207 **Supplementary tables**

208 **Table S1**. Retention time, ions (m/z) and specific abundance for each amino acid

N°	Amino acids	Retention time in minutes*	Identification ions (m/z) and abundance (%)	Quantitation ions (m/z)
1	L-Alanine	8.51±0.03	116(100)+73(53.6)	116
2	L-Glycine	9.35±0.03	102(100)+73(68.4)	102
3	Sarcosine	12.22±0.02	116(100)+73(52.0)	116
4	L-Valine	12.29±0.02	144(100)+73(40.6)	144
5	L-Leucine	14.40±0.02	158(100)+73(42.4)	158
6	L-Isouleucine	15.25±0.02	158(100)+73(50.4)	158
7	L-Serine	17.60±0.02	73(100)+204(75.2)	204
8	L-Threonine	21.83±0.02	73(100)+218(46.0)	218
9	L-Methionine	21.9±0.02	176(100)+128(60.0)	176
10	L-Aspartic acid	20.24±0.02	73(100)+232(68.4)	232
11	L-Proline	21.15±0.02	156(100)+73(53.6)	156
12	L-Cysteine	22.15±0.02	73(100)+220(88.8)	220
13	L-Glutamic acid	22.99±0.03	246(100)+128(32.4)	246
14	L-Phenylalanine	23.00±0.02	218(100)+192(71.2)	218
15	L-Asparagine	23.75±0.03	116(92.40)+231(51.2)	231
16	L-Lysine	24.45±0.03	84(100)+156(55.6)	156

209 *Mean ± standard deviation (n=10). Adapted from de Paiva *et al*., 2013
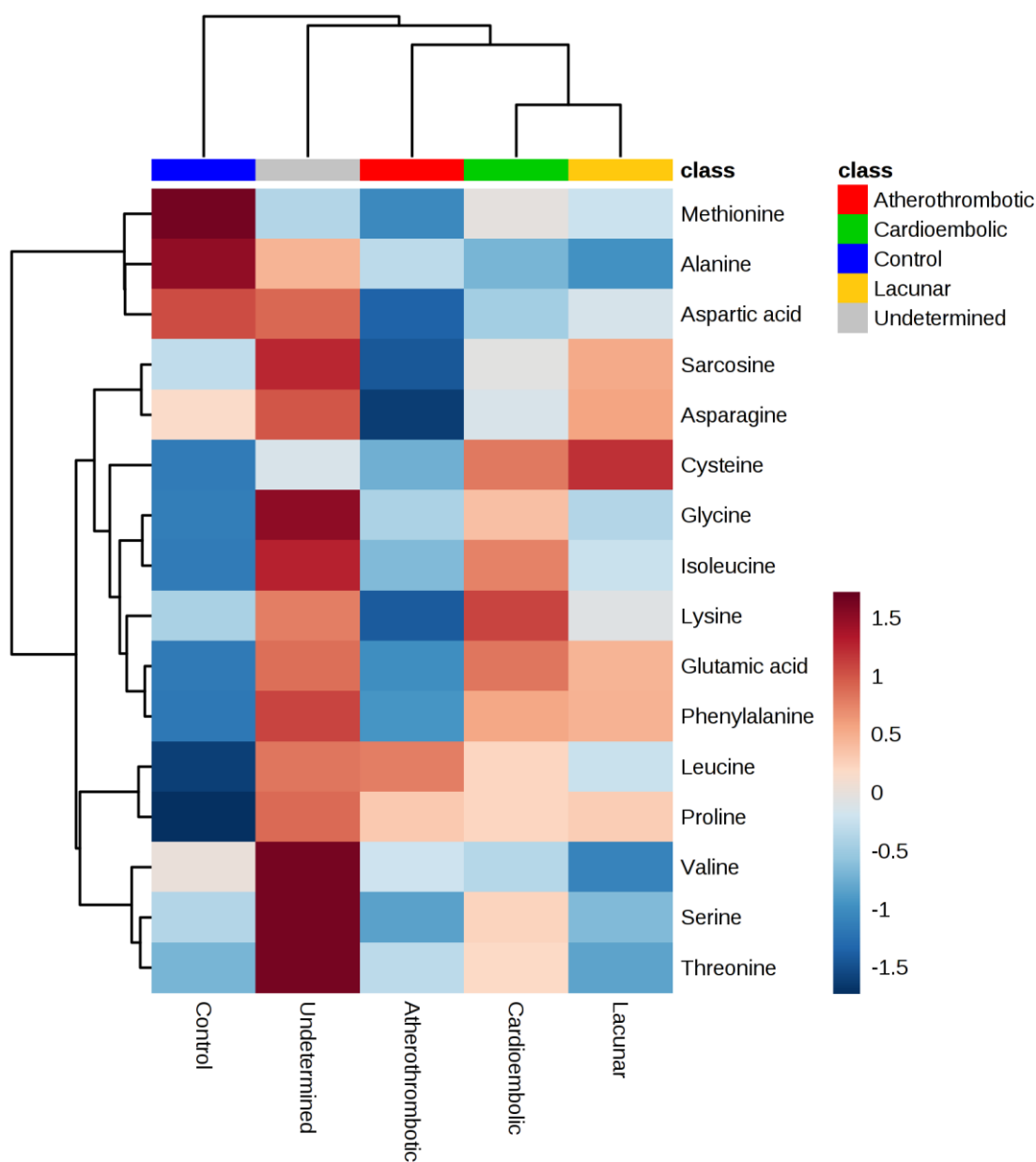
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Figure S1. Heatmap of the ischemic stroke amino acid dataset. The colors represent the
concentration of metabolites. The subtypes of ischemic stroke and controls are represented
in horizontal axis and amino acids in vertical axis; and are separated using hierarchical
clustering (Ward's algorithm), with the dendrogram being scaled to represent the distance
between each branch (distance measure: Euclidean). The contrast in the average
concentrations of metabolites between the group of patients with stroke and healthy
individuals are being presented.