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🌐 Differential gene expression analysis

📄 In 1 collection

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Protocol status: Working
We use this protocol and it's working

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Abstract

Differential gene expression analysis from Kilfeather, Khoo et al., 2024

Troubleshooting

Protocol

1   Differential gene expression analysis in TRAP samples (including calculation of gene enrichment and depletion, relative to tissue homogenate RNA) was performed using DESeq2 (v1.36.0, RRID:SCR_015687) in R (v4.2.1, RRID:SCR_001905) with Bioconductor (v3.15, RRID:SCR_006442). Adaptive shrinkage of log fold change estimates was performed using ashr. The following settings were changed from defaults: minReplicatesForReplace = Inf, cooksCutoff = Inf, filterFun = ihw, lfcThreshold = $\log_2(1.05)$. Genes were classed as significantly differentially expressed with an FDR-adjust P value < 0.01. Protein-protein interactions were obtained using STRINGdb (version 11) with a minimum confidence threshold of 0.4.