raw con_sp.hsa.canonical.isoforms protein_groups 30m_vs_ud 1h_vs_ud + 6h_vs_ud 0.2 \times 1d_vs_ud X 0.1 Leading logFC dim 2 0.0 -0.1 -0.2 -0.3 -0.2 0.0 0.2 0.4 0.6 Leading logFC dim 1