**Supplemental Information**

**Methods and Materials**

*Growth Factor Content Assay*

 Growth factor analysis was performed on five donors of micronized dHACM (EpiFix®, MiMedx), five donors of “chorion-free cryopreserved amnion and amniotic fluid” (FloGraft® FREEDOM, Applied Biologics, LLC), and five donors of “placental tissue matrix” (PX50®, Skye Biologics, Inc.). All samples were sent to the independent contract research organization and content was measured using a multiplex ELISA array (Human Cytokine Array Q1000, RayBiotech). Concentrations for each factor in
amnion and amniotic fluid” and “placental tissue matrix” products were normalized to the concentration of that corresponding factor measured in dHACM and reported as a mean percentage value ± standard deviation.

*Synoviocyte Hyaluronic Acid (HA) Gene Expression and Production*

 Human fibroblast-like Synoviocytes (HFLS) isolated from normal synovium, osteoarthritic (OA) synovium and rheumatoid arthritic (RA) synovium (Cell Applications) were cultured at 37°C, 5% CO2 and 20% humidity in human synoviocyte basal medium containing growth supplement (Complete media, Cell Applications) until 80% confluent. For HA gene expression experiments, HFLS from normal, OA and RA synovium were lifted from adherent culture using TrypLE (Gibco) and plated at 15,000 cells/well in a 24-well microplate and allowed to attach overnight. Treatment groups were prepared by suspending micronized dHACM allografts (EpiFix®, MiMedx) at 35 mg/mL in synoviocyte basal medium and were allowed to extract overnight at 4°C (n=5 donors). The following day, extracts were collected by centrifuging samples for 10 minutes at 3000 rcf, after which, supernatants were filtered through a 0.22μm syringe filter. Supernatants were diluted to 10 mg/mL in and 1 mg/mL in basal media and synoviocytes were then treated with the 10 mg/mL extract, the 1mg/mL extract, basal media, or complete media. Cells were incubated for 72 hours at 37°C, 5% CO2 and 20% humidity. After 72 hours, RNA was extracted using a GeneJET RNA Purification Kit (Thermo Scientific) and quantified using a NanoDrop 2000 spectrophotometer (Thermo Scientific). Reverse transcription to cDNA was performed using a Maxima First Strand cDNA Synthesis Kit (Thermo Scientific). Quantitative polymerase chain reaction (qPCR) amplification for each gene target was performed on a QuantStudio 7 System (Life Technologies) using predesigned TaqMan Gene Expression assays for hyaluronic acid synthase 1 (HAs1), HAs2, and eukaryotic 18s ribosomal RNA (Life Technologies). The 2-∆∆Ct method was used to determine relative expression of dHACM treated synoviocytes compared to basal media-treated synoviocytes with eukaryotic 18s ribosomal RNA as an endogenous housekeeping control.

For HA production experiments, HFLS from normal, OA and RA synovium were lifted from adherent culture using TrypLE (Gibco) and plated at 2500 cells/well in a 96-well microplate and allowed to attach overnight. Treatment groups were prepared and cells were treated as previously described for gene expression experiments (n=5 donors). Cell-free treatment groups containing 10 mg/mL or 1 mg/mL extracts were included as blank controls during HA measurements. After 72 hours, supernatants were collected and stored at -80°C until assayed for HA production. Cells were rinsed with PBS and cell number was measured using a CyQUANT® Cell Proliferation Assay Kit (ThermoFisher). HA production was measured using a Hyaluronan Quantikine enzyme-linked immunosorbent assays (ELISA) Kit (R&D Systems). HA readings for each well were subtracted by cell-free blanks (for extract treatment groups) and normalized to cell number.

*Statistical Analysis*

 All values were reported as mean ± standard deviation, and statistical analyses were performed in Minitab (v17.1). For growth factor content data, non-normalized values were compared using a two-way analysis of variance (ANOVA). For HA gene expression and production, values were compared within for each cell type using a one-way ANOVA. For each ANOVA, pairwise comparisons were made using a Tukey’s *post hoc* test. Significant differences were assigned when p ≤ 0.05.