**SUPPLEMENT**

*Kessenikh E.D., Bykova K.M., Murashko E.A., Dubrovskii Ya.A., Dorofeykov V.V., Savvina I.A.* (2025) Metabolomic profiling of patients with sepsis-associated encephalopathy. Biomeditsinskaya Khimiya, **71**(6), 441-453.
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Figure S1 shows unsupervised hierarchical clustering of significantly altered metabolites ($p < 0.05$ with Benjamini-Hochberg FDR correction) between the control group and the patients with SAE. Rows represent differentially abundant metabolites; columns represent individual plasma samples. The color scale illustrates the relative abundance of each metabolite (red indicates up-regulation, blue indicates down-regulation relative to the mean). Clustering reveals distinct metabolic profiles that separate the experimental groups.

Figure S2 shows Receiver Operating Characteristic (ROC) curves evaluating the diagnostic performance of individual significantly altered metabolites for discriminating between the control group and patients with SAE. The Area Under the Curve (AUC) values with 95% confidence intervals are indicated on the graph.

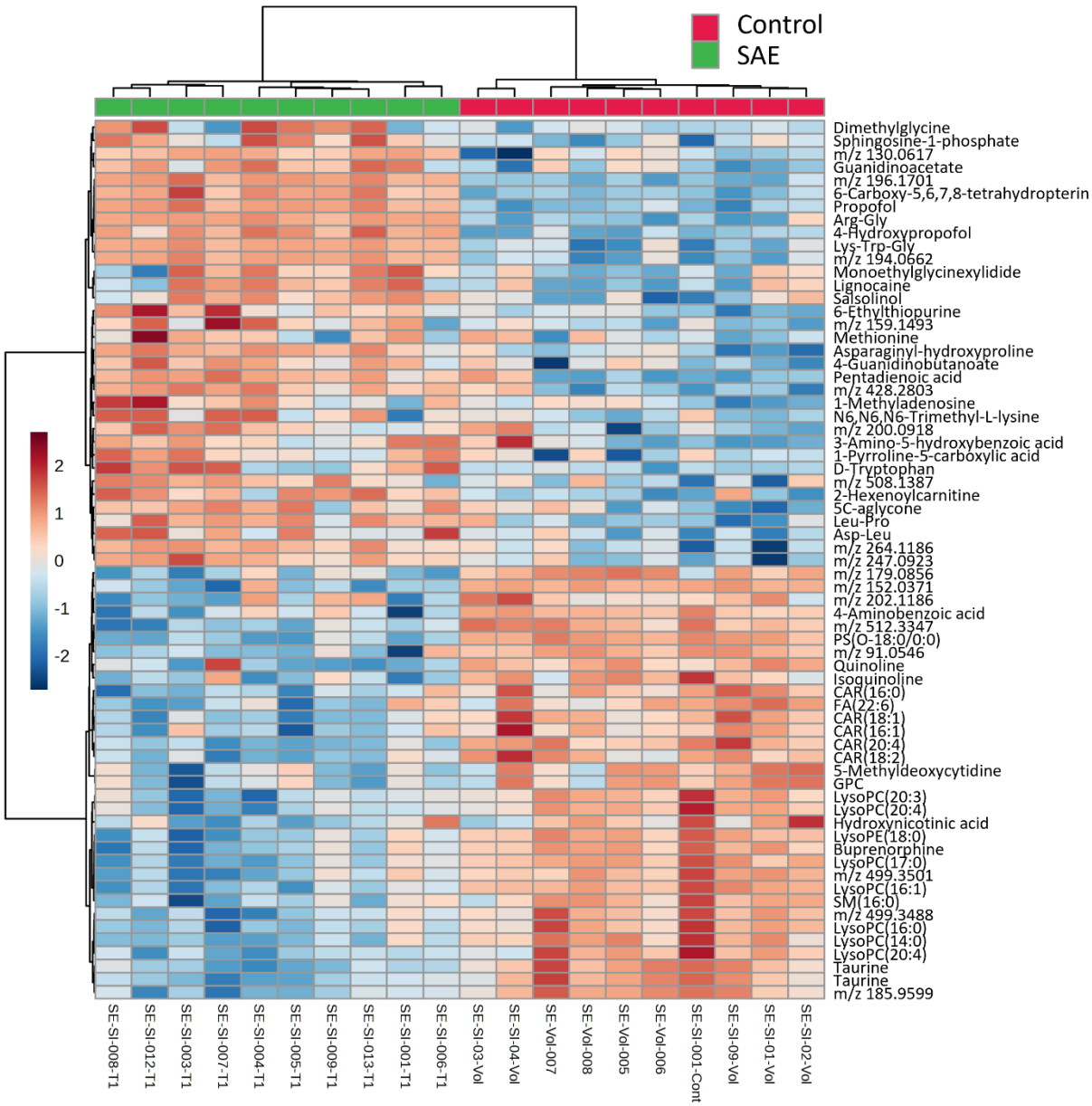


Figure S1. Heatmap of significant metabolites distinguishing control and sepsis-associated encephalopathy (SAE) groups. Control samples are labeled in red, sepsis samples in green. Metabolite abundance is represented by a color gradient (blue: decreased, red: increased).

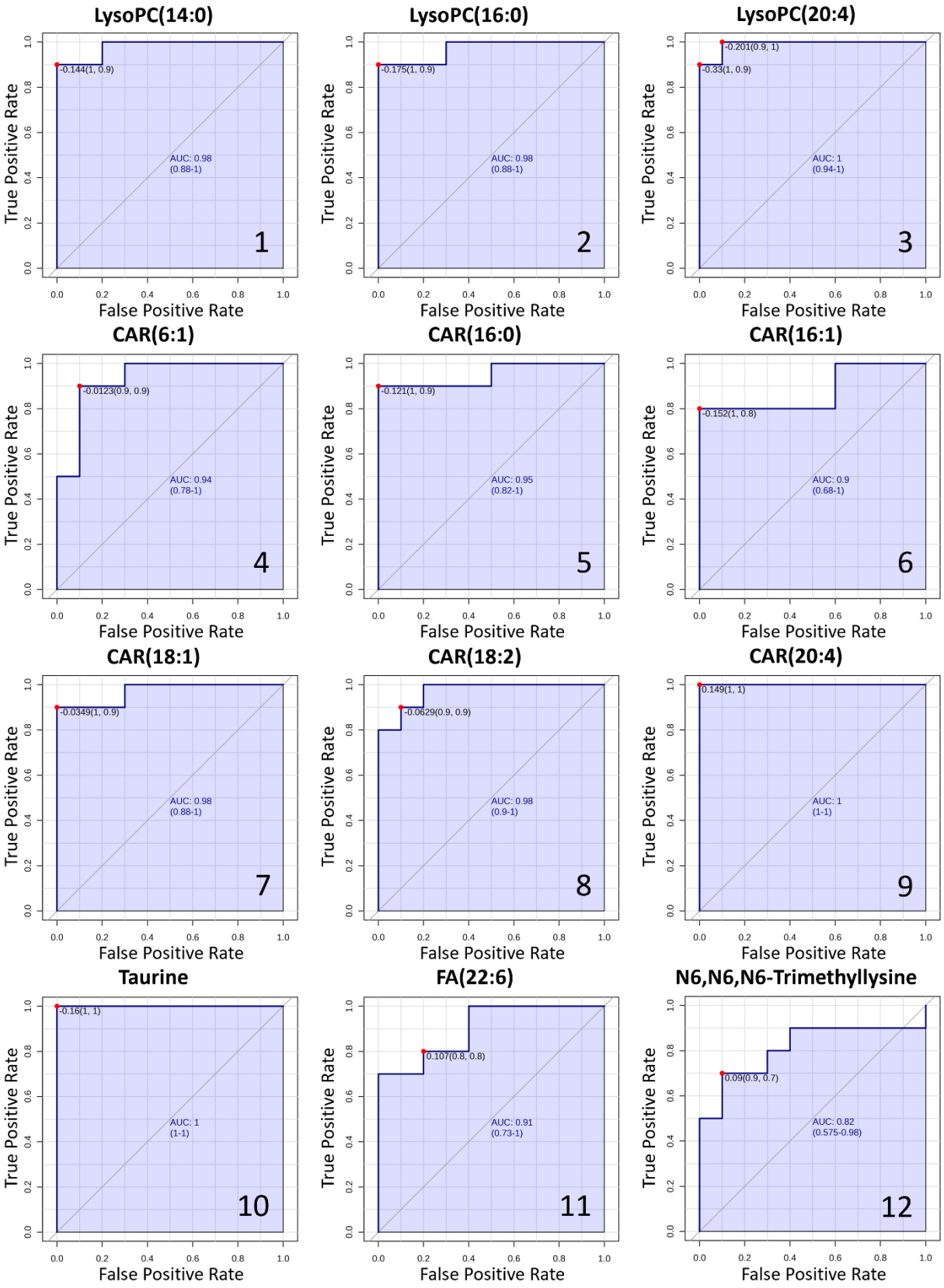


Figure S2. Diagnostic performance of significant metabolites. ROC curves for individual metabolites discriminating control subjects from patients with sepsis-associated encephalopathy (SAE): 1 – LysoPC(14:0); 2 – LysoPC(16:0); 3 – LysoPC(20:4n6); 4 – CAR(6:1); 5 – CAR(16:0); 6 – CAR(16:1); 7 – CAR(18:1); 8 – CAR(18:2); 9 – CAR(20:4); 10 – Taurine; 11 – DHA (Docosahexaenoic acid); 12 – TML (Trimethyllysine). The Area Under the Curve (AUC) values with 95% confidence intervals are provided. The Y-axis shows Sensitivity (True Positive Rate), and the X-axis shows 1 – Specificity (False Positive Rate).