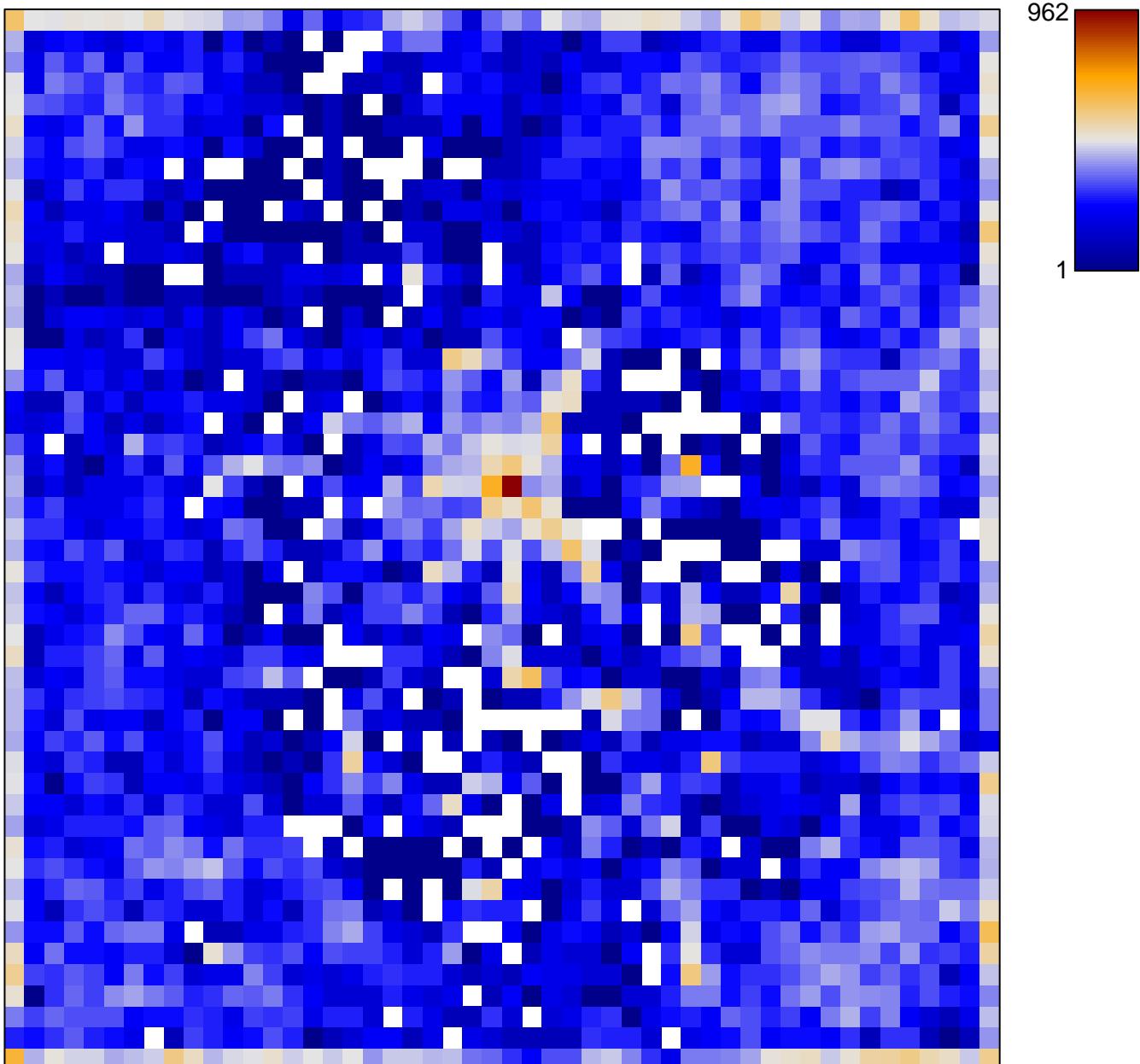
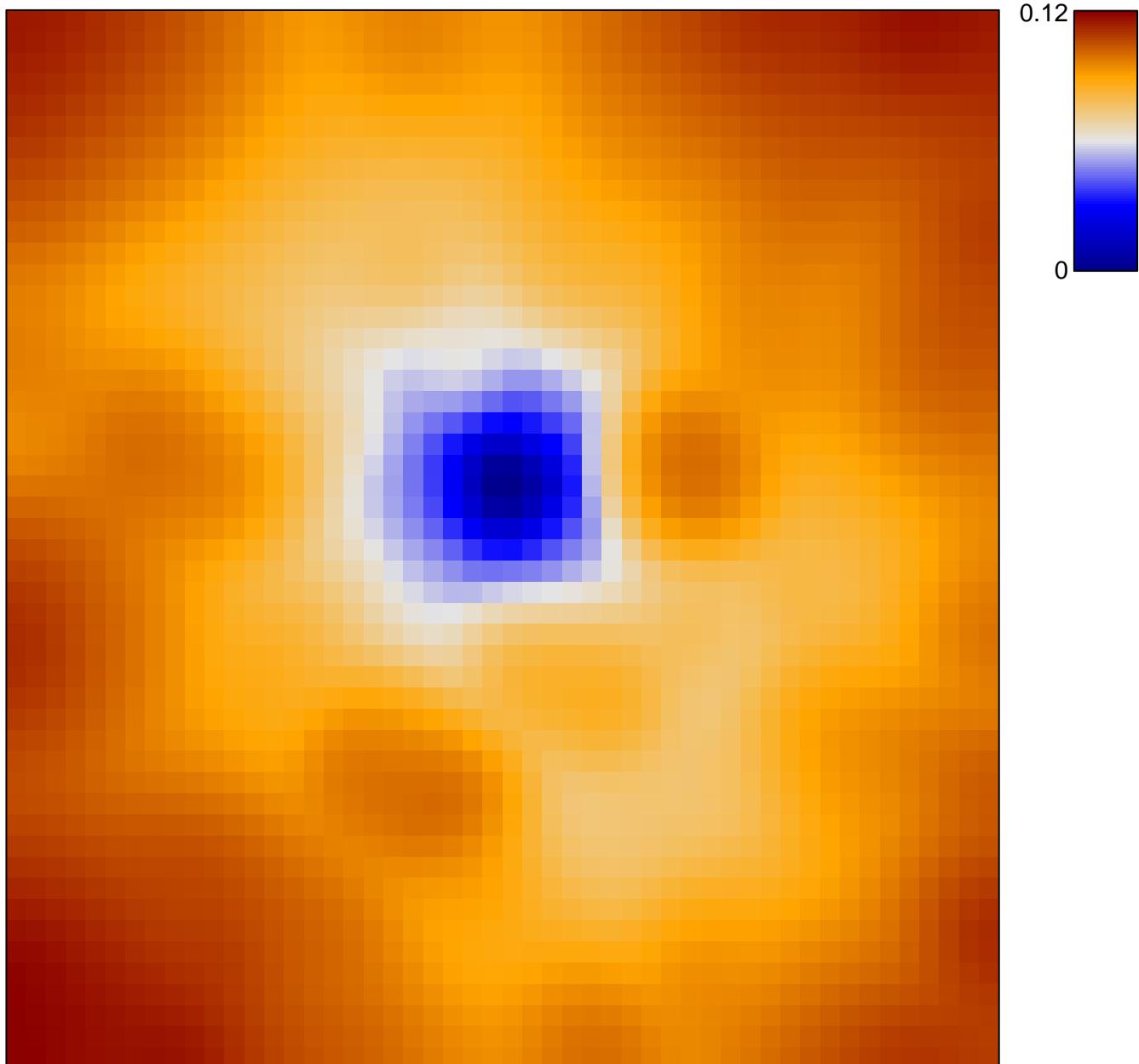


# Population Map



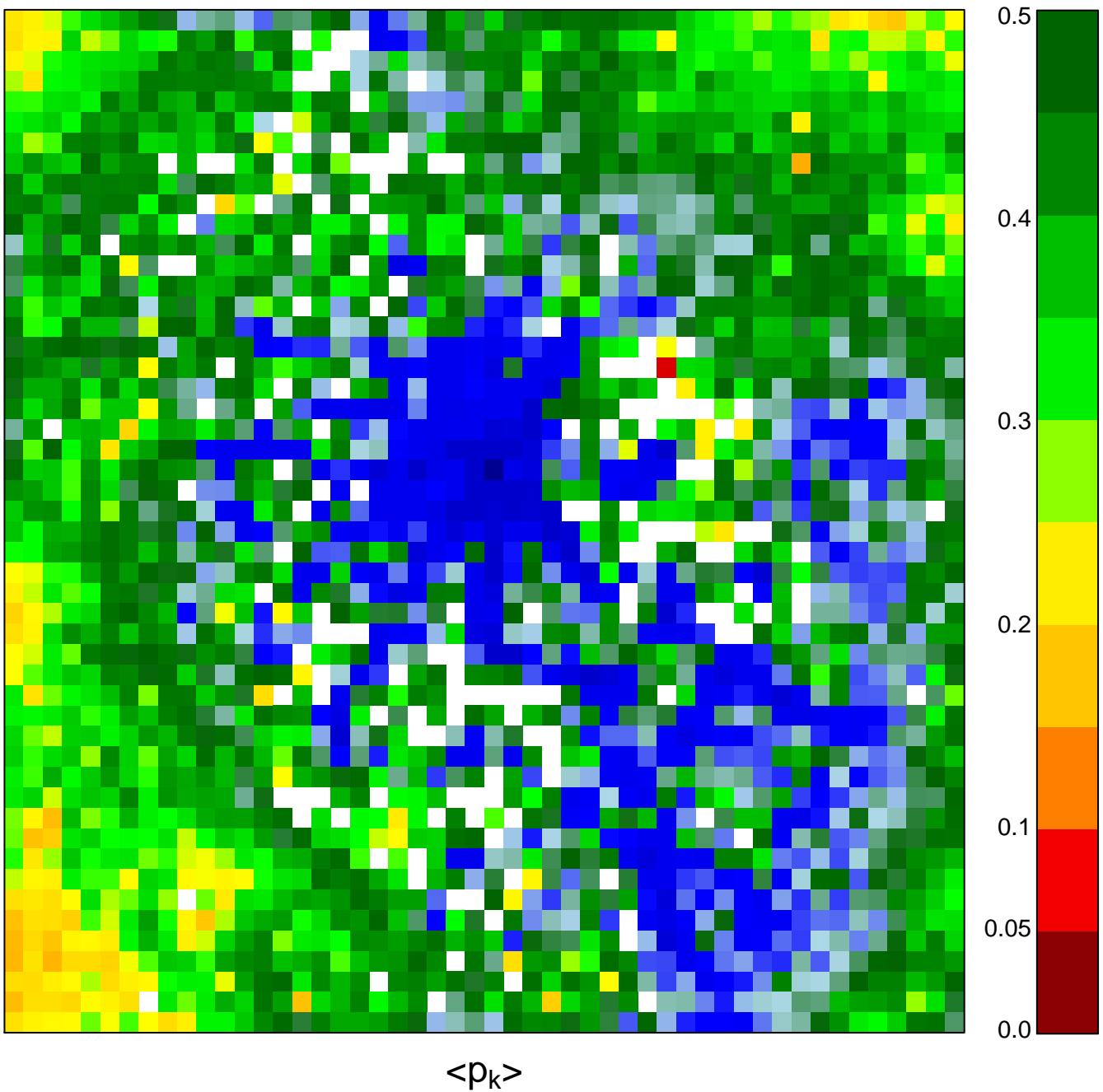
$\log (\# \text{ genes in metagene})$

# Metagene Variance Map

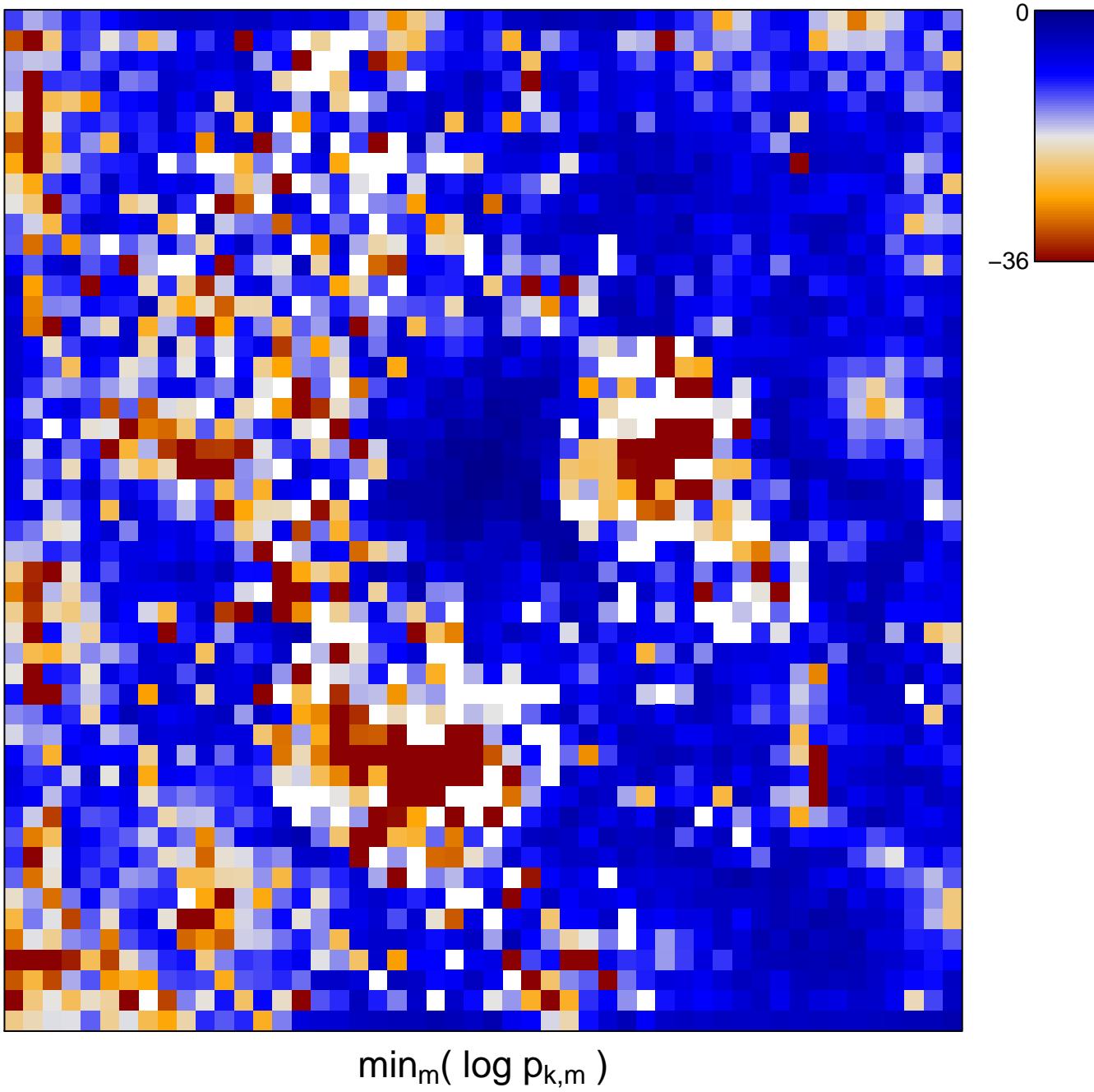


$\log$  ( metagene variance )

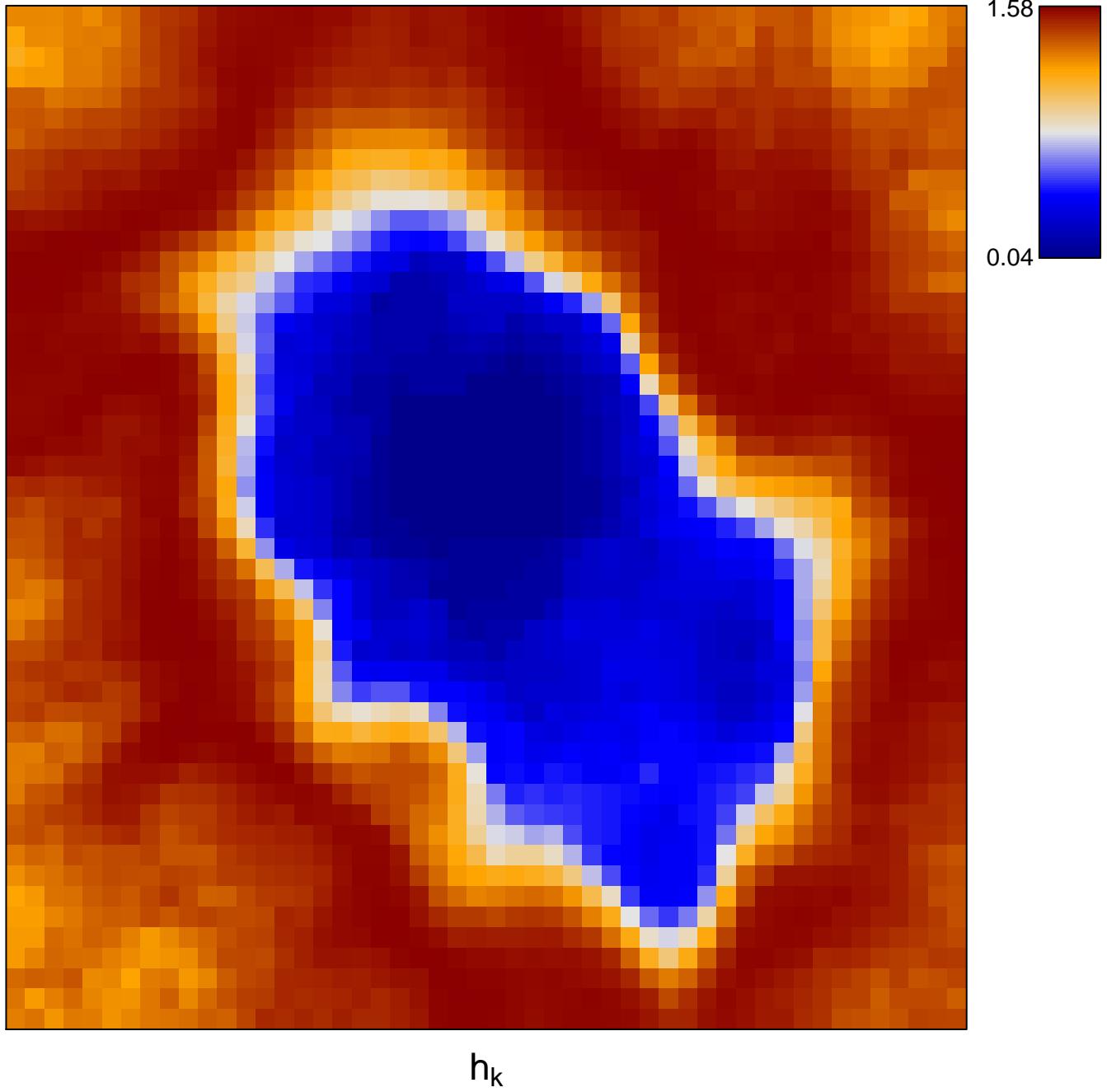
# Metagene Significance Map



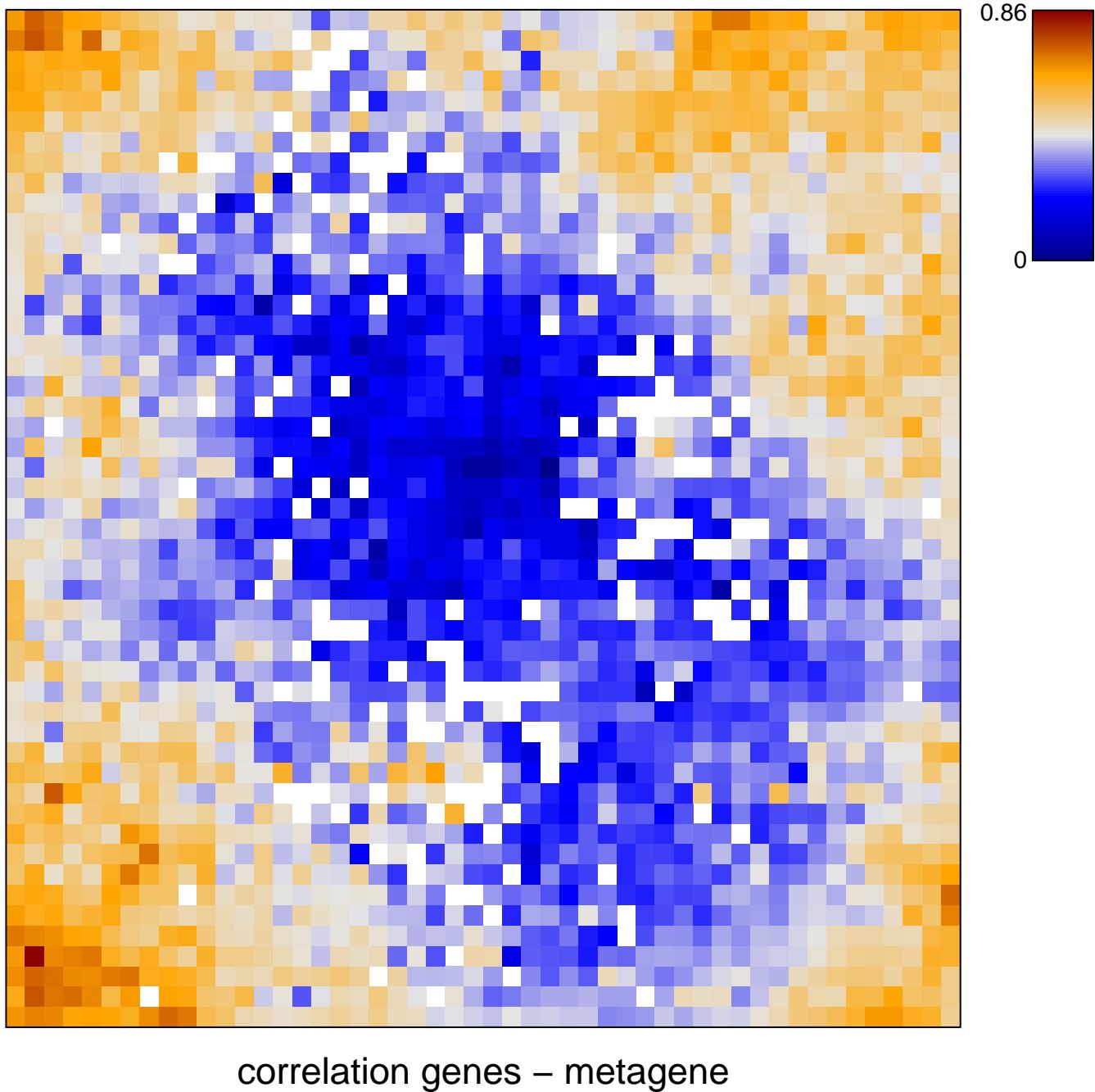
# Metagene Significance Map



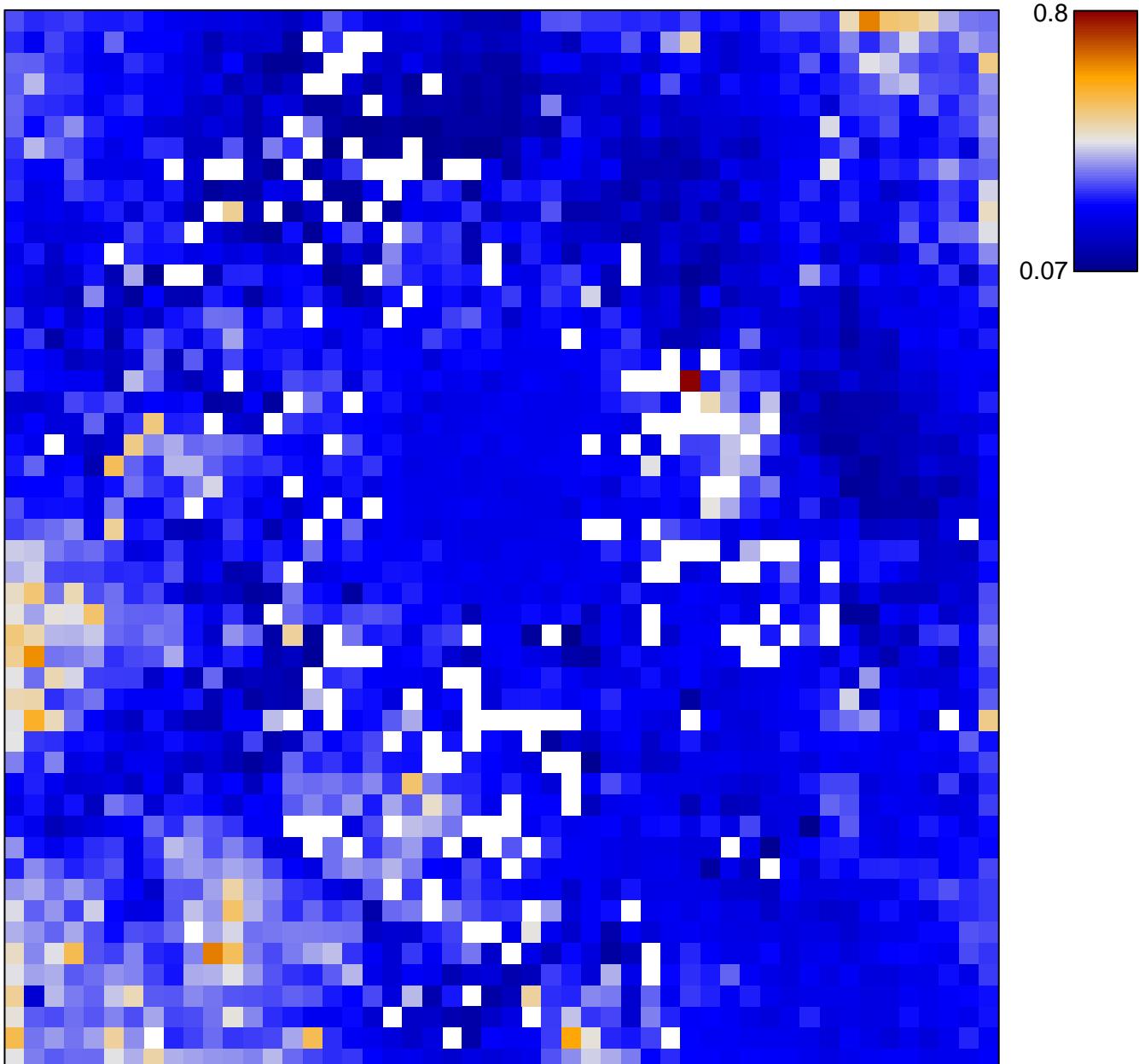
# Standard Metagene Entropy Map



# Gene–Metagene Covariance Map

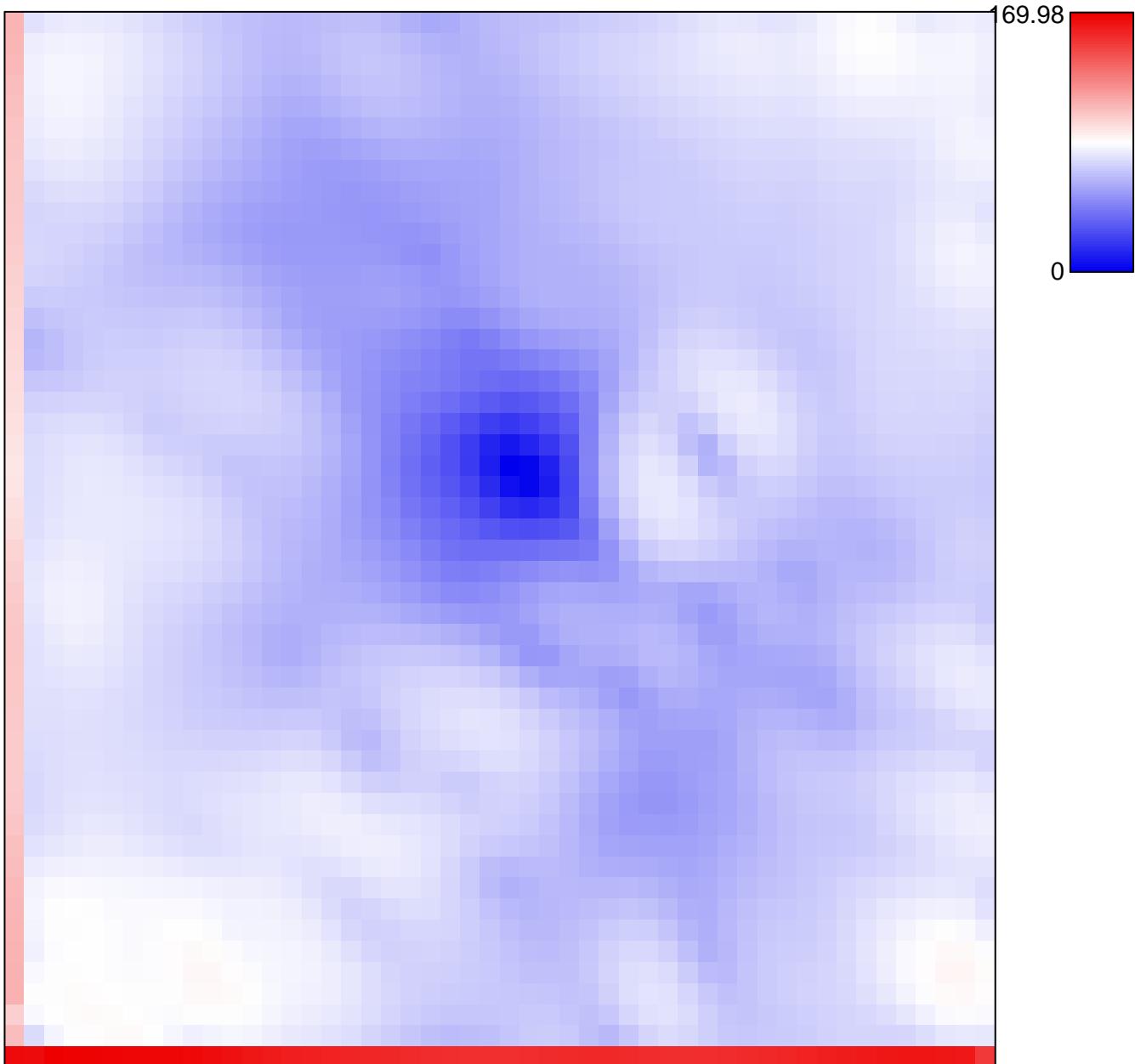


# Deviation Map



deviation genes – metagene

# Distance Map



deviation of adjacent metagenes