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SUPPORTING INFORMATION

Integration of metabolomics and transcriptomics to reveal metabolic characteristics and key targets associated with cisplatin resistance in non-small cell lung cancer

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Figure S1. PLS-DA sore plots and permutation analysis of A549/DDP (-) and A549/DDP (+) in ESI⁺ (A,B) and ESI ⁻ (C,D) modes.



Figure S2. PLS-DA sore plots and permutation analysis of A549 (-) and A549 (+) in ESI⁺ (A,B) and ESI ⁻ (C,D) modes.



Figure S3. PLS-DA sore plots and permutation analysis of A549 (+) and A549/DDP (+) in ESI⁺ (A,B) and ESI⁻ (C,D) modes.

Table S1. Identified metabolites in four groups (A549/DDP (-) VS A549/DDP (+), A549 (-) VS A549 (+), A549 (-) VS A549/DDP (-), A549 (+) VS A549/DDP (+)) based on UPLC-QTOF/MS.

M. (1) 17(Compound	A549/DDP(+)/	A549(+)/	A549/DDP (-) /	A549/DDP(+)/
Metabolites		A549/DDP(-)	A549(-)	A549 (-)	A549(+)
Malic acid	C4H6O5		1.569884634		0.632979569
Pyroglutamic acid	C5H7NO3		1.712726896		0.519511213
Citric acid	C6H8O7		1.583702756	0.686935484	0.472433709
Cys-Gly	C5H10N2O3S	0.88286327	1.477065766	0.755046715	0.451302187
N-acetylaspartate	C6H9NO5		1.755301234	0.599740492	0.36103926
Glutathione	C10H17N3O6S		1.636018766	0.742459007	0.433685751
Glutamate	C5H9NO4		2.005853639	0.823088815	0.484745253
Glutathione, oxidized	C20H32N6O12S2		1.993794444	0.5669591	0.303561382
threonate	C5H4N4O		1.949089668	0.427910377	0.245499005
Proline	C5H9NO2		1.515451031	0.543159996	0.340452905
Methionine	C5H11NO2S		1.572347379	0.352272269	0.223750496
Leucine	C6H13NO2		1.766841136	0.337800599	0.203229424
Tryptophan	C11H12N2O2		1.418563298	0.280034187	0.202749625
Phenylalanine	C9H11NO2		1.333741267	0.253337006	0.195052688
Valine	C5H11NO2		1.692251003	0.293496888	0.190441565
Tyrosine	C9H11NO3			0.240397451	0.178995778
Pantothenic Acid	C9H17NO5			0.2077143	0.176641307
Phosphocholine	C5H14NO4P			0.248512428	0.183715816
LysoPC(16:0)	C24H50NO7P			5.126478041	0.460760534
PC(16:0/22:5(4Z,7Z,10Z,13Z,16Z))	C46H82NO8P		4.368294498	2.823897618	0.586823833
LysoPC(18:1(11Z))	C26H52NO7P		7.203022065	2.059725778	0.24126696



Figure S4. The impact pathway analysis of A549 (-) and A549 (+) metabolites based on HMDB database.



Figure S5. The impact pathway analysis of A549 (+) and A549/DDP (+) metabolites based on HMDB database.



Figure S6. (A) Western blot bands of RRM2B in A549/DDP treated with negative siRNA (mock) and siRRM2B candidates. (B) Western blot bands of OPLAH in A549/DDP treated with negative siRNA (mock) and siOPLAH candidates.