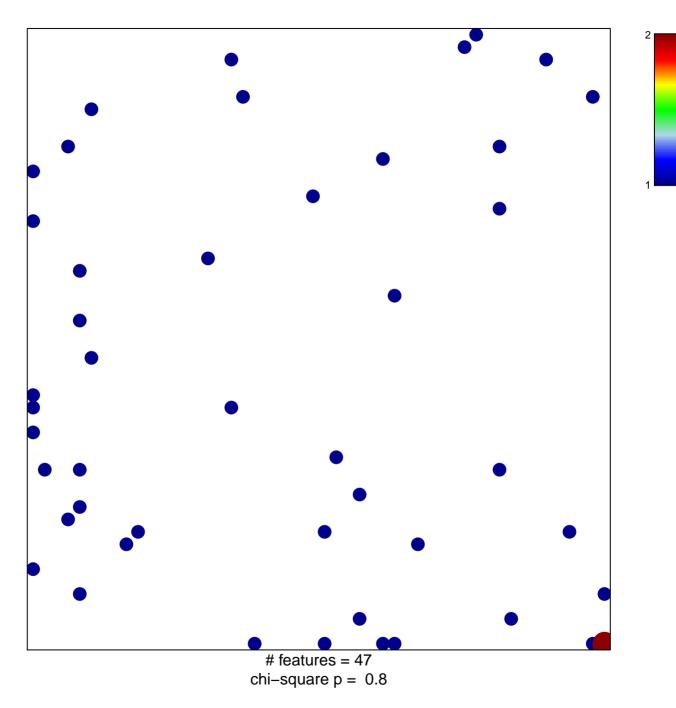
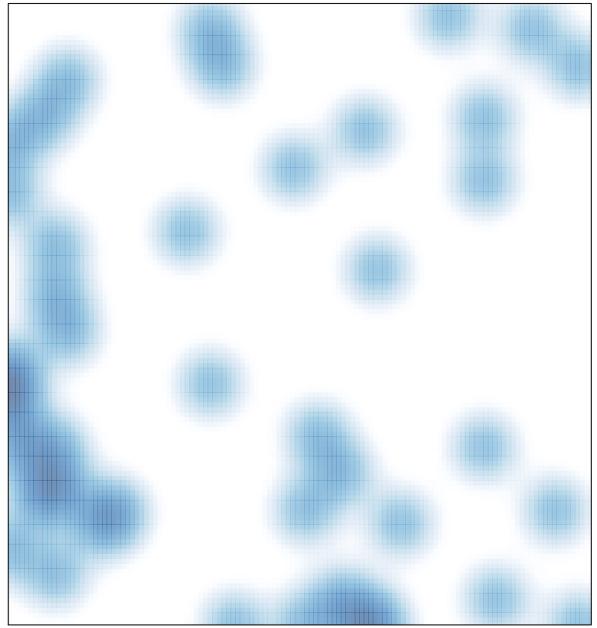
ZHAN\_MULTIPLE\_MYELOMA\_CD1\_AND\_CD2\_DN



## ZHAN\_MULTIPLE\_MYELOMA\_CD1\_AND\_CD2\_DN



# features = 47, max = 2