Gene	Protein functional domains	Functional group	1° screen Z-score	Re-Screen Z-score
Nrx-1	EGF/Laminin; Nrx-1, Concanavalin A-like lectins/glucanases; Nrx-1	Cell adhesion	4.94	**-2.28**
CR18748	Immunoglobulin; CG18748	Cell adhesion	-2.05	**-4.29**
CG31646	LACHESIN, Immunoglobulin C-2 type	Cell adhesion	2.74	**-2.27**
c(3)G	MYOSIN HEAVY CHAIN-RELATED (PTHR23160)	Cytoskeletal	-2.12	**-3.32**
fbp	Sugar phosphatases; fbp	Metabolism - carbohydrate	-2.49	**-3.50**
CG5432	Fructose-bisphosphate aldolase	Metabolism - carbohydrate	-3.24	**-3.34**
CG7304	Nucleotide-diphospho-sugar transferases; CG7304, Glycosyl transferase, family 2	Metabolism - carbohydrate	-2.36	**-2.34**
CG1893	Phospholipid Scrablase 1, 2	Metabolism - lipid	-2.23	**-14.07**
CG3961	Firefly luciferase-like; CG3961, AMP-dependent synthetase and ligase	Metabolism - lipid	-2.82	**-2.02**
CG30499	RIBULOSE-5-PHOSPHATE-3-EPIMERASE	Metabolism - others	-2.45	**-2.56**
CG32699	ACETYLTRANSFERASE-RELATED	Metabolism - others	-2.66	**-4.94**
Lrr47	Leucine rich repeat 47	Others	2.42	**-2.17**
kin17	Antigenic Determinant of RecA Protein Homolog	Others	-3.65	**-20.84**
CG32030	ARM repeat; CG5797, Formin Homology 2 Domain	Others	-2.67	**-3.97**
CG8773	Membrane alanyl dipeptidase, family M1	Protease	-2.58	**-3.82**
CG8329	Chymotrypsin serine protease family (S1)	Protease	-2.02	**-3.48**
Pros26.4	AAA ATPase superfamily, P-loop containing nucleotide triphosphate hydrolas	Proteasome	-3.66	**-13.69**
Prosbeta2	Multispecific proteases of the proteasome, Proteasome B-type subunit	Proteasome	-3.93	**-12.05**
Prosalpha7	Proteasome A-type subunit, Multispecific proteases of the proteasome	Proteasome	-2.89	**-15.46**
Tbp-1	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-4.01	**-9.53**
Rpt4	P-loop containing nucleotide triphosphate hydrolas,	Proteasome	-4.23	**-5.78**
Rpt3	P-loop containing nucleotide triphosphate hydrolas,	Proteasome	-4.76	**-29.02**
Rpt1	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-2.42	**-32.10**
Rpn6	Tetratricopeptide repeat (TPR); Rpn6	Proteasome	-4.10	**-39.53**
Rpn9		Proteasome	-2.39	**-5.91**
Rpn2	ARM repeat; Rpn2	Proteasome	-2.86	**-16.79**
Rpn12		Proteasome	-2.29	**-22.85**
Rpn11	Also called DmS13	Proteasome	-2.28	**-44.69**
Rpn1	ARM repeat; Rpn1	Proteasome	-2.17	**-18.95**
CG7546	Scythe/BAT3; Ubiquitin-like; CG7546	Proteasome	-3.00	**-2.92**
CG17735	HECT domain, ARM repeat; CG17735	Protein modification-Ubiquitin ligase	-4.99	**-2.34**
CG9475	P-loop containing nucleotide triphosphate hydrolas, AAA ATPase superfamily	Proteasome	-3.10	**-18.05**
CG6204	P-loop containing nucleotide triphosphate hydrolas	Proteasome	2.35	**-2.84**
CG10845	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-2.70	**-4.74**
CG30382, Prosalpha6	Proteasome A-type subunit, Multispecific proteases	Proteasome	-3.29	**-13.30**
Fkbp13	FKBP-like; EF-hand	Protein modification - folding	-2.05	**-3.54**
Pgant35A	Polypeptide N-acetyl-glycosyl transferase	Protein modification - glycosylation	-2.18	**-8.09**
Su(var)2-10	SUMO LIGASE	Protein modification - Sumoylation	-2.18	**-7.65**
CG10107	SUMO/Sentrin/Ubl1 specific protease, Cysteine proteinases; CG10107	Protein modification -	-2.91	**-5.12**

		Sumoylation		
Bruce	Ubiquitin conjugating enzyme; Inhibitor of apoptosis (IAP) repeat;	Protein modification - Ubiquitin conjugating enzyme	-2.93	**-16.57**
UbcD4	Ubiquitin-conjugating enzymes, Ubiquitin conjugating enzyme; UbcD4	Protein modification - Ubiquitin conjugating enzyme	-2.37	**-4.31**
skpB	POZ domain; skpB, Skp1-Skp2 dimerization domains; skpB	Protein modification - Ubiquitin conjugating enzyme	5.23	**-23.31**
CG11700	Ubiquitin-like; CG11700	Protein modification - Ubiquitin conjugating enzyme	-3.66	**-26.85**
CG11321	RING Finger Protein 31-Related	Protein modification - Ubiquitin conjugating enzyme	-2.12	**-5.92**
CG5604	HECT domain, Ankyrin repeat; CG5604,	Protein modification - Ubiquitin conjugating enzyme	-2.71	**-9.55**
eIF-5C	eIF4-gamma/eIF5/eIF2-epsilon	protein syntesis	-2.22	**-2.63**
eIF-3p66	Eukaryotic translation initiation factor	protein syntesis	-3.32	**-5.21**
eIF-2alpha	S1 RNA binding domain	protein syntesis	-2.08	**-26.85**
ctp	Dynein light chain type 1, Intra cellular protein trafficing	Protein transport	-3.95	**-6.98**
Nup154	Nuclear Pore complex	Protein transport	3.35	**-3.04**
Sec61alpha	SecY protein	Protein transport	-2.55	**-3.98**
Rtnl1	RETICULON-RELATE	Protein transport	-2.02	**-2.98**
CG33214	SELECTIN LIGAND RELATED	Protein transport	-2.60	**-10.00**
CG10050, Pbprp4	Pbprp4: Insect pheromon/odorant-binding proteins; Pbprp4	Protein transport	-2.09	**-3.38**
ImpL3	NAD(P)-binding Rossmann-fold domains, L-lactate dehydrogenase,	Re-dox	-2.32	**-3.23**
phr	N-terminal domain of DNA photolyase; phr, FAD-binding (C-terminal)	Re-dox	-2.85	**-4.07**
ple	Biopterin-dependent aromatic amino acid hydroxylase, monoxygenases,	Re-dox	-2.80	**-45.49**
CG7277	Aromatic-ring hydroxylase (flavoprotein monooxygena, UbiH/COQ6 monooxygenase family, FAD/NAD(P)-binding domain;	Re-dox	-3.73	**-16.57**
CG6012	Glucose/ribitol dehydrogenase, NAD(P)-binding Rossmann-fold domains	Re-dox	-2.01	**-8.10**
Cyp49a1	Cytochrome P450 enzyme, E-class P450 group IV,	Re-dox	-2.39	**-5.06**
CG8888	Short-chain dehydrogenase/reductase (SDR) superfami, NAD(P)-binding Rossmann-fold domains	Re-dox	-2.37	**-7.58**
CG11208	DHS-like NAD/FAD-binding domain; Thiamin diphosphate-binding fold (THDP-binding)	Re-dox	-2.56	**-4.44**
Txl	Thioredoxin, Thioredoxin-like; Txl	Re-dox	-3.11	**-37.50**
CG3301	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; NAD(P)-binding Rossmann-fold domain	Re-dox	-2.55	**-7.88**
CG11790	Thioredoxin-like; CG11790, Thioredoxin	Re-dox	-2.72	**-5.25**
CG30427	NAD(P)-binding Rossmann-fold domains; CG2858	Re-dox	-2.20	**-6.38**
GstE7	Thioredoxin-like; CG17531, Glutathione S-transferases, C-terminal domain; CG1	Re-dox	-2.29	**-11.88**
CG10803		RNA binding	-2.20	**-2.84**
CG9107	RNA-binding domain, RBD; CG9107	RNA binding	-2.52	**-5.36**
Dcr-2	Dicer; Endodeoxyribonuclease	RNA processing	-2.60	**-8.14**
CG3808	RNA methyl transferase	RNA processing	-2.45	**-2.29**
AGO2		RNA processing	-2.68	**-12.76**

CG32533	ATP- dependent RNA helicase	RNA processing	-2.50	**-3.99**
neuroligin	Esterase/lipase/thioesterase, neuroligin	Signal transduction	-2.15	**-20.15**
Ac13E	Adenylyl and guanylyl cyclase catalytic domain; Ac, Guanylate cyclase	Signal transduction	-2.45	**-3.45**
CBP	sarcoplasmic calcium-binding protein;CBP	Signal transduction	-2.11	**-3.28**
PGRP-SA	Bacteriophage T7 lysozyme (Zn amidase); PGRP-SA	Signal transduction	2.25	**-8.95**
CG7227	Scavenger Receptor Class B Type-1 (SR-B1)	Signal transduction	2.65	**-7.45**
Or30a	G-protein coupled receptor	Signal transduction	-2.55	**-10.26**
CG10481	G-protein coupled receptor; XPR1	Signal transduction	-2.12	**-3.83**
CG8834	AMP-dependent synthetase and ligase, Firefly luciferase-like; CG8834	Signal transduction	-2.42	**-3.43**
CG7365	Phospholipase B	Signal transduction	-2.31	**-7.35**
PGRP-LB	Bacteriophage T7 lysozyme (Zn amidase); PGRP-LB	Signal transduction	-3.57	**-2.52**
CG4115	C-type lectin-like; CG4115	Signal transduction	-3.21	**-2.18**
CG7702	Leu-rich Transmembrane Protein	Signal transduction	-2.20	**-7.11**
CG7000	Scavenger Receptor Class B Type-1 (SR-B1)	Signal transduction	2.55	**-3.19**
lectin-46Ca	Galactose-Specific C-Type Lectin	Signal transduction	-2.54	**-2.79**
CG32912	Peptidoglycan-recognition protein-LD isoform 2	Signal transduction	-2.23	**-3.06**
vap	RAS GTPase activating protein	Signal transduction - GAP	-2.35	**-22.35**
CCKLR-17 D3	Neuropeptide Y receptor, Rhodopsin-like GPCR superfamily	Signal transduction - GPCR	-2.85	**-3.04**
Nipped-A	Phosphatidylinositol 3- and 4-kinase, Protein kinase-like (PK-like);	Signal transduction - kinase	-3.40	**-8.82**
htl	Fibroblast Growth Factor Receptor, Tyrosine protein kinase	Signal transduction - kinase	-2.03	**-2.80**
Strn-Mlck	Serine/Threonine protein kinase family, Tyrosine kinase catalytic domain	Signal transduction - kinase	-2.80	**-12.24**
Tak1	TGFβ activated kinase; Serine/Threonine protein kinase family	Signal transduction - kinase	2.94	**-8.70**
Mbs	Protein Phosphatase 1 Regulatory subunit 12B	Signal transduction - phosphatase	3.11	**-10.39**
ssh	Dual specificity protein phosphatase, (Phosphotyrosine protein) phosphatases II	Signal transduction - phosphatase	4.24	**-10.31**
CG7556	Phosphotyrosine protein) phosphatases II; CG7556	Signal transduction - phosphatase	2.70	**-22.42**
cnc	bZIP (Basic-leucine zipper) transcription factor fa, Binding domain of Skn-1; cnc	Transcription factor	-4.13	**-5.23**
Jra	cAMP response element binding (CREB) protein, bZIP (Basic-leucine zipper) transcription factor fa, Jun transcription factor, Binding domain of Skn-1; Jra	Transcription factor	-2.58	**-4.21**
kay	Fos transforming protein, bZIP (Basic-leucine zipper) transcription factor fa, Binding domain of Skn-1; kay	Transcription factor	3.95	**-2.40**
pnr	GATA-type zinc finger domain, Zinc-finger GCS-type	Transcription factor	-2.54	**-3.68**
tup	Insulin Gene Enhancer Protein, Homeobox domain	Transcription factor	-2.32	**-4.92**
ush	Friend of GATA2-Related, Zinc finger, C2H2 type,	Transcription factor	-3.43	**-8.81**
yemalpha	Nucleic acid binding	Transcription factor	-2.47	**-11.07**
wdn	C2H2 and C2HC zinc fingers	Transcription factor	-2.42	**-2.85**
CG6769	Zinc finger, C2H2 type, U1-like zinc finger	Transcription factor	-2.03	**-71.41**
CG3119	Homeobox transcription factor, N-Acetylgalactoseamine-Alpha-R-beta 1,3-Galactosyltransferase	Transcription factor	-2.02	**-7.47**
CG4621	YL-1 PROTEIN (TRANSCRIPTION FACTOR-LIKE 1)	Transcription factor	-2.78	**-20.60**
CG8079	SMAD/FHA domain; CG8079, D111/G-patch domain	Transcription factor	-2.01	**-18.96**
CG10494	Myb DNA binding domain	Transcription factor	-3.60	**-2.97**
CG6272	bZIP transcription factor	Transcription factor	-2.21	**-3.89**
CG14712	Zinc finger, C2H2 type	Transcription factor	2.61	**-13.75**
CG5641	Interleukin Enhancer Binding Factor 2	Transcription factor	-2.54	**-4.53**

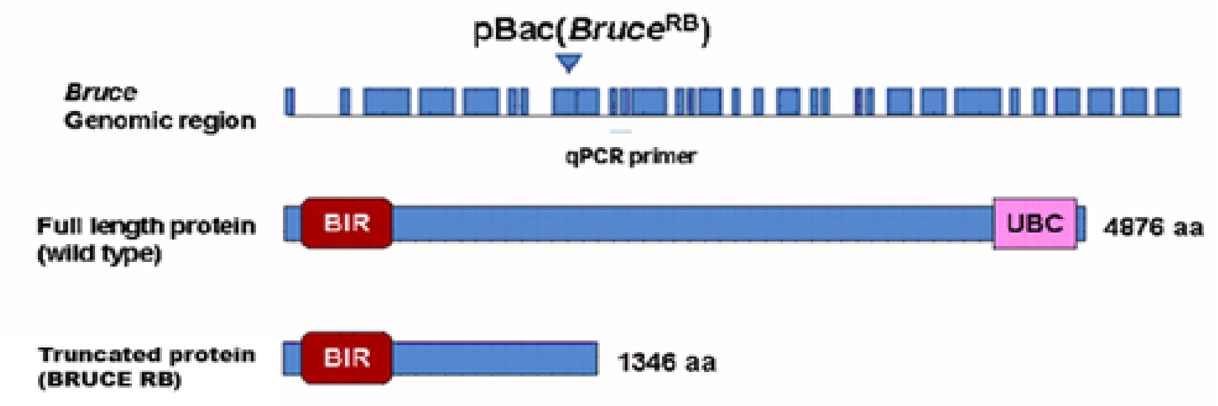
ppk23	Amiloride-sensitive sodium channel	Transport - ion	-2.95	**-2.18**
CG9887	Solute Carrier Family 17, (Glu Transporter 2, 3)	Transport - ion	-2.05	**-2.56**
CG9324	Voltage-Gated K Channel Beta Subunit 4.1-Related	Transport - ion	-3.48	**-18.22**
CG17274	Periplasmic binding protein-like II; Ionotropic glutamate receptor	Transport - ion	-2.01	**-6.98**
CG31722	Eukaryotic porin	Transport - ion	-2.09	**-6.51**
ppk11	Amiloride-sensitive sodium channel	Transport - ion	-2.34	**-6.50**
PebIII	Chemosensory Protein-Related	Transporter	-3.51	**-8.72**
ScpX	Sterol carrier protein 2 (SCP2); ScpX, Thiolase-like; ScpX	Transporter	-2.39	**-5.09**
CG5002	Sulfate transporter	Transporter	-2.05	**-3.00**
CG9444	PTR peptide transporters (PTR2)	Transporter	-3.26	**-4.23**
swa	swallow;swa	Unknown	-2.80	**-3.47**
Eig71Ec		Unknown	-2.71	**-2.10**
slv	Nodulin MTN3-Related	Unknown	-2.03	**-4.21**
CG31705		Unknown	4.73	**-4.92**
CG12636	Lipase/lipooxygenase domain; BG:DS07721.6	Unknown	-2.07	**-12.63**
CG2233		Unknown	-2.01	**-3.06**
CG15321		Unknown	2.62	**-6.30**
CG15043		Unknown	2.33	**-2.25**
CG33253		Unknown	2.04	**-2.11**
CG11943		Unknown	2.02	**-6.45**
CG3625	Androgen Induced Protein-Related	Unknown	-4.21	**-12.48**
CG8813		Unknown	-2.90	**-4.12**
CG7382		Unknown	-2.44	**-6.11**
CG9207		Unknown	3.22	**-11.23**
CG3818		Unknown	-2.36	**-17.62**
CG17105		Unknown	-3.04	**-7.00**
CG16850		Unknown	-2.15	**-3.07**
CG10176		Unknown	-2.10	**-11.80**
CG15161		Unknown	-3.72	**-18.70**
CG13964		Unknown	-8.79	**-4.82**
CG8237		Unknown	2.21	**-4.95**
CG13228		Unknown	-3.89	**-6.44**
CG13321		Unknown	-2.29	**-4.06**
CG13324		Unknown	-2.73	**-22.50**
CG5773		Unknown	-2.02	**-3.58**
CG10625		Unknown	-2.14	**-3.32**
CG10063		Unknown	2.78	**-23.88**
CG8616		Unknown	-2.14	**-3.42**
CG13738		Unknown	2.82	**-3.12**
CG13444		Unknown	-2.22	**-4.73**
CG7484		Unknown	-2.13	**-5.20**
CG14608	Tachycitin; Chitin binding domain	Unknown	-2.31	**-2.52**
CG11694		Unknown	3.33	**-5.91**
CG6791	C2H2 and C2HC zinc fingers; CG6791, Zinc finger, C2H2 type	Unknown	-3.11	**-3.24**
CG5866		Unknown	-2.46	**-4.46**
CG5451	WD-repeat protein	Unknown	-2.18	**-3.16**
CG15684		Unknown	-2.52	**-2.43**
CG17298		Unknown	-2.04	**-3.09**

CG10011	Ankyrin repeat; CG10011	Unknown	-2.66	**-8.59**
CG11877		Unknown	-2.68	**-3.64**
CG17169		Unknown	-3.69	**-2.15**
CG33254		Unknown	-2.48	**-2.06**
CG12617		Unknown	2.65	**-3.03**
CG18870		Unknown	-2.13	**-11.01**
CG30053		Unknown	4.08	**-6.61**
CG31869		Unknown	-2.90	**-8.23**
CG32462		Unknown	-2.52	**-3.77**
Sgs1	Salivary gland secretion 1;Sgs1	Unknown	2.68	**-5.62**
endos		Unknown	-2.11	**-5.76**

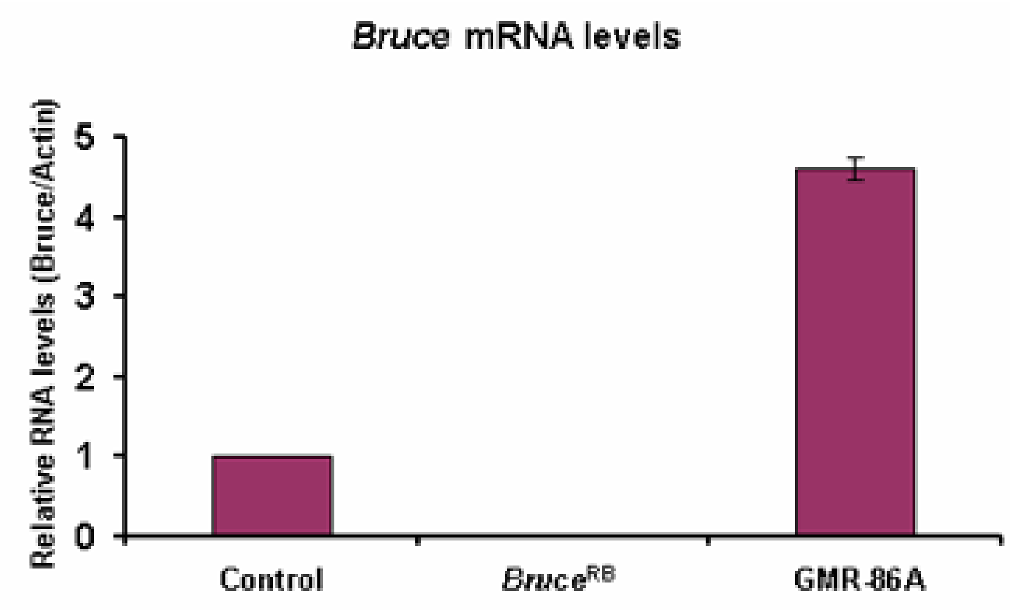
Table S1: Functional classification of genes that regulate light dependent Cry degradation. The genes that inhibit Cry-Luc degradation in S2 cells were re-confirmed by the secondary screen were annotated and classified into distinct functional groups by using flybase and GO annotation tools.

Suppplemental Fig S1: (**A**) Schematic diagram showing the *Bruce* genomic region: Exons and introns are indicated along with the piggyBac insertion in exon 8. The probe used for quantitative RT-PCR (RT-qPCR) is indicated. The full length Bruce protein containing the N-terminal BIR or inhibitor of apoptosis repeat and the C-terminal UBC domain are shown. The piggyBac insertion resulting in premature transcription termination is predicted to produce a truncated protein of 1346 amino acids lacking the critical UBC domain. (**B**) *Bruce* mRNA levels are significantly reduced in *Bruce*$^{\mathrm{RB}}$ mutants. RT-qPCR of *Bruce* mRNA in control flies, *Bruce*$^{\mathrm{RB}}$ mutants and a line over-expressing *Bruce* in the eye. These data were averaged from 2 independent experiments.

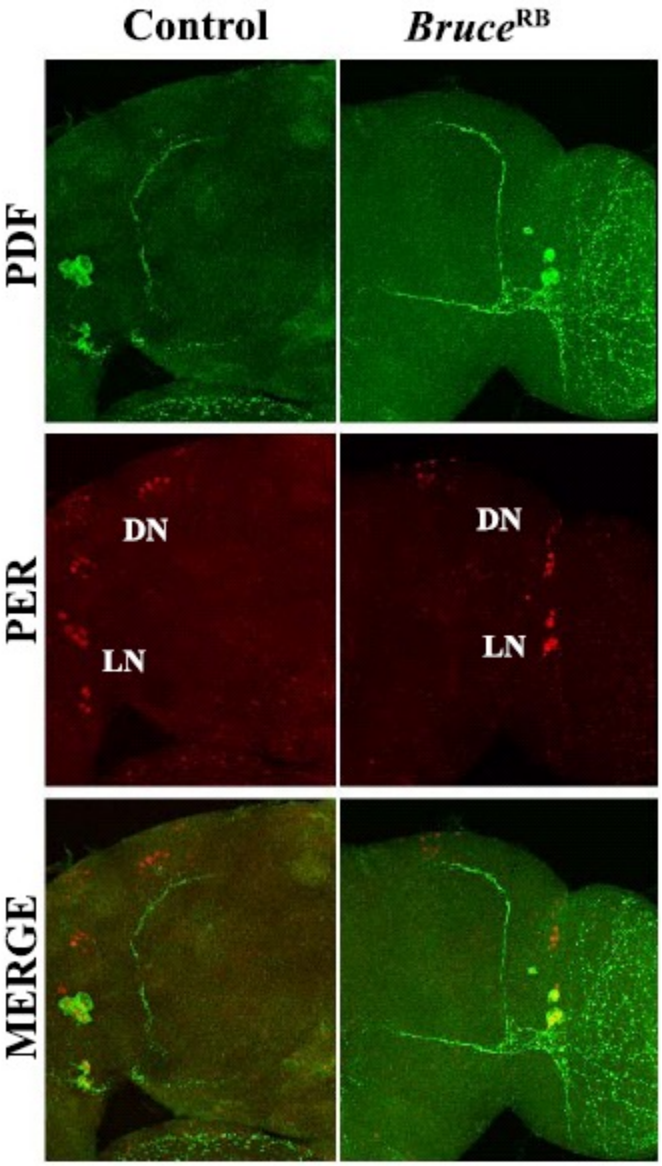
A



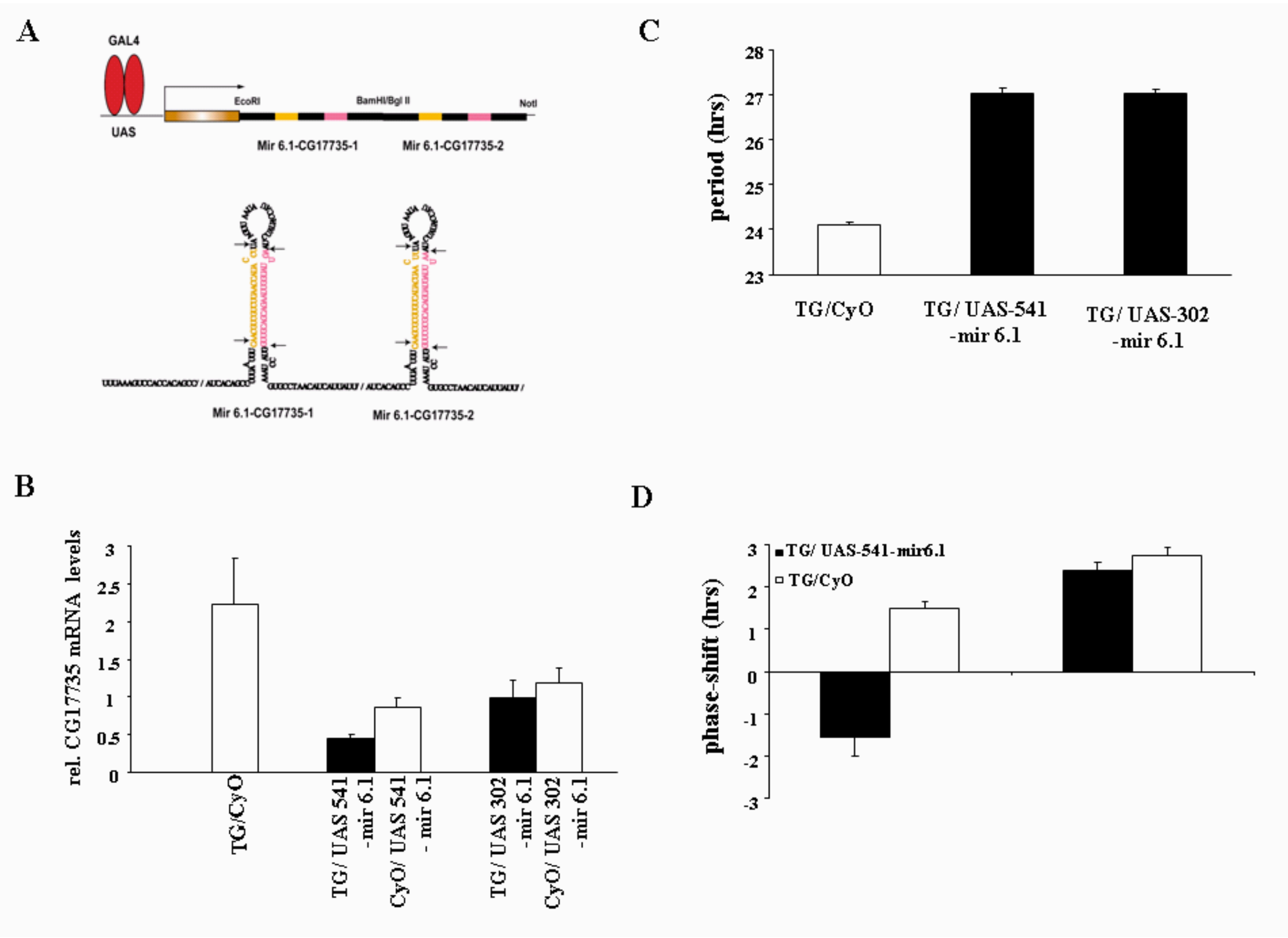
B



Supplemental Fig S2: Morphology of clock cells and clock gene expression in *Bruce*^{RB} mutants: Adult fly brains showing that PDF neurons and projections are unaffected in *Bruce*^{RB} mutants. Both the dorso-lateral and ventro-lateral neurons (LNs) and the dorsal neuron clusters (DNs) are unaffected as examined by PER staining at ZT2. 6 fly heads were examined for each genotype.

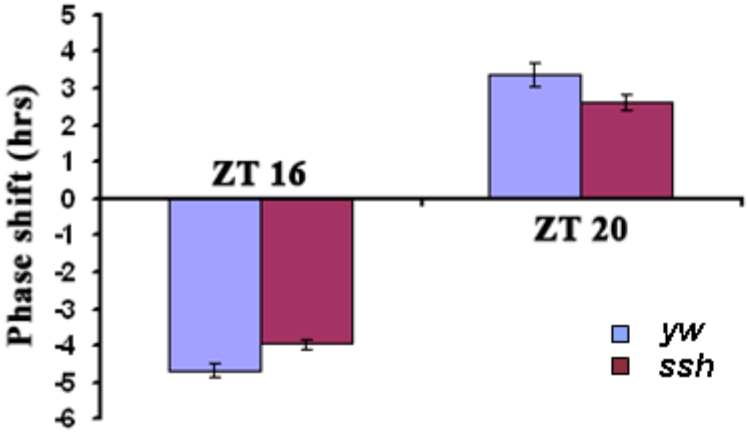


Supplemental Fig S3: (A) Schematic representation of the mir 6.1-CG17735-hybrid construct. The two mir6.1 based CG17735 haripins are indicated. The GAL4 expressed from the circadian clock promoter *tim* is also represented. **(B)** Real time qPCR quantification of CG17735 mRNA levels in the heads of flies expressing mir 6.1-CG17735. The CG17735 mRNA levels are significantly lower ($p<0.001$) in the fly heads expressing mir 6.1-CG17735 than the sibling (UAS-mir 6.1-CG17735/CyO) and parental controls (TG/CyO). **(C)** Free-running period of TG/UAS mir 6.1-CG17735 and TG/CyO. The circadian period of both TG/UAS mir6.1-CG17735 flies (line 541, n=31 and line 302, n=26) are significantly greater (**$p<0.001$) compared to the control lines (TG/CyO) (n=56). **(D)** Light induced phase shifts are almost similar in TG/UAS mir 6.1-CG17735 flies compared to the parental controls (TG/CyO). Control or mir 6.1-CG17735 expressing flies were given a short light pulse (~2500 lux for 2 min) at ZT20 and ZT22 on the last day of light:dark cycle (LD). The phase delay (negative values) and advances are plotted. Error bars represent standard error of the mean. Genotypes of flies used in each data set are indicated. The TG/UAS mir 6.1-CG17735 flies (line 541, n=24) as compared to the controls (n=24) showed significantly (**$p < 0.001$, by t- test) reduced phase shifts at ZT20, however at ZT22 the phase-shifts obtained for both genotypes are comparable.



Supplemental Fig S3

Supplemental Fig S4: Behavioral phase shifts in *ssh* mutant flies. The behavioral phase advance at late night (ZT 20) in *ssh* hypomophic mutant (*ssh*$^{1\text{-}6}$/*ssh*^{51}) flies was marginally decreased when compared to the control (*y w*) flies, however this difference was not statistically significant (n=14 & 15 respectively). At early night time point (ZT 16) there was also a marginal decrease in the phase delay (P=0.005) (n=16 & 14 respectively).



Gene	Protein functional domains	Functional group	1° screen Z-score	Re-Screen Z-score
Nrx-1	EGF/Laminin; Nrx-1, Concanavalin A-like lectins/glucanases; Nrx-1	Cell adhesion	4.94	**-2.28**
CR18748	Immunoglobulin; CG18748	Cell adhesion	-2.05	**-4.29**
CG31646	LACHESIN, Immunoglobulin C-2 type	Cell adhesion	2.74	**-2.27**
c(3)G	MYOSIN HEAVY CHAIN-RELATED (PTHR23160)	Cytoskeletal	-2.12	**-3.32**
fbp	Sugar phosphatases; fbp	Metabolism - carbohydrate	-2.49	**-3.50**
CG5432	Fructose-bisphosphate aldolase	Metabolism - carbohydrate	-3.24	**-3.34**
CG7304	Nucleotide-diphospho-sugar transferases; CG7304, Glycosyl transferase, family 2	Metabolism - carbohydrate	-2.36	**-2.34**
CG1893	Phospholipid Scrablase 1, 2	Metabolism - lipid	-2.23	**-14.07**
CG3961	Firefly luciferase-like; CG3961, AMP-dependent synthetase and ligase	Metabolism - lipid	-2.82	**-2.02**
CG30499	RIBULOSE-5-PHOSPHATE-3-EPIMERASE	Metabolism - others	-2.45	**-2.56**
CG32699	ACETYLTRANSFERASE-RELATED	Metabolism - others	-2.66	**-4.94**
Lrr47	Leucine rich repeat 47	Others	2.42	**-2.17**
kin17	Antigenic Determinant of RecA Protein Homolog	Others	-3.65	**-20.84**
CG32030	ARM repeat; CG5797, Formin Homology 2 Domain	Others	-2.67	**-3.97**
CG8773	Membrane alanyl dipeptidase, family M1	Protease	-2.58	**-3.82**
CG8329	Chymotrypsin serine protease family (S1)	Protease	-2.02	**-3.48**
Pros26.4	AAA ATPase superfamily, P-loop containing nucleotide triphosphate hydrolas	Proteasome	-3.66	**-13.69**
Prosbeta2	Multispecific proteases of the proteasome, Proteasome B-type subunit	Proteasome	-3.93	**-12.05**
Prosalpha7	Proteasome A-type subunit, Multispecific proteases of the proteasome	Proteasome	-2.89	**-15.46**
Tbp-1	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-4.01	**-9.53**
Rpt4	P-loop containing nucleotide triphosphate hydrolas,	Proteasome	-4.23	**-5.78**
Rpt3	P-loop containing nucleotide triphosphate hydrolas,	Proteasome	-4.76	**-29.02**
Rpt1	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-2.42	**-32.10**
Rpn6	Tetratricopeptide repeat (TPR); Rpn6	Proteasome	-4.10	**-39.53**
Rpn9		Proteasome	-2.39	**-5.91**
Rpn2	ARM repeat; Rpn2	Proteasome	-2.86	**-16.79**
Rpn12		Proteasome	-2.29	**-22.85**
Rpn11	Also called DmS13	Proteasome	-2.28	**-44.69**
Rpn1	ARM repeat; Rpn1	Proteasome	-2.17	**-18.95**
CG7546	Scythe/BAT3; Ubiquitin-like; CG7546	Proteasome	-3.00	**-2.92**
CG17735	HECT domain, ARM repeat; CG17735	Protein modification-Ubiquitin ligase	-4.99	**-2.34**
CG9475	P-loop containing nucleotide triphosphate hydrolas, AAA ATPase superfamily	Proteasome	-3.10	**-18.05**
CG6204	P-loop containing nucleotide triphosphate hydrolas	Proteasome	2.35	**-2.84**
CG10845	P-loop containing nucleotide triphosphate hydrolas	Proteasome	-2.70	**-4.74**
CG30382, Prosalpha6	Proteasome A-type subunit, Multispecific proteases	Proteasome	-3.29	**-13.30**
Fkbp13	FKBP-like; EF-hand	Protein modification - folding	-2.05	**-3.54**
Pgant35A	Polypeptide N-acetyl-glycosyl transferase	Protein modification - glycosylation	-2.18	**-8.09**
Su(var)2-10	SUMO LIGASE	Protein modification - Sumoylation	-2.18	**-7.65**
CG10107	SUMO/Sentrin/Ubl1 specific protease, Cysteine proteinases; CG10107	Protein modification - Sumoylation	-2.91	**-5.12**
Bruce	Ubiquitin conjugating enzyme; Inhibitor of apoptosis (IAP) repeat;	Protein modification -	-2.93	**-16.57**

		Ubiquitin conjugating enzyme		
UbcD4	Ubiquitin-conjugating enzymes, Ubiquitin conjugating enzyme; UbcD4	Protein modification - Ubiquitin conjugating enzyme	-2.37	**-4.31**
skpB	POZ domain; skpB, Skp1-Skp2 dimerization domains; skpB	Protein modification - Ubiquitin conjugating enzyme	5.23	**-23.31**
CG11700	Ubiquitin-like; CG11700	Protein modification - Ubiquitin conjugating enzyme	-3.66	**-26.85**
CG11321	RING Finger Protein 31-Related	Protein modification - Ubiquitin conjugating enzyme	-2.12	**-5.92**
CG5604	HECT domain, Ankyrin repeat; CG5604,	Protein modification - Ubiquitin conjugating enzyme	-2.71	**-9.55**
eIF-5C	eIF4-gamma/eIF5/eIF2-epsilon	protein syntesis	-2.22	**-2.63**
eIF-3p66	Eukaryotic translation initiation factor	protein syntesis	-3.32	**-5.21**
eIF-2alpha	S1 RNA binding domain	protein syntesis	-2.08	**-26.85**
ctp	Dynein light chain type 1, Intra cellular protein trafficing	Protein transport	-3.95	**-6.98**
Nup154	Nuclear Pore complex	Protein transport	3.35	**-3.04**
Sec61alpha	SecY protein	Protein transport	-2.55	**-3.98**
Rtnl1	RETICULON-RELATE	Protein transport	-2.02	**-2.98**
CG33214	SELECTIN LIGAND RELATED	Protein transport	-2.60	**-10.00**
CG10050, Pbprp4	Pbprp4: Insect pheromon/odorant-binding proteins; Pbprp4	Protein transport	-2.09	**-3.38**
ImpL3	NAD(P)-binding Rossmann-fold domains, L-lactate dehydrogenase,	Re-dox	-2.32	**-3.23**
phr	N-terminal domain of DNA photolyase; phr, FAD-binding (C-terminal)	Re-dox	-2.85	**-4.07**
ple	Biopterin-dependent aromatic amino acid hydroxylase, monoxygenases,	Re-dox	-2.80	**-45.49**
CG7277	Aromatic-ring hydroxylase (flavoprotein monooxygena, UbiH/COQ6 monooxygenase family, FAD/NAD(P)-binding domain;	Re-dox	-3.73	**-16.57**
CG6012	Glucose/ribitol dehydrogenase, NAD(P)-binding Rossmann-fold domains	Re-dox	-2.01	**-8.10**
Cyp49a1	Cytochrome P450 enzyme, E-class P450 group IV,	Re-dox	-2.39	**-5.06**
CG8888	Short-chain dehydrogenase/reductase (SDR) superfami, NAD(P)-binding Rossmann-fold domains	Re-dox	-2.37	**-7.58**
CG11208	DHS-like NAD/FAD-binding domain; Thiamin diphosphate-binding fold (THDP-binding)	Re-dox	-2.56	**-4.44**
Txl	Thioredoxin, Thioredoxin-like; Txl	Re-dox	-3.11	**-37.50**
CG3301	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; NAD(P)-binding Rossmann-fold domain	Re-dox	-2.55	**-7.88**
CG11790	Thioredoxin-like; CG11790, Thioredoxin	Re-dox	-2.72	**-5.25**
CG30427	NAD(P)-binding Rossmann-fold domains; CG2858	Re-dox	-2.20	**-6.38**
GstE7	Thioredoxin-like; CG17531, Glutathione S-transferases, C-terminal domain; CG1	Re-dox	-2.29	**-11.88**
CG10803		RNA binding	-2.20	**-2.84**
CG9107	RNA-binding domain, RBD; CG9107	RNA binding	-2.52	**-5.36**
Dcr-2	Dicer; Endodeoxyribonuclease	RNA processing	-2.60	**-8.14**
CG3808	RNA methyl transferase	RNA processing	-2.45	**-2.29**
AGO2		RNA processing	-2.68	**-12.76**
CG32533	ATP- dependent RNA helicase	RNA processing	-2.50	**-3.99**
neuroligin	Esterase/lipase/thioesterase, neuroligin	Signal transduction	-2.15	**-20.15**

Ac13E	Adenylyl and guanylyl cyclase catalytic domain; Ac, Guanylate cyclase	Signal transduction	-2.45	**-3.45**
CBP	sarcoplasmic calcium-binding protein;CBP	Signal transduction	-2.11	**-3.28**
PGRP-SA	Bacteriophage T7 lysozyme (Zn amidase); PGRP-SA	Signal transduction	2.25	**-8.95**
CG7227	Scavenger Receptor Class B Type-1 (SR-B1)	Signal transduction	2.65	**-7.45**
Or30a	G-protein coupled receptor	Signal transduction	-2.55	**-10.26**
CG10481	G-protein coupled receptor; XPR1	Signal transduction	-2.12	**-3.83**
CG8834	AMP-dependent synthetase and ligase, Firefly luciferase-like; CG8834	Signal transduction	-2.42	**-3.43**
CG7365	Phospholipase B	Signal transduction	-2.31	**-7.35**
PGRP-LB	Bacteriophage T7 lysozyme (Zn amidase); PGRP-LB	Signal transduction	-3.57	**-2.52**
CG4115	C-type lectin-like; CG4115	Signal transduction	-3.21	**-2.18**
CG7702	Leu-rich Transmembrane Protein	Signal transduction	-2.20	**-7.11**
CG7000	Scavenger Receptor Class B Type-1 (SR-B1)	Signal transduction	2.55	**-3.19**
lectin-46Ca	Galactose-Specific C-Type Lectin	Signal transduction	-2.54	**-2.79**
CG32912	Peptidoglycan-recognition protein-LD isoform 2	Signal transduction	-2.23	**-3.06**
vap	RAS GTPase activating protein	Signal transduction - GAP	-2.35	**-22.35**
CCKLR-17D3	Neuropeptide Y receptor, Rhodopsin-like GPCR superfamily	Signal transduction - GPCR	-2.85	**-3.04**
Nipped-A	Phosphatidylinositol 3- and 4-kinase, Protein kinase-like (PK-like);	Signal transduction - kinase	-3.40	**-8.82**
htl	Fibroblast Growth Factor Receptor, Tyrosine protein kinase	Signal transduction - kinase	-2.03	**-2.80**
Strn-Mlck	Serine/Threonine protein kinase family, Tyrosine kinase catalytic domain	Signal transduction - kinase	-2.80	**-12.24**
Tak1	TGFβ activated kinase; Serine/Threonine protein kinase family	Signal transduction - kinase	2.94	**-8.70**
Mbs	Protein Phosphatase 1 Regulatory subunit 12B	Signal transduction - phosphatase	3.11	**-10.39**
ssh	Dual specificity protein phosphatase, (Phosphotyrosine protein) phosphatases II	Signal transduction - phosphatase	4.24	**-10.31**
CG7556	Phosphotyrosine protein) phosphatases II; CG7556	Signal transduction - phosphatase	2.70	**-22.42**
cnc	bZIP (Basic-leucine zipper) transcription factor fa, Binding domain of Skn-1; cnc	Transcription factor	-4.13	**-5.23**
Jra	cAMP response element binding (CREB) protein, bZIP (Basic-leucine zipper) transcription factor fa, Jun transcription factor, Binding domain of Skn-1; Jra	Transcription factor	-2.58	**-4.21**
kay	Fos transforming protein, bZIP (Basic-leucine zipper) transcription factor fa, Binding domain of Skn-1; kay	Transcription factor	3.95	**-2.40**
pnr	GATA-type zinc finger domain, Zinc-finger GCS-type	Transcription factor	-2.54	**-3.68**
tup	Insulin Gene Enhancer Protein, Homeobox domain	Transcription factor	-2.32	**-4.92**
ush	Friend of GATA2-Related, Zinc finger, C2H2 type,	Transcription factor	-3.43	**-8.81**
yemalpha	Nucleic acid binding	Transcription factor	-2.47	**-11.07**
wdn	C2H2 and C2HC zinc fingers	Transcription factor	-2.42	**-2.85**
CG6769	Zinc finger, C2H2 type, U1-like zinc finger	Transcription factor	-2.03	**-71.41**
CG3119	Homeobox transcription factor, N-Acetylgalactoseamine-Alpha-R-beta 1,3- Galactosyltransferase	Transcription factor	-2.02	**-7.47**
CG4621	YL-1 PROTEIN (TRANSCRIPTION FACTOR-LIKE 1)	Transcription factor	-2.78	**-20.60**
CG8079	SMAD/FHA domain; CG8079, D111/G-patch domain	Transcription factor	-2.01	**-18.96**
CG10494	Myb DNA binding domain	Transcription factor	-3.60	**-2.97**
CG6272	bZIP transcription factor	Transcription factor	-2.21	**-3.89**
CG14712	Zinc finger, C2H2 type	Transcription factor	2.61	**-13.75**
CG5641	Interleukin Enhancer Binding Factor 2	Transcription factor	-2.54	**-4.53**
ppk23	Amiloride-sensitive sodium channel	Transport - ion	-2.95	**-2.18**
CG9887	Solute Carrier Family 17, (Glu Transporter 2, 3)	Transport - ion	-2.05	**-2.56**
CG9324	Voltage-Gated K Channel Beta Subunit 4.1-Related	Transport - ion	-3.48	**-18.22**

CG17274	Periplasmic binding protein-like II; Ionotropic glutamate receptor	Transport - ion	-2.01	**-6.98**
CG31722	Eukaryotic porin	Transport - ion	-2.09	**-6.51**
ppk11	Amiloride-sensitive sodium channel	Transport - ion	-2.34	**-6.50**
PebIII	Chemosensory Protein-Related	Transporter	-3.51	**-8.72**
ScpX	Sterol carrier protein 2 (SCP2); ScpX, Thiolase-like; ScpX	Transporter	-2.39	**-5.09**
CG5002	Sulfate transporter	Transporter	-2.05	**-3.00**
CG9444	PTR peptide transporters (PTR2)	Transporter	-3.26	**-4.23**
swa	swallow;swa	Unknown	-2.80	**-3.47**
Eig71Ec		Unknown	-2.71	**-2.10**
slv	Nodulin MTN3-Related	Unknown	-2.03	**-4.21**
CG31705		Unknown	4.73	**-4.92**
CG12636	Lipase/lipooxygenase domain; BG:DS07721.6	Unknown	-2.07	**-12.63**
CG2233		Unknown	-2.01	**-3.06**
CG15321		Unknown	2.62	**-6.30**
CG15043		Unknown	2.33	**-2.25**
CG33253		Unknown	2.04	**-2.11**
CG11943		Unknown	2.02	**-6.45**
CG3625	Androgen Induced Protein-Related	Unknown	-4.21	**-12.48**
CG8813		Unknown	-2.90	**-4.12**
CG7382		Unknown	-2.44	**-6.11**
CG9207		Unknown	3.22	**-11.23**
CG3818		Unknown	-2.36	**-17.62**
CG17105		Unknown	-3.04	**-7.00**
CG16850		Unknown	-2.15	**-3.07**
CG10176		Unknown	-2.10	**-11.80**
CG15161		Unknown	-3.72	**-18.70**
CG13964		Unknown	-8.79	**-4.82**
CG8237		Unknown	2.21	**-4.95**
CG13228		Unknown	-3.89	**-6.44**
CG13321		Unknown	-2.29	**-4.06**
CG13324		Unknown	-2.73	**-22.50**
CG5773		Unknown	-2.02	**-3.58**
CG10625		Unknown	-2.14	**-3.32**
CG10063		Unknown	2.78	**-23.88**
CG8616		Unknown	-2.14	**-3.42**
CG13738		Unknown	2.82	**-3.12**
CG13444		Unknown	-2.22	**-4.73**
CG7484		Unknown	-2.13	**-5.20**
CG14608	Tachycitin; Chitin binding domain	Unknown	-2.31	**-2.52**
CG11694		Unknown	3.33	**-5.91**
CG6791	C2H2 and C2HC zinc fingers; CG6791, Zinc finger, C2H2 type	Unknown	-3.11	**-3.24**
CG5866		Unknown	-2.46	**-4.46**
CG5451	WD-repeat protein	Unknown	-2.18	**-3.16**
CG15684		Unknown	-2.52	**-2.43**
CG17298		Unknown	-2.04	**-3.09**
CG10011	Ankyrin repeat; CG10011	Unknown	-2.66	**-8.59**
CG11877		Unknown	-2.68	**-3.64**
CG17169		Unknown	-3.69	**-2.15**
CG33254		Unknown	-2.48	**-2.06**

CG12617		Unknown	2.65	**-3.03**
CG18870		Unknown	-2.13	**-11.01**
CG30053		Unknown	4.08	**-6.61**
CG31869		Unknown	-2.90	**-8.23**
CG32462		Unknown	-2.52	**-3.77**
Sgs1	Salivary gland secretion 1;Sgs1	Unknown	2.68	**-5.62**
endos		Unknown	-2.11	**-5.76**

Table S1: Functional classification of genes that regulate light dependent Cry degradation. The genes that inhibit Cry-Luc degradation in S2 cells were re-confirmed by the secondary screen were annotated and classified into distinct functional groups by using flybase and GO annotation tools.