Supplemental Material to:

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Identification of Atg5-dependent transcriptional changes and increases in mitochondrial mass in Atg5-deficient T lymphocytes

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Figure S1

![Graph showing percent survival over weeks post reconstitution for Atg5/F/F Cre+ and Atg5/F/F Cre- mice. The graph indicates a significant difference (p<0.0001) between the two groups. The y-axis represents percent survival ranging from 0 to 100, and the x-axis represents weeks post reconstitution ranging from 0 to 32. The Atg5/F/F Cre+ group has a lower percent survival compared to the Atg5/F/F Cre- group.]

Figure S2

![Image showing gel electrophoresis results for Atg5/F/F Cre+ and Atg5/F/F Cre- mice. The gel bands are labeled as Flox and Deleted.]

- *Atg5/F/F Cre* (n=34)
- *Atg5/F/F Cre* (n=25)
Supplementary Figure 3

A

Literature co-citation analysis using terms associated with mitochondrial functions

B

292 of 699 differentially expressed genes have PubMed citations for the terms searched
Supplemental Figure 1. *Atg5*<sup>−/−</sup> chimeras have decreased survival compared with *Atg5*<sup>+/+</sup> chimeras. The survival of Atg5 chimeric mice was recorded up to 31 weeks post-irradiation and stem cell reconstitution. The p value between the *Atg5*<sup>−/−</sup> and *Atg5*<sup>+/+</sup> survival curves is shown. Data pooled from 4 independently generated batches of reconstituted chimeras.

Supplemental Figure 2. Recombination of the *Atg5*<sup>flox</sup> allele in *Atg5*<sup>F/F Cre+</sup> thymocytes. PCR analysis performed on DNA isolated from thymocyte of *Atg5*<sup>F/F Cre+</sup> and *Atg5*<sup>F/F Cre−</sup> mice to determine recombination of the *Atg5*<sup>flox</sup> locus. Two mice are shown of each genotype. Representative gel from 4 independent experiments.

Supplemental Figure 3. Matrices generated from literature co-citation analysis of differentially expressed genes and citation terms associated with mitochondrial and cellular functions. (A) Mitochondrial functions and (B) general cellular processes or specific T-lineage immune functions, displayed as a heatmap. The intensity of red on the heatmap denotes the extent to which each gene is co-cited with each specific term in the PubMed database.