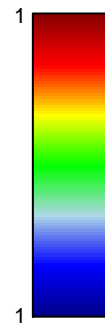
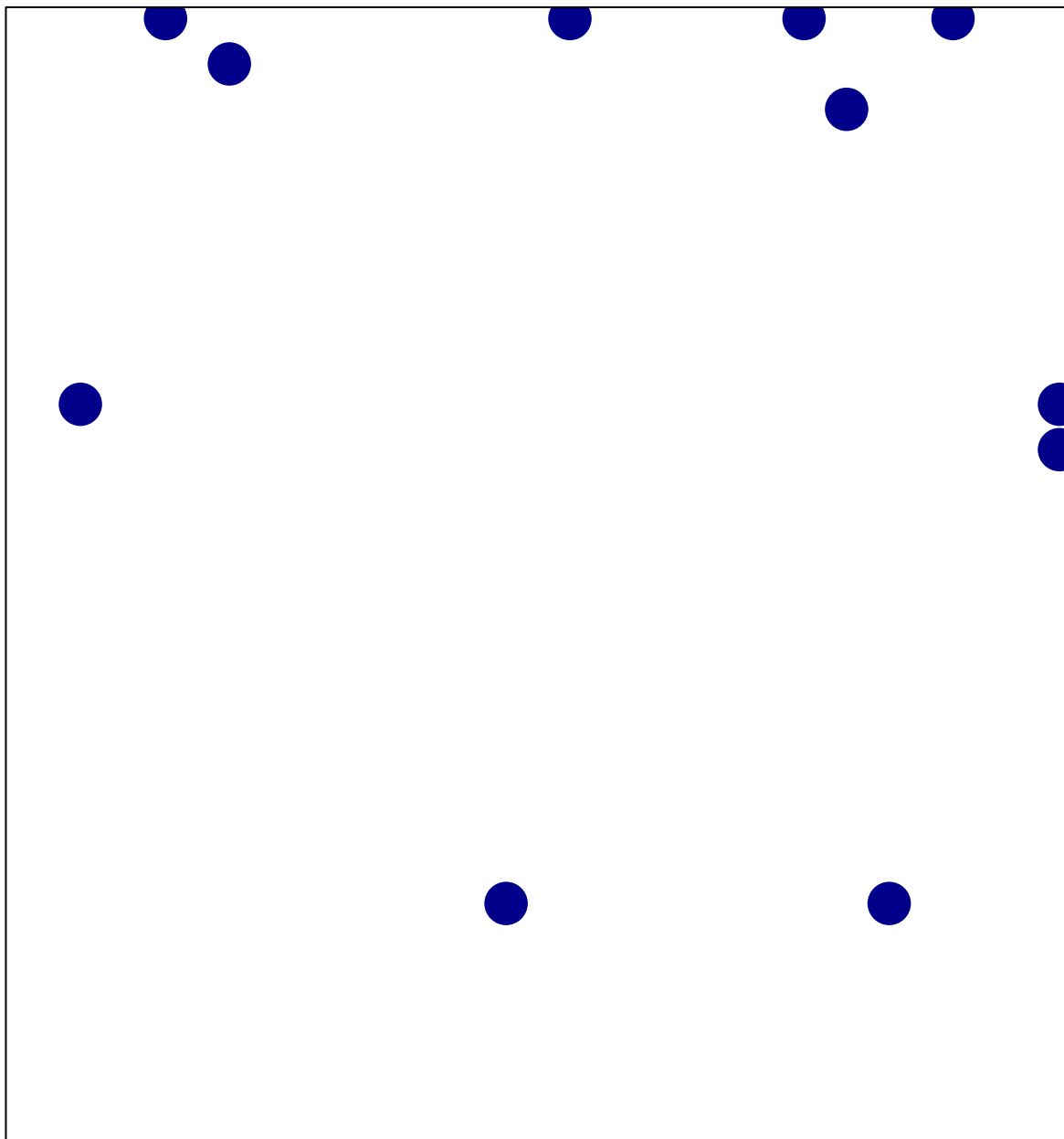
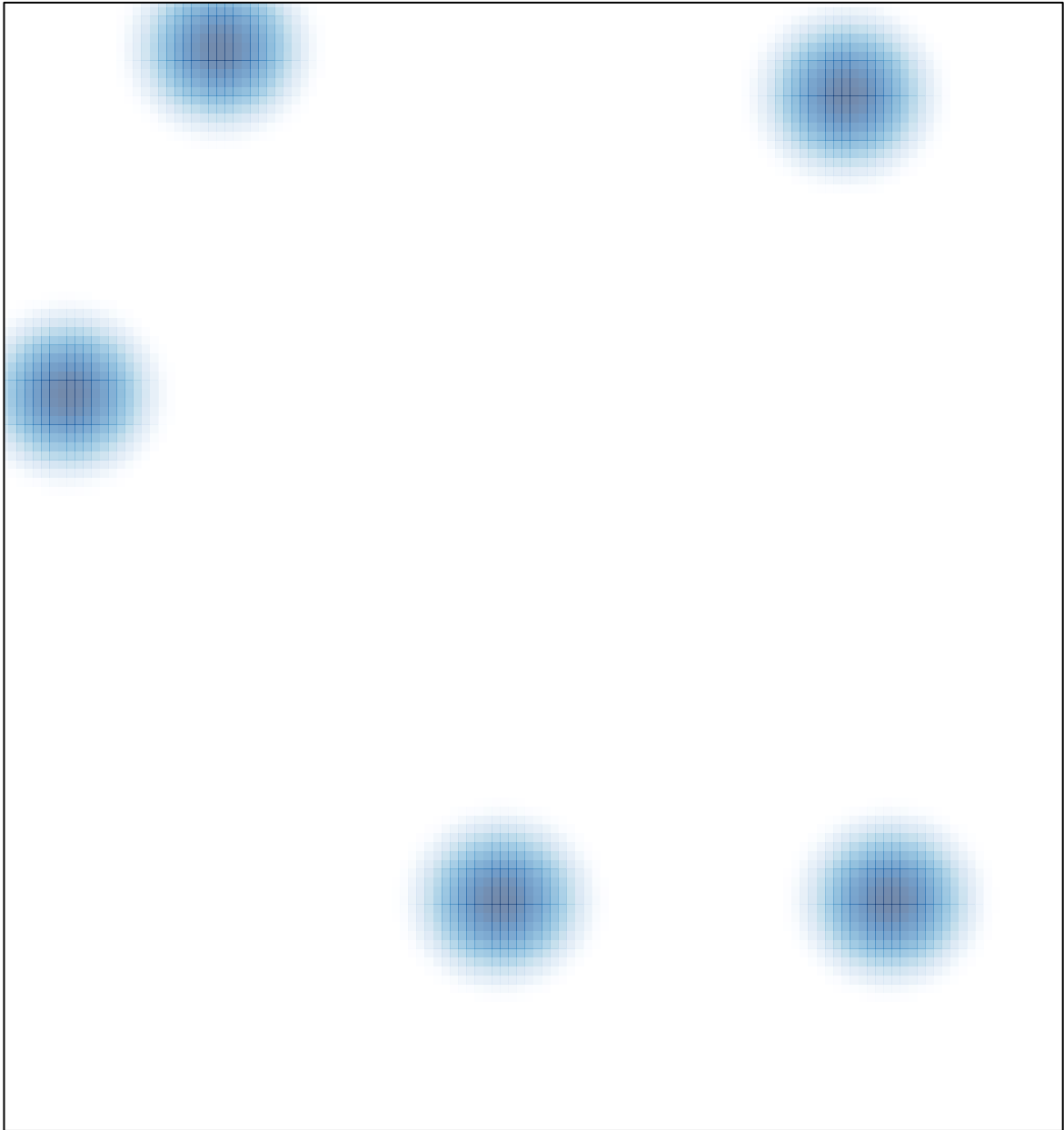


WILLSCHER_GBM_LTSmut_proteomics-B_UP



features = 11
chi-square p = 0.8

WILLSCHER_GBM_LTSmut_proteomics-B_UP



features = 11 , max = 1