Supplementary materials

The reagents and materials used were as follows: LC-MS grade water (H_2O), acetonitrile (CAN), methanol (MeOH), 0.1% formic acid (FA) in water, and 2-chlorophenylalanine (Shanghai Sinopharm Group Chemical Reagent Co., Ltd.). Furthermore, we used a refrigerated centrifuge (H1650-W, Changsha Xiangyi Centrifuge Instrument Co., Ltd.), mixer (QL-866, Haimen Qilin Bell Instrument Manufacturing Co., Ltd.), pure water instrument (Arium® mini, Germany Sartorius Group), vacuum concentrator (53050, Eppendorf AG, Germany), a liquid chromatography system (AcquityUPLC, Waters Technology Co., Ltd., USA), and a content spectrometer (Orbitrap XL, Thermo Fisher Scientific, USA).

The fecal supernatant samples were prepared as follows: 100 mg of feces were taken in a 2 ml tube, and 500 μL of double distilled H_2O (4℃) was added. This was mixed well for 1 min, followed by adding 1 ml of methanol (-20℃) and vortexing for 30 s. This sample was then placed in an ultrasonic machine, exposed to room temperature (18℃-25℃) for 10 min, placed on ice for 30 min, and then centrifuged at 13,000*g* (centrifuge radius, 90 mm) at 4°C for 10 min. Then, 1200 μL of the supernatant was transferred to a new centrifuge tube, and the sample was concentrated using a vacuum centrifugal concentrator; finally, 400 μL of 2-chlorophenylalanine (0.02‰) methanol aqueous solution (1:1, 4℃) was added to dissolve the sample, which was filtered through a 0.22-μm membrane to obtain the test sample.

The mass spectrometry platform was established as follows: Feces samples were collected from the same patient, and parallel samples were prepared, followed by a precision inspection. We used the AcquityUPLC liquid chromatograph and the LTQ-Orbitrap XL mass spectrometer at Suzhou Panomic Biomedical Technology Co., Ltd. to explore and optimize the liquid chromatography-mass spectrometry (LC/MS) analysis conditions and performed methodological analysis. For the inspection, the compound species were identified by comparative matching evaluation; the metabolomics data

of biological samples were analyzed by partial least squares-discriminant analysis using the ProteoWizard software (Version 3.0.9134, ProteoWizard, Palo Alto, CA). Pattern recognition was performed, and the response permutation test was used to verify whether the model passed the fitting verification. The LC/MS software system was used to control the quality of the acquired data. Finally, a stable LC/MS-based metabolome full-spectrum analysis platform for biological samples was established.

The chromatographic conditions were as follows: An AcquityUPLC HSST3 1.8 μm (2.1 × 150 mm) chromatographic column was used, and the autosampler temperature was set at 4°C. The flow rate was 0.25 ml/min, and the column temperature was 40°C. Here, 5 μl of the sample was injected for gradient elution, and the mobile phase used was 0.1% FA in water (A)–0.1% FA in acetonitrile (B). The gradient elution program is 0-1 min, 2% B; 1-9.5 min, 2%-50% B; 9. 5-14 min, 50%-98% B; 14-15 min, 98% B; 15-15.5 min, 98%-2% B; and 15.5-17 min, 2% B.

The mass spectrometry conditions were as follows: The instrument used was an LTQ-Orbitrap XL mass spectrometer (Thermo Fisher Scientific), and electrospray was the ion source. Both positive and negative ionization modes were used, with the positive ion spray voltage being 4.80 kV and the negative ion spray voltage being 4.50 kV. The sheath and auxiliary gas flow rates were 45 arb (arbitrary unit, gas flow unit) and 15 arb, respectively. The capillary temperature was 325°C; the capillary voltage was 35 V/-15 V; and the tube lens voltage was 50 V/-50 V. The full scan was performed at a resolution of 60,000 m/Δm, and the scanning range was 89-1000 (mass-to-charge ratio). Data-dependent acquisition MS/MS experiments were performed with collision-induced dissociation scan. The collision voltage was 30 eV. Dynamic exclusion was used to remove unnecessary MS/MS information (dynamic exclusion time, 15 s).

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Supplementary Table 1 Changes in body weight and body composition of patients with cervical cancer during the periradiation period

	T0	T2	T4	Tf
Body weight (kg)	56.12±1.18	54.40±1.14	52.26±1.10	49.63±1.04
Skeletal muscle content (%)	46.96±4.23	45.72±3.91	43.28±3.79	41.44±3.76
Body fat content (%)	22.20±0.40	22.20±0.40	21.20±0.40	20.50±0.30
BMI (Kg/m^2)	21.30±0.34	20.74±0.33	19.92±0.31	18.92±0.30
Phase angle (^{o})	5.13±0.09	4.99±0.09	4.79±0.08	4.55±0.08
Serum albumin (g/L)	38.46±0.31	36.92±0.29	35.44±0.28	33.67±0.27
Serum prealbumin (mg/L)	302.88±9.62	290.76±9.22	279.16±8.86	265.22±8.41
NRS 2002 score	1.24±0.52	1.60±0.70	2.12±0.77	2.96±0.53

BMI: Body mass index; NRS: Nutritional risk screening.

Supplementary Table 2 121 differential metabolites identified in stool samples

Compound	Molecular Weight	Compound	Molecular Weight	Compound	Molecular Weight
2-Ketobutyric acid	102.0911	Ascorbic acid	175.0244	Nandrolone	275.2001
Choline	104.1067	3-Isopropylmalic acid	175.0606	Stearidonic acid	277.216
Styrene	105.0697	Suberic acid	175.0963	Linoleic acid	281.2471
Creatinine	114.066	N-Formyl-L-methionine	176.0381	N1,N12-Diacetylspermine	287.2432
N-Acetylpyrrolidine	114.0911	L-Tyrosine	182.0807	Lauroyl diethanolamide	288.2529
gamma-Caprolactone	115.0751	Glycylleucine	189.123	Androstanedione	289.2563
5-Aminopentanoic acid	118.0867	N-alpha-Acetyllysine	189.1231	Aspartame	295.1282
Phenylethylamine	122.0962	Kynurenic acid	190.0497	alpha-dimorphecolic acid	295.2256
Nicotinic acid	124.0389	N-Acetylglutamic acid	190.0707	Enterolactone	297.111
Citraconic acid	129.0196	Indole-3-propionic acid	190.0861	Ricinoleic acid	297.2412
Ketoleucine	129.0558	N-Acetyl-L-methionine	192.0688	Arachidonic acid	303.1328
Pipecolic acid	130.0858	Gluconic acid	195.0501	Eicosapentaenoic acid	303.2312
Glutaric acid	131.0352	1,7-Dimethyluric acid	195.0513	gamma-Glutamyltyrosine	311.1231
2-Ethyl-2-Hydroxybutyric	131.0715	N-Acetylhistidine	198.0849	13-L-Hydroperoxylinoleic acid	311.2203

acid					
Creatine	132.0752	xi-5-Dodecanolide	199.1691	Octadecanedioic acid	313.2358
L-Leucine	132.1018	p-Chlorophenylalanine	200.0469	alpha-CMBHC	319.1888
L-Malic acid	133.0145	Alanyl-Leucine	201.1234	Cytidine monophosphate	324.216
Ornithine	133.0969	Asymmetric dimethylarginine	203.15	N,N-Dimethylsphing-4-enine	328.3204
2-Methylbenzoic acid	135.0451	Xanthurenic acid	206.0446	Cyclic AMP	330.0573
p-Aminobenzoic acid	138.0547	5-Methoxyindoleacetate	206.0842	Melibiose	341.1065
Methylglutaric acid	145.0503	N-Acetyl-L-phenylalanine	208.0966	7-Dehydrocholesterol	385.3418
N-Acetylcadaverine	145.1334	Eudesmic acid	211.0598	Artemetin	387.1067
4-Acetamidobutanoic acid	146.0808	Isoproterenol	212.1281	Deoxycholic acid	393.2994
N-Methylisoleucine	146.1172	Pantothenic acid	220.1174	Cholic acid	407.2788
L-Glutamine	147.0763	Traumatic acid	227.1275	Allocholic acid	407.2788
L-Lysine	147.1124	Dodecanedioic acid	229.1431	PE(14:0/0:0)	426.2608
trans-Cinnamic acid	149.0595	Fenfluramine	232.1287	LysoPE(15:0/0:0)	440.2761
L-Methionine	150.0582	Alanyl-dl-Phenylalanine	237.1231	Quercitrin	447.2039

p-Hydroxyphenylacetic acid	153.1271	CMPF	241.1068	LysoPE(16:1(9Z)/0:0)	452.2762
3-Hydroxyanthranilic acid	154.0496	Mefenamic acid	241.9991	PE(16:0/0:0)	454.2917
Orotic acid	155.0093	1,11-Undecanedicarboxylic acid	243.1583	Phosphatidylethanolamine lyso alkenyl 18:1	462.2982
Protocatechuic acid	155.1063	2-Hydroxymyristic acid	243.1947	PE(17:1(9Z)/0:0)	466.2918
Aminoadipic acid	160.0612	Chrysin	253.0699	Glycyrrhetinic acid	471.3456
Tryptamine	161.107	Daidzein	255.0648	Folinic acid	474.1712
Phenylpyruvic acid	163.0395	Gamma-Glu-Leu	261.144	PE(18:1(9Z)/0:0)	480.3074
Formylanthranilate	164.0349	Phenylalanylproline	263.1389	PG(16:0/0:0)[U]	483.2712
L-Phenylalanine	164.0713	Farnesyl acetone	263.2366	PE(19:1(9Z)/0:0)	494.3227
4-Hydroxycinnamic acid	165.0542	Inosine	269.0874	Taurodeoxycholic acid	498.2962
3-(3-Hydroxyphenyl)propanoic acid	165.0553	Phloretin	273.0745	Taurocholic acid	516.2972
1-Methylxanthine	167.0562	6-Phosphogluconic acid	275.0208	FAD	784.1499
Norepinephrine	170.0808				