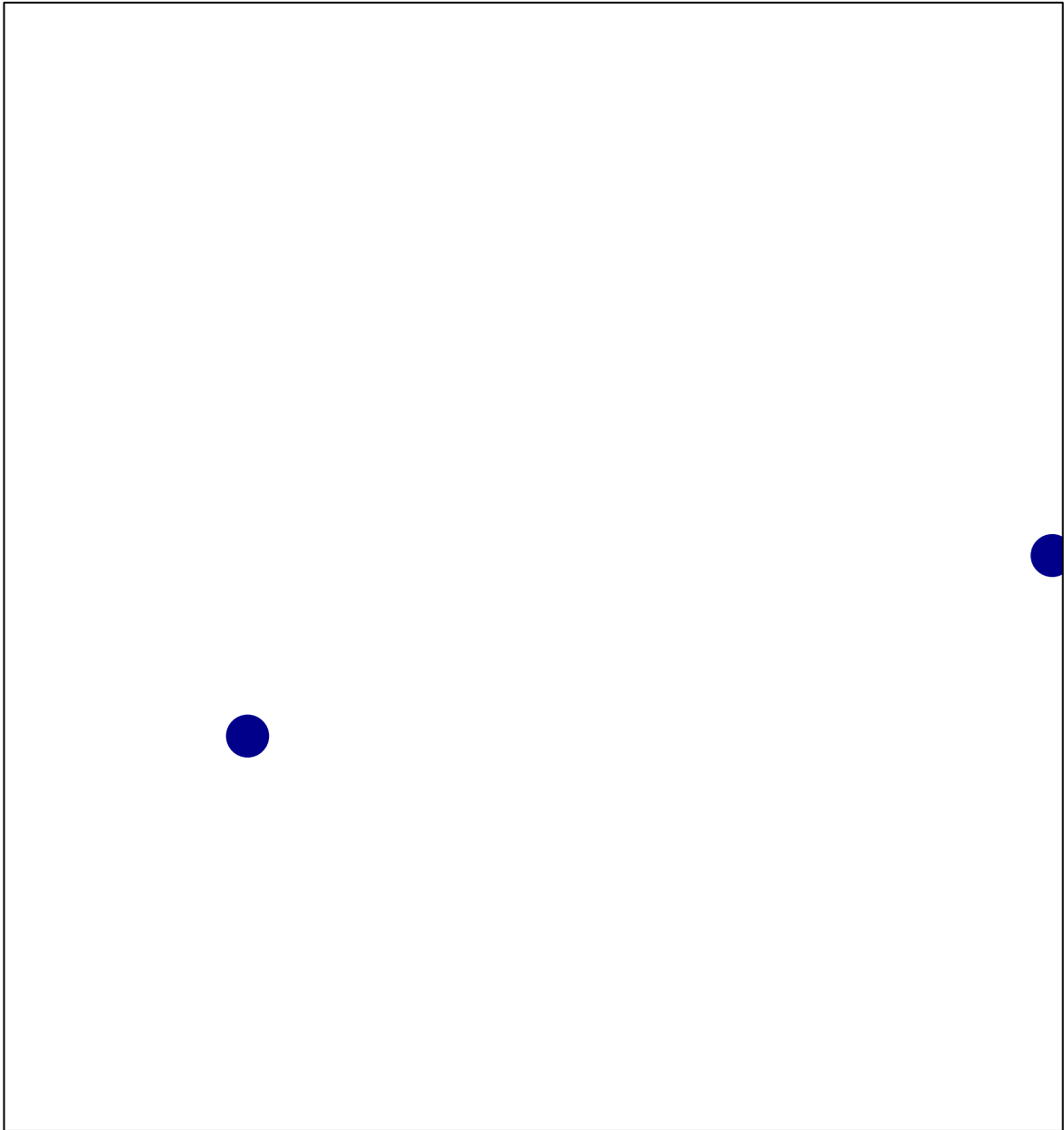
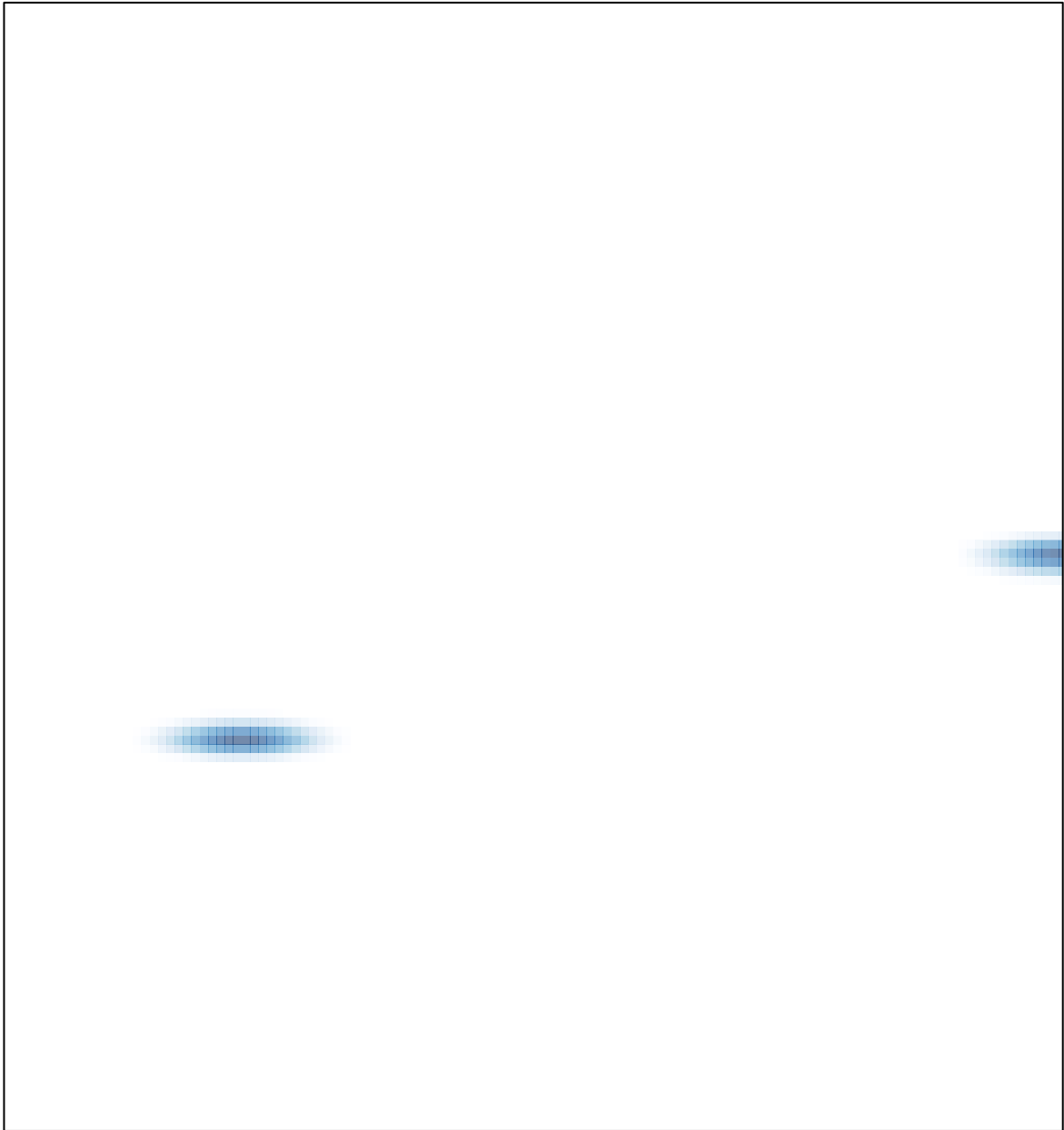


willscher_GBM_LTSwt_proteomics-E_DOWN



features = 2
chi-square p = 0.84

willscher_GBM_LTSwt_proteomics-E_DOWN



features = 2 , max = 1