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**Figure S1.** Protein-protein interaction (PPI) network graphs a) Protein-protein interaction (PPI) network graph with 178 nodes and 631 interactions. b) Protein-protein interaction (PPI) network graph with 141 nodes and 540 interactions after the elimination of nodes and clusters disconnected from the main network. Node size represents the degree parameter (large nodes = high degree value). Colors represent the betweenness parameter (red = high betweenness centrality, blue = low betweenness centrality)

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**Figure S2.** Enrichment analysis of cellular components grouped using the Cytoscape ClueGO application. a) Network of enriched proteins and associated cellular components. b) Percentage of genes associated to each term. c) Percentage of terms per group. Colors = Gene ontology groups

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**Figure S3.** Enrichment analysis of molecular functions grouped using the Cytoscape ClueGO application. a) Network of enriched proteins and associated molecular functions. b) Percentage of genes associated to each term. c) Percentage of terms per group. Colors = Gene ontology groups

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**Figure S4.** CytoHubba analyses. a) The ten proteins with the highest values of degree represented in a subnetwork. Red = high degree value. b) The ten proteins with the highest values of closeness centrality represented in a subnetwork. Red = high closeness centrality value. c) The five interacting proteins in the intersection between the degree (a) and closeness centrality (b) subnetworks