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Gene set enrichment analysis

In 1 collection

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

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Abstract

Gene set enrichment analysis from Kilfeather, Khoo et al., 2024

Troubleshooting

Protocol

1 No statistical methods were used to predetermine sample sizes, but our sample sizes for TRAP analyses surpass those reported in previous publications[23,28,87] and our sample sizes for Stereo-seq samples are comparable with or exceed those of similar spatial transcriptomic datasets[11]. All statistical analyses were performed with R (v4.2.1) and Python (v3.9). All *P* values were modified to an FDR of 1, 5 or 10 % as described in the text with the Benjamini & Hochberg method.