raw con_sp.hsa.canonical.isoforms peptides 30m_vs_ud 9.0 1h_vs_ud + 6h_vs_ud × 1d_vs_ud 0.4 Leading logFC dim 2 0.2 0.0 -0.2 -0.4 9.0--0.5 0.5 0.0 Leading logFC dim 1