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