raw con_sp.hsa.canonical.isoforms_trembl protein_groups 0.3 30m_vs_ud 1h_vs_ud + 6h_vs_ud × 1d_vs_ud 0.2 Leading logFC dim 2 0.1 0.0 -0.1 -0.2 -0.2 0.0 0.2 0.4 Leading logFC dim 1