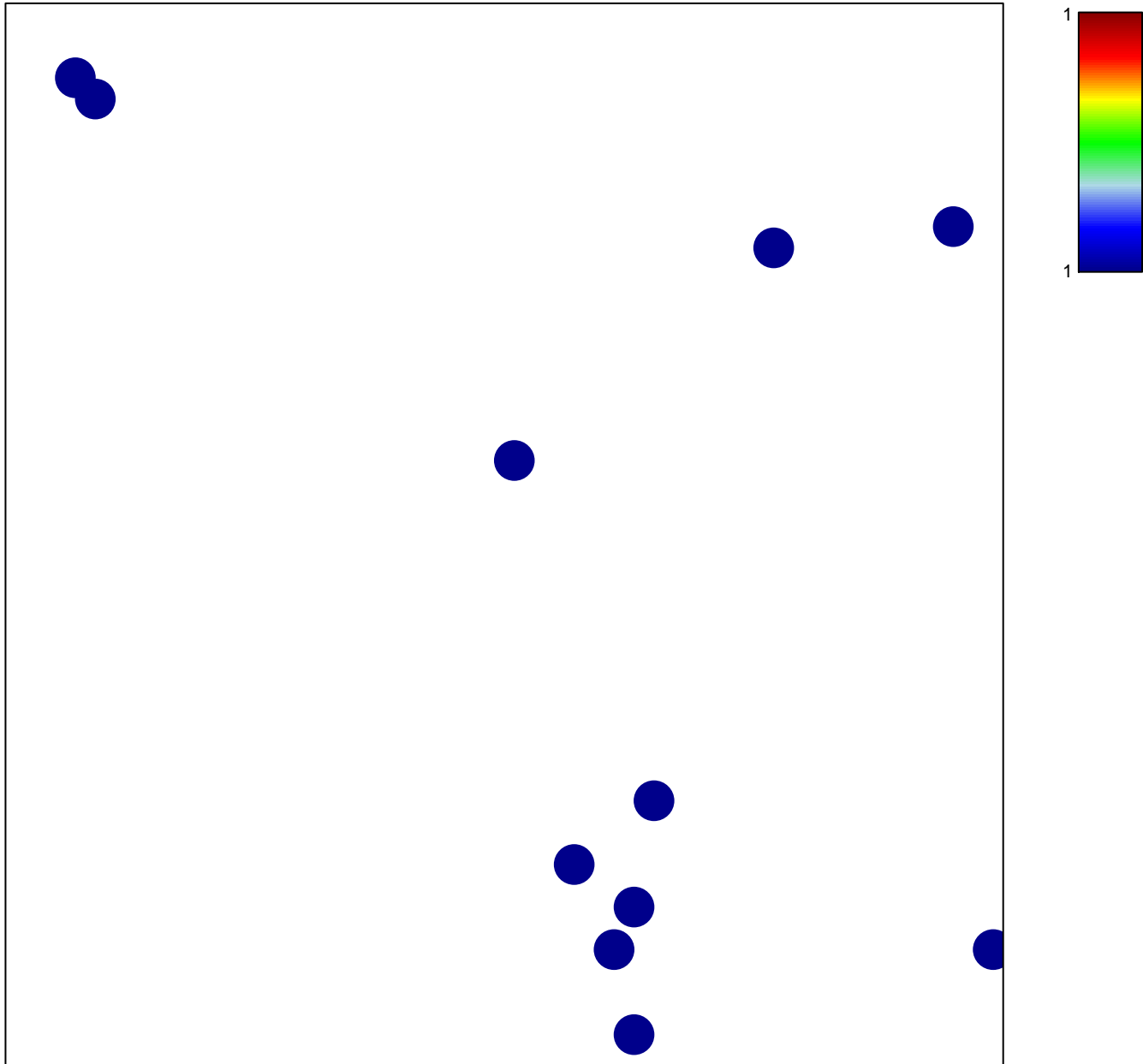
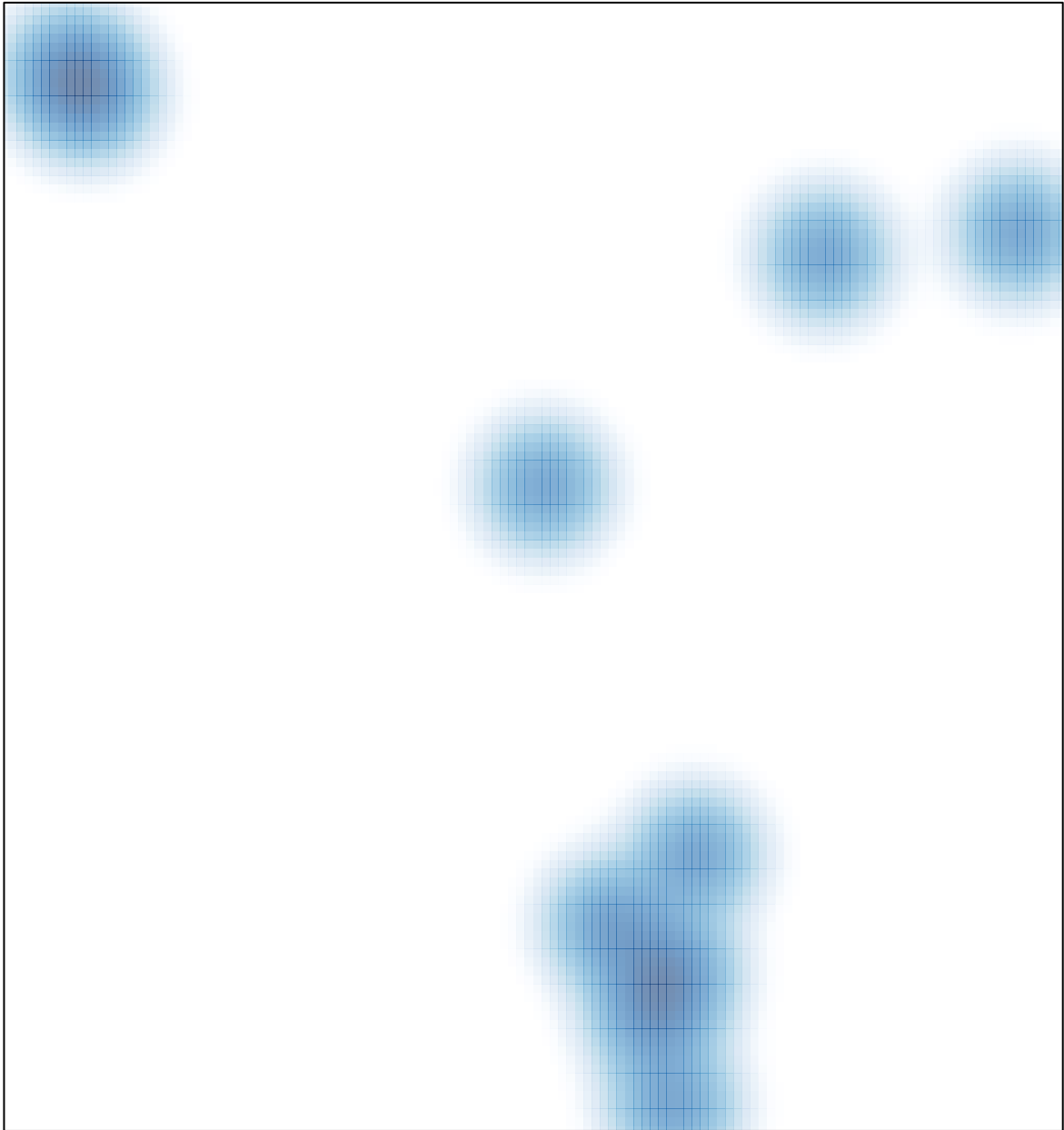


# nucleosome binding



# features = 11  
chi-square p = 0.84

# nucleosome binding



# features = 11 , max = 1