**Supplementary Materials**

**2D chitosan-based films: a proteomic mass spectrometry study of chondrocyte differentiation processes as a function of cell-biomaterial interactions**

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**Technical and combined coefficients of variation (CV%) between experimental conditions in shotgun proteomics.**

A diagram of different types of musical instruments

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**Figure S1.** Violin plot for the comparison of technical and combined CV % between experimental conditions.

**Gene expression analysis of cartilage markers.**

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**Figure S2**. Gene expression of *Coll1*, *Coll2,* *Acan* , *Coll6* and *COMP* in freshly isolated chondrocytes (IS), cultured in adhesion on tissue culture dish (P), on chitosan film (F), and on chitosan film+hyaluronic acid (F+HA) for 2 weeks. \*: *p* value < 0.05; \*\*: *p* value < 0.01.

**Gene expression analysis of transcription factors.**

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**Figure S3**. Gene expression of *Sox9*, *RUNX2*, *ALK5* and *SMAD2* in freshly isolated chondrocytes (IS), cultured in adhesion on tissue culture dish (P), on chitosan film (F), and on chitosan film+hyaluronic acid (F+HA) for 2 weeks. \*: *p* value < 0.05; \*\*: *p* value < 0.01.

**Volcano plots for pairwise comparison in proteomics.**

A graph of different colored shapes

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A diagram of a graph

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**Figure S4**. Fold change and statistical significance in pairwise comparison. Proteins are represented by all the precursor peptides identified by shotgun proteomics.

**Differential expression of actin organization markers.**

A diagram of different types of numbers

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**Figure S5**. Fold change and statistical significance of actin organization protein markers in pairwise comparison. Proteins are represented by all the precursor peptides identified by shotgun proteomics.

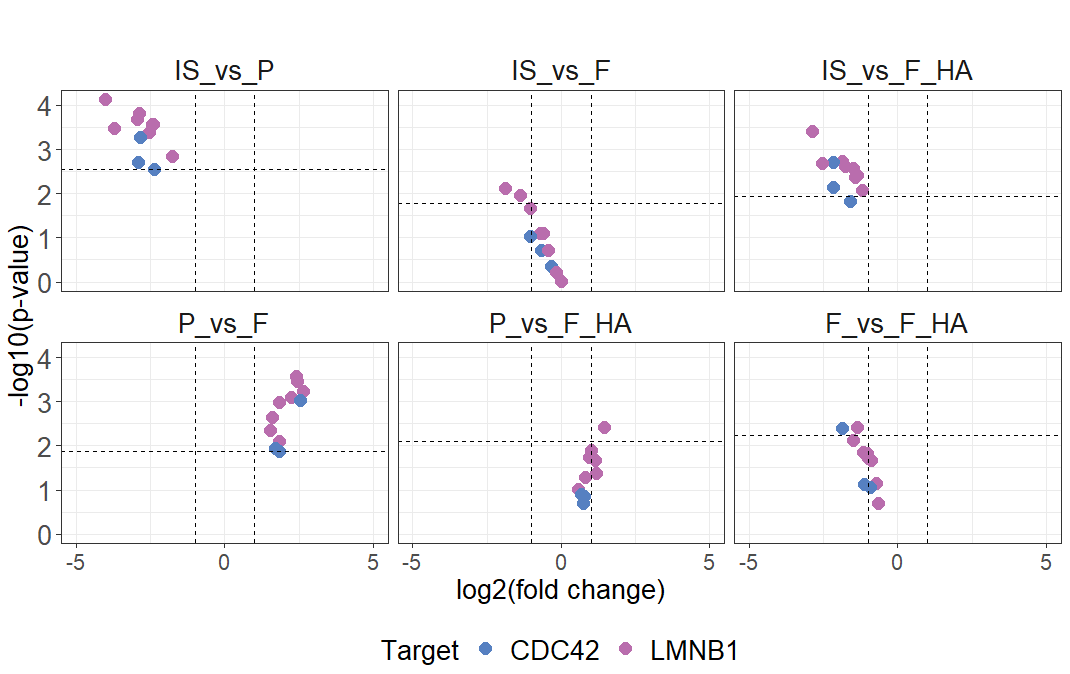
**Differential expression of cell adhesion markers.**

A graph of different types of numbers

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**Figure S6**. Fold change and statistical significance of cell adhesion protein markers in pairwise comparison. Proteins are represented by all the precursor peptides identified by shotgun proteomics.

**Differential expression of cytoskeletal-nuclear remodeling markers.**



**Figure S7**. Fold change and statistical significance of cytoskeletal-nuclear remodeling markers in pairwise comparison. Proteins are represented by all the precursor peptides identified by shotgun proteomics.

**Gene ontology enrichment analysis of DEPs in cells grown on biomaterials.**

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**Figure S8**. GO enrichment analysis of F and F+HA significant proteins on GO biological process annotation set. GO0002486/2476/1916 terms belong to immune system response, while GO0001732 is related to translation initiation.