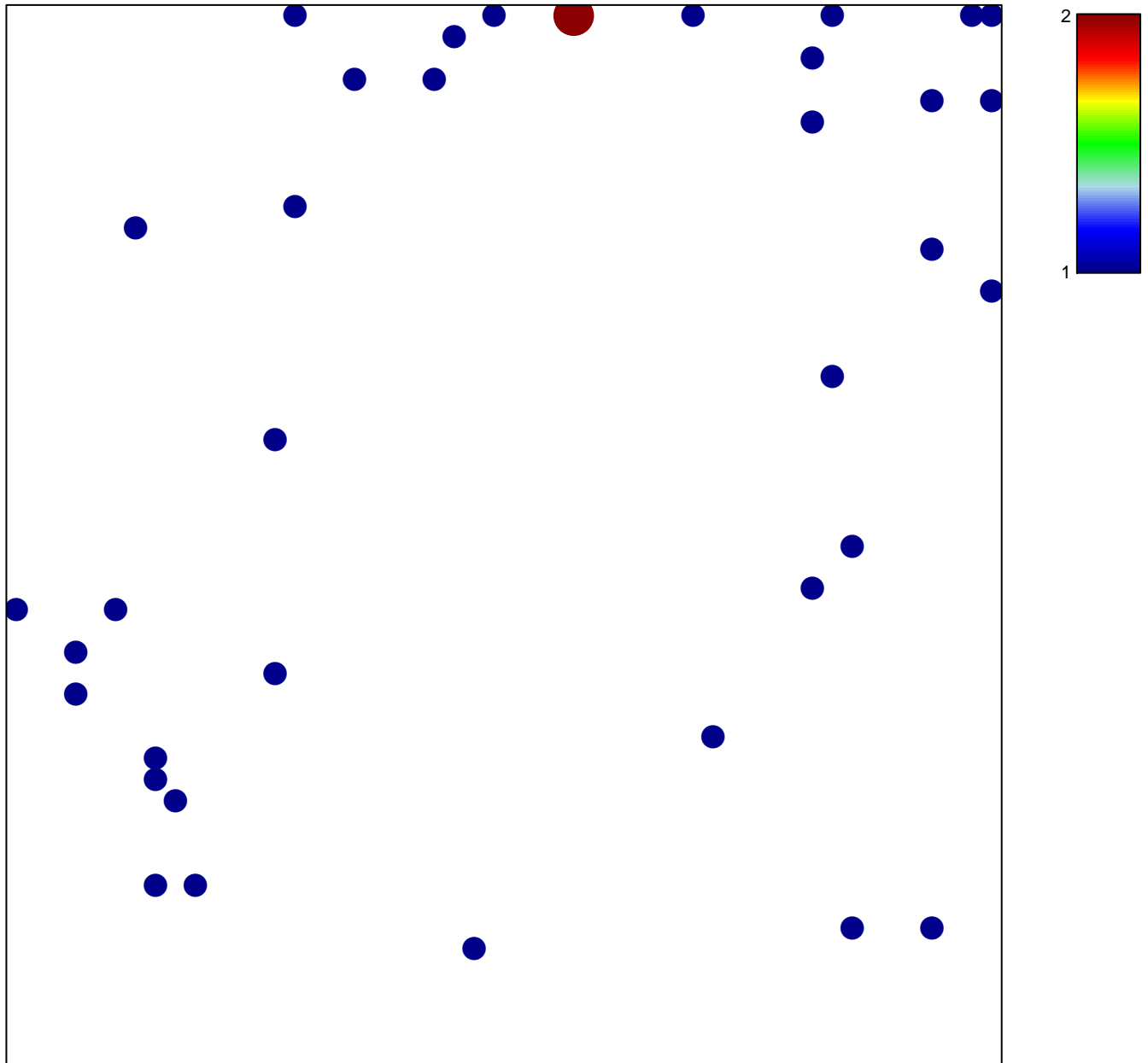


willscher_GBM_proteomics_wtOnly_SpotH



features = 37
chi-square p = 0.8

willscher_GBM_proteomics_wtOnly_SpotH



features = 37 , max = 2