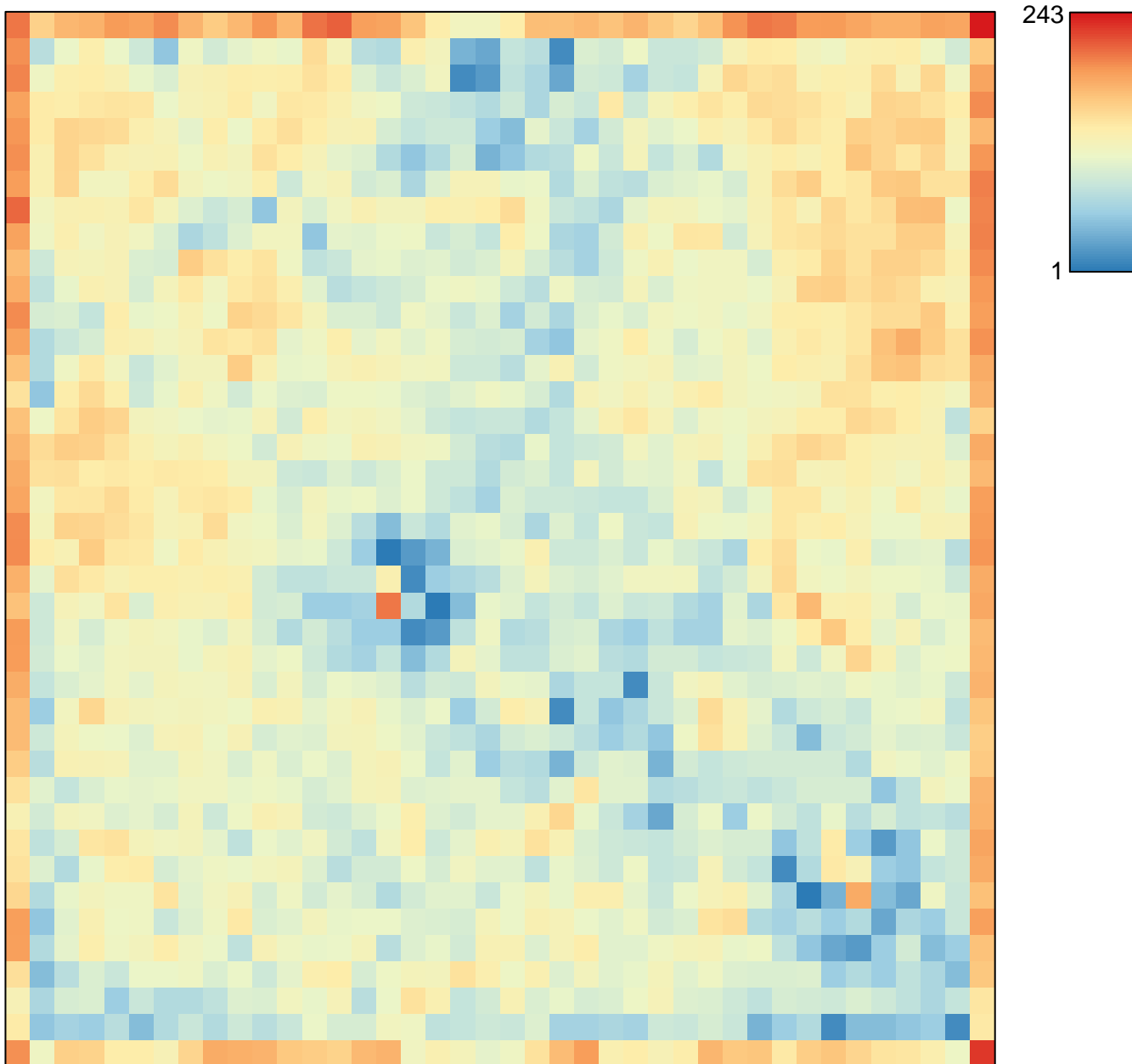
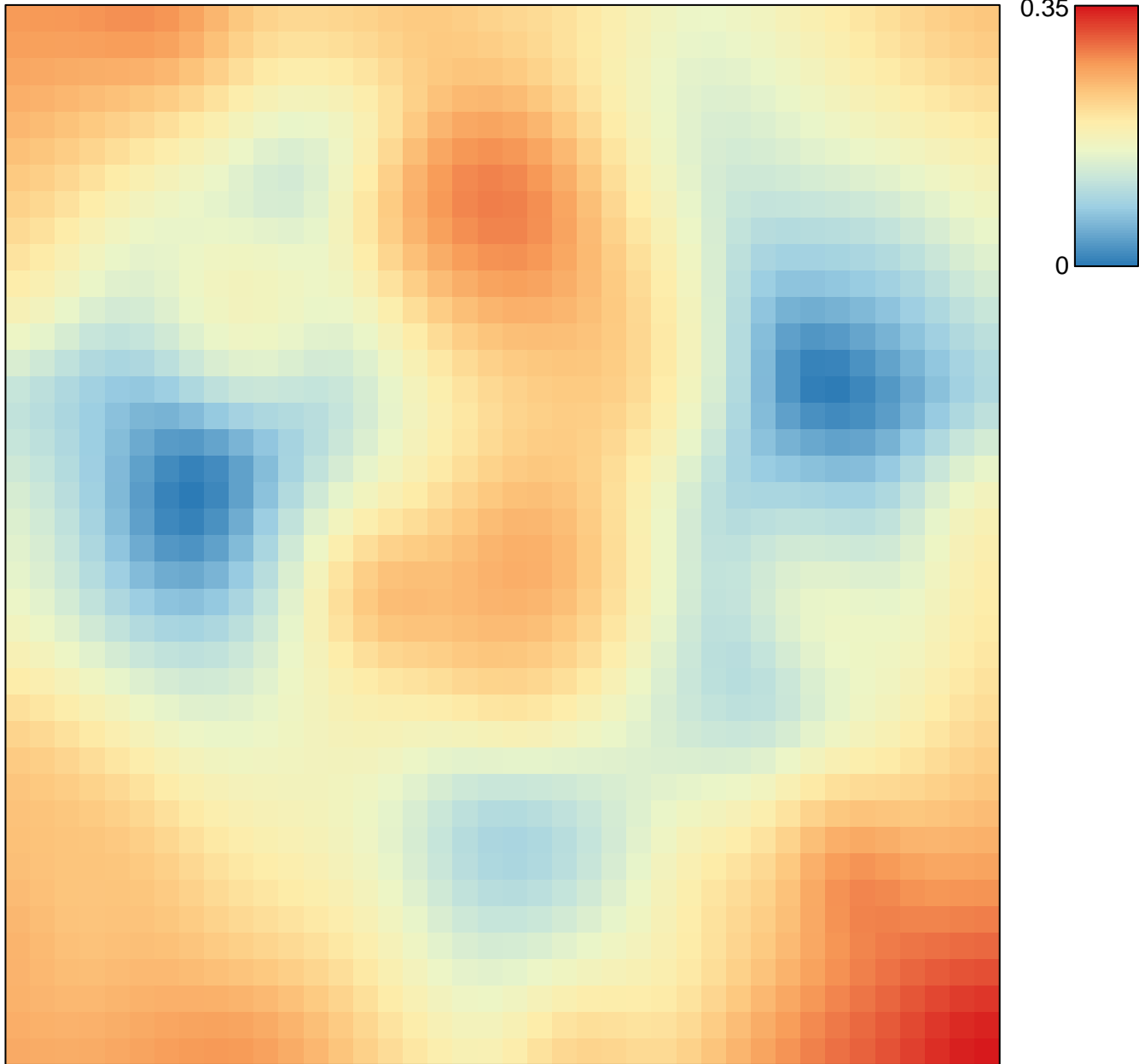


# Population Map



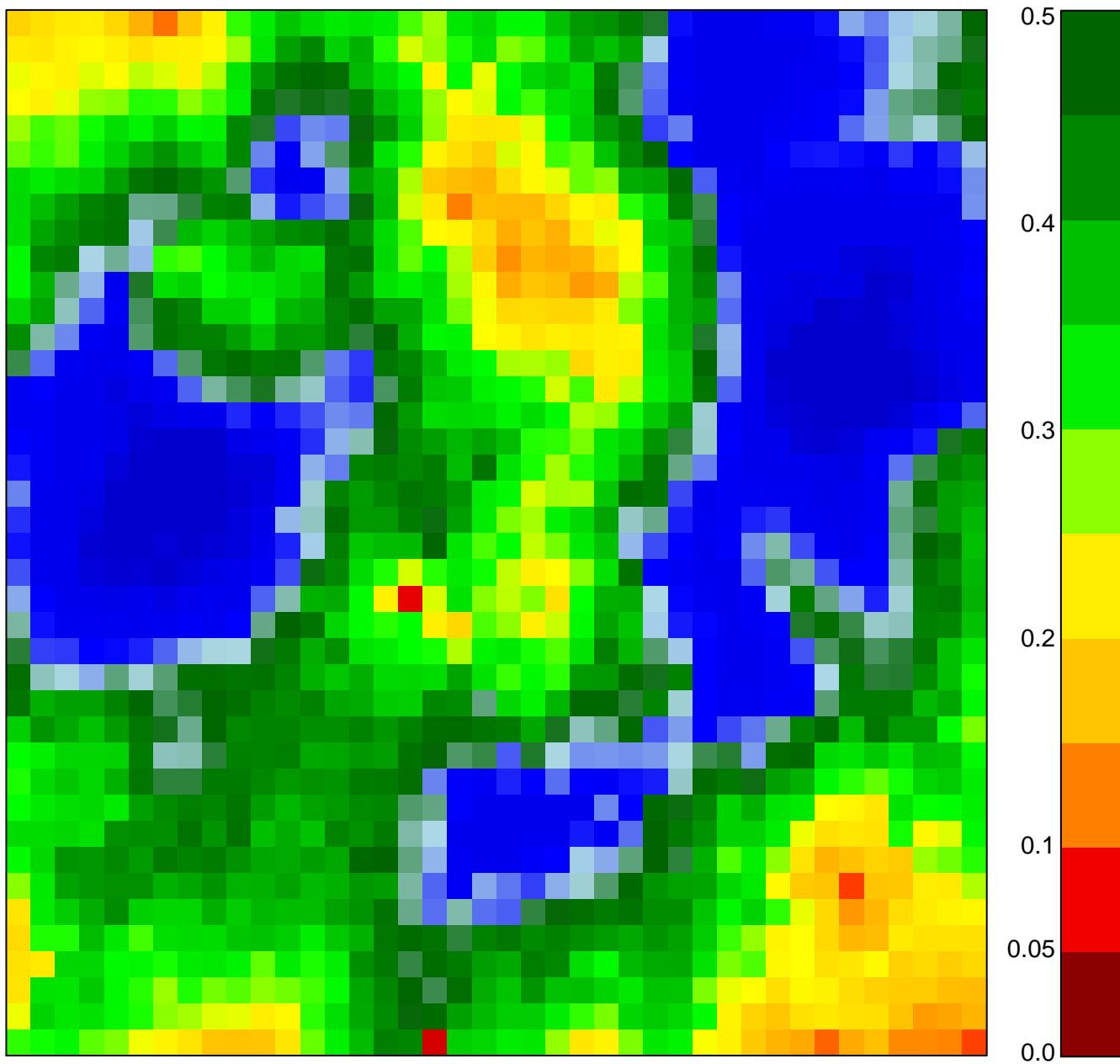
$\log ( \# \text{ genes in metagene } )$

# Metagene Variance Map



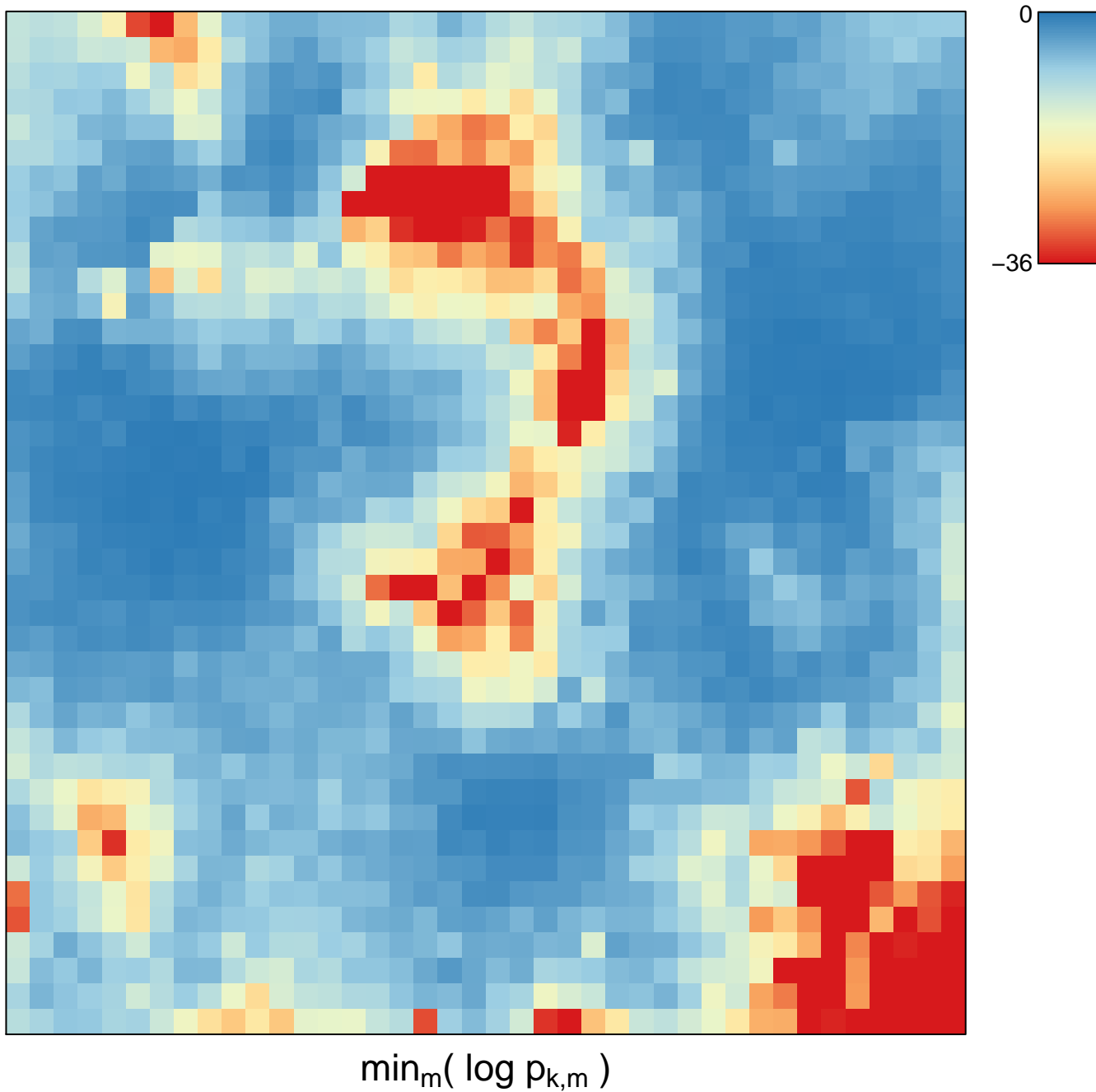
$\log(\text{metagene variance})$

# Metagene Significance Map

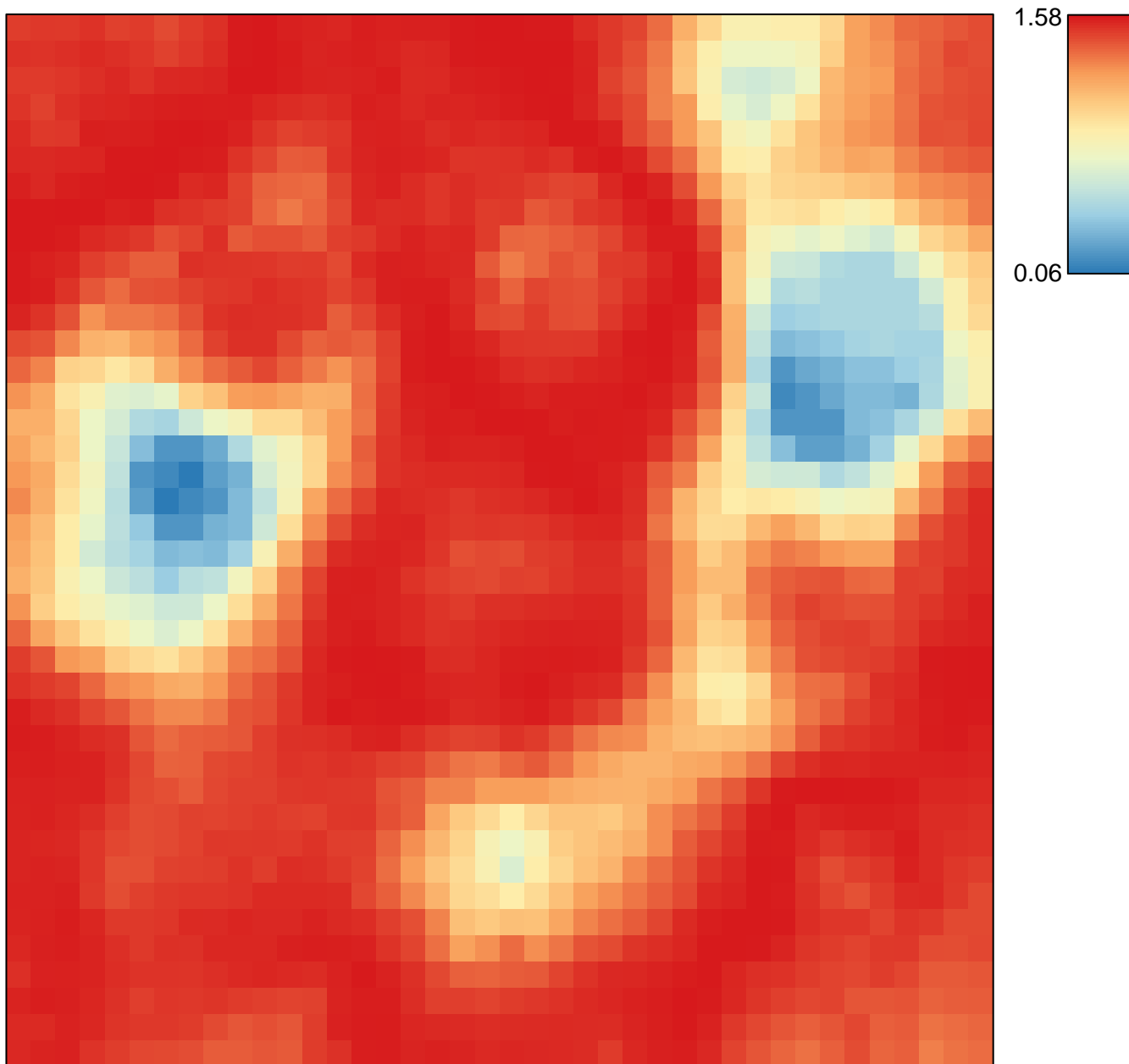


$\langle p_k \rangle$

# Metagene Significance Map

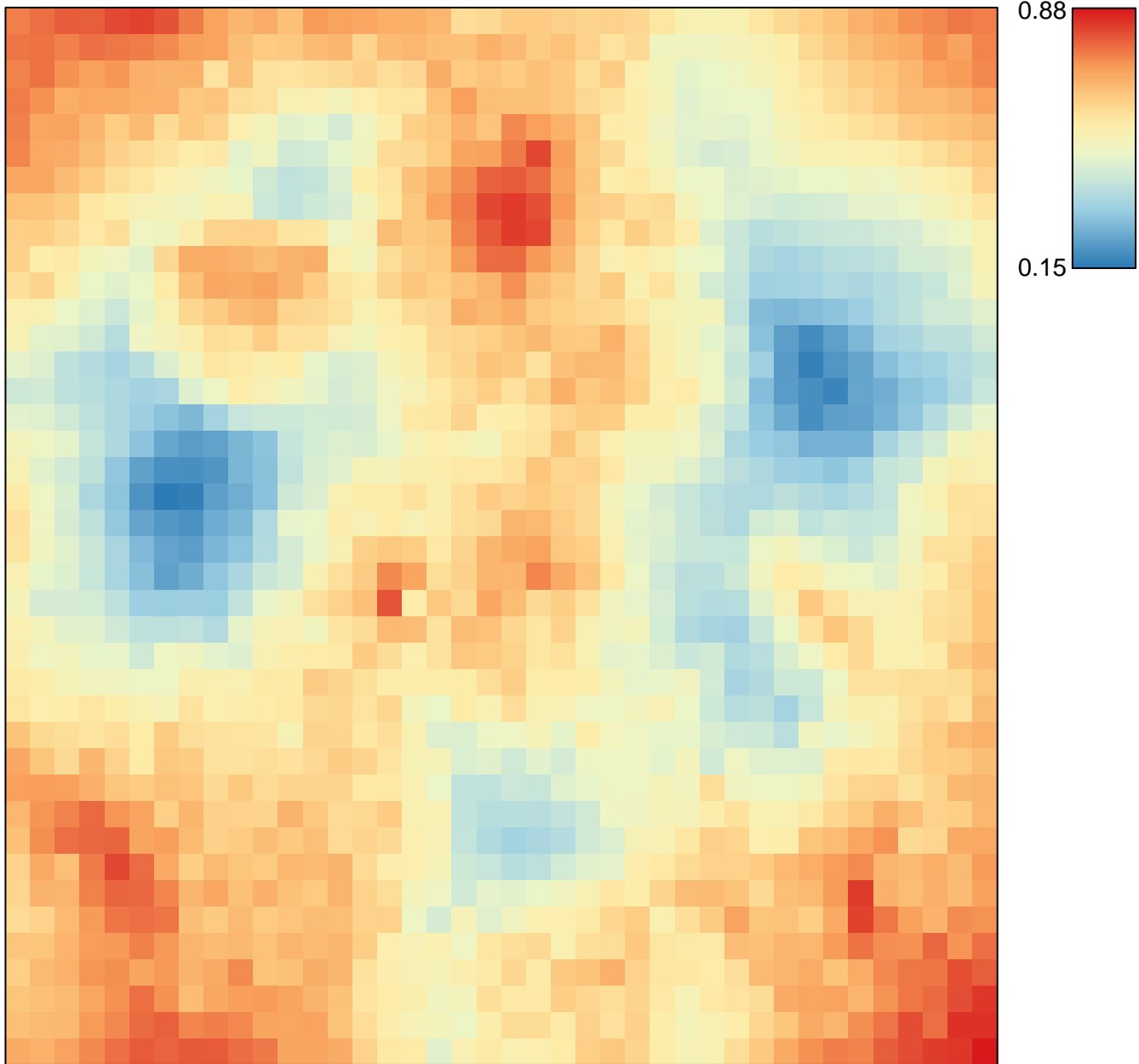


# Standard Metagene Entropy Map



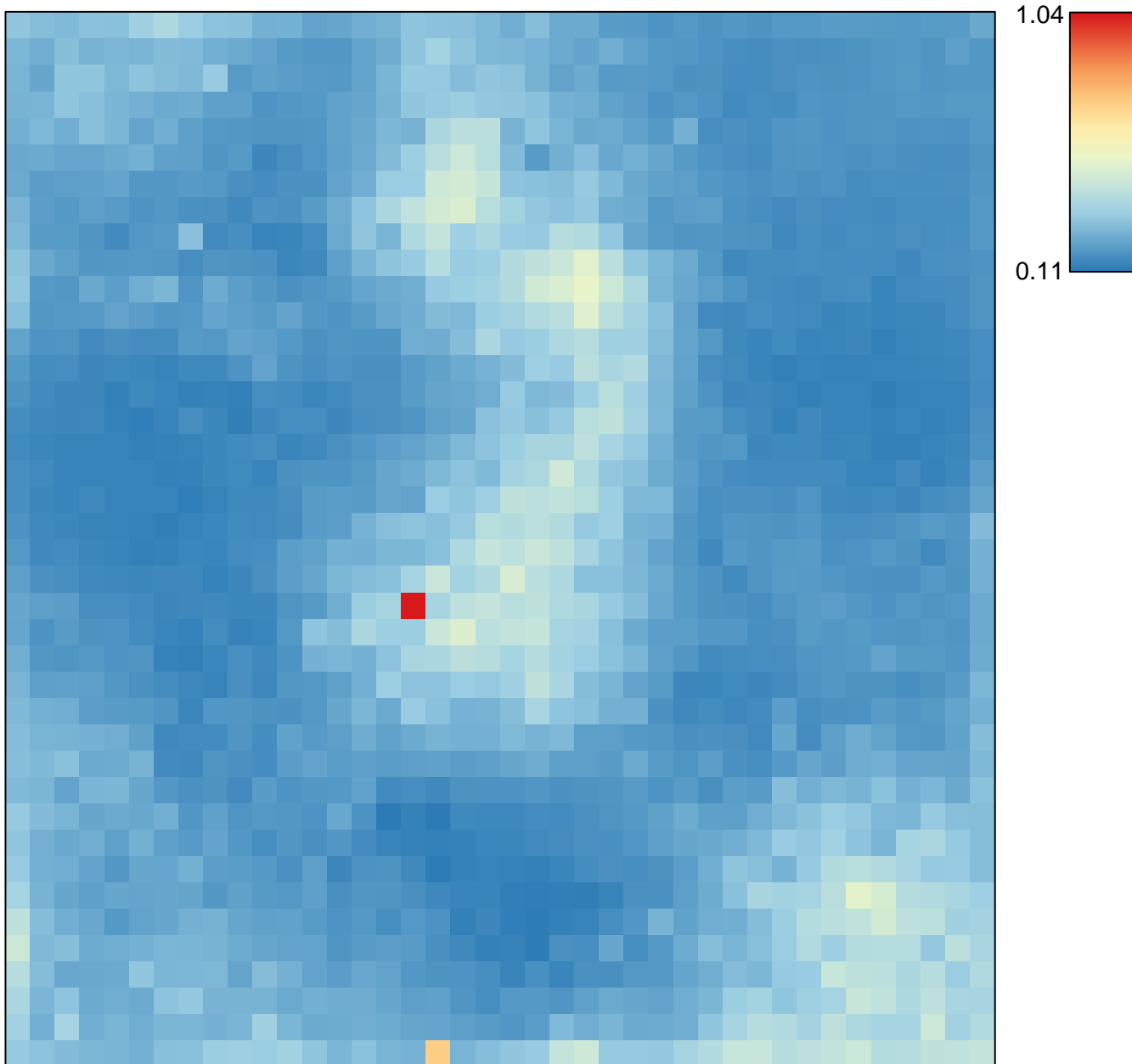
$h_k$

# Gene–Metagene Covariance Map



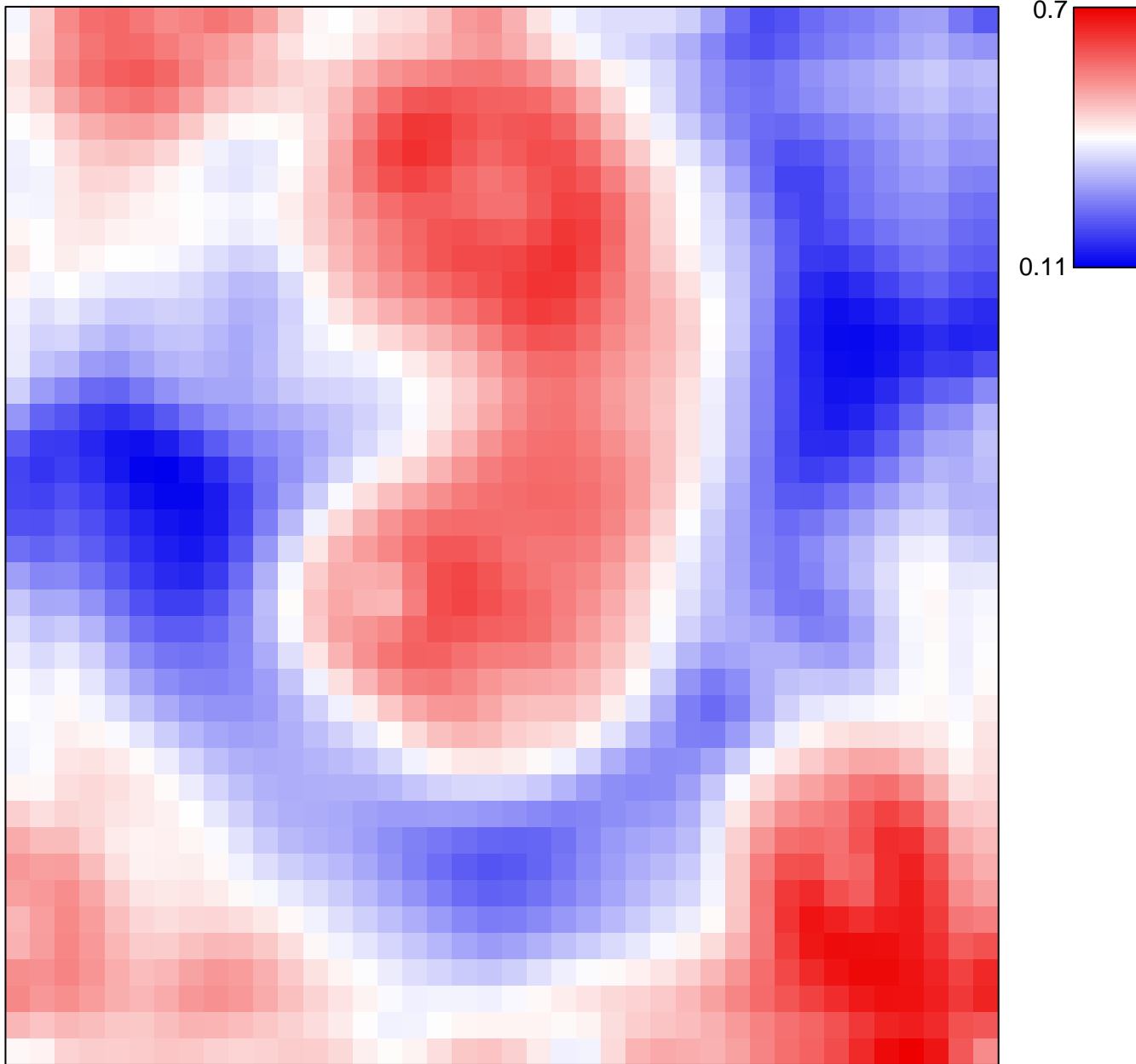
correlation genes – metagene

# Deviation Map



deviation genes – metagene

# Distance Map



deviation of adjacent metagenes