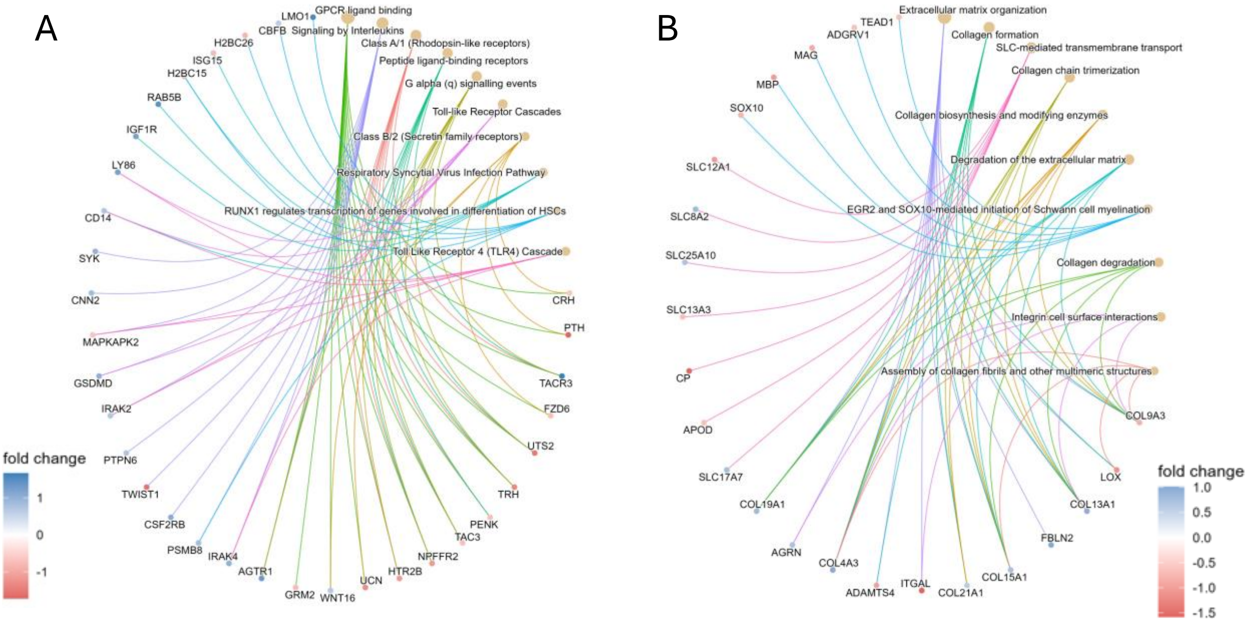

Supplementary Figure 5. Circular category network plots. Top 10 enriched pathways and their associated genes when using differentially expressed genes from *Figure 3A* (**A**) and *Figure 3B* **(B)**. Pathway terms (categories) are arranged in the top right of the circle, while genes form the remainder of the circle. Coloured edges connect each gene to the pathways in which it participates and overlapping coloured edges emphasizes genes that are members of multiple pathways. Node (outer circles) colour indicates the gene's $\log_2$ fold change between LPS + Vehicle vs control (A), and LPS + IL-1Ra vs LPS + Vehicle (B) (red: downregulated, blue: upregulated).