MDS normalised, hc =2 con_sp.hsa.canonical.isoforms peptides 0.5 30m_vs_ud 1h_vs_ud + 6h_vs_ud \times 1d_vs_ud Leading logFC dim 2 0.0 -0.5 -1.0 -0.5 0.0 0.5 1.0 Leading logFC dim 1