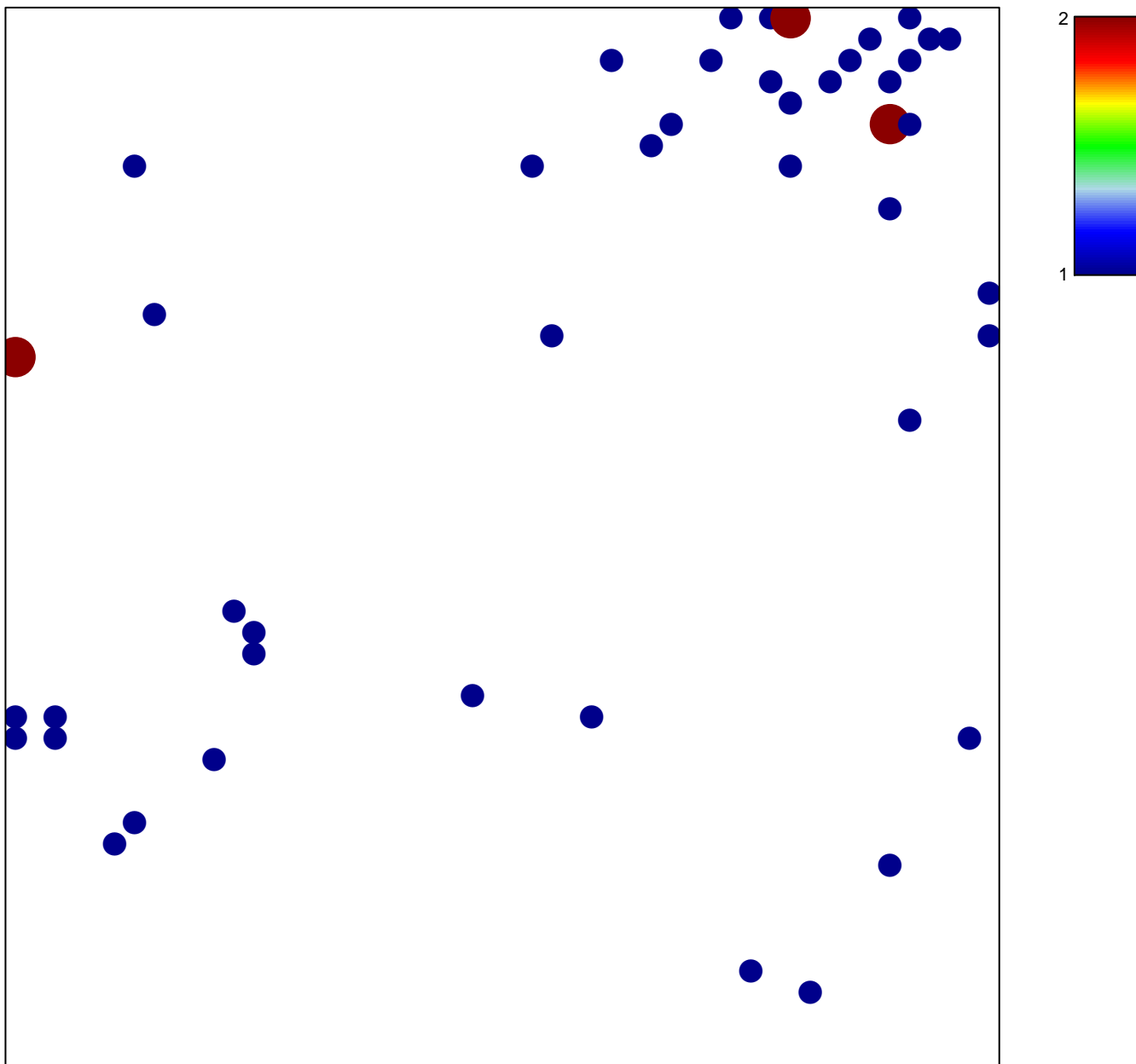
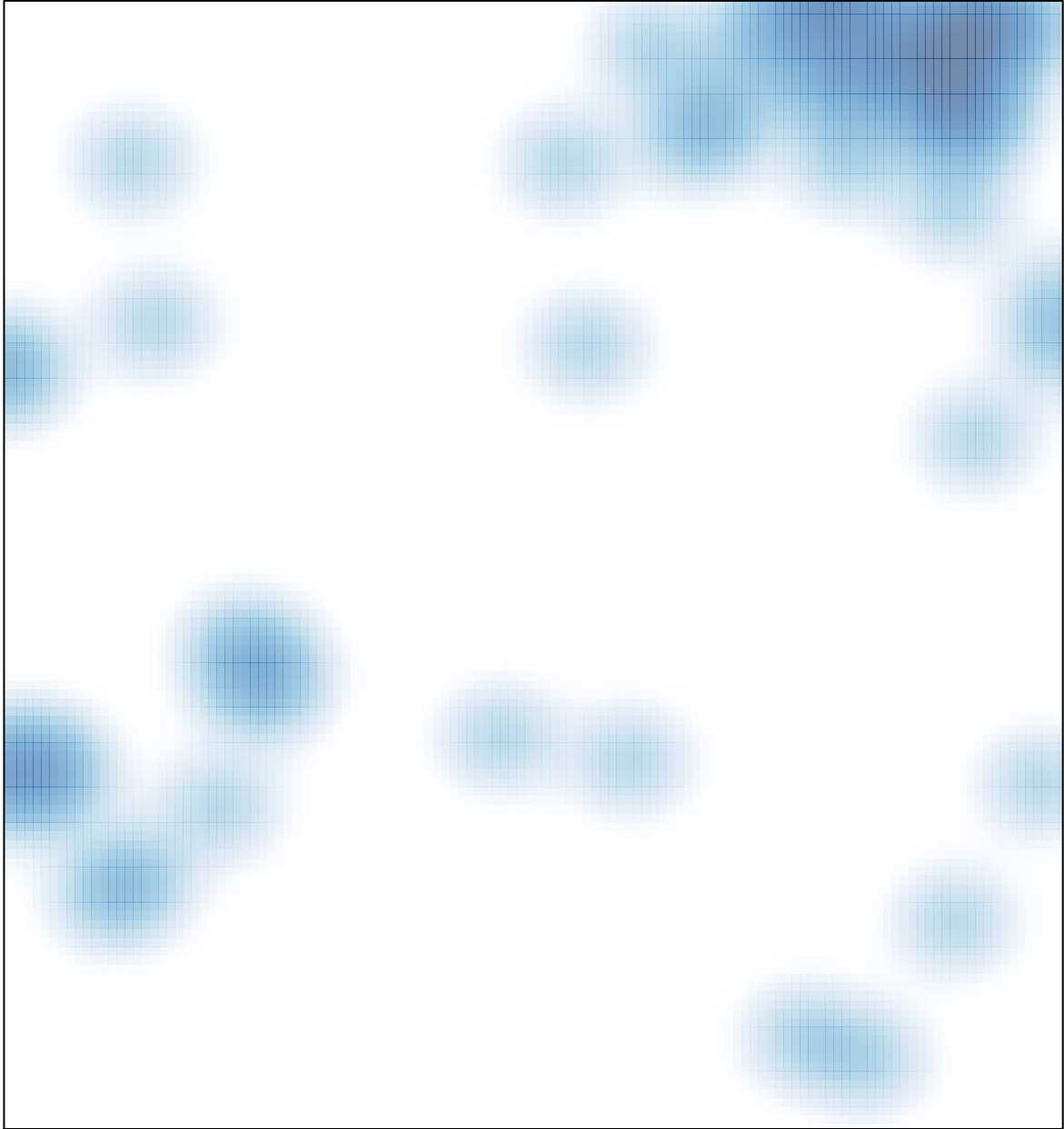


transcription-coupled nucleotide-excision repair



features = 48
chi-square p = 0.8

transcription-coupled nucleotide-excision repair



features = 48 , max = 2