



Figure S2: Over-represented functional categories with p -values < 0.001 in the GO-term enrichment analysis were used to generate a treemap colored by functional category with REVIGO (Supek *et al.* 2011) between MP vs. NMP (1.), between MP-MF vs. NMP-MF (2.), between MP vs. MP-MF (3.), between NMP vs. NMP-MF (4.). The size of each rectangle is proportional to the p -value for its category. UniprotKB was used to determine Gene Ontology Biological Process (A.) and Molecular Functions (B.) that were over-represented among genes DE between the corresponding contrast.