



**S3 Fig. Summary of the 1232 statistically overrepresented GO terms from Biological Processes ontology.** Obtained terms are grouped and annotated to their representative based on a semantic similarity measure through REVIGO web server [1] using default parameters. Area of each representative rectangle is inversely proportional to the p-value obtained in the hypergeometric test. The treemap was generated with *treemap* package [2].

[1] F. Supek, M. Bošnjak, N. Škunca, and T. Šmuc, “REVIGO summarizes and visualizes long lists of gene ontology terms.,” *PLoS One*, vol. 6, no. 7, p. e21800, Jan. 2011.

[2] M. Tennekes, “treemap: Treemap Visualization. R package version 2.4-1.” 2016.