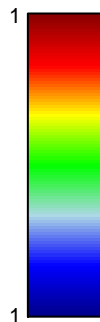
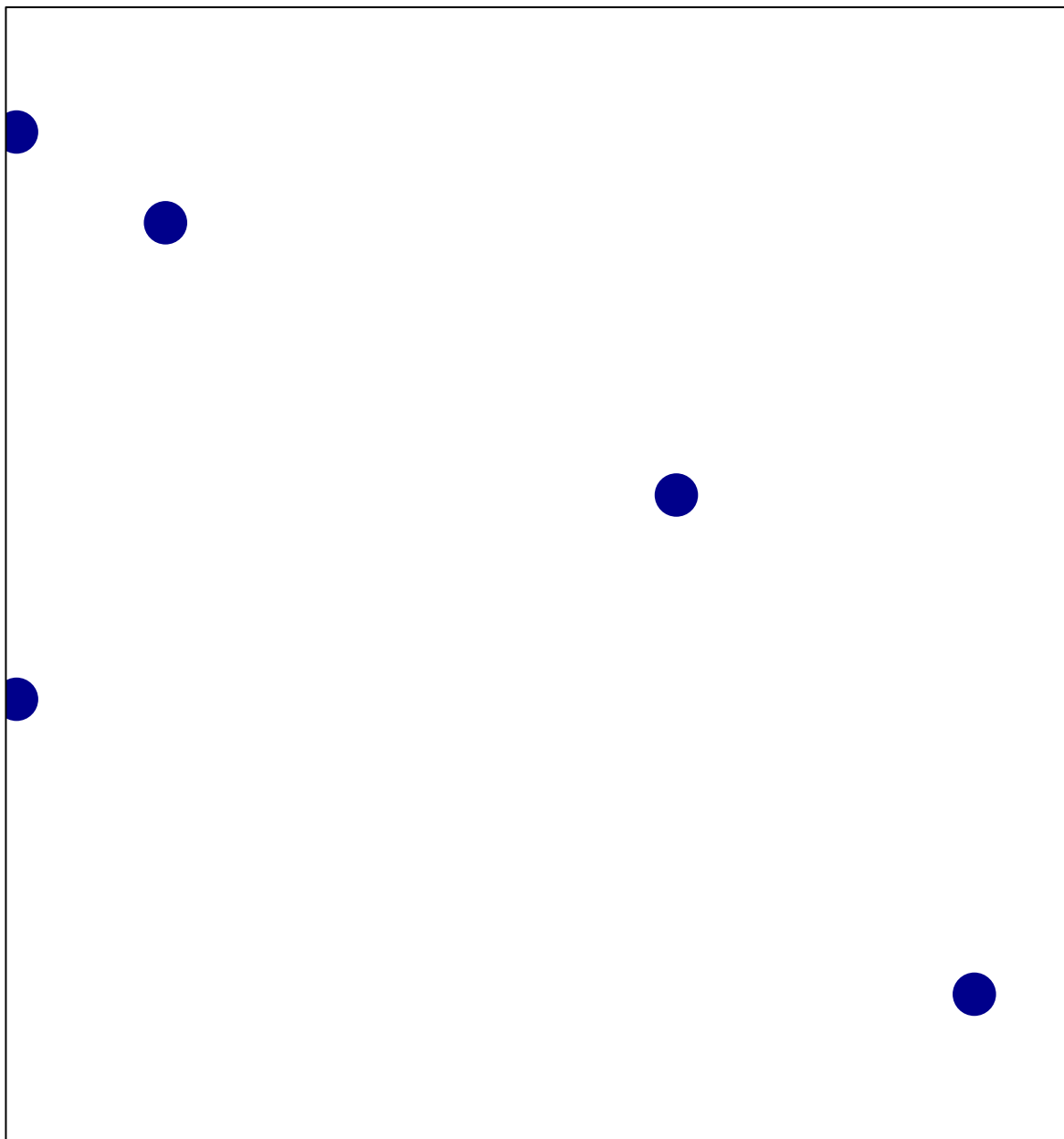
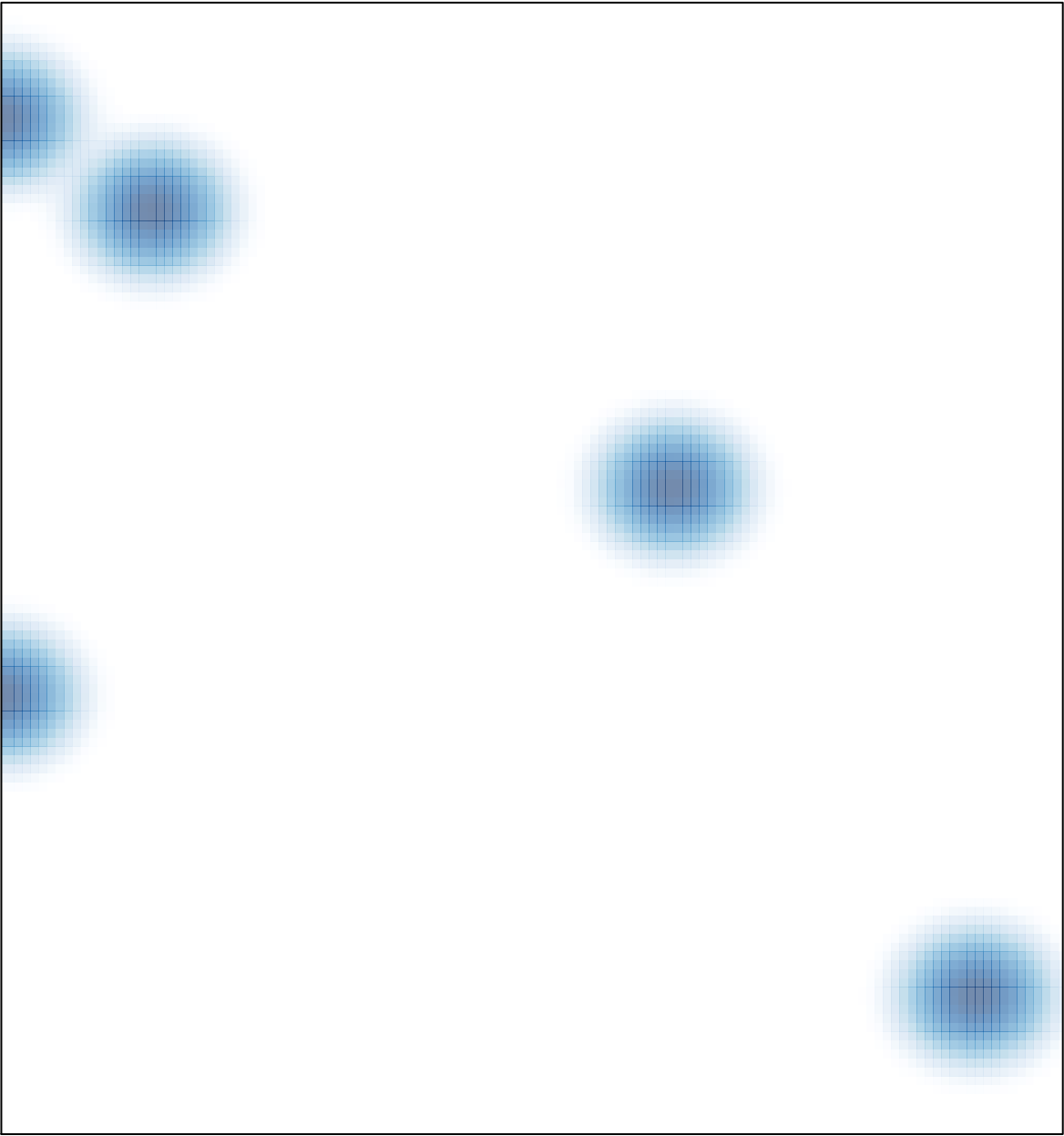


# Hewish\_dMMR-secondary-mutations\_Transcriptional\_regulation



# features = 5  
chi-square p = 0.83

# h\_dMMR-secondary-mutations\_Transcriptional\_reg



# features = 5 , max = 1