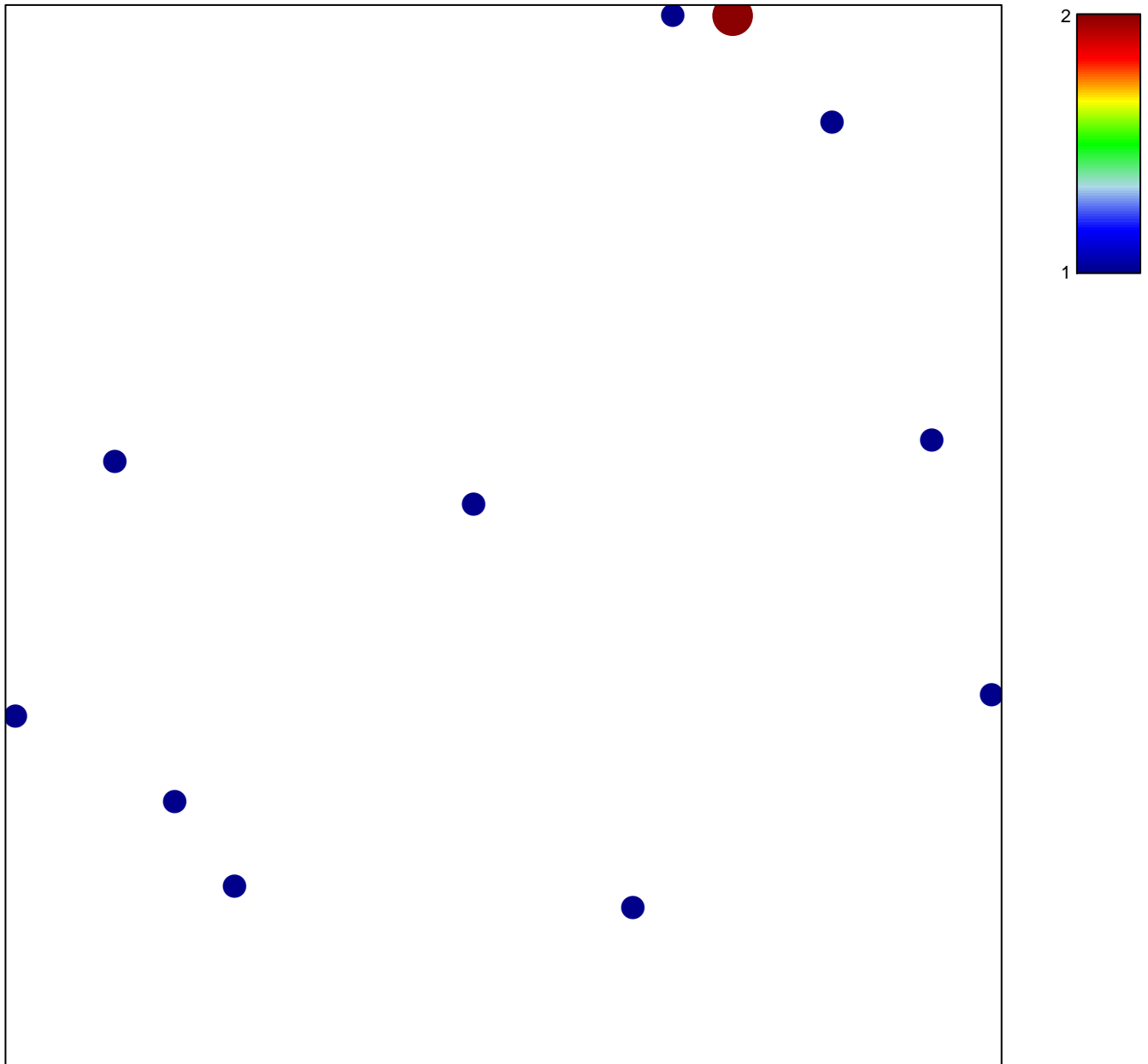
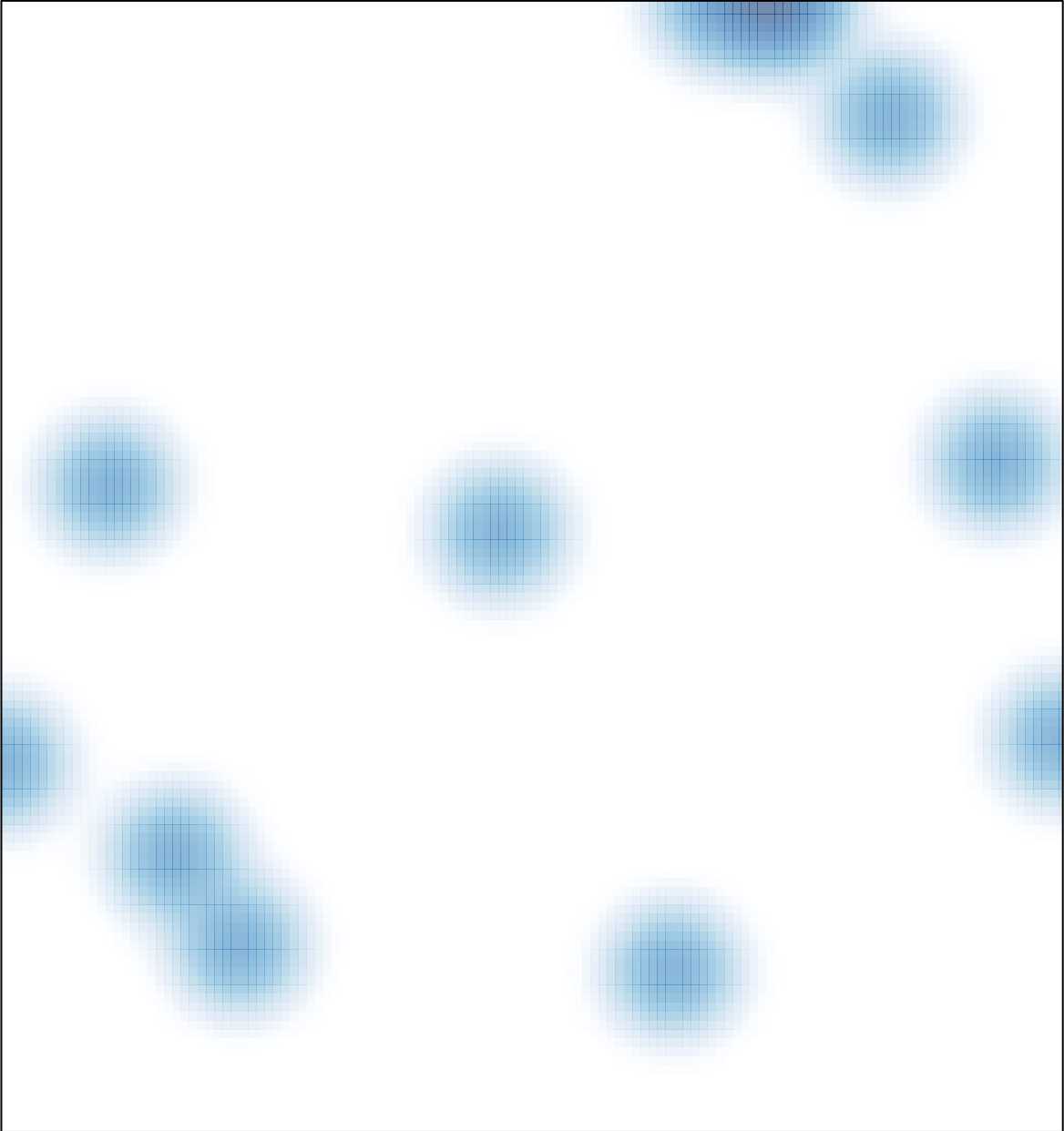


# willscher\_GBM\_STSwt\_proteomics-B\_DOWN



# features = 12  
chi-square p = 0.83

# willscher\_GBM\_STSwt\_proteomics-B\_DOWN



# features = 12 , max = 2