

Figure S1.

A.

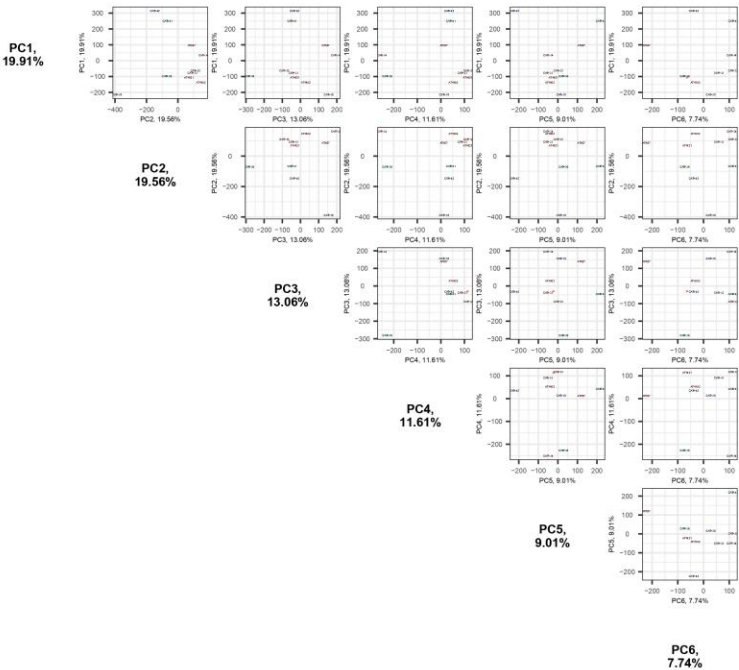
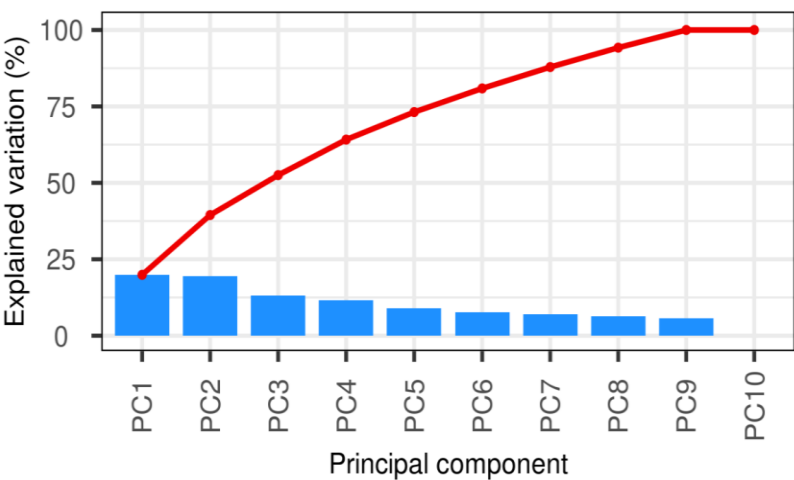
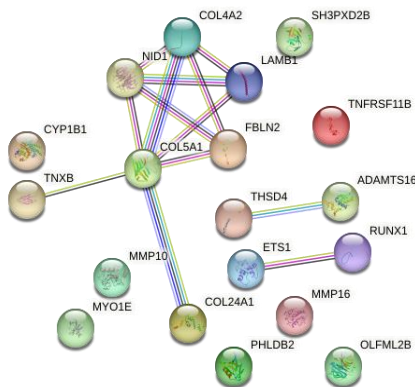


Figure S1: Scree plot that shows the cumulative variance explained by each principal component (PC).

Figure S2.

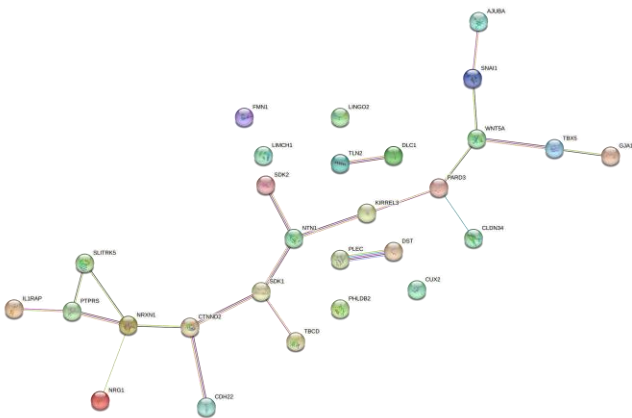
A.

Extracellular matrix organization



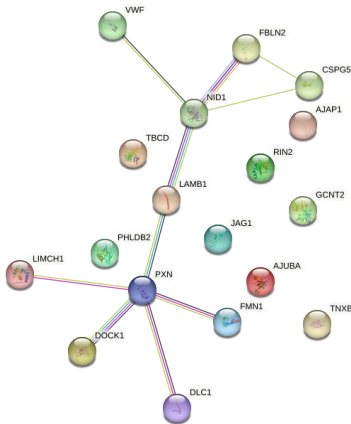
Number of nodes: 19	Number of edges: 13
Average node degree: 1.37	Expected number of edges: 1
Avg.local clustering coefficient: 0.526	PPI enrichment p-value: 3.04e-10

Cell junction assembly



Number of nodes: 28	Number of edges: 21
Average node degree: 1.5	Expected number of edges: 4
Avg.local clustering coefficient: 0.482	PPI enrichment p-value: 3.19e-09

Cell-substrate adhesion



Number of nodes: 18	Number of edges: 10
Average node degree: 1.11	Expected number of edges: 2
Avg.local clustering coefficient: 0.398	PPI enrichment p-value: 1.05e-05

Figure S2: Functional protein association networks using STRING plots of the gens implicated in the extracellular matrix organization, the cell junction assembly and the cell-substrate adhesion processes