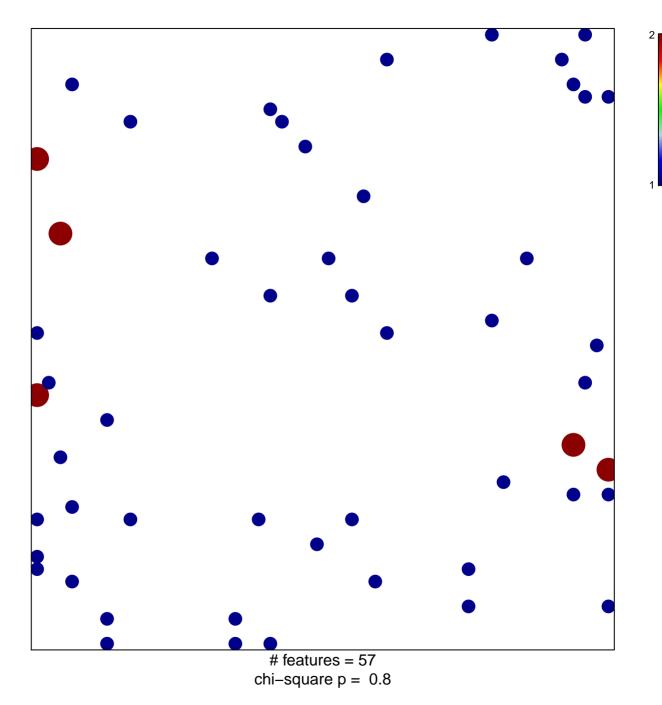
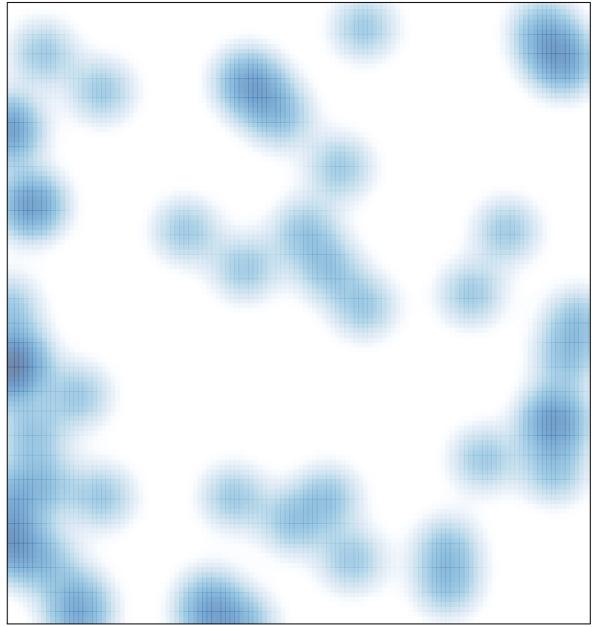
**REACTOME\_SPHINGOLIPID\_METABOLISM** 



## **REACTOME\_SPHINGOLIPID\_METABOLISM**



# features = 57 , max = 2