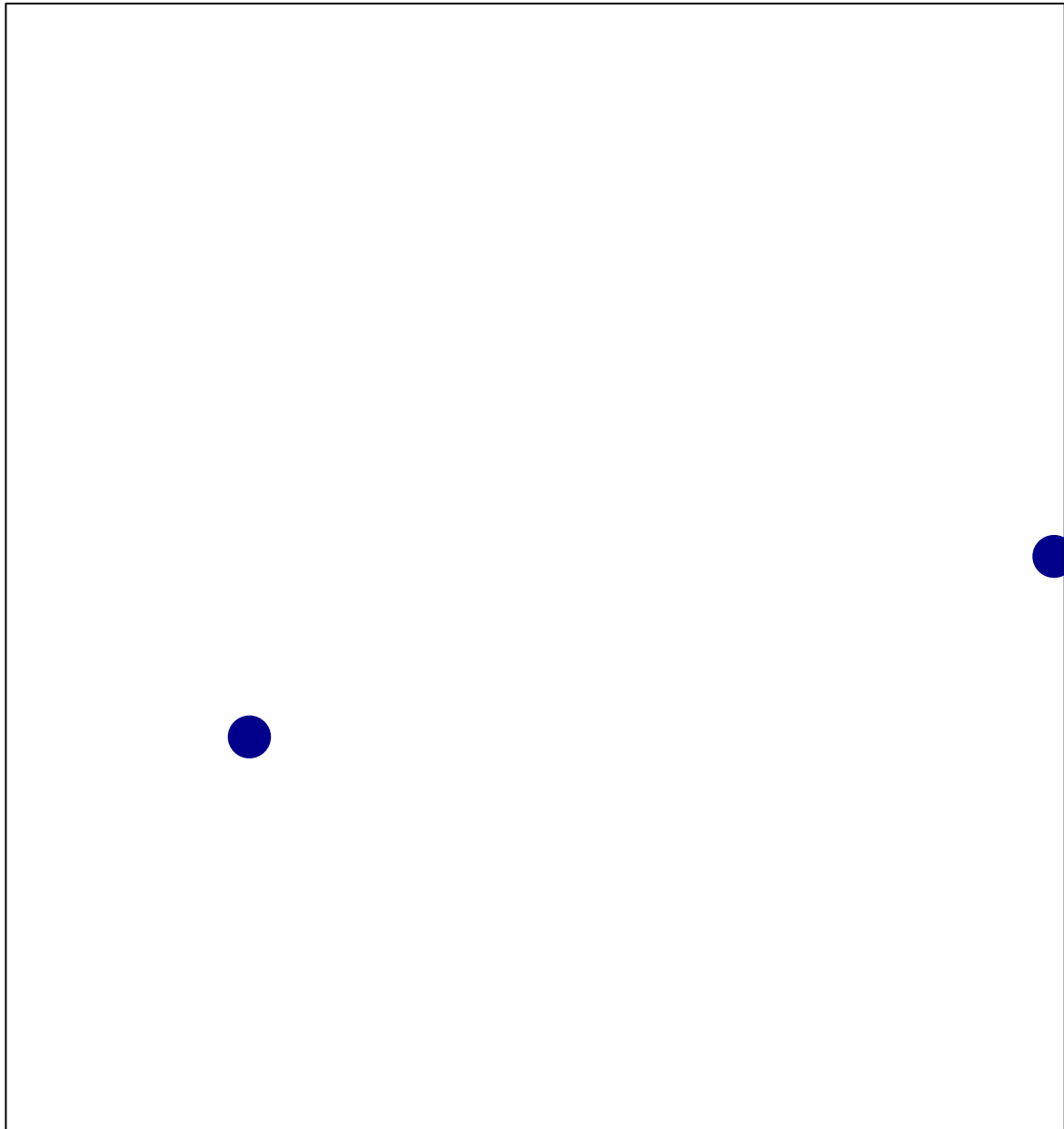
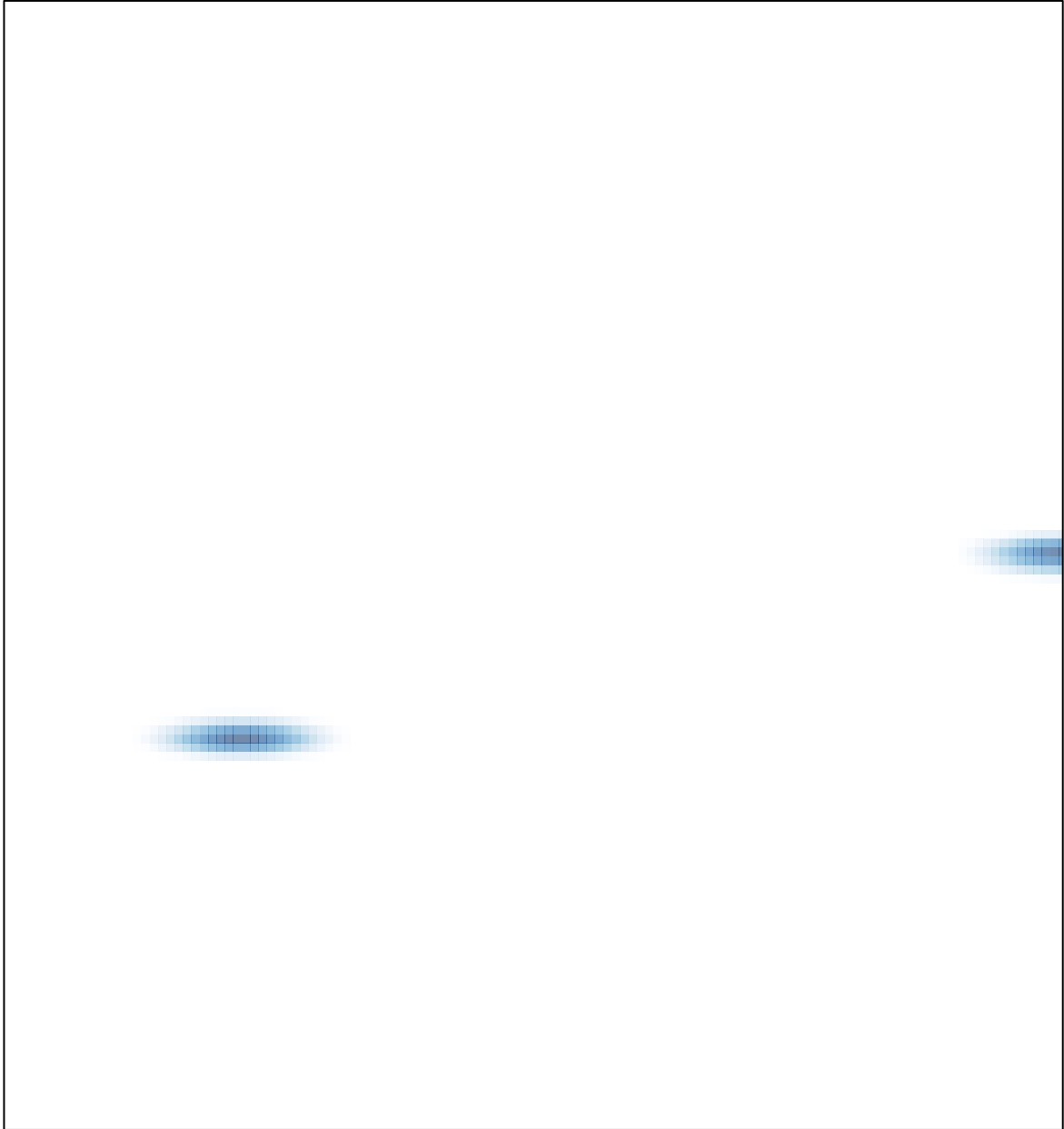


willscher_GBM_LTSmut_proteomics-E_UP



features = 2
chi-square p = 0.84

willscher_GBM_LTSmut_proteomics-E_UP



features = 2 , max = 1