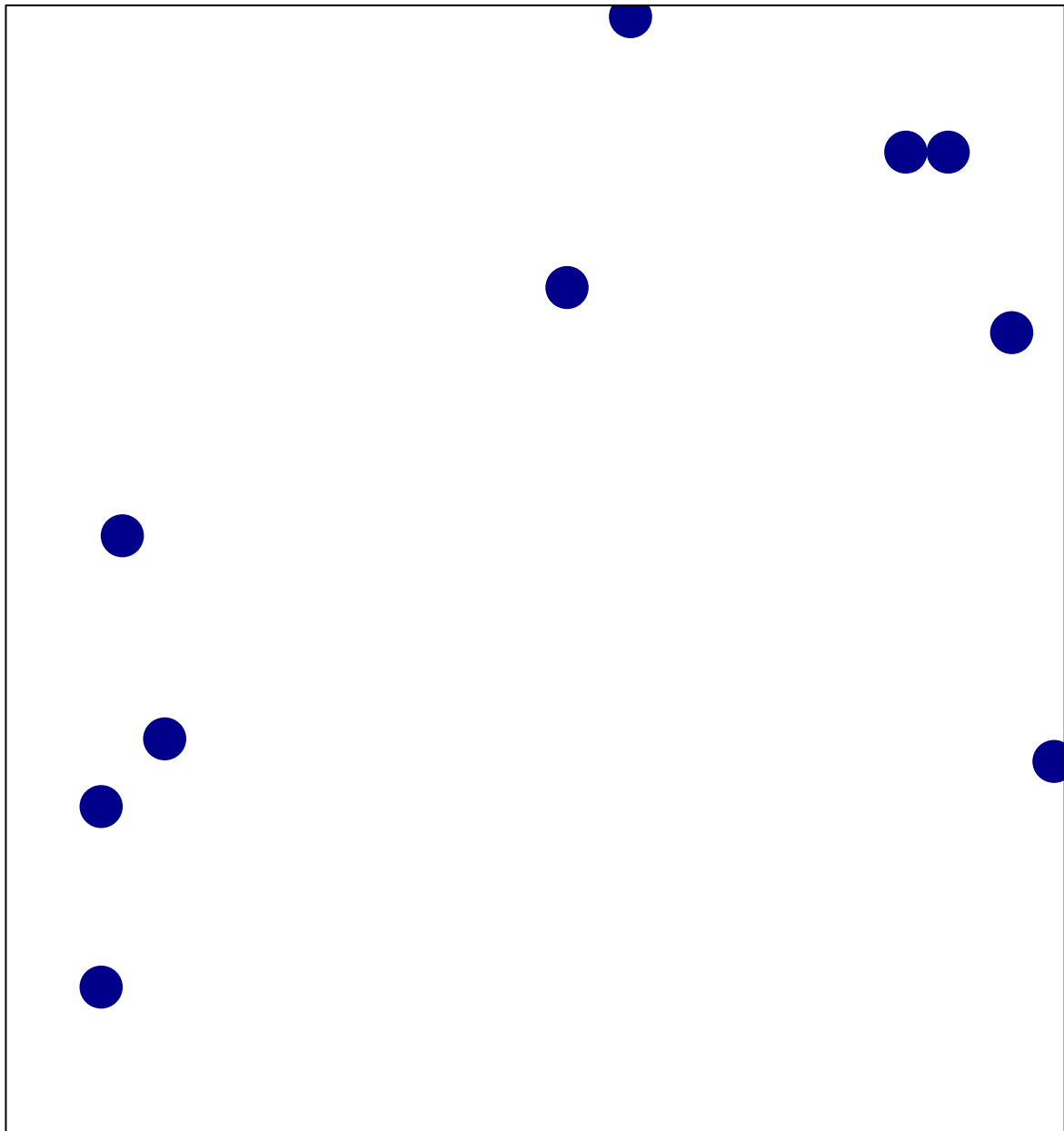
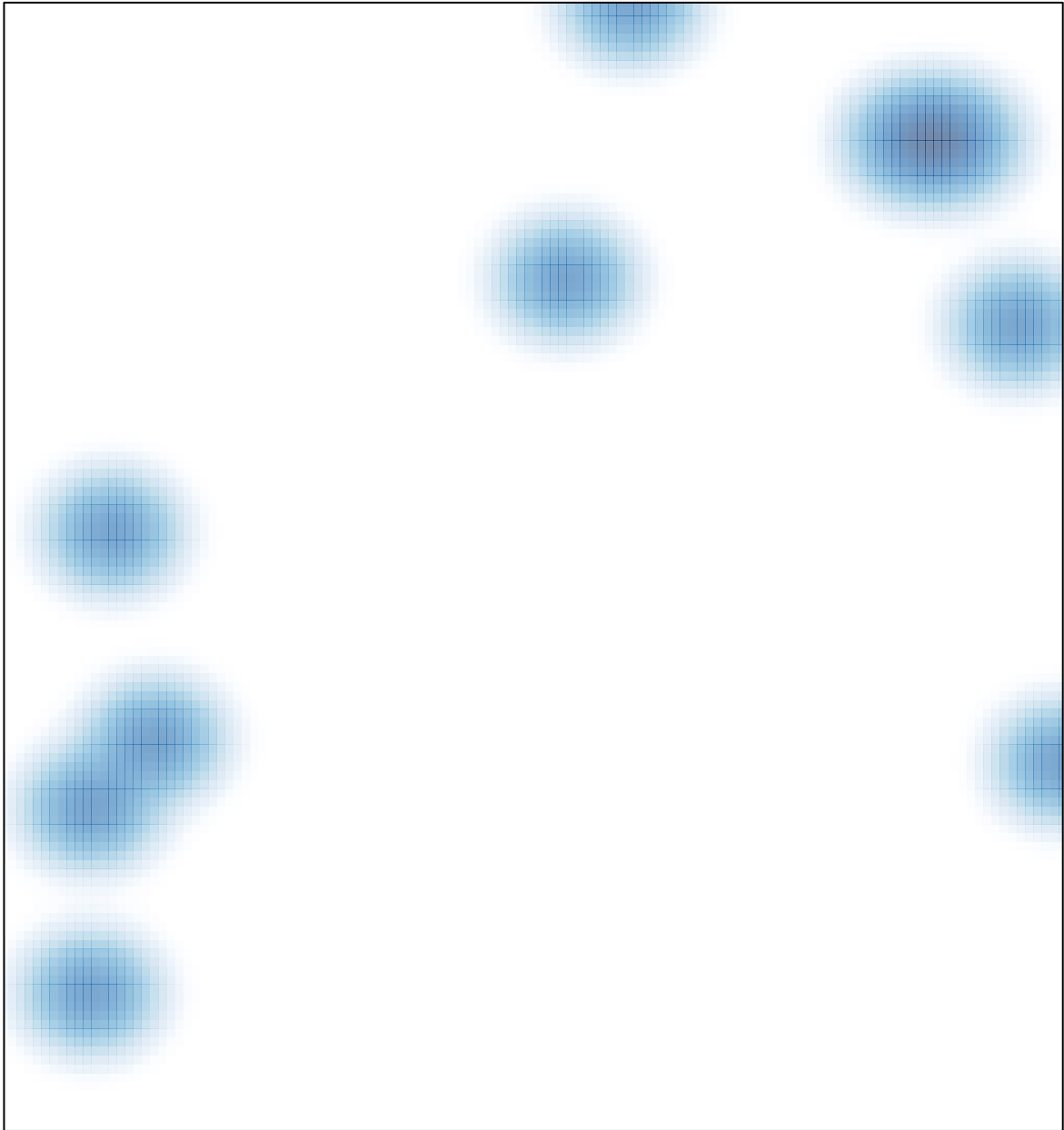


willscher_GBM_LTSmut_proteomics-A_UP



features = 10
chi-square p = 0.84

willscher_GBM_LTSmut_proteomics-A_UP



features = 10 , max = 1