Table S1. **Comparison of essential autophagy genes in the *D. melanogaster* larval fat body and *l(2)mbn* cells**

Yeast gene	CG number	Flybase designation	Required for autophagy in larval fat body[a]	Required for autophagy in *l(2)mbn* cells
Atg1	*CG10967*	*DmAtg1*	Yes	Yes
Atg2	*CG1241*	*DmAtg2*	Yes	Yes
Atg3	*CG6687*	*DmAtg3*		Yes
Atg4	*CG6194*		No	Yes
	CG4428	*DmAtg4*		No
Atg5	*CG1643*	*DmAtg5*	Yes	Yes
Atg6	*CG5429*	*DmAtg6*	Variable	Yes
Atg7	*CG5489*	*DmAtg7*	Yes	Yes
Atg8	*CG32672*	*DmAtg8a*	No	Yes
	CG12334	*DmAtg8b*		Yes
Atg9	*CG3615*	*DmAtg9*		No
Atg12	*CG10861*	*DmAtg12*	Yes	Yes
Atg18	*CG7986*	*DmAtg18*	Yes	Yes
	CG8678		No	No

The fat body data were generated from a study by Scott R. et al. (Scott, R.C., O. Schuldiner, and T.P. Neufeld. 2004. *Dev. Cell.* 7:167–178) RNAi of 11 *DmAtg* genes showed a significant reduction in LTG high cells ($P < 0.05$), which indicates that these *DmAtg* genes are required for autophagy in *l(2)mbn* cells.

[a] Scott, R.C., O. Schuldiner, and T.P. Neufeld. 2004. Role and regulation of starvation-induced autophagy in the *Drosophila* fat body. *Dev. Cell.* 7:167–178.

Table S2. **Sequences of primers used for the preparation of dsRNAs**

Gene Name	Amplicon length	Forward primer sequence	Reverse primer sequence
Atg1 (CG10967)	701	TAATACGACTCACTATAGGTGCGGCTCTCCCATGTATATG	TAATACGACTCACTATAGGTGATTTTGTTGCTGCTGTGGAC
Atg2 (CG1241)	705	TAATACGACTCACTATAGGCCCATGATAGCCAAGCACAAT	TAATACGACTCACTATAGGCCGAGTAGCGAAGGTAACTTGC
Atg3 (CG6687)	713	TAATACGACTCACTATAGGATGTGGCCGAATATCTGACG	TAATACGACTCACTATAGGACATCTGTTCCACGGTCAGTG
CG6194	703	TAATACGACTCACTATAGGCTTTCCAAGTTGACCGACGA	TAATACGACTCACTATAGGACCACAATCTCATCGATCTGCT
Atg4 (CG4428)	714	TAATACGACTCACTATAGGACATTCCCCGAAGAAACACC	TAATACGACTCACTATAGGTGCGTGGTATGAGGATCTAGGT
Atg5 (CG1643)	633	TAATACGACTCACTATAGGAGCCGGAGCCTTTCTATCTGA	TAATACGACTCACTATAGGTCGGACATCCATTGCAGTTG
Atg6 (CG5428)	713	TAATACGACTCACTATAGGGCTGGAGAAGATTAGCGTGCA	TAATACGACTCACTATAGGTAATGGTACCGAAATGCCCG
Atg7 (CG5489)	724	TAATACGACTCACTATAGGCCATTGAAGTTTCTTGGCCTG	TAATACGACTCACTATAGGAAGCCTAAAGCTGCGTTGATG
Atg8 (CG32672)	351	TAATACGACTCACTATAGGTCCAATACAAGGAGGAGCACG	TAATACGACTCACTATAGGCATGCCGTAAACATTCTCATCG
CG12334	287	TAATACGACTCACTATAGGCCAGTACAAGAAGGACCACTCG	TAATACGACTCACTATAGGAAGTGCTCCTGGTACAGTGCA
Atg9 (CG3615)	703	TAATACGACTCACTATAGGACCTTGACTCGTTCTTCTCGC	TAATACGACTCACTATAGGCAGCTCCGTTTGATTGCTTC
Atg12 (CG10861)	265	TAATACGACTCACTATAGGTTTGTATCCTTCTGAACGCCAC	TAATACGACTCACTATAGGTCATGTGCGTATCGATTTAGCC
Atg18 (CG7986)	724	TAATACGACTCACTATAGGAGGACATGAAGGTGGTGCACA	TAATACGACTCACTATAGGCGTGCCTCTTTATTAGCTGGC
CG8678	707	TAATACGACTCACTATAGGCAAGGTGGAGGAGATATTCGC	TAATACGACTCACTATAGGCAGAATTTTCGGACTTGGCA
Pten	718	TAATACGACTCACTATAGGTTGGAAGAGAATCATGCCCAG	TAATACGACTCACTATAGGTGTTCCATCGGACTCGCAA
Tsc1	709	TAATACGACTCACTATAGGCCGATTTATCCCTTGTTGGTG	TAATACGACTCACTATAGGCCGATTTATCCCTTGTTGGTG
Tsc2	716	TAATACGACTCACTATAGGGTGAATGGATCGACGGTAGCT	TAATACGACTCACTATAGGCCTGATAATCGGTGTCGTGTTC
RheB	502	TAATACGACTCACTATAGGTGACCCCACCATTGAGAACA	TAATACGACTCACTATAGGTATTTCCAACAGTTCGGCCG
Tor	700	TAATACGACTCACTATAGGCAAGGATCAGAAAGGCGTGAC	TAATACGACTCACTATAGGAAGAAGCGTTATGCAGGCAA
S6k	713	TAATACGACTCACTATAGGACAGCTCTGCGAGGAGAATGT	TAATACGACTCACTATAGGCTCGATGGTCTTCTTGCGATT
rpr	227	TAATACGACTCACTATAGGTTCTACATACCCGATCAGGCG	TAATACGACTCACTATAGGTGGACTATTGGTTTTCCCCGT
hid	703	TAATACGACTCACTATAGGAAATCTTCCAGTATCCGCCG	TAATACGACTCACTATAGGTGGCAGACTGGATTATTGCTG
grim	387	TAATACGACTCACTATAGGTGGCCATCGCCTATTTCATAC	TAATACGACTCACTATAGGACGTCGTCCTCATCGTTGTTC
sickle	316	TAATACGACTCACTATAGGTGACGGAATACAAACTGGTCGT	TAATACGACTCACTATAGGCACCAGTGTGTAAAATGCATCG
Ras	486	TAATACGACTCACTATAGGGGCCATTCCATTTTTCGAAG	TAATACGACTCACTATAGGCCTGCGGTTGTATTTGAACG
phl	710	TAATACGACTCACTATAGGACCCGCGAGAATATTGATGC	TAATACGACTCACTATAGGATCGGCACTCTATTGGCACAC
rl	495	TAATACGACTCACTATAGGAGTTTGTCTCATTTCAGTATGTT	TAATACGACTCACTATAGGCTTGCATACCTTCCATTCCC
th	704	TAATACGACTCACTATAGGCCAAACCGGCATGTACTTCA	TAATACGACTCACTATAGGAGCTGACCCTTCATCAGCTTG
Bruce	723	TAATACGACTCACTATAGGTACACAGAACGTCCCGCTGT	TAATACGACTCACTATAGGCATCGGCGAACTTCTCGTATG
debcl	718	TAATACGACTCACTATAGGCAAGTTCAAGTCCTCGTCGCT	TAATACGACTCACTATAGGCGTTGTCGATCAGCCAGTAGAC
buffy	626	TAATACGACTCACTATAGGTGGAGATTACGTGGAGCAAGG	TAATACGACTCACTATAGGCTTTCTCGCCAATTGCGAAC
Ark	726	TAATACGACTCACTATAGGGTCCAGGATATGCCGAAATCA	TAATACGACTCACTATAGGAGTGACCTGCTTGAACCGTGT
p53	590	TAATACGACTCACTATAGGTCTCCAATGATGTGAGTGCTCC	TAATACGACTCACTATAGGTCTGCAGCAGCCATTCCTTA
Nc	514	TAATACGACTCACTATAGGATCGCGAGCATATACGCAAG	TAATACGACTCACTATAGGAATATGGCACTATCCCCACCA
Ice	714	TAATACGACTCACTATAGGAGTACAACATGCGCCACAAGA	TAATACGACTCACTATAGGGTCAGCATGGTGGTTATGCAG
Dcp-1	705	TAATACGACTCACTATAGGTGCGTAACCAGAAACTACGGAG	TAATACGACTCACTATAGGGGAATGGTCGAGTAGGAGAAG
Damm	695	TAATACGACTCACTATAGGATGTATCTGCCCGAAAGAACAG	TAATACGACTCACTATAGGCATAGTTGACCTTCGTTCGACC
Dredd	722	TAATACGACTCACTATAGGCAGCGAGTGCAATTTATCGG	TAATACGACTCACTATAGGCGGAGCGTTACTAATGATGGTG
dream	701	TAATACGACTCACTATAGGAGTTTGAACGGCGTCTCCTT	TAATACGACTCACTATAGGTTCCACTTTGCACTTCAGCTG
decay	704	TAATACGACTCACTATAGGCGAGGACACATACGAGAATTGC	TAATACGACTCACTATAGGATTCGACTGGTACTCGTAGGCC
Hs	708	TAATACGACTCACTATAGGATTGGAGACACCTTCAGACTCG	TAATACGACTCACTATAGGAGTCCTGTGCTATGTCCCTCCT
hid_2	601	TAATACGACTCACTATAGGCCGAGCAAAAACTTGACTTGAG	TAATACGACTCACTATAGGGGTACATCCTGACCCACTCGTA
Ras_2	565	TAATACGACTCACTATAGGCACGGCAATTAAATTGGTGC	TAATACGACTCACTATAGGCGCATATACTGATCCCGCAT
phl_2	709	TAATACGACTCACTATAGGACGAGCACCTTGAAACACAATC	TAATACGACTCACTATAGGCGCCAACAGTTCGTACATCAC
rl_2	141	TAATACGACTCACTATAGGAATTCGAGCGGATCAGTAG	TAATACGACTCACTATAGGCATGCCATAAGCTCCTTCA
Dcp-1_2	489	TAATACGACTCACTATAGGTCAACAATGGCTCCTGGTACAT	TAATACGACTCACTATAGGTTTCTATTGGCAAGGTCTCGC
debcl_2	465	TAATACGACTCACTATAGGCACTGCCCGTTGAAATTCAGA	TAATACGACTCACTATAGGTTGCTGCTGAGGCCTTTGTT
Ark_2	662	TAATACGACTCACTATAGGGATCATTCGATGACGCTTACGC	TAATACGACTCACTATAGGGGGCATTCCAAGCAGTTGAATC
p53_2	370	TAATACGACTCACTATAGGAATGATAGCCGAGACTGCGAC	TAATACGACTCACTATAGGTCACCGTTAAACGCCTTACG
Bruce_2	693	TAATACGACTCACTATAGGTCCCTGGCTGAGAAGCATATC	TAATACGACTCACTATAGGTTATCACGTTGGCACCAGTGT
Ice_2	415	TAATACGACTCACTATAGGCAGCCCAACGATCACACAGAT	TAATACGACTCACTATAGGCACTATCGCTGTGATTCTGCG
buffy_2	481	TAATACGACTCACTATAGGCCACACTACATTCCGCATCAC	TAATACGACTCACTATAGGAACGTGTGTGTTGATGCCACT