

Amino acid metabolism in estrogen receptor-positive breast cancer

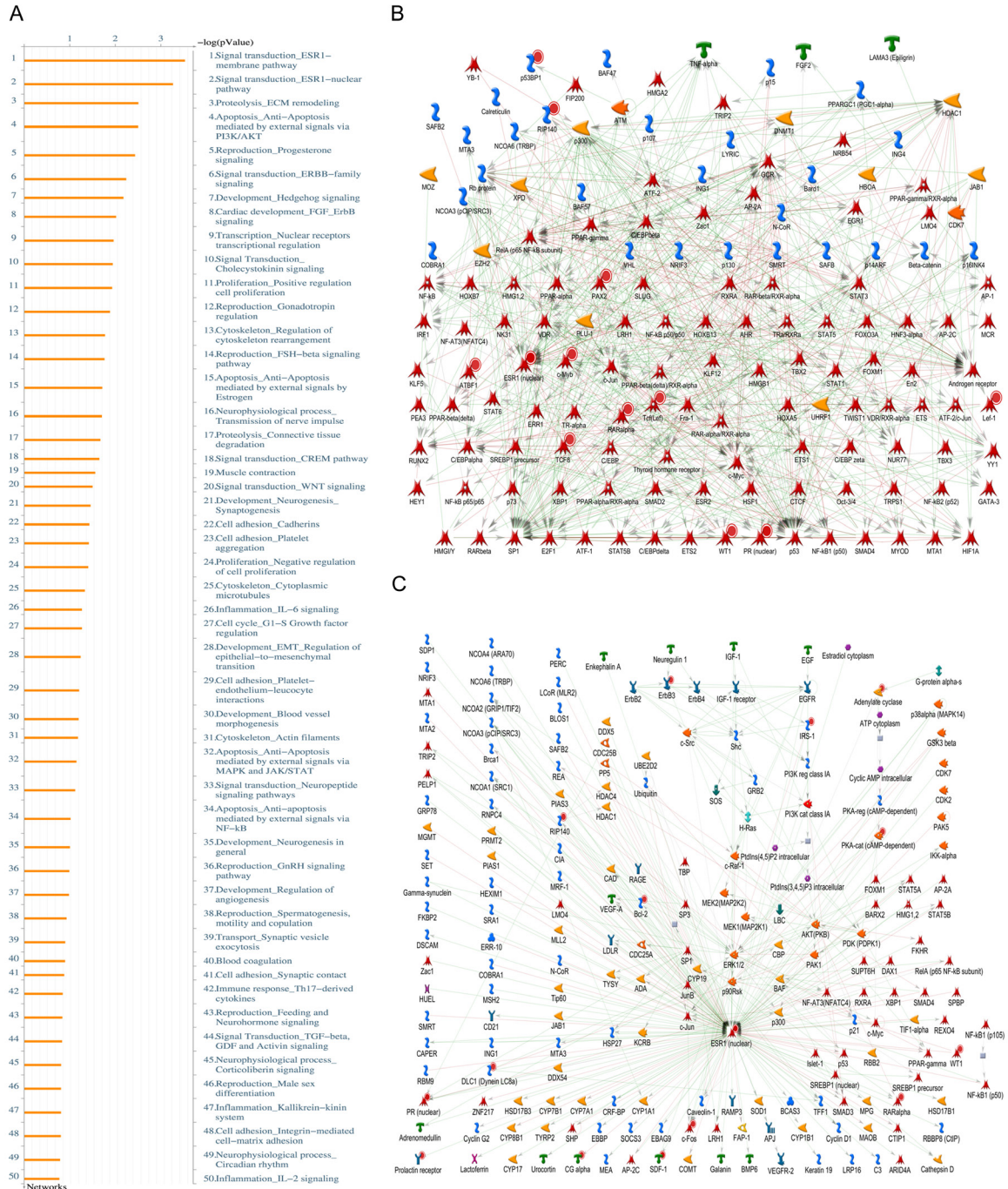


Figure S1. The METABRIC, TCGA, and GSE11352 databases were compared, and highly expressed genes from ER⁺ patients were uploaded to the MetaCore database for disease and biomarker analysis. A. Significant “positive-regulation” genes (upregulation) among the TCGA and METABRIC clinical ER⁺ patient databases and the GSE11352 (MCF7-Estradiol/MCF7-Con) database were uploaded to the MetaCore database for downstream pathway analysis. B. “Breast neoplasm transcription regulation”, C. “Signal transduction ESR1-nuclear pathway” and other related genes were significantly upregulated in the ER⁺ patient group and the MCF7-estradiol group.

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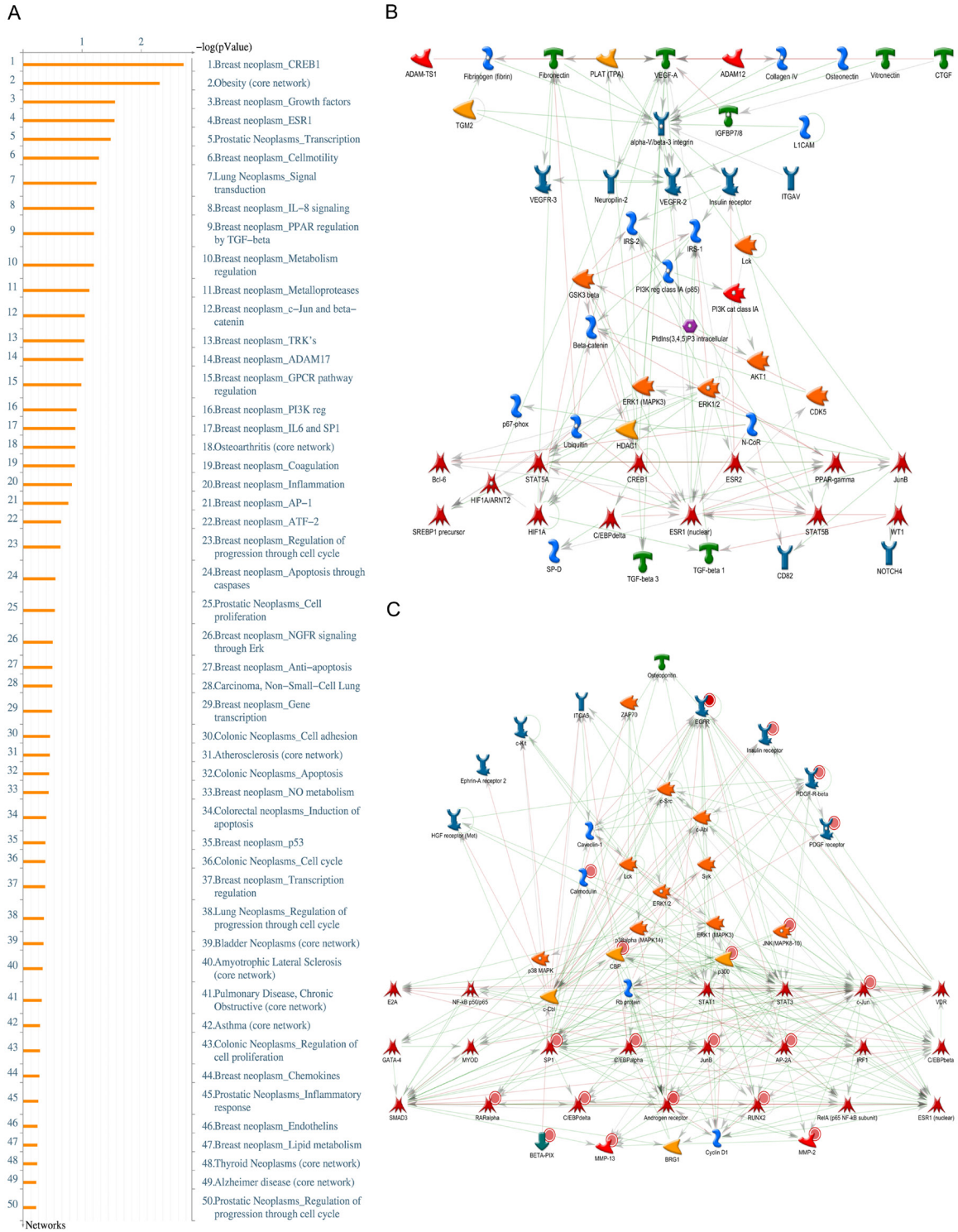
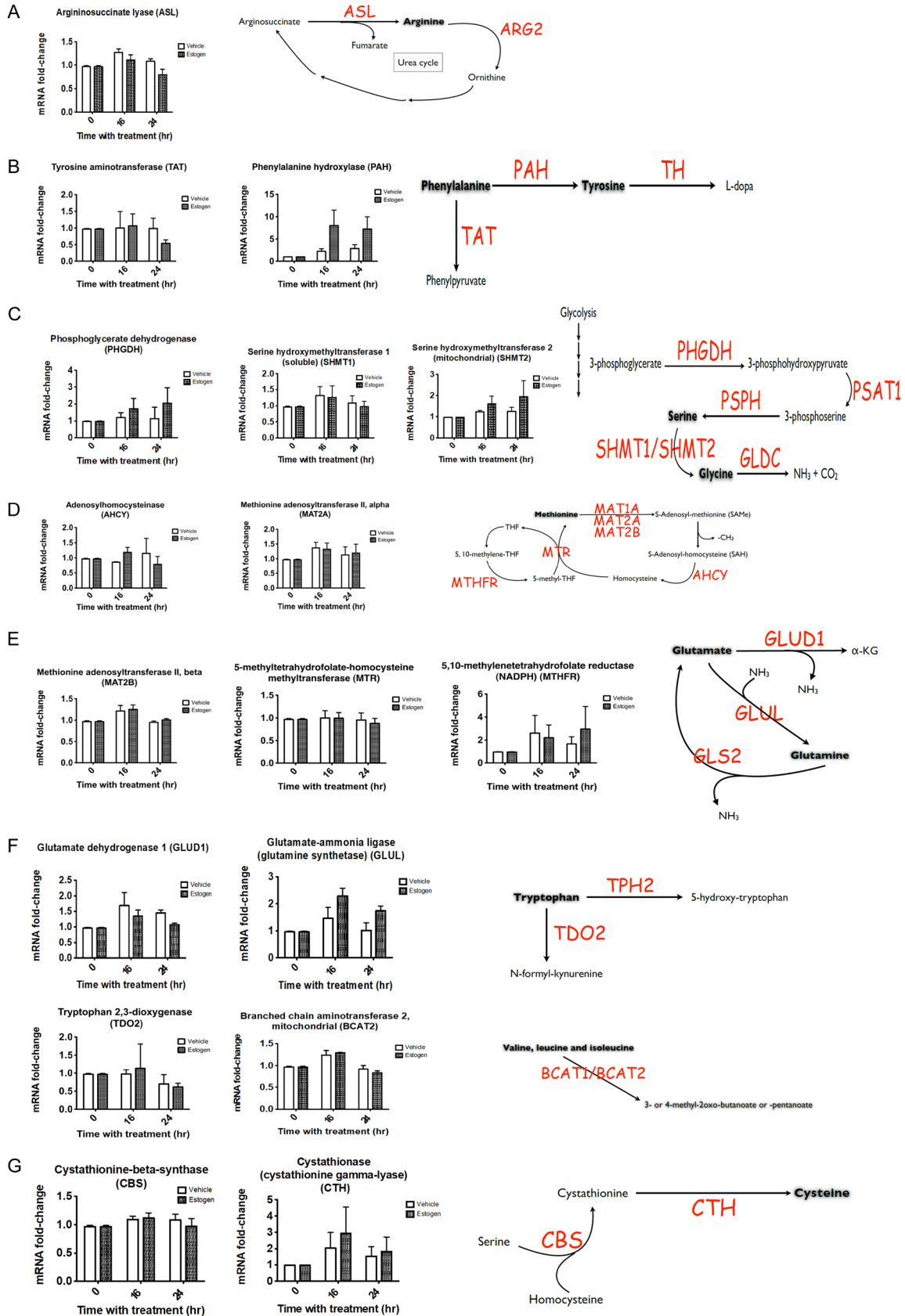


Figure S2. Comparing the upregulated genes between the estradiol treatment and control groups and exploring the potential networks. (A) The GSE11352 database describes disease biomarker networks, where control MCF-7 groups (12C, 24C, and 48C) were compared with estradiol treatment for 12 (12E), 24 (24E), or 48 hour (48E) in MCF-7 cells, (B) “Breast neoplasm ESR1” and other related pathways are significantly upregulated in the estradiol group. (C) Novel downstream pathways identified in the estradiol treatment group, such as “breast neoplasm metabolism regulation”.

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Figure S3. The mRNA expression levels of amino acid metabolism genes in the MCF-7 cell line. MCF-7 cells were seeded and treated with 10 nM estradiol for 16-18 hours. Total RNA was extracted, and amino acid metabolic genes were analyzed by RT-qPCR, using the mRNA of PGR, which is activated by the estrogen receptor, as a positive control. A. Argininosuccinate lyase/ASL. B. Tyrosine aminotransferase/TAT; phenylalanine hydroxylase/PAH. C. Phosphoglycerate dehydrogenase/PHGDH; serine hydroxymethyltransferase 1/SHMT1; serine hydroxymethyltransferase 2/SHMT2. D. Adenosylhomocysteinase/AHCY; methionine adenosyltransferase 2A/MAT2A. E. Methionine adenosyltransferase 2B/MAT2B; 5-methyltetrahydrofolate-homocysteine methyltransferase/MTR. F. Glutamate dehydrogenase 1/GLUD1; glutamate-ammonia ligase/GLUL; tryptophan 2,3-dioxygenase/TDO2; branched-chain amino acid transaminase 2/BCAT2. G. Cystathionine-beta-synthase/CBS; cystathionine gamma-lyase/CTH.