

CORRECTION

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Correction: Integration of metabolites from meta-analysis with transcriptome reveals enhanced *SPHK1* in PDAC with a background of pancreatitis

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Following publication of the original article [1], the authors identified a typesetting error. Figure 2 was published in incomplete form. Figure 2E-G were erroneously omitted. The complete Fig. 2 has been published in this correction. The original article [1] has been updated.

Reference

1. Ketavarapu V, Ravikanth V, Sasikala M, et al. Integration of metabolites from meta-analysis with transcriptome reveals enhanced SPHK1 in PDAC with a background of pancreatitis. *BMC Cancer*. 2022;22:792. <https://doi.org/10.1186/s12885-022-09816-6>.

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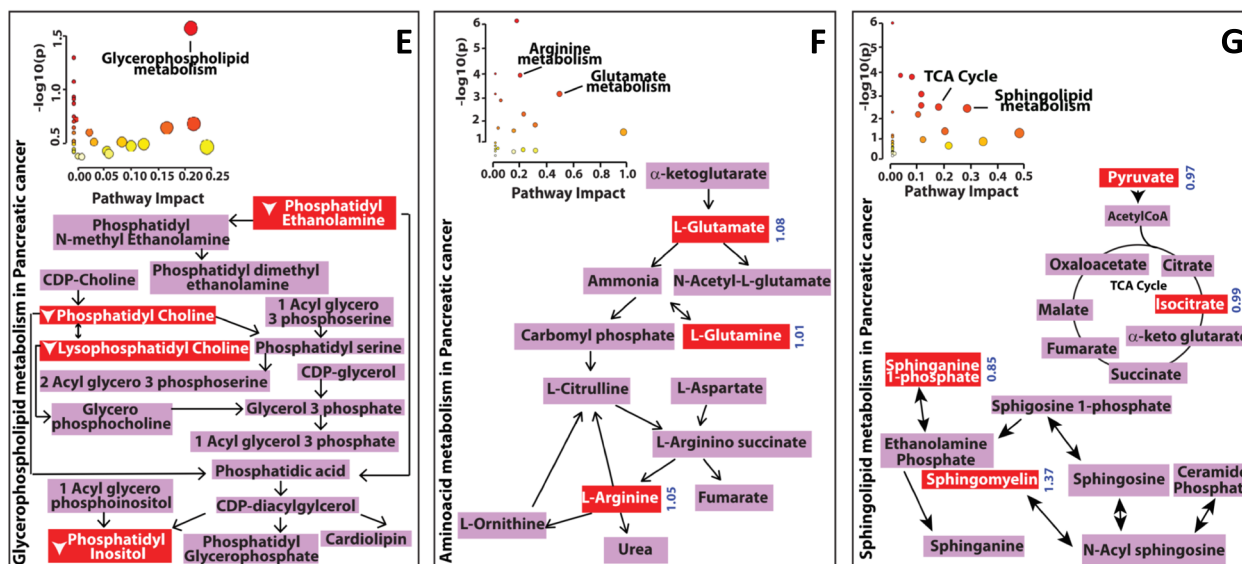
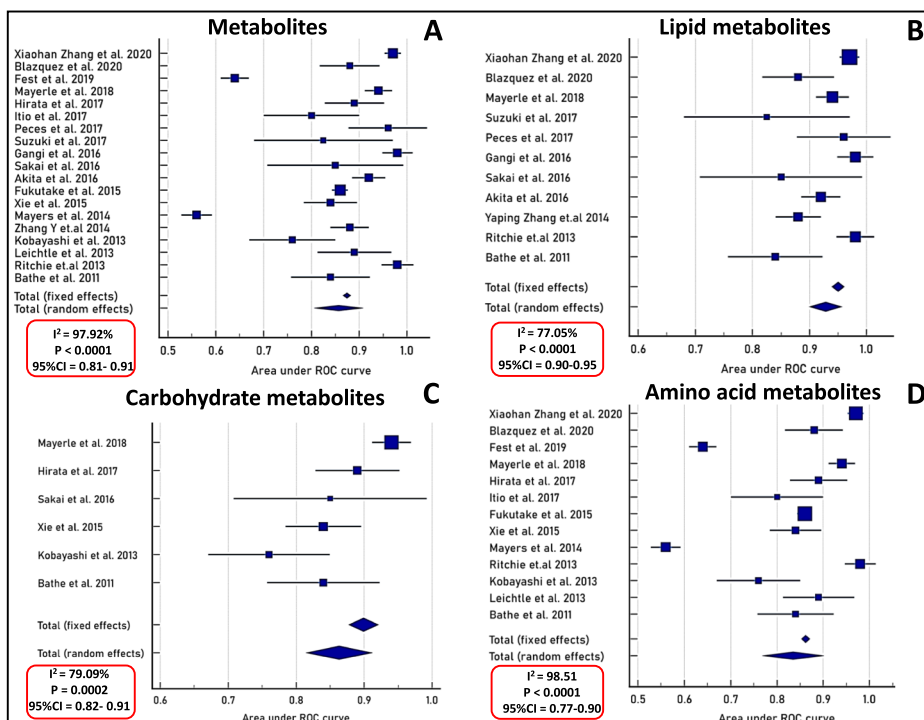


Fig. 2 Forest plots of altered metabolites identified in meta-analysis (A) Forest plot of 19 metabolomic studies using AUC values and computed standard error. Heterogeneity (I^2) was assessed for fixed and random effects (B) Forest plot of lipid metabolites retrieved from 11 studies (C) Forest plot of carbohydrate metabolites retrieved from 6 studies (D) Forest plot of amino acid metabolites retrieved from 13 studies. Metabolic pathway analysis using metaboAnalyst identified (E) Enriched glycerophospholipid pathway for circulatory metabolites detected in healthy control and PDAC. Metabolites marked in red are altered in PDAC patients as compared to healthy controls (F) metaboAnalyst analysis identified enriched arginine and glutamate metabolism for circulatory metabolites detected in PDAC as compared to healthy controls/chronic pancreatitis. Metabolites are marked in red and their fold changes are in blue color (G) metaboAnalyst analysis identified enriched sphingomyelin pathway and TCA cycle for circulatory metabolites detected in PDAC and CP patients. Metabolites are marked in red and their fold changes are in blue color