Supplementary Figure 1. The top network for plasma (A) and synovial fluid (B) EV DE miRNAs overlaid with PTOA-relevant canonical pathways. Figures generated are graphical representations of molecules identified in our data 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.