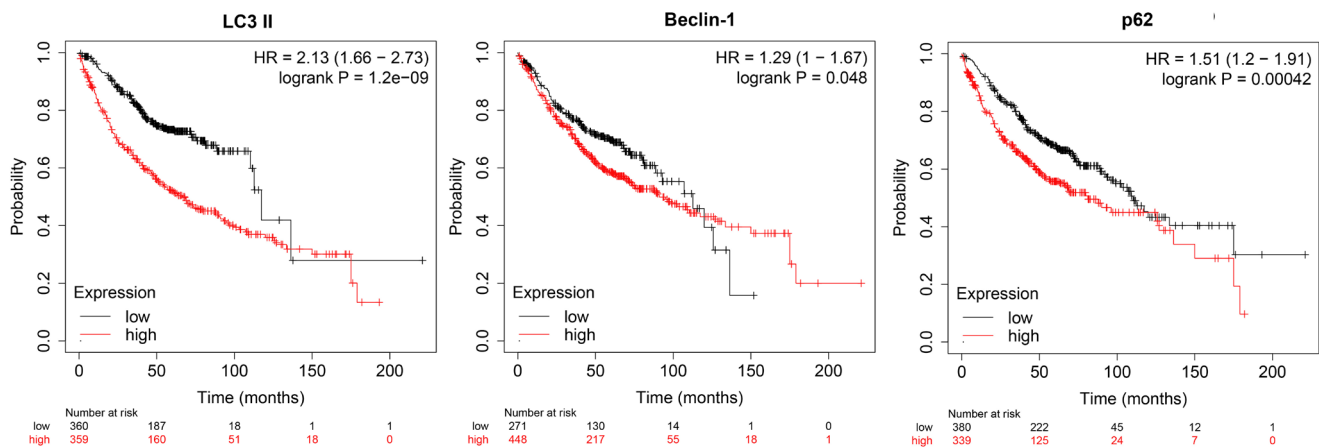


Table S1 The forward and reverse primer sequences of autophagy RT2 Profiler™ PCR Array

Primers	5' to 3'
Cav1-F	GCGACCCTAAACACCTCAAC
Cav1-R	ATGCCGTCAAAACTGTGTGTC
Actin-F	CATGTACGTTGCTATCCAGGC
Actin-R	CTCCTTAATGTCACGCACGAT
AKT1-F	GTCATCGAACGCACCTCCAT
AKT1-R	AGCTTCAGGTACTCAAACCTCGT
AMBRA1-F	TGGGGAGGTTAGGATTTGGGA
AMBRA1-R	GAGCCGTAGGGTGGAAAGC
APP-F	GCCCTGCGGAATTGACAAAG
APP-R	CCATCTGCATAGTCTGTGCTG
ATG10-F	ATAAGATGCGACTGCTACAGGG
ATG10-R	CAATGCTCAGCCATGATGTGAT
ATG12-F	TAGAGCGAACACGAACCATCC
ATG12-R	CACCTGCCCCAACTCATAGAGA
ATG16L1-F	AACGCTGTGCAGTTCAGTCC
ATG16L1-R	AGCTGCTAAGAGGTAAGATCCA
ATG16L2-F	TTAGCAGCAACTTACAACCAGG
ATG16L2-R	ACACCACGCTATTACAGTAGGA
ATG3-F	GATGGCGGATGGGTAGATACA
ATG3-R	TCTTCACATAGTCTGAGCAATC
ATG4A-F	TGCTGGTTGGGGATGTATGC
ATG4A-R	GCGTTGGTATCTTTGGGTTGT
ATG4B-F	GGTGTGGACAGATGATCTTGC
ATG4B-R	CCAACTCCCATTTGCGCTATC
ATG4C-F	ACCCCAACAATTTCTCTGAAGG
ATG4C-R	GTCCATACCAATCTCCTGCTTTT
ATG4D-F	CCAGCCCACTGTGGATGTC
ATG4D-R	AAGCCCACGGTACAGCTTG
ATG5-F	AGAAGCTGTTTCGTCTGTGG
ATG5-R	AGGTGTTTCCAACATTGGCTC
ATG7-F	ATGATCCCTGTAACCTAGCCCA
ATG7-R	CACGGAAGCAAACTTCAAC
ATG9A-F	CCAGAATACATGGTGGCACT
ATG9A-R	GTCCCCAGAAAGAGGATCAGC
ATG9B-F	TGTGCTCACCGTCTACGAC
ATG9B-R	GGGAGGTAGTGCATGTGGG
BAD-F	CCCAGAGTTTGAGCCGAGTG
BAD-R	CCCATCCCTTCGTCTGCTCCT
BAK1-F	CATCAACCGACGCTATGACTC
BAK1-R	GTCAGGCCATGCTGGTAGAC
BAX-F	CCCAGAGGTTCTTTTCCGAG
BAX-R	CCAGCCCATGATGGTCTGAT
BCL2L1-F	GACTGAATCGGAGATGGAGACC
BCL2L1-R	GCAGTCAAACTCGTCGCCT
BECN1-F	ACCTCAGCCGAAGACTGAAG
BECN1-R	AACAGCGTTTGTAGTTCTGACA
BID-F	ATGGACCGTAGCATCCCTCC
BID-R	GTAGGTGCGTAGGTTCTGGT
BNIP3-F	TGAGTCTGGACGGAGTAGCTC
BNIP3-R	CCCTGTTGGTATCTTGTGGTGT
CASP3-F	GAAATGTGGAATTGATGCGTGA
CASP3-R	CTACAACGATCCCCTCTGAAAAA
CASP8-F	CCAGAGACTCCAGGAAAAGAGA
CASP8-R	GATAGAGCATGACCCTGTAGGC
CDKN1B-F	TAATTGGGGCTCCGGCTAACT
CDKN1B-R	TGCAGGTCGCTTCCTTATTC
CDKN2A-F	ATGGAGCCTTCGGCTGACT
CDKN2A-R	GTAACATTCGGTGGTTGGG
CLN3-F	GCCTCTCCCTTCGGGAAAG
CLN3-R	CCCTGTTTAATGAAATACTCGGC
CTSB-F	AGAGTTATGTTTACCAGGACCT
CTSB-R	GATGCAGATCCGGTCAGAGA
CTSD-F	ATTCAGGGCGAGTACATGATCC
CTSD-R	CGACACCTTGAGCGTGTAG
CTSS-F	TGACAACGGCTTTCCAGTACA
CTSS-R	GGCAGCACGATATTTGAGTCAT
CXCR4-F	ACGCCACCAACAGTCAGAG
CXCR4-R	AGTCGGGAATAGTCAGCAGGA
DAPK1-F	GAGTTTGTGCTCCTGAGATAGT
DAPK1-R	GCTTAGTGTCTCCAAGAAATGGG
DRAM1-F	AGTGCTTGATTGGTGGGATG
DRAM1-R	GATGGACTGTAGGAGCGTGTA
DRAM2-F	CTGTGCTTACCCTTGGTATGGG
DRAM2-R	GCACTTACTCCACACAGATAAC
EIF2AK3-F	GGAACGAGAGCGGATTTATT
EIF2AK3-R	ACTATGTCCATTATGGCAGCTC
EIF4G1-F	CCCGAAAAGAACCCAGCAAG
EIF4G1-R	TTCCCTCGATCCTTATCAGC
ESR1-F	GAAAGGTGGGATACGAAAAGACC
ESR1-R	GCTGTTCTTCTTAGAGCGTTTGA
FADD-F	GTGGCTGACCTGGTACAAGAG
FADD-R	GGTAGATGCGTCTGAGTCCAT
FAS-F	AGATTGTGTGATGAAGGACATGG
FAS-R	TGTTGCTGGTGAAGTGTGATT
GAA-F	TGCCCTCGCAGTATATCACAG
GAA-R	GAGACCCGTAGAGGTTCCG
GABARAP-F	AGAAGAGCATCCGTTGAGAA
GABARAP-R	CCAGGTCTCCTATCCGAGCTT
GABARAPL1-F	ATGAAGTTCCAGTACAAGGAGGA
GABARAPL1-R	GCTTTTGGAGCCTTCTTACAAT
GABARAPL2-F	AGGTCTCAGGCTCTCAGATTG
GABARAPL2-R	ACAGGAAGATCGCCTTTTCAGA
HDAC1-F	CGCCCTCACAAGCCAATG
HDAC1-R	CTGCTTGTGCTACTCCGACA
HDAC6-F	ACCCAGTGTCTCTATTCTC
HDAC6-R	CCTGGTTCCAAGGCACATTGA
HGS-F	GAGACAGAAGTCCAGTACACT
HGS-R	CGTTGAGATACCGTCCGAG
HSP90AA1-F	GCTTGACCAATGACTGGGAAG
HSP90AA1-R	AGCTCCTCACAGTTATCCATGA
HSPA8-F	ACTCCAAGCTATGTCGCCTTT
HSPA8-R	TGGCATCAAAAACCTGTGTTGGT
HTT-F	GCTCTTAGGCTTACTCGTTCCT
HTT-R	TTCCCTGTCACTCCGAAGCTG
IFNG-F	TCGGTAACTGACTTGAATGTCCA
IFNG-R	TCGCTTCCCTGTTTTAGCTGC
IGF1-F	GCTCTCAGTTGTTGTTGGGA
IGF1-R	GCCTCCTTAGATCACAGCTCC
INS-F	GCAGCCTTTGTGAACCAACAC
INS-R	CCCCGCACACTAGGTAGAGA
IRGM-F	CCTCACCTCCTACTGAGCTG
IRGM-R	GTTTTGGCAAGCATCACATGATT
LAMP1-F	CACGAGAAATGCAACACGTTAC
LAMP1-R	GGGTGCCACTAACACATCTGTAT
MAP1LC3A-F	AACATGAGCGAGTTGGTCAAG
MAP1LC3A-R	GCTCGTAGATGTCGCGGAT
MAP1LC3B-F	AAGGCGCTTACAGCTCAATG
MAP1LC3B-R	CTGGGAGGCATAGACCATGT
MAPK14-F	CTGTTGGACGTTTTTACACCTGC
MAPK14-R	AGACCTCGGAGAAATTTGGTAGA
MAPK8-F	TGTTGGAATCAAGCACCTTC
MAPK8-R	AGGCGTCATCATAAACTCGTTC
MTOR-F	TCCGAGAGATGATCAAGAGG
MTOR-R	CACCTTCCACTCCTATGAGGC
NFKB1-F	GAAGCAGCAATGACAGAGGC
NFKB1-R	GCTTGGCGGATTAGCTCTTTT
NPC1-F	GTCTCCGAGTACACTCCCATC
NPC1-R	CGCAGTAATGAAGACCAGCGA
PIK3C3-F	GTCTGGCCTAATGTAGAAGCAG
PIK3C3-R	GGCAAGACGGCTCATCTGAT
PIK3CG-F	GGCGAAAACGCCCATCAAAA
PIK3CG-R	GACTCCCGTGCAGTCAATCC
PIK3R4-F	GCTCTTAGGCGAGTATGTGCG
PIK3R4-R	GATGTCCCAGTACGCAACTCC
PRKAA1-F	GGCACGCCATACCTTGAT
PRKAA1-R	TCTTCTCTGTCACAGCAAATAA
PTEN-F	TTTGAAGACCATAACCACCAC
PTEN-R	ATTACACCAGTTCGTCCTTTT
RAB24-F	TCTGGGTGAAGGAACTGCG
RAB24-R	ACTGACGTAATCCTCTGCCAC
RB1-F	CACCTTTGTAACGCCTTCTGT
RB1-R	CACGTTTGAATGCTCCTGAACA
RGS19-F	GGCGCAGTCTTTTGAACAGC
RGS19-R	GCCTTCTCGTCTACCACATGC
RPS6KB1-F	AGAACTCTGGCTCGAAAGGT
RPS6KB1-R	CGACAGGTGTCTGACGTGTAA
SNCA-F	AAGAGGGTGTCTCTATGAGGC
SNCA-R	GCTCCTCCAACATTTGTCACTT
SQSTM1-F	GACTACGACTTGTGTAGCGTC
SQSTM1-R	AGTGTCCGTGTTTACCTTCC
TGFB1-F	CAATTCCTGGCGATACCTCAG
TGFB1-R	GCACAACCTCCGGTGACATCAA
TGM2-F	CGTGACCAACTACAACCTCGG
TGM2-R	CATCCACGACTCCACCCAG
TMEM74-F	AAATAACAGCGGAACGGAAAGT
TMEM74-R	CTTGGGACCCTCATTTTGGATT
TNF-F	GAGGCCAAGCCCTGGTATG
TNF-R	CGGGCCGATTGATCTCAGC
TNFSF10-F	TGCGTGTGATCGTGTCTTCC
TNFSF10-R	GCTCGTTGGTAAAGTACACGTA
ULK1-F	CCAGAGCAACATGATGGCG
ULK1-R	CCTTCCCGTGTAGTGCTG
ULK2-F	GTGGTATTCGCATCAAAATAGCG
ULK2-R	CACAAGTACAGCCTTAGCATATA
UVRAG-F	CTTGGGTACAGCAGATTATGC
UVRAG-R	CATCGTAAAGAAATTCGAAACACAG
WIPI1-F	AACAGGTCTATGTCTCTCTCT
WIPI1-R	CTCATGGGCAGCAATAGTGC
bcl2-F	GGTGGGTGCATGTGTGG
bcl2-R	CGGTTTCAAGTACTCAGTCACTC
TP53-F	GAGGTTGGCTCTGACTGTACC
TP53-R	TCCGTCACAGTAGATTACCAC

**Table S2** The expression profiles of 84 genes via autophagy RT2 Profiler™ PCR Array in H358-IRR and A549-IRR cells

Gene name	H358R-siNC	H358R-sicav1	Foldchange	Gene name	A549R-siNC	A549R-sicav1	Foldchange
<i>IGF1</i>	0.6983	1.5453	2.2129	<i>GAA</i>	0.3839	2.4228	6.3104
<i>CASP8</i>	0.8044	1.6487	2.0497	<i>CDKN2A</i>	0.2858	1.4915	5.219
<i>CTSD</i>	0.551	0.9734	1.7666	<i>IFNG</i>	0.4703	1.6279	3.4613
<i>SQSTM1</i>	0.2858	0.4954	1.7336	<i>IGF1</i>	0.6133	1.2875	2.0994
<i>GABARAPL1</i>	1	1.5294	1.5294	<i>Tp53</i>	0.9446	1.7918	1.8968
<i>ATG9B</i>	0.4307	0.6575	1.5266	<i>LAMP1</i>	0.8471	1.5695	1.8528
<i>HDAC6</i>	1	1.4852	1.4852	<i>TGM2</i>	0.2416	0.4354	1.8022
<i>BCL2L1</i>	0.5207	0.7624	1.4644	<i>tnfsf10</i>	0.9945	1.7918	1.8018
<i>CASP3</i>	1	1.4201	1.4201	<i>FAS</i>	1.3471	2.4228	1.7985
<i>MAP1LC3A</i>	0.0888	0.1245	1.4024	<i>TGFB1</i>	1.0247	1.7918	1.7486
<i>HSP90AA1</i>	0.8754	1.2158	1.3889	<i>GABARAPL1</i>	0.8727	1.503	1.7221
<i>CLN3</i>	0.7175	0.963	1.3421	<i>PIK3C3</i>	0.3255	0.5546	1.7036
<i>IFNG</i>	1	1.3018	1.3018	<i>SNCA</i>	0.009	0.015	1.6734
<i>ATG4A</i>	1	1.283	1.283	<i>HGS</i>	0.9768	1.6245	1.6631
<i>MAPK14</i>	1	1.2771	1.2771	<i>BID</i>	1.1697	1.9193	1.6409
<i>CXCR4</i>	0.3389	0.4229	1.248	<i>HTT</i>	0.7118	1.1225	1.577
<i>EIF2AK3</i>	1	1.2359	1.2359	<i>ATG10</i>	0.8286	1.2813	1.5463
<i>rb1</i>	1	1.2285	1.2285	<i>MAPK14</i>	0.8386	1.2941	1.5431
<i>GABARAPL2</i>	0.8704	1.041	1.196	<i>RGS19</i>	1.1394	1.6973	1.4896
<i>GAA</i>	0.153	0.1827	1.1943	<i>ATG4A</i>	1.1794	1.7491	1.483
<i>BAD</i>	0.7227	0.861	1.1915	<i>MAP1LC3A</i>	1.4372	2.0599	1.4333
<i>DRAM1</i>	0.7594	0.9022	1.1881	<i>DRAM1</i>	1.6987	2.4228	1.4263
<i>CTSB</i>	0.5014	0.5222	1.0415	<i>BCL2L1</i>	1.3625	1.9193	1.4087
<i>MTOR</i>	1	1.0342	1.0342	<i>ATG5</i>	1.0312	1.4508	1.4069
<i>BAX</i>	1	0.9878	0.9878	<i>MTOR</i>	0.9046	1.2663	1.3998
<i>MAP1LC3B</i>	1	0.9807	0.9807	<i>ulk1</i>	1.0789	1.5038	1.3939
<i>APP</i>	1	0.9635	0.9635	<i>BNIP3</i>	0.3849	0.5344	1.3883
<i>HDAC1</i>	0.8404	0.8096	0.9634	<i>FADD</i>	1.1882	1.6052	1.3509
<i>FADD</i>	1	0.9615	0.9615	<i>CTSB</i>	1.8356	2.4228	1.3199
<i>FAS</i>	0.578	0.5435	0.9402	<i>APP</i>	1.2544	1.5981	1.2739
<i>ATG12</i>	1	0.934	0.934	<i>GABARAPL2</i>	1.9313	2.4228	1.2545
<i>ulk1</i>	1.0696	0.9792	0.9155	<i>ATG4C</i>	0.6484	0.8116	1.2517
<i>ATG10</i>	1	0.9053	0.9053	<i>ATG4B</i>	0.4759	0.589	1.2377
<i>MAPK8</i>	1	0.8975	0.8975	<i>RPS6KB1</i>	1.1394	1.395	1.2243
<i>CTSS</i>	0.0357	0.0317	0.8881	<i>uvrag</i>	1.1394	1.378	1.2094
<i>HTT</i>	1	0.8858	0.8858	<i>HSP90AA1</i>	1.4372	1.7367	1.2085
<i>ATG5</i>	1	0.8769	0.8769	<i>ATG16L1</i>	1.0045	1.2131	1.2076
<i>PRKAA1</i>	1	0.8687	0.8687	<i>PRKAA1</i>	1.2067	1.4002	1.1603
<i>BNIP3</i>	1	0.8652	0.8652	<i>CTSS</i>	1.9933	2.306	1.1569
<i>PIK3C3</i>	1	0.8624	0.8624	<i>ATG12</i>	1.1872	1.3501	1.1372
<i>INS</i>	0	0	0.8371	<i>AMBRA1</i>	1.0988	1.2467	1.1346
<i>NPC1</i>	1	0.8263	0.8263	<i>CASP8</i>	0.422	0.4722	1.1191
<i>HGS</i>	1	0.8142	0.8142	<i>PIK3R4</i>	0.8909	0.9597	1.0772
<i>ATG4C</i>	1	0.8135	0.8135	<i>BAX</i>	1.4835	1.5929	1.0738
<i>uvrag</i>	0.5926	0.4726	0.7974	<i>MAPK8</i>	1.2524	1.3168	1.0514
<i>wIP1</i>	0.3429	0.2707	0.7894	<i>ATG16L2</i>	1.6052	1.6678	1.039
<i>RAB24</i>	1	0.7831	0.7831	<i>RAB24</i>	0.4017	0.4147	1.0323
<i>ulk2</i>	1.0696	0.8279	0.774	<i>HDAC6</i>	1.8965	1.9245	1.0147
<i>ATG4B</i>	1	0.7719	0.7719	<i>PTEN</i>	1.4372	1.4301	0.9951
<i>RPS6KB1</i>	0.9358	0.7198	0.7692	<i>EIF2AK3</i>	1.0597	1.0521	0.9928
<i>EIF4G1</i>	1	0.7685	0.7685	<i>ATG3</i>	1.6052	1.5929	0.9923
<i>PTEN</i>	0.9577	0.7154	0.747	<i>SQSTM1</i>	1.1394	1.1286	0.9905
<i>BAK1</i>	1	0.7396	0.7396	<i>CTSD</i>	1.9933	1.9268	0.9666
<i>PIK3R4</i>	1	0.7254	0.7254	<i>MAP1LC3B</i>	0.9613	0.9268	0.9641
<i>ATG9A</i>	1	0.7232	0.7232	<i>bcl2</i>	0.0534	0.0505	0.9458
<i>ATG4D</i>	1	0.7039	0.7039	<i>ATG9A</i>	0.5719	0.5381	0.941
<i>AMBRA1</i>	1	0.6932	0.6932	<i>ATG7</i>	1.6052	1.4953	0.9315
<i>NFKB1</i>	1	0.6692	0.6692	<i>ulk2</i>	1.0374	0.9658	0.931
<i>ATG3</i>	0.9163	0.6125	0.6684	<i>NPC1</i>	0.7955	0.737	0.9264
<i>ATG7</i>	0.8802	0.5876	0.6676	<i>BAK1</i>	0.957	0.8862	0.926
<i>tnf</i>	0.4778	0.3141	0.6574	<i>wIP1</i>	1.1394	1.0203	0.8955
<i>TGM2</i>	1.0696	0.7005	0.655	<i>HDAC1</i>	1.9933	1.7508	0.8784
<i>BID</i>	0.458	0.2856	0.6236	<i>rb1</i>	0.9387	0.8225	0.8762
<i>ATG16L2</i>	0.9889	0.5985	0.6052	<i>DRAM2</i>	1.9933	1.7366	0.8712
<i>TGFB1</i>	0.5944	0.3526	0.5932	<i>NFKB1</i>	1.3553	1.1671	0.8612
<i>RGS19</i>	0.6267	0.3623	0.5781	<i>BECN1</i>	1.3699	1.1671	0.8519
<i>ATG16L1</i>	1	0.5675	0.5675	<i>CXCR4</i>	1.9933	1.6413	0.8234
<i>BECN1</i>	1	0.5667	0.5667	<i>CLN3</i>	1.9933	1.4943	0.7497
<i>DRAM2</i>	0.4974	0.278	0.559	<i>GABARAP</i>	2.3098	1.7238	0.7463
<i>AKT1</i>	1	0.533	0.533	<i>AKT1</i>	1.1044	0.7944	0.7193
<i>HSPA8</i>	1	0.5283	0.5283	<i>DAPK1</i>	1.9933	1.4317	0.7183
<i>DAPK1</i>	0.1014	0.0495	0.4883	<i>HSPA8</i>	0.9573	0.6844	0.7149
<i>bcl2</i>	1.0696	0.5189	0.4852	<i>EIF4G1</i>	1.2991	0.9053	0.6969
<i>GABARAP</i>	1	0.4851	0.4851	<i>ATG4D</i>	1.0755	0.7241	0.6733
<i>TP53</i>	0.9615	0.3957	0.4116	<i>CASP3</i>	1.7132	1.027	0.5995
<i>CDKN2A</i>	0.8455	0.3124	0.3695	<i>CDKN1B</i>	1.9933	1.0897	0.5467
<i>SNCA</i>	1.0696	0.3748	0.3504	<i>TMEM74</i>	0.1052	0.0566	0.538
<i>TMEM74</i>	1.0696	0.3716	0.3474	<i>BAD</i>	1.6052	0.7489	0.4665
<i>tnfsf10</i>	0.0519	0.0156	0.3002	<i>ATG9B</i>	2.991	1.3867	0.4636
<i>LAMP1</i>	1	0.2301	0.2301	<i>TNF</i>	2.991	1.2547	0.4195
<i>IRGM</i>	0.9146	0.1409	0.154	<i>IRGM</i>	2.991	0.0741	0.0248
<i>CDKN1B</i>			N/A	<i>ESR1</i>			N/A
<i>ESR1</i>			N/A	<i>PIK3CG</i>			N/A
<i>PIK3CG</i>			N/A	<i>INS</i>			N/A



**Figure S1** The overall survival analysis based on expression of LC3 II, Beclin-1 and p62. LC3 II, Microtubule associated protein 1 light chain 3 II; p62, Sequestosome 1.