



**Supplementary Figure S4. Differentially expressed matrisome proteins in synovial sarcoma (SS) cases (n=42) that either received preoperative treatment or were untreated.** (a) Heatmap of 54 matrisome proteins significantly upregulated in treated samples compared to untreated samples (fold change > 2, false discovery rate < 0.01). Samples in the heatmap are arranged by treatment type (untreated, chemotherapy alone (Chemo), radiotherapy and chemotherapy (RT+Chemo), and radiotherapy alone (RT)). (b) Breakdown of 54 upregulated matrisome into 6 matrisome classes. (c) Over-representation analysis of upregulated KEGG pathways in SS cases that received preoperative treatment compared to untreated cases. (d) Protein-protein interaction networks constructed using STRINGdb, including KEGG pathway annotations. Box plots show log<sub>2</sub> normalised expression of selected matrisome proteins within each of the two KEGG pathway annotations in SS cases split by treatment type. ns = non significant, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001. SS = synovial sarcoma, ECM = extracellular matrix.