**Western Blot data:**

Each sheet included the data aligned to the specific protein investigated. Data is shown as target protein expression normalised to total protein per run (3x runs). All three points have been plotted with mean and standard deviation found for three runs.

**TEM data:**

The first sheet shows minimum diameter. A varying number of images were taken for each sample from 1 of 3 runs. Each image contained a varying number of fibrils, each number shown is the mean minimum diameter from each fibril within the image. All mean fibril diameters from each run have been plotted on the graph with the median and standard deviation found across the three runs.

The minimum diameter frequency was found using all fibril diameters and splitting into bin centres encompassing two minimum diameters i.e. 15≤x≤16 nm. The percentage of fibrils within the bin centre compared to the total number of fibrils was then found and plotted as a histogram.

**Alignment data:**

Using the ImageJ plugin ‘OrientationJ’ the angle of the fibres from fluorescent imaging of the tissue engineered structures was discovered. The angle was normalised to act between -90 and 90° by minusing 180° from any fibril with an orientation of >90° or adding 180° to any fibril with an orientation <90°, this meant that 0° represented the most aligned fibre. The number of fibres within a bin centre (e.g. -90≤x≤-80) was found as a percentage of the overall fibres and the mean and standard deviation was found across the images taken. The mid region was plotted as a line histogram above the x-axis and the anchor region as a line histogram below the x-axis. The control mid region was super imposed on all experimental conditions. One way ANOVA was used to compare the percentage of fibres at each bin centre between the anchor point and mid region for each sample (internal control) and the control mid region vs the experimental mid region.

**qPCR data:**

Each sheet included the data aligned to the specific gene investigated. Data is shown as target protein expression normalised to total protein per run (3x runs). All three points have been plotted with mean and standard deviation found for three runs.

**ALP data:**

Each data point represents the ALP expression in the media from individual samples on the stated time point. Each point has been plotted and the mean and standard deviation found. The experimental conditions have been compared on each time point through statistical analysis of the means.

**Mechanical testing data:**

Each sheet represents the mechanical test being investigated. For max strain, max stress, Young’s modulus and rate of relaxation each value per experimental condition represents an individual run. Each run has been plotted and the mean and standard deviation found and used for statistical analysis. The percentage energy lost was analysed in the same way except using four runs rather than three. The hysteresis sheet was used to give a representative profile for each experimental group with the fixed strain values plotted against the variable strain values for each experimental condition. The stress relaxation sheet shows stress values at set time points and would be plotted as time on the x-axis and stress on the y-axis for each experimental condition, with staggered y values to separate the conditions.