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GWAS prioritization analysis

In 1 collection

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

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Abstract

GWAS prioritization analysis from Kilfeather, Khoo et al., 2024

Troubleshooting

Protocol

1 A list of 303 genes (sourced from Nalls et al., 2019 supplementary materials), containing SNPs at an $r^2 > 0.5$ and located within ±1 Mb of 107 common risk variants for sporadic PD was used for prioritization analysis. To convert between human and mouse gene symbols, homologene (v1.4.68.19.3.27, RRID:SCR_002924) and biomaRt (v2.52.0, RRID:SCR_019214) were used. TRAP enrichment (measured as the product of the $\log_2$ fold-change and FDR-adjusted *P* value) and specificity indices for DAT-TRAP samples were used for gene prioritization, per lead SNP.