Supplementary Figure 3. Top-scoring networks derived from the 596 putative mRNA targets in synovial fluid EVs derived from joints with and without PTOA. (A) IPA identified a top network, “Cellular Development, Cellular Growth and Proliferation, Connective Tissue Development and Function” with a score of 59. (B) The “Cell Death and Survival, Cellular Movement, Gene Expression” network, with a score of 46, shows molecules linked to their respective canonical pathways. Both networks are overlaid with relevant biological functions contained within the gene sets. Figures generated are graphical representations of molecules identified in our data and predicted mRNA targets in their respective networks. Molecule color indicates upregulation (red) or downregulation (green). Cellular function color denotes predicted activation (orange), inhibition (blue), or those which could not be predicted (gray) in PTOA. Intensity of color is directly proportionate to fold-change. Legends to the main features in the networks are shown.