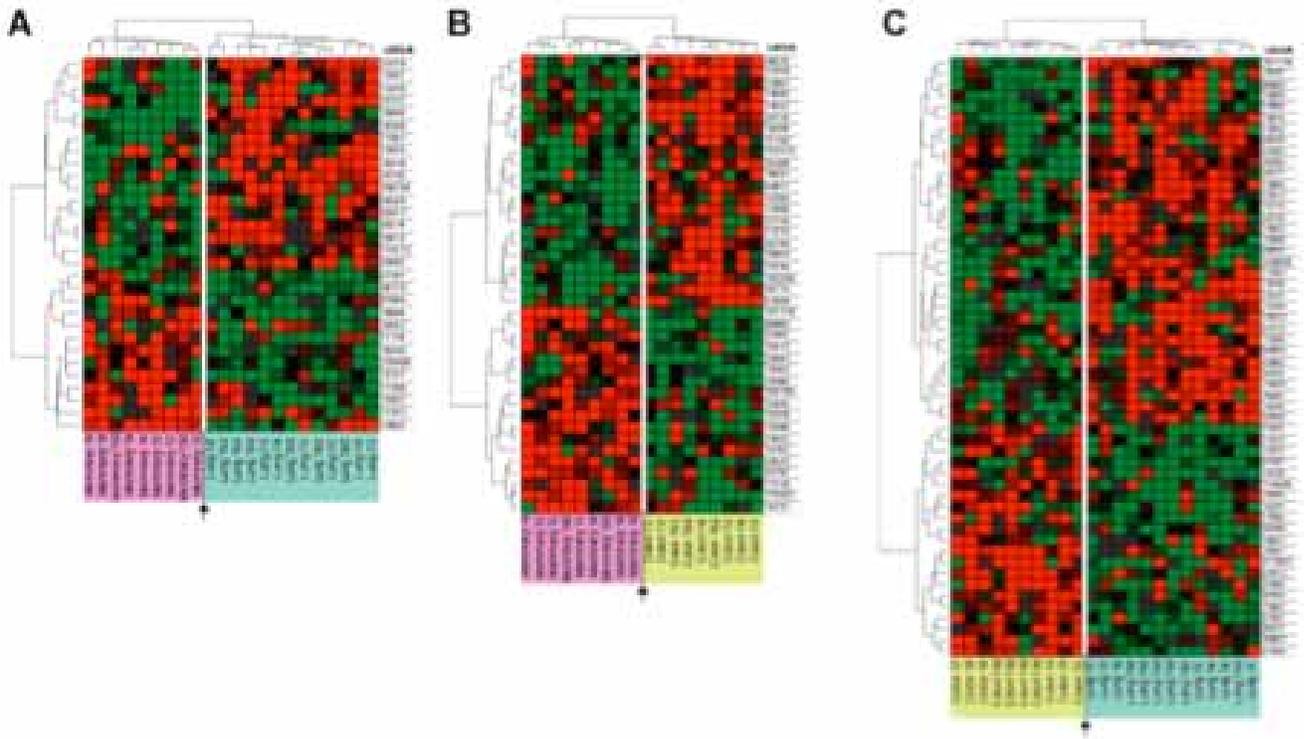
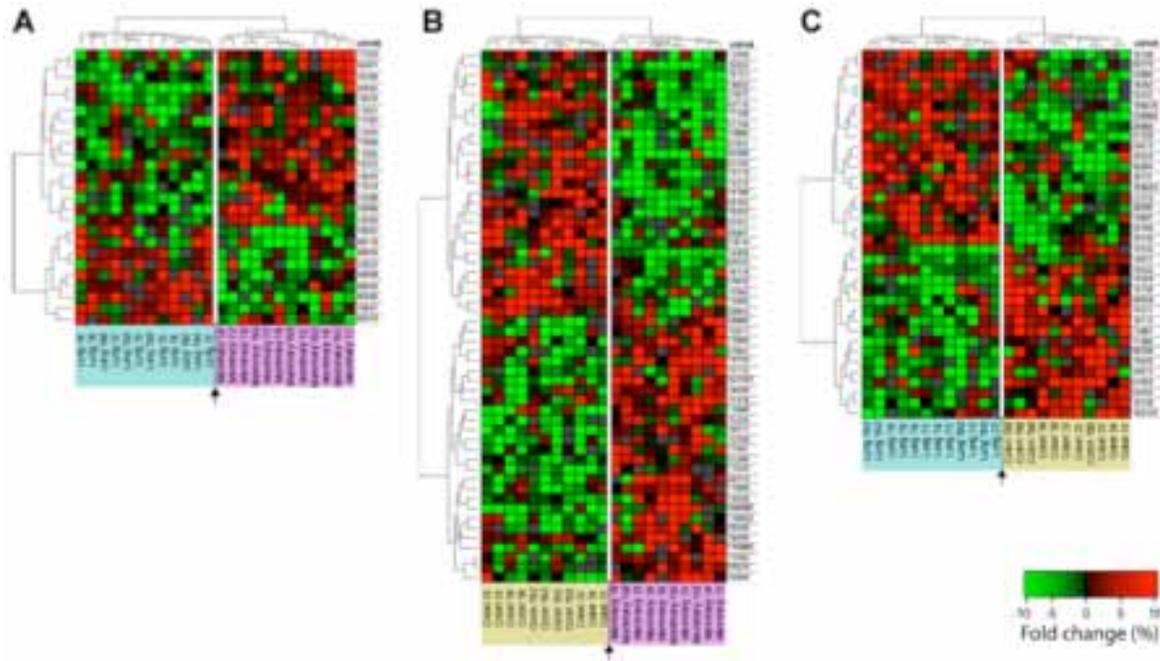


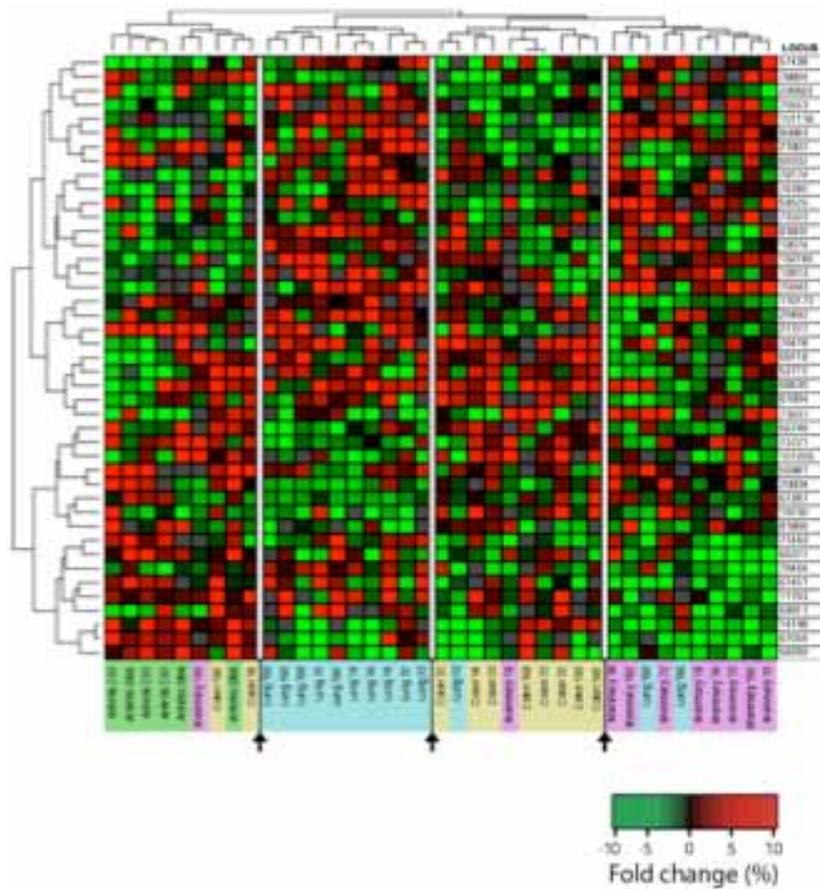
Supplementary Fig. (1). Hierarchical heatmap of hypothalamic samples: Comparisons are based on the subset of differentially expressed genes between the paired models, mammary and lung (A.), colon and mammary (B). Each column represents a sample and each row a single gene. Red indicates up-regulation, green down-regulation, and black no change. The white line marks the subdivision into the two dominant clusters of samples. Sample labels indicate cancer model (cyan, yellow and magenta for lung, colon and mammary cancer models, respectively) and time point.



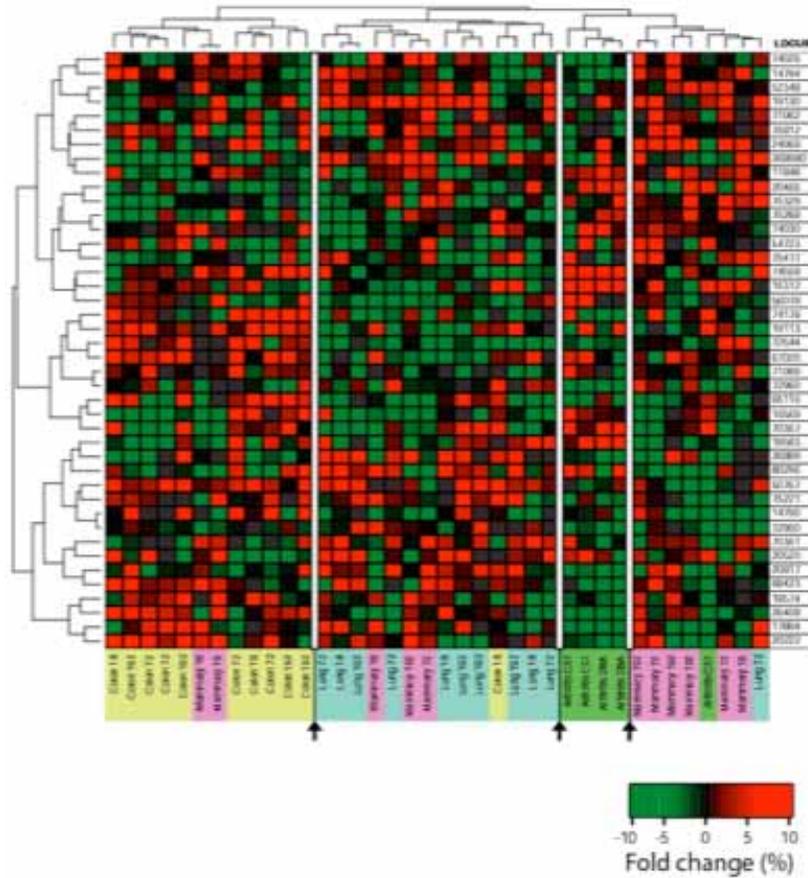
Supplementary Fig. (2). Hierarchical heatmap of cortical samples: Comparisons are based on the subset of differentially expressed genes between the paired models, mammary and lung (A), colon and mammary (B) and colon and lung (C). For more details see supplementary Fig. (1).



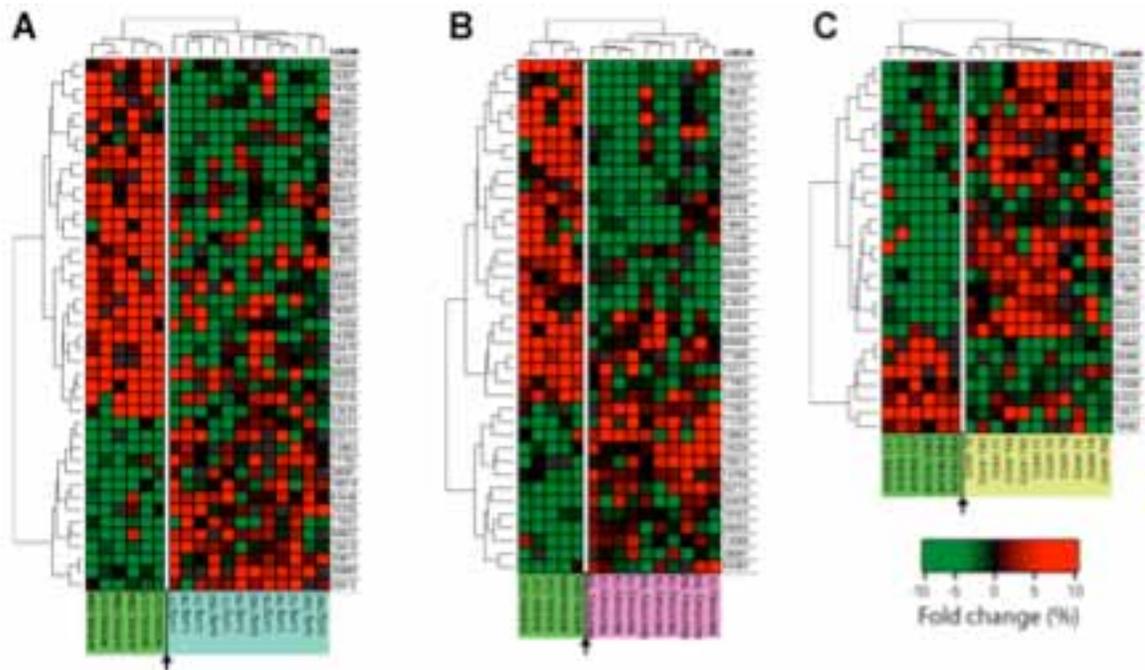
Supplementary Fig. (3). Hierarchical heatmap of Midbrain samples: Comparisons are based on the subset of differentially expressed genes between the paired models, mammary and lung (A), colon and mammary (B) and colon and lung (C). For more details see supplementary Fig. (1).



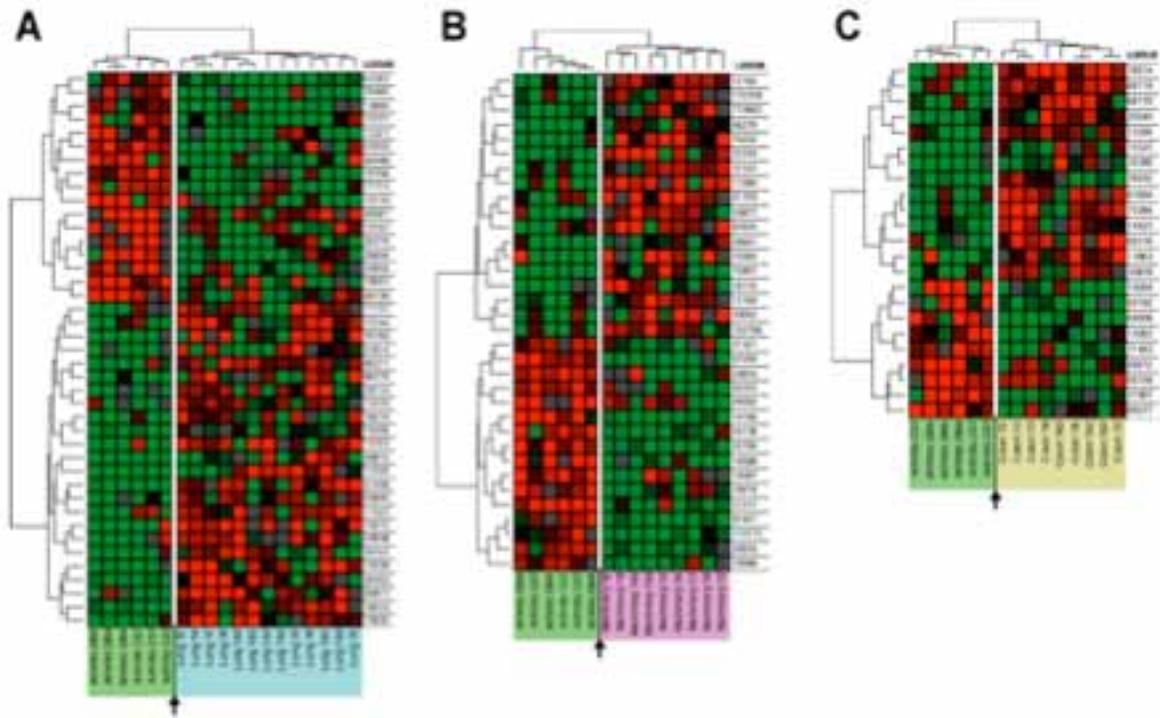
Supplementary Fig. (4). Hierarchical cluster analysis of cortical samples: obtained from the arthritis and cancer models based on the 10 top-ranked genes from each pair-wise comparison. Each column represents a sample and each row a single gene. Red indicates up-regulation, green down-regulation, and black no change. The white line marks the subdivision into the dominant clusters of samples. Sample labels indicate disease model (green, cyan, magenta and yellow for arthritis, lung, mammary and colon cancer models, respectively) and time point.



Supplementary Fig. (5). Hierarchical cluster analysis of Midbrain samples: obtained from the arthritis and cancer models based on the 10 top-ranked genes from each pair-wise comparison. For more details see supplementary Fig. (4).



Supplementary Fig. (6). Hierarchical heatmap of cortical samples: from arthritis and each of the three different cancer models: Lung (A) mammary (B) and colon (C), based on the subset of differentially expressed genes between the different paired models. Each column represents a sample and each row a single gene. Red indicates up-regulation, green down-regulation, and black no change. The white line marks the subdivision into the two dominant clusters of samples. Sample labels indicate the disease model (green, cyan, yellow and magenta for arthritis, lung, colon, and mammary cancer models respectively) and time point.



Supplementary Fig. (7). Hierarchical heatmap of Midbrain samples: from arthritis and each of the three different cancer models: Lung (A) mammary (B) and colon (C), based on the subset of differentially expressed genes between the different paired models. For more details see supplementary Fig. (6).