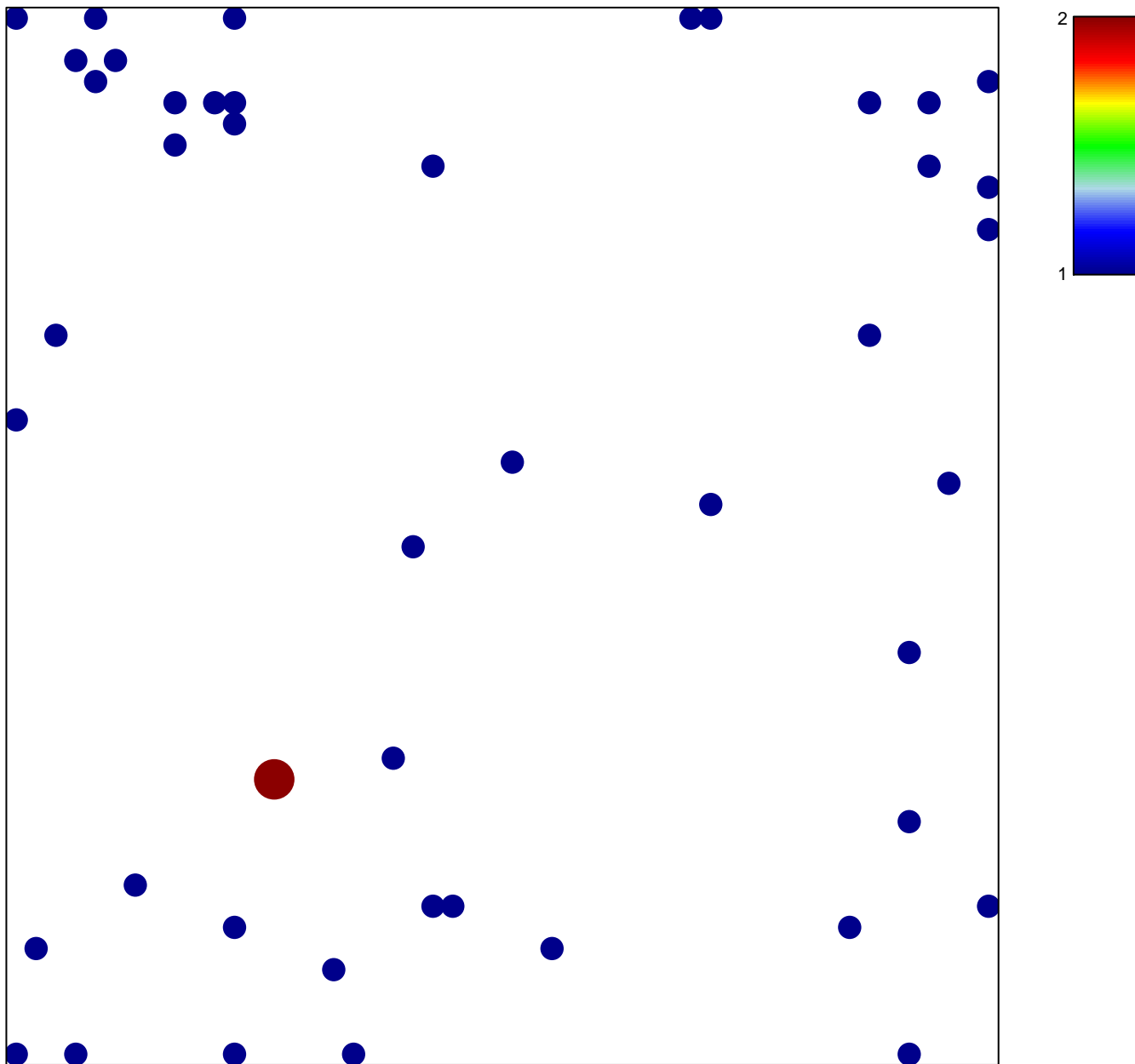
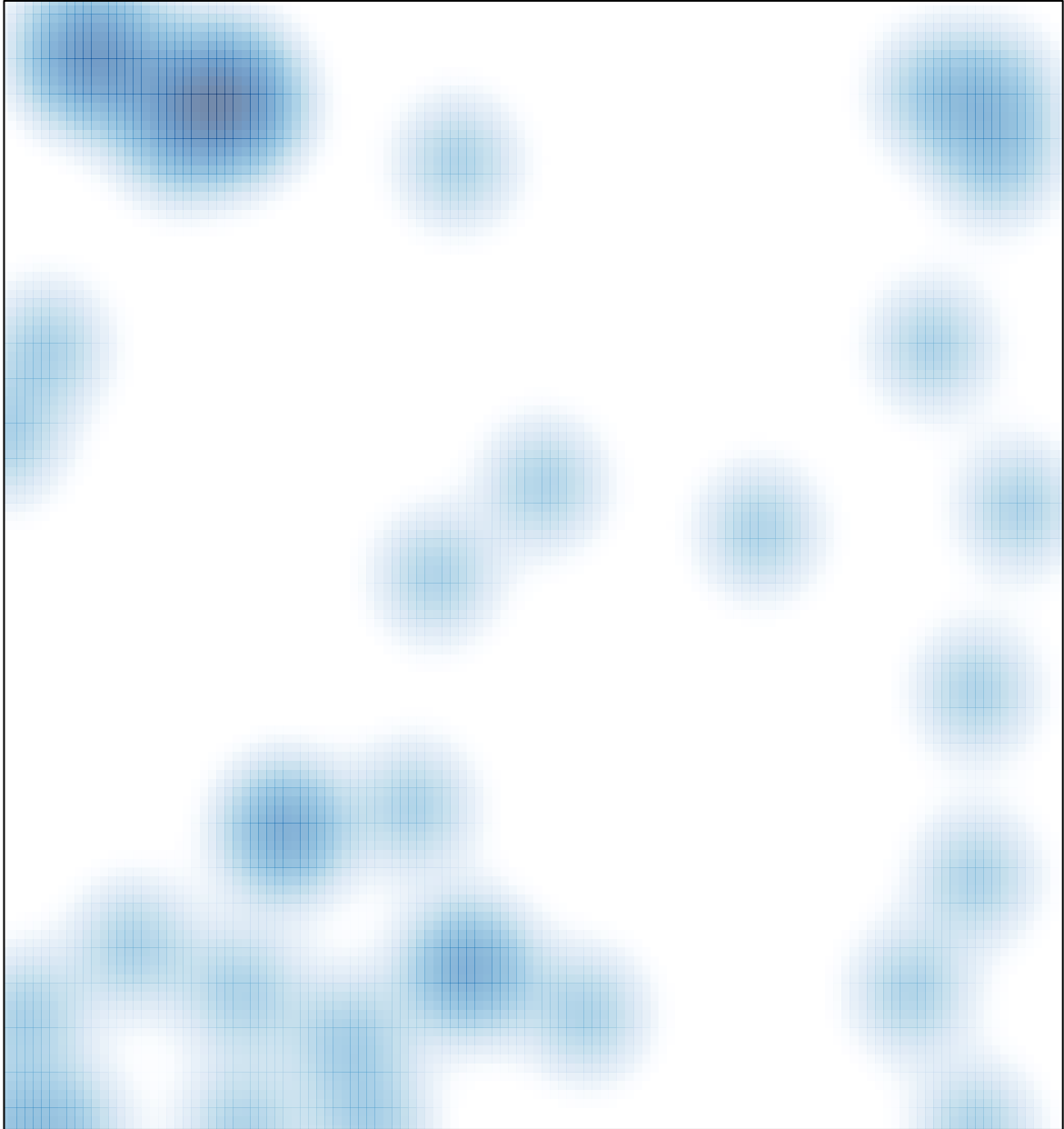


# methylated histone binding



# features = 46  
chi-square p = 0.8

# methyated histone binding



# features = 46 , max = 2