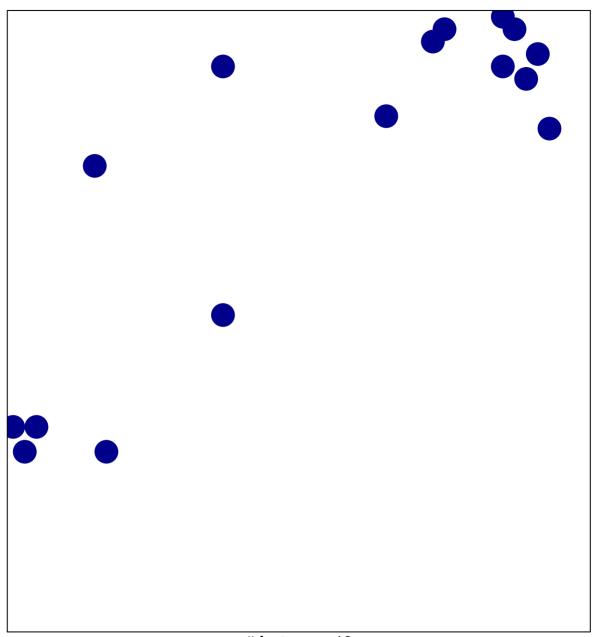
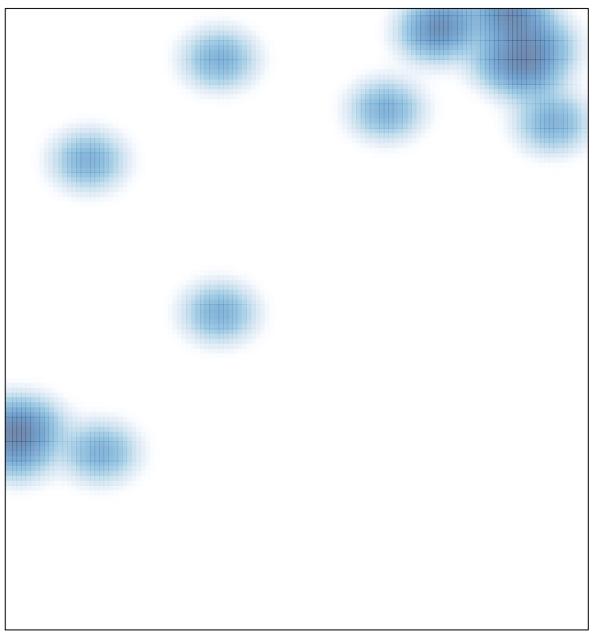
## ZHAN\_MULTIPLE\_MYELOMA\_SUBGROUPS



# features = 16 chi-square p = 0.84

## ZHAN\_MULTIPLE\_MYELOMA\_SUBGROUPS



# features = 16, max = 1