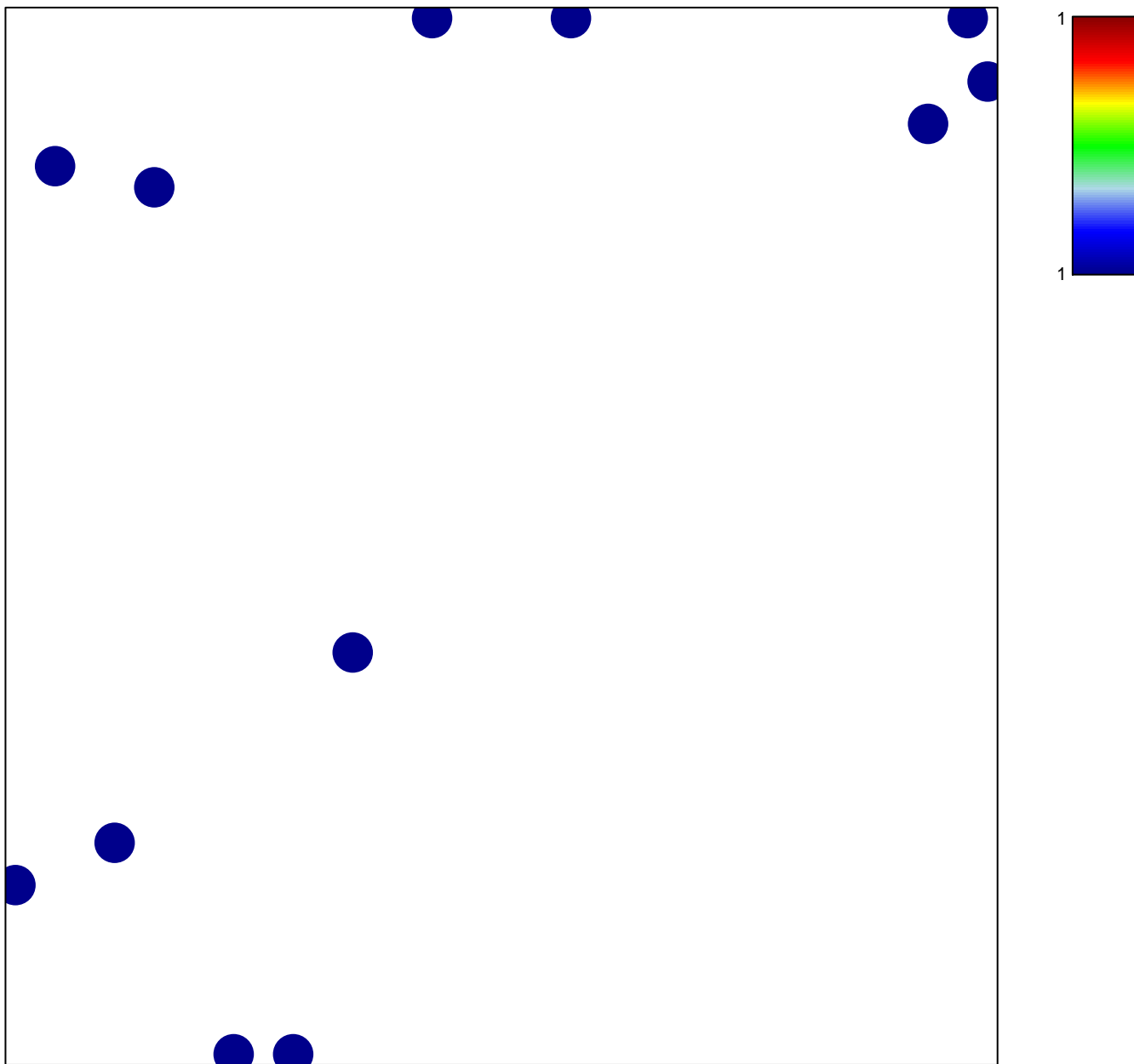


TOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE_NUCLEOTIDE_REPLACEMENT_P



features = 12
chi-square p = 0.83

N_OF_AP_SITES_VIA_THE_SINGLE_NUCLEOTIDE_I



features = 12 , max = 1