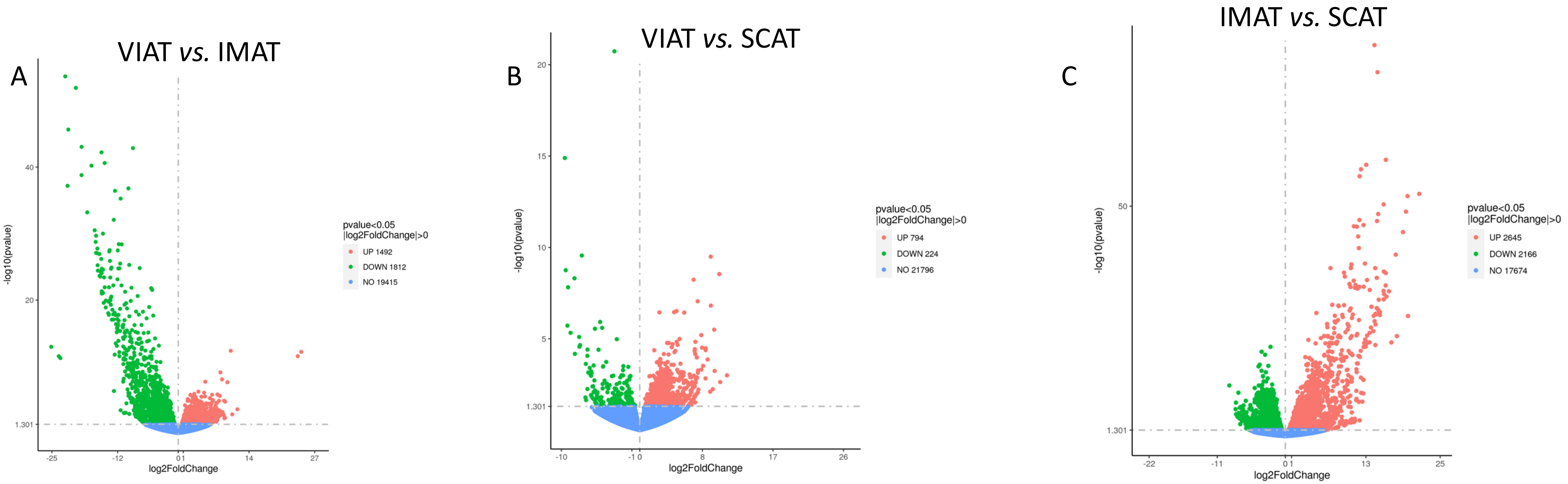

Figure 1.) Volcano plots of differentially expressed genes in VIAT vs IMAT, VIAT vs SCAT, and IMAT vs SCAT in beef cattle (n=4) obtained through transcriptome analysis. A.) VIAT has 1492 genes upregulated and 1812 downregulated compared to IMAT. B.) VIAT has 794 upregulated genes and 224 downregulated genes compared to SCAT. C.) IMAT has 2645 upregulated genes and 2166 downregulated genes compared to SCAT.

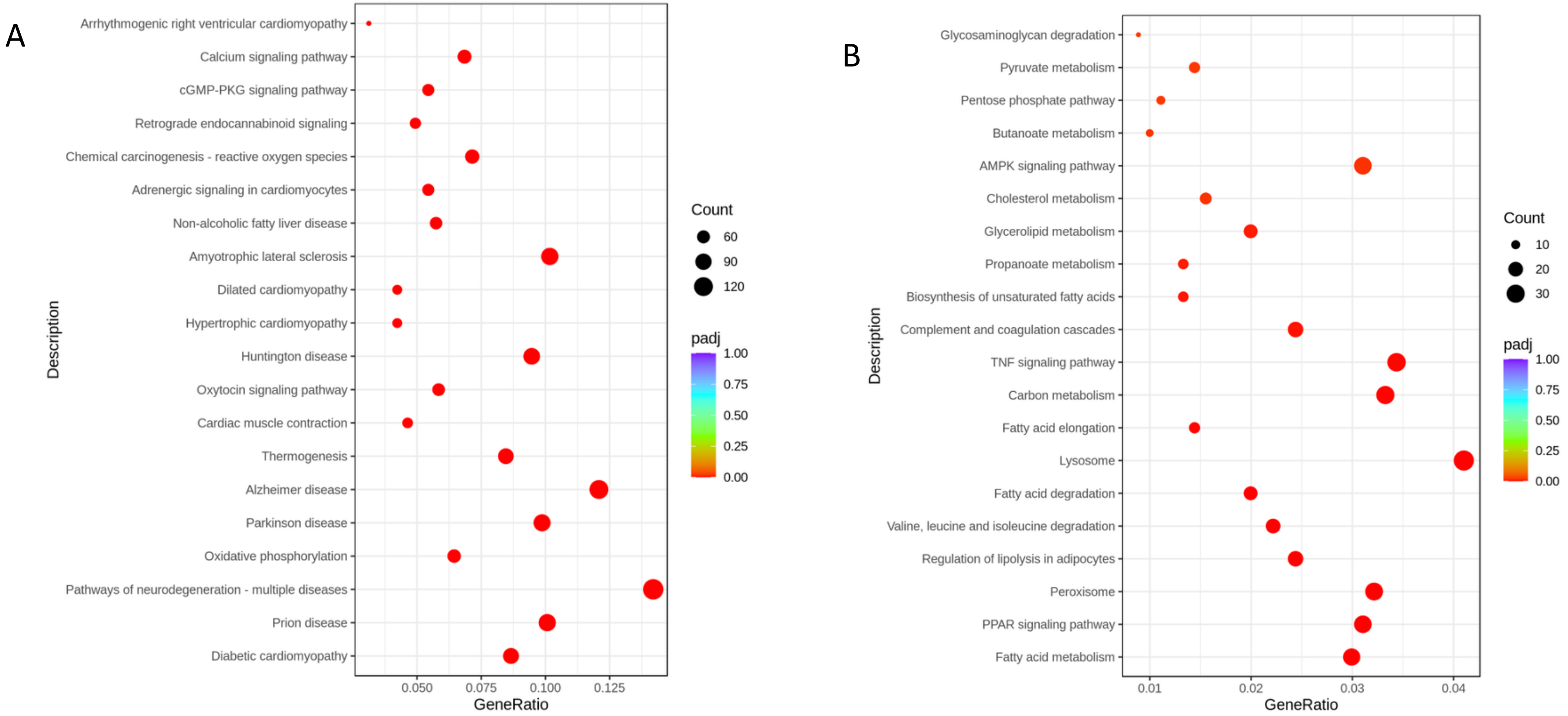

Figure 2.) KEGG pathways for IMAT *vs.* SCAT in beef cattle. A.) Upregulated KEGG pathways for IMAT vs SCAT show increased oxidative phosphorylation and thermogenesis. B.) Downregulated KEGG pathways for IMAT vs. SCAT show SCAT has increased fatty acid synthesis and adipocyte regulators.

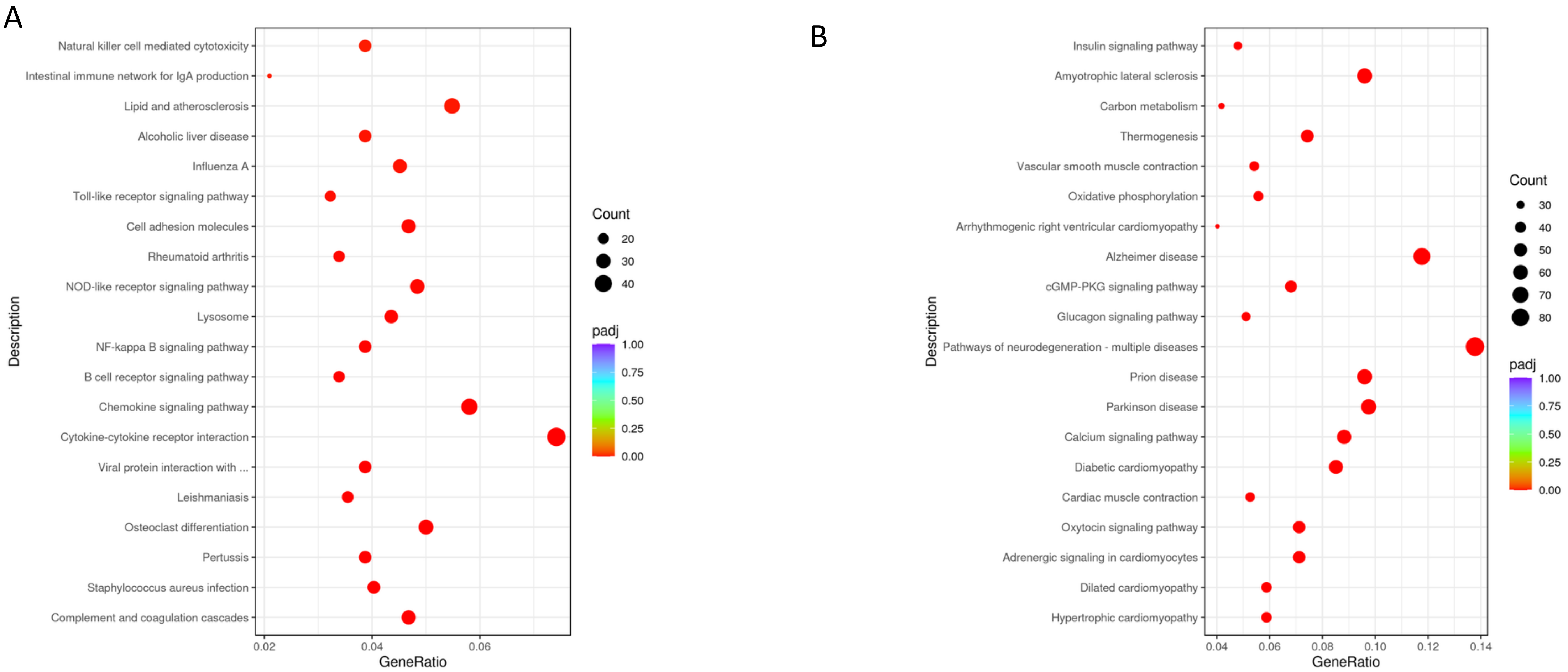

Figure 3.) KEGG pathways for VIAT *vs.* IMAT in beef cattle. A.) Upregulated KEGG pathways for VIAT vs. IMAT show immune pathways such as B Cell receptor, Chemokine, and NOD-like receptor Pathways. B.) Downregulated KEGG pathways for VIAT vs. IMAT show IMAT has increased pathways for oxidative phosphorylation, thermogenesis, and the glucagon signaling pathway.

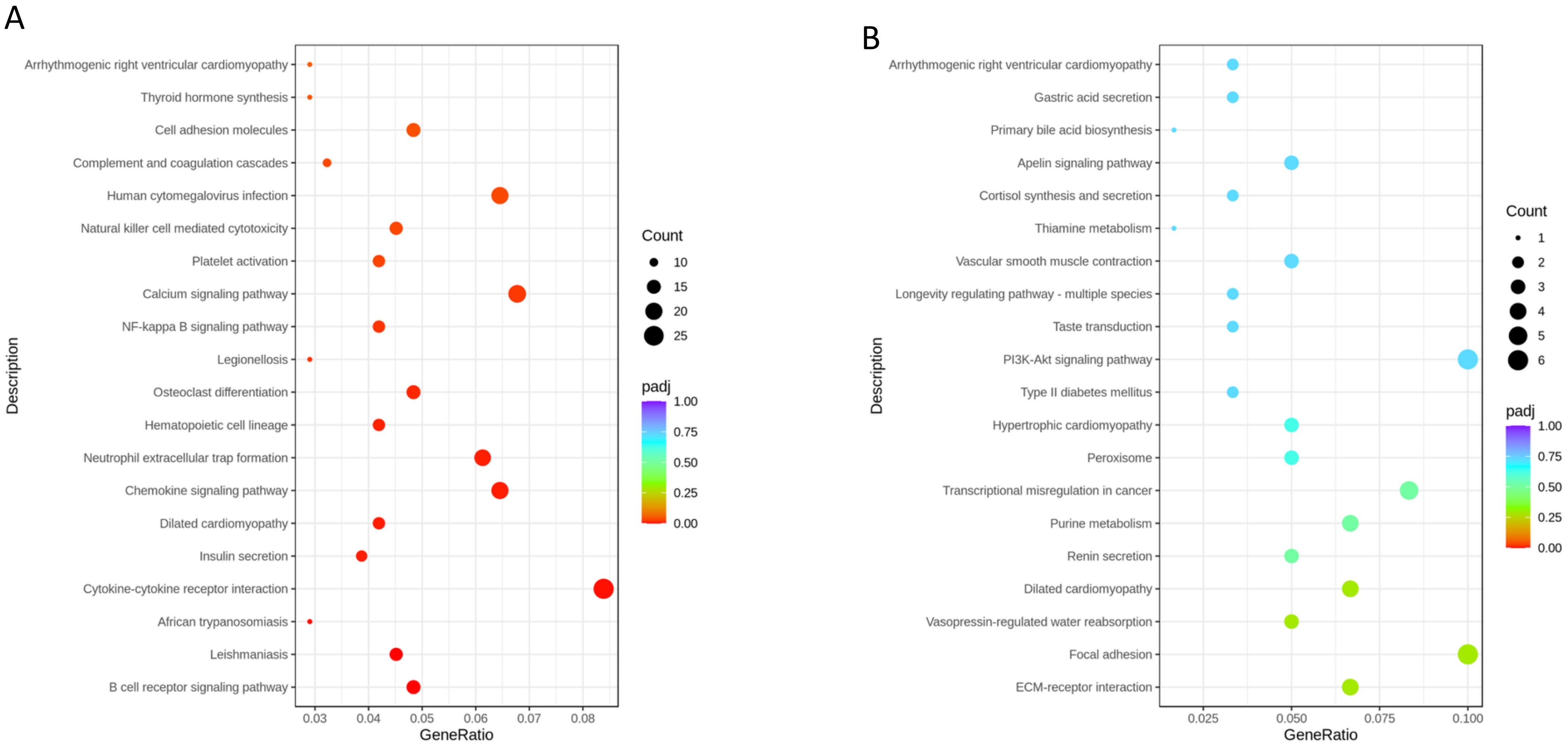

Figure 4.) KEGG pathways of VIAT *vs.* SCAT in beef AT. A.) VIAT has upregulated pathways for cell adhesion, immune cell signaling, and Insulin Secretion compared to SCAT. B.) Downregulated KEGG pathways in VIAT *vs.* SCAT are not statistically significant.

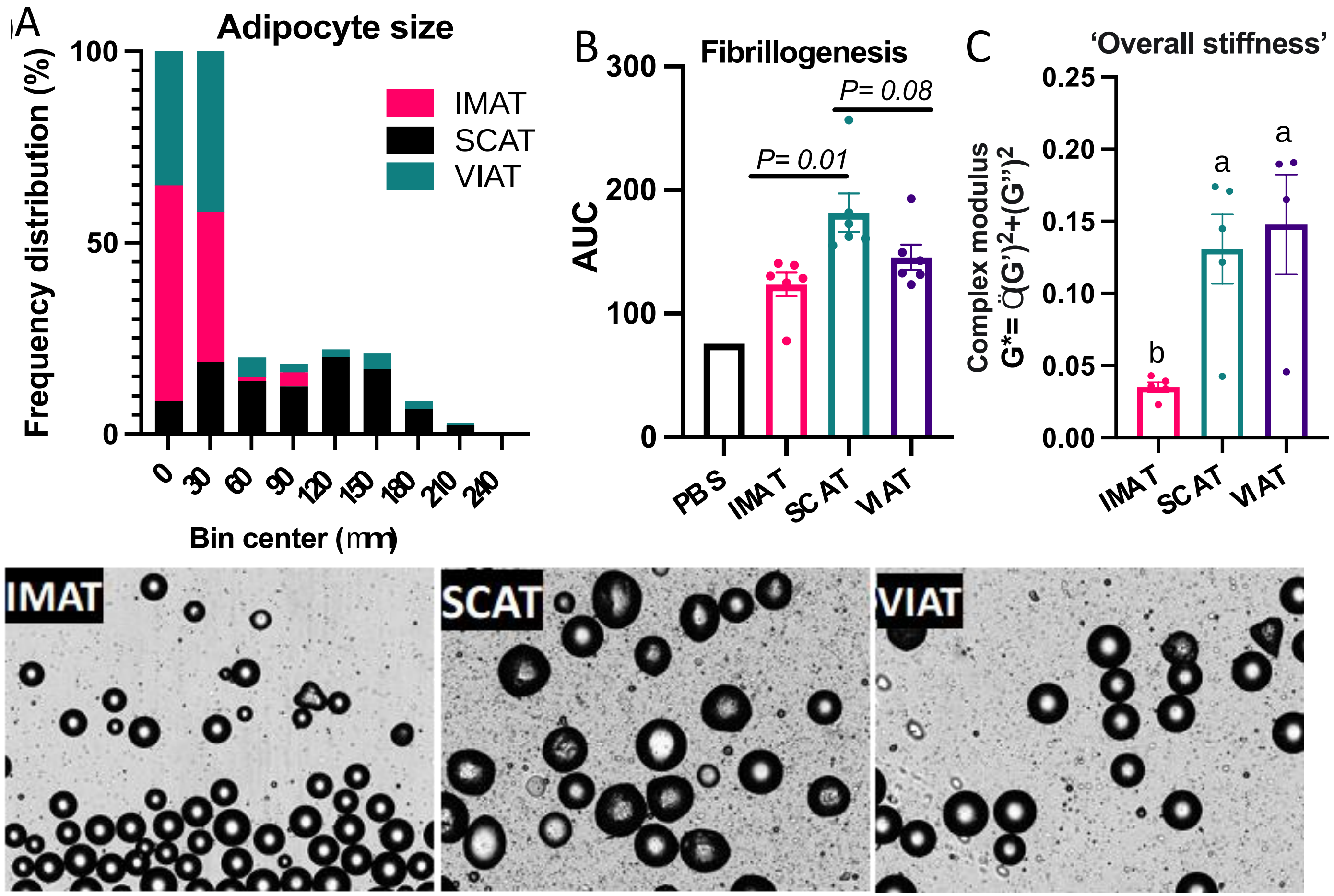

Figure 5. (A) Frequency distribution of buoyant adipocytes from IMAT, SCAT and VIAT of beef cattle measured in a K2 cellometer (Nexcelom). Statistical analysis: SCAT x IMAT: P=0.002; SCAT x VIAT: P=0.002; IMAT x VIAT: P=0.85. (B) Calculated area under the curve (AUC) of collagen I fibrillogenesis in IMAT, SCAT and VIAT. PBS was used as a control. (C) Complex modulus of beef IMAT, SCAT and VIAT obtained from rheological analysis.