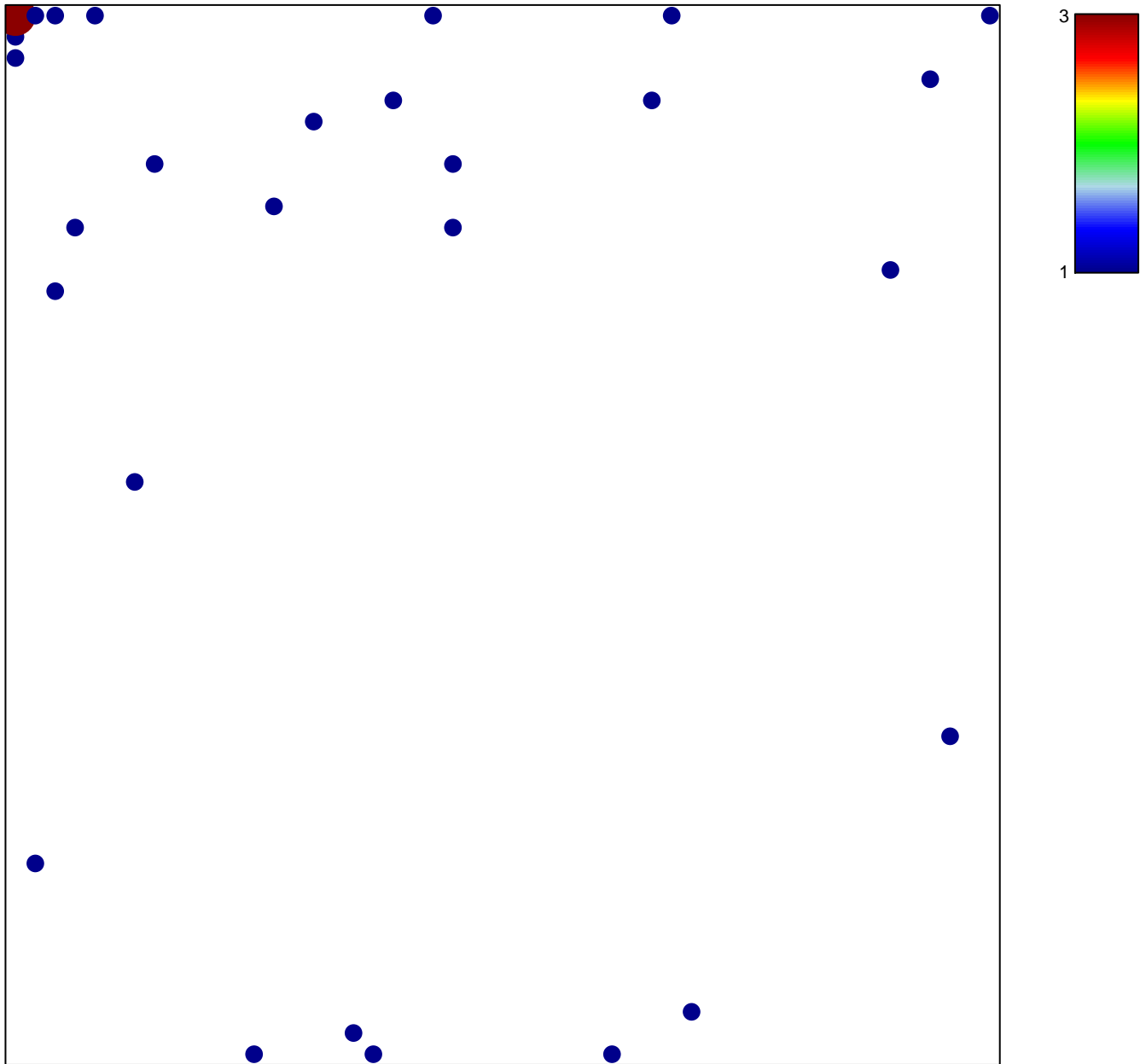
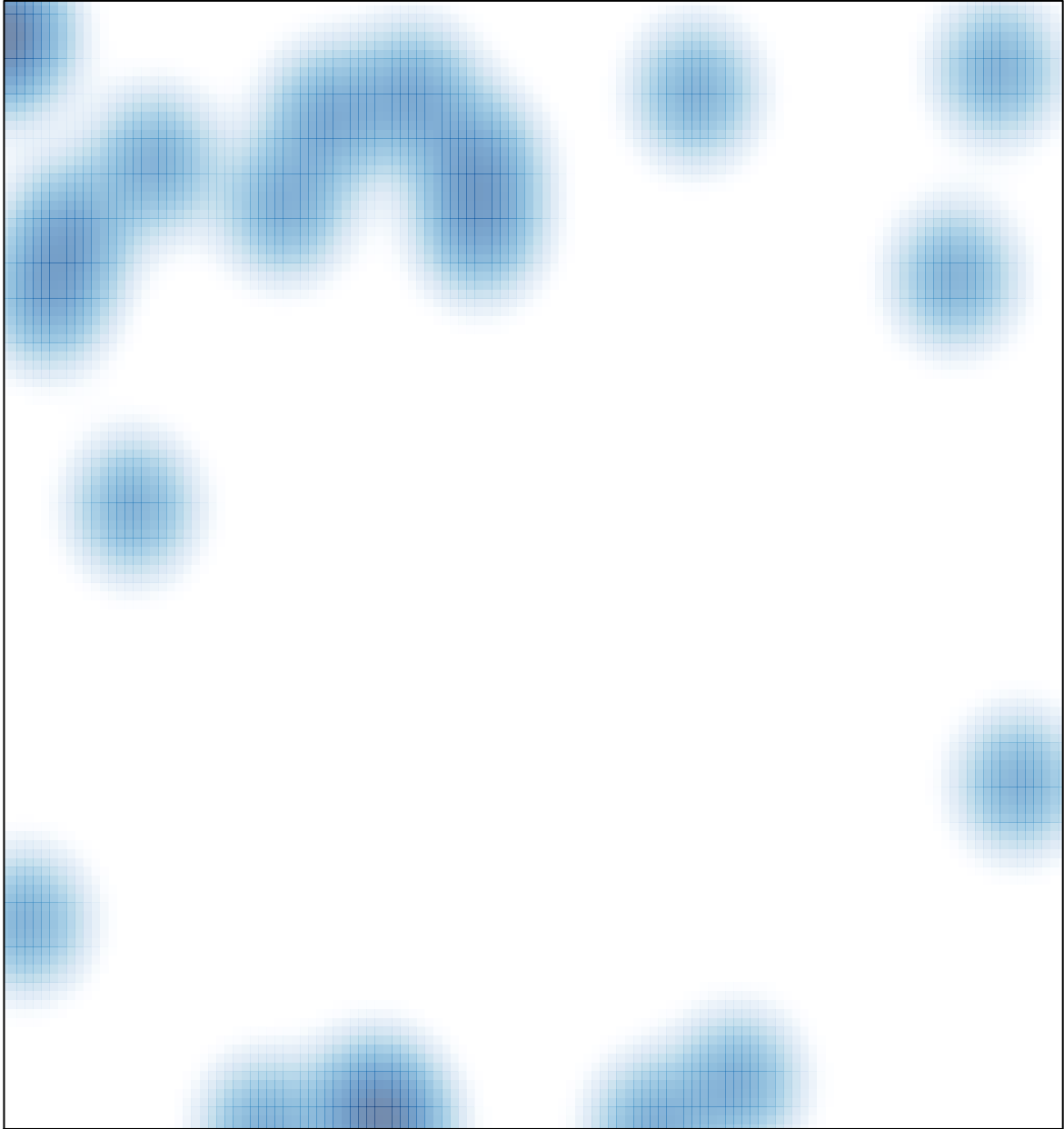


# ZHAN\_MULTIPLE\_MYELOMA\_SUBGROUPS



# features = 30  
chi-square p = 0.77

# ZHAN\_MULTIPLE\_MYELOMA\_SUBGROUPS



# features = 30 , max = 3