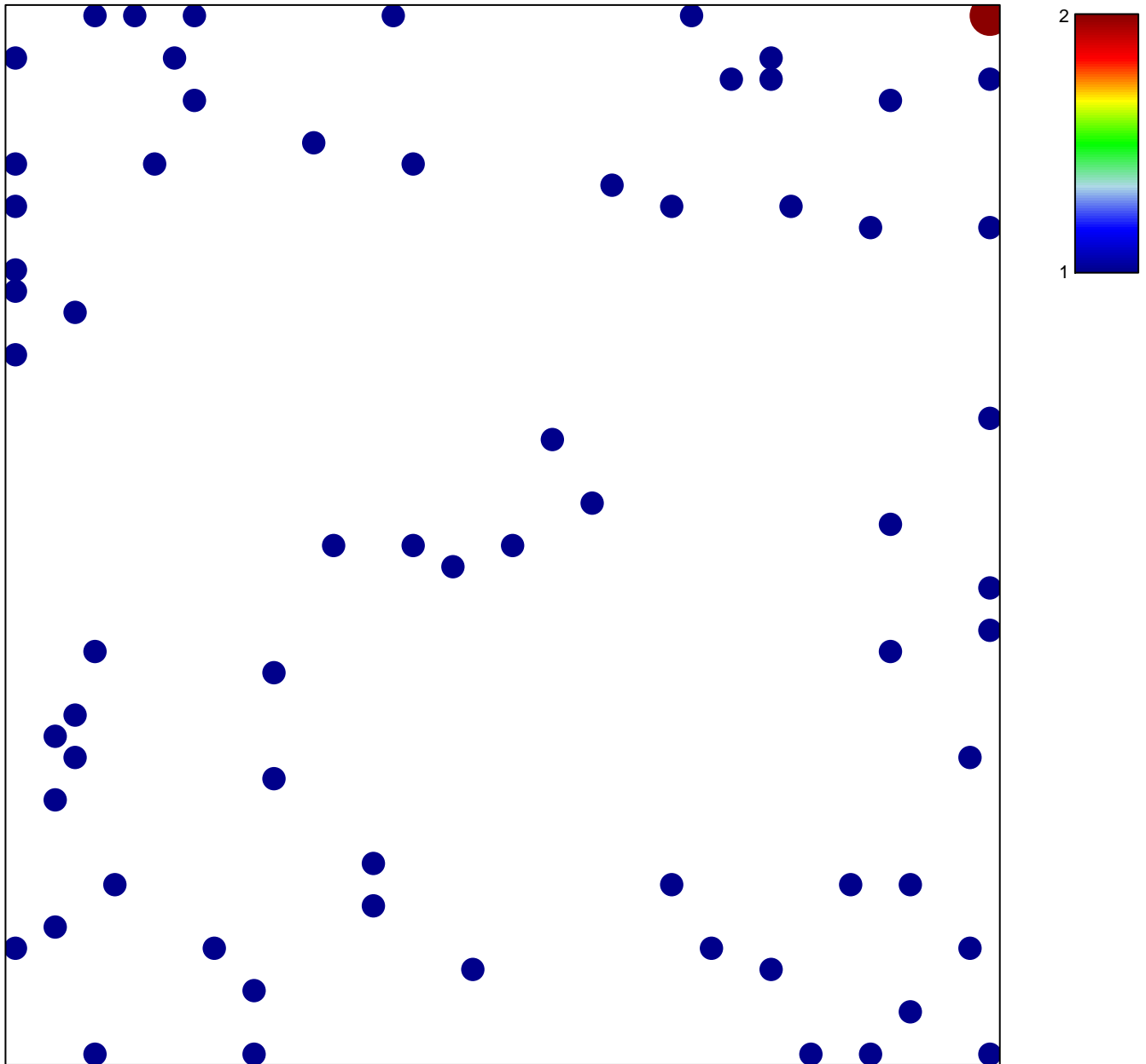
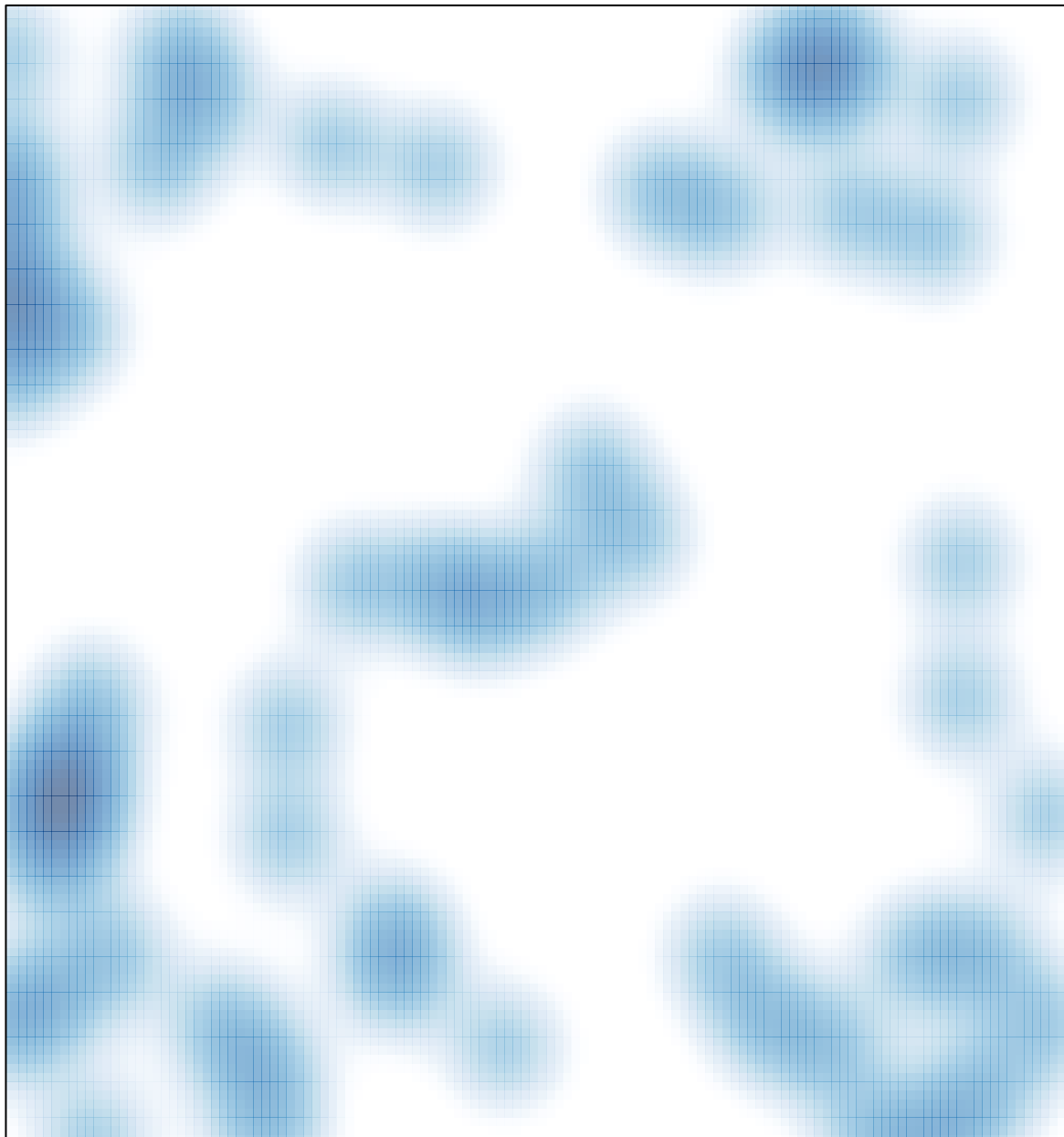


BILANGES_SERUM_SENSITIVE_GENES



features = 68
chi-square p = 0.8

BILANGES_SERUM_SENSITIVE_GENES



features = 68 , max = 2