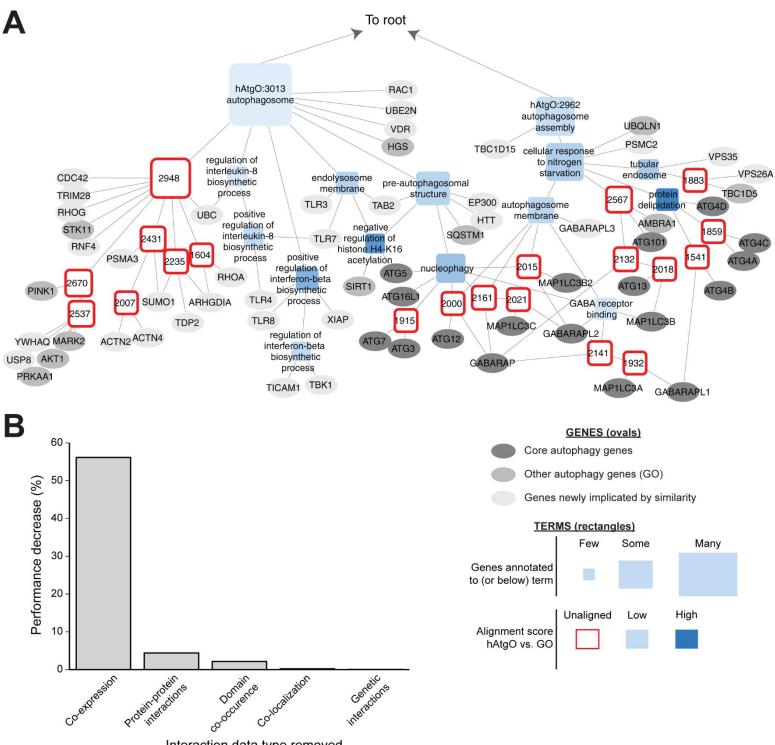


**Figure S1. Performance degradation as interactions are removed, related to Figure 3B.** Performance degradation as more interactions of the indicated type (color) are cumulatively excluded. The mean degradation (point) and standard deviation (error bars) are calculated over 50 random sets of interactions.



Interaction data type removed



hAtgO:3013:"autophagosome", hAtgO:2962:"autophagosome assembly", their descendants and gene annotations are displayed. (**B**) Performance decrease in hAtgO when all data of one type are excluded from the model. Performance is measured as the Pearson correlation between pairwise similarity scores derived from integrated data versus GO. 

 Table S1. Newly generated genetic interaction data, related to Figures 3C, D. Calculated genetic interaction S-scores provided for

 3 static and 3 differential conditions.

 Table S2. Curation of AtgO 2.0 term names, related to Figure 4. Atg 2.0 term names were curated from prior knowledge to

 describe known biology underlying a term, if possible. Gene names, literature and comments are included here. See also Figure 5.

**Table S3. AtgO files, related to Figure 4 and Figure S2.** Full AtgO 2.0 and Atg 1.0 are provided in parent-child format. Each row represents an edge, where column 1 is the parent term, column 2 is the child term, column 3 is the relation type (term-term or gene) and column 4 indicates the data-derived gene similarity value at which the parent term was created.