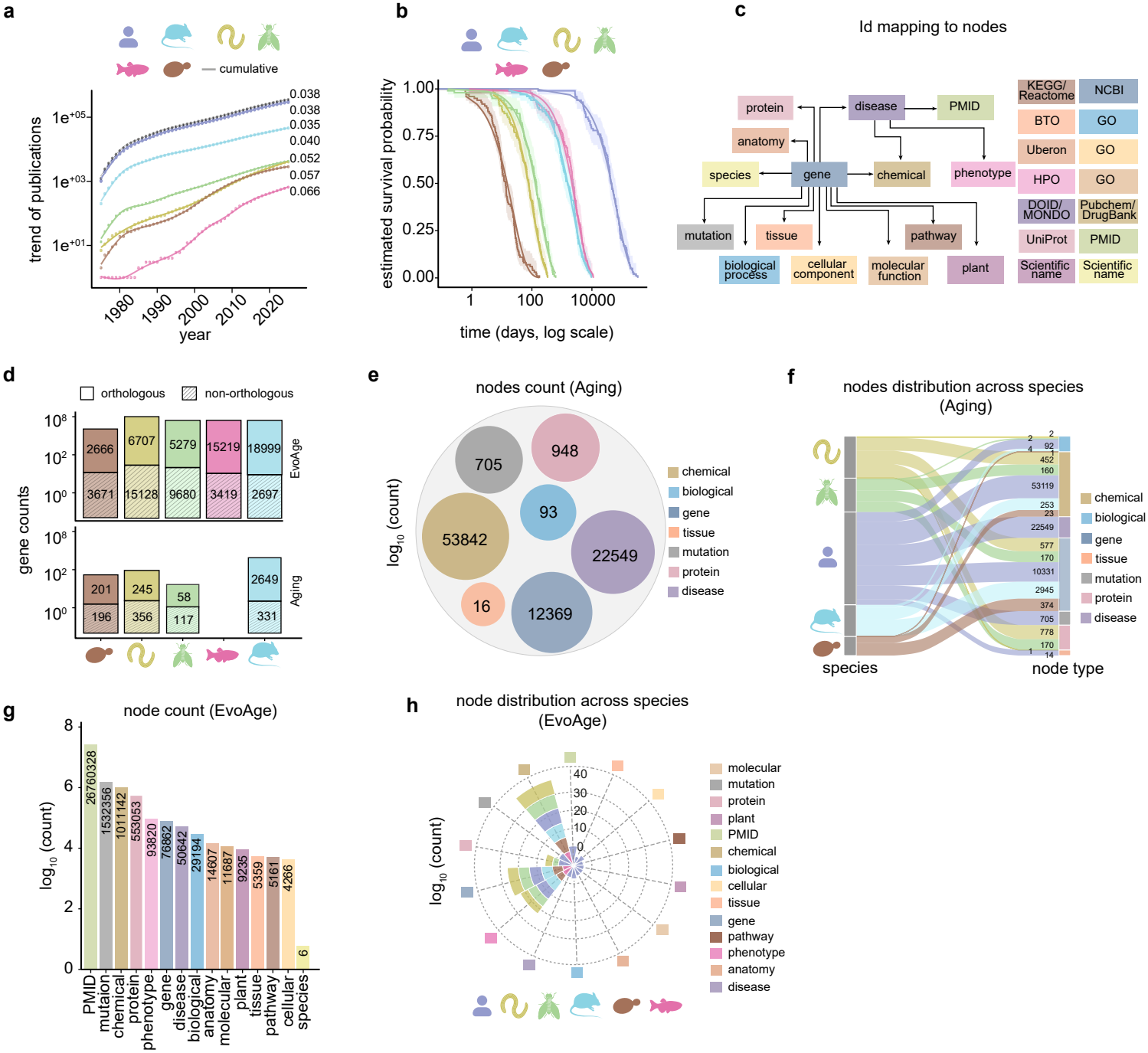

Supplementary figure 1

Supplementary Figure 1: Multi-Species Framework and Baseline Characterization of the Aging KG

(a) Cumulative publication trends for aging research (1975-2023) by model organism (y-axis, log scale). **(b)** Fitted Weibull survival curves comparing the lifespans of the six model organisms. The X-axis shows time in days (log scale). Shaded areas represent 95% CIs. **(c)** The EvoAge-KG schema, showing 15 node types and their inter-relationships. The index details the standard identifier (e.g., NCBI, UniProt, DOID) used for the harmonization of each node type. **(d)** Stacked bar chart of gene counts (log scale) for model organisms, showing the number of genes with ("ortho," solid) and without ("non-ortho," hatched) a mapped human ortholog. **(e)** Bubble plot of absolute node counts for the 7 primary node types in the baseline 'Aging' KG. The area of a circle is proportional to the log10 count. **(f)** Alluvial plot showing the distribution of nodes in the 'Aging' KG by species (left) and node type (right). **(g)** Bar chart of absolute node counts for all 15 entity types in the final EvoAge-KG (y-axis, log10 scale). **(h)** Radar plot illustrating the node type distribution (log10 count) for each of the six model organisms in the final EvoAge-KG.