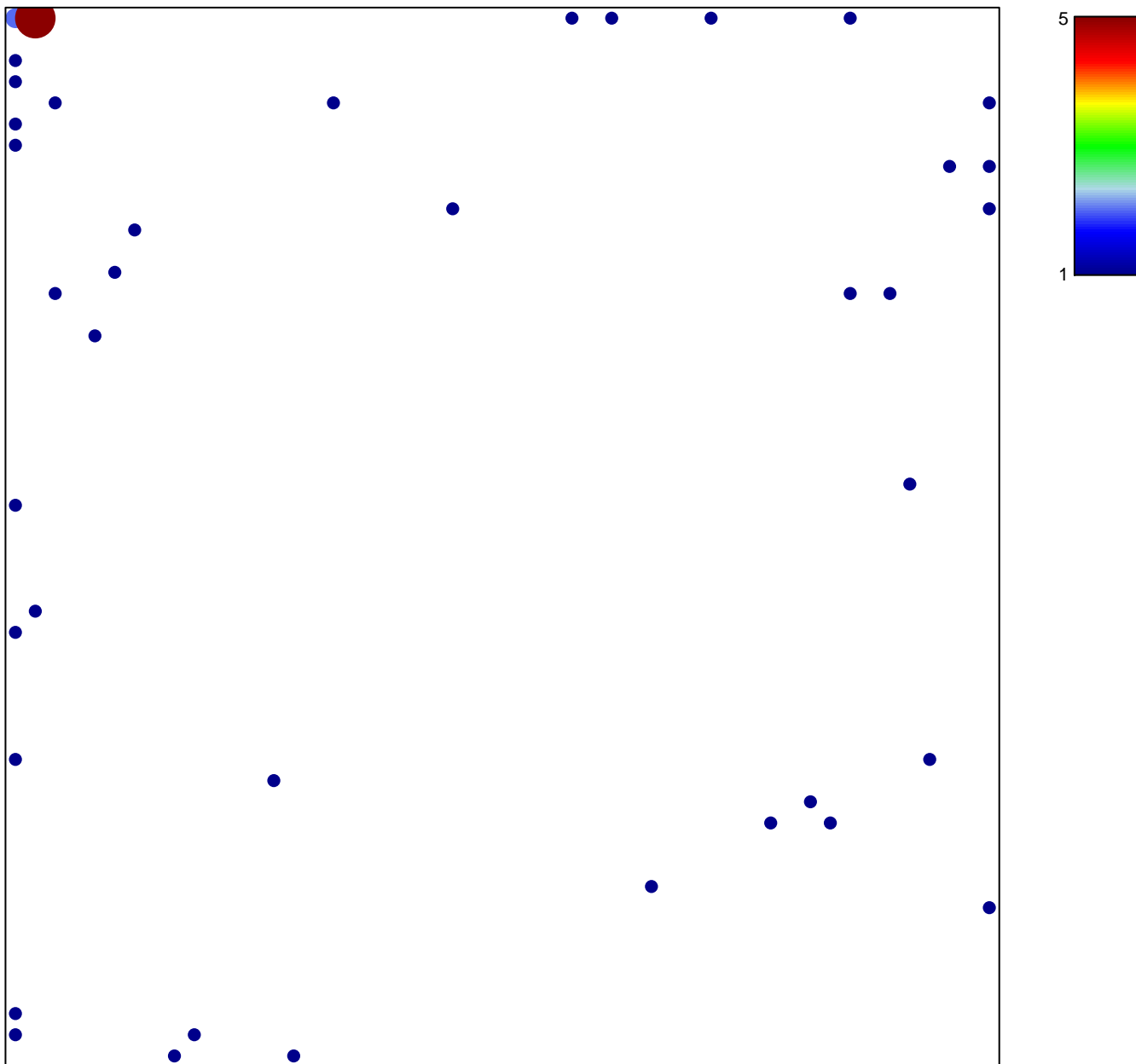
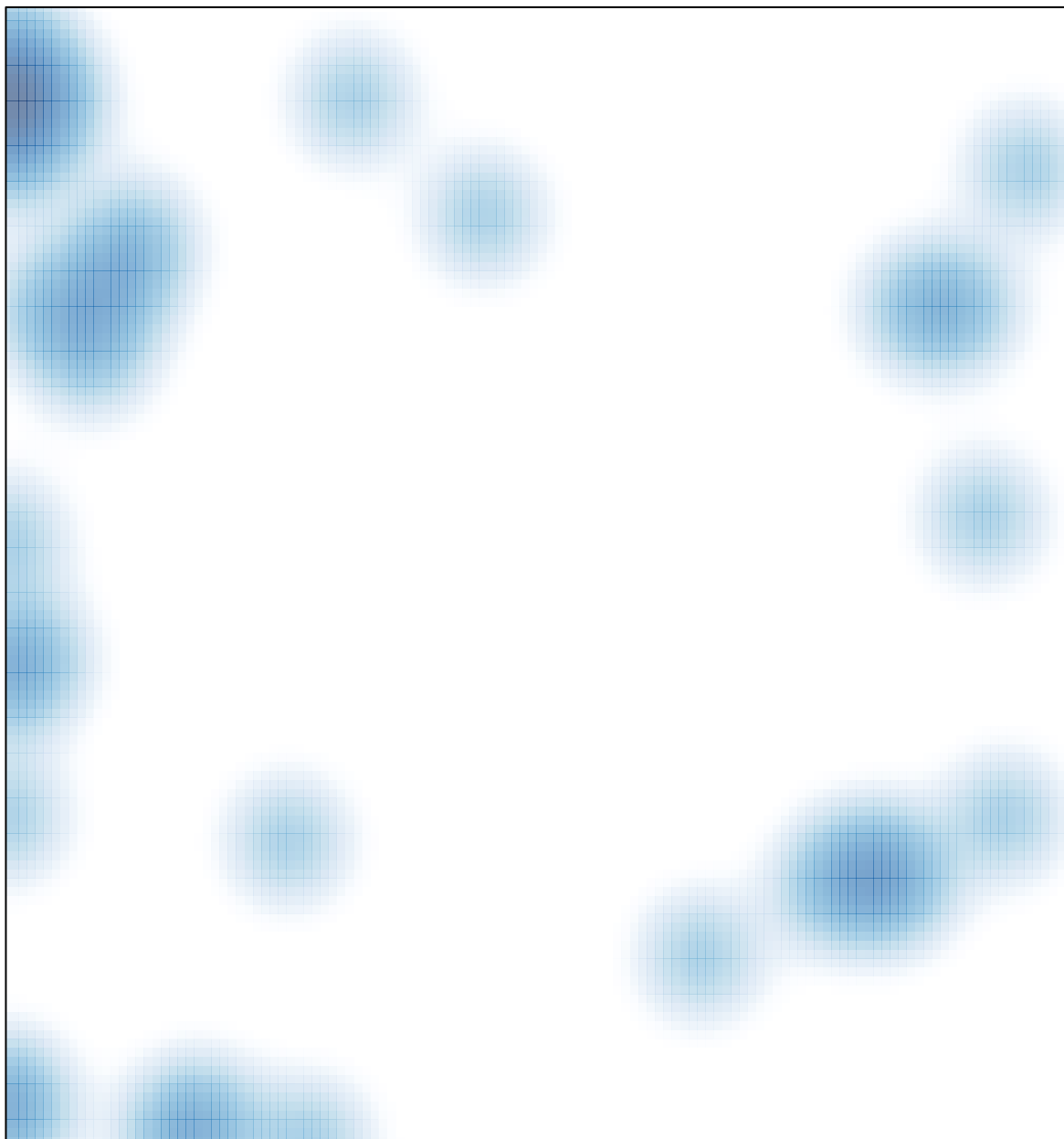


transcription-coupled nucleotide-excision repair



features = 45
chi-square p = 0.72

transcription-coupled nucleotide-excision repair



features = 45 , max = 5