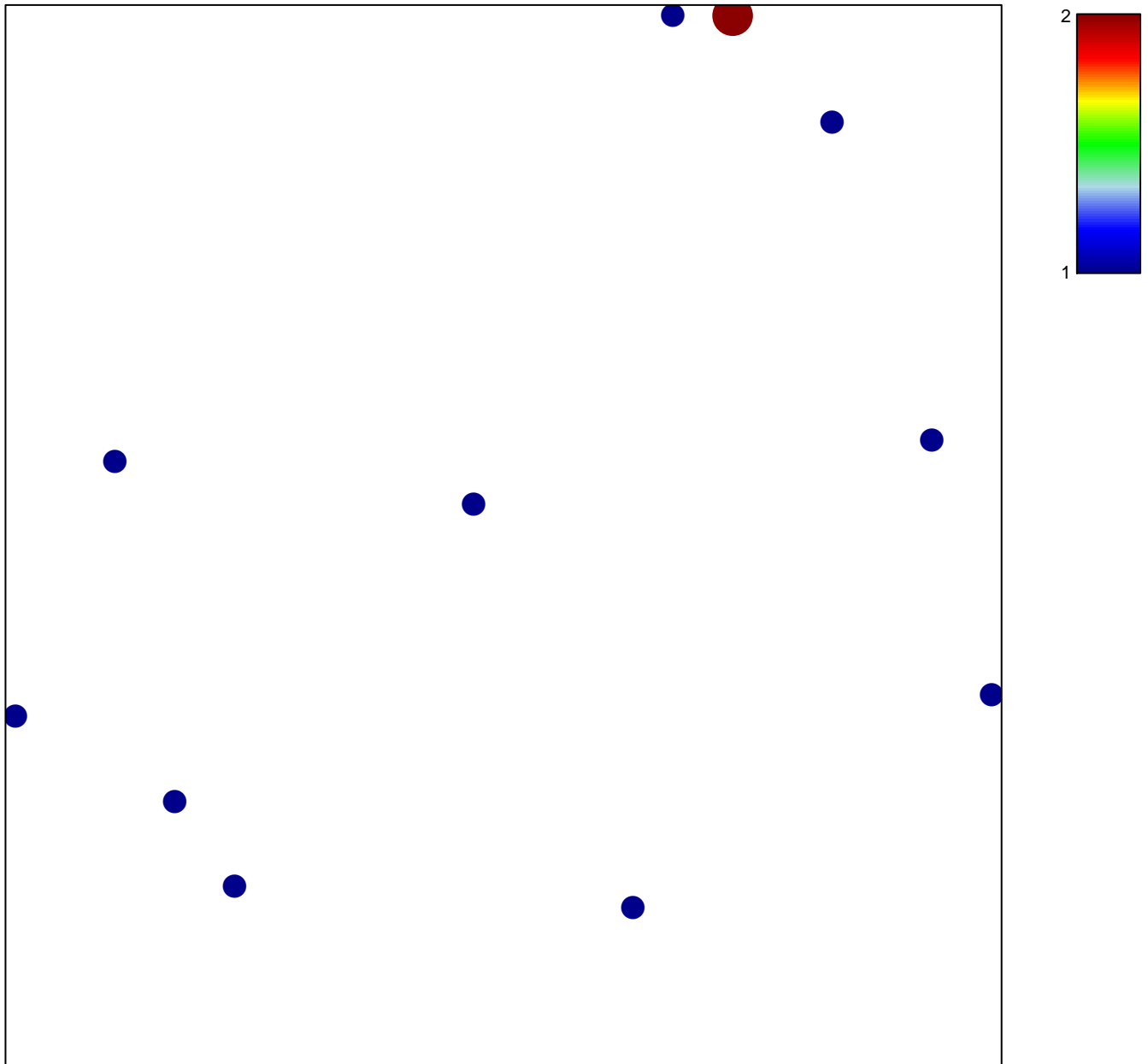
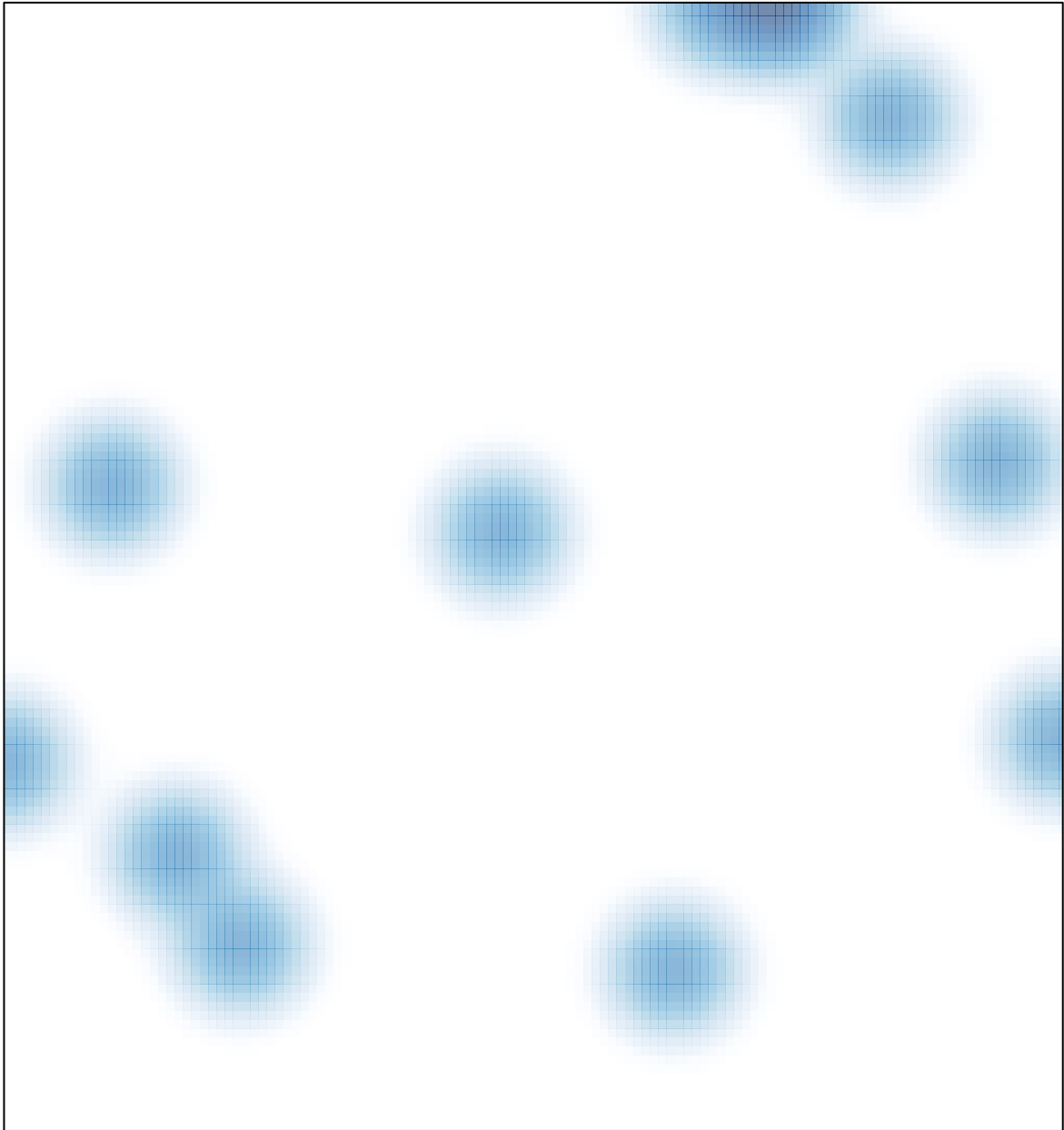


willscher_GBM_LTSmut_proteomics-B_UP



features = 12
chi-square p = 0.83

willscher_GBM_LTSmut_proteomics-B_UP



features = 12 , max = 2