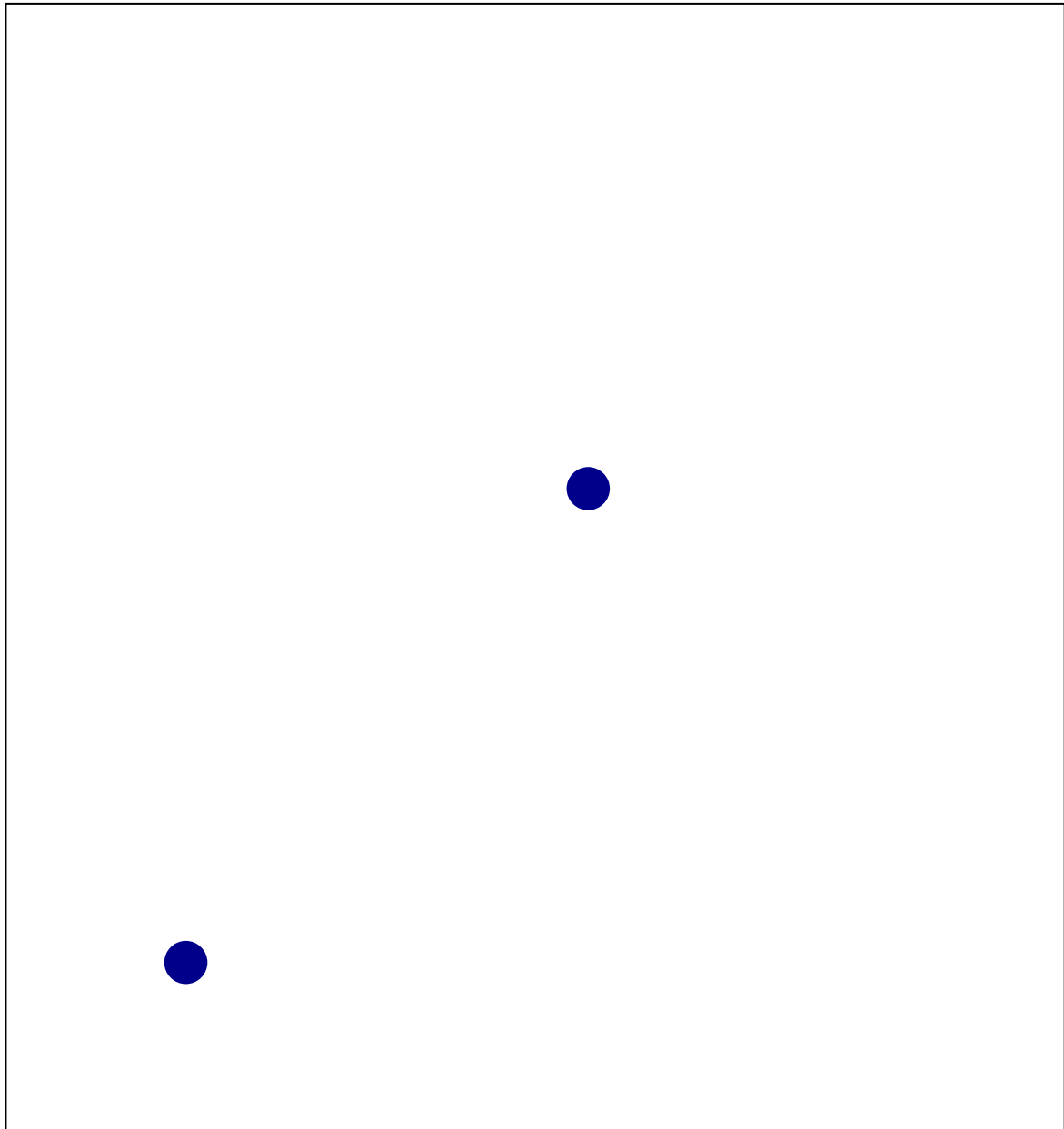
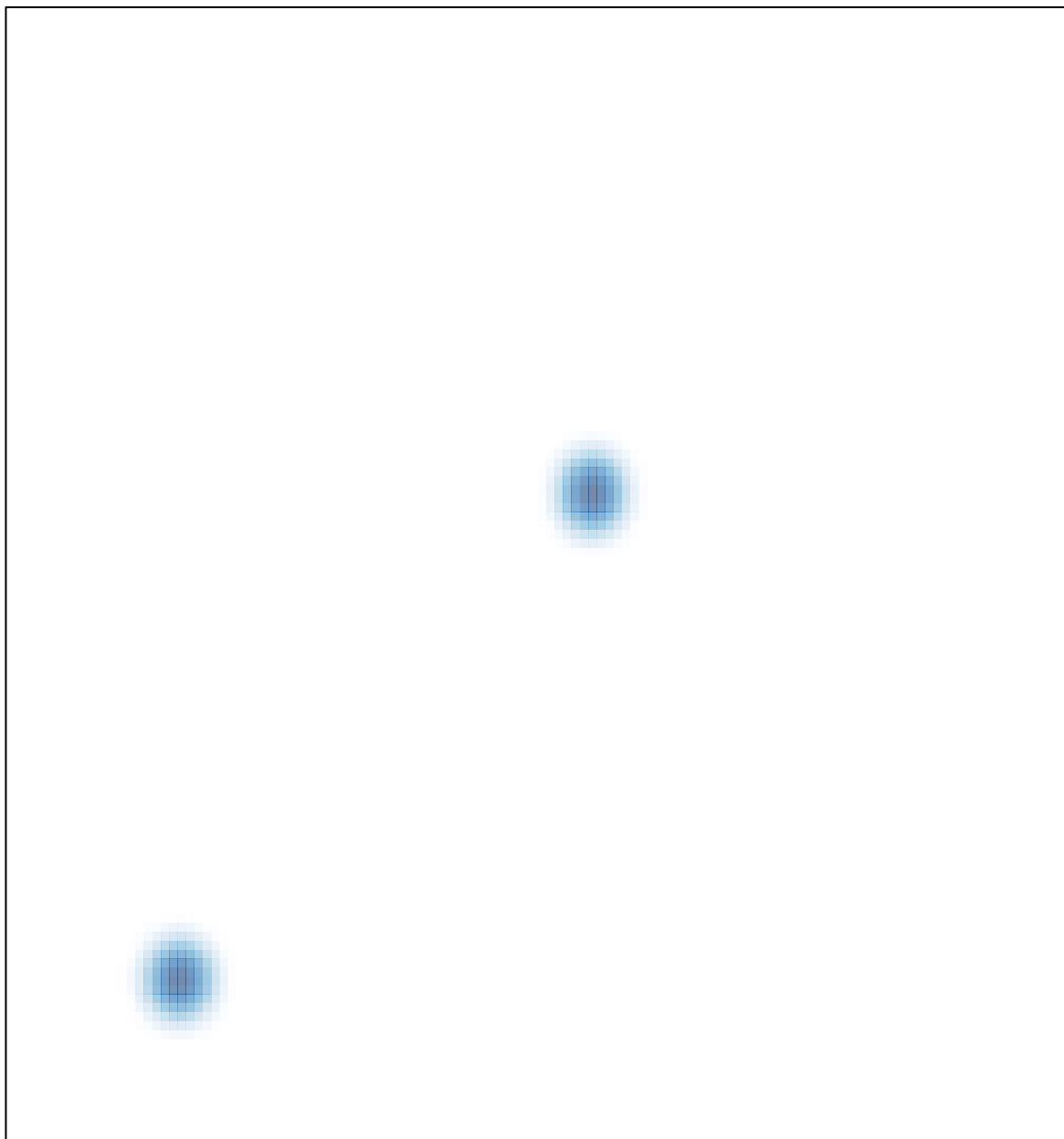


# WILLSCHER\_GBM\_LTSwt\_proteomics-M\_UP



# features = 2  
chi-square p = 0.84

# WILLSCHER\_GBM\_LTSwt\_proteomics-M\_UP



# features = 2 , max = 1