代谢组学助力疾病诊断标志物的筛查

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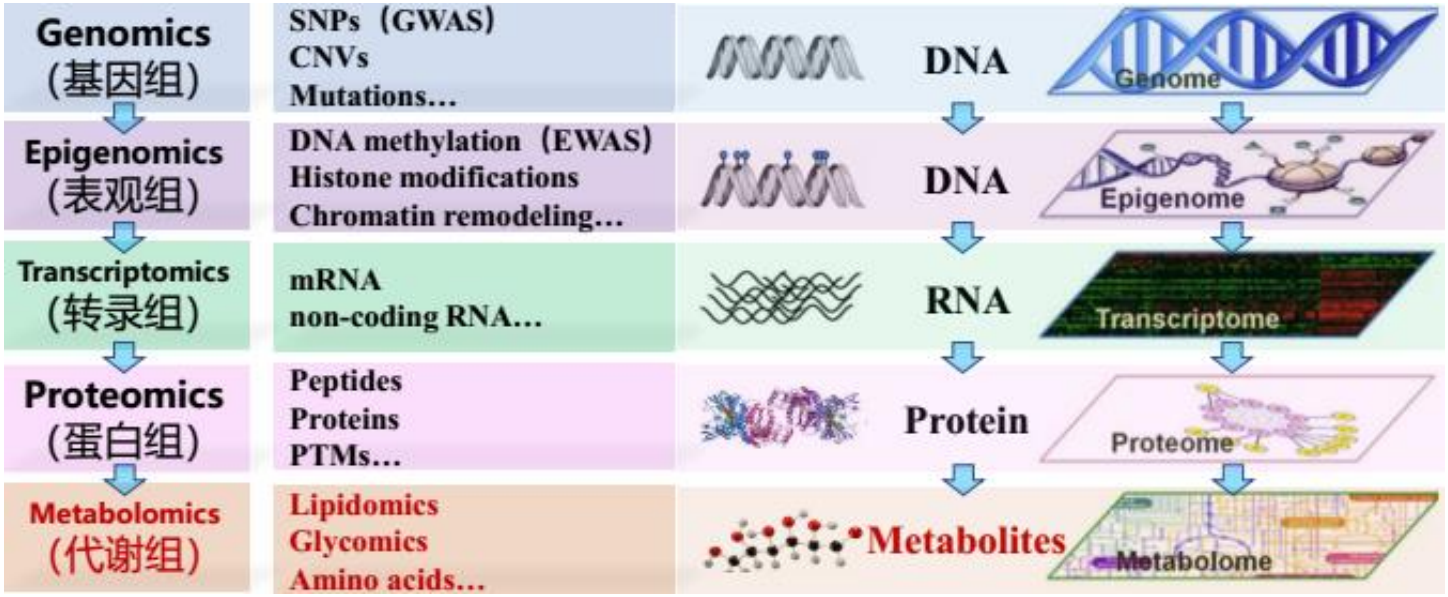
一、什么是代谢组学？

代谢组学主要研究生物体在生物刺激、病理生理障碍或遗传信息发生改变等情况下整体动态代谢的变化。其研究对象是相对分子量小于1000的小分子代谢产物。它是继基因组学和蛋白质组学之后发展起来的一门新型学科。



二、代谢组学的检测平台

NMR平台

GC-MS平台

LC-MS平台

二、代谢组学的检测平台

分析技术	灵敏度	优势	缺点
核磁共振 NMR	10^{-6} mol	样品量需求小；样品处理简单，对样品破坏性小；特异性、分辨率高	检测动态范围有限；灵敏度低；硬件投资巨大
气质联用 GC-MS	10^{-12} mol	分辨率高；选择性好；数据库较健全	样品处理过程复杂，难挥发性物质需要衍生化；不适用于分析热不稳定和大分子量的代谢物。
液质联用 LC-MS	10^{-15} mol	灵敏度高；分辨率高	数据库不健全，有待完善

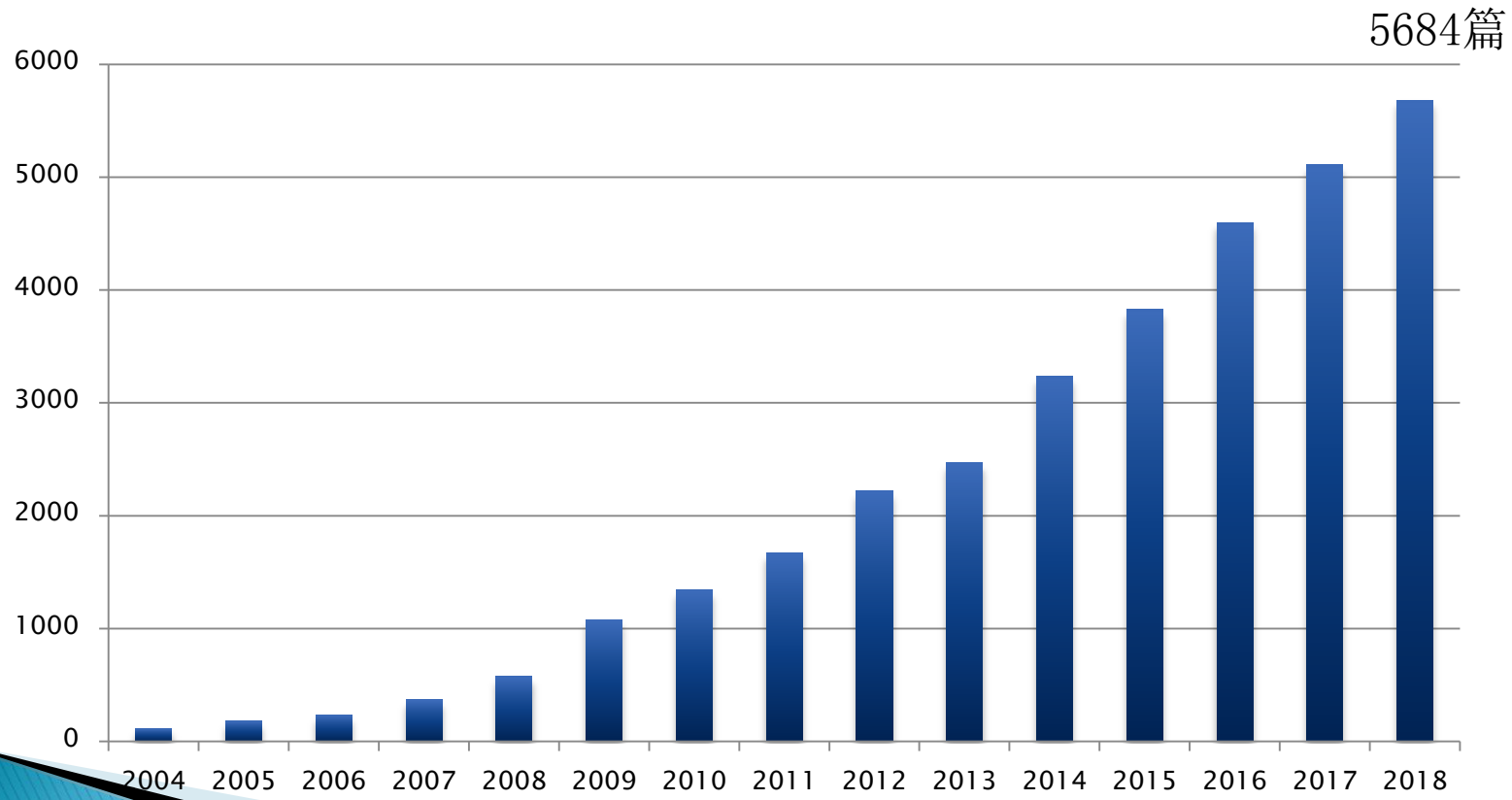
三、代谢组学的研究方法

1. **非靶向代谢组学**：在特定分析条件下，对某种生物样品中的**全部**代谢物进行检测分析。通过非靶向代谢组学研究能获得**大量复杂多效的代谢物信息**，是相对开放的分析方法，常用于**探究未知的生理模式和发现可能的生物标志物。**

2. **靶向代谢组学**：是对生物样品中的某个或几个特定组分进行分析，能对提出的科学假设做针对性研究，也可**对前期筛选的潜在生物标志物进行验证。**

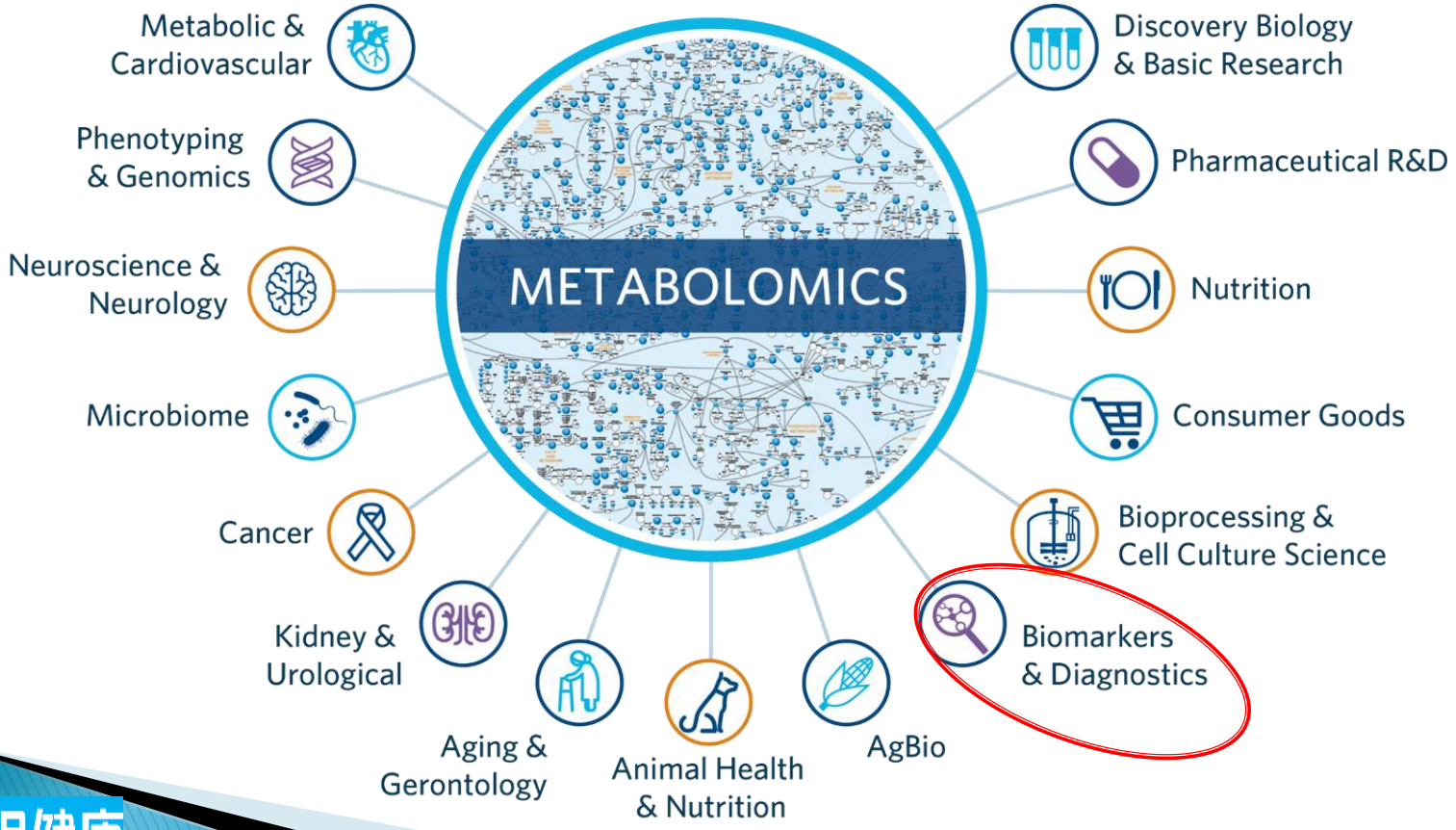
四、代谢组学的应用

Pubmed 检索关键词“Metabolomics OR Metabolome ”，统计近15年代谢组学相关文章。代谢组学相关文章呈逐年递增趋势，2018年代谢组学文章达5684篇，比2017年增长11.2%。



四、代谢组学的应用

代谢组学被广泛应用于医学、生物科学、食品、农业等各个领域



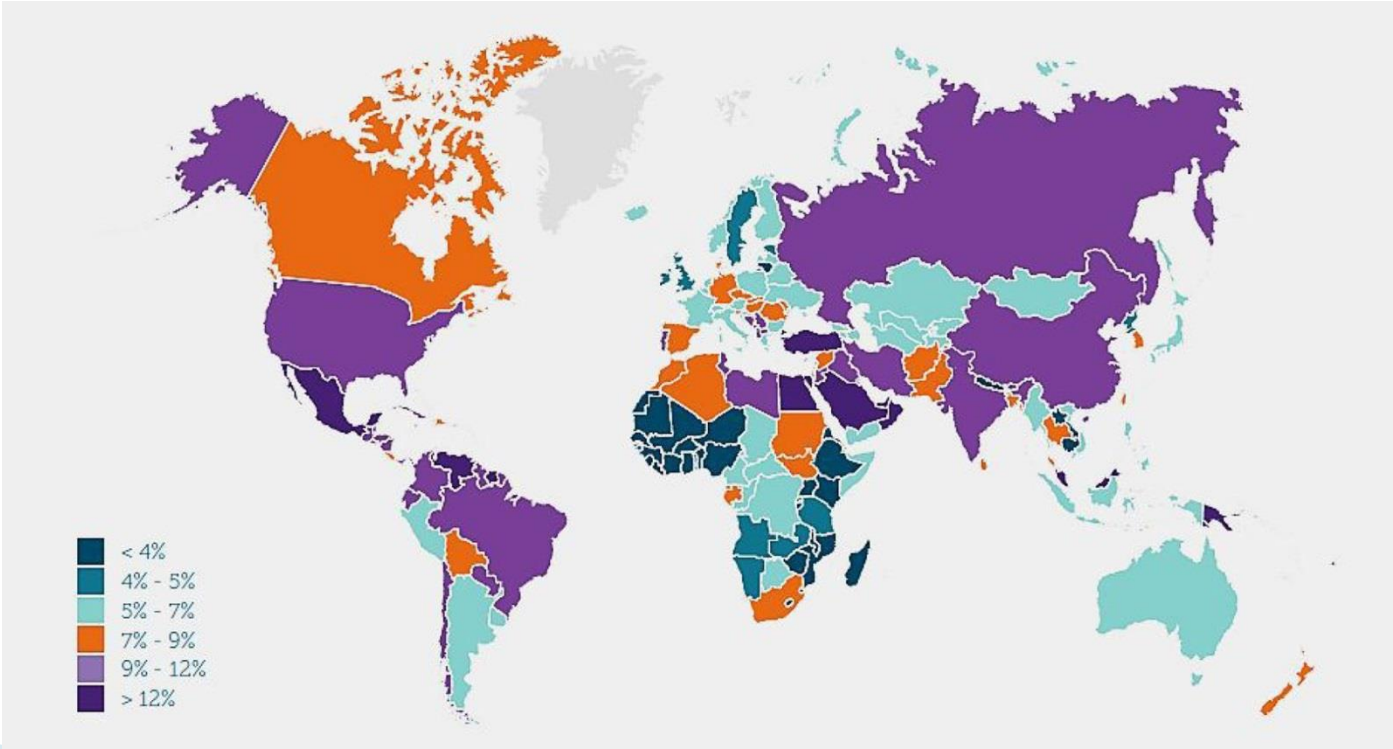
五、疾病诊断和诊断标志物的筛查

代谢组学

- 内分泌疾病：糖尿病等
- 肿瘤：肝癌、前列腺癌等
- 心血管疾病：冠心病、高血压等
- 自身免疫性疾病：RA、SLE等

1. 代谢组学在糖尿病诊断中的作用

糖尿病是一种复杂的代谢紊乱疾病，与胰岛素抵抗，受损胰岛素信号，β 细胞功能紊乱，血糖异常，脂类代谢改变，亚临床验证和氧化应激增加等相关。其发生发展过程中代谢物特征的改变**对于了解其病理过程以及发现潜在的生物标志物和药物靶点是非常重要的**。



International Diabetes Federation. IDF Diabetic Atlas 7th Edition 2015.

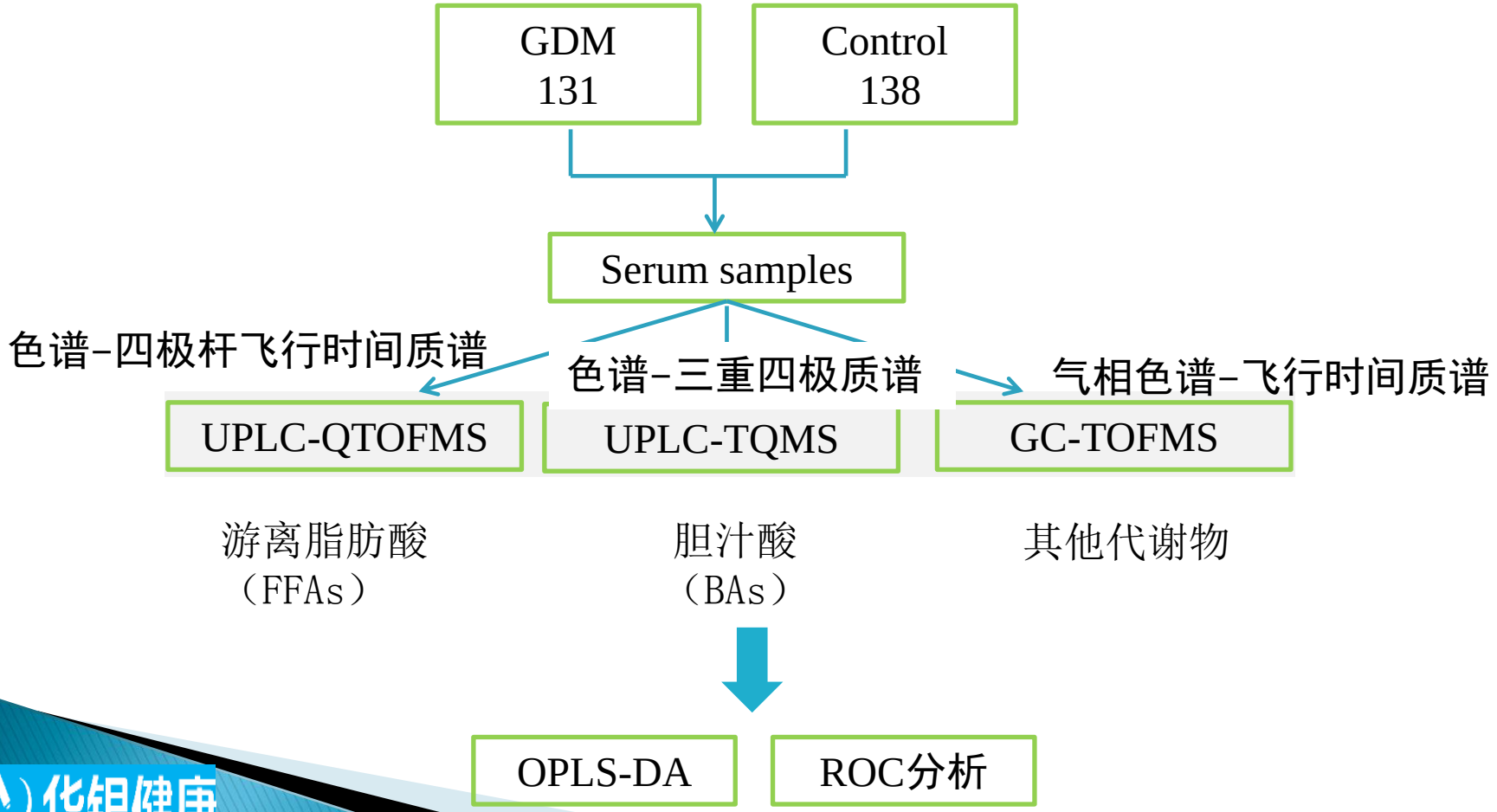
Mol Cell Proteomics. 2018 Mar;17(3):431-441. doi: 10.1074/mcp.RA117.000121. Epub 2017 Dec 27.

Development of Multimarker Diagnostic Models from Metabolomics Analysis for Gestational Diabetes Mellitus (GDM).

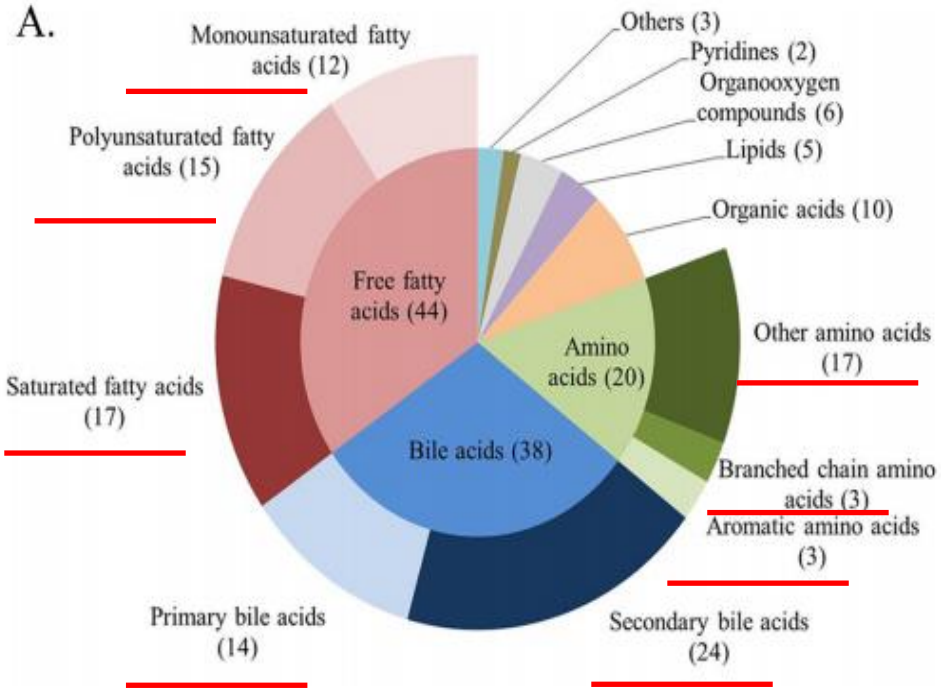
IF:5.236，2018

上海交通大学附属第六人民医院内分泌科糖尿病重点实验室

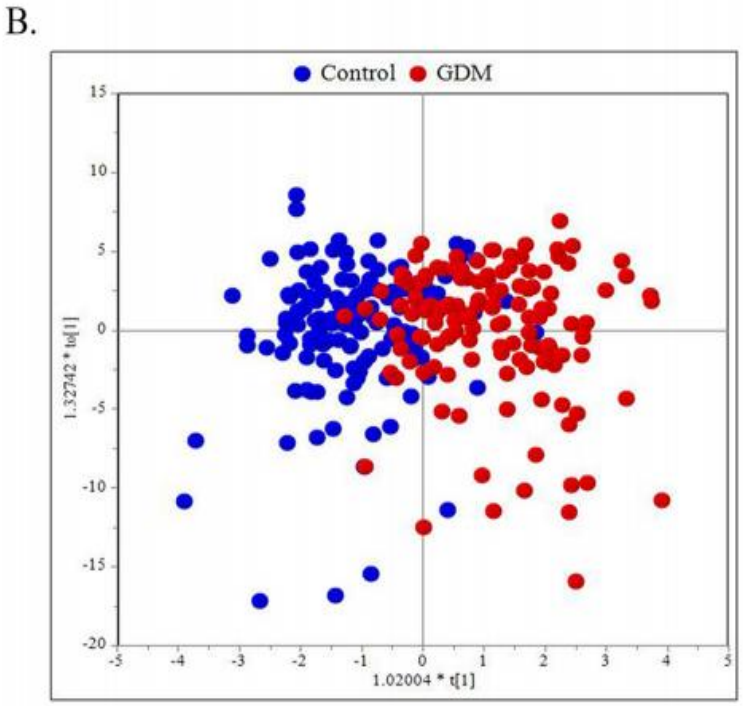
通过代谢组学分析建立妊娠期糖尿病的诊断模型



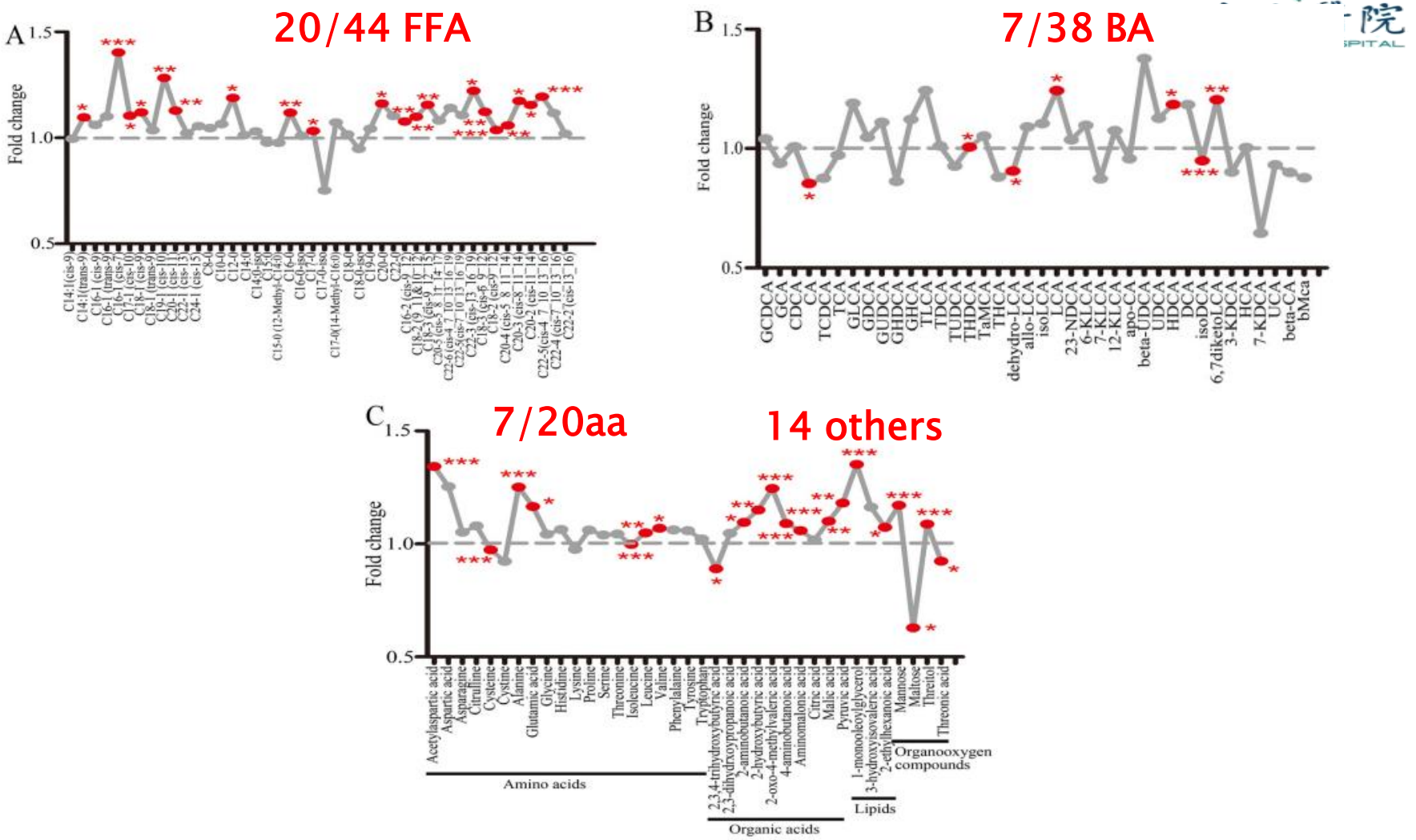
妊娠期糖尿病患者和对照人群的血清代谢谱存在差异



Pie chart displays metabolite types and subtypes measured in our research



The OPLS-DA scores plot shows the groupings of control (blue), and GDM (red) subjects based on all metabolite profiles.



Fold change plot of metabolites (GDM/control).

Fold change plot of (*A*) free fatty acids, (*B*) bile acids and (*C*) other metabolites.

建立妊娠期糖尿病多变量诊断模型

Model	Variables included in the model	AUC (95% CI)	*p value*
Metabolites			
1	N-acetylaspartic acid, 2-Oxo-4-methylvaleric acid, C16:1 (cis-7), 6,7-diketoLCA	0.740 (0.680–0.799)	<0.001
2	N-acetylaspartic acid, alanine, C16:1 (cis-7), 6,7-diketoLCA	0.740 (0.681–0.800)	<0.001
3	N-acetylaspartic acid, 1-monooleoyl glycerol, C16:1 (cis-7), 6,7-diketoLCA	0.738 (0.679–0.798)	<0.001
4	N-acetylaspartic acid, C16:1 (cis-7), 6,7-diketoLCA	0.732 (0.672–0.792)	<0.001
5	N-acetylaspartic acid, 1-monooleoyl glycerol, 6,7-diketoLCA, 2-oxo-4-methylvaleric acid	0.722 (0.661–0.783)	<0.001
6	N-acetylaspartic acid, 1-monooleoyl glycerol, C16:1 (cis-7), 2-oxo-4-methylvaleric acid	0.721 (0.661–0.781)	<0.001
BMI and metabolites			
7	BMI, 2-oxo-4-methylvaleric acid, n-acetylaspartic acid, 6,7-diketoLCA	0.744 (0.685–0.803)	<0.001
8	BMI, 2-oxo-4-methylvaleric acid, n-acetylaspartic acid, C16:1 (cis-7)	0.743 (0.685–0.802)	<0.001
9	BMI, 2-oxo-4-methylvaleric acid, C16:1 (cis-7), 6,7-diketoLCA	0.740 (0.681–0.800)	<0.001
10	BMI, n-acetylaspartic acid, alanine, C16:1 (cis-7)	0.740 (0.681–0.798)	<0.001
11	BMI, n-acetylaspartic acid, 1-monooleoyl glycerol, C16:1 (cis-7)	0.740 (0.681–0.799)	<0.001
12	BMI, n-acetylaspartic acid, C16:1 (cis-7)	0.732 (0.672–0.791)	<0.001
BMI, biochemical markers and metabolites			
13	BMI, RBP4, n-acetylaspartic acid, C16:1 (cis-7)	0.751 (0.693–0.809)	<0.001
14	BMI, Cys C, n-acetylaspartic acid, 6,7-diketoLCA	0.749 (0.691–0.808)	<0.001
15	BMI, ChE, n-acetylaspartic acid, C16:1 (cis-7)	0.748 (0.690–0.806)	<0.001
16	BMI, Cys C, n-acetylaspartic acid, C16:1 (cis-7)	0.747 (0.689–0.805)	<0.001
17	BMI, Cys C, RBP 4, n-acetylaspartic acid	0.743 (0.683–0.803)	<0.001
18	BMI, Cys C, n-acetylaspartic acid	0.731 (0.671–0.792)	<0.001

***$p < 0.001$ from ROC analysis.

建立妊娠期糖尿病多变量诊断模型

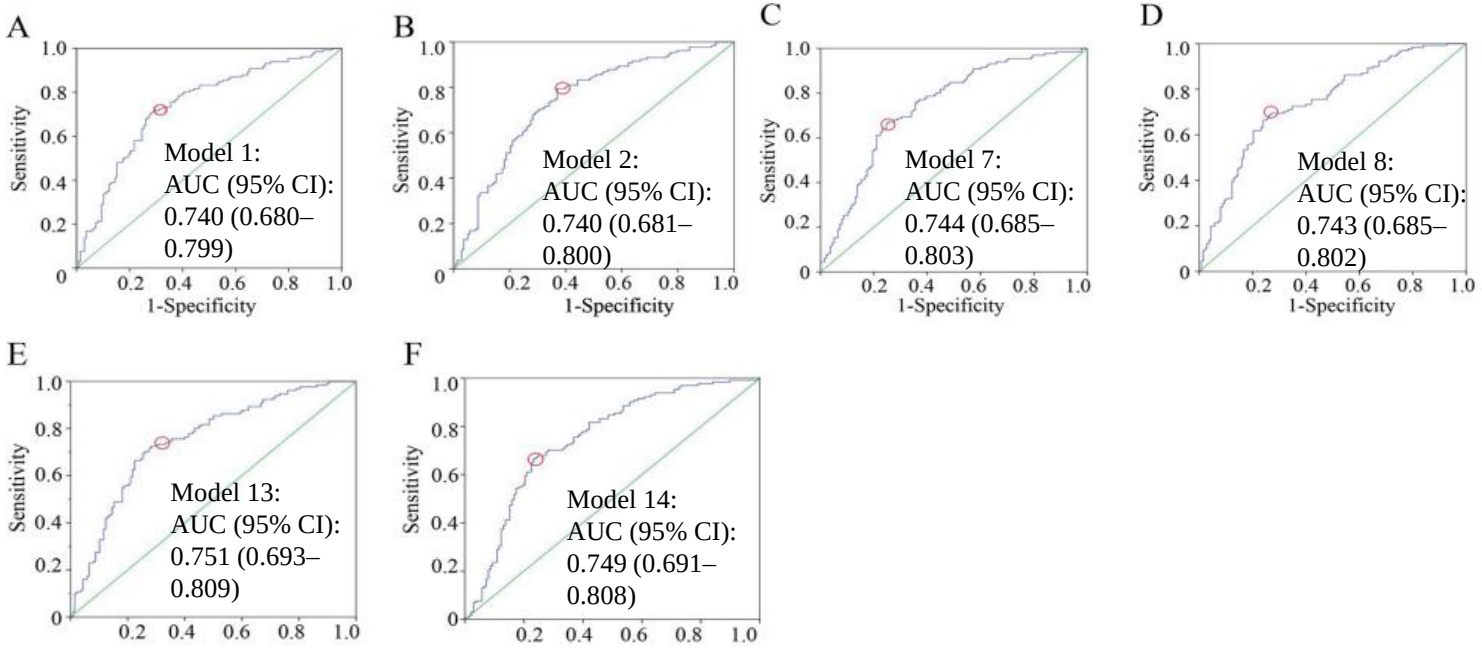


TABLE IV

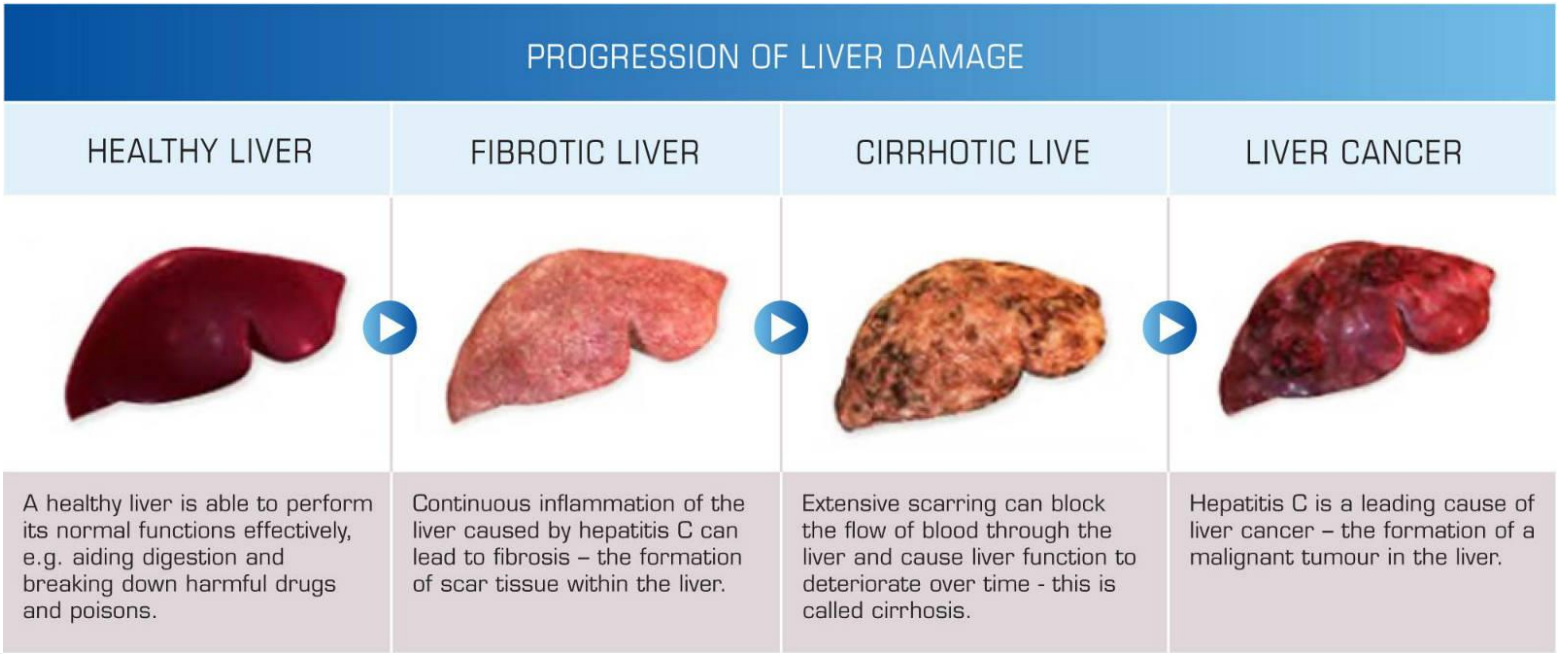
PPV and NPV calculations of multimarker models. PPV, positive predictive value; NPV, negative predictive value

Model	Sensitivity (%)	Specificity (%)	5% prevalence		10% prevalence	
			PPV (%)	NPV (%)	PPV (%)	NPV (%)
1	71.0	71.7	11.7	97.9	21.8	95.7
2	79.4	63.0	10.1	98.3	19.3	96.5
7	66.4	75.4	12.5	97.7	23.1	95.3
8	69.5	73.2	12.0	97.9	22.4	95.6
13	72.5	71.7	11.9	98.0	22.2	95.9
14	67.2	76.1	12.9	97.8	23.8	95.4

2. 代谢组学在肝癌诊断中的作用

南方醫院 NANFANG HOSPITAL

肝癌是全世界范围内最普遍的一种肿瘤，2014年最新的全球癌症统计数据显示，每年原发性肝癌新发病例发展中国家占83.7%，死亡病例发展中国家占83.4%。而我国是肝癌发病重灾区，患病率和死亡率占亚洲近70%，居亚洲之首。肝癌的早期诊断对于防治肝癌至关重要。



华银健康 HUAYIN HEALTH

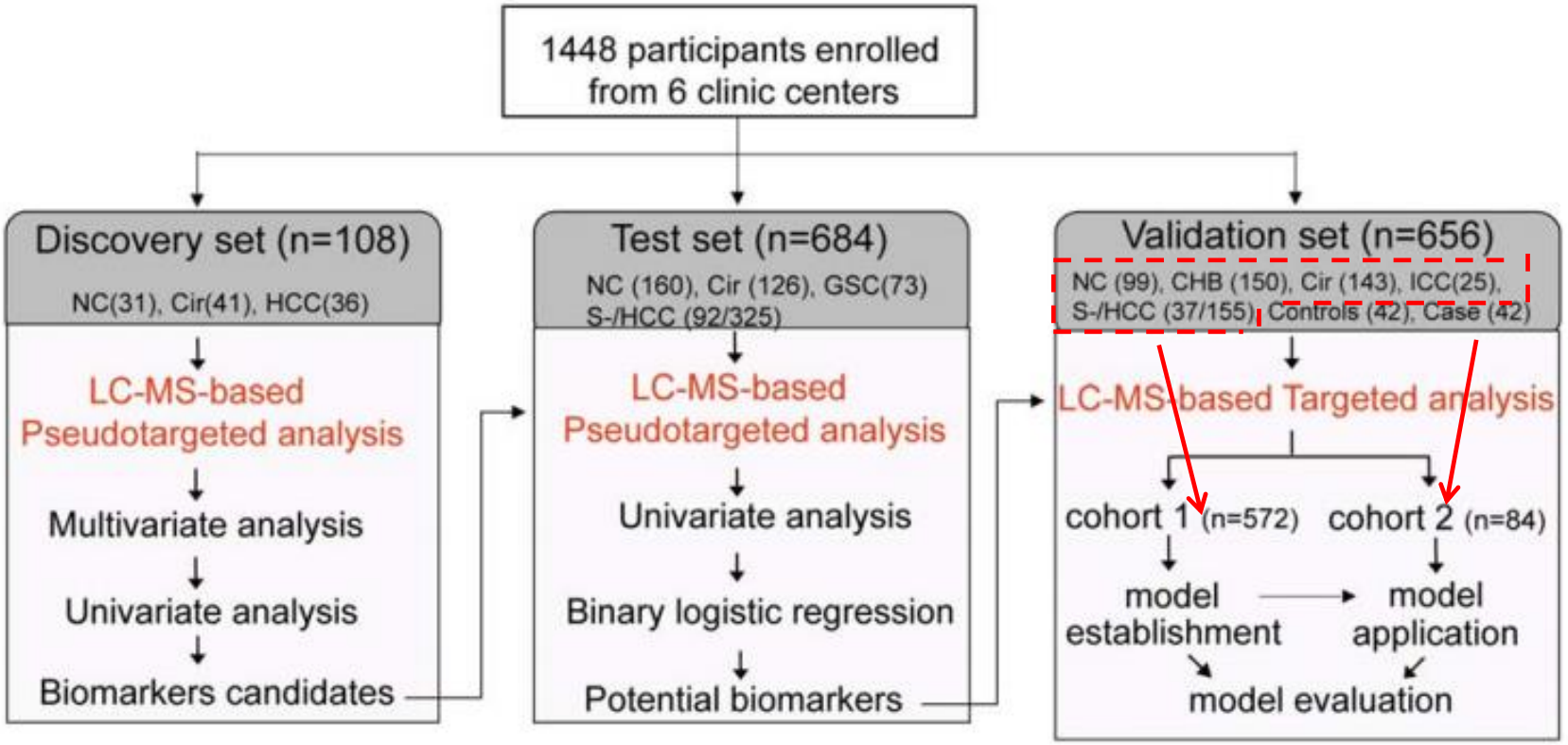
A Large - scale, multicenter serum metabolite biomarker identification study for the early detection of hepatocellular carcinoma

IF:14.079，2017

Ping Luo, Peiyuan Yin, Rui Hua, Yexiong Tan, Zaifang Li, Gaokun Qiu, Zhenyu Yin, Xingwang Xie, Xiaomei Wang, Wenbin Chen, Lina Zhou, Xiaolin Wang, Yanli Li, Hongsong Chen, Ling Gao, Xin Lu, Tangchun Wu ✉, Hongyang Wang ✉, Junqi Niu ✉, Guowang Xu ✉

中科院大连化学物理研究所代谢组研究分析中心主任**许国旺院士团队**

大规模、多中心血清代谢标志物在肝癌早期诊断中的应用

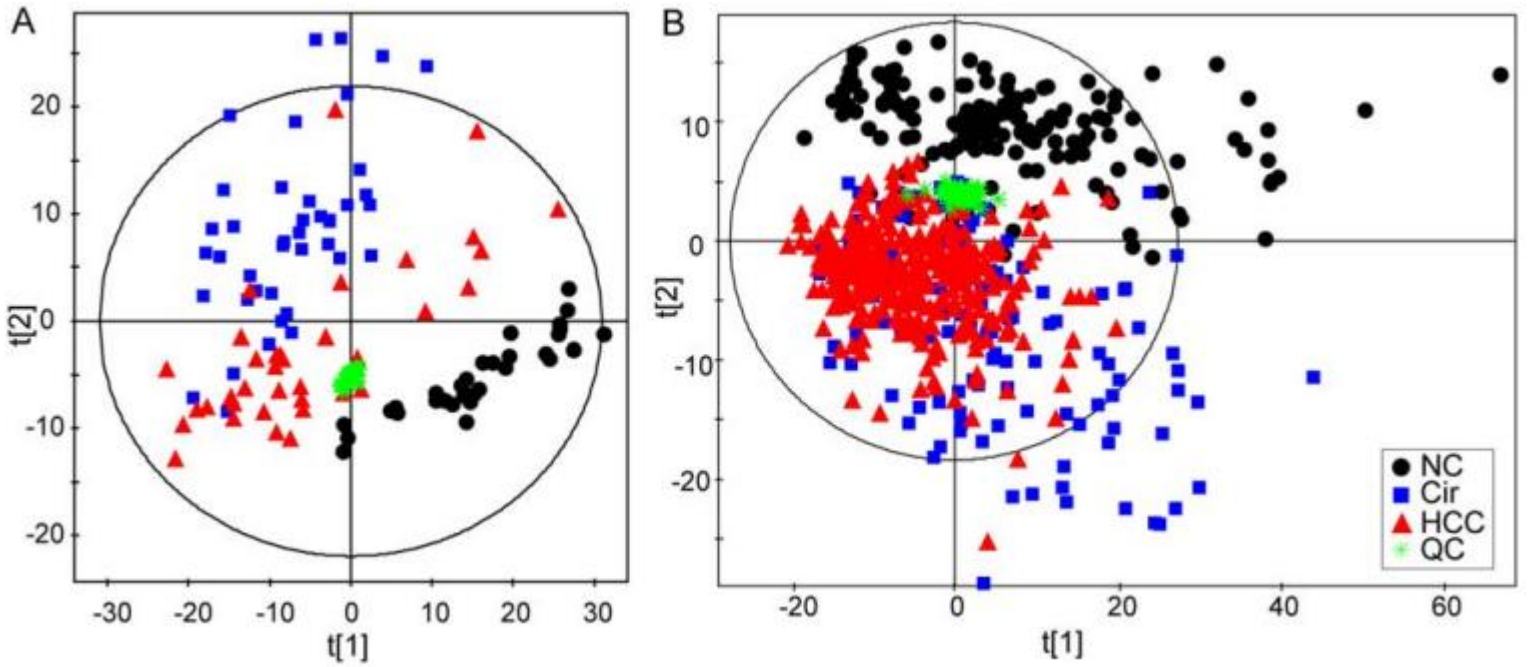


发现阶段　测试阶段　验证阶段

https://aasldpubs.onlinelibrary.wiley.com/doi/full/10.1002/hep.29561

血清代谢谱区分肝细胞癌患者和各组对照人群的能力

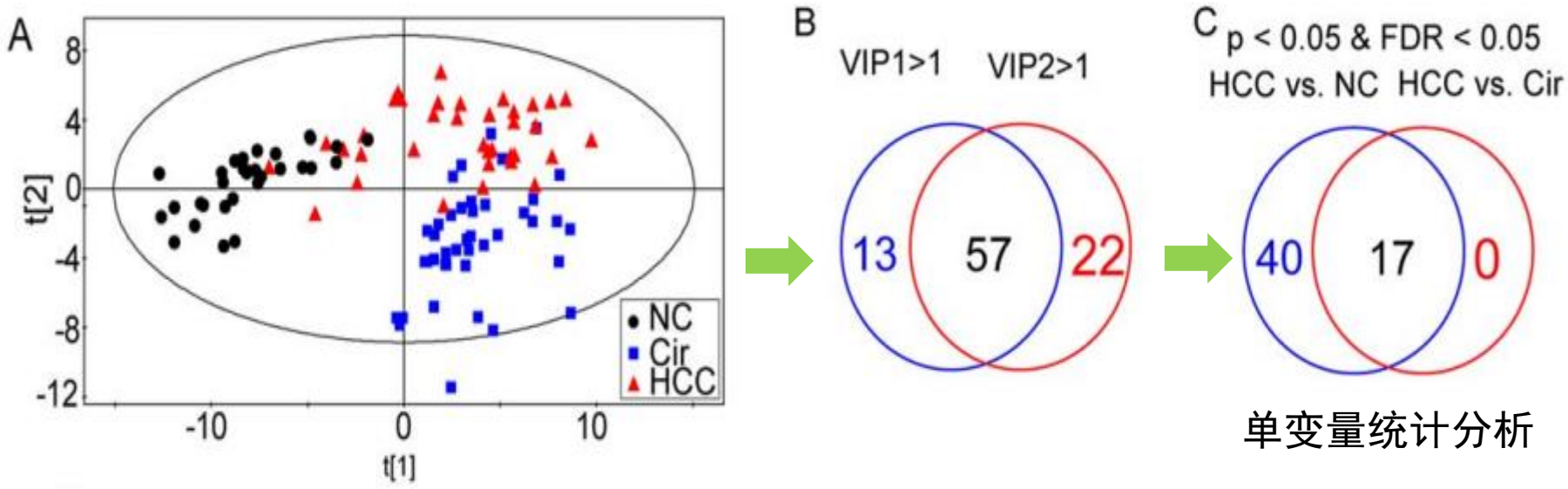
Discovery set **Test set**



Score plots of principal component analysis (PCA) based on the combinational data of ESI+ and ESI- modes from the discovery set (A) and the test set (B).

筛选潜在的HCC生物标志物—step1

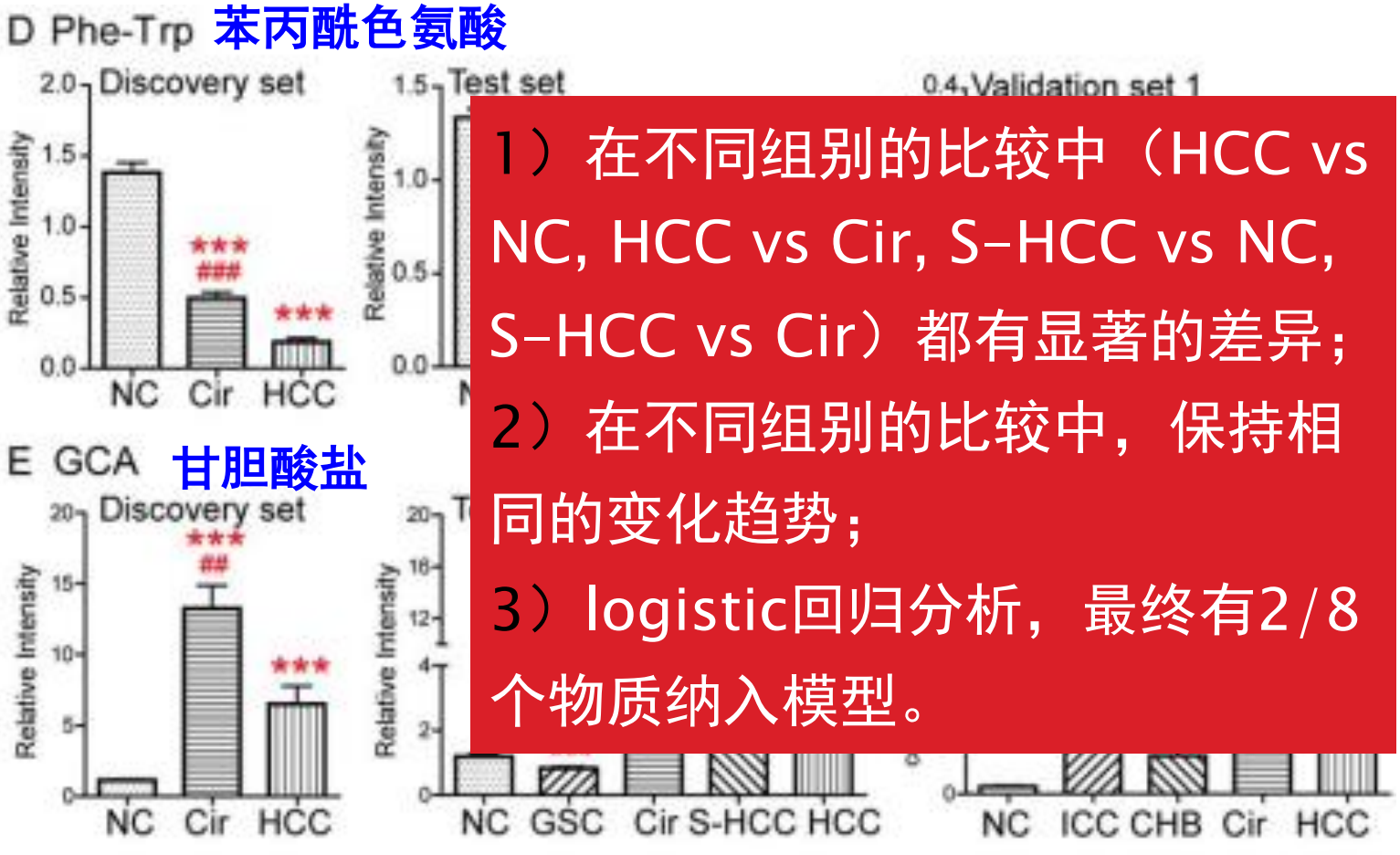
Discovery set



单变量统计分析

(A) Partial least squares discriminant analysis score plot based on NC, Cir, and HCC groups in the discovery set. (B) Venn diagram displays variables with VIP values >1 on two principal components (VIP1 and VIP2).

筛选潜在的HCC代谢标志物—step2



1）在不同组别的比较中（HCC vs NC, HCC vs Cir, S-HCC vs NC, S-HCC vs Cir）都有显著的差异；

2）在不同组别的比较中，保持相同的变化趋势；

3）logistic回归分析，最终有2/8个物质纳入模型。

(A) Trp (D) and GCA (E) in the discovery, test, and validation sets, respectively. *P < 0.05, **P < 0.01, and ***P < 0.001 when compared with NC/controls, respectively; #P < 0.05, ##P < 0.01, and ###P < 0.001 when compared with HCC, respectively.

代谢标志物对HCC诊断潜能的评估与验证

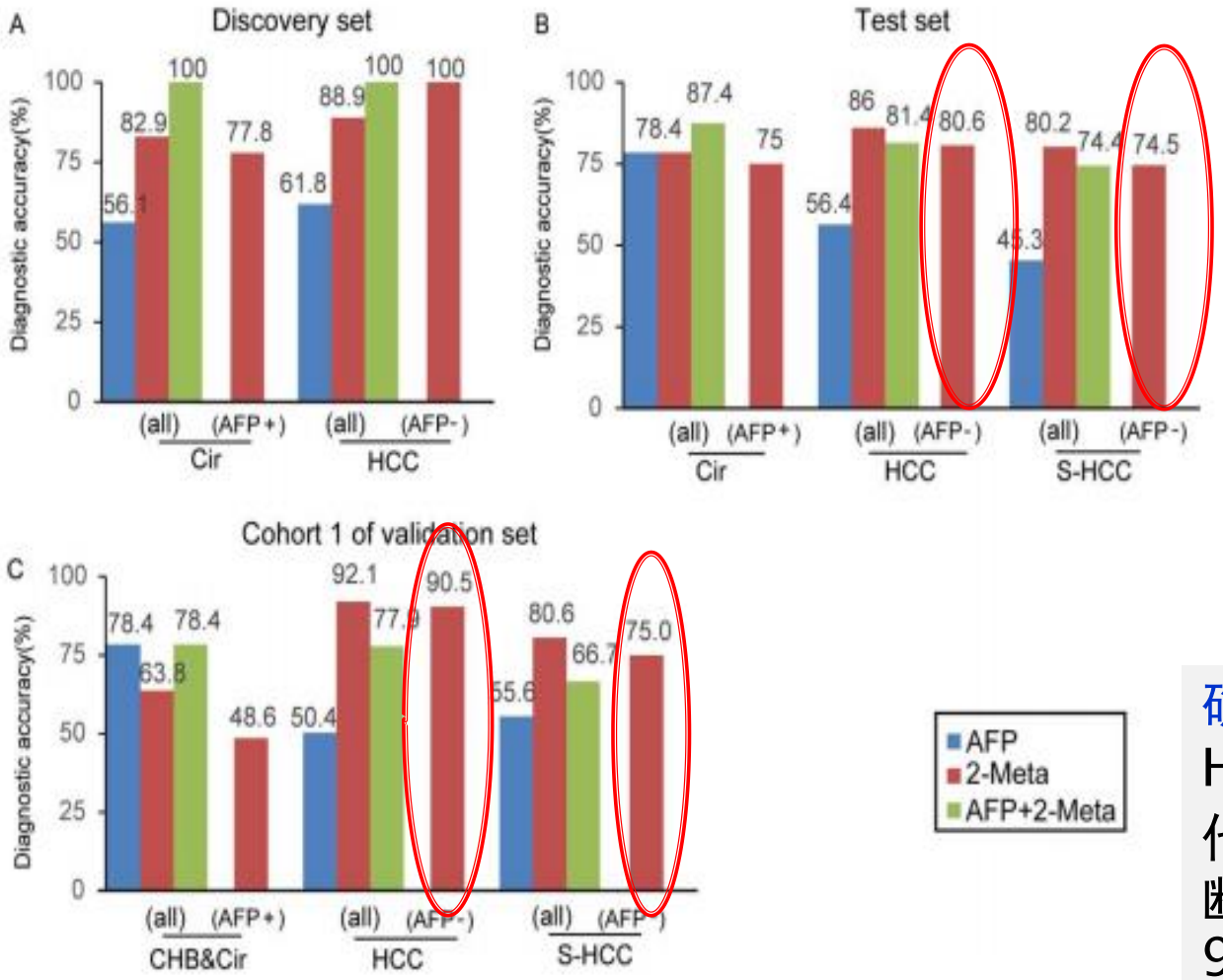
TABLE 2. Results of Measurement of the Serum Metabolite Panel, AFP, or Both in the Diagnosis of HCC

	Discovery Set			Test Set			Validation Set (Cohort 1)		
	AUC (95% CI)	Sensitivity (%)	Specificity (%)	AUC (95% CI)	Sensitivity (%)	Specificity (%)	AUC (95% CI)	Sensitivity (%)	Specificity (%)
HCC versus non-HCC									
2-Meta	0.951 (0.914-0.989)	88.9	88.9	0.936 (0.917-0.955)	88.6	85.7	0.875 (0.846-0.905)	91.6	72.2
HCC versus Cir									
2-Meta	0.930 (0.871-0.988)	88.9	82.9	0.892 (0.856-0.929)	86	78.4	0.807 (0.753-0.861)	92.1	52.8
AFP	0.657	61.8	56.1	0.725	56.4	78.4	0.650	50.4	73.2
2-Meta+AF									
HCC versus (									
2-Meta									
AFP									
2-Meta+AF									
S-HCC versus									
2-Meta									
AFP									
2-Meta+AF				(0.820-0.919)			(0.688-0.861)		
S-HCC versus (CHB and Cir)									
2-Meta	—	—	—	—	—	—	0.771 (0.689- 0.854)	80.6	63.8
AFP	—	—	—	—	—	—	0.711 (0.614-0.808)	55.6	78.4
2-Meta+AFP	—	—	—	—	—	—	0.801 (0.722-0.878)	66.7	78.4

Abbreviations: CI, confidence interval; 2-Meta, serum metabolite panel.

1. 代谢物构建的诊断模型能很好地区分HCC与非HCC；
2. 区分HCC与Cir的能力比AFP强；
3. 区分S-HCC与Cir的效能比AFP更好。

AFP阴性代谢标志物对HCC和s-HCC诊断的潜能



筛查组：AFP阴性(AFP<20 ng/ml)的HCC和s-HCC患者，代谢物诊断模型的诊断准确率分别达80.6%和74.5%。

确认组：AFP阴性HCC和s-HCC患者，代谢物诊断模型的诊断准确率分别达90.5%和75.0%

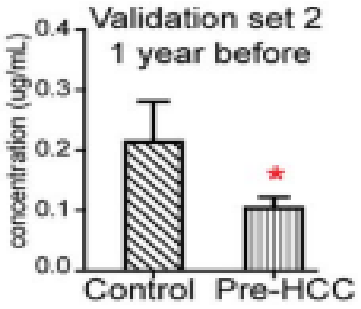
血清代谢模型可以预测（提前1年）肝癌的发生

TABLE 3. Performance of Serum Metabolite Panel, AFP, or Both in Prediction of HCC by Year Before Clinical Diagnosis in Cohort 2 of the Validation Set

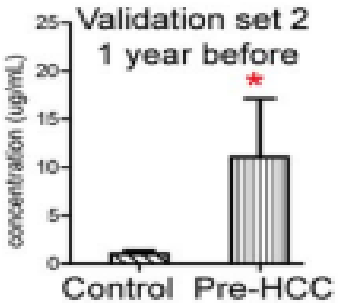
	1 Year Before (n = 10 × 2)	1.5 Years Before (n = 16 × 2)	2 Years Before (n = 28 × 2)	2.5 Years Before (n = 37 × 2)	3 Years Before (n = 42 × 2)
2-Meta					
AUC	0.790	0.738	0.689	0.647	0.635
(95% CI)	(0.581-0.999)	(0.557-0.920)	(0.550-0.828)	(0.522-0.773)	(0.513-0.751)
Sensitivity (%)	80.0	75.0	75.0	70.3	71.4
Specificity (%)	80.0	68.8	57.1	51.4	47.6
AFP					
AUC	0.740	0.674	0.633	0.619	0.622
(95% CI)	(0.518-0.962)	(0.482-0.866)	(0.482 -0.783)	(0.489-0.750)	(0.500-0.745)
Sensitivity (%)	40.0	37.5	28.6	27.0	26.2
Specificity (%)	100.0	93.8	96.4	97.3	97.6
2-Meta&AFP					
AUC	0.880	0.789	0.742	0.726	0.721
(95% CI)	(0.723-1.037)	(0.618-0.961)	(0.610-0.874)	(0.608-0.844)	(0.610-0.833)
Sensitivity (%)	60.0	68.8	64.3	64.9	64.3
Specificity (%)	100.0	87.5	78.6	78.4	78.6

Abbreviations: CI, confidence interval; 2-Meta, serum metabolite panel.

苯丙酰色氨酸

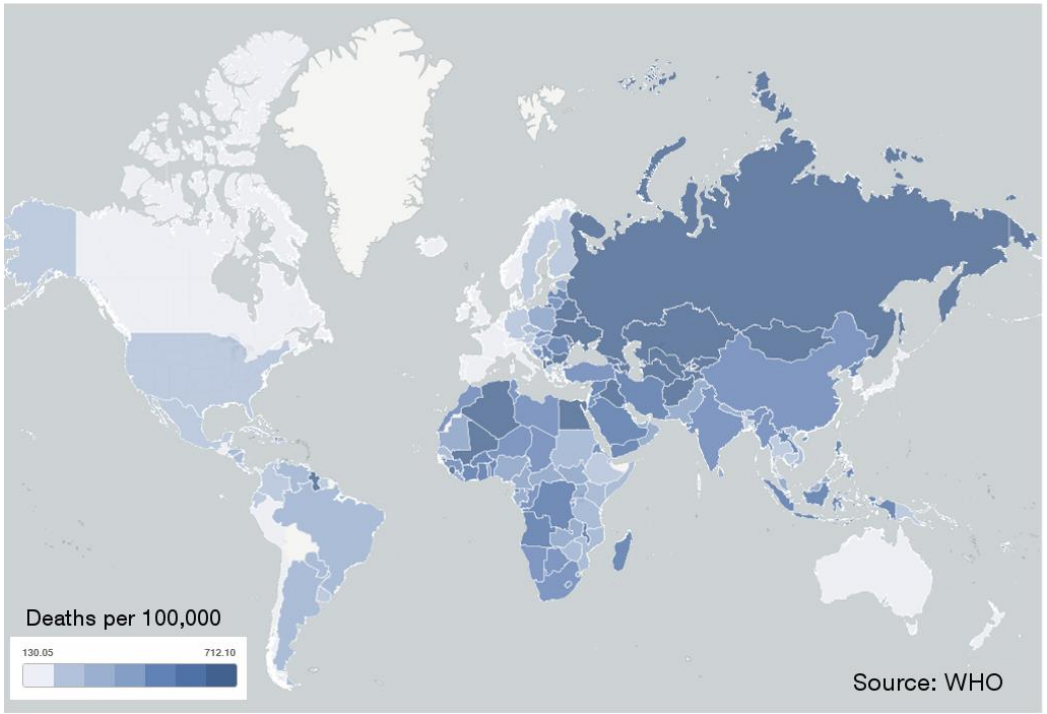


甘胆酸盐



3. 代谢组学在CVD诊断中的作用

心血管疾病（CVD）是一种严重威胁中老年人健康的常见病，具有高患病率、高致残率和高死亡率的特点。心血管疾病的发生与不良的饮食和生活习惯密切相关，不合理的膳食与机体代谢相互作用，促使机体多种代谢途径发生改变，因此**心血管疾病的发生和发展与机体的代谢密切相关**。



Deaths from cardiovascular disease around the world per, based on 2012 WHO data.

Circulation. 2018 Feb 20; 137(8): 841–853.
doi: 10.1161/CIRCULATIONAHA.117.029468
PMID: 29459470

IF：18.881，2018

南方醫院 NANFANG HOSPITAL

Metabolic Predictors of Incident Coronary Heart Disease in Women

女性冠心病的代谢预测因子 （美国马萨诸塞州布列根和妇女医院）

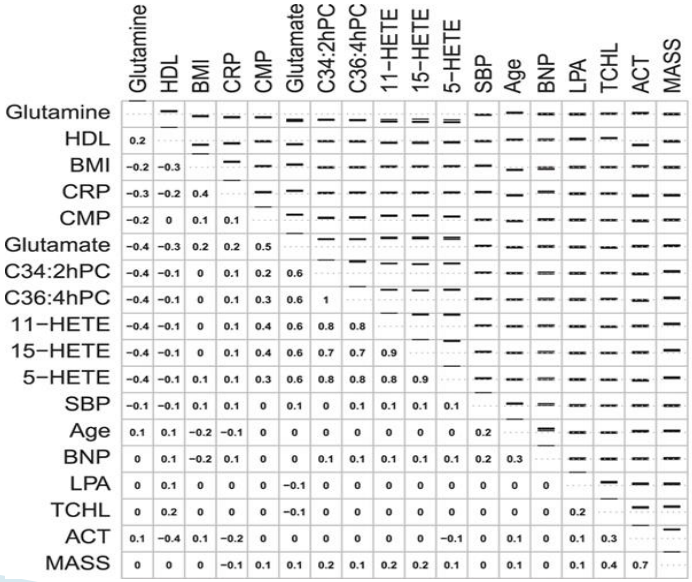
◆ WHI-OS（发现集）：
472例绝经后冠心病妇女
472例对照
◆ WHI-HT（验证集）：
312例绝经后冠心病妇女
315例对照
◆ PREDIMED（独立队列验证）
980例参与者
3种饮食干预：
- 补充天然橄榄油的地中海饮食干预
- 补充坚果的地中海饮食干预
- 低脂饮食

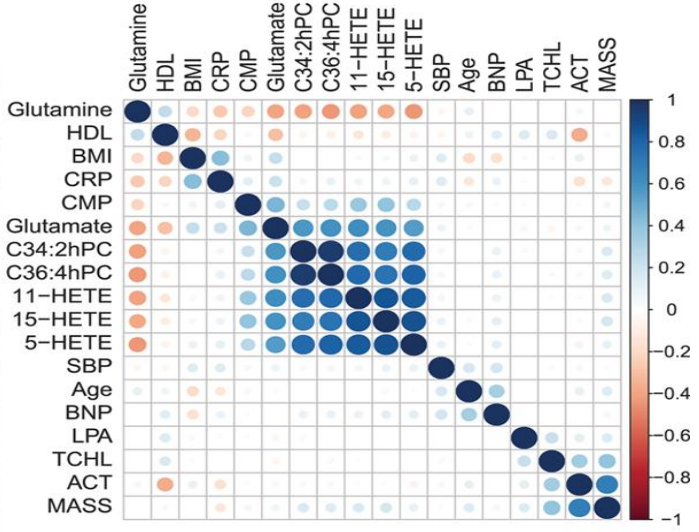
实验技术
- HILIC正负离子模式：水溶性代谢物
- C8正离子模式：极性和非极性血脂
- C18负离子模式：游离脂肪酸和胆汁酸

数据分析
- Logistic回归
- 受试者工作特征曲线（ROC）分析
- 相关性网络分析

代谢物与CHD疾病风险相关

通过筛查集和验证发现C34：2羟基磷脂酰胆碱、 C36:4羟基磷脂酰胆碱，5-羟基二十碳四烯酸(HETE)，15-HETE，11-HETE，谷氨酸、胞嘧啶核苷酸(CMP)**七个物质与 CHD 的风险正相关，谷氨酰胺与 CHD 风险负相关**。





代谢物可用于预测女性冠心病

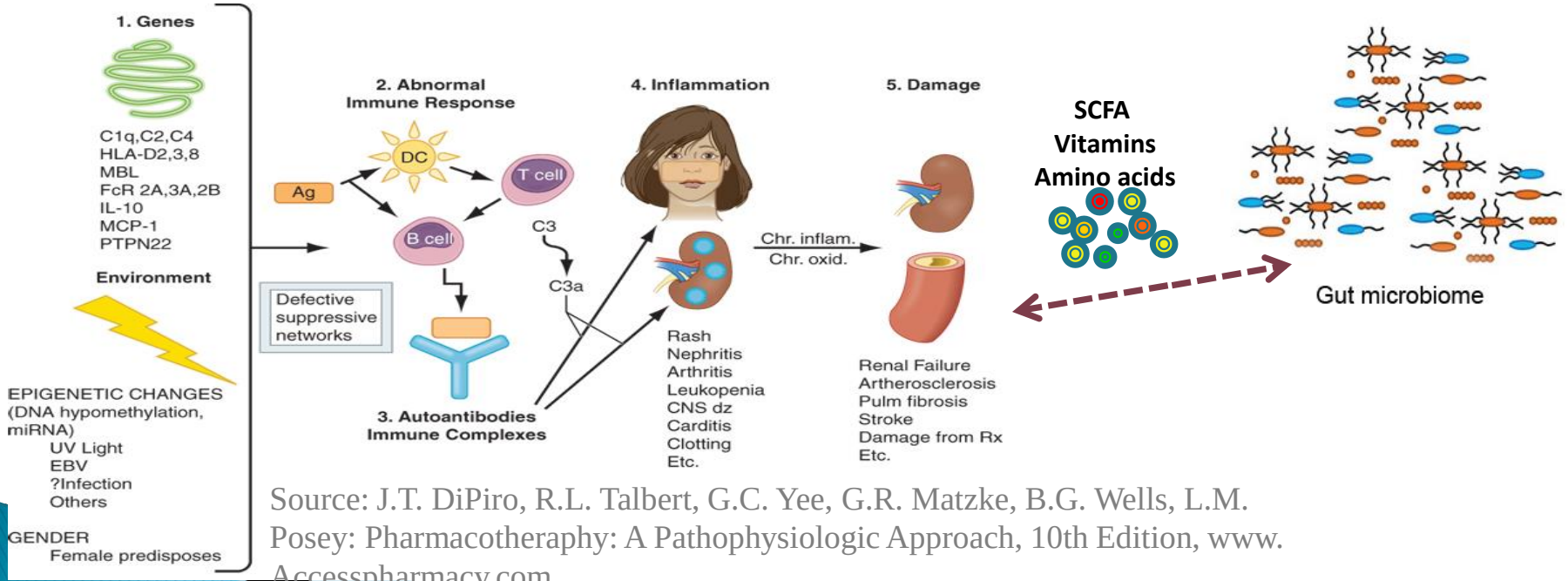
Table 3. Validation of Metabolites Among Men and Women in PREDIMED

Metabolite	All CVD* (N=980, 230 cases)		CVD Men Only* (139 cases)		CVD Women Only* (91 cases)		Interaction by Sex *P* Value
	Hazard Ratio (95% CI)	*P* Value	Hazard Ratio (95% CI)	*P* Value	Hazard Ratio (95% CI)	*P* Value	
C34:2 Hydroxy-PC	1.40 (1.15–1.70)	0.0008	1.16 (0.90–1.51)	0.26	1.79 (1.30–2.46)	0.0004	0.013
C36:4 Hydroxy-PC	1.36 (1.12–1.66)	0.0002	1.14 (0.86–1.49)	0.366	1.67 (1.22–2.29)	0.0015	0.026
Glutamate	1.48 (1.22–1.80)	0.00009	1.39 (1.04–1.84)	0.024	1.64 (1.19–2.24)	0.0022	0.32
Glutamine	0.84 (0.64–1.11)	0.22	0.83 (0.59–1.19)	0.32	0.79 (0.50–1.26)	0.33	0.65

对CHD高危男性和女性进行PREDIMED实验以测试研究结果的普适性，采用的两种检测方法能检测出8个代谢物中的4个，其中**谷氨酸、C34:2羟基PC 和 C36:4羟基PC**的确能增加CHD风险。**3个代谢物与女性CHD存在强相关性，在男性中只有谷氨酸存在显著相关**。

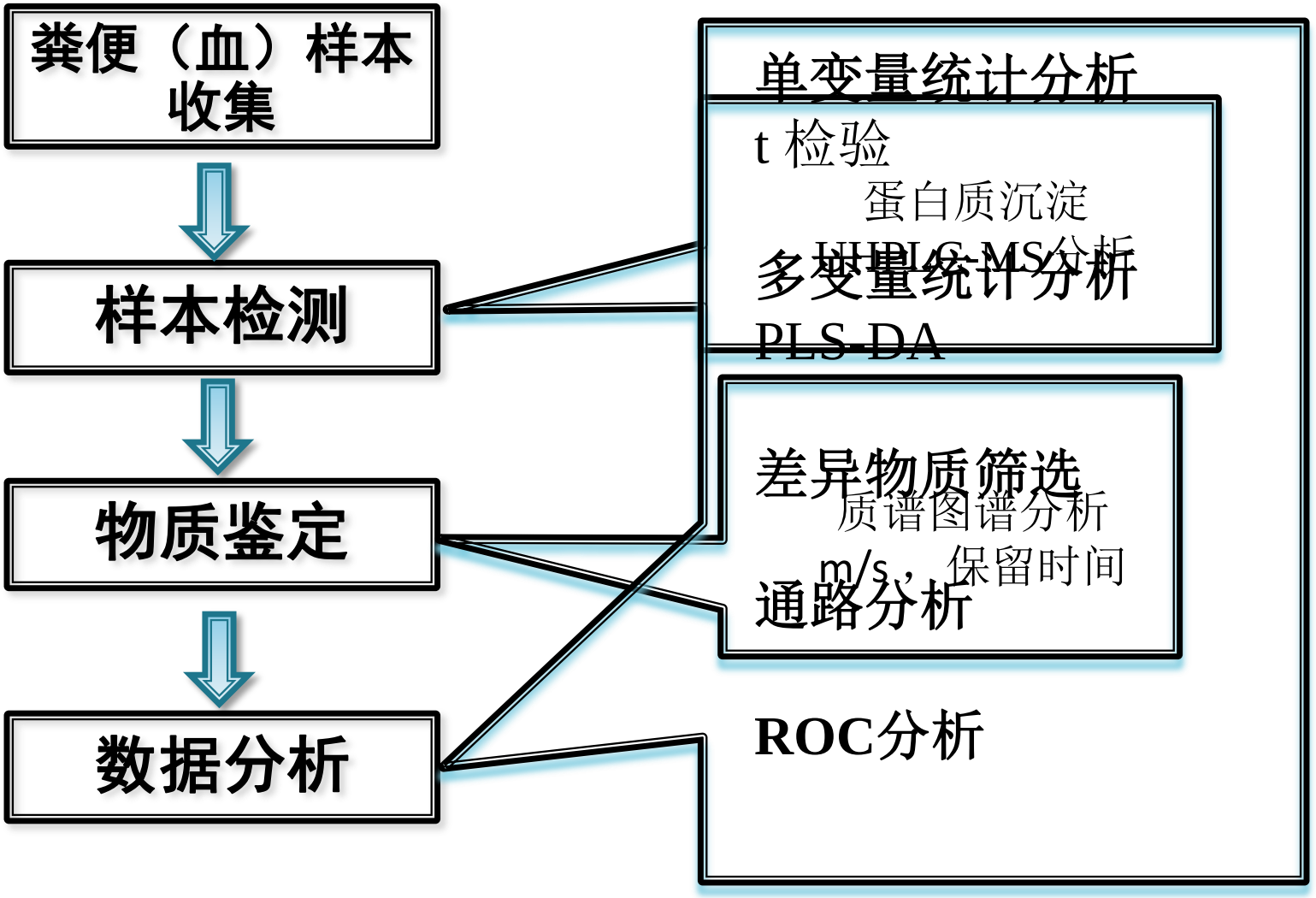
4. 代谢组学在SLE诊断中的作用

- 系统性红斑狼疮（SLE）一种以产生自身抗体为特征的慢性自身免疫性炎症性疾病，好发于育龄期女性，男女比例约为1:9；
- 病因复杂，常认为遗传、免疫、激素和环境因素导致疾病易感性；
- 临床诊断依靠临床表现和自身抗体检测



Source: J.T. DiPiro, R.L. Talbert, G.C. Yee, G.R. Matzke, B.G. Wells, L.M. Posey: Pharmacotheraphy: A Pathophysiologic Approach, 10th Edition, www.Accesspharmacy.com

检测方案


粪便（血）样本收集
样本检测
物质鉴定
数据分析
单变量统计分析
t 检验
蛋白质沉淀
UHPLC-MS分析
多变量统计分析
PLS-DA
差异物质筛选
质谱图谱分析
m/s，保留时间
通路分析
ROC分析

SLE患者粪便非靶向代谢组学研究

研究对象：32例SLE患者　　26例健康对照

检测平台：超高效液相色谱（AB Ekspert UltraLC 110）

高分辨质谱（AB Triple TOF 5600+）

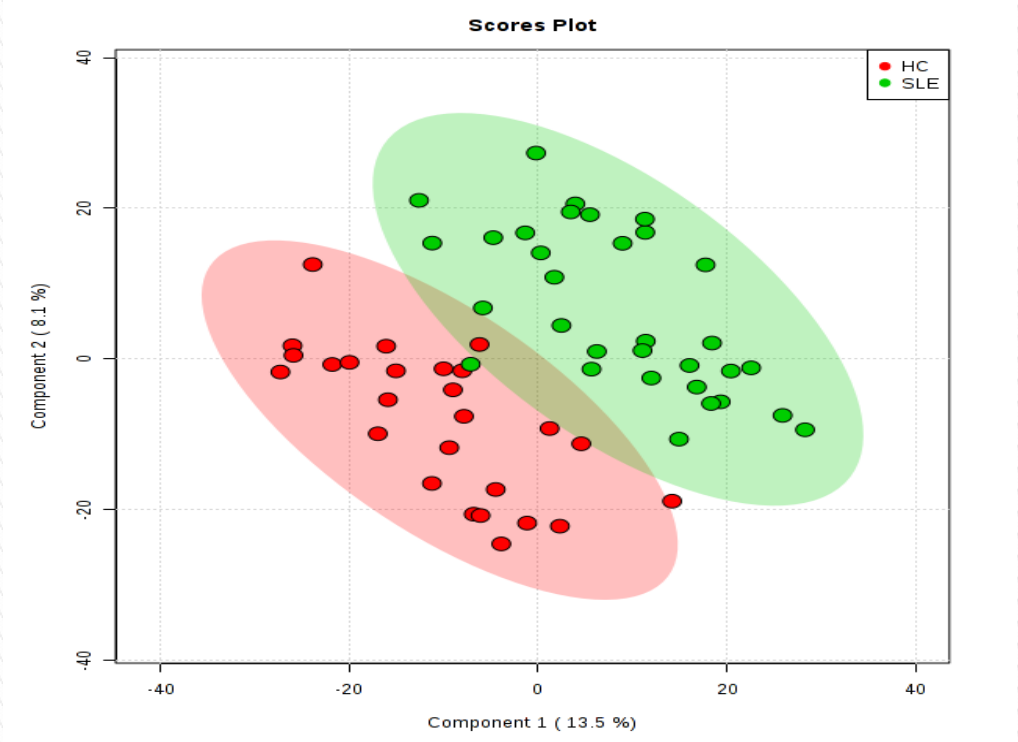


图1　SLE组及HC组PLS-DA（偏最小二乘法)得分图

两组分离趋势明显

粪便差异代谢物　　VIP>1, p<0.05　代谢物的筛选条件

序号	Metabolite	中文名	p	VIP	Change	参与代谢
1	Proline	脯氨酸	0.002	2.08	Up	氨基酸代谢
2	L-Tyrosine	L-酪氨酸	0.007	1.79	Up	氨基酸代谢
3	L-Methionine	L-蛋氨酸	0.015	1.63	Up	氨基酸代谢
4	L-Asparagine	L-天冬酰胺酸	0.037	1.40	Up	氨基酸代谢
5	Dl-Pipecolinic acid	2-哌啶酸	0.033	1.43	Up	氨基酸代谢
6	Glycyl-L-Proline	甘氨酰脯氨酸	0.014	1.64	Up	氨基酸代谢
7	D-Ala-D-ala	D-丙氨酰-D-丙氨酸	0.022	1.54	Down	氨基酸代谢
8	L-Carnosine	L-肌肽	0.010	1.72	Up	氨基酸代谢
9	Xanthurenic acid	黄尿酸	0.004	1.90	Up	氨基酸代谢
10	Kynurenic acid	犬尿喹啉酸	0.025	1.51	Up	氨基酸代谢
11	Lauryl diethanolamide	月桂酰二乙醇胺	0.028	1.48	Down	脂肪酸代谢
12	1,2-Dioleoyl-Rac-Glycerol	1，2-二油酸基- Rac -甘油	0.004	1.90	Up	甘油脂代谢
13	MG 22:6	甘油一酯	0.049	1.33	Up	甘油脂代谢
14	MG 16:5	甘油一酯	0.018	1.59	Up	甘油脂代谢
15	SQDG 26:5		0.005	1.87	Down	甘油脂代谢
16	lysoPE 16:0	溶血磷脂酰乙醇胺	0.025	1.51	Up	甘油磷脂代谢
17	lysoPC 22:5	溶血磷脂酰胆碱	0.002	2.05	Up	甘油磷脂代谢
18	PG 27:2	磷脂酰甘油	0.000	2.50	Up	甘油磷脂代谢
19	Adenosine	腺苷	0.001	2.12	Down	嘌呤代谢
20	Adenosine 5'-Diphosphate	5’—二磷酸腺苷	0.002	2.06	Down	嘌呤代谢
21	Trigonelline	葫芦巴碱	0.043	1.36	Down	维生素代谢
22	Thiamine pyrophosphate	焦磷酸硫胺素	0.033	1.43	Down	维生素代谢
23	Mucic acid	粘液酸	0.030	1.46	Down	其他

23个差异代谢物，15↑，8↓

差异性的代谢产物进行聚类分析

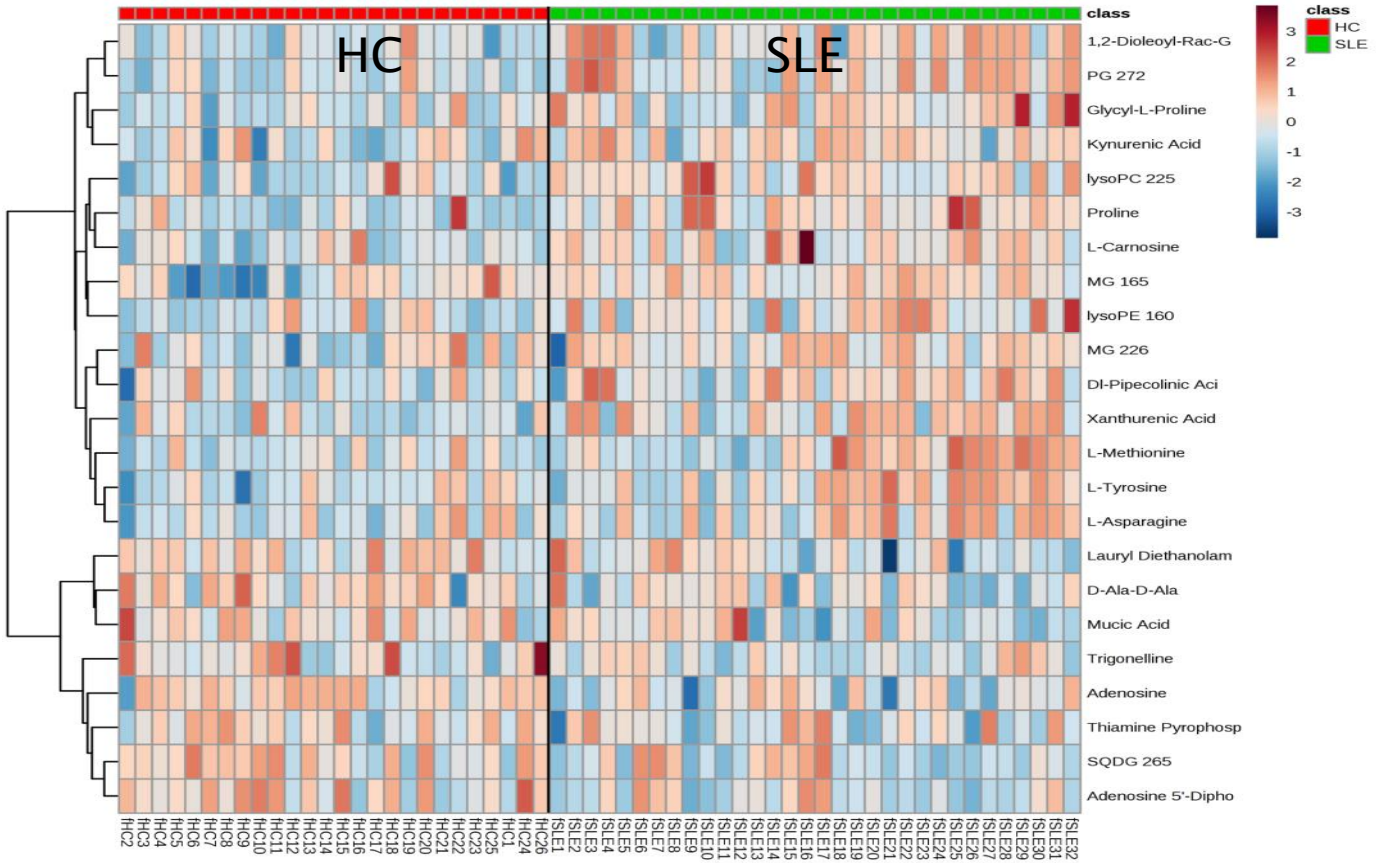
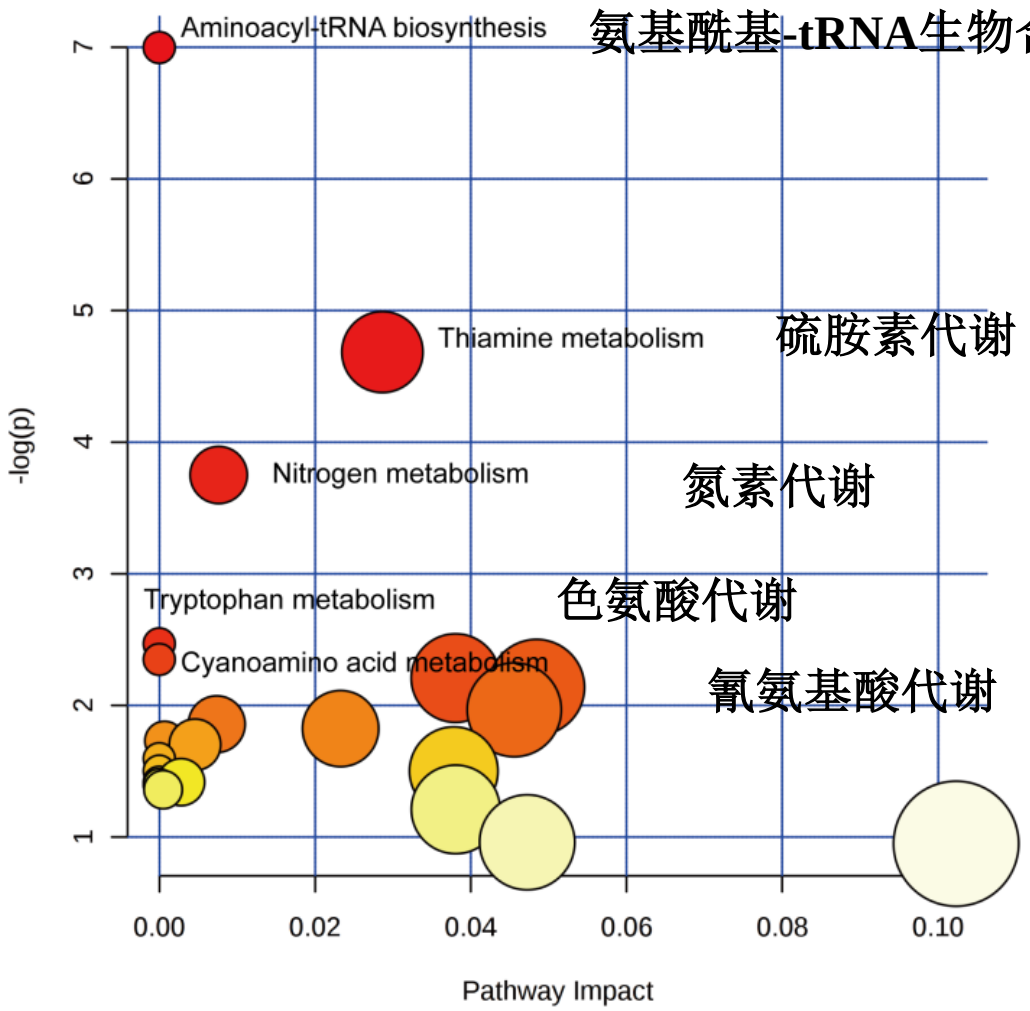


图2　SLE组和HC组粪便差异代谢物热图

代谢通路分析　　P<0.1



用Metaboanalys3.0软件对差异代谢物质进行了代谢通路分析，富集到23条代谢通路。

图3 SLE组和HC组粪便差异代谢物通路分析

粪便差异代谢物诊断效能评估

序号	Metabolite	中文名	AUC	Sensitivity	Specificity
1	PG 27:2	磷脂酰甘油	0.787	84.4%	65.4%
2	Adenosine	腺苷	0.748	71.9%	73.1%
3	Proline	脯氨酸	0.755	75.0%	73.1%
4	Adenosine 5'-Diphosphate	5’—二磷酸腺苷	0.732	59.4%	80.8%
5	lysoPC 22:5	溶血磷脂酰胆碱	0.754	81.2%	69.2%
6	Xanthurenic acid	黄尿酸	0.716	68.7%	73.1%
7	1,2-Dioleoyl-rac-glycerol	1，2-二油酸基- Rac -甘油	0.730	75.0%	76.9%
8	SQDG 26:5		0.716	62.5%	80.8%
9	L-Carnosine	L-肌肽	0.715	59.4%	84.6%
10	L-Tyrosine	L-酪氨酸	0.671	46.9%	92.3%
11	Glycyl-L-proline	甘氨酰脯氨酸	0.681	78.1%	61.5%
12	L-Methionine	L-蛋氨酸	0.653	53.1%	80.8%
13	MG 16:5	甘油一酯	0.632	96.9%	34.6%
14	D-Ala-D-Ala	D-丙氨酰-D-丙氨酸	0.695	81.2%	57.7%
15	Kynurenic acid	犬尿酸	0.686	68.7%	73.1%

选取 VIP>1的前15个物质进行ROC曲线分析，AUC>0.7有9个。为了提高诊断效能，将15个差异代谢物进行回归分析，筛选出PG27：2和脯氨酸进入模型 。

粪便差异代谢物诊断效能评估

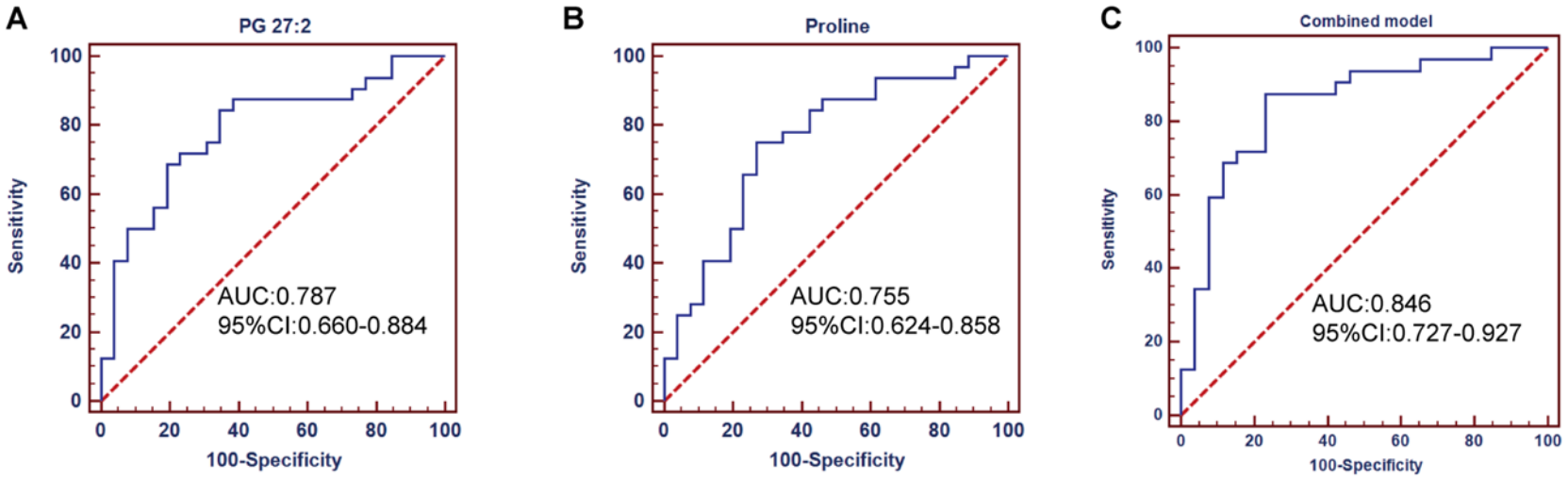


图4　粪便PG 27:2、脯氨酸及联合模型 ROC 分析

A　PG 27:2：　AUC= 0.787　灵敏度：84.4%　特异度：65.4%

B　Proline：　AUC= 0.755　灵敏度：75.0%　特异度：73.1%

C　联合模型：　AUC=0.846　灵敏度：　87.5%　特异度：　76.9%

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Fecal Metabolomics and Potential Biomarkers for Systemic Lupus Erythematosus

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The role of metabolomics in autoimmune diseases has been a rapidly expanding area in researches over the last decade, while its pathophysiologic impact on systemic lupus erythematosus (SLE) remains poorly elucidated. In this study, we analyzed the metabolic profiling of fecal samples from SLE patients and healthy controls based on ultra-high-performance liquid chromatography equipped with mass spectrometry for exploring the potential biomarkers of SLE. The results showed that 23 differential metabolites and 5 perturbed pathways were identified between the two groups, including aminoacyl-tRNA biosynthesis, thiamine metabolism, nitrogen metabolism, tryptophan metabolism, and cyanoamino acid metabolism. In addition, logistic regression and ROC analysis were used to establish a diagnostic model for distinguishing SLE patients from healthy controls. The combined model of fecal PG 27:2 and proline achieved an area under the ROC curve of 0.846, and had a good diagnostic efficacy. In the present study, we analyzed the correlations between fecal metabolic perturbations and SLE pathogenesis. In summary, we firstly illustrate the comprehensive metabolic profiles of feces in SLE patients, suggesting that the fecal metabolites could be used as the potential non-invasive biomarkers for SLE.

Keywords: feces, metabolomics, biomarker, systemic lupus erythematosus, liquid chromatography, mass spectrometry

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INTRODUCTION

Systemic lupus erythematosus (SLE) is an autoimmune disease with persistent inflammation that affects multiple organ systems, characterized by high morbidity and low quality of life. The etiological factors and pathogenesis of SLE are still not completely understood (1). However, a lot of evidences suggest that the gut microbiome takes an important role in inflammatory and

- 另外做了SLE病人血清代谢产物的筛选，并进行了靶向验证，文章正在整理中。

总结：

疾病的代谢谱用于疾病的诊断是今后的一个发展方向！

谢谢聆听