

Table S1 The list of the significant 114 differentially expressed ARGs

<i>ACTG2</i>	<i>BIRC5</i>	<i>CCL2</i>	<i>EEF1A2</i>	<i>FOXO1</i>	<i>MAP2K1</i>	<i>NLRP3</i>	<i>PKN3</i>	<i>RET</i>	<i>SLC36A1</i>	<i>TRAF2</i>	<i>UGT2B15</i>
<i>ALPI</i>	<i>BLK</i>	<i>CDK1</i>	<i>EPHA2</i>	<i>GABARAPL1</i>	<i>MAP2K3</i>	<i>NRG1</i>	<i>PLCG1</i>	<i>RIPK4</i>	<i>SLC3A1</i>	<i>TRAF5</i>	<i>UGT2B28</i>
<i>ALPL</i>	<i>BRSK1</i>	<i>CDKN2A</i>	<i>EPHA3</i>	<i>HCK</i>	<i>MELK</i>	<i>NRG2</i>	<i>PLD1</i>	<i>RPS6KA6</i>	<i>SLC7A10</i>	<i>TUSC1</i>	<i>UGT2B7</i>
<i>ANK3</i>	<i>BRSK2</i>	<i>DAPK2</i>	<i>EPHB1</i>	<i>HDAC4</i>	<i>MYC</i>	<i>NRG3</i>	<i>PNCK</i>	<i>SEC24B</i>	<i>SLC7A11</i>	<i>UGT1A1</i>	<i>VPS45</i>
<i>APOL1</i>	<i>CAMK2B</i>	<i>DES</i>	<i>EPHB2</i>	<i>IKBKE</i>	<i>MYD88</i>	<i>NTRK2</i>	<i>POC1A</i>	<i>SERPINA1</i>	<i>SLC7A6</i>	<i>UGT1A10</i>	
<i>ARHGAP10</i>	<i>CAPN11</i>	<i>DIRAS3</i>	<i>ERBB4</i>	<i>ITGA6</i>	<i>MYLK</i>	<i>NVL</i>	<i>PPP2R2C</i>	<i>SHC3</i>	<i>SLC7A8</i>	<i>UGT1A6</i>	
<i>ARHGAP42</i>	<i>CAPN12</i>	<i>DLC1</i>	<i>FGFR1</i>	<i>JUN</i>	<i>MYO3A</i>	<i>PAK7</i>	<i>PPP2R3B</i>	<i>SIK1</i>	<i>SPHK1</i>	<i>UGT1A9</i>	
<i>ARHGEF4</i>	<i>CAPN13</i>	<i>DNM3</i>	<i>FGFR2</i>	<i>KLHL17</i>	<i>NAMPT</i>	<i>PEA15</i>	<i>PRKAA2</i>	<i>SIPA1L3</i>	<i>TMEM74</i>	<i>UGT2A1</i>	
<i>AURKA</i>	<i>CAPN6</i>	<i>E2F1</i>	<i>FGR</i>	<i>KLHL2</i>	<i>NLRP12</i>	<i>PGA3</i>	<i>PRKCB</i>	<i>SLC1A1</i>	<i>TNIK</i>	<i>UGT2A3</i>	
<i>AXL</i>	<i>CAPN8</i>	<i>E2F2</i>	<i>FOS</i>	<i>LPIN2</i>	<i>NLRP14</i>	<i>PINK1</i>	<i>RCAN1</i>	<i>SLC1A2</i>	<i>TP73</i>	<i>UGT2B10</i>	

ARGs, autophagy-related genes.

Table S2 GO analyses results for the differentially expressed ARGs

ID	Ontology	Description	Gene ratio	BgRatio	P value	P.adjust	q value	Gene ID	Count	Rich factor
GO:0052695	BP	Cellular glucuronidation	9/112	19/18,670	6.37E-16	1.73E-12	1.30E-12	<i>UGT1A1/UGT1A10/UGT1A6/UGT1A9/UGT2A1/UGT2A3/UGT2B15/UGT2B28/UGT2B7</i>	9	0.47
GO:0046777	BP	Protein autophosphorylation	18/112	235/18,670	3.25E-15	4.42E-12	3.31E-12	<i>AURKA/BLK/CAMK2B/DAPK2/EPHB1/ERBB4/FGFR1/FGFR2/FGR/HCK/JUN/MELK/MYO3A/NLRP12/NTRK2/PINK1/SIK1/TNIK</i>	18	0.08
GO:0006063	BP	Uronic acid metabolic process	9/112	24/18,670	8.80E-15	5.98E-12	4.48E-12	<i>UGT1A1/UGT1A10/UGT1A6/UGT1A9/UGT2A1/UGT2A3/UGT2B15/UGT2B28/UGT2B7</i>	9	0.38
GO:0019585	BP	Glucuronate metabolic process	9/112	24/18,670	8.80E-15	5.98E-12	4.48E-12	<i>UGT1A1/UGT1A10/UGT1A6/UGT1A9/UGT2A1/UGT2A3/UGT2B15/UGT2B28/UGT2B7</i>	9	0.38
GO:0018108	BP	Peptidyl-tyrosine phosphorylation	17/112	363/18,670	5.60E-11	2.89E-08	2.16E-08	<i>AXL/BLK/EPHA2/EPHA3/EPHB1/EPHB2/ERBB4/FGFR1/FGFR2/FGR/HCK/MAP2K1/MAP2K3/MELK/NRG1/NTRK2/RET</i>	17	0.05
GO:0018212	BP	Peptidyl-tyrosine modification	17/112	366/18,670	6.37E-11	2.89E-08	2.16E-08	<i>AXL/BLK/EPHA2/EPHA3/EPHB1/EPHB2/ERBB4/FGFR1/FGFR2/FGR/HCK/MAP2K1/MAP2K3/MELK/NRG1/NTRK2/RET</i>	17	0.05
GO:0052697	BP	Xenobiotic glucuronidation	5/112	11/18,670	3.19E-09	1.24E-06	9.28E-07	<i>UGT1A1/UGT1A10/UGT1A6/UGT1A9/UGT2B28</i>	5	0.45
GO:0015807	BP	L-amino acid transport	8/112	67/18,670	6.33E-09	2.15E-06	1.61E-06	<i>SLC1A1/SLC1A2/SLC36A1/SLC3A1/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	8	0.12
GO:0051090	BP	Regulation of DNA-binding transcription factor activity	15/112	432/18,670	4.64E-08	1.27E-05	9.55E-06	<i>CDKN2A/FOS/HCK/HDAC4/JUN/MYD88/NLRP12/NLRP3/PINK1/PRKCB/RIPK4/SIK1/SPHK1/TRAF2/TRAF5</i>	15	0.09
GO:0003333	BP	Amino acid transmembrane transport	8/112	86/18,670	4.69E-08	1.27E-05	9.55E-06	<i>SLC1A1/SLC1A2/SLC36A1/SLC3A1/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	8	0.03
GO:1903825	BP	Organic acid transmembrane transport	9/112	135/18,670	1.21E-07	2.74E-05	2.05E-05	<i>PRKAA2/SLC1A1/SLC1A2/SLC36A1/SLC3A1/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	9	0.07
GO:1905039	BP	Carboxylic acid transmembrane transport	9/112	135/18,670	1.21E-07	2.74E-05	2.05E-05	<i>PRKAA2/SLC1A1/SLC1A2/SLC36A1/SLC3A1/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	9	0.07
GO:0006865	BP	Amino acid transport	9/112	145/18,670	2.23E-07	4.67E-05	3.50E-05	<i>NTRK2/SLC1A1/SLC1A2/SLC36A1/SLC3A1/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	9	0.06
GO:0043491	BP	Protein kinase B signaling	11/112	269/18,670	6.57E-07	0.000127654	9.57E-05	<i>AXL/CCL2/EPHA2/ERBB4/FGFR1/FGFR2/NRG1/NRG2/NTRK2/PINK1/RET</i>	11	0.04
GO:1902475	BP	L-alpha-amino acid transmembrane transport	6/112	53/18,670	7.43E-07	0.000134715	0.000100969	<i>SLC1A1/SLC1A2/SLC7A10/SLC7A11/SLC7A6/SLC7A8</i>	6	0.11
GO:0071496	BP	Cellular response to external stimulus	12/112	339/18,670	9.19E-07	0.000156212	0.000117081	<i>AXL/FOS/FOXO1/GABARAPL1/HDAC4/ITGA6/JUN/MYD88/NAMPT/PRKAA2/SIK1/SLC1A2</i>	12	0.04
GO:0005996	BP	Monosaccharide metabolic process	11/112	292/18,670	1.47E-06	0.000234962	0.000176104	<i>FOXO1/SIK1/UGT1A1/UGT1A10/UGT1A6/UGT1A9/UGT2A1/UGT2A3/UGT2B15/UGT2B28/UGT2B7</i>	11	0.04
GO:0009812	BP	Flavonoid metabolic process	4/112	15/18,670	1.59E-06	0.000240461	0.000180226	<i>UGT1A1/UGT1A10/UGT1A6/UGT1A9</i>	4	0.27
GO:0034599	BP	Cellular response to oxidative stress	11/112	302/18,670	2.04E-06	0.000289709	0.000217137	<i>AXL/CDK1/FOS/FOXO1/JUN/MELK/PINK1/PRKAA2/SLC7A11/SPHK1/TRAF2</i>	11	0.04
GO:0051896	BP	Regulation of protein kinase B signaling	10/112	244/18,670	2.13E-06	0.000289709	0.000217137	<i>AXL/EPHA2/ERBB4/FGFR1/FGFR2/NRG1/NRG2/NTRK2/PINK1/RET</i>	10	0.04

GO, Gene Ontology; ARGs, autophagy-related genes; BP, biological process.

Table S3 KEGG pathway analyses results for the differentially expressed ARGs

ID	Description	Gene ratio	BgRatio	P value	P.adjust	q value	Gene ID	Count	Rich factor
hsa00053	Ascorbate and aldarate metabolism	10/88	27/8,048	1.05E-13	2.13E-11	1.10E-11	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.37
hsa00040	Pentose and glucuronate interconversions	10/88	34/8,048	1.53E-12	1.55E-10	8.06E-11	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.29
hsa00860	Porphyrin and chlorophyll metabolism	10/88	42/8,048	1.60E-11	1.08E-09	5.62E-10	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.24
hsa00140	Steroid hormone biosynthesis	10/88	61/8,048	8.29E-10	4.21E-08	2.18E-08	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.16
hsa04012	ErbB signaling pathway	11/88	85/8,048	1.56E-09	6.32E-08	3.27E-08	816/2066/3725/5604/4609/3084/9542/10718/5335/5579/53358	11	0.13
hsa00830	Retinol metabolism	10/88	68/8,048	2.51E-09	8.50E-08	4.41E-08	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.15
hsa00982	Drug metabolism—cytochrome P450	10/88	71/8,048	3.88E-09	1.13E-07	5.84E-08	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.14
hsa00980	Metabolism of xenobiotics by cytochrome P450	10/88	76/8,048	7.68E-09	1.95E-07	1.01E-07	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.13
hsa00983	Drug metabolism—other enzymes	10/88	79/8,048	1.13E-08	2.55E-07	1.32E-07	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.13
hsa05204	Chemical carcinogenesis	10/88	82/8,048	1.63E-08	3.31E-07	1.72E-07	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.12
hsa04976	Bile secretion	10/88	90/8,048	4.06E-08	7.50E-07	3.89E-07	54658/54575/54578/54600/10941/79799/7365/7366/54490/7364	10	0.11
hsa05167	Kaposi sarcoma-associated herpesvirus infection	12/88	189/8,048	8.57E-07	1.45E-05	7.52E-06	1869/1870/2353/23710/3055/9641/3725/5604/4609/5335/1827/7186	12	0.06
hsa05161	Hepatitis B	11/88	162/8,048	1.32E-06	1.86E-05	9.65E-06	332/1869/1870/2353/9641/3725/5604/5606/4609/4615/5579	11	0.08
hsa05135	Yersinia infection	10/88	130/8,048	1.33E-06	1.86E-05	9.65E-06	6347/2353/3725/5604/5606/4615/114548/5335/27330/7186	10	0.07
hsa05214	Glioma	8/88	75/8,048	1.37E-06	1.86E-05	9.65E-06	816/1029/1869/1870/5604/5335/5579/53358	8	0.11
hsa01521	EGFR tyrosine kinase inhibitor resistance	8/88	79/8,048	2.05E-06	2.60E-05	1.35E-05	558/2263/5604/3084/9542/5335/5579/53358	8	0.1
hsa04010	MAPK signaling pathway	14/88	294/8,048	3.11E-06	3.72E-05	1.93E-05	1969/2066/2260/2263/2353/3725/5604/5606/4609/4615/4915/5579/27330/7186	14	0.05
hsa05219	Bladder cancer	6/88	41/8,048	4.76E-06	5.37E-05	2.78E-05	1029/23604/1869/1870/5604/4609	6	0.15
hsa04621	NOD-like receptor signaling pathway	10/88	181/8,048	2.55E-05	0.000272775	0.000141444	6347/23710/9641/3725/4615/10135/91662/114548/7186/7188	10	0.06
hsa04722	Neurotrophin signaling pathway	8/88	119/8,048	4.32E-05	0.000438944	0.000227609	816/3725/5604/4915/5335/27330/53358/7161	8	0.07

KEGG, Kyoto Encyclopedia of Genes and Genomes; ARGs, autophagy-related genes.

Table S4 Univariate Cox regression analysis results for the differentially expressed ARGs significantly related to the OS outcomes of HCC patients

Gene symbol	Coef	SE	z	P	HR	HRse	HRz	HRp	HRCILL	HRCIUL
<i>BIRC5</i>	0.758	0.195	3.885	0	2.134	0.416	2.724	0.006	1.548	2.941
<i>PNCK</i>	0.678	0.194	3.498	0	1.969	0.382	2.541	0.011	1.432	2.708
<i>E2F2</i>	0.665	0.192	3.463	0.001	1.944	0.373	2.53	0.011	1.418	2.666
<i>SLC7A11</i>	0.586	0.191	3.072	0.002	1.796	0.343	2.325	0.02	1.313	2.458
<i>CDK1</i>	0.58	0.19	3.048	0.002	1.786	0.34	2.313	0.021	1.306	2.442
<i>MELK</i>	0.548	0.19	2.888	0.004	1.73	0.328	2.223	0.026	1.266	2.364
<i>E2F1</i>	0.517	0.191	2.702	0.007	1.676	0.321	2.11	0.035	1.224	2.296
<i>AURKA</i>	0.501	0.189	2.649	0.008	1.651	0.312	2.084	0.037	1.209	2.253
<i>SLC36A1</i>	0.499	0.191	2.619	0.009	1.648	0.314	2.062	0.039	1.204	2.255
<i>CDKN2A</i>	0.447	0.188	2.372	0.018	1.563	0.294	1.913	0.056	1.147	2.131
<i>UGT1A6</i>	0.447	0.19	2.349	0.019	1.564	0.298	1.894	0.058	1.143	2.138
<i>BRSK1</i>	0.424	0.19	2.234	0.025	1.528	0.29	1.821	0.069	1.118	2.088
<i>VPS45</i>	0.398	0.189	2.109	0.035	1.489	0.281	1.74	0.082	1.092	2.032
<i>SPHK1</i>	0.386	0.188	2.052	0.04	1.471	0.277	1.703	0.089	1.08	2.005
<i>NTRK2</i>	-0.391	0.189	-2.074	0.038	0.676	0.128	-2.538	0.011	0.496	0.922
<i>DLC1</i>	-0.424	0.19	-2.228	0.026	0.654	0.125	-2.775	0.006	0.479	0.895
<i>RIPK4</i>	-0.425	0.19	-2.233	0.026	0.654	0.124	-2.783	0.005	0.478	0.894
<i>CAPN11</i>	-0.434	0.189	-2.29	0.022	0.648	0.123	-2.867	0.004	0.475	0.885
<i>PLD1</i>	-0.436	0.19	-2.286	0.022	0.647	0.123	-2.865	0.004	0.473	0.885
<i>DNM3</i>	-0.44	0.189	-2.332	0.02	0.644	0.122	-2.929	0.003	0.472	0.878
<i>FOXO1</i>	-0.453	0.192	-2.364	0.018	0.635	0.122	-2.991	0.003	0.464	0.871
<i>LPIN2</i>	-0.578	0.191	-3.027	0.002	0.561	0.107	-4.099	0	0.41	0.768
<i>GABARAPL1</i>	-0.616	0.192	-3.202	0.001	0.54	0.104	-4.426	0	0.394	0.741

ARGs, autophagy-related genes; OS, overall survival; HCC, hepatocellular carcinoma; coef, coefficient; SE, standard error; HR, hazard ratio; HRse, hazard ratio standard error; HRz, hazard ratio z-score; HRp, hazard ratio P value; HRCILL, hazard ratio confidence interval lower limit; HRCIUL, hazard ratio confidence interval upper limit.