0.7116
Glut1 vs. Caα1D	0.006813	-0.01752 to 0.03114	No	ns	0.8502
SUR1 vs. Caα1D	-0.002230	-0.02788 to 0.02342	No	ns	0.9942

Extended Data Figure 4j

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Fed	23	8	8
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Starved	23	7	9
w-; LexAop-CD8-GFP-2A-CD8-GFP/+; UAS-mLexA-VP16-NFAT, LexAop-rCD2-GFP/ CN-Gal4	M	Refed	23	6	8

Statistics - One-way ANOVA with Tukey post hoc test

Relative GFP intensity: Cell body – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	0.8945	0.03049 to 1.759	Yes	*	0.0415
Fed vs. Refed	-0.009132	-0.8982 to 0.8799	No	ns	0.9996
Starved vs. Refed	-0.9036	-1.768 to -0.03962	Yes	*	0.0393

Extended Data Figure 5a

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	10	10
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Relative intensity of Syt-GFP: Neurites to IPCs - Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	2.684	0.9643 to 4.404	Yes	**	0.0018
Fed vs. Refed	0.5297	-0.9952 to 2.055	No	ns	0.6667
Starved vs. Refed	-2.155	-3.842 to -0.4671	Yes	*	0.0105

Extended Data Figure 5b

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	6	6
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	6	6

Statistics - One-way ANOVA with Tukey post hoc test

Relative intensity of Syt-GFP: Neurites to CC – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	5.470	2.484 to 8.455	Yes	***	0.0006
Fed vs. Refed	-0.05580	-3.041 to 2.930	No	ns	0.9987
Starved vs. Refed	-5.525	-8.624 to -2.427	Yes	***	0.0008

Extended Data Figure 5c

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	10	10
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Length of branch: Neurites to IPCs – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	16.36	-10.51 to 43.24	No	ns	0.3005
Fed vs. Refed	-12.01	-35.84 to 11.82	No	ns	0.4331
Starved vs. Refed	-28.37	-54.74 to -2.001	Yes	*	0.0332

Extended Data Figure 5d

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	6	6
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	6	6

Statistics - One-way ANOVA with Tukey post hoc test

Length of branch: Neurites to CC – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	137.8	71.72 to 203.9	Yes	***	<0.0001
Fed vs. Refed	30.47	-28.13 to 89.07	No	ns	0.4110
Starved vs. Refed	-107.3	-172.2 to -42.50	Yes	**	0.0010

Extended Data Figure 5f-h

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of animals)	Sample size (n) (# of CCs)
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Fed	23	10	10
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Starved	23	7	7
w-; Crz-Gal4/+; UAS-Syt-GFP/+	M	Refed	23	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Extended Data Figure 5f

Number of Syt+ puncta: Dorsal lateral area – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	0.4857	-5.561 to 6.532	No	ns	0.9782
Fed vs. Refed	3.018	-2.343 to 8.379	No	ns	0.3550
Starved vs. Refed	2.532	-3.400 to 8.465	No	ns	0.5451

Extended Data Figure 5g

Number of Syt+ puncta: Medial lateral area – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	0.7143	-12.90 to 14.32	No	ns	0.9906
Fed vs. Refed	2.000	-10.07 to 14.07	No	ns	0.9107
Starved vs. Refed	1.286	-12.07 to 14.64	No	ns	0.9688

Extended Data Figure 5h

Number of Syt+ puncta: SEZ – Fed vs. Starved vs. Refed

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Fed vs. Starved	-0.1667	-14.38 to 14.04	No	ns	0.9995
Fed vs. Refed	2.818	-9.206 to 14.84	No	ns	0.8292
Starved vs. Refed	2.985	-10.98 to 16.95	No	ns	0.8556

Extended Data Figure 6b

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Negative Control	*w-; UAS-GCaMP6s/+; CN-Gal4/+*	M	Fed	2.5 mM ATP	10	10
Positive control-UAS	*w-; UAS-GCaMP6s/+ ; CN-Gal4/ UAS-P2X*$_2$	M	Fed	2.5 mM ATP	7	7
Positive control-LexA	*w-; R20F11-LexA/ LexAop-GCaMP6s ; LexAop-P2X*$_2$*/+*	M	Fed	2.5 mM ATP	11	11

Statistics - One-way ANOVA with Tukey post hoc test

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Negative Control vs. UAS-P2X$_2$	-400.9	-562.9 to -238.9	Yes	***	<0.0001
Negative Control vs. LexAop-P2 X$_2$	-354.3	-527.7 to -180.9	Yes	***	0.0003
UAS-P2X$_2$ vs. LexAop-P2X$_2$	46.64	-138.9 to 232.2	No	ns	0.7881

Extended Data Figure 6c-f

Sample size

Experiments	Genotype	Gender	Feeding status	Treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Negative Control	*w-; UAS-GCaMP6s/+; Dh44-Gal4/+*	M	Fed	2.5 mM ATP	3	3
Positive control	*w-; UAS-GCaMP6s/ Dh44-LexA; Dh44-Gal4/ LexAop-P2X*$_2$	M	Fed	2.5 mM ATP	4	4
Experimental (Dh44 to CN)	*w-; UAS-GCaMP6s/ Crz-Gal4; Dh44-LexA/ LexAop-P2X*$_2$	M	Fed	2.5 mM ATP	7	7
Experimental (CN to Dh44)	*w-; UAS-GCaMP6s/ R20F11-LexA; Dh44-Gal4/ LexAop-P2X*$_2$	M	Fed	2.5 mM ATP	4	16

Extended Data Figure 7f

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-; +/+; UAS-Kir2.1, dilp2-HA-FLAG/ CN-Gal4, dilp2-HA-FLAG	M	Fed	23	6	60
w-; +/+; UAS-Kir2.1, dilp2-HA-FLAG/ dilp2-HA-FLAG	M	Fed	23	6	60

Statistics – Unpaired two-tailed t test

UAS-Kir2.1/CN-Gal4; dilp2-HA vs. UAS-Kir2.1/+; dilp2-HA

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=9.792, df=10
Mean of column A	27.16
Mean of column B	47.26
Difference between means (B - A) ± SEM	20.10 ± 2.053
95% confidence interval	15.53 to 24.67
R squared (eta squared)	0.9056

Extended Data Figure 7h

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-; +/+; CN-Gal4/+	M	Fed	23	3	60
w-; +/+; UAS-Kir2.1/+	M	Fed	23	9	60
w-; +/+; UAS-Kir2.1/CN-Gal4	M	Fed	23	9	60

Statistics - One-way ANOVA with Tukey post hoc test

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	2.558	-25.43 to 30.54	No	ns	0.9705
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	-40.94	-68.92 to -12.96	Yes	**	0.0041
UAS-Kir2.1/+ vs. UAS-Kir2.1/CN-Gal4	-43.50	-63.28 to -23.71	Yes	***	<0.0001

Extended Data Figure 8c

Sample size

Experiments	Genotype	Gender	Feeding status	treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control	*w-; R20F11-LexA/ UAS-GCaMP6s; dilp2-Gal4/ +*	M	Fed	100 μM Glibenclamide	5	28
Experimental	*w-; R20F11-LexA/ UAS-GCaMP6s; dilp2-Gal4/ LexAop-TNT*	M	Fed	100 μM Glibenclamide	9	44

Statistics – Unpaired two-tailed t test

Max ΔF/F (%): Control vs. Experimental

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=5.970, df=70
Mean of column A	280.4
Mean of column B	45.71
Difference between means (B - A) ± SEM	-234.6 ± 39.30
95% confidence interval	-313.0 to -156.3
R squared (eta squared)	0.3374

Extended Data Figure 9c

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; Crz-Gal4/+; +/+	M	Fed	23	3	28
w-; UAS-Crz-RNAi(2)/+; +/+	M	Fed	23	3	38
w-; Crz-Gal4/ UAS-Crz-RNAi(2); +/+	M	Fed	23	5	36
w-; +/+; UAS-Crz-RNAi(3)/+	M	Fed	23	4	30
w-; Crz-Gal4/+; UAS-Crz-RNAi(3)/+	M	Fed	23	5	34
w-; Crz-Gal4/+; +/+	M	Starved	23	6	32
w-; UAS-Crz-RNAi(2)/+; +/+	M	Starved	23	4	36
w-; Crz-Gal4/ UAS-Crz-RNAi(2); +/+	M	Starved	23	12	48
w-; +/+; UAS-Crz-RNAi(3)/+	M	Starved	23	6	34
w-; Crz-Gal4/+; UAS-Crz-RNAi(3)/+	M	Starved	23	4	38

* The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *Crz-Gal4 X UAS-Crz-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. Crz-RNAi(2)/+	15.14	-9.731 to 40.02	No	ns	0.2496
Crz-Gal4/+ vs. Crz-RNAi(2)/Crz-Gal4	16.13	-6.116 to 38.38	No	ns	0.1574
Crz-RNAi(2)/+ vs. Crz-RNAi(2)/Crz-Gal4	0.9885	-21.26 to 23.24	No	ns	0.9912

Group 2 (Starved, *Crz-Gal4 X UAS-Crz-RNAi(2)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. Crz-RNAi(2)/+	18.72	-29.47 to 66.90	No	ns	0.5938
Crz-Gal4/+ vs. Crz-RNAi(2)/Crz-Gal4	3.785	-33.54 to 41.11	No	ns	0.9641
Crz-RNAi(2)/+ vs. Crz-RNAi(2)/Crz-Gal4	-14.93	-58.03 to 28.16	No	ns	0.6589

Group 3 (Fed, *Crz-Gal4 X UAS-Crz-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. Crz-RNAi(3)/+	30.01	-15.24 to 75.26	No	ns	0.2080
Crz-Gal4/+ vs. Crz-RNAi(3)/Crz-Gal4	8.101	-35.17 to 51.37	No	ns	0.8624
Crz-RNAi(3)/+ vs. Crz-RNAi(3)/Crz-Gal4	-21.91	-61.66 to 17.83	No	ns	0.3191

Group 4 (Starved, *Crz-Gal4 X UAS-Crz-RNAi(3)*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Crz-Gal4/+ vs. Crz-RNAi(3)/+	0.000	-18.10 to 18.10	No	ns	>0.9999
Crz-Gal4/+ vs. Crz-RNAi(3)/Crz-Gal4	-15.71	-35.94 to 4.525	No	ns	0.1396
Crz-RNAi(3)/+ vs. Crz-RNAi(3)/Crz-Gal4	-15.71	-35.94 to 4.525	No	ns	0.1396

Extended Data Figure 9d

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)*
w-; CrzR-Gal4/+; +/+	M	Starved	23	5	42
w-; CrzR-Gal4/+; UAS-CrzR-RNAi(44310GD)/+	M	Starved	23	4	33
w-; CrzR-Gal4/ UAS-CrzR-RNAi(108506); +/+	M	Starved	23	4	42
w-; CrzR-Gal4/+; UAS-CrzR-RNAi(46713GD)/+	M	Starved	23	4	41

***** The number of files(n) stated in this table is the number of flies that was used in one of the all trials. For all the details, please check the raw data.

Statistics – Unpaired two-tailed t test

CrzR-Gal4/+ vs. UAS-CrzR-RNAi(44310GD)/ CrzR-Gal4

Unpaired t test	
P value	0.4259
P value summary	ns
Significantly different (P < 0.05)?	No
One- or two-tailed P value?	Two-tailed
t, df	t=0.8453, df=7
Mean of column A	70.48
Mean of column B	78.59
Difference between means (B - A) ± SEM	8.116 ± 9.601
95% confidence interval	-14.59 to 30.82
R squared (eta squared)	0.09263

CrzR-Gal4/+ vs. UAS-CrzR-RNAi(108506)/ CrzR-Gal4

Unpaired t test	
P value	0.0500
P value summary	ns
Significantly different (P < 0.05)?	No
One- or two-tailed P value?	Two-tailed
t, df	t=2.364, df=7
Mean of column A	70.48
Mean of column C	91.67
Difference between means (C - A) ± SEM	21.19 ± 8.962
95% confidence interval	-0.004105 to 42.38
R squared (eta squared)	0.4440

CrzR-Gal4/+ vs. UAS-CrzR-RNAi(46713GD)/ CrzR-Gal4

Unpaired t test	
P value	0.1299
P value summary	ns
Significantly different (P < 0.05)?	No
One- or two-tailed P value?	Two-tailed
t, df	t=1.716, df=7
Mean of column A	70.48
Mean of column D	87.44
Difference between means (D - A) ± SEM	16.96 ± 9.884
95% confidence interval	-6.411 to 40.33
R squared (eta squared)	0.2961

Extended Data Figure 9e

Sample size

Genotype	Gender	Feeding status	30 min incubation	Sample size (N) (# of brains)	Sample size (n) (# of cells)
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM sucrose	4	4
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM D-glucose	5	5
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM D-glucose + 0.5 μM TTX	7	7
w-; Crz-Gal4/UAS-mCD8:GFP; +/+	M	18 hr Starved	80 mM L-glucose	6	6

Statistics - One-way ANOVA with Tukey post hoc test

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
AHL vs. D-Glc	-0.07431	-0.4422 to 0.2936	No	ns	0.9395
AHL vs. D-Glc/TTX	-0.07488	-0.4186 to 0.2688	No	ns	0.9257
AHL vs. L-Glc	-0.06021	-0.4142 to 0.2938	No	ns	0.9624
D-Glc vs. D-Glc/TTX	-0.0005688	-0.3217 to 0.3205	No	ns	>0.9999
D-Glc vs. L-Glc	0.01411	-0.3180 to 0.3462	No	ns	0.9994
D-Glc/TTX vs. L-Glc	0.01467	-0.2904 to 0.3198	No	ns	0.9991

Extended Data Figure 10b

Sample size

Experiments	Genotype	Gender	Feeding status	treatment	Sample size (N) (# of brains)	Sample size (n) (# of cells)
Control	*w-; UAS-GCaMP6s/+; dilp2-Gal4/ +*	M	Fed	DMSO only	5	27
Experimental	*w-; UAS-GCaMP6s/+; dilp2-Gal4/ +*	M	Fed	80 μM sNPF	8	31

Statistics – Unpaired two-tailed t test

Max ΔF/F (%): Control (DMSO) vs. sNPF

Unpaired t test	
P value	<0.0001
P value summary	***
Significantly different (P < 0.05)?	Yes
One- or two-tailed P value?	Two-tailed
t, df	t=5.502, df=56
Mean of column A	-1.817
Mean of column B	93.70
Difference between means (B - A) ± SEM	95.51 ± 17.36
95% confidence interval	60.74 to 130.3
R squared (eta squared)	0.3509

Extended Data Figure 10c

Sample size

Genotype	Gender	Feeding status	Incubated Temperature (°C)	Sample size (N) (# of trials)	# of flies in each trial (n)
w-; +/+; CN-Gal4/+	M	Fed	23	14	30
w-; +/+; UAS-Kir2.1/+	M	Fed	23	12	30
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Fed	23	7	30
w-; +/+; CN-Gal4/+	M	Starved	23	6	30
w-; +/+; UAS-Kir2.1/+	M	Starved	23	6	30
w-; +/+; UAS-Kir2.1/ CN-Gal4	M	Starved	23	7	30

Statistics - One-way ANOVA with Tukey post hoc test

Group 1 (Fed, *CN-Gal4 X UAS-Kir2.1*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	1.741	-5.214 to 8.696	No	ns	0.8120
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	-10.65	-18.84 to -2.470	Yes	**	0.0086
UAS-Kir2.1/+ vs. UAS-Kir2.1/CN-Gal4	-12.39	-20.80 to -3.987	Yes	**	0.0029

Group 2 (Starved, *CN-Gal4 X UAS-Kir2.1*)

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
CN-Gal4/+ vs. UAS-Kir2.1/+	3.508	-4.121 to 11.14	No	ns	0.4777
CN-Gal4/+ vs. UAS-Kir2.1/CN-Gal4	-7.859	-15.21 to -0.5076	Yes	*	0.0353
UAS-Kir2.1/+ vs. UAS-Kir2.1/CN-Gal4	-11.37	-18.72 to -4.016	Yes	**	0.0029

Supplementary Table 2

Fly lines that were used in this study.

Drosophila strains	**Source**	**Identifier**
w^{1118}	Bloomington *Drosophila* stock center	BL6326
VT58471-Gal4 (VT058471)	Vienna *Drosophila* Resource Center	201682
VT43147-Gal4 (VT043147)	Vienna *Drosophila* Resource Center	203711
VT19059-Gal4 (VT019059)	Vienna *Drosophila* Resource Center	50816
VT44330-Gal4 (VT044330)	Vienna *Drosophila* Resource Center	204632
VT61919-Gal4 (VT061919)	Vienna *Drosophila* Resource Center	205399
VT30597-Gal4 (VT030587)	Vienna *Drosophila* Resource Center	202274
VT60736-Gal4 (VT060736)	Vienna *Drosophila* Resource Center	202781
VT42831-Gal4 (VT042831)	Vienna *Drosophila* Resource Center	205009
VT6394-Gal4 (VT006394)	Vienna *Drosophila* Resource Center	201211
VT28326-Gal4 (VT028326)	Vienna *Drosophila* Resource Center	204776
VT20739-Gal4 (VT020739)	Vienna *Drosophila* Resource Center	204908
VT43145-Gal4 (VT043145)	Vienna *Drosophila* Resource Center	204212
VT55827-Gal4 (VT055827)	Vienna *Drosophila* Resource Center	200416
VT22112-Gal4 (VT022112)	Vienna *Drosophila* Resource Center	201255
VT26149-Gal4 (VT026149)	Vienna *Drosophila* Resource Center	204563
VT6395-Gal4 (VT006395)	Vienna *Drosophila* Resource Center	215038
VT0465-Gal4 (VT00465)	Vienna *Drosophila* Resource Center	203732
Crz-Gal4	Lee et al.,2008	N/A
UAS-Kir2.1	Bloomington *Drosophila* stock center	BL6595
Tub-Gal80^{ts}	Bloomington *Drosophila* stock center	BL7018
Cha-Gal80 (ChAT-Gal80)	Kimamoto,2002	N/A
UAS-mCD8:GFP	Bloomington *Drosophila* stock center	BL32186
UAS-Denmark, UAS-Syt-eGFP	Bloomington *Drosophila* stock center	BL33065
R20F11-LexA	Bloomington *Drosophila* stock center	BL52569
LexAop-FLP	Shang et al.,2008	N/A
UAS-FRT-stop-FRT-smGFP	Nern et al.,2015	N/A
UAS-FRT-stop-FRT-activeTNT	von Philipsborn et al.,2011	N/A
LexAop-GFP (LexAop-rCD2-GFP)	Bloomington *Drosophila* stock center	BL66687
LexAop-TNT (13XLexAop-IVS-TNT:HA)	Karuppudurai et al.,2014	N/A
UAS-GCaMP6s (20XUAS-IVS-GCaMP6s)	Bloomington *Drosophila* stock center	BL42746
CalexA (LexAop-CD2::GFP; UAS-mLexA-VP16-NFAT,LexAop-CD8::GFP-2A-CD8::GFP)	Masuyama et al.,2012	N/A
UAS-nurexin-GFP1-10	Chen et al.,2014	N/A
UAS-Hex-C-RNAi(3)	Bloomington *Drosophila* stock center	BL35338
UAS-Hex-T2-RNAi(3)	Bloomington *Drosophila* stock center	BL47331
UAS-Hex-A-RNAi(3)	Bloomington *Drosophila* stock center	BL35155
UAS-SUR1-RNAi(2)	Bloomington *Drosophila* stock center	BL62746
UAS-SUR1-RNAi(3)	Bloomington *Drosophila* stock center	BL36087
UAS-Ca-α1D-RNAi(3)	Bloomington *Drosophila* stock center	BL33413
UAS-Glut1-RNAi(3)	Bloomington *Drosophila* stock center	BL28645
UAS-Glut4EF-RNAi(3)	Bloomington *Drosophila* stock center	BL57461
UAS-sut1-RNAi(2)	Bloomington *Drosophila* stock center	BL65964
UAS-sut2-RNAi(2)	Bloomington *Drosophila* stock center	BL64861
UAS-slv-RNAi(3)	Bloomington *Drosophila* stock center	BL29388
UAS-smvt-RNAi(2)	Bloomington *Drosophila* stock center	BL63568
LexAop-CD4-GFP11	Chen et al.,2014	N/A
UAS-P2X$_2$	Lima and Miesenbock,2005	N/A
LexAop-P2X$_2$	Bloomington *Drosophila* stock center	BL76030
dilp2-Gal4 (Ilp-Gal4.R)	Bloomington *Drosophila* stock center	BL37516
dilp2-lexA	Li et al.,2015	N/A
LexAop-GCaMP6s (13XLexAop-IVS-GCaMP6s-p10)	Bloomington *Drosophila* stock center	BL44590
UAS-Syt-GFP (UAS-IVS-Syn21-GFP-p10)	Pfeiffer et al.,2012	N/A
Dh44-Gal4	Dus et al.,2015	N/A
Dh44-LexA	Dus et al.,2015	N/A
dilp2 -HA-FLAG knock-in	Park et al.,2015	N/A
LexAop-syb-GFP1-10	Macpherson, L. J. et al.,2015	N/A
UAS-CD4-GFP11	Macpherson, L. J. et al.,2015	N/A
AKH-Gal4 (AKH-Gal4.L)	Bloomington *Drosophila* stock center	BL25684
UAS-Arclight	Cao, G. et al.,2016	N/A
UAS-sNPF-RNAi(2)	Lee et al.,2004	N/A
UAS-sNPF-RNAi(3)	Bloomington *Drosophila* stock center	BL25867
UAS-sNPFR-DN (dominant negative)	Lee et al.,2008	N/A
CrzR(receptor)-Gal4	Tayler et al.,2012	N/A
UAS-Crz-RNAi(GD)	Vienna *Drosophila* Resource Center	30670
UAS-Crz-RNAi(KK)	Vienna *Drosophila* Resource Center	106876
UAS-CrzR-RNAi (44310GD)	Vienna *Drosophila* Resource Center	44310
UAS-CrzR-RNAi (108506)	Vienna *Drosophila* Resource Center	108506
UAS-CrzR-RNAi (46713GD)	Vienna *Drosophila* Resource Center	46713

Supplementary Table 3

Quantitative value (Top 3 precursor intensity) of peptide intensity in hemolymph of the control (*UAS-Kir2.1/+*) and experimental (*UAS-Kir2.1/ CN-Gal4*) flies.

Trial 1

Identified Proteins (226)	**Accession Number**	**Alternate ID**	**Molecular Weight**	**Control – Trial1**	**Exp – Trial 1**
Neuropeptide-like 2 OS=Drosophila melanogaster GN=Nplp2 PE=1 SV=1	NPLP2_DROME	Nplp2	9 kDa	5.57E+09	5.85E+09
CG16712, isoform B OS=Drosophila melanogaster GN=CG16712 PE=2 SV=1	Q9VQT8_DROME	CG16712	9 kDa	2.00E+09	2.26E+08
Accessory gland-specific peptide 57Da OS=Drosophila melanogaster GN=Mst57Da PE=2 SV=1	MS57A_DROME	Mst57Da	7 kDa	1.65E+09	3.30E+07
Odorant-binding protein 99c OS=Drosophila melanogaster GN=Obp99c PE=2 SV=1	Q9VAI9_DROME	Obp99c	17 kDa	8.85E+08	3.46E+08
RT02906p OS=Drosophila melanogaster GN=Sfp79B PE=2 SV=1	B4ZJA5_DROME	Sfp79B	4 kDa	8.78E+08	1.76E+07
CG5804-PA OS=Drosophila melanogaster GN=CG5804 PE=2 SV=1	Q9VSP9_DROME	CG5804	9 kDa	2.55E+08	6.15E+07
CG4944-PA, isoform A OS=Drosophila melanogaster GN=cib PE=1 SV=1	O97428_DROME	cib	14 kDa	2.41E+08	5.93E+07
RH08789p OS=Drosophila melanogaster GN=ssp7 PE=2 SV=1	Q8IR95_DROME	ssp7	10 kDa	1.94E+08	1.62E+08
Drosomycin OS=Drosophila melanogaster GN=Drs PE=1 SV=1	DMYC_DROME	Drs	8 kDa	1.41E+08	5.79E+07
General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2	OB99A_DROME	Obp99a	16 kDa	7.52E+07	2.42E+07
Protein bangles and beads OS=Drosophila melanogaster GN=bnb PE=1 SV=1	BNB_DROME	bnb	46 kDa	5.71E+07	9.08E+07
CG1648, isoform B OS=Drosophila melanogaster GN=CG1648 PE=4 SV=1	A1Z7Z4_DROME (+1)	CG1648	24 kDa	5.32E+07	4.28E+08
12 kDa FK506-binding protein OS=Drosophila melanogaster GN=FK506-bp2 PE=3 SV=2	FKB12_DROME	FK506-bp2	12 kDa	4.46E+07	5.13E+07
LD45324p OS=Drosophila melanogaster GN=Prx5 PE=2 SV=1	Q960M4_DROME	Prx5	20 kDa	3.79E+07	1.16E+08
General odorant-binding protein 56a OS=Drosophila melanogaster GN=Obp56a PE=1 SV=1	OB56A_DROME	Obp56a	15 kDa	3.70E+07	4.87E+08
Protein Turandot A OS=Drosophila melanogaster GN=TotA PE=1 SV=1	TOTA_DROME	TotA	14 kDa	3.63E+07	1.22E+08
Drosomycin-like 5 OS=Drosophila melanogaster GN=Drsl5 PE=2 SV=1	Q9VZR2_DROME	Drsl5	8 kDa	3.60E+07	2.25E+07
CG34215 OS=Drosophila melanogaster GN=CG34215 PE=4 SV=1	A8DY49_DROME	CG34215	11 kDa	2.92E+07	4.93E+08
Immune-induced peptides OS=Drosophila melanogaster GN=IM10 PE=1 SV=2	IM10_DROME	IM10	29 kDa	2.49E+07	4.65E+07
Ductus ejaculatorius peptide 99B OS=Drosophila melanogaster GN=Dup99B PE=1 SV=2	DEJP_DROME	Dup99B	6 kDa	2.43E+07	4.35E+07
Probable elongation factor 1-beta OS=Drosophila melanogaster GN=Ef1beta PE=1 SV=3	EF1B_DROME	Ef1beta	24 kDa	1.70E+07	1.59E+07
Crammer OS=Drosophila melanogaster GN=cer PE=1 SV=1	A1ZBK7_DROME	cer	9 kDa	1.42E+07	6.64E+07
Accessory gland-specific peptide 26Aa OS=Drosophila melanogaster GN=Acp26Aa PE=2 SV=2	MS2A_DROME	Acp26Aa	30 kDa	1.25E+07	2.54E+07
CG30395 OS=Drosophila melanogaster GN=CG30395 PE=4 SV=2	Q8MLV0_DROME	CG30395	98 kDa	1.09E+07	5.39E+07
Niemann-Pick type C-2g OS=Drosophila melanogaster GN=Npc2g PE=4 SV=1	Q9VA42_DROME	Npc2g	17 kDa	9897700	4.16E+07
CG2862, isoform B OS=Drosophila melanogaster GN=CG2862 PE=4 SV=1	Q86BQ4_DROME (+1)	CG2862	14 kDa	8433100	2568100
CG15067, isoform A OS=Drosophila melanogaster GN=CG15067 PE=4 SV=1	A1ZB61_DROME	CG15067	16 kDa	8212300	4.78E+07
Accessory gland protein Acp36DE OS=Drosophila melanogaster GN=Acp36DE PE=2 SV=1	A36DE_DROME	Acp36DE	102 kDa	7758200	1.42E+07
Jonah 44E OS=Drosophila melanogaster GN=Jon44E PE=2 SV=1	Q7JX43_DROME (+6)	Jon44E	30 kDa	6730100	5517100
Eukaryotic translation initiation factor 4G, isoform B OS=Drosophila melanogaster GN=eIF4G PE=4 SV=1	A8DZ29_DROME (+1)	eIF4G	211 kDa	6085200	2358600
CG13023, isoform A OS=Drosophila melanogaster GN=CG13023 PE=4 SV=1	Q9VVC0_DROME	CG13023	45 kDa	5827000	8082400
Obp44a OS=Drosophila melanogaster GN=Obp44a PE=2 SV=1	Q7K084_DROME	Obp44a	16 kDa	5182900	3.37E+07
CG18594 OS=Drosophila melanogaster GN=Pebp1 PE=2 SV=1	Q9VD01_DROME	Pebp1	20 kDa	5054400	8933800
CG31872, isoform A OS=Drosophila melanogaster GN=CG17093 PE=2 SV=2	Q9VKT1_DROME	CG17093	119 kDa	4836500	1564200
Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2	PEB3_DROME	PebIII	15 kDa	4505000	1.41E+07
CG15369, isoform B OS=Drosophila melanogaster GN=CG15369 PE=4 SV=1	Q9W370_DROME	CG15369	13 kDa	3566400	1.38E+07
BG642312, isoform A OS=Drosophila melanogaster GN=BG642312 PE=2 SV=1	Q0E8H8_DROME	BG642312	9 kDa	3248800	2.59E+08
Accessory gland protein Acp63F OS=Drosophila melanogaster GN=Acp63F PE=2 SV=2	A63F_DROME	Acp63F	9 kDa	3059300	5187700
Sarcoplasmic calcium binding protein 1	Q8MSI2	Scp1	21kDa	2925300	3.06E+08
CG15635 OS=Drosophila melanogaster GN=CG15635 PE=4 SV=4	Q9VR13_DROME	CG15635	115 kDa	2481000	1.05E+08
Ribosomal protein S10b, isoform D OS=Drosophila melanogaster GN=RpS10b PE=4 SV=1	M9NEQ9_DROME (+1)	RpS10b	18 kDa	2213900	6.42E+07
Fat-body protein 1 OS=Drosophila melanogaster GN=Fbp1 PE=2 SV=2	FBP1_DROME (+1)	Fbp1	120 kDa	2031100	5636700
CG15201 OS=Drosophila melanogaster GN=CG15201 PE=2 SV=1	Q9VZ24_DROME	CG15201	13 kDa	1914900	3183100
Fondue, isoform D OS=Drosophila melanogaster GN=fon PE=4 SV=1	M9PDP3_DROME (+2)	fon	58 kDa	1824500	4504100
NEDD8 OS=Drosophila melanogaster GN=Nedd8 PE=1 SV=1	NEDD8_DROME	Nedd8	9 kDa	1742500	3338000
CG9928, isoform B OS=Drosophila melanogaster GN=CG9928-RA PE=2 SV=1	Q9VK39_DROME	CG9928-RA	11 kDa	1476000	5.65E+07
Triosephosphate isomerase OS=Drosophila melanogaster GN=Tpi PE=1 SV=3	TPIS_DROME	Tpi	27 kDa	1118600	1.05E+07
CG9691, isoform B OS=Drosophila melanogaster GN=CG9691 PE=2 SV=1	Q9W306_DROME	CG9691	13 kDa	901760	2.65E+07

Ran, isoform B OS=Drosophila melanogaster GN=Ran PE=4 SV=1	A4V4A5_DROME (+1)	Ran	25 kDa	793740	4721400
CG15293, isoform A OS=Drosophila melanogaster GN=CG15293 PE=4 SV=1	Q9V3Y7_DROME	CG15293	37 kDa	751880	2.71E+07
Fructose-bisphosphate aldolase OS=Drosophila melanogaster GN=Ald PE=2 SV=1	A4V3G1_DROME (+1)	Ald	40 kDa	694770	4.58E+07
CG3982-PA OS=Drosophila melanogaster GN=CG3982 PE=4 SV=2	Q9VSY3_DROME	CG3982	37 kDa	665920	1.21E+07
Aldose 1-epimerase OS=Drosophila melanogaster GN=CG10467-RA PE=2 SV=1	Q9VRU1_DROME	CG10467-RA	40 kDa	581540	6818700
CG2720-PA OS=Drosophila melanogaster GN=Hop PE=2 SV=1	Q9VPN5_DROME	Hop	56 kDa	436770	6351100
CG16885 OS=Drosophila melanogaster GN=CG16885 PE=2 SV=1	Q8SZM2_DROME	CG16885	29 kDa	198680	1591600
CG11395 OS=Drosophila melanogaster GN=CG11395 PE=2 SV=1	Q7K533_DROME	CG11395	49 kDa	162220	5.45E+07
GH08696p OS=Drosophila melanogaster GN=wupA PE=2 SV=1	A4V4Q6_DROME (+2)	wupA	25 kDa	0	3.38E+08
Enolase, isoform F OS=Drosophila melanogaster GN=Eno PE=3 SV=1	E1JHR5_DROME (+1)	Eno	47 kDa	0	1.68E+08
Myosin heavy chain, non-muscle OS=Drosophila melanogaster GN=zip PE=1 SV=2	MYSN_DROME (+2)	zip	237 kDa	0	1.54E+08
CG11400 OS=Drosophila melanogaster GN=CG11400 PE=2 SV=1	Q7JV39_DROME	CG11400	22 kDa	0	1.05E+08
CG17919 OS=Drosophila melanogaster GN=CG17919 PE=2 SV=1	Q9VI09_DROME	CG17919	23 kDa	0	5.55E+07
Anon1A4 OS=Drosophila melanogaster GN=Df31 PE=2 SV=1	O16043_DROME	Df31	19 kDa	0	4.22E+07
Poly(U)-specific endoribonuclease homolog OS=Drosophila melanogaster GN=CG2145 PE=1 SV=1	ENDOU_DROME	CG2145	64 kDa	0	3.05E+07
CG6409, isoform B OS=Drosophila melanogaster GN=CG6409 PE=2 SV=2	Q9VTC3_DROME	CG6409	40 kDa	0	2.74E+07
Alpha-amylase A OS=Drosophila melanogaster GN=Amy-p PE=2 SV=1	AMYA_DROME (+1)	Amy-p	54 kDa	0	2.63E+07
CON__ENSEMBL:ENSP00000377550	CON__ENSEMBL:ENSP00000377550 (+5)		?	0	2.44E+07
Probable isoaspartyl peptidase/L-asparaginase CG7860 OS=Drosophila melanogaster GN=CG7860 PE=1 SV=1	ASGL1_DROME	CG7860	35 kDa	0	2.43E+07
CG31883 OS=Drosophila melanogaster GN=CG31883 PE=4 SV=1	Q9VLB4_DROME	CG31883	33 kDa	0	2.31E+07
Ypsilon schachtel, isoform B OS=Drosophila melanogaster GN=yps PE=4 SV=1	M9NFR5_DROME (+1)	yps	37 kDa	0	2.11E+07
Superoxide dismutase [Cu-Zn] OS=Drosophila melanogaster GN=Sod PE=3 SV=1	M9PF91_DROME (+1)	Sod	17 kDa	0	1.83E+07
Calmodulin OS=Drosophila melanogaster GN=Cam PE=1 SV=2	CALM_DROME	Cam	17 kDa	0	1.65E+07
CG16713-PA OS=Drosophila melanogaster GN=CG16713-RA PE=2 SV=1	Q9VQT7_DROME	CG16713-RA	9 kDa	0	1.55E+07
ATP synthase subunit d, mitochondrial OS=Drosophila melanogaster GN=ATPsyn-d PE=2 SV=2	ATP5H_DROME	ATPsyn-d	20 kDa	0	1.21E+07
CG9119 OS=Drosophila melanogaster GN=CG9119 PE=2 SV=1	Q9W0J9_DROME	CG9119	36 kDa	0	9529000
Sh3beta, isoform E OS=Drosophila melanogaster GN=Sh3beta PE=4 SV=1	M9MRQ6_DROME (+3)	Sh3beta	54 kDa	0	7870800
CG18179 OS=Drosophila melanogaster GN=CG18179 PE=2 SV=1	Q9VT24_DROME (+1)	CG18179	29 kDa	0	7232900
Cytochrome b5 OS=Drosophila melanogaster GN=Cyt-b5 PE=2 SV=1	CYB5_DROME	Cyt-b5	15 kDa	0	6953400
FI21560p1 OS=Drosophila melanogaster GN=wdp PE=2 SV=1	Q9W266_DROME	wdp	75 kDa	0	6199700
CG3777, isoform A OS=Drosophila melanogaster GN=EG:125H10.1 PE=2 SV=2	O76874_DROME	EG	94 kDa	0	5354100
Putative hydroxypyruvate isomerase OS=Drosophila melanogaster GN=Gip PE=1 SV=1	HYI_DROME	Gip	29 kDa	0	5027800
CG5010-PA OS=Drosophila melanogaster GN=CG5010 PE=2 SV=1	Q9VX77_DROME	CG5010	17 kDa	0	3982200
Eukaryotic translation initiation factor 4G2 OS=Drosophila melanogaster GN=eIF4G2 PE=4 SV=2	Q9VCH1_DROME	eIF4G2	227 kDa	0	3954900
Cathepsin L OS=Drosophila melanogaster GN=Cp1 PE=2 SV=2	CATL_DROME	Cp1	42 kDa	0	3386300
EH domain containing protein OS=Drosophila melanogaster GN=Past1 PE=2 SV=1	Q8T6I0_DROME (+1)	Past1	61 kDa	0	3256500
CG32521, isoform I OS=Drosophila melanogaster GN=CG32521 PE=4 SV=1	M9PI18_DROME (+1)	CG32521	30 kDa	0	3242700
GH14088p OS=Drosophila melanogaster GN=Ser7 PE=2 SV=1	Q9W314_DROME	Ser7	44 kDa	0	3077900
CG33307, isoform B OS=Drosophila melanogaster GN=BG:DS00941.11 PE=2 SV=1	Q961T9_DROME	BG	20 kDa	0	2720700
60 kDa heat shock protein, mitochondrial OS=Drosophila melanogaster GN=Hsp60 PE=1 SV=3	CH60_DROME	Hsp60	61 kDa	0	2648400
CG6028 OS=Drosophila melanogaster GN=CG6028 PE=2 SV=1	Q95SI7_DROME	CG6028	32 kDa	0	1699600
CG9915, isoform B OS=Drosophila melanogaster GN=CG9915 PE=4 SV=1	A8JV07_DROME	CG9915	91 kDa	0	1693200
CG1342 OS=Drosophila melanogaster GN=Spn100A PE=3 SV=1	Q9VA48_DROME	Spn100A	73 kDa	0	1677200
CG5791 OS=Drosophila melanogaster GN=CG5791 PE=2 SV=1	Q9VD48_DROME	CG5791	10 kDa	0	1534000
Viking, isoform A OS=Drosophila melanogaster GN=vkg PE=4 SV=1	Q9VMV5_DROME	vkg	194 kDa	0	1358800
AT19138p OS=Drosophila melanogaster GN=CG30109 PE=2 SV=1	Q6NLJ9_DROME	CG30109	10 kDa	0	1236300
Proteasomal ubiquitin receptor ADRM1 homolog OS=Drosophila melanogaster GN=Rpn13 PE=1 SV=1	ADRM1_DROME	Rpn13	42 kDa	0	1219500
Nucleosome remodeling factor-38kD, isoform B OS=Drosophila melanogaster GN=Nurf-38 PE=4 SV=1	B7YZQ7_DROME (+1)	Nurf-38	33 kDa	0	1135000
Beta-lactamase-like protein 2 homolog OS=Drosophila melanogaster GN=CG12375 PE=2 SV=1	LACB2_DROME	CG12375	33 kDa	0	1039400
CCHC-type zinc finger protein CG3800 OS=Drosophila melanogaster GN=CG3800 PE=1 SV=1	Y3800_DROME	CG3800	18 kDa	0	1014900
Total Precursor Intensity of Top 3 Peptides				**1.24E+10**	**1.13E+10**

Trial 2

Identified Proteins (252/256)	Accession Number	Alternate ID	Molecular Weight	Control – Trial 2	Exp – Trial 2
Sarcoplasmic calcium-binding protein 1, isoform A	Q8MSI2	Scp1	21.6kDa	3.30E+09	1.53E+09
Enolase, isoform F OS=Drosophila melanogaster GN=Eno PE=3 SV=1	E1JHR5_DROME (+1)	Eno	47 kDa	1.93E+09	5.36E+08
Neuropeptide-like 2 OS=Drosophila melanogaster GN=Nplp2 PE=1 SV=1	NPLP2_DROME	Nplp2	9 kDa	1.56E+09	1.11E+10
Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Drosophila melanogaster GN=Gapdh2 PE=1 SV=2	G3P2_DROME (+1)	Gapdh2	35 kDa	9.04E+08	6.36E+08
CG34215 OS=Drosophila melanogaster GN=CG34215 PE=4 SV=1	A8DY49_DROME	CG34215	11 kDa	8.67E+08	3.25E+08
Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Drosophila melanogaster GN=Gapdh1 PE=2 SV=2	G3P1_DROME	Gapdh1	35 kDa	8.04E+08	8.55E+08
Nucleoside diphosphate kinase OS=Drosophila melanogaster GN=awd PE=1 SV=3	NDKA_DROME	awd	17 kDa	6.79E+08	2.95E+08
CG16712, isoform B OS=Drosophila melanogaster GN=CG16712 PE=2 SV=1	Q9VQT8_DROME	CG16712	9 kDa	3.33E+08	7644500
CG12493, isoform B OS=Drosophila melanogaster GN=CG12493 PE=4 SV=1	M9PHF9_DROME (+1)	CG12493	32 kDa	3.27E+08	0
CG17919 OS=Drosophila melanogaster GN=CG17919 PE=2 SV=1	Q9VI09_DROME	CG17919	23 kDa	2.88E+08	8.41E+07
Sh3beta, isoform E OS=Drosophila melanogaster GN=Sh3beta PE=4 SV=1	M9MRQ6_DROME (+3)	Sh3beta	54 kDa	2.51E+08	7.24E+07
Short stop, isoform H OS=Drosophila melanogaster GN=shot PE=4 SV=1	A1Z9J3_DROME	shot	990 kDa	2.23E+08	0
Fructose-bisphosphate aldolase OS=Drosophila melanogaster GN=Ald PE=2 SV=1	A4V3G1_DROME (+1)	Ald	40 kDa	1.95E+08	4.78E+08
Protein bangles and beads OS=Drosophila melanogaster GN=bnb PE=1 SV=1	BNB_DROME	bnb	46 kDa	1.87E+08	2.66E+07
CG44008, isoform A OS=Drosophila melanogaster GN=CG44008 PE=4 SV=1	M9PBA3_DROME	CG44008	9 kDa	1.35E+08	7.50E+07
Rha OS=Drosophila melanogaster GN=rha PE=4 SV=1	Q9VBR7_DROME	rha	152 kDa	1.29E+08	1.86E+07
CG6028 OS=Drosophila melanogaster GN=CG6028 PE=2 SV=1	Q95SI7_DROME	CG6028	32 kDa	1.27E+08	6015000
CG4944-PA, isoform A OS=Drosophila melanogaster GN=cib PE=1 SV=1	O97428_DROME	cib	14 kDa	1.26E+08	6.20E+07
Odorant-binding protein 99c OS=Drosophila melanogaster GN=Obp99c PE=2 SV=1	Q9VAI9_DROME	Obp99c	17 kDa	1.18E+08	7.17E+07
CG30395 OS=Drosophila melanogaster GN=CG30395 PE=4 SV=2	Q8MLV0_DROME	CG30395	98 kDa	1.12E+08	1.53E+07
Calmodulin OS=Drosophila melanogaster GN=Cam PE=1 SV=2	CALM_DROME	Cam	17 kDa	1.11E+08	6.38E+07
Chitinase-like protein Idgf4 OS=Drosophila melanogaster GN=Idgf4 PE=2 SV=1	IDGF4_DROME	Idgf4	49 kDa	1.09E+08	1.82E+07
Anon1A4 OS=Drosophila melanogaster GN=Df31 PE=2 SV=1	O16043_DROME	Df31	19 kDa	9.14E+07	5.62E+07
CG7998 OS=Drosophila melanogaster GN=Mdh2 PE=2 SV=1	Q9VEB1_DROME	Mdh2	35 kDa	8.70E+07	1.24E+08
CG7966 OS=Drosophila melanogaster GN=CG7966 PE=4 SV=2	Q9VFZ4_DROME	CG7966	55 kDa	7.92E+07	0
MIP08680p OS=Drosophila melanogaster GN=vib PE=2 SV=1	Q9VDY8_DROME	vib	31 kDa	7.13E+07	3117000
Cathepsin L OS=Drosophila melanogaster GN=Cp1 PE=2 SV=2	CATL_DROME	Cp1	42 kDa	6.55E+07	6756100
General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2	OB99A_DROME	Obp99a	16 kDa	6.50E+07	0
Aconitate hydratase OS=Drosophila melanogaster GN=Irp-1B PE=3 SV=1	Q9VGZ3_DROME	Irp-1B	99 kDa	5.82E+07	1.72E+07
CG18594 OS=Drosophila melanogaster GN=Pebp1 PE=2 SV=1	Q9VD01_DROME	Pebp1	20 kDa	5.69E+07	3.56E+07
CG1532, isoform B OS=Drosophila melanogaster GN=CG1532 PE=4 SV=1	Q9VRD4_DROME	CG1532	32 kDa	5.24E+07	5.53E+07
CG18135, isoform E OS=Drosophila melanogaster GN=CG18135 PE=4 SV=1	M9PI96_DROME (+4)	CG18135	73 kDa	5.10E+07	1.11E+08
CG5804-PA OS=Drosophila melanogaster GN=CG5804 PE=2 SV=1	Q9VSP9_DROME	CG5804	9 kDa	4.97E+07	6.44E+07
Heat shock 70 kDa protein cognate 4 OS=Drosophila melanogaster GN=Hsc70-4 PE=1 SV=3	HSP7D_DROME	Hsc70-4	71 kDa	4.89E+07	1.12E+07
Putative hydroxypyruvate isomerase OS=Drosophila melanogaster GN=Gip PE=1 SV=1	HYI_DROME	Gip	29 kDa	4.57E+07	1.91E+07
Transient-receptor-potential-like protein OS=Drosophila melanogaster GN=trpl PE=1 SV=2	TRPL_DROME	trpl	128 kDa	4.02E+07	0
Eip55E OS=Drosophila melanogaster GN=Eip55E PE=2 SV=1	Q7JXZ2_DROME	Eip55E	43 kDa	3.97E+07	0
Cytochrome b5 OS=Drosophila melanogaster GN=Cyt-b5 PE=2 SV=1	CYB5_DROME	Cyt-b5	15 kDa	3.62E+07	4085100
Probable isoaspartyl peptidase/L-asparaginase CG7860 OS=Drosophila melanogaster GN=CG7860 PE=1 SV=1	ASGL1_DROME	CG7860	35 kDa	3.45E+07	1.44E+07
Adenylosuccinate synthetase OS=Drosophila melanogaster GN=AdSS PE=2 SV=1	PURA_DROME	AdSS	49 kDa	3.36E+07	3.54E+07
Angiotensin-converting enzyme-related protein OS=Drosophila melanogaster GN=Acer PE=1 SV=1	ACER_DROME (+1)	Acer	73 kDa	3.09E+07	1.32E+07
CG9119 OS=Drosophila melanogaster GN=CG9119 PE=2 SV=1	Q9W0J9_DROME	CG9119	36 kDa	3.05E+07	7.75E+07
Ribosomal protein S10b, isoform D OS=Drosophila melanogaster GN=RpS10b PE=4 SV=1	M9NEQ9_DROME (+1)	RpS10b	18 kDa	3.05E+07	1052700
Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2	PEB3_DROME	PebIII	15 kDa	3.04E+07	2.51E+07
LD45324p OS=Drosophila melanogaster GN=Prx5 PE=2 SV=1	Q960M4_DROME	Prx5	20 kDa	2.74E+07	0
Glutactin OS=Drosophila melanogaster GN=Glt PE=1 SV=2	GLT_DROME (+1)	Glt	119 kDa	2.54E+07	0
Accessory gland-specific peptide 26Aa OS=Drosophila melanogaster GN=Acp26Aa PE=2 SV=2	MS2A_DROME	Acp26Aa	30 kDa	2.49E+07	0
Dietary and metabolic glutamate transporter OS=Drosophila melanogaster GN=dmGlut PE=2 SV=2	Q9VKC9_DROME	dmGlut	54 kDa	2.36E+07	0
CG16713-PA OS=Drosophila melanogaster GN=CG16713-RA PE=2 SV=1	Q9VQT7_DROME	CG16713-RA	9 kDa	2.07E+07	2668100
CG10031 OS=Drosophila melanogaster GN=CG10031 PE=4 SV=2	Q9VQU0_DROME	CG10031	14 kDa	1.96E+07	202910
CG9391, isoform C OS=Drosophila melanogaster GN=CG9391 PE=2 SV=1	Q7KTW5_DROME	CG9391	31 kDa	1.92E+07	5073800
CG4365, isoform C OS=Drosophila melanogaster GN=CG4365 PE=3 SV=1	Q8IPU3_DROME (+2)	CG4365	39 kDa	1.77E+07	8736000
GH04080p OS=Drosophila melanogaster GN=PPO1 PE=2 SV=1	Q7K2W6_DROME	PPO1	79 kDa	1.75E+07	9099000

Esterase 6, isoform B OS=Drosophila melanogaster GN=Est-6 PE=2 SV=1	C9QP21_DROME (+1)	Est-6	61 kDa	1.55E+07	5.72E+07
Obp44a OS=Drosophila melanogaster GN=Obp44a PE=2 SV=1	Q7K084_DROME	Obp44a	16 kDa	1.53E+07	2.16E+08
DnaJ-like-2, isoform A OS=Drosophila melanogaster GN=Droj2 PE=2 SV=1	Q9VFV9_DROME	Droj2	45 kDa	1.44E+07	0
Eukaryotic translation initiation factor 5 OS=Drosophila melanogaster GN=eIF5 PE=1 SV=1	IF5_DROME	eIF5	52 kDa	1.44E+07	0
Guanylate cyclase OS=Drosophila melanogaster GN=Gyc32E PE=3 SV=1	A8DYZ3_DROME (+1)	Gyc32E	134 kDa	1.33E+07	0
CG5397, isoform A OS=Drosophila melanogaster GN=CG5397 PE=2 SV=1	Q9VPZ5_DROME	CG5397	71 kDa	1.27E+07	0
General odorant-binding protein 19d OS=Drosophila melanogaster GN=Obp19d PE=2 SV=2	OB19D_DROME	Obp19d	17 kDa	1.23E+07	4.39E+07
CG31872, isoform A OS=Drosophila melanogaster GN=CG17093 PE=2 SV=2	Q9VKT1_DROME	CG17093	119 kDa	1.10E+07	947160
Muscle-specific protein 300 kDa, isoform G OS=Drosophila melanogaster GN=Msp300 PE=4 SV=1	M9MRJ4_DROME (+1)	Msp300	1508 kDa	1.07E+07	0
CG4797, isoform B OS=Drosophila melanogaster GN=CG4797 PE=2 SV=2	Q8MLQ7_DROME (+1)	CG4797	59 kDa	1.07E+07	0
Ran, isoform B OS=Drosophila melanogaster GN=Ran PE=4 SV=1	A4V4A5_DROME (+1)	Ran	25 kDa	1.02E+07	2.81E+07
RH08789p OS=Drosophila melanogaster GN=ssp7 PE=2 SV=1	Q8IR95_DROME	ssp7	10 kDa	1.01E+07	5.59E+07
Glutathione S transferase S1, isoform C OS=Drosophila melanogaster GN=GstS1 PE=2 SV=1	A4UZL5_DROME (+1)	GstS1	28 kDa	9817000	8.64E+07
Moesin, isoform K OS=Drosophila melanogaster GN=Moe PE=2 SV=1	C7LAH9_DROME (+3)	Moe	76 kDa	9339400	1549700
CG18446 OS=Drosophila melanogaster GN=CG18446 PE=2 SV=1	Q7JZC5_DROME	CG18446	55 kDa	9275600	0
Niemann-Pick type C-2g OS=Drosophila melanogaster GN=Npc2g PE=4 SV=1	Q9VA42_DROME	Npc2g	17 kDa	8460600	1.26E+07
FI04779p OS=Drosophila melanogaster GN=HBS1 PE=2 SV=2	Q9W074_DROME	HBS1	74 kDa	8268000	0
GH01724p OS=Drosophila melanogaster GN=p47 PE=2 SV=1	Q7K3Z3_DROME	p47	43 kDa	8248000	0
Isocitrate dehydrogenase [NADP] OS=Drosophila melanogaster GN=Idh PE=3 SV=2	B7Z0E0_DROME (+4)	Idh	54 kDa	8098400	3.65E+08
Jonah 44E OS=Drosophila melanogaster GN=Jon44E PE=2 SV=1	Q7JX43_DROME (+5)	Jon44E	30 kDa	7952900	0
Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster GN=Cyp1 PE=1 SV=2	PPIA_DROME	Cyp1	25 kDa	7729600	2.17E+07
CG15201 OS=Drosophila melanogaster GN=CG15201 PE=2 SV=1	Q9VZ24_DROME	CG15201	13 kDa	7232300	1.46E+07
Doublesex-Mab related 99B OS=Drosophila melanogaster GN=dmrt99B PE=2 SV=1	Q9VAI8_DROME	dmrt99B	55 kDa	6996900	3.25E+07
Seminal fluid protein 87B OS=Drosophila melanogaster GN=Sfp87B PE=2 SV=1	B4ZJA7_DROME	Sfp87B	10 kDa	6973300	2.61E+07
LD21576p OS=Drosophila melanogaster GN=Nap1 PE=2 SV=1	Q9W1G7_DROME	Nap1	43 kDa	6897500	0
CG30197 OS=Drosophila melanogaster GN=CG30197 PE=2 SV=1	Q8MKJ5_DROME	CG30197	12 kDa	6873300	1.29E+07
CG6852, isoform C OS=Drosophila melanogaster GN=CG6852 PE=2 SV=1	Q9VVT6_DROME	CG6852	12 kDa	6705200	0
FI21560p1 OS=Drosophila melanogaster GN=wdp PE=2 SV=1	Q9W266_DROME	wdp	75 kDa	6577300	7604900
Transferrin OS=Drosophila melanogaster GN=Tsf1 PE=3 SV=1	Q9VWV6_DROME	Tsf1	72 kDa	6432800	4.21E+08
CG11784 OS=Drosophila melanogaster GN=GstE13 PE=2 SV=1	Q7JVI6_DROME	GstE13	26 kDa	6397800	0
CG17032, isoform B OS=Drosophila melanogaster GN=CG17032 PE=2 SV=1	Q9VUV8_DROME	CG17032	31 kDa	5991800	5644700
GH13304p OS=Drosophila melanogaster GN=Pglym78 PE=2 SV=2	Q9VAN7_DROME	Pglym78	29 kDa	5446300	6.91E+07
CG11400 OS=Drosophila melanogaster GN=CG11400 PE=2 SV=1	Q7JV39_DROME	CG11400	22 kDa	5000100	5.42E+07
CG14430-PA OS=Drosophila melanogaster GN=bou PE=2 SV=1	Q9W3T7_DROME	bou	17 kDa	4840600	0
A kinase anchor protein 200, isoform G OS=Drosophila melanogaster GN=Akap200 PE=4 SV=1	Q86BM5_DROME (+2)	Akap200	88 kDa	4620400	6386900
CG11089 OS=Drosophila melanogaster GN=CG11089 PE=2 SV=1	Q9VC18_DROME	CG11089	63 kDa	4326100	6900600
Bifocal, isoform D OS=Drosophila melanogaster GN=bif PE=4 SV=1	M9PGW8_DROME (+4)	bif	124 kDa	4320100	0
BG642312, isoform A OS=Drosophila melanogaster GN=BG642312 PE=2 SV=1	Q0E8H8_DROME	BG642312	9 kDa	4312400	1227900
Rab8, isoform B OS=Drosophila melanogaster GN=Rab8 PE=3 SV=1	M9NEE8_DROME (+1)	Rab8	20 kDa	4262600	0
Myosin light chain cytoplasmic, isoform B OS=Drosophila melanogaster GN=Mlc-c PE=4 SV=1	M9NEW1_DROME (+1)	Mlc-c	17 kDa	4207900	0
Cystatin-like protein OS=Drosophila melanogaster GN=Cys PE=2 SV=2	CYTL_DROME	Cys	13 kDa	4124400	1.98E+07
CG12811 OS=Drosophila melanogaster GN=CG12811 PE=2 SV=1	Q9VH37_DROME	CG12811	23 kDa	4105500	0
CG33307, isoform B OS=Drosophila melanogaster GN=BG:DS00941.11 PE=2 SV=1	Q961T9_DROME	BG	20 kDa	4041600	0
Alpha-amylase A OS=Drosophila melanogaster GN=Amy-p PE=2 SV=1	AMYA_DROME (+1)	Amy-p	54 kDa	3983600	1.20E+08
Neural lazarillo, isoform B OS=Drosophila melanogaster GN=NLaz PE=4 SV=1	M9PBN2_DROME (+1)	NLaz	27 kDa	3832200	0
Total Precursor Intensity of Top 3 Peptides				**1.45E+10**	**1.87E+10**

Trial 3, 4, and 5

Identified Proteins	Accession Number	Gene Name	Mr/kDa	Control – Trial 3	Exp – Trial 3	Control – Trial 4	Exp – Trial 4	Control – Trial 5	Exp – Trial 5
Neuropeptide-like 2 OS=Drosophila melanogaster GN=Nplp2 PE=1 SV=1	NPLP2_DROME	Nplp2	9 kDa	1.24E+11	1.63E+11	1.10E+11	9.92E+10	1.05E+11	1.14E+11
Protein bangles and beads OS=Drosophila melanogaster GN=bnb PE=1 SV=1	BNB_DROME	bnb	46 kDa	1.39E+09	2.58E+09	1.30E+09	4.88E+09	1.20E+09	4.13E+09
Accessory gland protein Acp36DE OS=Drosophila melanogaster GN=Acp36DE PE=2 SV=1	A36DE_DROME	Acp36DE	102 kDa	2.52E+09	1.78E+09	2.64E+09	9.37E+08	1.90E+09	6.46E+08
CG1648, isoform B OS=Drosophila melanogaster GN=CG1648 PE=4 SV=1	A1Z7Z4_DROME (+1)	CG1648	24 kDa	1.71E+09	6.41E+08	6.54E+09	1.74E+09	6.16E+09	5.97E+08
Drosomycin OS=Drosophila melanogaster GN=Drs PE=1 SV=1	DMYC_DROME	Drs	8 kDa	7.35E+09	2.36E+10	5.73E+09	1.87E+10	3.74E+09	2.32E+10
Odorant-binding protein 99c OS=Drosophila melanogaster GN=Obp99c PE=2 SV=1	Q9VAI9_DROME	Obp99c	17 kDa	1.25E+10	1.63E+10	7.56E+09	7.80E+09	7.48E+09	1.17E+10
Accessory gland protein Acp62F OS=Drosophila melanogaster GN=Acp62F PE=2 SV=1	A62F_DROME	Acp62F	13 kDa	3.04E+09	3.19E+09	6.02E+09	2.87E+09	6.29E+09	3.65E+09
Ubiquitin-63E, isoform C OS=Drosophila melanogaster GN=Ubi-p63E PE=4 SV=1	A4V1F9_DROME (+5)	Ubi-p63E	86 kDa	8.41E+09	8.93E+09	3.07E+09	3.84E+09	1.10E+09	2.60E+09
Niemann-Pick type C-2g OS=Drosophila melanogaster GN=Npc2g PE=4 SV=1	Q9VA42_DROME	Npc2g	17 kDa	7.99E+09	1.30E+10	5.17E+09	7.93E+09	5.72E+09	8.62E+09
Arginine kinase, isoform G OS=Drosophila melanogaster GN=Argk PE=3 SV=2	A8JNP1_DROME (+1)	Argk	40 kDa	7.02E+08	3.14E+09	3.15E+09	6.79E+08	4.58E+09	4.48E+08
CG5804-PA OS=Drosophila melanogaster GN=CG5804 PE=2 SV=1	Q9VSP9_DROME	CG5804	9 kDa	1.24E+10	1.27E+10	1.40E+10	8.03E+09	1.16E+10	7.14E+09
CG2720-PA OS=Drosophila melanogaster GN=Hop PE=2 SV=1	Q9VPN5_DROME	Hop	56 kDa	8.54E+08	9.37E+08	1.12E+09	6.65E+08	7.11E+08	4.69E+08
CG16712, isoform B OS=Drosophila melanogaster GN=CG16712 PE=2 SV=1	Q9VQT8_DROME	CG16712	9 kDa	5.65E+10	2.92E+10	4.20E+10	5.00E+10	3.01E+10	3.05E+10
CG4944-PA, isoform A OS=Drosophila melanogaster GN=cib PE=1 SV=1	O97428_DROME	cib	14 kDa	2.54E+09	3.54E+09	2.13E+09	1.47E+09	1.86E+09	1.28E+09
CG30395 OS=Drosophila melanogaster GN=CG30395 PE=4 SV=2	Q8MLV0_DROME	CG30395	98 kDa	1.29E+09	1.14E+09	1.35E+09	3.20E+08	1.38E+09	2.84E+08
Phosphoglycerate kinase OS=Drosophila melanogaster GN=Pgk PE=3 SV=1	M9PCE0_DROME (+1)	Pgk	44 kDa	1.73E+09	2.43E+09	2.64E+09	2.27E+09	2.14E+09	1.17E+09
Probable elongation factor 1-beta OS=Drosophila melanogaster GN=Ef1beta PE=1 SV=3	EF1B_DROME	Ef1beta	24 kDa	9.95E+09	2.64E+09	8.76E+09	3.35E+09	4.08E+09	1.56E+09
Anon1A4 OS=Drosophila melanogaster GN=Df31 PE=2 SV=1	O16043_DROME	Df31	19 kDa	2.10E+08	2.61E+08	3.40E+08	9.18E+08	2.92E+08	5.44E+08
12 kDa FK506-binding protein OS=Drosophila melanogaster GN=FK506-bp2 PE=3 SV=2	FKB12_DROME	FK506-bp2	12 kDa	7.16E+09	4.96E+09	5.93E+09	1.07E+10	6.49E+09	1.31E+10
Acyl-CoA-binding protein homolog OS=Drosophila melanogaster GN=Dbi PE=2 SV=1	ACBP_DROME	Dbi	10 kDa	2.29E+09	3.28E+09	5.11E+09	2.09E+09	7.67E+08	7.31E+08
General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2	OB99A_DROME	Obp99a	16 kDa	2.92E+09	4.90E+09	2.09E+09	1.68E+09	1.65E+09	1.08E+09
Obp44a OS=Drosophila melanogaster GN=Obp44a PE=2 SV=1	Q7K084_DROME	Obp44a	16 kDa	1.37E+09	6.63E+08	1.83E+09	6.91E+08	1.78E+09	6.11E+08
CG34215 OS=Drosophila melanogaster GN=CG34215 PE=4 SV=1	A8DY49_DROME	CG34215	11 kDa	1.10E+09	1.27E+09	1.15E+09	1.44E+09	1.20E+09	5.65E+08
RH08789p OS=Drosophila melanogaster GN=ssp7 PE=2 SV=1	Q8IR95_DROME	ssp7	10 kDa	3.19E+09	3.51E+09	3.51E+09	8.15E+09	3.10E+09	9.26E+09
Aldose 1-epimerase OS=Drosophila melanogaster GN=CG10467-RA PE=2 SV=1	Q9VRU1_DROME	CG10467-RA	40 kDa	2.14E+08	1.29E+09	1.04E+08	9.32E+08	1.43E+08	1.48E+09
Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Drosophila melanogaster GN=Gpdh PE=3 SV=1	M9PC43_DROME	Gpdh	39 kDa	5.19E+08	1.36E+08	1.49E+09	2.59E+08	9.25E+08	8.30E+07
Bacchus, isoform B OS=Drosophila melanogaster GN=Bacc PE=2 SV=1	Q9VQF7_DROME	Bacc	15 kDa	5.51E+08	6.57E+08	9.56E+08	9.54E+08	6.57E+08	7.16E+08
Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Drosophila melanogaster GN=Gapdh2 PE=1 SV=2	G3P2_DROME (+1)	Gapdh2	35 kDa	1.02E+09	3.40E+08	2.11E+09	3.69E+08	2.57E+09	6.22E+07
Accessory gland protein Acp63F OS=Drosophila melanogaster GN=Acp63F PE=2 SV=2	A63F_DROME	Acp63F	9 kDa	2.63E+09	3.11E+09	3.78E+09	1.89E+09	2.34E+09	2.25E+09
CG6409, isoform B OS=Drosophila melanogaster GN=CG6409 PE=2 SV=2	Q9VTC3_DROME	CG6409	40 kDa	1.67E+08	6.74E+08	6.49E+08	7.75E+08	2.24E+08	8.18E+07
Hsc/Hsp70-interacting protein related, isoform B OS=Drosophila melanogaster GN=HIP-R PE=4 SV=1	E2QD63_DROME (+2)	HIP-R	41 kDa	1.79E+09	4.36E+08	1.26E+09	9.87E+08	1.29E+09	4.40E+08

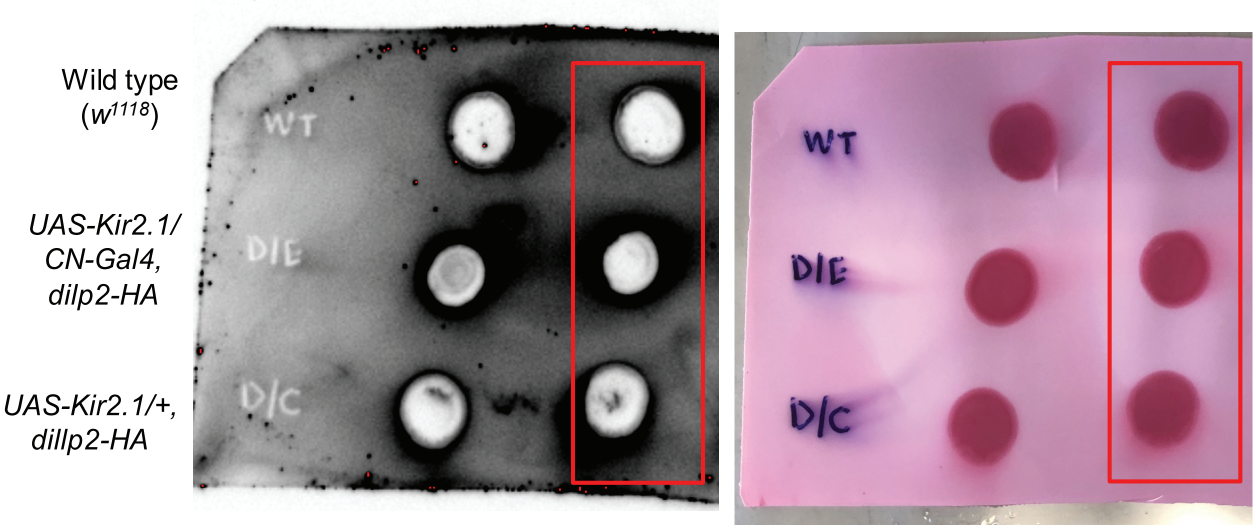
Accessory gland-specific peptide 57Da OS=Drosophila melanogaster GN=Mst57Da PE=2 SV=1	MS57A_DROME	Mst57Da	7 kDa	1.83E+10	1.06E+10	1.48E+10	3.82E+09	1.72E+10	4.00E+09
Adenylyl cyclase-associated protein OS=Drosophila melanogaster GN=capt PE=2 SV=2	Q9VPX6_DROME (+1)	capt	84 kDa	4.76E+08	4.36E+08	6.03E+08	5.73E+08	3.16E+08	1.53E+08
General odorant-binding protein 56d OS=Drosophila melanogaster GN=Obp56d PE=1 SV=2	OB56D_DROME	Obp56d	14 kDa	6.14E+08	7.37E+08	4.70E+08	8.74E+08	4.98E+08	9.45E+08
Protein Turandot A OS=Drosophila melanogaster GN=TotA PE=1 SV=1	TOTA_DROME	TotA	14 kDa	1.48E+09	5.23E+09	1.32E+09	2.40E+09	1.56E+09	3.84E+09
Fructose-bisphosphate aldolase OS=Drosophila melanogaster GN=Ald PE=2 SV=1	A4V3G1_DROME (+1)	Ald	40 kDa	1.07E+08	2.73E+08	1.71E+08	6.36E+08	1.23E+08	1.54E+09
CG44008, isoform A OS=Drosophila melanogaster GN=CG44008 PE=4 SV=1	M9PBA3_DROME	CG44008	9 kDa	1.96E+09	9.82E+08	2.23E+09	3.35E+09	2.31E+09	1.38E+09
CG15369, isoform B OS=Drosophila melanogaster GN=CG15369 PE=4 SV=1	Q9W370_DROME	CG15369	13 kDa	2.20E+08	1.01E+09	1.30E+08	3.52E+08	1.24E+08	4.34E+08
Triosephosphate isomerase OS=Drosophila melanogaster GN=Tpi PE=1 SV=3	TPIS_DROME	Tpi	27 kDa	1.49E+09	8.23E+08	2.02E+09	9.03E+08	1.91E+09	9.68E+08
Ductus ejaculatorius peptide 99B OS=Drosophila melanogaster GN=Dup99B PE=1 SV=2	DEJP_DROME	Dup99B	6 kDa	1.27E+10	7.81E+09	4.76E+09	2.07E+08	3.27E+09	2.16E+08
Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster GN=Cyp1 PE=1 SV=2	PPIA_DROME	Cyp1	25 kDa	2.74E+08	4.93E+08	6.58E+08	2.81E+08	4.51E+08	6.44E+08
AT30951p OS=Drosophila melanogaster GN=CG9920 PE=2 SV=1	Q9VFN5_DROME	CG9920	11 kDa	6.76E+08	1.60E+09	1.51E+09	2.12E+08	1.21E+09	2.41E+08
Odorant-binding protein 56g, isoform A OS=Drosophila melanogaster GN=Obp56g PE=4 SV=1	A1ZBQ3_DROME (+1)	Obp56g	14 kDa	5.76E+08	3.84E+08	8.04E+08	1.51E+08	8.79E+08	5.79E+08
Odorant binding protein c OS=Drosophila melanogaster GN=Obp51a PE=2 SV=1	Q7KE33_DROME	Obp51a	13 kDa	3.10E+09	1.96E+09	2.27E+09	6.87E+08	1.66E+09	7.37E+08
CG18594 OS=Drosophila melanogaster GN=Pebp1 PE=2 SV=1	Q9VD01_DROME	Pebp1	20 kDa	2.89E+08	2.79E+08	8.86E+08	0	1.78E+08	3.82E+07
CG8498, isoform B OS=Drosophila melanogaster GN=CG8498 PE=2 SV=1	Q9VLS4_DROME	CG8498	10 kDa	2.54E+08	7.84E+08	1.80E+09	1.19E+08	3.49E+08	1.09E+08
CG17278 OS=Drosophila melanogaster GN=CG17278 PE=2 SV=2	Q9VDG1_DROME	CG17278	9 kDa	2.82E+08	1.84E+08	2.50E+08	3.59E+08	2.32E+08	2.17E+08
General odorant-binding protein 56a OS=Drosophila melanogaster GN=Obp56a PE=1 SV=1	OB56A_DROME	Obp56a	15 kDa	3.77E+07	1.95E+09	2.38E+07	1.40E+09	5.69E+07	3.48E+09
GH15296p	Q8MSI2_DROME	Scp1	21.7kDa	2.38E+08	8.86E+07	3.67E+08	1.44E+08	3.07E+08	4.86E+08
Protein Turandot C OS=Drosophila melanogaster GN=TotC PE=1 SV=1	TOTC_DROME	TotC	14 kDa	9.56E+08	3.69E+08	8.11E+08	5.61E+08	8.63E+08	4.87E+08
CG11400 OS=Drosophila melanogaster GN=CG11400 PE=2 SV=1	Q7JV39_DROME	CG11400	22 kDa	4.82E+08	7.41E+08	7.35E+08	3.75E+08	7.06E+08	4.52E+08
CG14961 OS=Drosophila melanogaster GN=CG14961 PE=4 SV=1	Q9VZQ7_DROME	CG14961	101 kDa	8.49E+07	7.35E+08	4.91E+07	2.29E+08	4.49E+07	0
CG6503 OS=Drosophila melanogaster GN=CG6503 PE=2 SV=2	Q9VBF3_DROME	CG6503	7 kDa	4.05E+07	6.40E+09	1.15E+08	2.01E+07	0	0
CG16704, isoform B OS=Drosophila melanogaster GN=CG16704 PE=2 SV=1	Q9VQT5_DROME	CG16704	9 kDa	5.52E+09	1.15E+10	5.22E+09	1.17E+10	4.51E+09	1.36E+10
GH13304p OS=Drosophila melanogaster GN=Pglym78 PE=2 SV=2	Q9VAN7_DROME	Pglym78	29 kDa	9.42E+07	2.41E+07	3.24E+08	4.78E+07	2.39E+08	0
Crammer OS=Drosophila melanogaster GN=cer PE=1 SV=1	A1ZBK7_DROME	cer	9 kDa	1.51E+08	1.92E+08	1.25E+08	1.85E+08	1.09E+08	1.71E+08
CG18064-PA OS=Drosophila melanogaster GN=Met75Ca PE=4 SV=1	Q9V449_DROME	Met75Ca	6 kDa	6.80E+08	5.03E+08	1.92E+08	2.76E+08	1.27E+08	5.07E+07
Elongation factor 1-alpha 1 OS=Drosophila melanogaster GN=Ef1alpha48D PE=1 SV=2	EF1A1_DROME	Ef1alpha48D	50 kDa	1.34E+10	5.70E+09	1.20E+10	7.08E+09	1.32E+10	7.76E+09
CG13023, isoform A OS=Drosophila melanogaster GN=CG13023 PE=4 SV=1	Q9VVC0_DROME	CG13023	45 kDa	2.27E+08	3.34E+08	6.45E+07	2.08E+08	1.14E+08	1.20E+08
Enolase, isoform F OS=Drosophila melanogaster GN=Eno PE=3 SV=1	E1JHR5_DROME (+1)	Eno	47 kDa	5.13E+07	2.64E+08	1.64E+08	2.33E+08	1.19E+08	1.75E+08
CG34454 OS=Drosophila melanogaster GN=CG34018 PE=4 SV=1	A8JNG6_DROME	CG34018	14 kDa	6.58E+08	9.13E+08	4.97E+08	4.42E+08	4.86E+08	2.62E+08
CG31872, isoform A OS=Drosophila melanogaster GN=CG17093 PE=2 SV=2	Q9VKT1_DROME	CG17093	119 kDa	2.80E+08	9.88E+07	4.81E+08	3.75E+08	4.04E+08	3.84E+08
V-type proton ATPase subunit E OS=Drosophila melanogaster GN=Vha26 PE=2 SV=1	VATE_DROME	Vha26	26 kDa	2.15E+08	1.53E+08	2.28E+08	5.10E+08	3.14E+08	4.27E+08
Drosomycin-like 5 OS=Drosophila melanogaster GN=Drsl5 PE=2 SV=1	Q9VZR2_DROME	Drsl5	8 kDa	2.40E+09	4.12E+09	2.34E+09	1.84E+09	1.41E+09	1.44E+09
CG10527 OS=Drosophila melanogaster GN=CG10527 PE=4 SV=1	Q9W2M4_DROME	CG10527	32 kDa	2.57E+08	5.54E+08	5.06E+07	5.02E+08	3.77E+07	3.60E+08
Tequila, isoform G OS=Drosophila melanogaster GN=Tequila PE=4 SV=4	Q9VSU2_DROME	Tequila	309 kDa	2.35E+08	1.93E+08	0	1.18E+08	0	1.61E+08

Accessory gland-specific peptide 26Aa OS=Drosophila melanogaster GN=Acp26Aa PE=2 SV=2	MS2A_DROME	Acp26Aa	30 kDa	1.05E+09	7.99E+07	1.29E+09	0	7.88E+08	0
Aconitase, isoform B OS=Drosophila melanogaster GN=Acon PE=2 SV=2	Q9VIE8_DROME	Acon	85 kDa	5.96E+07	1.86E+08	4.14E+08	1.17E+08	2.68E+08	1.02E+08
CG3513-PA OS=Drosophila melanogaster GN=CG3513 PE=2 SV=1	Q9VQT6_DROME	CG3513	9 kDa	1.83E+09	1.75E+09	8.48E+08	1.07E+08	1.29E+08	0
Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2	APLP_DROME (+1)	Rfabg	373 kDa	2.30E+08	0	3.39E+07	3.74E+07	2.47E+07	1.64E+07
Transitional endoplasmic reticulum ATPase TER94 OS=Drosophila melanogaster GN=TER94 PE=1 SV=1	TERA_DROME	TER94	89 kDa	1.38E+08	5.04E+08	4.57E+08	4.77E+08	3.99E+08	2.20E+08
Elongation factor 2 OS=Drosophila melanogaster GN=EF2 PE=1 SV=4	EF2_DROME	EF2	94 kDa	2.04E+08	2.02E+07	1.54E+08	8.74E+07	9.67E+07	3.46E+07
Superoxide dismutase [Cu-Zn] OS=Drosophila melanogaster GN=Sod PE=1 SV=2	SODC_DROME	Sod	16 kDa	5.94E+07	2.44E+08	1.31E+08	2.02E+08	1.59E+08	2.56E+08
LD45324p OS=Drosophila melanogaster GN=Prx5 PE=2 SV=1	Q960M4_DROME	Prx5	20 kDa	6.67E+07	3.83E+08	1.29E+08	3.13E+08	1.64E+08	3.24E+08
Heat shock protein 83 OS=Drosophila melanogaster GN=Hsp83 PE=1 SV=1	HSP83_DROME (+1)	Hsp83	82 kDa	1.55E+08	1.58E+08	2.12E+08	4.08E+07	1.26E+08	3.10E+07
LD36265p (Fragment) OS=Drosophila melanogaster GN=UGP PE=2 SV=1	A5XCL5_DROME (+1)	UGP	58 kDa	4.01E+08	1.68E+09	2.00E+08	1.80E+08	2.88E+08	1.03E+09
Ribosomal protein LP0, isoform B OS=Drosophila melanogaster GN=RpLP0 PE=3 SV=1	M9PG76_DROME (+1)	RpLP0	34 kDa	4.38E+08	3.34E+08	4.37E+08	1.08E+07	4.35E+07	0
Odorant-binding protein 56e OS=Drosophila melanogaster GN=Obp56e PE=2 SV=1	Q7K088_DROME	Obp56e	14 kDa	1.33E+09	1.17E+09	4.76E+08	1.44E+09	3.43E+08	1.78E+09
CG9029-PA OS=Drosophila melanogaster GN=CG9029 PE=4 SV=1	Q9VML7_DROME	CG9029	12 kDa	3.96E+08	1.31E+08	9.96E+08	5.82E+07	9.42E+08	7.61E+07
CG7834, isoform A OS=Drosophila melanogaster GN=CG7834 PE=4 SV=1	Q0KHZ6_DROME	CG7834	27 kDa	1.48E+08	2.50E+08	3.77E+08	2.09E+08	3.78E+08	2.18E+08
CG18815, isoform D OS=Drosophila melanogaster GN=CG18815-RA PE=2 SV=1	C0PDF4_DROME (+2)	CG18815-RA	24 kDa	1.22E+08	1.86E+08	2.03E+08	8.48E+07	6.18E+07	1.28E+08
Actin-5C OS=Drosophila melanogaster GN=Act5C PE=1 SV=4	ACT1_DROME (+1)	Act5C	42 kDa	8.96E+08	1.35E+09	1.23E+09	5.45E+08	1.05E+09	5.18E+08
General odorant-binding protein 99b OS=Drosophila melanogaster GN=Obp99b PE=2 SV=1	OB99B_DROME	Obp99b	17 kDa	3.03E+07	1.34E+08	1.26E+07	9.89E+07	2.06E+07	1.00E+08
Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Drosophila melanogaster GN=Gapdh1 PE=2 SV=2	G3P1_DROME	Gapdh1	35 kDa	2.62E+09	1.90E+09	4.52E+09	1.16E+09	5.10E+09	3.53E+08
CG9691, isoform B OS=Drosophila melanogaster GN=CG9691 PE=2 SV=1	Q9W306_DROME	CG9691	13 kDa	9.97E+07	4.60E+07	1.64E+08	2.67E+08	1.03E+08	2.77E+07
CG15293, isoform A OS=Drosophila melanogaster GN=CG15293 PE=4 SV=1	Q9V3Y7_DROME	CG15293	37 kDa	3.45E+08	1.15E+09	0	2.39E+08	1.92E+08	3.07E+08
CG16885 OS=Drosophila melanogaster GN=CG16885 PE=2 SV=1	Q8SZM2_DROME	CG16885	29 kDa	1.03E+08	1.94E+08	9.14E+07	6.33E+07	4.18E+07	4.56E+07
60 kDa heat shock protein homolog 2, mitochondrial OS=Drosophila melanogaster GN=Hsp60C PE=2 SV=2	CH60C_DROME	Hsp60C	62 kDa	0	3.69E+07	1.39E+08	1.09E+08	7.56E+07	1.10E+07
Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2	PEB3_DROME	PebIII	15 kDa	6.44E+07	1.88E+08	2.35E+08	1.48E+08	2.17E+08	4.49E+08
CG8036, isoform D OS=Drosophila melanogaster GN=CG8036 PE=4 SV=1	Q7KSU6_DROME (+1)	CG8036	63 kDa	7.85E+08	1.41E+08	1.96E+09	2.38E+08	1.55E+09	2.24E+08
CG31883 OS=Drosophila melanogaster GN=CG31883 PE=4 SV=1	Q9VLB4_DROME	CG31883	33 kDa	4.15E+08	4.32E+08	2.73E+08	0	1.40E+08	0
Immune-induced peptides OS=Drosophila melanogaster GN=IM10 PE=1 SV=2	IM10_DROME	IM10	29 kDa	0	8.42E+08	0	1.61E+08	0	3.17E+08
CG30197 OS=Drosophila melanogaster GN=CG30197 PE=2 SV=1	Q8MKJ5_DROME	CG30197	12 kDa	1.01E+08	2.96E+07	1.90E+08	1.28E+08	1.24E+08	4597800
LD11278p OS=Drosophila melanogaster GN=Prx2540-1 PE=2 SV=1	A1Z892_DROME (+1)	Prx2540-1	25 kDa	1.85E+08	3.70E+07	1.59E+08	2.90E+07	9.66E+07	0
RT02906p OS=Drosophila melanogaster GN=Sfp79B PE=2 SV=1	B4ZJA5_DROME	Sfp79B	4 kDa	3.71E+09	2.08E+09	5.36E+09	0	9.82E+09	0
Poly(U)-specific endoribonuclease homolog OS=Drosophila melanogaster GN=CG2145 PE=1 SV=1	ENDOU_DROME	CG2145	64 kDa	7.41E+08	1.48E+09	5.79E+08	5.41E+08	5.20E+08	7.14E+08
CG7054 OS=Drosophila melanogaster GN=CG7054 PE=1 SV=1	Q9VD02_DROME	CG7054	20 kDa	3.34E+08	7.94E+08	4.19E+08	5.53E+08	3.37E+08	5.11E+08
CG10576, isoform A OS=Drosophila melanogaster GN=CG10576 PE=4 SV=1	Q9VRP2_DROME	CG10576	43 kDa	1.22E+08	4.91E+08	6.76E+07	1.07E+08	2.10E+08	8.79E+07
60S acidic ribosomal protein P2 OS=Drosophila melanogaster GN=RpLP2 PE=1 SV=1	RLA2_DROME	RpLP2	12 kDa	1.96E+08	1.85E+08	1.07E+08	0	2.85E+07	2.86E+07
Deoxyuridine triphosphatase, isoform B OS=Drosophila melanogaster GN=dUTPase PE=2 SV=1	Q8IPB1_DROME (+1)	dUTPase	18 kDa	1.63E+08	8.92E+07	1.23E+08	1.22E+08	1.52E+08	5.56E+07
Total Precursor Intensity of Top 3 Peptides				**3.66E+11**	**4.01E+11**	**3.34E+11**	**2.96E+11**	**2.98E+11**	**2.97E+11**

Supplementary Figure 1

Uncropped scans of gel images for the dot blot assay

Extended Data Figure 7e



Extended Data Figure 7g