

SUPPLEMENTARY TABLES

Supplementary Table 1. Cox regression analysis of 72 differentially expressed autophagy-related genes in gliomablastoma patients

Gene	Univariate analysis			Multivariate analysis		
	HR	z	pvalue	HR	z	pvalue
CXCR4	1.12752231	1.36150731	0.17335342	-	-	-
MAP1LC3C	1.09214902	1.51592606	0.12953805	-	-	-
IL24	1.09055155	1.02655736	0.30462894	-	-	-
CASP1	1.09631446	1.05763629	0.29022129	-	-	-
APOL1	1.03878724	0.56953867	0.56899063	-	-	-
PARK2	1.1116884	1.05253107	0.29255596	-	-	-
GRID1	0.96610039	-0.4636662	0.64288692	-	-	-
RB1CC1	1.05469152	0.4335599	0.66460806	-	-	-
WDFY3	0.97232968	-0.2591414	0.79552617	-	-	-
EGFR	0.96155822	-0.9756129	0.32925635	-	-	-
ERBB2	1.15572387	1.78927734	0.07357016	-	-	-
NRG3	1.02157032	0.41012589	0.6817136	-	-	-
HDAC1	0.9681987	-0.2503851	0.80228957	-	-	-
CASP4	1.27332956	2.31674033	0.02051788	-	-	-
MAPK8IP1	1.01901845	0.2236201	0.82305292	-	-	-
RPTOR	1.06053203	0.55691437	0.57758593	-	-	-
AMBRA1	1.10502149	0.88581859	0.37571529	-	-	-
SERPINA1	1.15201256	1.96520121	0.04939095	-	-	-
DAPK2	1.15644409	1.62702842	0.10373106	-	-	-
CASP3	1.19157365	1.61187975	0.10698811	-	-	-
DIRAS3	1.16347952	2.53110692	0.01137032	-	-	-
IFNG	1.21783781	1.31300654	0.18918075	-	-	-
PINK1	1.11048638	0.9324178	0.35112065	-	-	-
ATG2B	1.02325887	0.21985061	0.82598751	-	-	-
BIRC5	1.03313466	0.47552664	0.63441165	-	-	-
CTSB	1.31560381	2.54009925	0.0110821	-	-	-
ITGB1	1.04985848	0.45753454	0.64728688	-	-	-
MAPK1	0.92472275	-0.7449741	0.45628737	-	-	-
IKBKB	1.08210872	0.59394047	0.55255193	-	-	-
MAPK8	0.91317847	-0.9090328	0.36333282	-	-	-
PRKCQ	0.93580259	-0.8419977	0.39978924	-	-	-
ULK1	1.16006405	1.17391162	0.24043043	-	-	-
DRAM1	1.21266735	1.9069304	0.0565296	-	-	-
FKBP1B	1.37459207	2.92057153	0.0034939	-	-	-
GNB2L1	0.83523584	-1.2999676	0.19361207	-	-	-
MAPK3	1.12040281	0.81243541	0.41654183	-	-	-
NRG1	1.14389011	2.74819125	0.0059925	1.14157962	2.66231234	0.00776058

ITGA3	1.19112653	2.68707229	0.00720814	1.14941814	2.02128687	0.04325008
VEGFA	1.08260766	1.50294174	0.13285407	-	-	-
MYC	0.9135298	-1.0194185	0.30800432	-	-	-
ATG4A	1.05172571	0.34005326	0.73381642	-	-	-
CDKN1A	1.10613952	1.36952825	0.17083421	-	-	-
GNAI3	0.9559024	-0.2984975	0.76532347	-	-	-
FAS	1.16693931	1.89196524	0.05849561	-	-	-
PRKCD	1.16153179	1.51380892	0.13007431	-	-	-
TP73	0.95783626	-0.8832974	0.37707559	-	-	-
TMEM74	1.02652779	0.43315698	0.66490073	-	-	-
MAPK9	1.11804113	0.81646607	0.41423362	-	-	-
ITPR1	1.21698874	1.86942202	0.06156412	-	-	-
CX3CL1	0.99173975	-0.0990952	0.92106272	-	-	-
IKBKE	1.2062973	1.64515448	0.09993796	-	-	-
HIF1A	0.93383523	-0.7361781	0.4616223	-	-	-
TUSC1	1.12449246	1.6239062	0.10439583	-	-	-
ULK2	1.0903667	0.79924586	0.42414787	-	-	-
CAMKK2	1.10383881	0.71073959	0.47724562	-	-	-
CDKN2A	0.96348157	-1.178491	0.23860092	-	-	-
DAPK1	0.99689091	-0.0375145	0.97007475	-	-	-
BAK1	0.93815456	-0.4304121	0.66689588	-	-	-
NAMPT	1.12745712	1.8547772	0.06362805	-	-	-
TSC1	0.96762564	-0.3495673	0.72666347	-	-	-
EIF4EBP1	1.0262793	0.20731651	0.83576268	-	-	-
TP53	0.92835436	-0.8075141	0.41937034	-	-	-
MAP1LC3A	1.39894856	3.17692527	0.00148845	1.30823622	2.46357359	0.01375597
CASP8	1.08199498	0.71583924	0.47409062	-	-	-
RGS19	1.21061651	1.30953568	0.19035296	-	-	-
CCR2	1.11426965	1.70918135	0.08741736	-	-	-
PRKAR1A	1.1494814	1.06072757	0.28881373	-	-	-
GABARAPL1	1.13059973	1.18350566	0.23660881	-	-	-
P4HB	1.35062977	2.14162036	0.03222404	-	-	-
PTK6	0.95966931	-0.6245504	0.53226621	-	-	-
BAX	1.06447347	0.52869632	0.59701613	-	-	-
TP63	1.12260577	2.22352058	0.02618072	-	-	-

Please browse Full Text version to see the data of Supplementary Tables 2 and 3.

Supplementary Table 2. GSEA reports for high ITGA3, MAP1LC3A, and NRG1 expression groups in TCGA-GBM cohort.

Supplementary Table 3. GSEA reports for ATG-based high-risk and low-risk group in TCGA-GBM cohort.