Explanation of sample naming found in biochemical data .xls files

Bovine\_DNAassay\_results.xls

T30C2, T31C2, T32C2, T33C2, T34C2, T35C2 = Tail disc level C2-C3 from tail no 30 to 35. C2-C3 samples served as cellular control tissue

T30C1, T31C1, T32C1, T33C1, T34C1, T35C1 = Tail disc level C1-C2 from tail no 30 to 35. C1-2 samples were decellularised.

NP = nucleus pulposus; iAF = inner annulus fibrosusu; oAF = outer annulus fibrosus; EP = endplate

Bovine\_GAGassay\_results.xls

Cellular tissue is shown as “C2” (meaning that the disc level is C2-C3) and individual GAG concentration are detailed for each tail number (T30 to 35).

Decellularised tissue is shown as “C1” (disc level C1-C2) and individual GAG concentration are detailed for each tail number (T30 to 35).

NP = nucleus pulposus; iAF = inner annulus fibrosusu; oAF = outer annulus fibrosus

Human\_DNAassay\_results.xls

S1, S2 and S3 = Spine/donor 1,2 and 3

For each donor spine, two thoracic discs were decellularised (Spine levels T1-2 and T5-6). For each donor spine, two thoracic discs acted as cellular controls (Spine levels T2-3 and T6-7).

NP = nucleus pulposus; iAF = inner annulus fibrosusu; oAF = outer annulus fibrosus; EP = endplate; VB = vertebral bone

Human\_GAGassay\_result.xls

For each donor spine, two thoracic discs were decellularised (Spine levels T1-2 and T5-6). For each donor spine, two thoracic discs acted as cellular controls (Spine levels T2-3 and T6-7).

NP = nucleus pulposus; iAF = inner annulus fibrosusu; oAF = outer annulus fibrosus

Explanation of DNA assay results for both bovine and human samples

Nanodrop readings (in the “raw” data tab of the spreadsheet) in ng/ul were converted to ng/mg dry weight: Average ng/ul results of sample (detected by nonodrop apparatus) were multiplied by the sample elution volume and divided by the dry weight of the original sample. This is shown in the “processed” results tab for cellular and decellularised tissue. The “collated” tab shows the results for both cellular and decellularised samples along with descriptive statistics.

Explanation of GAG assay results for both bovine and human samples

Absorbance values of standards (in “raw” data tab) were normalised by subtracting blank/background values. A standard curve was produced from which the concentration of unknown samples was calculated in ug/ml. This value was corrected for the dilution factor (multiplied by dilution factor of unknown sample) and the original volume of digested sample (multiplied by original volume of sample). The resulting value was converted to ug of GAG per mg dry tissue weight by dividing by the dry weight of original digested sample used in the analysis. This is shown in the “processed” results tab in the spreadsheets for cellular and decellularised samples. The “collated” tab shows the results for both cellular and decellularised samples along with descriptive statistics.