BOR-Papers in Press. Published on July 14, 2010 as DOI: 10.1095/biolreprod.110.084889

READ_ME file for Supplemental Online Material for

BIOLREPROD/2010/084889

Microarray-Based Analysis of Cell-Cycle Gene Expression During Spermatogenesis in the Mouse by Dipanwita Roy Choudhury, Chris Small, Yufeng Wang, Paul R. Mueller, Vivienne I. Rebel, Michael D. Griswold, and John R. McCarrey

The Supplemental Data online at www.biolreprod.org shows noninteractive material for reference only. For the complete interactive database described below, you must go to http://darwin.cbi.utsa.edu/mccarreylab

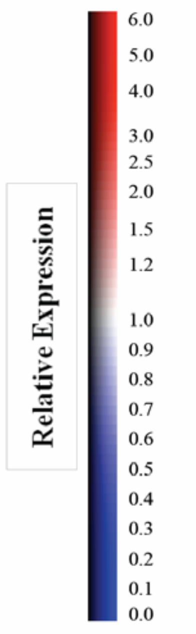
This database consists of two parts. The first part is the actual literature based cell cycle phase-specific networks, containing interaction information and gene information for all members of the network. The second part consists of expression maps, where genes in phase-specific network that are up-regulated by 1.5X are color coded with red.

How to browse the interactive database:

1. You can open any HTML file for a phase of cell cycle (e.g., G0-G1_html_map [G0-G1_map.doc]) and its corresponding expression map for the same phase (e.g., G0-G1_expression_map.ppt) at the same time. Genes that are color coded in red are up-regulated by 1.5X in that particular cell type.

2. In the interactive HTML map, you can click on the gene name on the map to get more information about the gene. You can also click on interaction nodes to read references about the interaction. Please see the Pathway Key for the legends for different nodes, edges, and relationships.

3. The color bar above each gene in the maps indicates the relative extent of differential expression between cell types. Red indicates up-regulated expression, blue indicates down-regulated expression, and white indicates little or no significant change in expression level.



03/16/2010