



Figure S1 Quality control and normalization of scRNA-seq data (GSE134520). (A) nCount and nFeature of RNA expression range and percentages of mitochondria and ribosomes in NAG and EGC groups. (B) VlnPlot of cutoff value of nCount and nFeature of RNA expression and percentage of mitochondria in NAG and EGC groups. (C) Highly variable genes in EGC and NAG groups. (D) Between-group and phase (G1, G2M, and S) batch effect removal for EGC and NAG in UMAP, tSNE, and PCA plots. NAG, nonatrophic gastritis; EGC, early gastric cancer; PC, principal component; tSNE, t-distributed stochastic neighbor embedding; UMAP, uniform manifold approximation and projection; scRNA-seq, single-cell RNA sequencing; PCA, principal component analysis.

Table S2 Predictive analysis of cimifugin-anticancer drug interactions in multiple cancer cells

Drug A	Drug B	Drug A SMILES	Drug B SMILES	MolWt drug A	MolWt drug B	Heavy Atom Count drug A	Heavy Atom Count drug B	Ring Count drug A	Ring Count drug B	Num Rotatable Bonds drug A	Num Rotatable Bonds drug B	Donor Count drug A	Donor Count drug B	Acceptor Count drug A	Acceptor Count drug B	MolLogP drug A	MolLogP drug B	MELANOMA prediction	OVARIAN prediction	GENERAL prediction	LUNG prediction	BREAST prediction	COLON prediction	PROSTATE prediction
Cimifugin	Capecitabine	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	CCCCCOC(=O)NC1=NC(=O)N(C=C1F)C2C(C(O2)C)O)O	306.314	359.354	22	25	3	2	3	6	2	3	5	8	1.3683	0.7602	Antagonistic	Antagonistic	Antagonistic	Synergistic	Synergistic	Synergistic	
Cimifugin	Cisplatin	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	N.N.Cl[Pt]Cl	306.314	300.046	22	5	3	0	3	0	2	2	5	0	1.3683	1.7005	Synergistic	Synergistic	Synergistic	Antagonistic	Synergistic	Synergistic	
Cimifugin	5-FU	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	C1=C(C(=O)NC(=O)N1)F	306.314	130.078	22	9	3	1	3	0	2	2	5	3	1.3683	-0.7977	Antagonistic	Antagonistic	Synergistic	Antagonistic	Synergistic	Synergistic	
Cimifugin	Irinotecan	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	CCC1=C2CN3C(=CC4=C(C3=O)COC(=O)C4(CC)O)C2=NC5=C1C=C(C=C5)OC(=O)N6CCC(CC6)N7CCCCC7	306.314	586.689	22	43	3	7	3	4	2	3	5	7	1.3683	4.0911	Antagonistic	Antagonistic	Synergistic	Synergistic	Antagonistic	Antagonistic	
Cimifugin	Oxaliplatin	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	C1CCC(C(1)[NH-])[NH-].C(=O)(C(=O)O)O.[Pt+2]	306.314	397.288	22	15	3	1	3	0	2	2	5	4	1.3683	1.5551	Synergistic	Synergistic	Antagonistic	Synergistic	Antagonistic	Synergistic	
Cimifugin	Paclitaxel	CC(C)(C1CC2=C(O1)C=C3C(=C2OC)C(=O)C=C(O3)CO)O	CC1=C2C(C(=O)C3(C(CC4C(C3C(C(C2(C)C(CC1OC(=O)C(C(C5=CC=CC=C5)NC(=O)C6=CC=CC=C6)O)O)OC(=O)C7=CC=CC=C7)CO4)OC(=O)C)OC(=O)C)OC(=O)C	306.314	853.918	22	62	3	7	3	10	2	4	5	14	1.3683	3.7357	Antagonistic	Synergistic	Antagonistic	Antagonistic	Antagonistic	Synergistic	

SMILES, simplified molecular input line entry system; MolWt, molecular weight; NumRotatableBonds, number of rotatable bonds; MolLogP, molecular logarithm of partition coefficient; 5-FU, 5-fluorouracil.

Table S3 Eight core genes, cell types, and KEGG metabolic pathways mapping list

Gene name	Cell type	KEGG metabolic pathway	P value
AKR1B10	PMC	Folate biosynthesis	9.67E-08
	T cell	Folate biosynthesis	9.67E-08
	PMC	Fructose and mannose metabolism	0.057448
	T cell	Fructose and mannose metabolism	0.057448
	PMC	Galactose metabolism	0.001346
	T cell	Galactose metabolism	0.001346
	PMC	Glycerolipid metabolism	0.005303
	T cell	Glycerolipid metabolism	0.005303
	PMC	Pentose and glucuronate interconversions	0.060829
	T cell	Pentose and glucuronate interconversions	0.060829
AKR1C2	PMC	Chemical carcinogenesis—DNA adducts	0.000226
	PMC	Chemical carcinogenesis—reactive oxygen species	0.000527
	PMC	Steroid hormone biosynthesis	0.005303
AKR1C3	PMC	Arachidonic acid metabolism	0.005137
	PMC	Chemical carcinogenesis—reactive oxygen species	0.000527
	PMC	Folate biosynthesis	9.67E-08
	PMC	Ovarian steroidogenesis	0.08747
	PMC	Steroid hormone biosynthesis	0.005303
CA2	PMC	Collecting duct acid secretion	0.047238
	PMC	Nitrogen metabolism	0.029991
	PMC	Proximal tubule bicarbonate reclamation	0.040374
CBR1	PMC	Arachidonic acid metabolism	0.005137
	T cell	Arachidonic acid metabolism	0.005137
	PMC	Chemical carcinogenesis—DNA adducts	0.000226
	T cell	Chemical carcinogenesis—DNA adducts	0.000226
	PMC	Chemical carcinogenesis—reactive oxygen species	0.000527
	T cell	Chemical carcinogenesis—reactive oxygen species	0.000527
	PMC	Folate biosynthesis	9.67E-08
	T cell	Folate biosynthesis	9.67E-08
	PMC	Metabolism of xenobiotics by CYP	8.73E-06
	T cell	Metabolism of xenobiotics by CYP	8.73E-06
GSTA1	PMC	Chemical carcinogenesis—DNA adducts	0.000226
	PMC	Drug metabolism—CYP	0.000256
	PMC	Drug metabolism—other enzymes	0.008699
	PMC	Glutathione metabolism	0.004499
	PMC	Metabolism of xenobiotics by CYP	8.73E-06
MAOB	Endocrine cell	Drug metabolism—CYP	0.000256
	CMP	Drug metabolism—CYP	0.000256
	Endocrine cell	Glycine, serine and threonine metabolism	0.069232
	CMP	Glycine, serine and threonine metabolism	0.069232
	Endocrine cell	Histidine metabolism	0.000675
	CMP	Histidine metabolism	0.000675
	Endocrine cell	Phenylalanine metabolism	0.000353
	CMP	Phenylalanine metabolism	0.000353
	Endocrine cell	Tyrosine metabolism	0.001815
	CMP	Tyrosine metabolism	0.001815
PDE2A	Endocrine cell	Glycine, serine and threonine metabolism	0.069232

KEGG, Kyoto Encyclopedia of Genes and Genomes; CMP, common myeloid progenitor; CYP, cytochrome P450; PMC, pit mucous cell.