

Supplementary Materials: Effects of Different Exercise Modes on the Urinary Metabolic Fingerprint of Men with and without Metabolic Syndrome

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Table S1. Important metabolites in explaining the PLS-DA models of the comparison of exercise modes in each group separately.

	MetS	Healthy		
	2 h	2 h	2 h	4 h
	CME vs. RE	HIE vs. CME	CME vs. RE	CME vs. RE
Alanine	2.60 **		1.57	
4-Hydroxyphenyllactate		−0.62 **		
Citrate	−0.37 *			
Creatine		−0.46 **	0.59	
Glutamate				−0.49 *
Guanine	2.10 ***		0.94	
Homocysteine	5.12 *			
Hypoxanthine	12.88 **	−0.75 ***	8.35 ***	6.45 **
Inosine			32.92 *	4.86 *
Lactate	92.88 **	−0.95 **	48.67 ***	
Monoisoamylamine			1.07 *	
Pyruvate	11.58 **		18.68 **	
Trimethylamine	0.81 **			
Tryptamine			1.15 *	
Uracil				−0.35 *
Uridine			−0.41 *	−0.50 *

Numbers indicate fold change and appear wherever a metabolite contributed to the discrimination. For example, the first number, 2.60, means that the value in RE was 2.60 fold higher than the value in CME. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, significant difference following Student's t test.

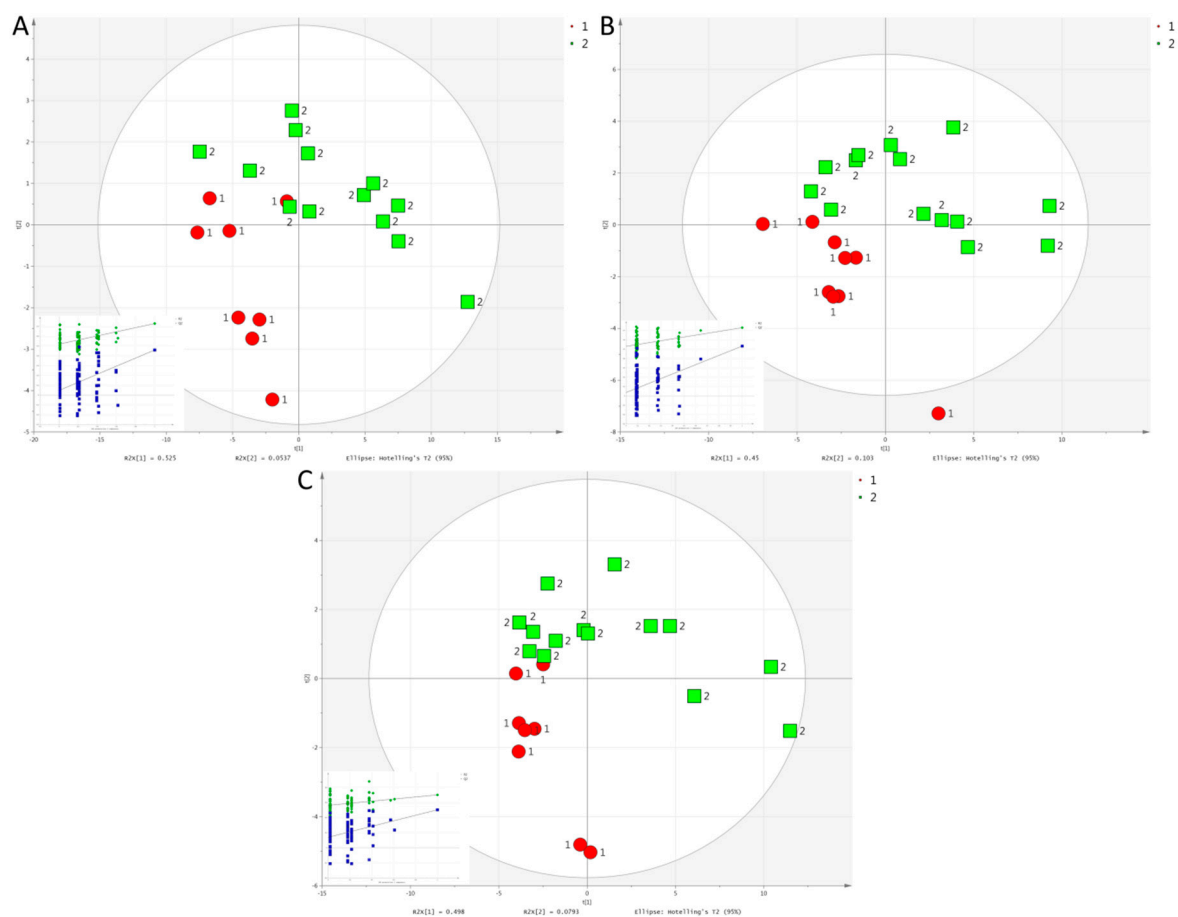


Figure S1. Score plots for the PLS-DA models of MetS (red circles) vs. Healthy (green squares) for: (A) HIIE at 2 h; (B) HIIE at 4 h; and (C) RE at 2 h. Inserts are permutation plots. R2X (cum), R2Y (cum), Q2Y (cum), and CV-ANOVA p value were: (A) 0.579, 0.723, 0.459, and 3.58×10^{-2} ; (B) 0.554, 0.730, 0.533, and 5.84×10^{-3} ; and (C) 0.577, 0.702, 0.504, and 2.46×10^{-2} , respectively.

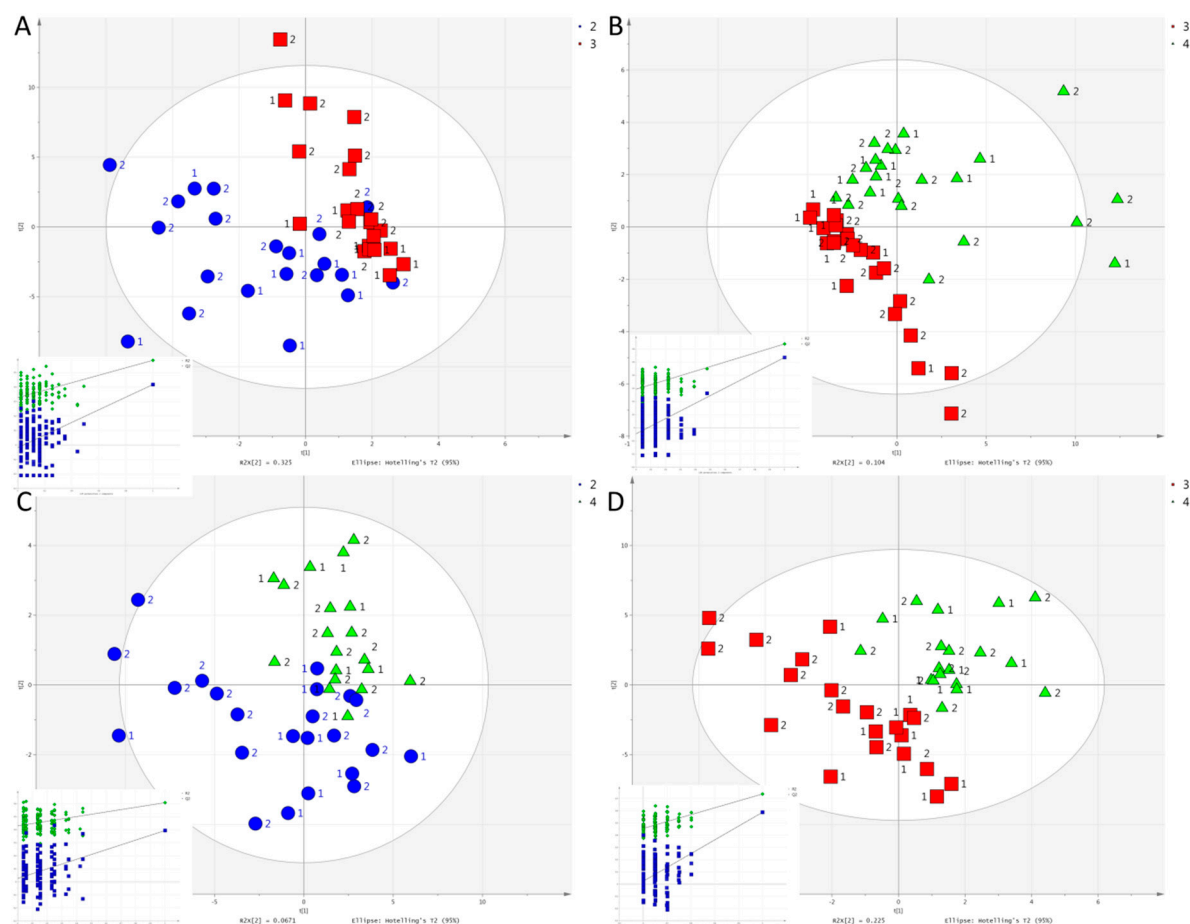


Figure S2. Score plots for the PLS-DA models of pair wise comparisons of exercise modes: **(A)** at 2 h HIIE (blue circles) vs. CME (red squares); **(B)** at 2 h CME (red squares) vs. RE (green triangles); **(C)** at 4 h HIIE (blue circles) vs. RE (green triangles); and **(D)** at 4 h CME (red squares) vs. RE (green triangles). Inserts are permutation plots. The MetS group is represented as 1 and the Healthy group as 2. R2X (cum), R2Y (cum), Q2Y (cum), and CV-ANOVA p value were: **(A)** 0.572, 0.584, 0.414, and 2.26×10^{-4} ; **(B)** 0.570, 0.638, 0.535, and 3.29×10^{-6} ; **(C)** 0.467, 0.607, 0.394, and 9.62×10^{-4} ; and **(D)** 0.467, 0.737, 0.588, and 4.32×10^{-5} , respectively.

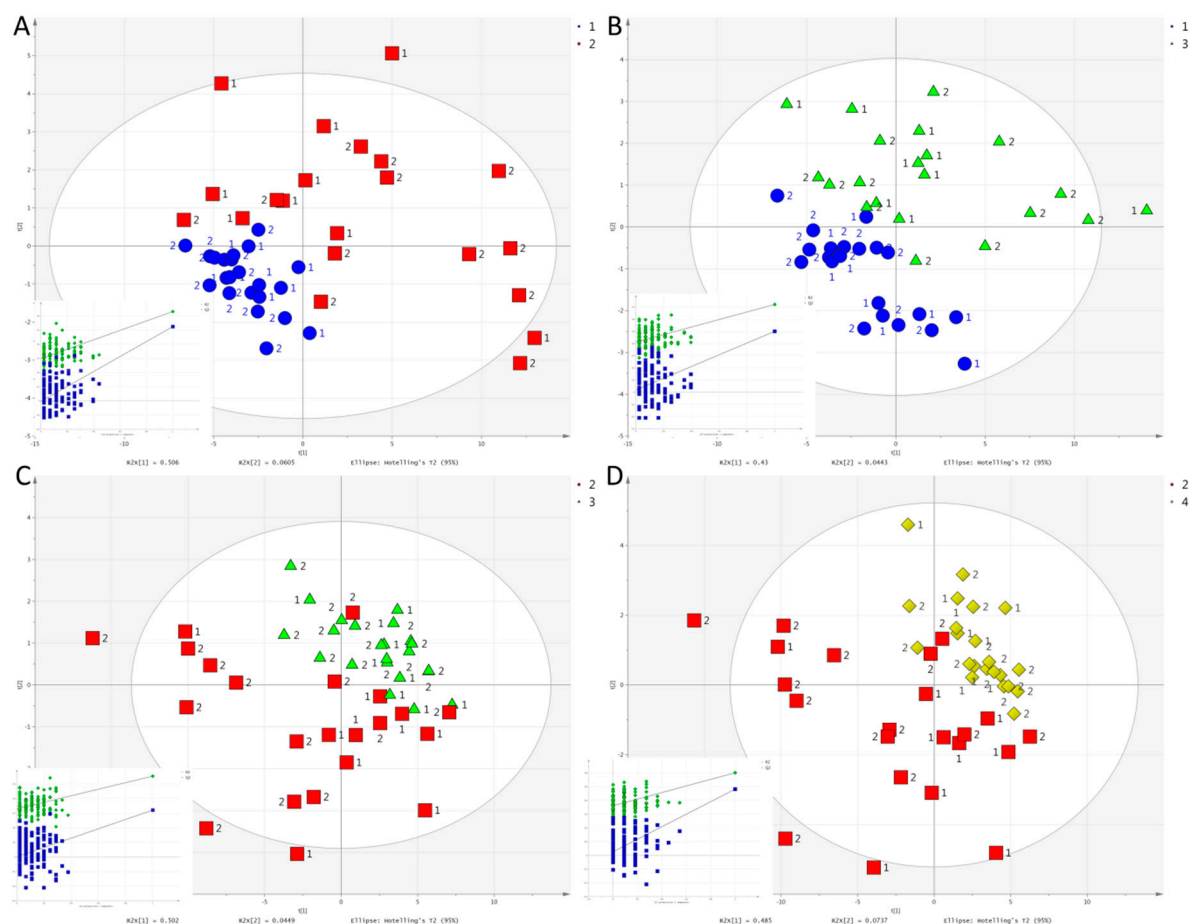


Figure S3. Score plots for the PLS-DA models of pair wise comparisons for HIIE: (A) 0 h (blue circles) vs. 2 h (red squares); (B) 0 h (blue circles) vs. 4 h (green triangles); (C) 2 h (red squares) vs. 4 h (green triangles); and (D) 2 h (red squares) vs. 24 h (yellow diamonds). Inserts are permutation plots. The MetS group is represented as 1 and the Healthy group as 2. R2X (cum), R2Y (cum), Q2Y (cum), and CV-ANOVA p value were: (A) 0.567, 0.631, 0.525, and 6.90×10^{-6} ; (B) 0.474, 0.722, 0.501, and 2.70×10^{-5} ; (C) 0.547, 0.554, 0.321, and 2.88×10^{-3} ; and (D) 0.559, 0.602, 0.483, and 1.81×10^{-5} , respectively.

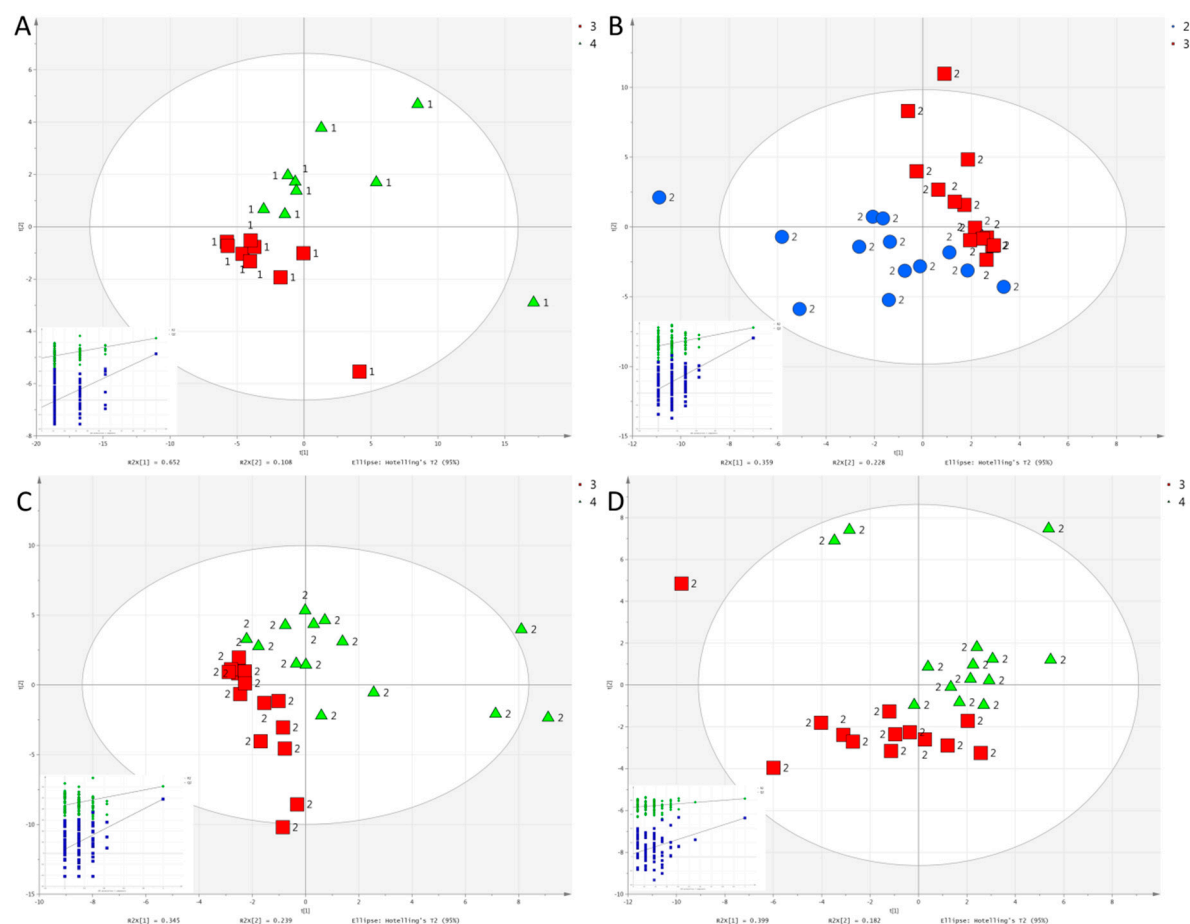


Figure S4. Score plots for the valid PLS-DA models of pair wise comparisons of exercise modes in each group separately: **(A)** MetS at 2 h, CME (red squares) vs. RE (green triangles); **(B)** Healthy at 2 h, HIIE (blue circles) vs. CME (red squares); **(C)** Healthy at 2 h, CME (red squares) vs. RE (green triangles); and **(D)** Healthy at 4 h, CME (red squares) vs. RE (green triangles). Inserts are permutation plots. The MetS group is represented as 1 and the Healthy group as 2. R2X (cum), R2Y (cum), Q2Y (cum), and CV-ANOVA p value were: **(A)** 0.813, 0.858, 0.641, and 4.08×10^{-2} ; **(B)** 0.587, 0.552, 0.464, and 1.15×10^{-3} ; **(C)** 0.584, 0.605, 0.490, and 1.53×10^{-3} ; and **(D)** 0.617, 0.823, 0.548, and 2.07×10^{-3} , respectively.