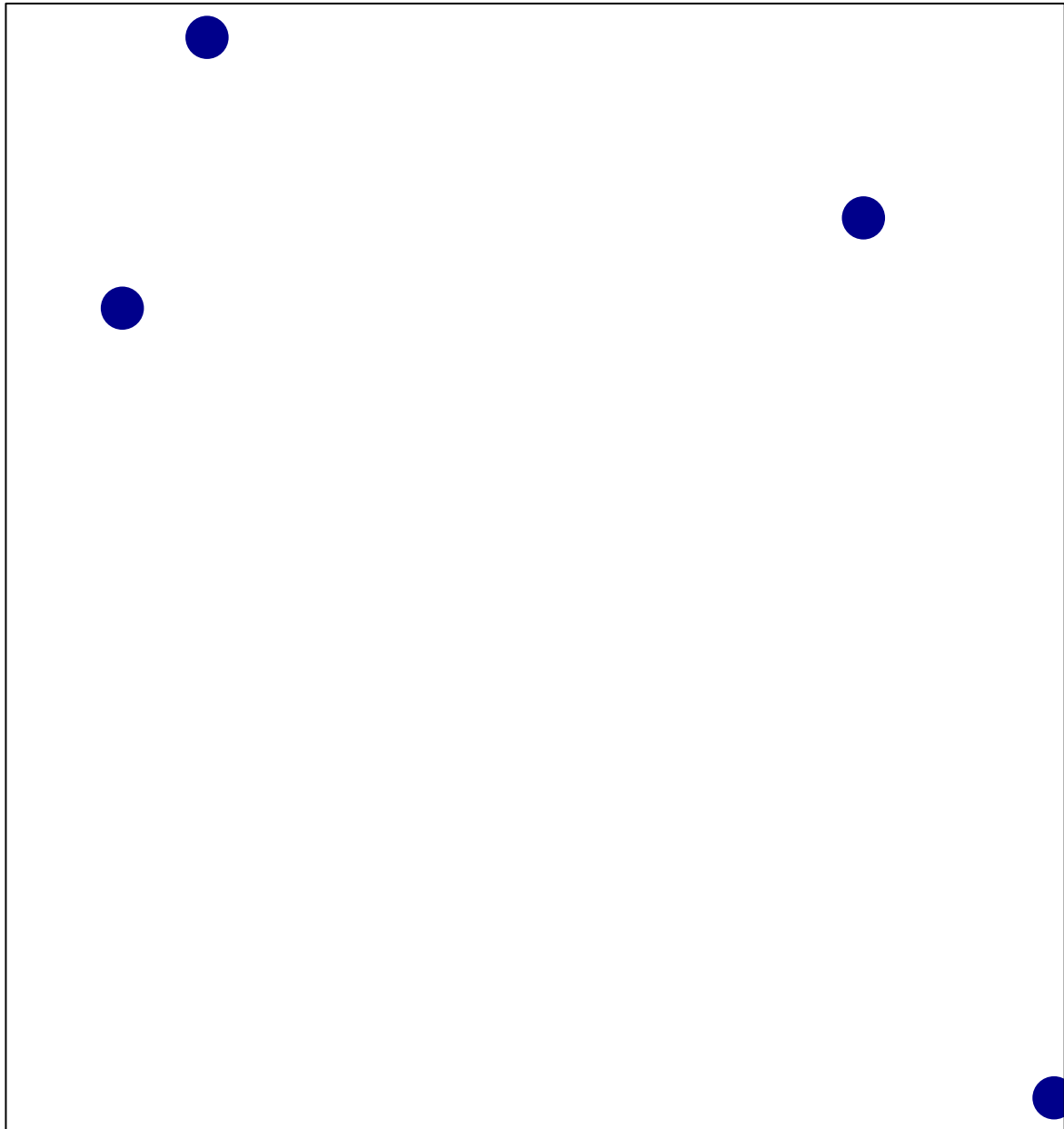
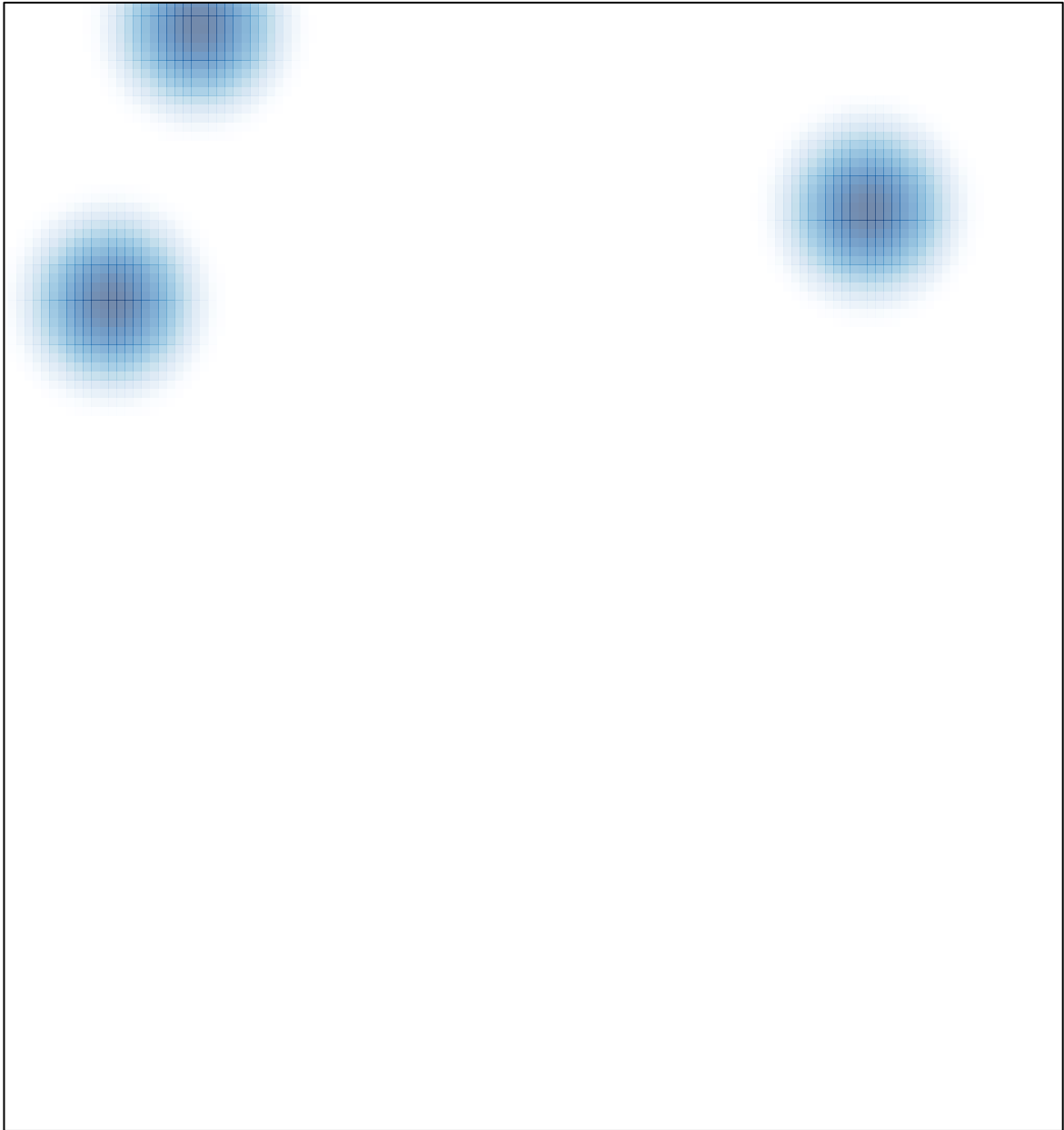


WILLSCHER_GBM_STSwt_proteomics-L_UP



features = 4
chi-square p = 0.85

WILLSCHER_GBM_STSwt_proteomics-L_UP



features = 4 , max = 1