



Article

Proteomic Analysis Reveals Differential Expression Profiles in Idiopathic Pulmonary Fibrosis Cell Lines

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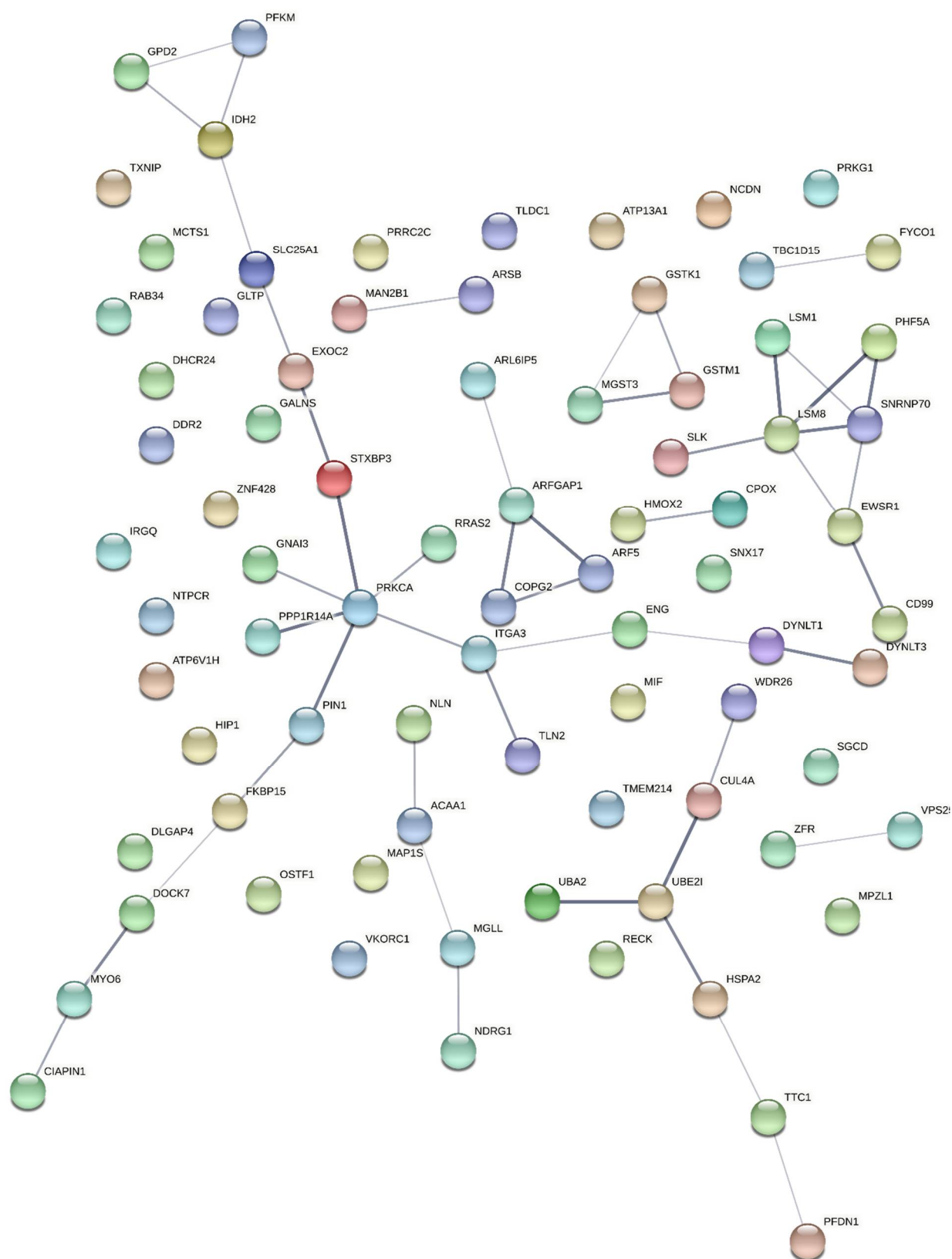


Figure S1. PPI network of the 80 proteins identified exclusively in the fibrotic groups (IPF-1 and IPF-2). The proteins were used to construct a PPI network using STRING software to visualize the interaction with tests such as network edge significance, and the active interaction sources were Text Extraction, Experiments, Database, Coexpression, Neighbourhood, Gene Fusion, and Cooccurrence, with a minimum required interaction score of medium confidence (0.4).

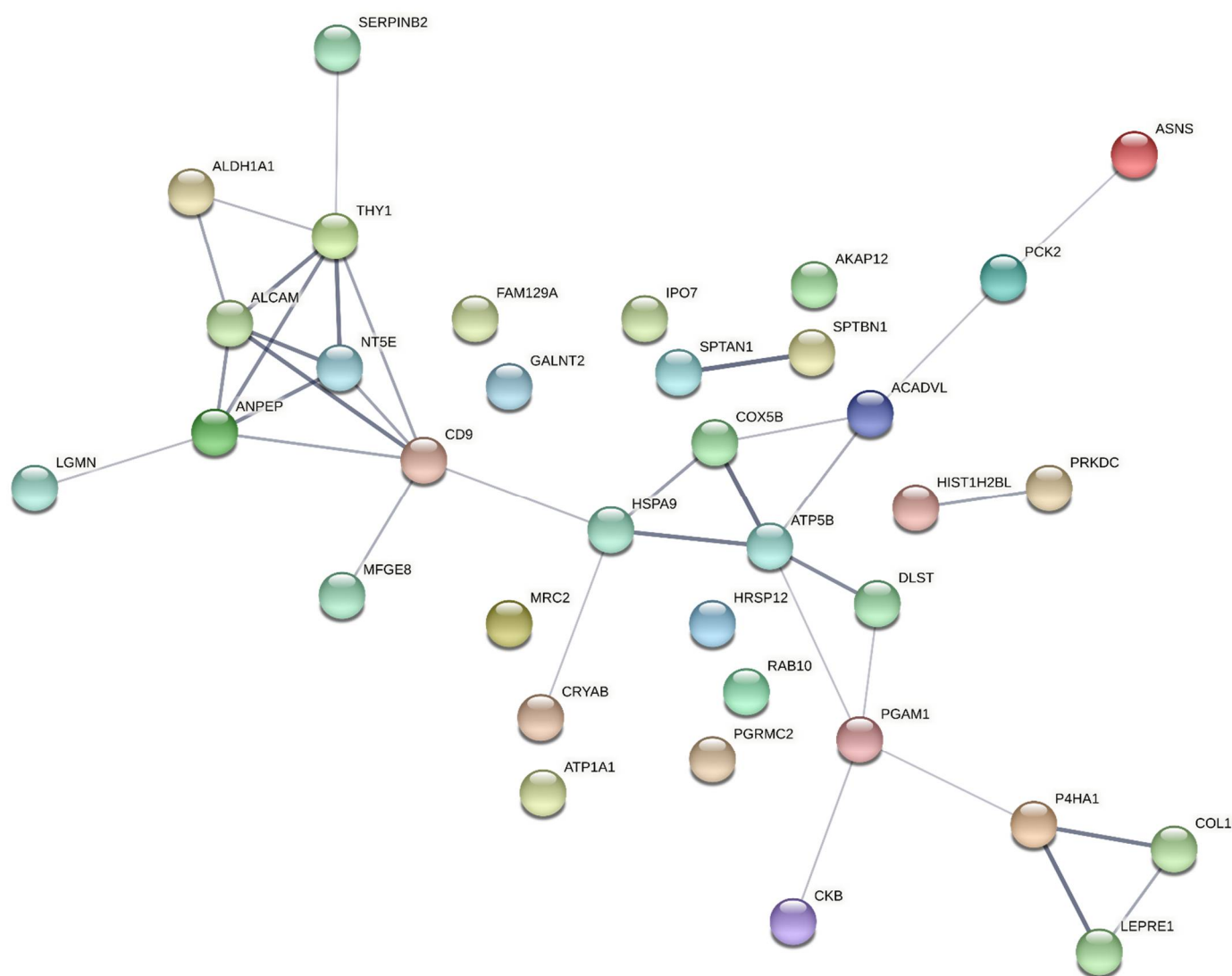


Figure S2. PPI network of DEPs in the fibrotic groups (IPF-1 and IPF-2). The proteins were used to construct a PPI network using STRING software to visualize the interaction with tests such as network edge significance and the active interaction sources were Text Extraction, Experiments, Database, Coexpression, Neighbourhood, Gene Fusion and Cooccurrence, with a minimum required interaction score of medium confidence (0.4).