Molecular BioSystems

PAPER

Supplement figure legends

Fig. 1. KEGG human metabolic pathway in control and stroke risk patients, and top ten pathways with most number of compound hits.

(a) Human metabolic pathway obtained from Kyoto Encyclopedia Genes and Genomics (KEGG). Black dots represent potentially affected metabolites linked to thrombotic stroke. **(b)** Top ten pathways with most number of compound hits in stroke risk patients or control group patients.

Fig. 2. Receiver operating characteristic (ROC) curve.

(a) ROC curve of catabolic pathway of lysine metabolites. **(b)** ROC curve of catabolic pathway of valine metabolites. **(c)** ROC curve of homocysteine sulfinic acid and ubiquinone.

Fig. 3. Intensities of 2-oxoglutarate and nicotinamide in control and stroke risk patients, and their correlation with diabetes metabolic or smoking.

(a) Relative concentrations of 2-oxoglutarate (*m/z* 215.02, $[M+HCOONa]^+$ in control and in stroke risk group. **(b)** Relative intensities of nicotinamide (*m/z* 207.02, $[M+HCOOK]^+$) in control and in stroke risk groups. **(c-d)** Comparison of relative intensities of 2-oxoglutarate and nicotinamide in diabetic and non-diabetic control subjects and in diabetic and non-diabetic stroke risk patients. **(e-f)** Comparison of relative intensities of 2-oxoglutarate and nicotinamide in smoker and non-smoker control subjects and in smoker and non-smoker stroke risk patients *Significant difference ($p < 0.05$).

Fig. 4. Valine catabolism pathway from KEGG and Mummichog, and intensities of valine and its catabolites in control and in stroke risk patients.

(a) Valine catabolism pathway obtained from the KEGG (ellipse) and Mummichog (rectangle). Arrows represent the compounds that are detected at low or high levels in stroke risk patients. **(b)** Concentrations of L-valine (*m/z* 118.09, $[M+H]^+$) in control and in stroke risk groups. **(c)** Concentrations of S-(2-methylpropionyl)-dihydrolipoamide-E (*m/z* 278.13, $[M+H]^+$) in control and in stroke risk group. **(d)** Concentrations of 2-oxoglutarate (*m/z* 215.02, $[M+HCOONa]^+$). *Significant difference ($p < 0.05$).

Fig. 5. Discrimination between features of control and stroke serum from validity population by OPLS-DA.

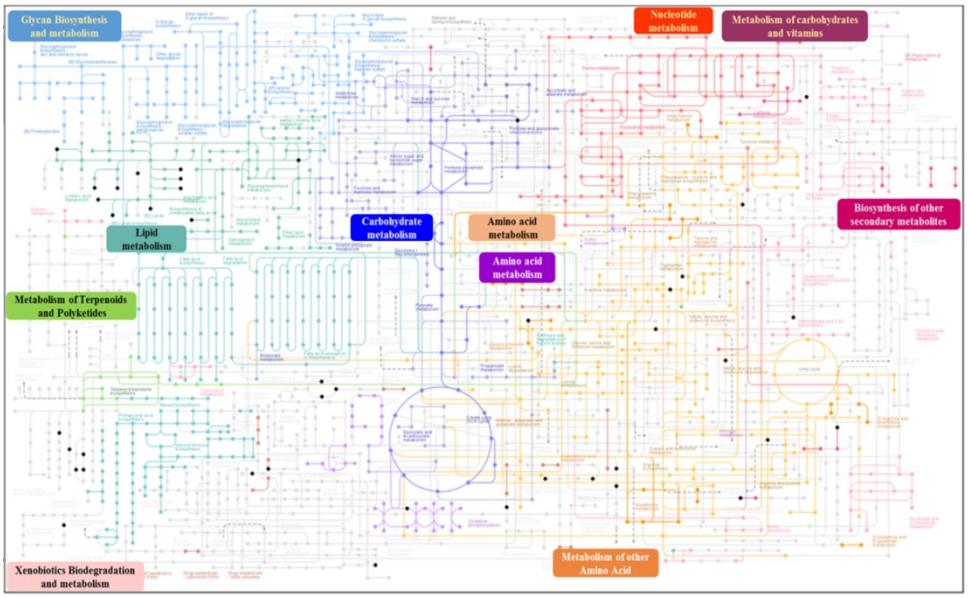
Control group is represented by blue circles and stroke risk patients are represented by red diamonds. **(a)** Score plot of control and stroke risk patient metabolic data showing a clear separation of groups. **(b)** The green dots signify metabolites with 95% association with the first two principal components. The gold circles represent the top 5% of these metabolites (403 *m/z*) that are most closely associated with control or stroke serum.

Fig. 6. Correlation analysis to identify compounds with specific pattern.

Correlation plot showing compounds that are significantly associated with a given feature (L-lysine). The compounds are represented as horizontal bars, with light pink indicating positive correlations with lysine and light blue indicating negative correlations.

Supplement Fig. 1

(a)



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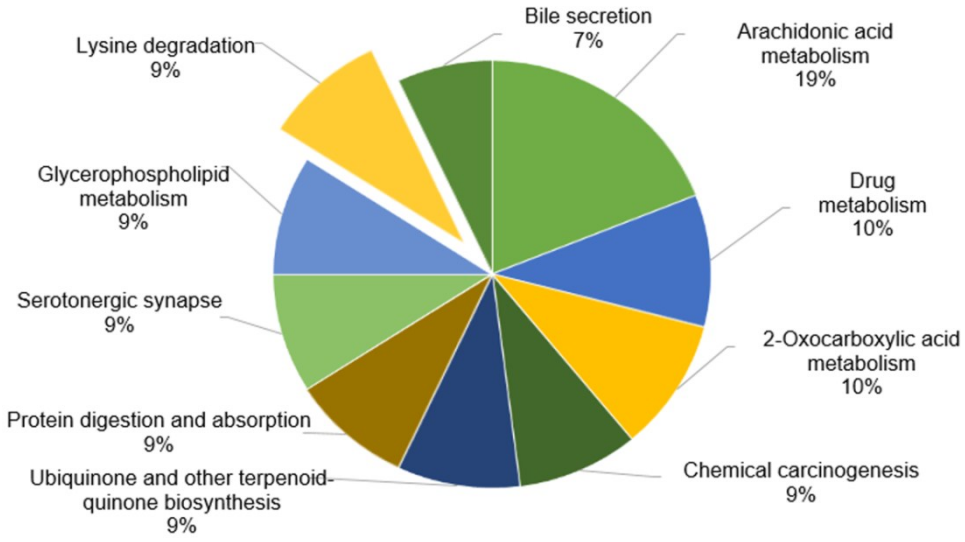
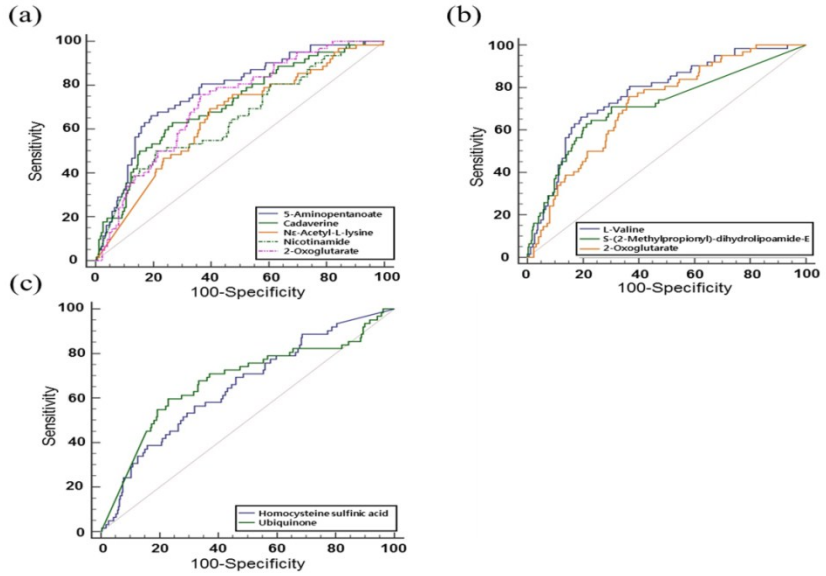


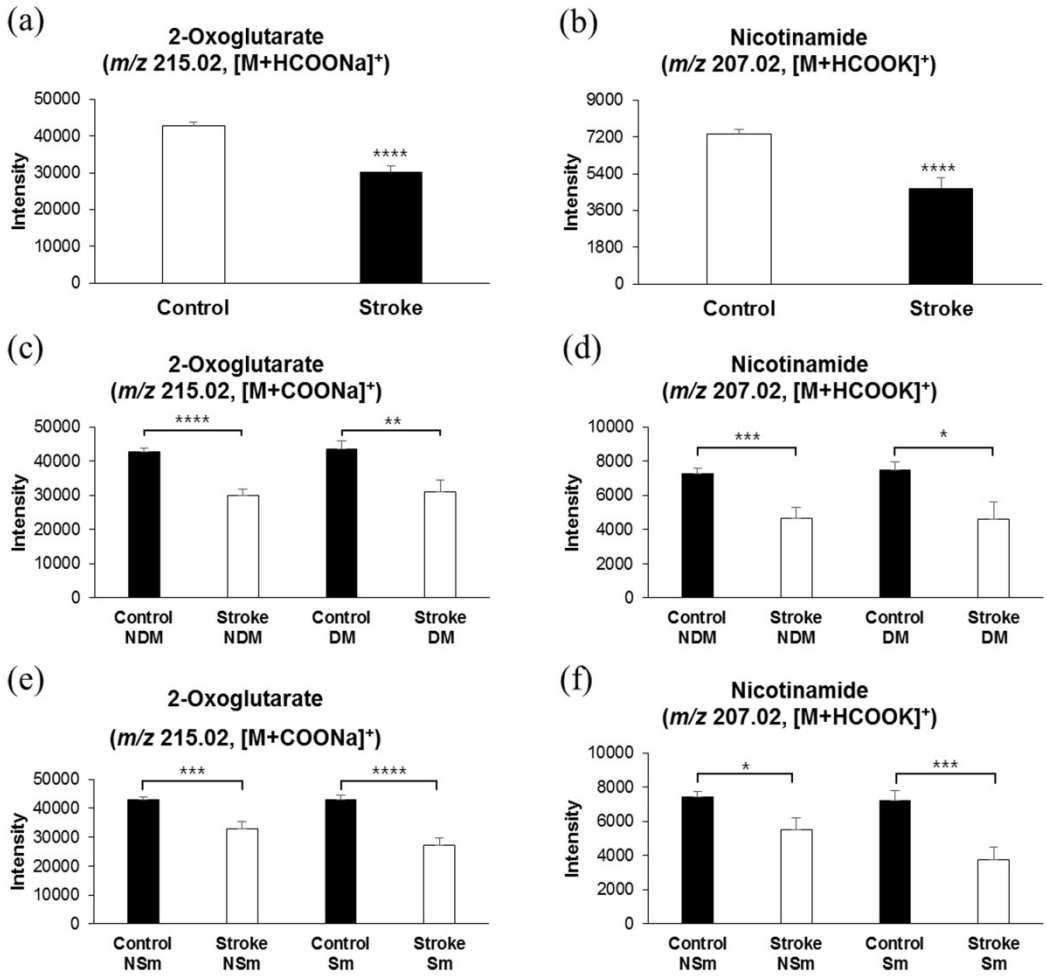
Supplement Fig. 2



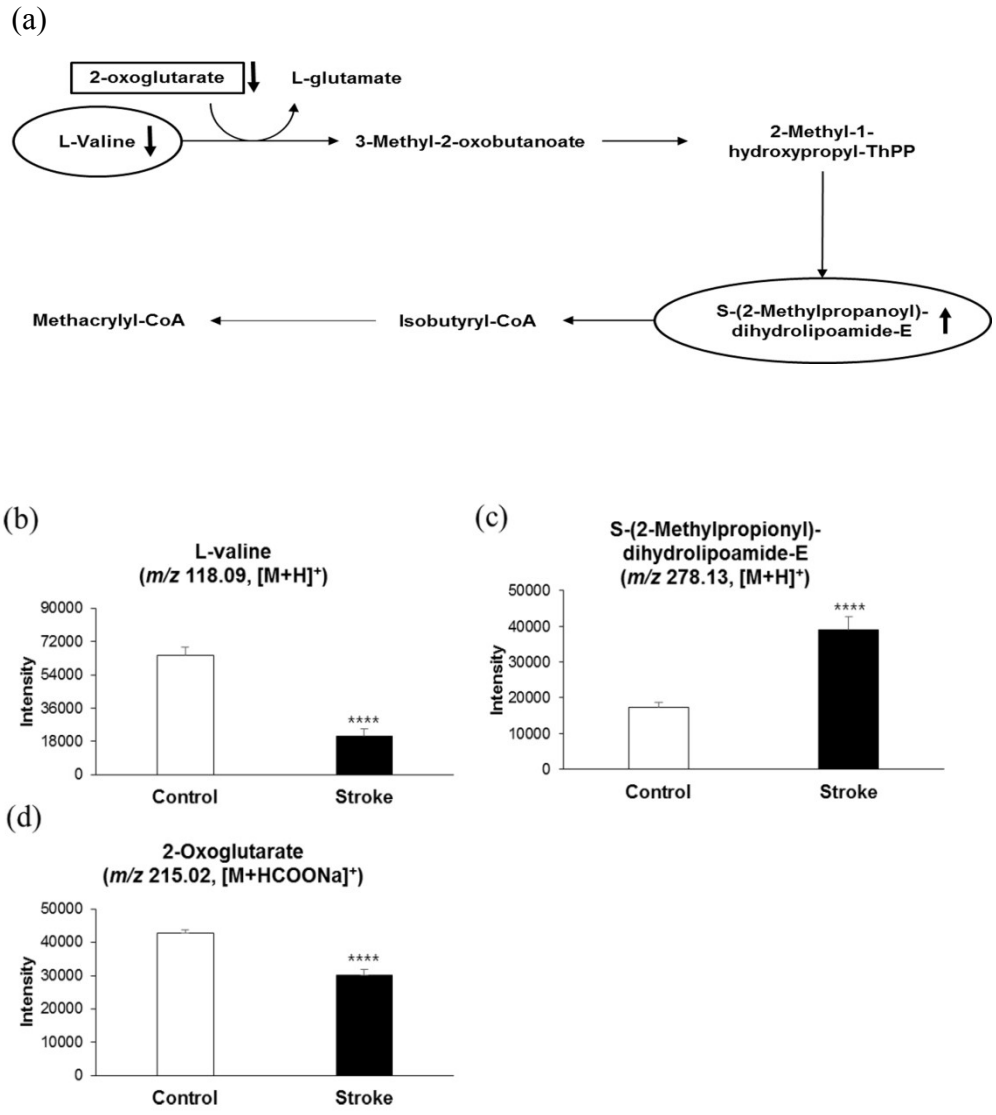
Supplement Table 1. Area under the ROC curve (AUC), sensitivity, and specificity at maximum Youden's index (*j*) in ROC curve.

Pathway	Metabolites	AUC	Sensitivity	Specificity
Lysine catabolic pathway	N6-Acetyl-L-lysine	0.651±0.0369	69.35	60.34
	5-Aminopentanoate	0.771±0.0316	66.13	80.75
	Cadaverine	0.711±0.0359	62.90	73.28
	2-Oxoglutarate	0.716±0.0324	75.81	63.51
	Nicotinamide	0.653±0.0391	50.00	79.02
Valine degradation pathway	L-Valine	0.771±0.0316	66.13	80.75
	S-(2-Methylpropionyl)-dihydrolipoamide-E	0.713±0.0384	62.90	78.74
	2-Oxoglutarate	0.716±0.0324	75.81	63.51
	Homocysteine sulfinic acid	0.651±0.0379	56.45	68.10
	Ubiquinone	0.677±0.0414	59.68	77.01

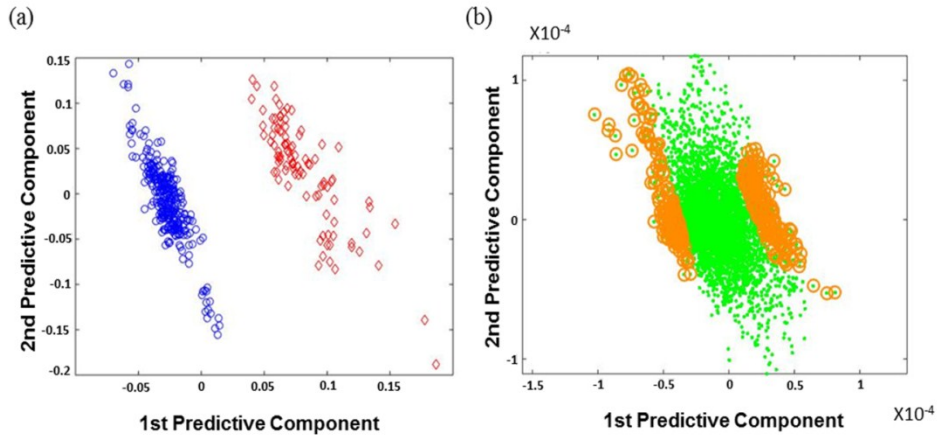
Supplement Fig. 3



Supplement Fig. 4



Supplement Fig. 5



Supplement Fig. 6