The heatmap and boxplots were generated using R(v4.1.1).

Top 20 highly and lowly expressed genes were extracted for each tumour type, Heatmap was generated using the log normalised expression (transcripts per million) counts of the top 20 highly and lowly expressed ECM genes identified separately for each tumour type.

Box plots were generated for the top 10 most expressed genes within each tumour type.

Comparison of the highly expressed ECM genes against the average expression of other ECM genes, inclusive of the entire cohort, was performed using paired t-tests under a significance level of 0.01. “NB\_top10\_COL1A1\_all”

Comparison of the highly expressed ECM genes against the average expression of other ECM genes, restricting the cohort to the Neuroblastoma tumor type, was performed using paired t-tests under a significance level of 0.05. “NB\_top10\_COL1A1\_all”