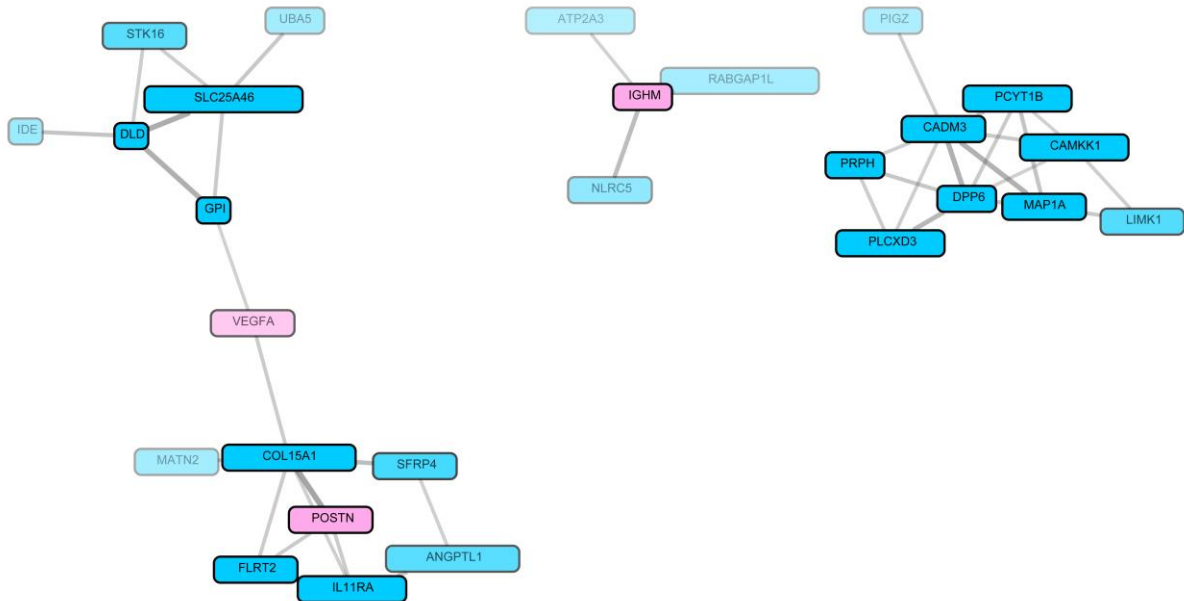


Supplemental Figure 1; Co-functionality network of genes downregulated in COPD patients

The co-functionality network shows the clustering of all genes that are downregulated in COPD lung tissue at $p < 0.001$. The clustering is based on the overlap in gene function as predicted by our GeneNetwork; i.e. close clustering means high overlap in predicted gene function.

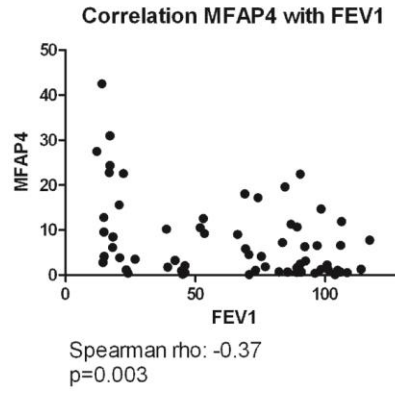
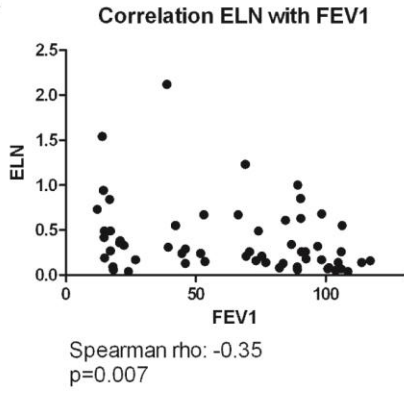


Supplemental Figure 2; Correlation between expression of elastogenesis genes and FEV1 in lung tissue

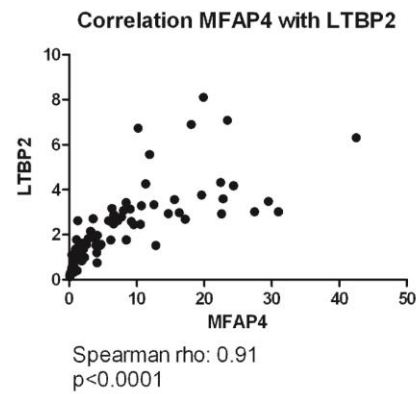
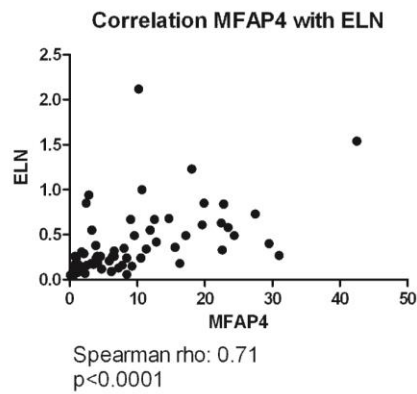
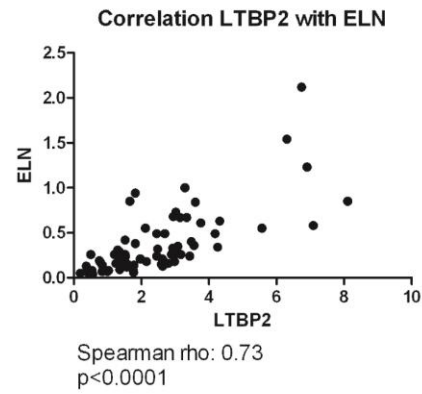
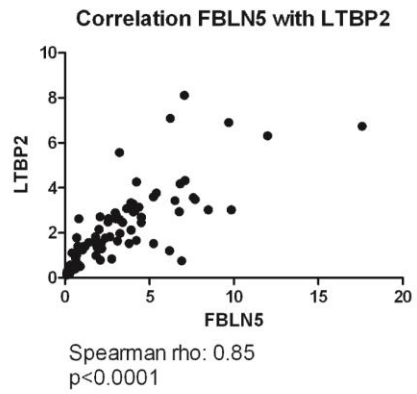
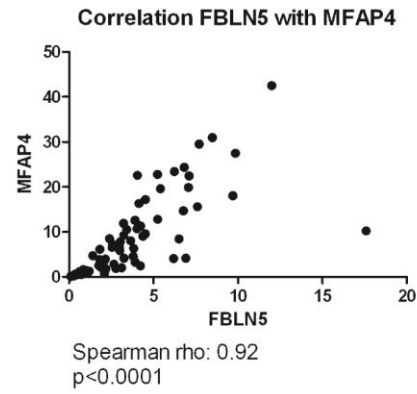
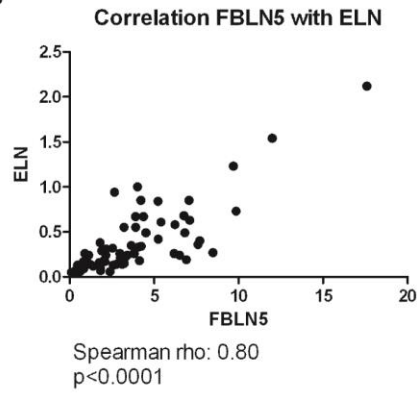
A) The negative correlation between the expression of ELN and MFAP4 in lung tissue and FEV1% predicted is shown. The result of the Spearman correlation is depicted below the figures.

B) The positive correlations between the expression of FBLN5, ELN, MFAP4 and LTBP2 in lung tissue measured by qRT-PCR is shown for the different gene combinations. The results of the Spearman correlations are depicted below the figures.

A



B



Supplemental Figure 3; Total protein levels of ELN and MFAP4 in lung tissue

ELN and MFAP4 protein levels relative to β -actin expression in lung tissue comparing COPD patients and non-COPD controls. The left graph shows the comparison between all COPD patients (closed symbols) and controls (open symbols). The right graph shows the subgroups based on smoking status and COPD stages. Differences between the groups were tested by Mann Whitney U tests. * = $p < 0.05$.

