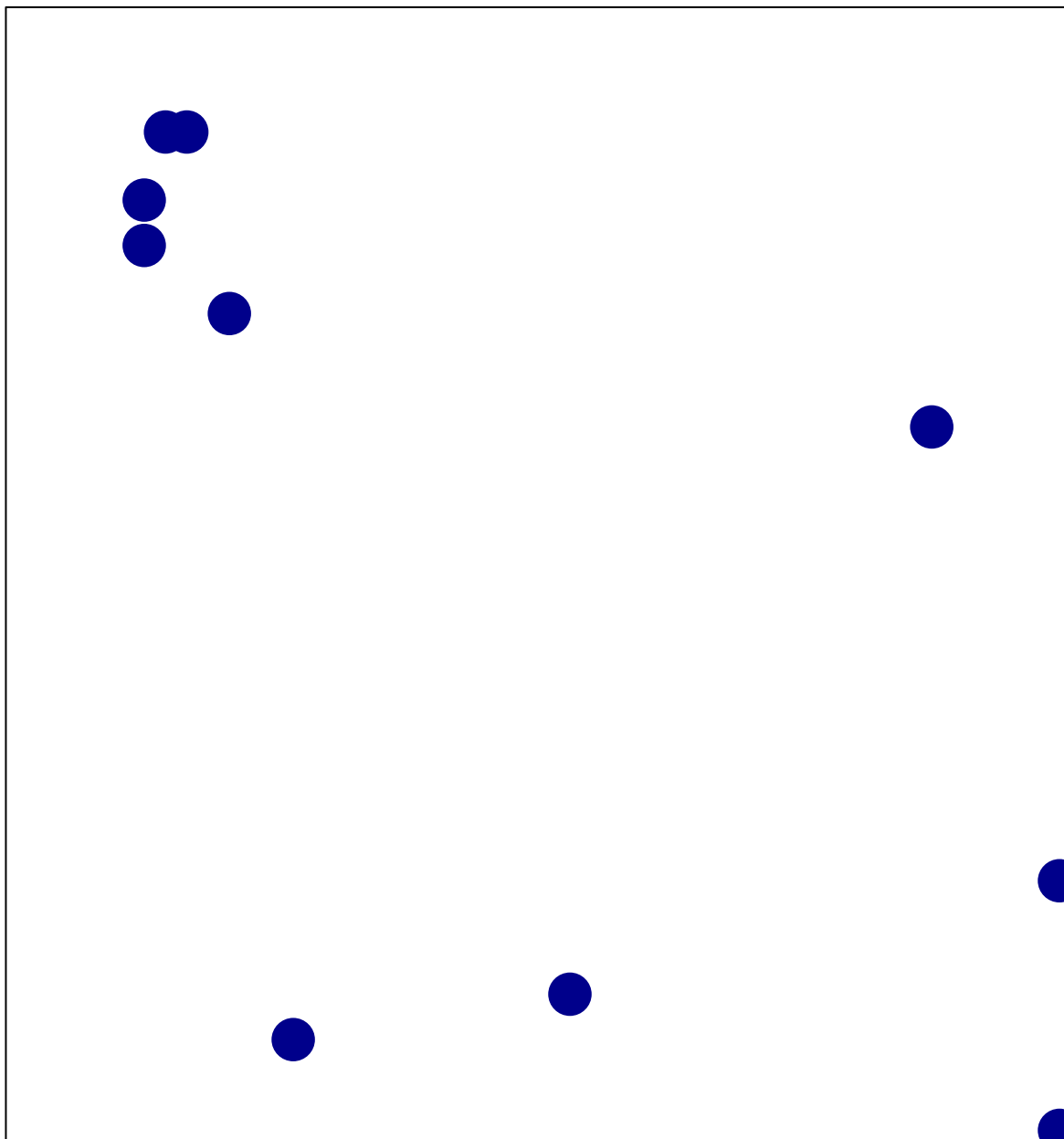
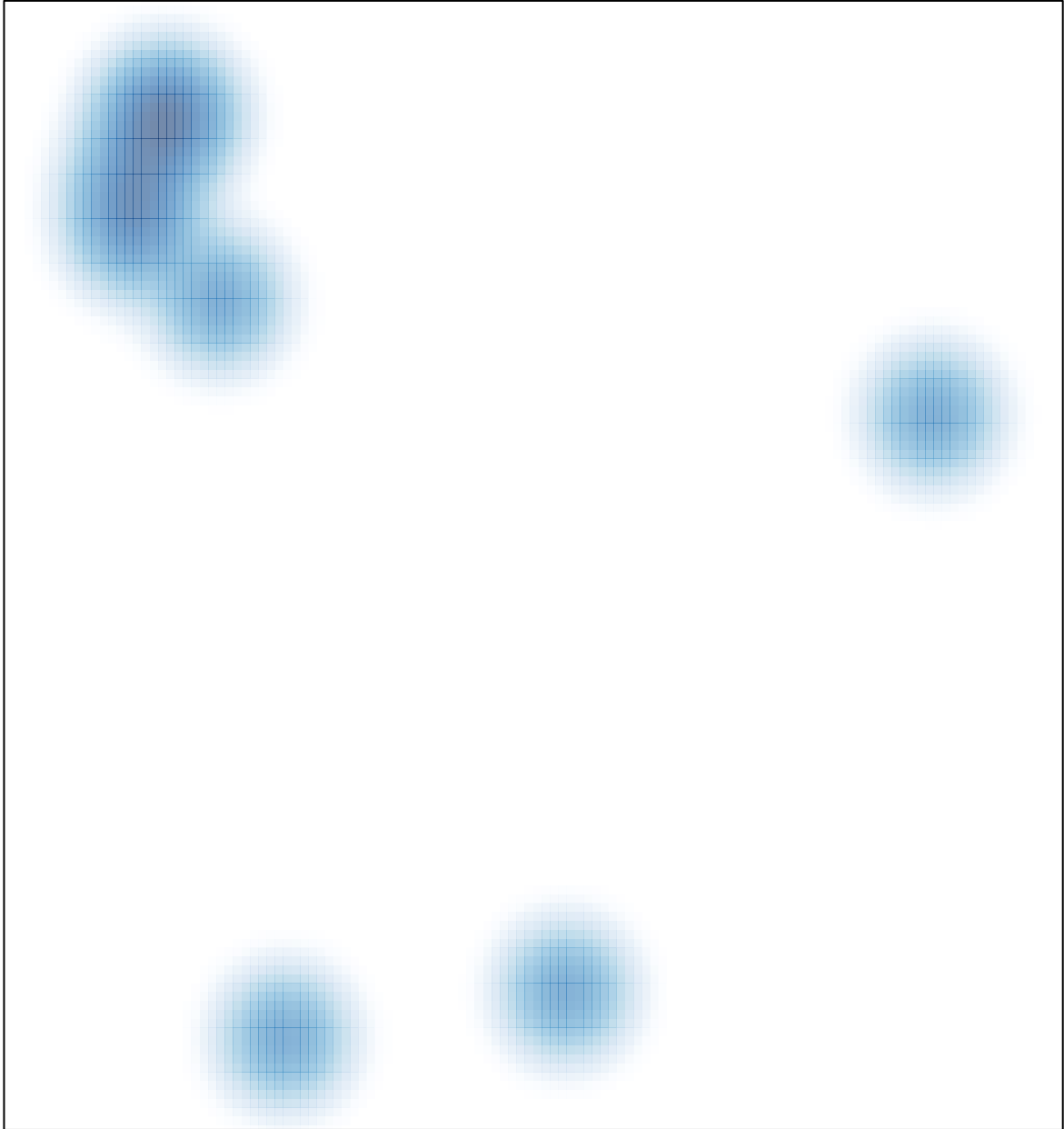


WILLSCHER_GBM_LTSmut_proteomics-A_UP



features = 10
chi-square p = 0.83

WILLSCHER_GBM_LTSmut_proteomics-A_UP



features = 10 , max = 1