**File S1 Autophagy-related gene from HADb**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| AMBRA1 | CCR2 | GRID1 | NRG1 | TMEM74 |
| APOL1 | CD46 | GRID2 | NRG2 | TNFSF10 |
| ARNT | CDKN1A | HDAC1 | NRG3 | TP53 |
| ARSA | CDKN1B | HDAC6 | P4HB | TP53INP2 |
| ARSB | CDKN2A | HGS | PARK2 | TP63 |
| ATF4 | CFLAR | HIF1A | PARP1 | TP73 |
| ATF6 | CHMP2B | HSP90AB1 | PEA15 | TSC1 |
| ATG10 | CHMP4B | HSPA5 | PELP1 | TSC2 |
| ATG12 | CLN3 | HSPA8 | PEX14 | TUSC1 |
| ATG16L1 | CTSB | HSPB8 | PEX3 | ULK1 |
| ATG16L2 | CTSD | IFNG | PIK3C3 | ULK2 |
| ATG2A | CTSL1 | IKBKB | PIK3R4 | ULK3 |
| ATG2B | CX3CL1 | IKBKE | PINK1 | USP10 |
| ATG3 | CXCR4 | IL24 | PPP1R15A | UVRAG |
| ATG4A | DAPK1 | IRGM | PRKAB1 | VAMP3 |
| ATG4B | DAPK2 | ITGA3 | PRKAR1A | VAMP7 |
| ATG4C | DDIT3 | ITGA6 | PRKCD | VEGFA |
| ATG4D | DIRAS3 | ITGB1 | PRKCQ | WDFY3 |
| ATG5 | DLC1 | ITGB4 | PTEN | WDR45 |
| ATG7 | DNAJB1 | ITPR1 | PTK6 | WDR45L |
| ATG9A | DNAJB9 | KIAA0226 | RAB11A | WIPI1 |
| ATG9B | DRAM1 | KIAA0652 | RAB1A | WIPI2 |
| ATIC | EDEM1 | KIAA0831 | RAB24 | ZFYVE1 |
| BAG1 | EEF2 | KIF5B | RAB33B |  |
| BAG3 | EEF2K | KLHL24 | RAB5A |  |
| BAK1 | EGFR | LAMP1 | RAB7A |  |
| BAX | EIF2AK2 | LAMP2 | RAC1 |  |
| BCL2 | EIF2AK3 | MAP1LC3A | RAF1 |  |
| BCL2L1 | EIF2S1 | MAP1LC3B | RB1 |  |
| BECN1 | EIF4EBP1 | MAP1LC3C | RB1CC1 |  |
| BID | EIF4G1 | MAP2K7 | RELA |  |
| BIRC5 | ERBB2 | MAPK1 | RGS19 |  |
| BIRC6 | ERN1 | MAPK3 | RHEB |  |
| BNIP1 | ERO1L | MAPK8 | RPS6KB1 |  |
| BNIP3 | FADD | MAPK8IP1 | RPTOR |  |
| BNIP3L | FAM48A | MAPK9 | SAR1A |  |
| C12orf44 | FAS | MBTPS2 | SERPINA1 |  |
| C17orf88 | FKBP1A | MLST8 | SESN2 |  |
| CALCOCO2 | FKBP1B | MTMR14 | SH3GLB1 |  |
| CAMKK2 | FOS | MTOR | SIRT1 |  |
| CANX | FOXO1 | MYC | SIRT2 |  |
| CAPN1 | FOXO3 | NAF1 | SPHK1 |  |
| CAPN10 | GAA | NAMPT | SPNS1 |  |
| CAPN2 | GABARAP | NBR1 | SQSTM1 |  |
| CAPNS1 | GABARAPL1 | NCKAP1 | ST13 |  |
| CASP1 | GABARAPL2 | NFE2L2 | STK11 |  |
| CASP3 | GAPDH | NFKB1 | Symbol |  |
| CASP4 | GNAI3 | NKX2-3 | TBK1 |  |
| CASP8 | GNB2L1 | NLRC4 | TM9SF1 |  |
| CCL2 | GOPC | NPC1 | TMEM49 |  |

**Table S1 Univariate cox results of ARlncRNAs based on TCGA-LUSC data.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| lncRNA | KM | B | SE | HR | HR.95L | HR.95H | p-value |
| AL035425.1 | 0.0160833 | 0.1238968 | 0.0623621 | 0.8834710 | 0.7818251 | 0.9983321 | 0.0469521 |
| LUCAT1 | 0.0274572 | 0.1181590 | 0.0524339 | 1.1254230 | 1.0155095 | 1.2472330 | 0.0242286 |
| FLJ46906 | 0.0062196 | 0.0688455 | 0.0280391 | 0.9334709 | 0.8835556 | 0.9862061 | 0.0140751 |
| AL049555.1 | 0.0138952 | 0.015940 | 0.0080465 | 0.9841794 | 0.9687799 | 0.9998237 | 0.0474936 |
| AL358472.2 | 0.0365389 | 0.3250618 | 0.1606993 | 0.7224827 | 0.5272783 | 0.9899539 | 0.0430943 |
| GS1-124K5.4 | 0.0251646 | 0.0558915 | 0.0270193 | 0.9456418 | 0.8968664 | 0.9970697 | 0.0385859 |
| LINC02001 | 0.0013664 | 0.0306445 | 0.0148349 | 0.9698202 | 0.9420279 | 0.9984325 | 0.0388557 |
| AL122125.1 | 0.0396307 | 0.2975697 | 0.1288432 | 0.7426208 | 0.5768934 | 0.9559576 | 0.0209131 |
| AC022150.2 | 0.0020426 | 0.1616821 | 0.0709641 | 1.1754865 | 1.0228523 | 1.3508974 | 0.0227048 |
| SFTA1P | 0.0043845 | 0.0149322 | 0.0071193 | 1.0150443 | 1.0009791 | 1.0293070 | 0.0359561 |
| AL021154.1 | 0.0166281 | 0.3335490 | 0.1671984 | 0.7163768 | 0.5162047 | 0.9941709 | 0.0460506 |
| AC019080.1 | 0.0025307 | 0.0761425 | 0.0377155 | 0.9266842 | 0.8606533 | 0.9977810 | 0.0435014 |
| CYP4F26P | 0.0069508 | 0.1545751 | 0.0658623 | 0.8567791 | 0.7530204 | 0.9748347 | 0.0189281 |
| AL035425.3 | 0.0064924 | 0.0452568 | 0.0214417 | 0.9557520 | 0.9164189 | 0.9967733 | 0.0347988 |
| AC025166.1 | 0.0454219 | 0.2779402 | 0.1380856 | 0.7573421 | 0.5777679 | 0.9927292 | 0.0441346 |
| AL138976.2 | 0.0207836 | 0.2451614 | 0.1024002 | 0.7825782 | 0.6402720 | 0.9565132 | 0.0166590 |
| AC068831.6 | 0.0464371 | 0.2406554 | 0.0969733 | 0.7861124 | 0.6500412 | 0.9506671 | 0.0130769 |
| AL391121.1 | 0.0010858 | 0.1286351 | 0.0591418 | 1.1372750 | 1.0128006 | 1.2770475 | 0.0296279 |
| AC254562.3 | 0.0070585 | 0.417754 | 0.1630329 | 0.6585227 | 0.4784063 | 0.9064514 | 0.0103950 |
| LINC01615 | 0.0476068 | 0.062048 | 0.0260815 | 1.0640078 | 1.0109839 | 1.1198128 | 0.0173689 |
| SNHG21 | 0.0002862 | 0.1702317 | 0.0794890 | 0.8434693 | 0.7217855 | 0.9856675 | 0.0322276 |
| AC253536.6 | 0.0102772 | 0.2896617 | 0.1395845 | 0.7485167 | 0.5693600 | 0.9840475 | 0.0379707 |
| AC106786.1 | 0.0119651 | 0.2612855 | 0.1121309 | 0.7700611 | 0.6181291 | 0.9593369 | 0.0197965 |
| TBX5-AS1 | 0.0203152 | 0.1724653 | 0.0872313 | 1.1882306 | 1.0014963 | 1.4097825 | 0.0480298 |
| GPRC5D-AS1 | 0.0055316 | 0.1494202 | 0.0685275 | 0.8612072 | 0.7529687 | 0.9850048 | 0.0292247 |
| AP006545.2 | 0.0028469 | 0.4786062 | 0.1698136 | 0.6196464 | 0.4442202 | 0.8643499 | 0.0048261 |
| AL033384.1 | 0.0323109 | 0.1180680 | 0.0582138 | 0.8886357 | 0.7928153 | 0.9960369 | 0.0425421 |

**Table S2 Gene set enrichment of gene ontology and KEGG pathway analysis results based on the signature of five ARlncRNAs.**

KEGG pathways upregulated in high risk group. (Top 20)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| NAME | SIZE | ES | NES | NOM p-val | FDR q-val | |
| KEGG\_PATHWAYS\_IN\_CANCER | 325 | 0.42748 | 1.78080 | 0.00000 | 0.02720 |
| KEGG\_NEUROACTIVE\_LIGAND\_RECEPTOR\_INTERACTION | 271 | 0.42945 | 1.78704 | 0.00000 | 0.02621 |
| KEGG\_MAPK\_SIGNALING\_PATHWAY | 267 | 0.41901 | 1.75845 | 0.00000 | 0.03033 |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 264 | 0.68900 | 2.43532 | 0.00000 | 0.00000 |
| KEGG\_REGULATION\_OF\_ACTIN\_CYTOSKELETON | 213 | 0.51938 | 2.14575 | 0.00000 | 0.00000 |
| KEGG\_FOCAL\_ADHESION | 199 | 0.65102 | 2.31420 | 0.00000 | 0.00000 |
| KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | 188 | 0.61453 | 2.28188 | 0.00000 | 0.00000 |
| KEGG\_ENDOCYTOSIS | 181 | 0.45767 | 1.93035 | 0.00000 | 0.01015 |
| KEGG\_JAK\_STAT\_SIGNALING\_PATHWAY | 155 | 0.58855 | 2.24599 | 0.00000 | 0.00000 |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 132 | 0.63656 | 2.31449 | 0.00000 | 0.00000 |
| KEGG\_TIGHT\_JUNCTION | 132 | 0.43398 | 1.83360 | 0.00000 | 0.01800 |
| KEGG\_CELL\_ADHESION\_MOLECULES\_CAMS | 131 | 0.69815 | 2.25947 | 0.00000 | 0.00000 |
| KEGG\_AXON\_GUIDANCE | 129 | 0.47176 | 1.85426 | 0.00000 | 0.01588 |
| KEGG\_LYSOSOME | 121 | 0.65095 | 2.15336 | 0.00000 | 0.00000 |
| KEGG\_LEUKOCYTE\_TRANSENDOTHELIAL\_MIGRATION | 116 | 0.68300 | 2.42025 | 0.00000 | 0.00000 |
| KEGG\_VASCULAR\_SMOOTH\_MUSCLE\_CONTRACTION | 114 | 0.46583 | 1.88595 | 0.00000 | 0.01258 |
| KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 108 | 0.54450 | 1.89040 | 0.00000 | 0.01182 |
| KEGG\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 102 | 0.54660 | 2.08415 | 0.00000 | 0.00119 |
| KEGG\_GNRH\_SIGNALING\_PATHWAY | 101 | 0.38912 | 1.63407 | 0.00000 | 0.05928 |
| KEGG\_MELANOGENESIS | 101 | 0.34906 | 1.48155 | 0.00000 | 0.10176 |

KEGG pathways upregulated in low risk group.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| NAME | SIZE | ES | NES | NOM p-val | FDR q-val |
| KEGG\_SPLICEOSOME | 127 | -0.5884 | -2.0380 | 0.0000 | 0.0170 |
| KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450 | 71 | -0.5508 | -1.9819 | 0.0000 | 0.0175 |
| KEGG\_RNA\_DEGRADATION | 59 | -0.5182 | -1.7919 | 0.0000 | 0.0432 |
| KEGG\_GLUTATHIONE\_METABOLISM | 49 | -0.5038 | -1.7227 | 0.0000 | 0.0625 |
| KEGG\_NUCLEOTIDE\_EXCISION\_REPAIR | 44 | -0.5794 | -1.8150 | 0.0000 | 0.0387 |
| KEGG\_RNA\_POLYMERASE | 29 | -0.5800 | -1.8365 | 0.0000 | 0.0349 |
| KEGG\_HOMOLOGOUS\_RECOMBINATION | 28 | -0.7554 | -2.0053 | 0.0000 | 0.0153 |
| KEGG\_GLYCOSYLPHOSPHATIDYLINOSITOL\_GPI\_ANCHOR\_BIOSYNTHESIS | 25 | -0.7012 | -2.0288 | 0.0000 | 0.0149 |
| KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450 | 69 | -0.5975 | -2.0849 | 0.0200 | 0.0611 |
| KEGG\_RETINOL\_METABOLISM | 64 | -0.4970 | -1.7472 | 0.0208 | 0.0557 |
| KEGG\_PARKINSONS\_DISEASE | 128 | -0.5927 | -1.9256 | 0.0213 | 0.0194 |
| KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | 79 | -0.4489 | -1.6694 | 0.0213 | 0.0854 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | 132 | -0.6340 | -2.0120 | 0.0217 | 0.0178 |
| KEGG\_PORPHYRIN\_AND\_CHLOROPHYLL\_METABOLISM | 40 | -0.5701 | -1.9543 | 0.0217 | 0.0183 |
| KEGG\_DNA\_REPLICATION | 36 | -0.6859 | -1.9071 | 0.0222 | 0.0221 |
| KEGG\_MISMATCH\_REPAIR | 23 | -0.6947 | -2.0715 | 0.0222 | 0.0340 |
| KEGG\_PENTOSE\_AND\_GLUCURONATE\_INTERCONVERSIONS | 28 | -0.6496 | -2.0574 | 0.0227 | 0.0226 |
| KEGG\_HUNTINGTONS\_DISEASE | 181 | -0.5156 | -1.9353 | 0.0233 | 0.0202 |
| KEGG\_ALZHEIMERS\_DISEASE | 166 | -0.4802 | -1.8456 | 0.0455 | 0.0314 |

Gene ontology terms upregulated in high risk group. (Top 20)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| NAME | SIZE | ES | NES | NOM p-val | FDR q-val |
| GO\_ENDOTHELIAL\_CELL\_PROLIFERATION | 184 | 0.600444 | 2.689750 | 0 | 0 |
| GO\_SPECIFIC\_GRANULE | 159 | 0.710602 | 2.651219 | 0 | 0 |
| GO\_POSITIVE\_REGULATION\_OF\_VASCULATURE\_DEVELOPMENT | 219 | 0.636391 | 2.632058 | 0 | 0 |
| GO\_POSITIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_PROLIFERATION | 108 | 0.632300 | 2.608887 | 0 | 0 |
| GO\_EPITHELIAL\_CELL\_APOPTOTIC\_PROCESS | 114 | 0.620563 | 2.599583 | 0 | 0 |
| GO\_ESTABLISHMENT\_OF\_ENDOTHELIAL\_BARRIER | 46 | 0.736491 | 2.576434 | 0 | 0 |
| GO\_REGULATION\_OF\_VASCULATURE\_DEVELOPMENT | 404 | 0.577970 | 2.567617 | 0 | 0 |
| GO\_LIPOPOLYSACCHARIDE\_MEDIATED\_SIGNALING\_PATHWAY | 59 | 0.720272 | 2.566856 | 0 | 0 |
| GO\_ENDOTHELIUM\_DEVELOPMENT | 131 | 0.626331 | 2.564729 | 0 | 0 |
| GO\_ACTOMYOSIN | 74 | 0.720546 | 2.562250 | 0 | 0 |
| GO\_RHO\_PROTEIN\_SIGNAL\_TRANSDUCTION | 140 | 0.644519 | 2.554861 | 0 | 0 |
| GO\_ENDOTHELIAL\_CELL\_MIGRATION | 262 | 0.560661 | 2.551415 | 0 | 0 |
| GO\_POSITIVE\_REGULATION\_OF\_EXTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY | 51 | 0.701859 | 2.548006 | 0 | 0 |
| GO\_BLOOD\_VESSEL\_REMODELING | 40 | 0.754788 | 2.543048 | 0 | 0 |
| GO\_CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | 213 | 0.664079 | 2.533833 | 0 | 0 |
| GO\_EXTRACELLULAR\_MATRIX\_DISASSEMBLY | 82 | 0.693339 | 2.524456 | 0 | 0 |
| GO\_SPECIFIC\_GRANULE\_MEMBRANE | 90 | 0.749925 | 2.521352 | 0 | 0 |
| GO\_ACTIN\_FILAMENT\_BUNDLE | 71 | 0.722392 | 2.519366 | 0 | 0 |
| GO\_LYMPH\_VESSEL\_MORPHOGENESIS | 20 | 0.840788 | 2.512942 | 0 | 0 |
| GO\_POSITIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION | 124 | 0.599242 | 2.512341 | 0 | 0 |

Gene ontology terms upregulated in low risk group. (Top 20)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| NAME | SIZE | ES | NES | NOM p-val | FDR q-val |
| GO\_U12\_TYPE\_SPLICEOSOMAL\_COMPLEX | 29 | -0.75702 | -2.23650 | 0 | 0.017292 |
| GO\_RNA\_METHYLATION | 83 | -0.63102 | -2.03911 | 0 | 0.07497 |
| GO\_NADH\_DEHYDROGENASE\_COMPLEX\_ASSEMBLY | 65 | -0.75559 | -2.04688 | 0 | 0.07539 |
| GO\_PROTEIN\_MANNOSYLATION | 23 | -0.69581 | -1.97206 | 0 | 0.07554 |
| GO\_U2\_SNRNP | 23 | -0.73207 | -2.05591 | 0 | 0.07599 |
| GO\_OXIDATIVE\_PHOSPHORYLATION | 146 | -0.67331 | -1.97431 | 0 | 0.07736 |
| GO\_PRECATALYTIC\_SPLICEOSOME | 53 | -0.67199 | -2.10158 | 0 | 0.07748 |
| GO\_INNER\_EAR\_RECEPTOR\_CELL\_DEVELOPMENT | 43 | -0.52451 | -2.00865 | 0 | 0.07893 |
| GO\_TRNA\_METHYLATION | 39 | -0.67463 | -1.96371 | 0 | 0.07941 |
| GO\_RESPIRATORY\_CHAIN\_COMPLEX\_IV\_ASSEMBLY | 25 | -0.78523 | -1.97545 | 0 | 0.07970 |
| GO\_U2\_TYPE\_SPLICEOSOMAL\_COMPLEX | 93 | -0.62481 | -1.98755 | 0 | 0.08110 |
| GO\_PRESPLICEOSOME | 17 | -0.72060 | -1.85295 | 0 | 0.08269 |
| GO\_NADH\_DEHYDROGENASE\_ACTIVITY | 46 | -0.74772 | -1.85635 | 0 | 0.08279 |
| GO\_PROTEIN\_O\_LINKED\_MANNOSYLATION | 18 | -0.67978 | -1.87549 | 0 | 0.08325 |
| GO\_MITOCHONDRIAL\_TRANSCRIPTION | 15 | -0.73133 | -1.99014 | 0 | 0.08380 |
| GO\_ENDORIBONUCLEASE\_ACTIVITY\_PRODUCING\_5\_PHOSPHOMONOESTERS | 29 | -0.66417 | -1.85641 | 0 | 0.08394 |
| GO\_TERMINATION\_OF\_RNA\_POLYMERASE\_II\_TRANSCRIPTION | 35 | -0.65433 | -1.87866 | 0 | 0.08412 |
| GO\_ATP\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY | 26 | -0.59403 | -1.84585 | 0 | 0.08442 |
| GO\_CYTOCHROME\_COMPLEX\_ASSEMBLY | 36 | -0.73799 | -1.88583 | 0 | 0.08458 |
| GO\_TETRAPYRROLE\_BIOSYNTHETIC\_PROCESS | 27 | -0.60001 | -1.87673 | 0 | 0.08495 |

**Supplementary Table3 correlation analysis of lncRNA and mRNA**

|  |  |  |  |
| --- | --- | --- | --- |
| EIF4EBP1 | AP006545.2 | 0.59908892 | 3.19E-50 |
| ATG4A | AL035425.3 | 0.48301969 | 1.05E-30 |
| CAPN10 | AC022150.2 | 0.39999618 | 1.04E-20 |
| IKBKB | AC106786.1 | 0.39751821 | 1.88E-20 |
| TSC2 | AC022150.2 | 0.38645259 | 2.50E-19 |
| ATG4B | AC022150.2 | 0.38439662 | 4.01E-19 |
| HDAC6 | AC022150.2 | 0.38252256 | 6.14E-19 |
| ATG2B | AL138976.2 | 0.36429133 | 3.36E-17 |
| GAPDH | GPRC5D-AS1 | 0.33683063 | 8.78E-15 |
| TSC1 | AC022150.2 | 0.32524468 | 7.83E-14 |
| ATG2A | AC022150.2 | 0.32348367 | 1.08E-13 |
| ATG16L2 | AC022150.2 | 0.31424867 | 5.73E-13 |
| GABARAPL1 | GPRC5D-AS1 | 0.30861711 | 1.54E-12 |
| PEX14 | AC022150.2 | 0.30305021 | 4.01E-12 |
| HDAC6 | AL138976.2 | 0.25033199 | 1.30E-08 |
| HDAC6 | AP006545.2 | 0.21431136 | 1.26E-06 |
| ATG2B | AL035425.3 | 0.19515704 | 1.06E-05 |
| TSC1 | AL138976.2 | 0.17470603 | 8.32E-05 |
| ATG2B | AC022150.2 | 0.14920493 | 0.00079812 |
| ATG4B | AP006545.2 | 0.1435863 | 0.00125615 |
| CAPN10 | AP006545.2 | 0.13589344 | 0.0022784 |
| ATG4B | AL138976.2 | 0.1337407 | 0.00267739 |
| TSC2 | AL138976.2 | 0.11327706 | 0.01108951 |
| ATG16L2 | AL138976.2 | 0.10324248 | 0.02068948 |
| PEX14 | AP006545.2 | 0.09731748 | 0.02924454 |
| GAPDH | AL035425.3 | 0.09543712 | 0.03252859 |
| TSC2 | AC106786.1 | 0.08892049 | 0.0464507 |
| ATG4A | AC106786.1 | 0.08815275 | 0.04838009 |
| PEX14 | LUCAT1 | -0.0925301 | 0.03822348 |
| EIF4EBP1 | AC022150.2 | -0.0948052 | 0.0337007 |
| ATG2A | LUCAT1 | -0.1087058 | 0.01482009 |
| TSC2 | GPRC5D-AS1 | -0.1353012 | 0.00238237 |
| PEX14 | GPRC5D-AS1 | -0.1577798 | 0.00038736 |
| GAPDH | AC022150.2 | -0.1742944 | 8.66E-05 |
| ATG2A | GPRC5D-AS1 | -0.2556346 | 6.24E-09 |