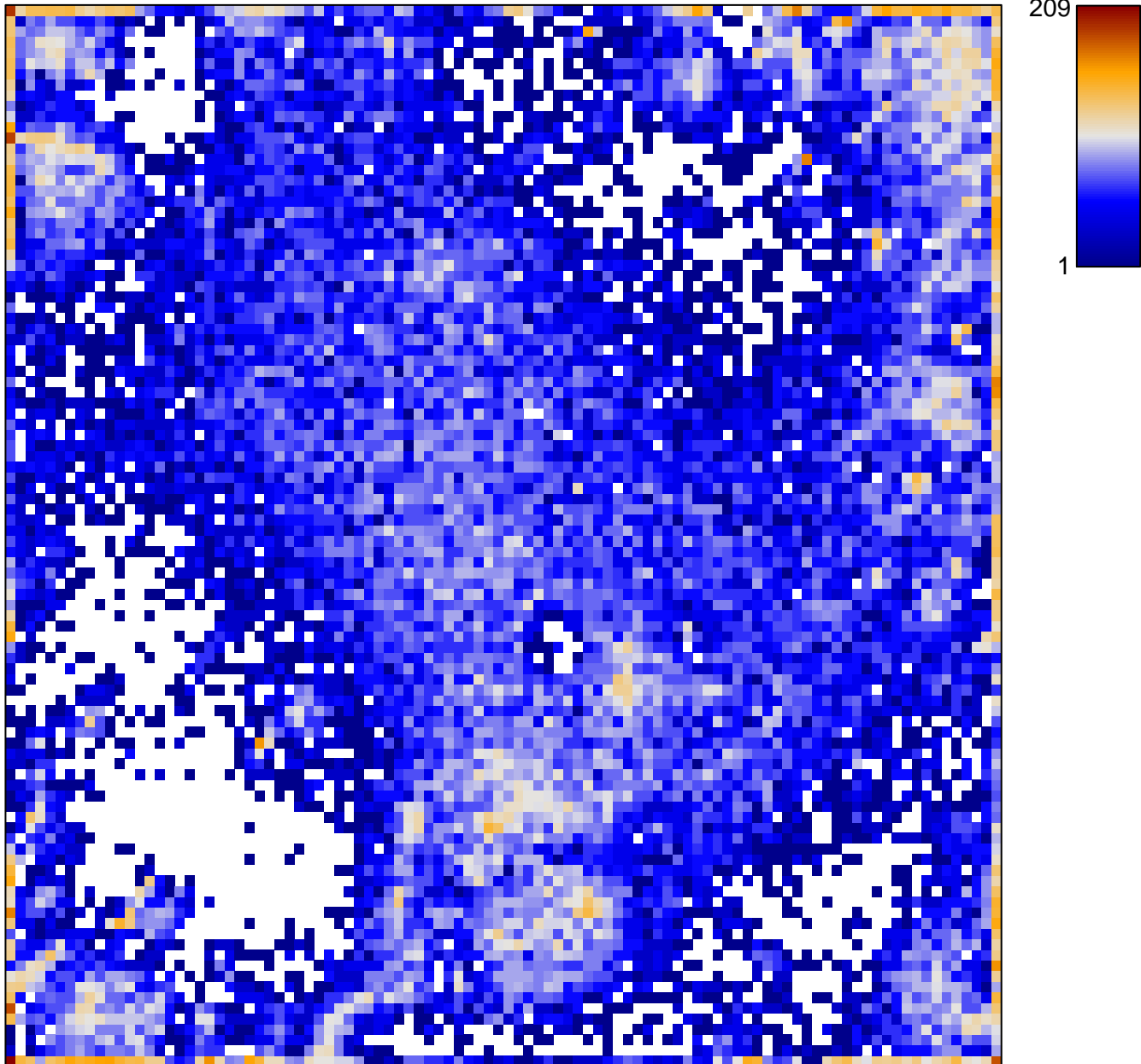
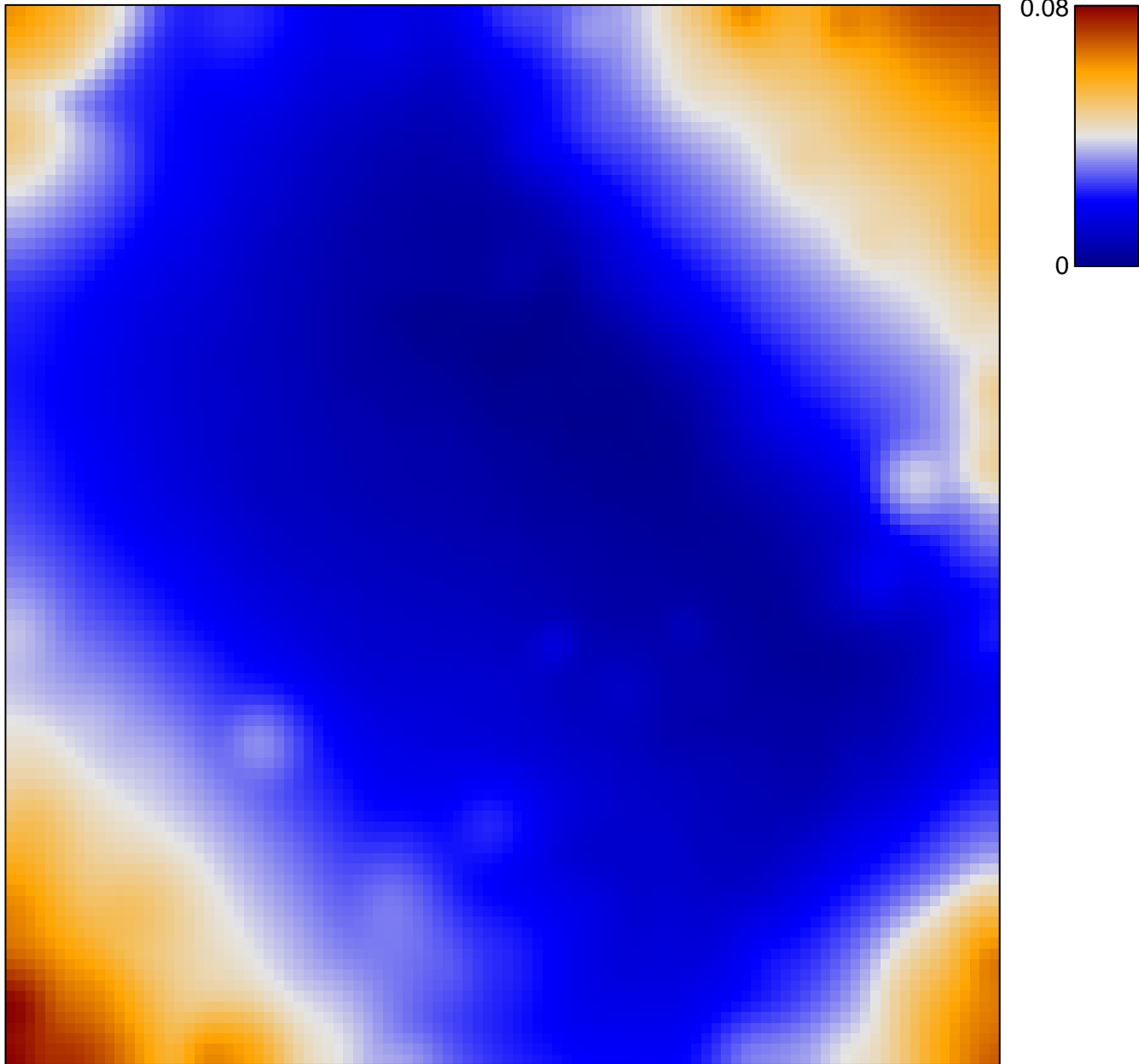


# Population Map



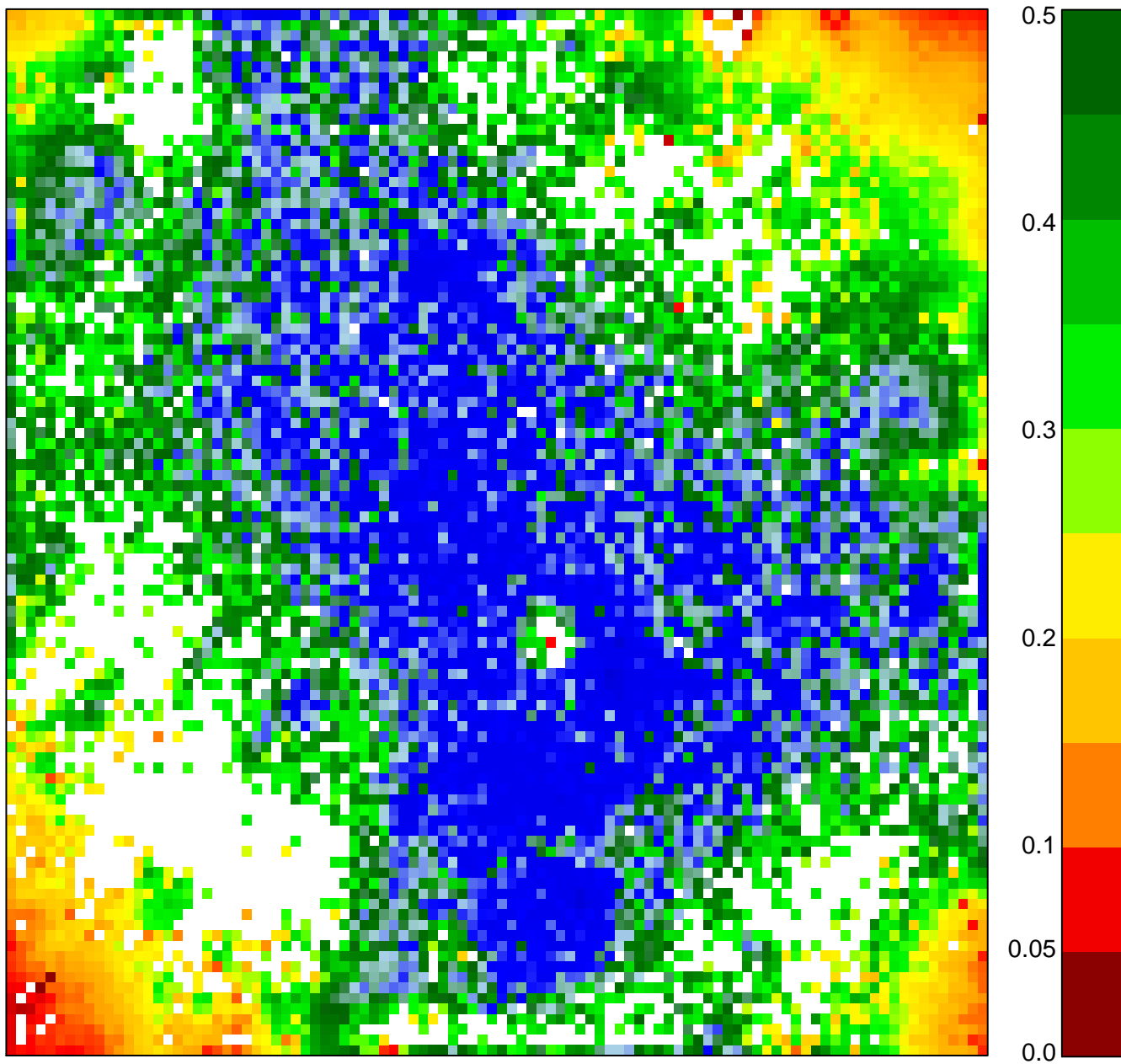
$\log ( \# \text{ genes in metagene } )$

# Metagene Variance Map



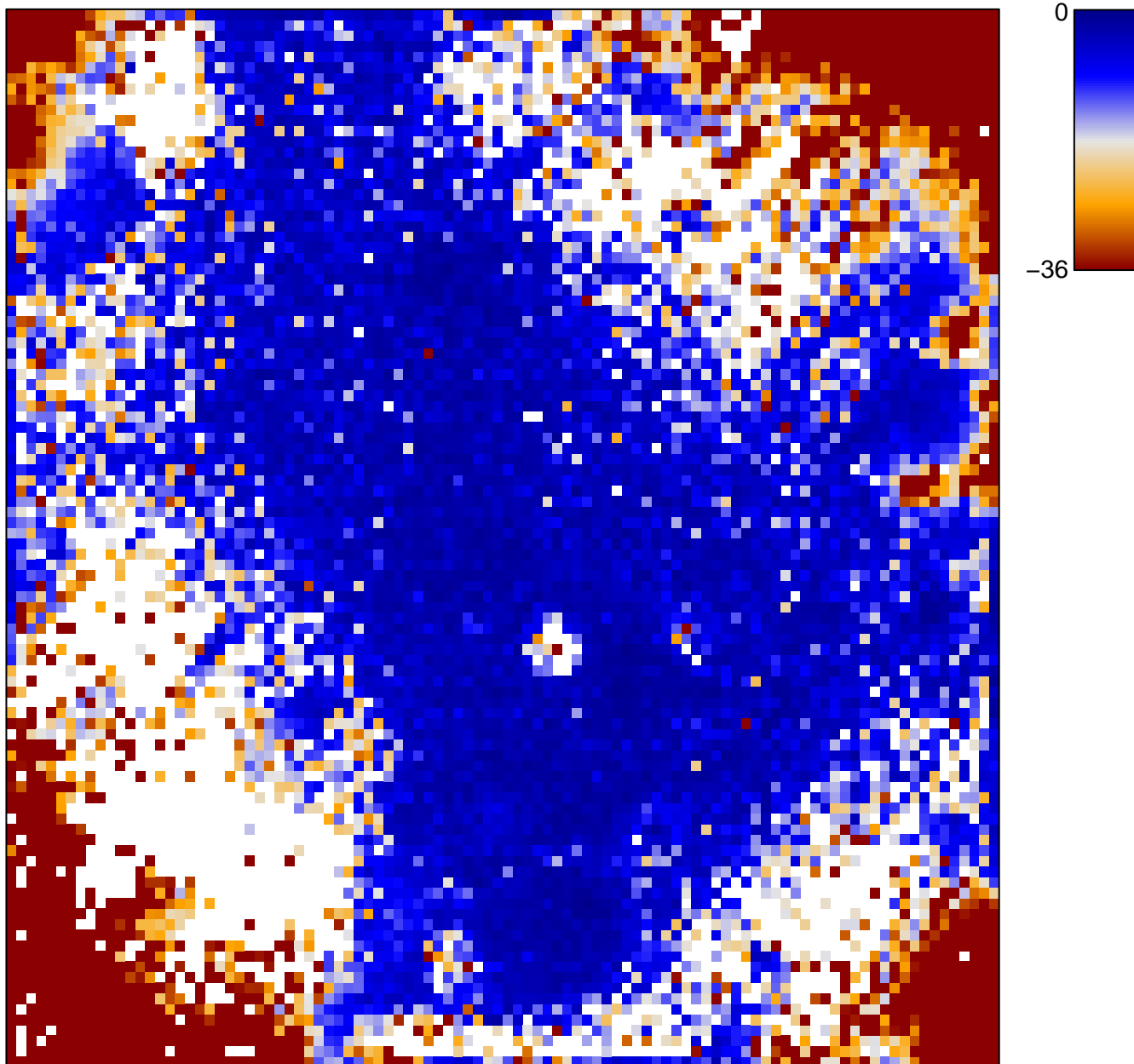
log ( metagene variance )

# Metagene Significance Map



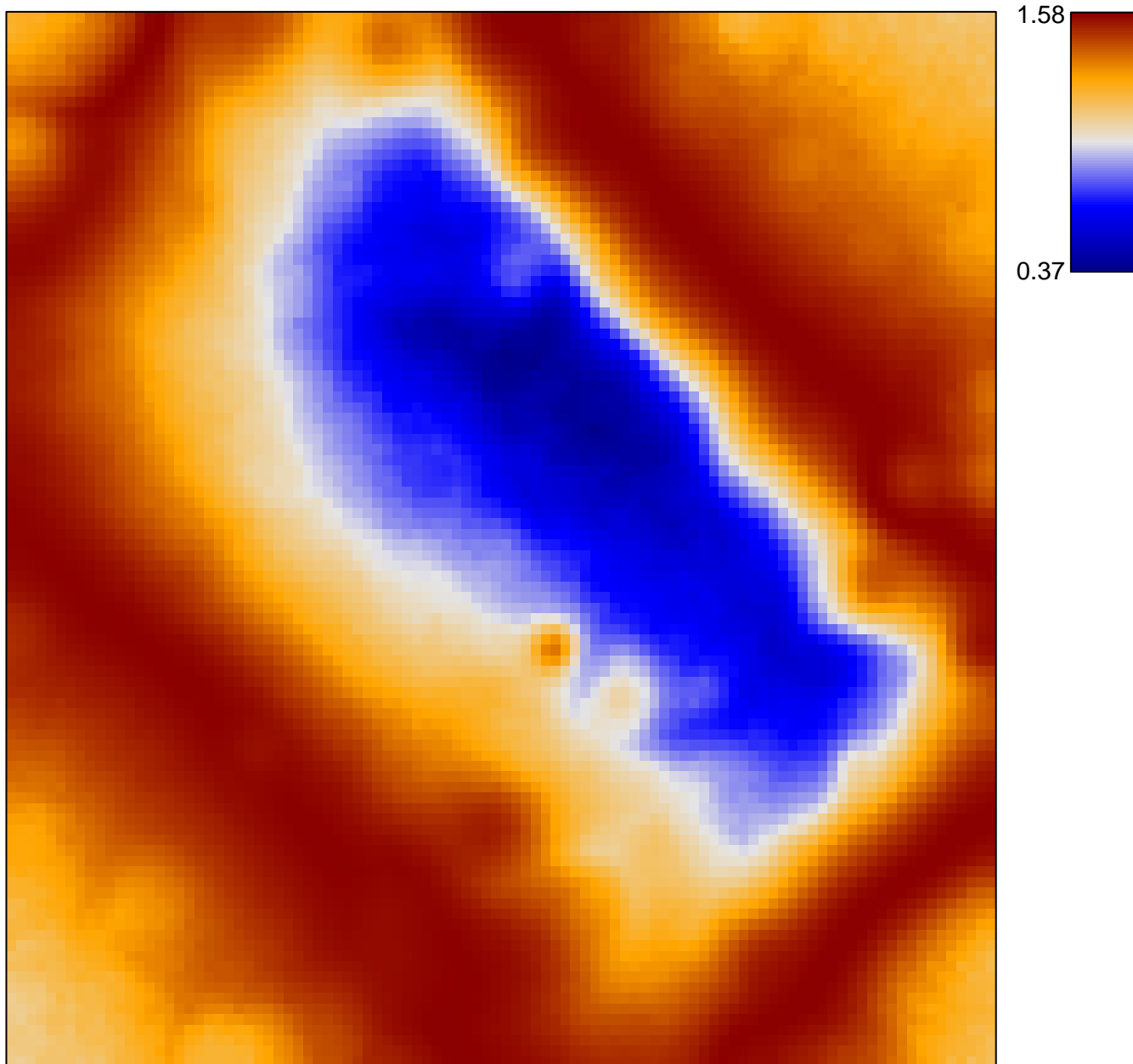
$\langle p_k \rangle$

# Metagene Significance Map



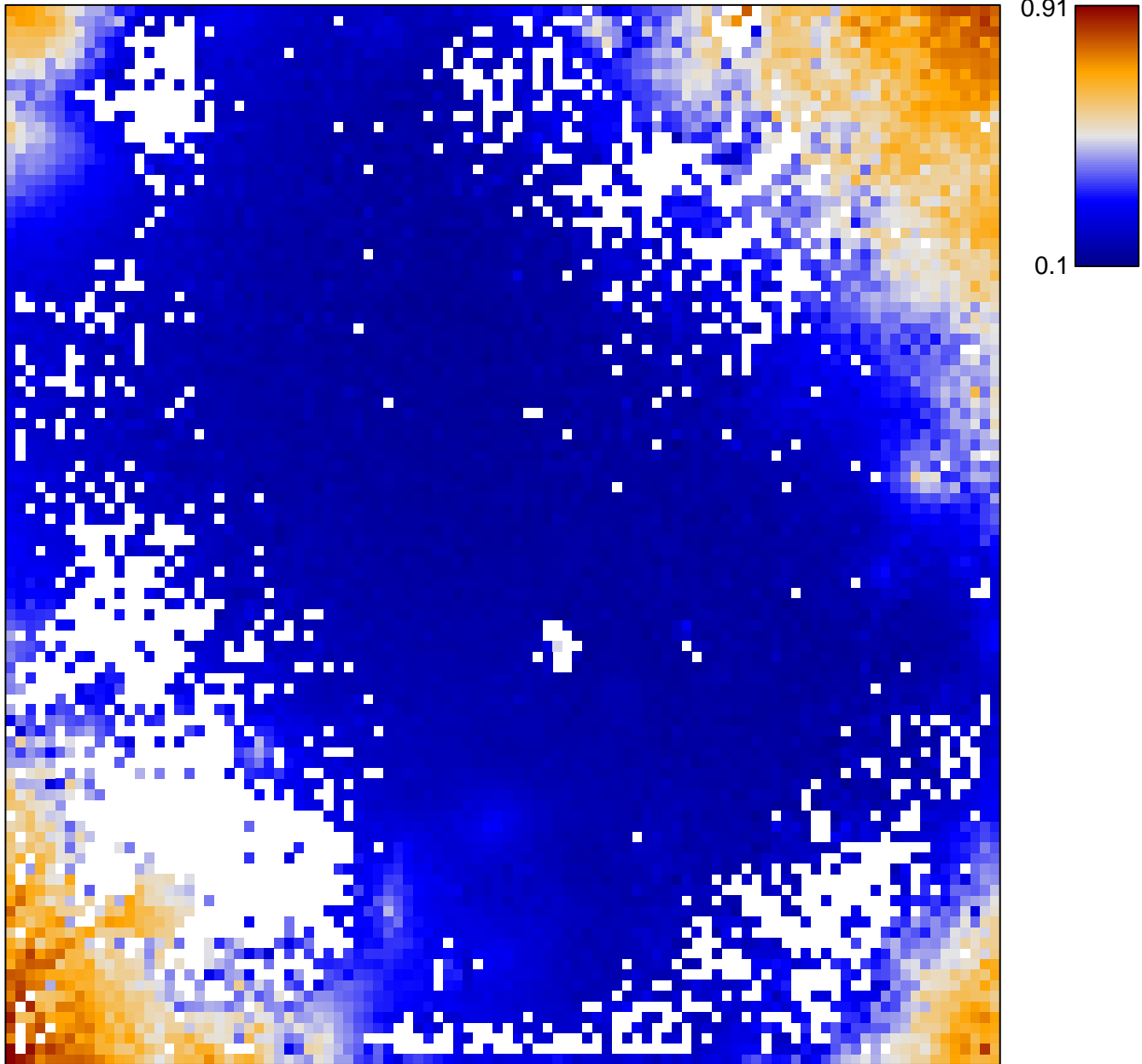
$\min_m(\log p_{k,m})$

# Standard Metagene Entropy Map



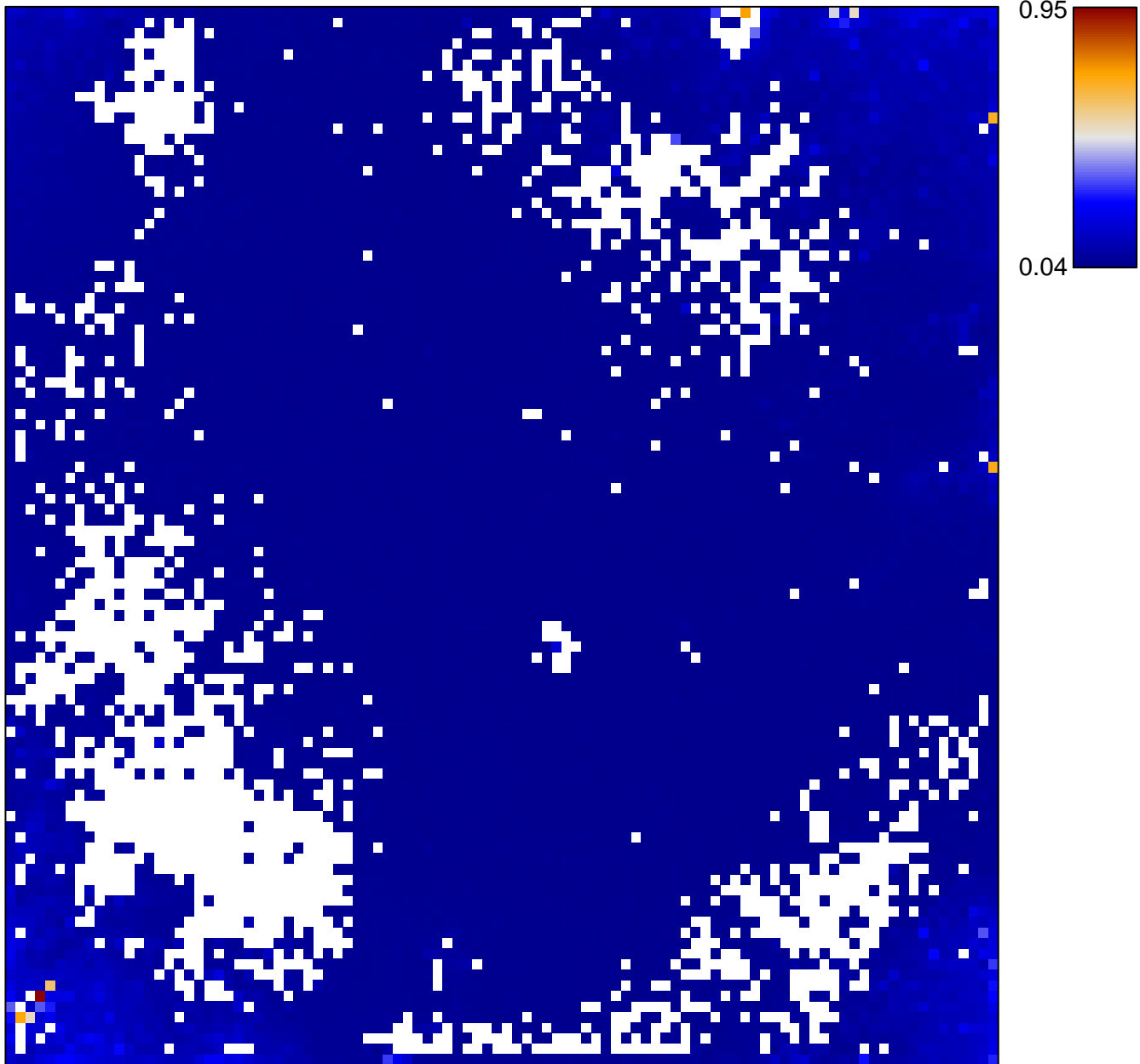
$h_k$

# Gene–Metagene Covariance Map



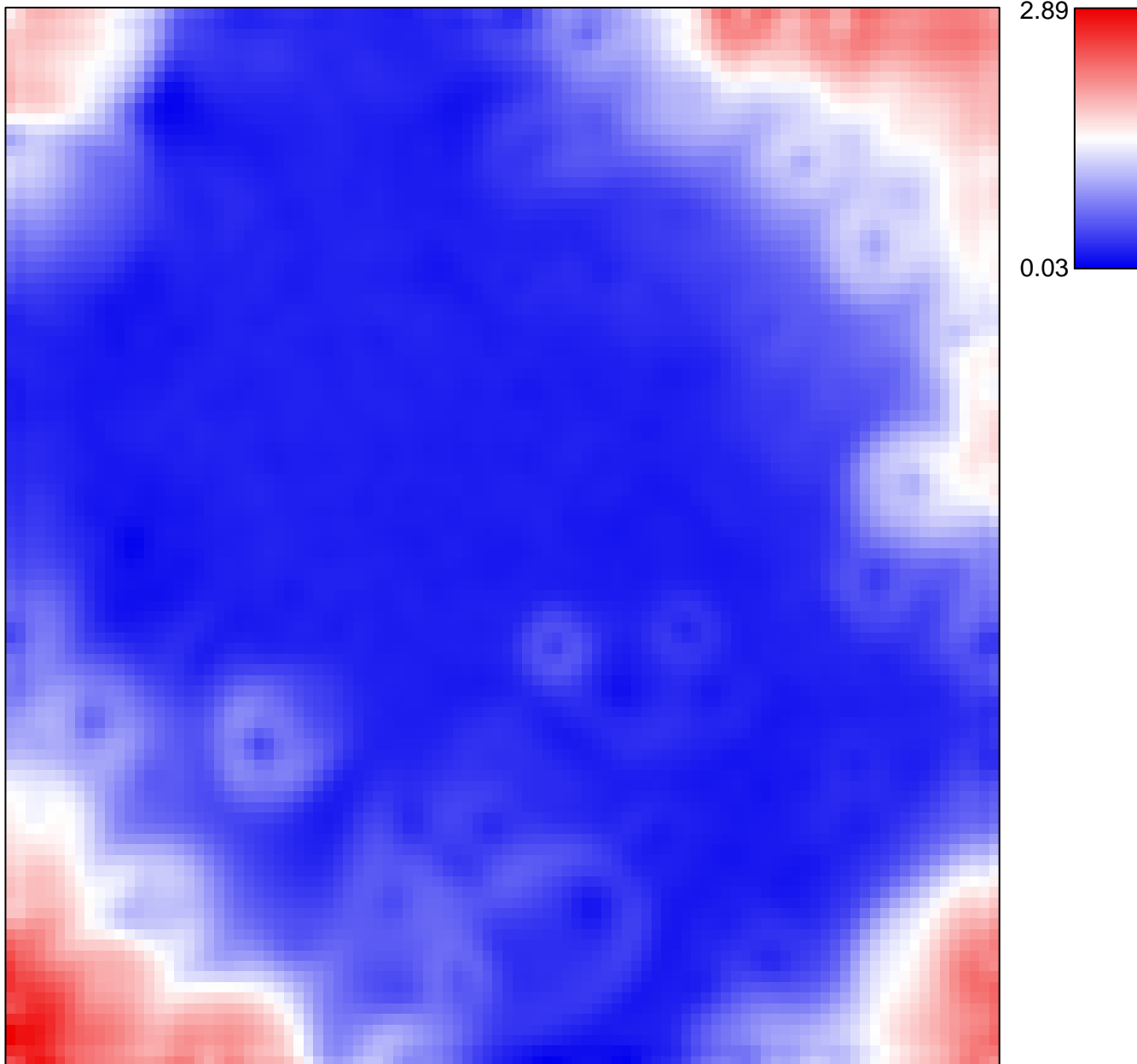
correlation genes – metagene

# Deviation Map



deviation genes – metagene

# Distance Map



deviation of adjacent metagenes