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SUPPLEMENTARY MATERIAL

corresponding to:

**Characterization of the *Autophagy related gene-8a (Atg8a)*
promoter in *Drosophila melanogaster***

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SUPPL. TABLE S1

2kb <i>atg8a</i> F	agcggccgcAACTAAACGGGCACCTTG
1.8kb <i>atg8a</i> F	agcggccgcGAGCGGCAGTGGTAGTCG
1.6kb <i>atga</i> F	agcggccgcCGTTCTCCATGTCATAGGTGGT
1.4kb <i>atga</i> F	agcggccgcACCACCTGCAGCAGATGC
1.2kb <i>atga</i> F	agcggccgcACCAATTGGTTGAACTTACCTTG
1.0kb <i>atga</i> F	agcggccgcCCTGAAACCATACTGATTGGC
0.8kb <i>atga</i> F	agcggccgcGCGAGTATGACGCGGTG
0.6kb <i>atga</i> F	agcggccgcCTTTTTGTTTTCTCCGTGCG
0.4kb <i>atga</i> F	agcggccgcTACCATTTAACGCGTACAACAAC
0.2kb <i>atga</i> F	agcggccgcCGAGTGCAGTACCACAGTG
qAtg2 FW	AAGTGGAAGCAGGAGATCCA
qAtg2 Rev	AATCACACCCATGTCGGAAT
qAtg3 FW	GCAATGTTCCCTGCTATCGT
qAtg3 Rev	TGTCGCTATCTGAGTGTGC
qAtg4a FW	CTTCTCCCTGCACTCGTTTC
qAtg4a Rev	CTCGGTTTGATGGGATGACT
qAtg4b FW	ACCTCGGATTCGGACTCTTT
qAtg4b Rev	CTCATTGGGTGCTCCACTTT
qAtg5 FW	GCACTACATGCCTGCCTGA
qAtg5 Rev	AGATTTCGAGGGGAATGTTT
qAtg6 FW	TTCCAGAAGGAGGTCGAGAA
qAtg6 Rev	TCCCCATTCAGGTTGGTTA
qAtg9 FW	AGCAGAAGCACGGATTCACA
qAtg9 Rev	GCAGTGCATCACAAGGCAA
qAtg12 FW	CAATGTGCCATCATCAAAA
qAtg12 Rev	CACGCCTGATTCTTGCACTA
qAtg18 FW	AGGTGACCGACGTGTTTAGC
qAtg101F	CGTTTCGACAGTTTTTGTATCTG
qAtg101R	CGACCGTGCCAATCGAGTAT
qAtg13F	GAACCTAAAGACAGGAGAGAGCA
qAtg13R	ACCCTCAGTCGTTTTCAGGGA

List of primers used in this study for cloning of *Atg8a* promoter fragments and for the qPCR of *Atgs* shown in Fig.1.

SUPPLEMENTARY TABLE S2

$\frac{yAtg8a^{KG07569(w+y+)}}{FM7c} ; \pm$ X $\frac{yw ; pCAtg8a(w+)}{Y pCAtg8a(w+)}$
 Virgin females + Males

F1 Genotypes

Transgenic lines	$\frac{yw}{FM7c} ; \frac{pCAtg8a}{+}$	$\frac{yAtg8a^{KG07569(w+y+)}}{FM7c} ; \frac{pCAtg8a(w+)}{+}$	$\frac{yAtg8a^{KG07569(w+y+)}}{Y} ; \frac{pCAtg8a(w+)}{+}$	$\frac{FM7c}{Y} ; \frac{pCAtg8a}{+}$
	Female (orange eyes, yellow body)	Female (red eyes, brown body)	Males (red eyes, brown body) rescue genotype	Males (white eyes, yellow body)
yw (control) n=56	19(33.92%)	27(48.21%)	0	10(17.85%)
0kb-pCAtg8a n=120	45(40.90%)	40(36.36%)	0	25(22.72%)
0.2kb-pCAtg8a n=109	34(30.9%)	30(27.27%)	25(22.72%)	21(19.09%)
0.4kb-pCAtg8a n=120	34(28.33%)	40(33.33%)	29(24.16%)	17(14.16%)
0.6kb-pCAtg8a n=136	39(28.67%)	36(26.47%)	35(25.73%)	26(19.11%)
0.8kb-pCAtg8a n=210	61(29.03%)	69(32.85%)	62(29.52%)	18(8.75%)
1.0kb-pCAtg8a n=133	37(29.12%)	41(32.28%)	34(26.77%)	21(16.53%)
1.2kb-pCAtg8a n=108	28(25.92%)	33(30.55%)	27(25%)	20(18.51%)
1.4kb-pCAtg8a n=147	45(30.60%)	41(27.89%)	38(25.85%)	23(15.64%)
1.6kb-pCAtg8a n=166	53(31.92%)	48(28.91%)	45(27.10%)	20(12.04%)
1.8kb-pCAtg8a n=121	39(32.22%)	31(25.61%)	28(23.14%)	23(19.03%)
2.0kb-pCAtg8a n=119	26(21.84%)	35(29.41%)	31(26.05%)	27(22.68%)

Table showing different genotypes obtained as F1 progeny in rescue experiments, and the total number of flies scored in each experiment. Percentages and sample size are shown in parentheses.