

Pheromone sensitivity
(absolute log fold)

0.16 ***

Upregulation in fertile
workers (log fold)

−0.04

0.05

Upregulation in queens
(log fold)

0.62 ***

0.11 *

0.17 ***

DNA methylation
(BiS−seq)

−0.07 *

−0.10 *

−0.13 ***

−0.29 ***

DNA methylation
(CpG depletion)

0.76 ***

−0.08 *

−0.12 *

−0.12 ***

−0.30 ***

Codon usage bias
(CAI)

0.70 ***

0.65 ***

−0.08 *

−0.13 **

−0.16 ***

−0.29 ***

Connectivity in the
transcriptome

0.46 ***

0.31 ***

0.32 ***

−0.14 *

−0.13 *

−0.28 ***

−0.21 ***

Log Expression level

0.19 ***

0.16 ***

0.12 ***

0.13 ***

0.19 ***

0.09 *

−0.39 ***

−0.11 ***

Connectivity in the
transcriptome

Codon usage bias
(CAI)

DNA methylation
(CpG depletion)

DNA methylation
(BiS−seq)

Upregulation in queens
(log fold)

Upregulation in fertile
workers (log fold)

Pheromone sensitivity
(absolute log fold)

Positive selection
(Gamma)