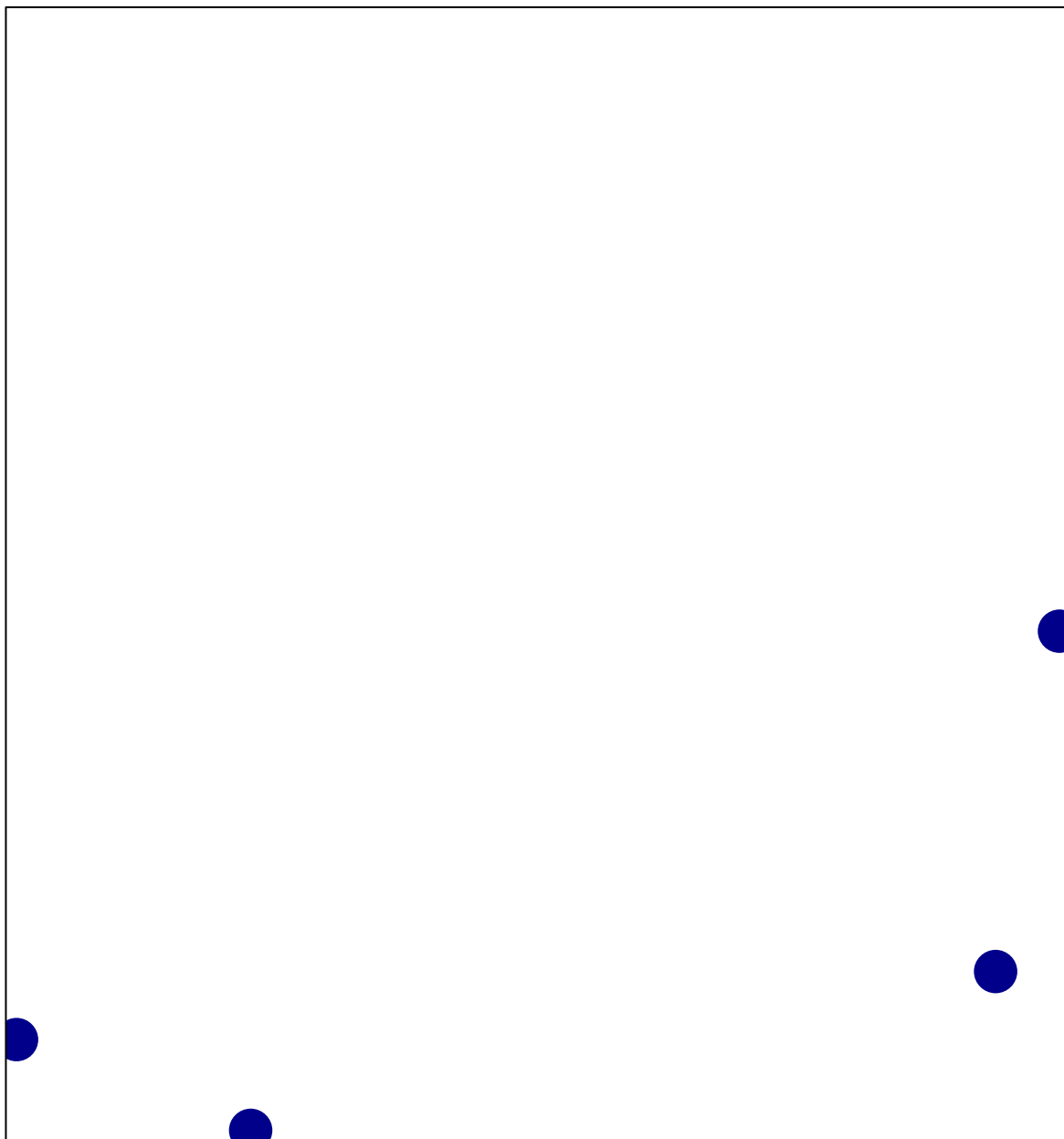


# Hewish\_dMMR-secondary-mutations\_Apoptosis



# features = 4  
chi-square p = 0.85

# Hewish\_dMMR-secondary-mutations\_Apoptosis



# features = 4 , max = 1