Figure S1 – Steady-state RNA levels of genes detected in the IPF lung. (A) Significance of genes (in ECM comparison) that are expressed in the IPF lung. (B-C) Cumulative p-value probability distributions are shown. The dotted line is the theoretical null distribution. The black line represents all genes except ECM region genes. The red line represents all ECM genes except those detected in the IPF lung (KS p-value for comparison to "All Genes"). The blue line represents all genes from the IPF lung except miRNA-29 targets (KS p-value for comparison to "ECM Genes"). The yellow line represents all IPF-detected miRNA-29 targets (KS p-value for comparison to "IPF Detected Proteins").
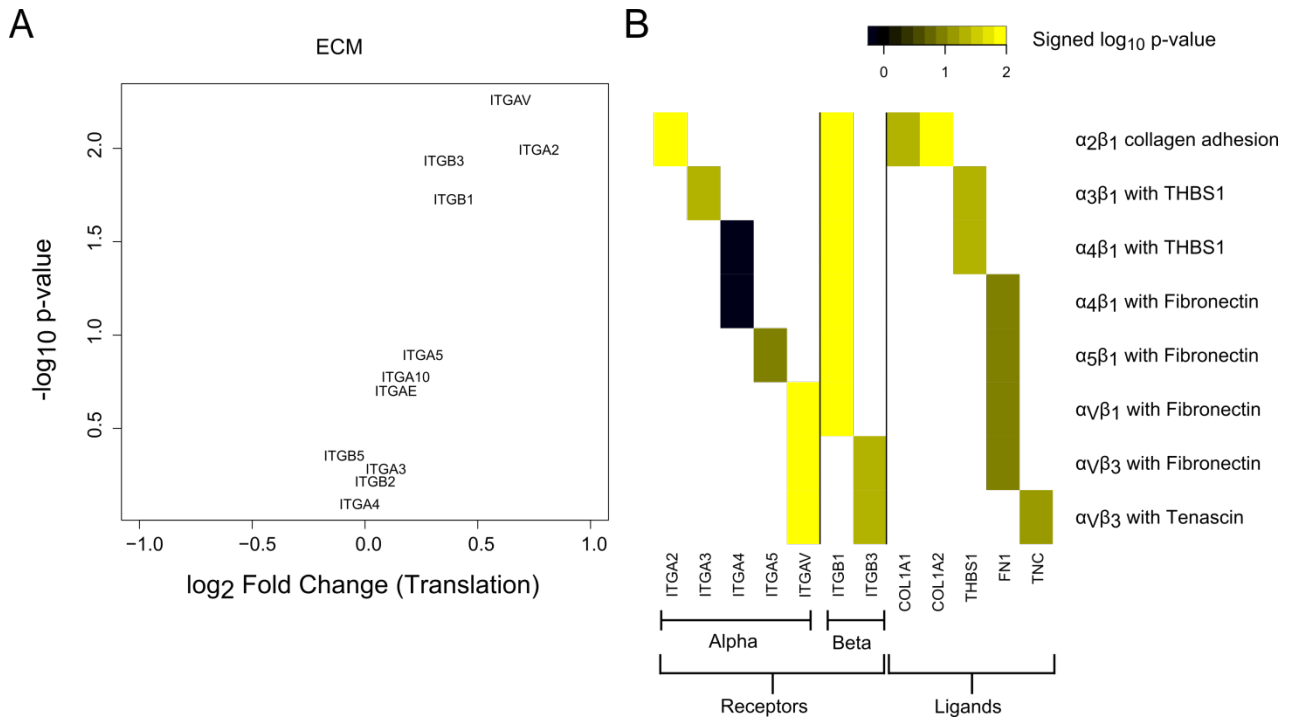
Figure S2 – Diseased ECM coordinately activates translation of integrin receptors and their ligands. (A) Volcano plot of changes due to IPF ECM of all detected integrins. (B) Heatmap of all annotated integrin binding reactions where both binding partners and the ligand were detected. On the left is the translational activation of the α integrin on IPF ECM. In the center is the translational activation of the β integrin. On the right is the translational activation of their cognate ligand(s).

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Table S1 – Genes significantly altered in polysome-associated RNA level on IPF ECM relative to control ECM.

ECM-regulated Translation Gene Ontologies:

	Ontology Name	Odds Ratio	p-value
GO:0071230	cellular response to amino acid stimulus	17.52	2.67×10^{-4}
GO:0022617	extracellular matrix disassembly	14.33	1.37×10^{-3}
GO:0031012	extracellular matrix	3.44	2.96×10^{-3}
GO:0005201	extracellular matrix structural constituent	5.14	3.99×10^{-3}
GO:0016525	negative regulation of angiogenesis	11.26	6.65×10^{-3}
GO:0030199	collagen fibril organization	11.26	6.65×10^{-3}
GO:0007411	axon guidance	3.36	8.65×10^{-3}
GO:0005509	calcium ion binding	2.84	8.77×10^{-3}

Co-regulated Translation Gene Ontologies:

	Ontology Name	Odds Ratio	p-value
GO:0031012	extracellular matrix	6.39	5.04×10^{-4}
GO:0042383	sarcolemma	26.75	1.68×10^{-3}
GO:0060041	retina development in camera-type eye	Inf	3.36×10^{-3}
GO:0005507	copper ion binding	13.43	5.43×10^{-3}
GO:0005198	structural molecule activity	10.75	8.35×10^{-3}
GO:0007528	neuromuscular junction development	33.82	9.72×10^{-3}

ECM-regulated Steady-state Gene Ontologies:

	Ontology Name	Odds Ratio	p-value
GO:0006954	inflammatory response	4.95	3.65×10^{-3}
GO:0016266	O-glycan processing	9.83	6.04×10^{-3}
GO:0043200	response to amino acid stimulus	21.64	7.05×10^{-3}

Co-regulated Steady-state Gene Ontologies:

	Ontology Name	Odds Ratio	p-value
GO:0005539	glycosaminoglycan binding	Inf	5.76×10^{-4}

Table S2 – Gene ontologies over-represented in the ECM-regulated and co-regulated subgroups of the translation and steady-state RNA profiles (see Figure 4)