**Supplementary Figure 2.** Top-scoring networks derived from the 602 putative mRNA targets in plasma EVs derived from control horses and horses with PTOA. (A) IPA identified “Cellular Function and Maintenance, Gene Expression, Protein Synthesis” as the top network with a score of 36. (B) The network “Cell Death and Survival, Cellular Movement, Organismal Injury and Abnormalities”, with a score of 22, 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.