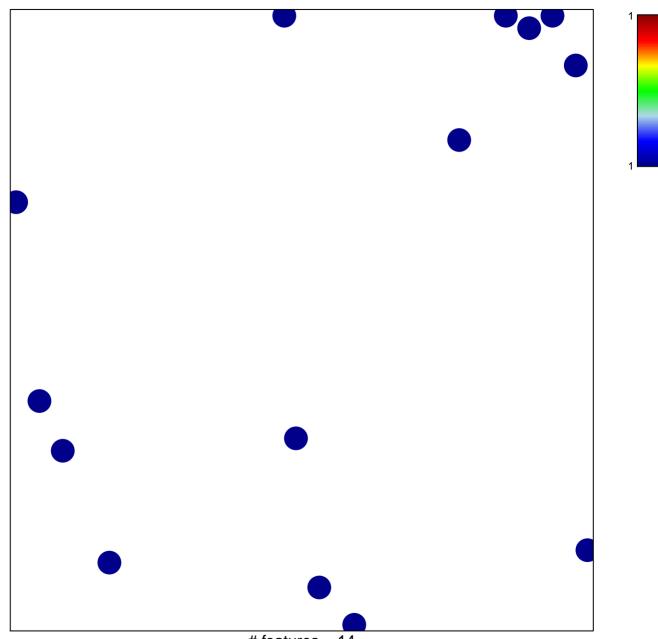
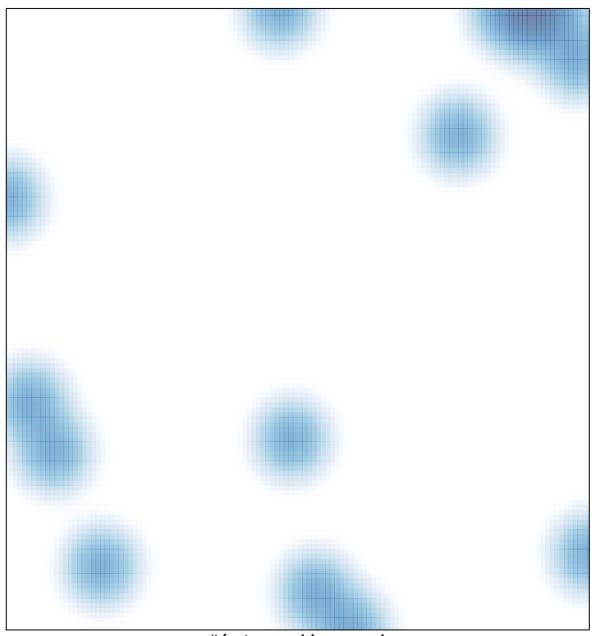
## REACTOME\_METABLISM\_OF\_NUCLEOTIDES



# features = 14 chi-square p = 0.85

## REACTOME\_METABLISM\_OF\_NUCLEOTIDES



# features = 14 , max = 1