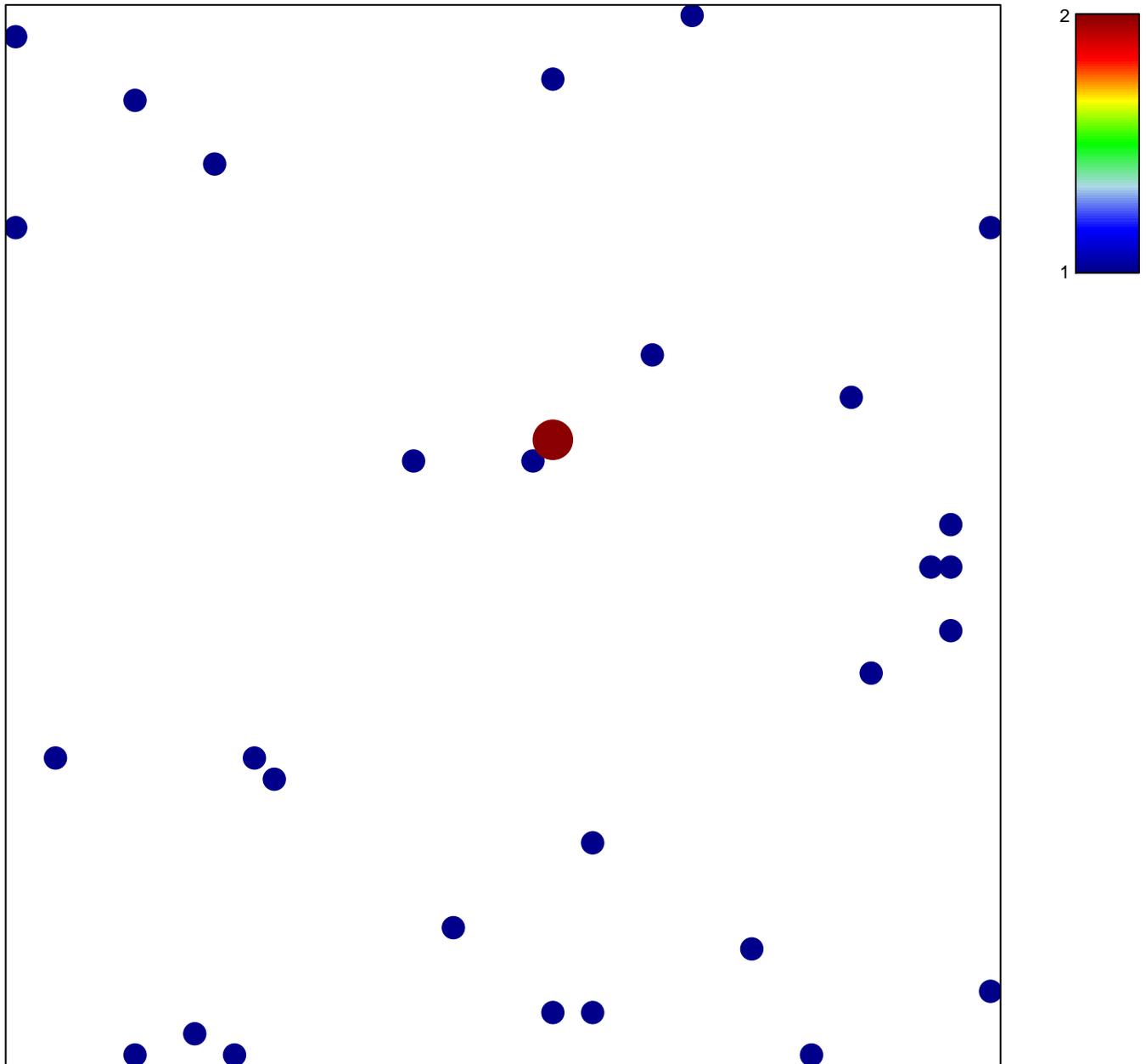
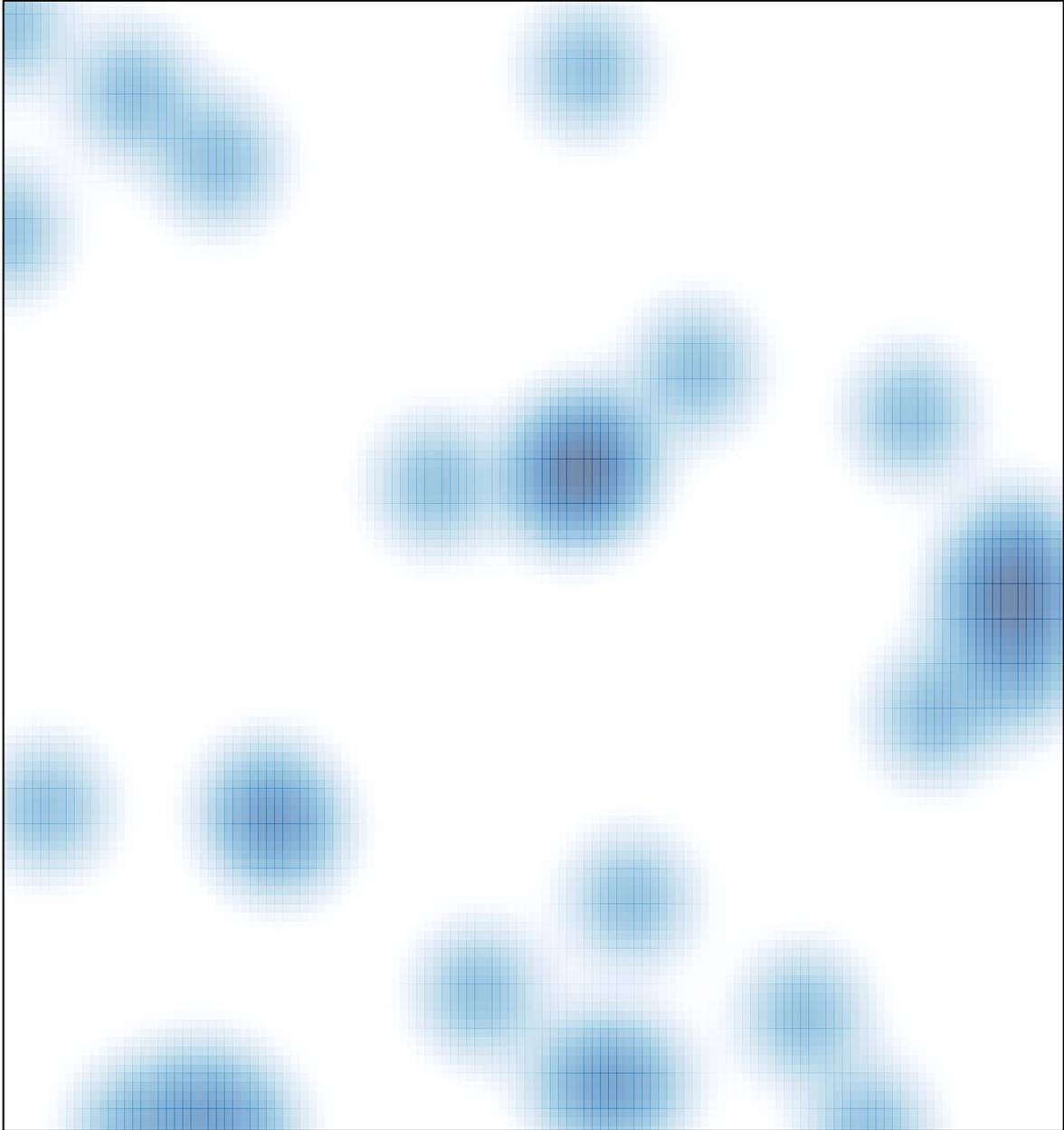


# transcription regulatory region sequence-specific DNA binding



# features = 31  
chi-square p = 0.83

# cription regulatory region sequence-specific DNA b



# features = 31 , max = 2