Figure S1. Biological process analysis of hub genes using the Biological Networks Gene Oncology tool. The color depth of nodes refers to the corrected P-value of ontologies. The size of nodes refers to the numbers of genes that are involved in the ontologies. P<0.01 was considered to indicate a statistically significant difference.

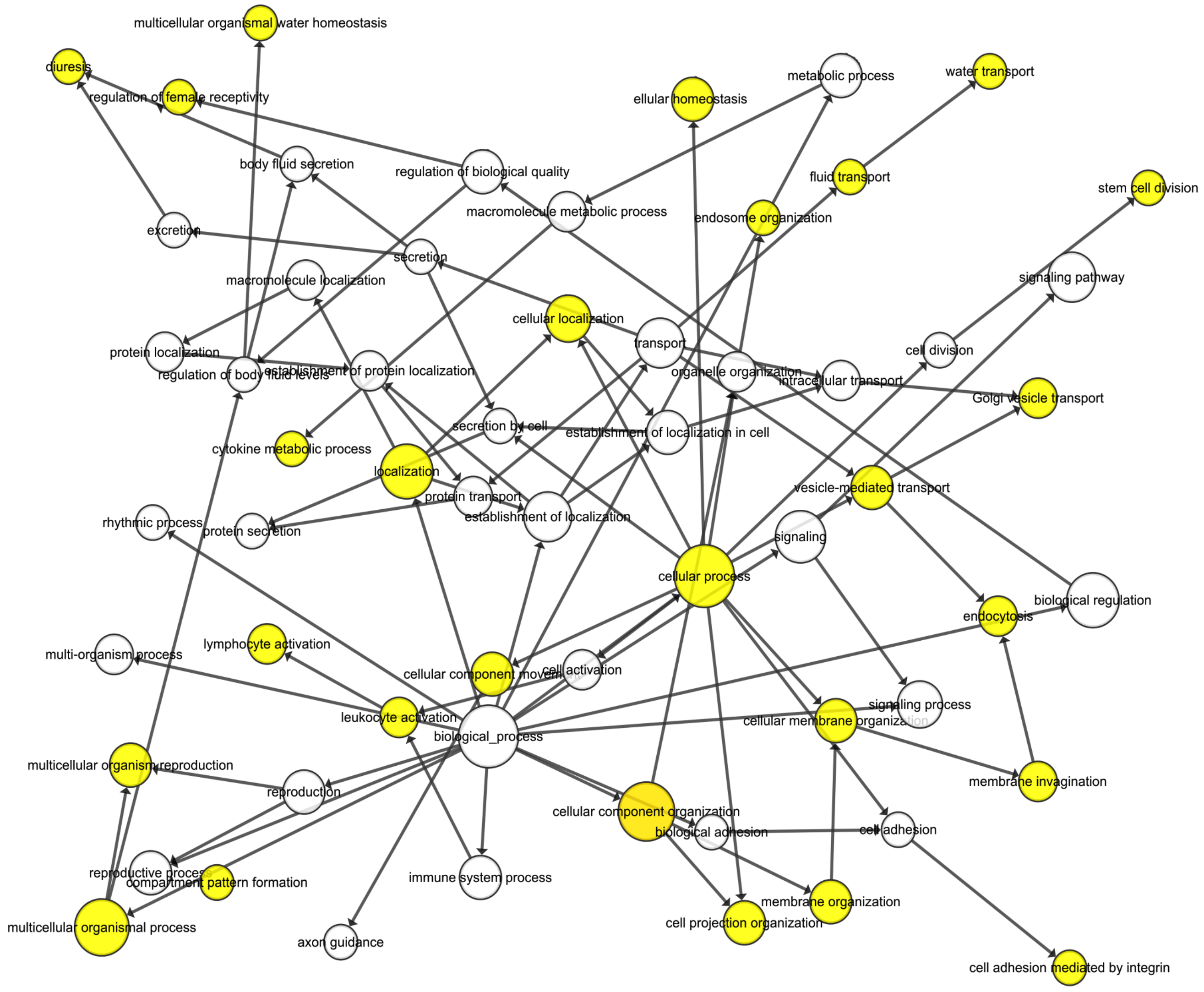

Figure S2. Cellular component analysis of hub genes using the Biological Networks Gene Oncology tool. The color depth of nodes refers to the corrected P-value of ontologies. The size of nodes refers to the numbers of genes that are involved in the ontologies. P<0.01 was considered to indicate a statistically significant difference.

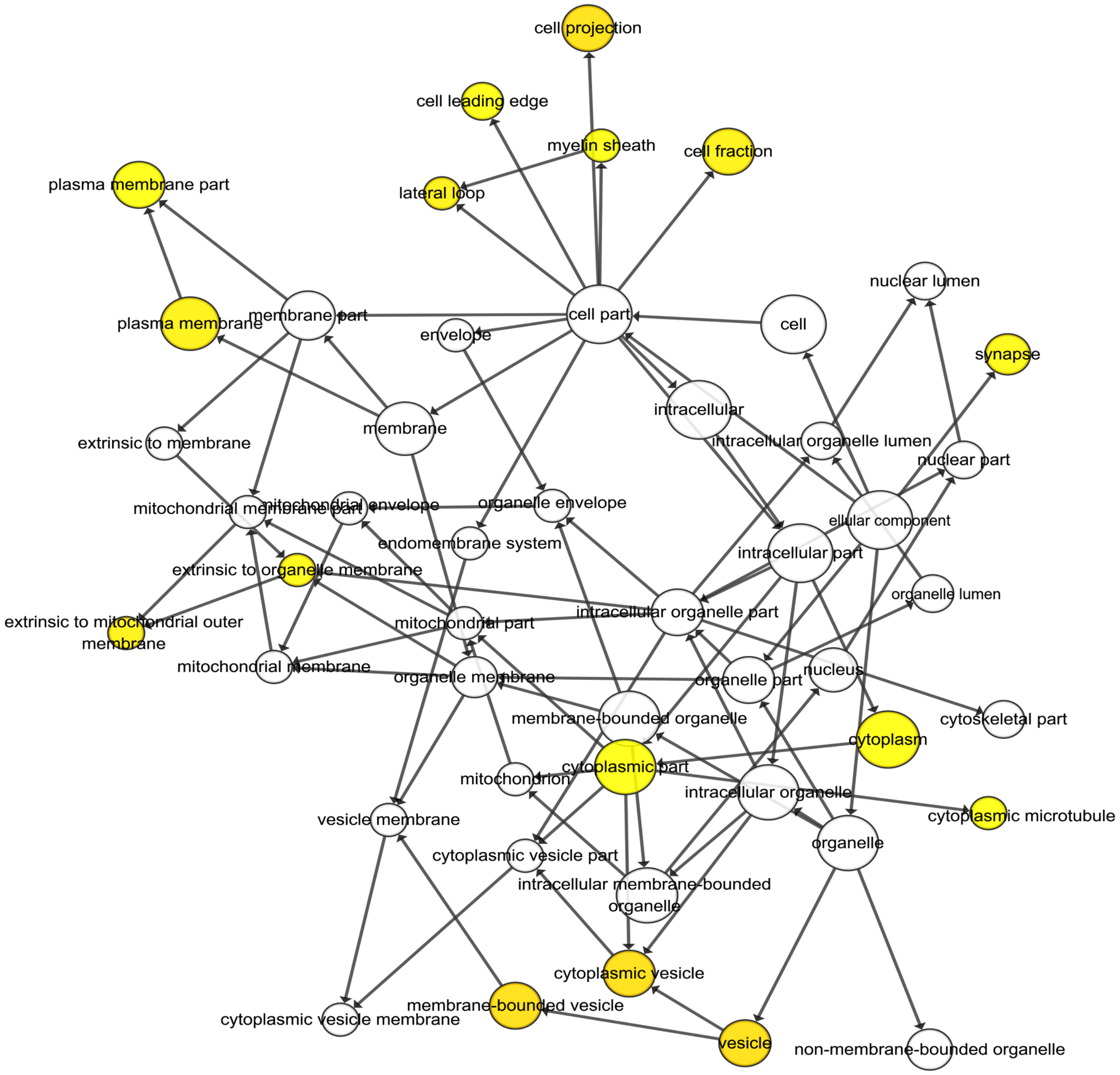

Figure S3. Molecular function analysis of hub genes using the Biological Networks Gene Oncology tool. The color depth of nodes refers to the corrected P-value of ontologies. The size of nodes refers to the numbers of genes that are involved in the ontologies. $P<0.01$ was considered to indicate a statistically significant difference.