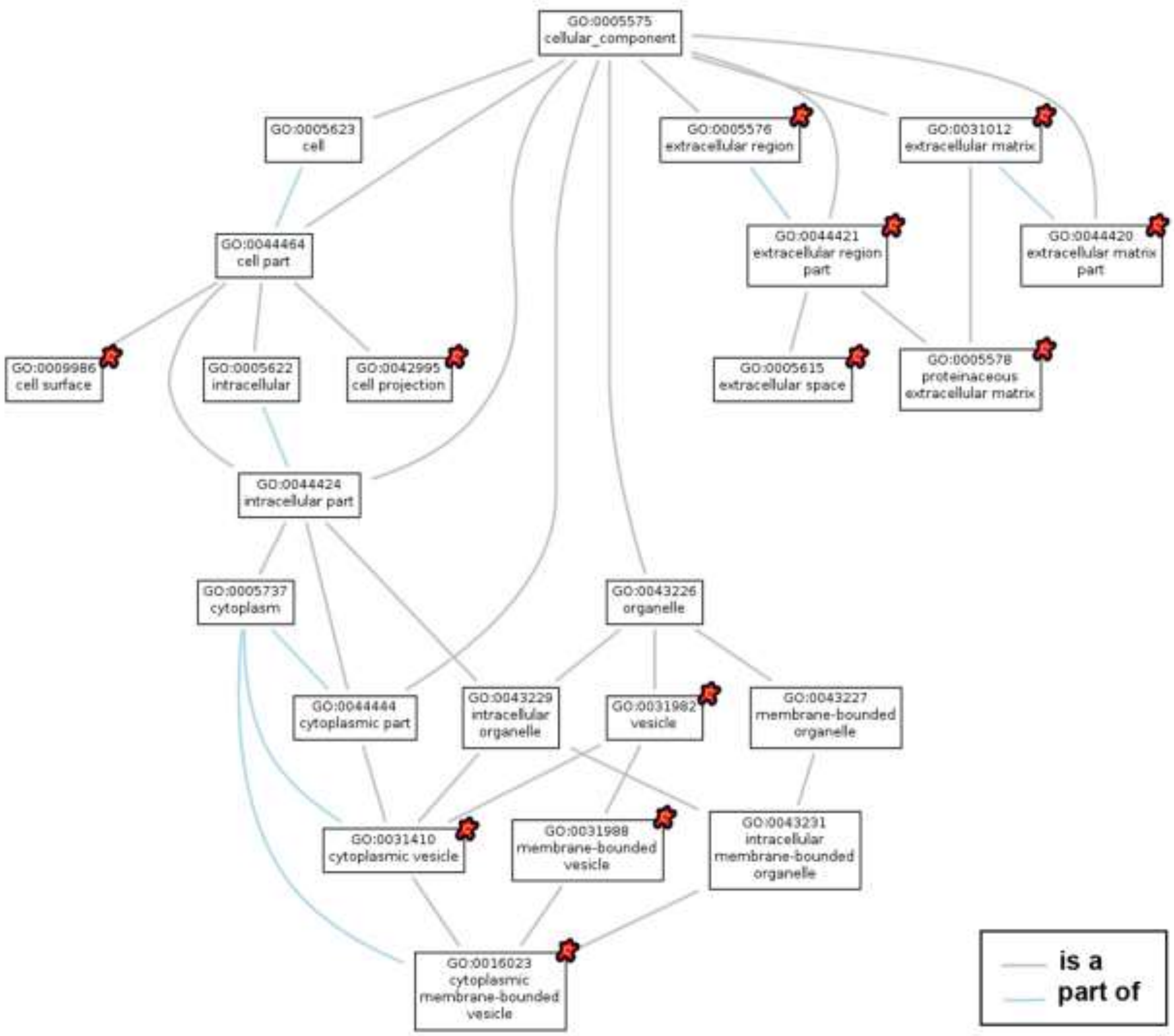

Fig. S1: Visualization of enriched proteins as determined by GO analysis demonstrates the clustering hierarchy. Red star indicates the GO classification of proteins that were altered 1.9 fold.

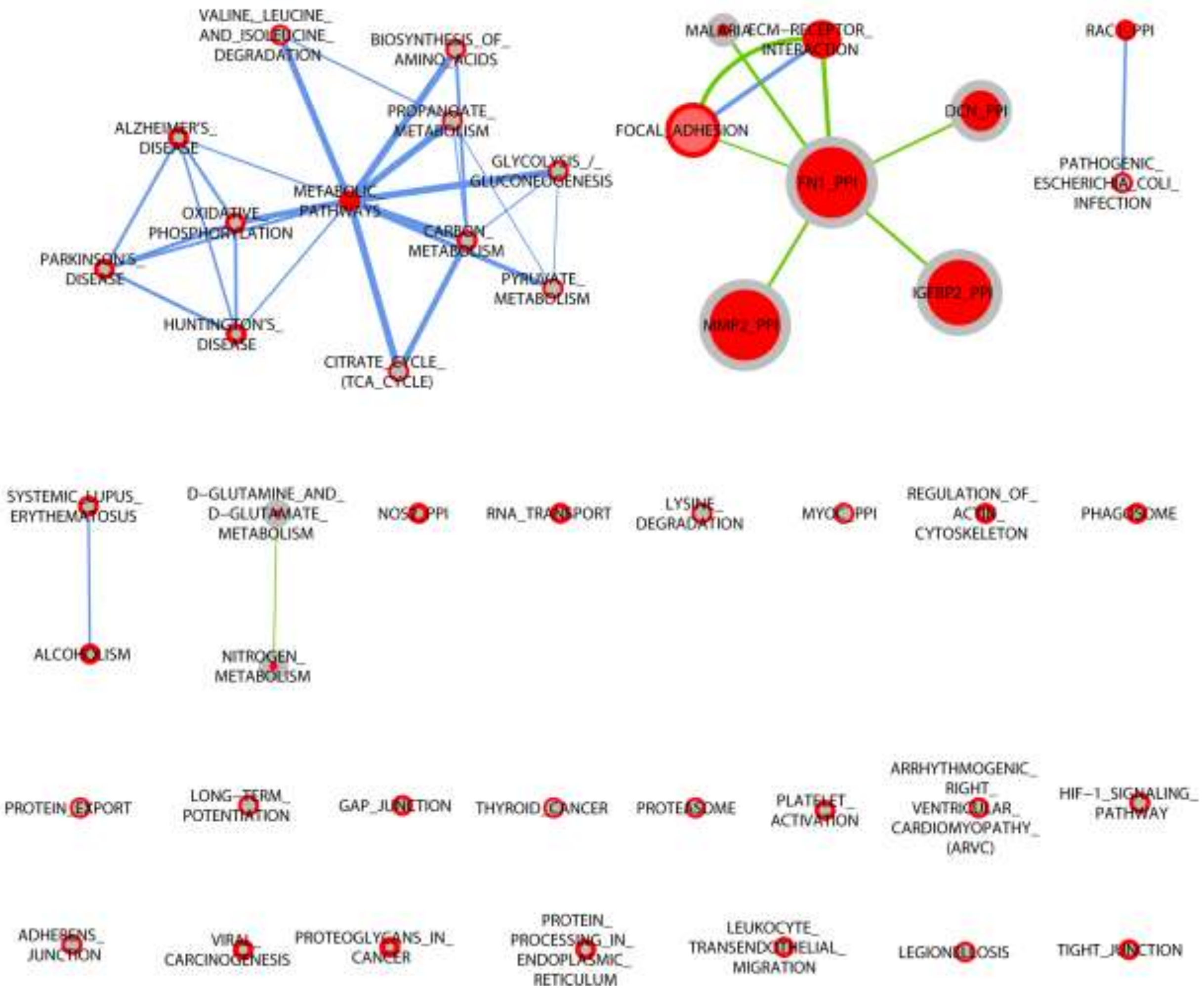

Fig. S2: Protein-protein interaction clusters of all proteins identified by KEGG pathway analysis of ECM proteins. In the pathway graph, the center part of the dot represents the enrichment of up-regulated genes and the outer layer of the dot corresponds to the enrichment of the down-regulated genes. Red-center at the nodes indicates that protein set is enriched in proteins that are up-regulated, gray indicates proteins that are not enriched in down-regulated group. Green edge color indicates that there are overlapped proteins (similarity) between the two nodes connecting the up-regulated proteins. Blue edge color indicates that there are overlapped proteins between the two nodes connecting the down-regulated proteins. If a node is solid red, which means that this gene set is enriched in both up- and down- regulated genes.