

Supplementary Table S1. Ferroptosis-related differentially expressed genes of ATL.

| genesymbol | adj.P.Val | logFC | Gene Title | id |
|------------|-----------|---------|--|-------|
| HBA1 | 1.29E-18 | 6.4372 | hemoglobin, alpha 1 | 35676 |
| NEDD4L | 2.16E-07 | 3.2987 | neural precursor cell expressed, developmentally down-regulated 4-like" | 16818 |
| TP63 | 5.12E-05 | 2.5939 | tumor protein p63 | 28920 |
| VLDLR | 6.82E-07 | 2.5599 | very low density lipoprotein receptor | 7516 |
| TF | 1.89E-14 | 2.4631 | transferrin | 792 |
| WWTR1 | 1.37E-07 | 2.1082 | WW domain containing transcription regulator 1 | 12258 |
| CAV1 | 2.23E-03 | 2.0759 | caveolin 1, caveolae protein, 22kDa" | 33242 |
| CREB5 | 5.15E-06 | 2.0431 | cAMP responsive element binding protein 5 | 35433 |
| RRM2 | 1.96E-04 | 1.9609 | ribonucleotide reductase M2 polypeptide | 21855 |
| GPT2 | 4.76E-05 | 1.8667 | glutamic pyruvate transaminase (alanine aminotransferase) 2 | 39644 |
| CDC25A | 7.30E-05 | 1.8540 | cell division cycle 25 homolog A (S. pombe) | 1097 |
| CAPG | 9.41E-09 | 1.8137 | capping protein (actin filament), gelsolin-like" | 18229 |
| MGST1 | 3.56E-04 | 1.6725 | microsomal glutathione S-transferase 1 | 6390 |
| PEX6 | 3.70E-08 | 1.6342 | peroxisomal biogenesis factor 6 | 9186 |
| CDKN2A | 1.06E-05 | 1.5771 | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)" | 1687 |
| TRIB2 | 5.89E-07 | 1.5699 | tribbles homolog 2 (Drosophila) | 22976 |
| MAPKAP1 | 1.40E-13 | 1.5590 | mitogen-activated protein kinase associated protein 1 | 24217 |
| MT1G | 3.01E-06 | 1.5454 | metallothionein 1G | 22896 |
| PDK4 | 2.52E-03 | 1.5406 | pyruvate dehydrogenase kinase, isozyme 4" | 42318 |
| MUC1 | 4.65E-06 | 1.5266 | mucin 1, cell surface associated" | 28892 |
| STEAP3 | 7.89E-05 | 1.5105 | STEAP family member 3 | 6929 |
| MAPK8 | 8.19E-09 | -1.5254 | mitogen-activated protein kinase 8 | 30035 |
| SLC7A5 | 4.83E-06 | -1.5717 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5" | 2090 |
| SCD | 2.41E-07 | -1.6331 | stearoyl-CoA desaturase (delta-9-desaturase) | 41666 |
| PARP11 | 5.61E-10 | -1.6501 | poly (ADP-ribose) polymerase family, member 11" | 26888 |
| STAT3 | 1.38E-09 | -1.7027 | signal transducer and activator of transcription 3 (acute-phase response factor) | 27157 |
| SLC7A11 | 5.83E-08 | -1.7518 | solute carrier family 7, (cationic amino | 32586 |

| | | | | |
|------------|----------|---------|--|-------|
| | | | acid transporter, y ⁺ system) member 11" | |
| ZFP36 | 2.06E-11 | -1.7783 | zinc finger protein 36, C3H type, homolog (mouse)" | 2800 |
| ZEB1 | 3.64E-07 | -1.8059 | zinc finger E-box binding homeobox 1 | 18088 |
| AKR1C3 | 3.02E-04 | -1.8111 | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)" | 42774 |
| BNIP3 | 1.14E-10 | -1.8593 | BCL2/adenovirus E1B 19kDa interacting protein 3 | 29331 |
| IFNG | 2.08E-04 | -1.8867 | interferon, gamma" | 16569 |
| LGMN | 3.06E-05 | -1.9617 | legumain | 39661 |
| GABARAP L1 | 6.59E-09 | -1.9746 | GABA(A) receptor-associated protein like 1 | 6174 |
| SOCS1 | 3.54E-12 | -2.0723 | suppressor of cytokine signaling 1 | 41081 |
| SETD1B | 3.29E-19 | -2.1030 | SET domain containing 1B | 39229 |
| RBMS1 | 1.85E-14 | -2.1612 | RNA binding motif, single stranded interacting protein 1" | 11523 |
| ENPP2 | 6.20E-06 | -2.1921 | ectonucleotide pyrophosphatase/phosphodiesterase 2 | 24072 |
| DPP4 | 1.48E-14 | -2.3504 | dipeptidyl-peptidase 4 | 12264 |
| USP35 | 6.58E-28 | -2.4351 | ubiquitin specific peptidase 35 | 19531 |
| CDKN1A | 2.48E-15 | -2.5308 | cyclin-dependent kinase inhibitor 1A (p21, Cip1)" | 15513 |
| SLC40A1 | 3.51E-08 | -2.7593 | solute carrier family 40 (iron-regulated transporter), member 1" | 19903 |
| LCN2 | 6.04E-07 | -2.7757 | lipocalin 2 | 33122 |
| IL1B | 3.82E-06 | -2.7949 | interleukin 1, beta" | 17980 |
| BEX1 | 3.17E-14 | -3.6296 | brain expressed, X-linked 1 | 38982 |
| SMAD7 | 3.03E-16 | -3.9545 | SMAD family member 7 | 351 |

Supplementary Table S2. The ferroptosis-related differentially expressed genes were divided into ferroptosis suppressor, driver, unclassified and marker

| suppressor | driver | unclassified | marker |
|------------|-----------|--------------|---------|
| BEX1 | SMAD7 | HBA1 | SLC40A1 |
| NEDD4L | IL1B | VLDLR | TF |
| LCN2 | TF | TF | |
| SLC40A1 | DPP4 | SETD1B | |
| TP63 | WWTR1 | RRM2 | |
| CDKN1A | SOCS1 | GPT2 | |
| TF | GABARAPL1 | BNIP3 | |
| USP35 | LGMN | CAPG | |
| ENPP2 | IFNG | SLC7A11 | |
| RBMS1 | ZEB1 | SLC7A5 | |
| CAV1 | SLC7A11 | STEAP3 | |
| CREB5 | PEX6 | | |
| RRM2 | CDKN2A | | |
| CDC25A | MAPK8 | | |
| AKR1C3 | | | |
| ZFP36 | | | |
| SLC7A11 | | | |
| STAT3 | | | |
| MGST1 | | | |
| PARP11 | | | |
| SCD | | | |
| TRIB2 | | | |
| MAPKAP1 | | | |
| MT1G | | | |
| PDK4 | | | |
| MUC1 | | | |

Supplementary Table S3. Autophagy-related differentially expressed genes of ATL.

| genesymbol | adj.P.Val | logFC | Gene Title | id |
|------------|-------------|---------|--|-------|
| TP63 | 5.12344E-05 | 2.5939 | tumor protein p63 | 28920 |
| LRRK2 | 4.87445E-06 | 2.2772 | leucine-rich repeat kinase 2 | 20217 |
| TP53INP1 | 1.04677E-11 | 1.9438 | tumor protein p53 inducible nuclear protein 1 | 36711 |
| CYB5A | 3.37088E-05 | 1.7382 | cytochrome b5 type A (microsomal) | 44466 |
| UBASH3B | 1.38957E-07 | 1.5932 | ubiquitin associated and SH3 domain containing, B | 36160 |
| TBC1D5 | 3.43742E-11 | 1.5848 | TBC1 domain family, member 5" | 39178 |
| CDKN2A | 1.06318E-05 | 1.5771 | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)" | 1687 |
| PDK4 | 0.002524317 | 1.5406 | pyruvate dehydrogenase kinase, isozyme 4" | 42318 |
| BIRC5 | 0.002498051 | 1.5288 | baculoviral IAP repeat-containing 5 | 28938 |
| MAPK8 | 8.18775E-09 | -1.5254 | mitogen-activated protein kinase 8 | 30035 |
| EEF2K | 3.30867E-08 | -1.5688 | eukaryotic elongation factor-2 kinase | 21439 |
| GPR18 | 1.63242E-07 | -1.7436 | G protein-coupled receptor 18 | 28002 |
| SNAI1 | 3.09973E-07 | -1.7720 | snail homolog 1 (Drosophila) | 1390 |
| BIRC2 | 9.04297E-27 | -1.9537 | baculoviral IAP repeat-containing 2 | 17712 |
| GABARAPL1 | 6.5943E-09 | -1.9746 | GABA(A) receptor-associated protein like 1 | 6174 |
| TNF | 1.95885E-06 | -2.0012 | tumor necrosis factor (TNF superfamily, member 2)" | 13025 |
| APP | 2.62527E-06 | -2.0422 | amyloid beta (A4) precursor protein | 20175 |
| SIK2 | 1.14839E-11 | -2.3187 | salt-inducible kinase 2 | 15147 |
| MAPT | 2.0207E-14 | -2.5343 | microtubule-associated protein tau | 20433 |
| BCL2L11 | 1.94785E-10 | -2.5709 | BCL2-like 11 (apoptosis facilitator) | 32463 |
| LZTS1 | 1.30016E-12 | -3.0211 | leucine zipper, putative tumor suppressor 1" | 32127 |
| LAPTM4B | 2.64801E-13 | -3.2081 | lysosomal protein transmembrane 4 beta | 22671 |
| CAMP | 1.13546E-06 | -3.3231 | cathelicidin antimicrobial peptide | 26579 |
| TBC1D4 | 9.798E-15 | -3.8369 | TBC1 domain family, member 4 | 4777 |
| CXCR3 | 2.57717E-19 | -3.8766 | chemokine (C-X-C motif) receptor 3 | 23155 |
| MID2 | 3.32244E-19 | -4.3439 | midline 2 | 23728 |

Supplementary Table S4. GO/KEGG enrichment analysis for Ferroptosis-related

| Ontology | ID | Description | p.adjust | Count | zscore |
|----------|------------|---|-------------|-------|--------------|
| BP | GO:0051348 | negative regulation of transferase activity | 2.42636E-05 | 9 | -0.333333333 |
| | | cellular response to external stimulus | 0.001053878 | 7 | -1.889822365 |
| | GO:0071496 | cellular response to chemical stress | 0.001518472 | 7 | -0.377964473 |
| | | negative regulation of phosphorylation | 2.42636E-05 | 10 | -0.632455532 |
| | GO:0042326 | regulation of epithelial cell differentiation | 4.16383E-05 | 7 | -0.377964473 |
| | | negative regulation of protein phosphorylation | 4.16383E-05 | 9 | -0.333333333 |
| | GO:0001933 | response to metal ion | 4.5611E-05 | 9 | -0.333333333 |
| | GO:0010038 | iron ion transport | 8.5108E-05 | 5 | -0.447213595 |
| | GO:0050863 | regulation of T cell activation | 0.001598328 | 7 | -1.889822365 |
| | GO:0006826 | apical part of cell | 0.064255189 | 6 | -0.816496581 |
| CC | GO:0045177 | protein kinase inhibitor activity | 0.002977318 | 4 | 0 |
| | | kinase inhibitor activity | 0.002977318 | 4 | 0 |
| | | iron ion binding | 0.002977318 | 5 | 0.447213595 |
| | | ferric iron binding | 0.017642478 | 2 | 1.414213562 |
| MF | GO:0008199 | cyclin-dependent protein serine/threonine kinase inhibitor activity | 0.017642478 | 2 | 0 |
| | | RNA polymerase II-specific DNA-binding transcription factor binding | 0.053844353 | 5 | -0.447213595 |
| | GO:0061629 | Ferroptosis | 0.007337061 | 4 | 0 |
| | GO:004216 | FoxO signaling pathway | 0.017693871 | 5 | -2.236067977 |
| KEGG | hsa04068 | MicroRNAs in cancer | 0.017693871 | 7 | -0.377964473 |
| | hsa04115 | p53 signaling pathway | 0.017693871 | 4 | 1 |
| | hsa05212 | Pancreatic cancer | 0.017693871 | 4 | -1 |
| | hsa05418 | Fluid shear stress and atherosclerosis | 0.017693871 | 5 | -0.447213595 |
| | | IL-17 signaling pathway | 0.023030109 | 4 | -2 |
| | hsa04657 | Th17 cell differentiation | 0.029027441 | 4 | -2 |
| | hsa04659 | HIF-1 signaling pathway | 0.029027441 | 4 | -1 |
| | hsa04066 | Human T-cell leukemia virus 1 infection | 0.041852069 | 5 | -0.447213595 |
| | | | | | |
| | hsa05166 | | | | |

Supplementary Table S5. GO/KEGG enrichment analysis for Autophagy-related

| ONTOLOGY | ID | Description | p.adjust | Count | zscore |
|----------|------------|---------------------------------|-------------|-------|--------------|
| BP | GO:0042594 | response to starvation | 0.000158625 | 6 | 0 |
| BP | GO:0048143 | astrocyte activation | 0.000480446 | 3 | -1.732050808 |
| | | positive regulation of cellular | | | |
| BP | GO:0031331 | catabolic process | 0.001812582 | 6 | -0.816496581 |
| BP | GO:0010506 | regulation of autophagy | 0.000158625 | 7 | -1.133893419 |
| | | regulation of cysteine-type | | | |
| | | endopeptidase activity | | | |
| BP | GO:0043281 | involved in apoptotic process | 0.000158625 | 6 | -0.816496581 |
| BP | GO:1901653 | cellular response to peptide | 0.000158625 | 7 | -1.889822365 |
| BP | GO:0001774 | microglial cell activation | 0.000158625 | 4 | -1 |
| | | regulation of cysteine-type | | | |
| BP | GO:2000116 | endopeptidase activity | 0.000158625 | 6 | -0.816496581 |
| | | leukocyte activation involved | | | |
| BP | GO:0002269 | in inflammatory response | 0.000158625 | 4 | -1 |
| MF | GO:0015631 | tubulin binding | 9.10484E-05 | 7 | -1.133893419 |
| MF | GO:0008017 | microtubule binding | 0.00012198 | 6 | -0.816496581 |
| MF | GO:0004857 | enzyme inhibitor activity | 0.008716538 | 5 | 0.447213595 |
| | | cysteine-type endopeptidase | | | |
| | | inhibitor activity involved in | | | |
| MF | GO:0043027 | apoptotic process | 0.012089896 | 2 | 0 |
| MF | GO:0051087 | chaperone binding | 0.012089896 | 3 | -0.577350269 |
| | | cysteine-type endopeptidase | | | |
| | | regulator activity involved in | | | |
| MF | GO:0043028 | apoptotic process | 0.033290429 | 2 | 0 |
| CC | GO:0005776 | autophagosome | 0.001729195 | 4 | 1 |
| CC | GO:0045121 | membrane raft | 0.0018998 | 5 | -1.341640786 |
| CC | GO:0098857 | membrane microdomain | 0.0018998 | 5 | -1.341640786 |
| KEGG | hsa04210 | Apoptosis | 0.000775323 | 5 | -1.341640786 |
| | | NOD-like receptor signaling | | | |
| KEGG | hsa04621 | pathway | 0.002229251 | 5 | -2.236067977 |
| KEGG | hsa04215 | Apoptosis - multiple species | 9.76225E-05 | 4 | -1 |
| KEGG | hsa01524 | Platinum drug resistance | 0.020240912 | 3 | 0.577350269 |
| KEGG | hsa05210 | Colorectal cancer | 0.026139473 | 3 | -0.577350269 |
| KEGG | hsa04931 | Insulin resistance | 0.03501896 | 3 | -1.732050808 |
| KEGG | hsa04668 | TNF signaling pathway | 0.03501896 | 3 | -1.732050808 |
| KEGG | hsa05145 | Toxoplasmosis | 0.03501896 | 3 | -1.732050808 |
| KEGG | hsa04068 | FoxO signaling pathway | 0.048627811 | 3 | -1.732050808 |

Supplementary Table S6. GO/KEGG enrichment analysis for Hub genes of Ferroptosis- and Autophagy-related DEGs.

| ONTOLOGY | ID | Description | p.adjust | Count | zscore |
|----------|------------|----------------------------------|-------------|-------|--------------|
| BP | GO:0061900 | glial cell activation | 1.17856E-08 | 6 | -1.632993162 |
| | | positive regulation of | | | |
| BP | GO:0045862 | proteolysis | 1.17856E-08 | 9 | -2.333333333 |
| BP | GO:0150076 | neuroinflammatory response | 2.2193E-08 | 6 | -1.632993162 |
| | | negative regulation of | | | |
| BP | GO:0045936 | phosphate metabolic process | 2.2193E-08 | 9 | -1.666666667 |
| BP | GO:0048143 | astrocyte activation | 1.17856E-08 | 5 | -2.236067977 |
| | | leukocyte activation involved in | | | |
| BP | GO:0002269 | inflammatory response | 1.72726E-07 | 5 | -1.341640786 |
| | | negative regulation of | | | |
| BP | GO:0042326 | phosphorylation | 1.72726E-07 | 8 | -1.414213562 |
| | | positive regulation of | | | |
| BP | GO:0032755 | interleukin-6 production | 3.67117E-06 | 5 | -2.236067977 |
| CC | GO:0045121 | membrane raft | 0.000544419 | 5 | -1.341640786 |
| CC | GO:0098857 | membrane microdomain | 0.000544419 | 5 | -1.341640786 |
| CC | GO:0030426 | growth cone | 0.010929308 | 3 | -0.577350269 |
| CC | GO:0097386 | glial cell projection | 0.010929308 | 2 | -1.414213562 |
| CC | GO:0030427 | site of polarized growth | 0.010929308 | 3 | -0.577350269 |
| KEGG | hsa04215 | Apoptosis - multiple species | 3.65445E-05 | 4 | -1 |
| KEGG | hsa04217 | Necroptosis | 3.65445E-05 | 6 | -2.449489743 |
| KEGG | hsa05145 | Toxoplasmosis | 0.000114108 | 5 | -2.236067977 |
| KEGG | hsa04068 | FoxO signaling pathway | 0.00017832 | 5 | -2.236067977 |
| KEGG | hsa04210 | Apoptosis | 0.00017832 | 5 | -1.341640786 |
| KEGG | hsa05321 | Inflammatory bowel disease | 0.000190727 | 4 | -2 |
| KEGG | hsa01524 | Platinum drug resistance | 0.000237581 | 4 | 0 |

Supplementary Table S7. GO/KEGG enrichment analysis for Hub genes of Ferroptosis- and Autophagy-related DEGs.

| ONTOLOGY | ID | Description | p.adjust | Count | zscore |
|----------|------------|--|-------------|-------|--------------|
| MF | GO:0004857 | enzyme inhibitor activity | 0.000162684 | 6 | 0 |
| MF | GO:0015631 | tubulin binding | 0.001488279 | 5 | -0.447213595 |
| MF | GO:0005126 | cytokine receptor binding | 0.002961663 | 4 | -2 |
| MF | GO:0008017 | microtubule binding | 0.002961663 | 4 | 0 |
| MF | GO:0051087 | chaperone binding | 0.002961663 | 3 | -0.577350269 |
| MF | GO:0019903 | protein phosphatase binding | 0.005940815 | 3 | -1.732050808 |
| MF | GO:0004866 | endopeptidase inhibitor activity | 0.007469973 | 3 | -0.577350269 |
| MF | GO:0030414 | peptidase inhibitor activity | 0.007469973 | 3 | -0.577350269 |
| MF | GO:0019902 | phosphatase binding | 0.007469973 | 3 | -1.732050808 |
| MF | GO:0061135 | endopeptidase regulator activity | 0.007469973 | 3 | -0.577350269 |
| MF | GO:0004861 | cyclin-dependent protein serine/threonine kinase inhibitor activity | 0.002468614 | 2 | 0 |
| MF | GO:0043027 | cysteine-type endopeptidase inhibitor activity involved in apoptotic process | 0.00368153 | 2 | 0 |
| MF | GO:0030291 | protein serine/threonine kinase inhibitor activity | 0.006503378 | 2 | 0 |
| MF | GO:0043028 | cysteine-type endopeptidase regulator activity involved in apoptotic process | 0.007469973 | 2 | 0 |
| MF | GO:0016538 | cyclin-dependent protein serine/threonine kinase regulator activity | 0.008964342 | 2 | 0 |