CORRECTION

Correction: Dysregulation of multiple metabolic networks related to brain transmethylation and polyamine pathways in Alzheimer disease: A targeted metabolomic and transcriptomic study

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During the process of revising the figures and ensuring they met the required standards for resolution/size, some of the line alignments in Fig 11 were lost or misaligned. See the corrected Fig 11 here.



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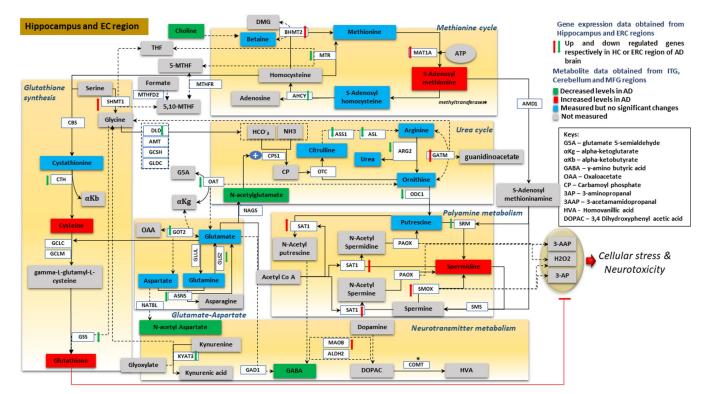


Fig 11. Integrated summary of alterations in metabolite concentrations and gene expression within metabolic pathways linked to transmethylation and polyamine synthesis/catabolism. Reactions within each of the six categories related to transmethylation and polyamine metabolism are shown within brown boxes [93-95]. Metabolites whose concentrations are increased in the AD ITG relative to controls are shown in red boxes; those that are reduced in AD are shown in green boxes. Metabolites whose concentrations were measured but did not differ between AD and control are indicated in blue boxes; metabolites whose concentrations were not assayed are shown in gray boxes. Red up and green down arrows indicate significantly increased and reduced gene expression in the ERC/hippocampus, respectively. AD, Alzheimer disease; AHCY, adenosylhomocysteinase; ALDH2, aldehyde dehydrogenase 2; AMD1, adenosylmethionine decarboxylase 1; AMT, aminomethyltransferase; ARG2, arginase 2; ASL, argininosuccinate lyase; ASNS, asparagine synthetase; ASS1, argininosuccinate synthase 1; BHMT2, betaine homocysteine smethyltransferase 2; CBS, cystathionine beta synthase; CN, Control; COMT, catechol-omethyltransferase; CPS1, carbamoyl phosphate synthase 1; CTH, cystathionine gamma-lyase; DLD, dihydrolipoamide dehydrogenase; ERC, entorhinal cortex; GAD1, glutamate decarboxylase 1; GATM, glycine amidino transferase; GCLC, glutamate cysteine ligase catalytic; GCLM, glutamate cysteine ligase modifier; GCSH, glycine cleavage system protein H; GLDC, glycine decarboxylase; GLS2, glutaminase 2; GLUL, glutamine synthetase; GOT2, glutamic oxaloacetic transaminase 2; GSS, GSH synthetase; HC, hippocampus; ITG, inferior temporal gyrus; KYAT3, kynurenine aminotransferase 3; MAT1A, methionine adenosyltransferase 1A; MFG, middle frontal gyrus; MOAB, monoamine oxidase B; MTHFD2, methylenetetrahydrofolate dehydrogenase 2; MTHFR, methylenetetrahydrofolate reductase: MTR. methyltransferase: NAT8L, n-acetyltransferase 8 like; OAT, ornithine aminotransferase: ODC1, ornithine decarboxylase 1; OTC, ornithine carbamoyltransferase; PAOX, polyamine oxidase; SAT1, spermidine/spermine n1-acetyltransferase 1; SHMT1, serine hydroxymethyl transferase 1; SMOX, spermine oxidase; SMS, spermine synthase; SRM, spermidine synthase.

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Reference

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