**Supplementary Table S1 The primer sequences of lncRNAs.**

|  |  |
| --- | --- |
| **LncRNA** | **sequences** |
| AC099850.3-F | CCCAGGTTCAAGTAACTGGGAC |
| AC099850.3-R | GACAATGCCTTGCCAAGGAATC |
| AC011978.1-F | GCAGTCGGATATTGGAGGAA |
| AC011978.1-R | TCTCCCCCAGCTAAATCTGA |
| CDKN2A-DT -F | CAGCGTGGACAGGAGCATCT |
| CDKN2A-DT -R | TGTGAGGTTGCGAATGACTGC |
| LINC01503-F | TGGTCATCTTTGGGTGGAGC |
| LINC01503-R | TGACCCAGTCTCCTGTCAGT |
| StarD4-AS1-F | GCCTGCCCTGTCAAAAGAAG |
| StarD4-AS1-R | GTGCTTCTGCTGTCTGGTTG |
| GAPDH-F | ACAACTTTGGTATCGTGGAAGG |
| GAPDH-R | GCCATCACGCCACAGTTTC |

**Supplementary Table S2 necroptosis -related genes**

|  |  |
| --- | --- |
| **Genes** | **Description** |
| FADD | Fas Associated Via Death Domain |
| FAS | Fas Cell Surface Death Receptor |
| FASLG | Fas Ligand |
| MLKL | Mixed Lineage Kinase Domain Like Pseudokinase |
| RIPK1 | Receptor Interacting Serine/Threonine Kinase 1 |
| RIPK3 | Receptor Interacting Serine/Threonine Kinase 3 |
| TLR3 | Toll Like Receptor 3 |
| TNF | Tumor Necrosis Factor |
| TSC1 | TSC Complex Subunit 1 |
| TRIM11 | Tripartite Motif Containing 11 |
| CASP8 | Caspase 8 |
| ZBP1 | Z-DNA Binding Protein 1 |
| MAPK8 | Mitogen-Activated Protein Kinase 8 |
| IPMK | Inositol Polyphosphate Multikinase |
| ITPK1 | Inositol-Tetrakisphosphate 1-Kinase |
| SIRT3 | Sirtuin 3 |
| MYC | MYC Proto-Oncogene, BHLH Transcription Factor |
| TNFRSF1A | TNF Receptor Superfamily Member 1A |
| TNFSF10 | TNF Superfamily Member 10 |
| TNFRSF1B | TNF Receptor Superfamily Member 1B |
| TRAF2 | TNF Receptor Associated Factor 2 |
| PANX1 | Pannexin 1 |
| OTULIN | OTU Deubiquitinase With Linear Linkage Specificity |
| CYLD | CYLD Lysine 63 Deubiquitinase |
| USP22 | Ubiquitin Specific Peptidase 22 |
| MAP3K7 | Mitogen-Activated Protein Kinase Kinase Kinase 7 |
| SQSTM1 | Sequestosome 1 |
| STAT3 | Signal Transducer And Activator Of Transcription 3 |
| DIABLO | Diablo IAP-Binding Mitochondrial Protein |
| DNMT1 | DNA Methyltransferase 1 |
| CFLAR | CASP8 And FADD Like Apoptosis Regulator |
| BRAF | B-Raf Proto-Oncogene, Serine/Threonine Kinase |
| AXL | AXL Receptor Tyrosine Kinase |
| ID1 | Inhibitor Of DNA Binding 1, HLH Protein |
| CDKN2A | Cyclin Dependent Kinase Inhibitor 2A |
| HSPA4 | Heat Shock Protein Family A (Hsp70) Member 4 |
| BCL2 | BCL2 Apoptosis Regulator |
| STUB1 | STIP1 Homology And U-Box Containing Protein 1 |
| FLT3 | Fms Related Receptor Tyrosine Kinase 3 |
| HAT1 | Histone Acetyltransferase 1 |
| SIRT2 | Sirtuin 2 |
| SIRT1 | Sirtuin 1 |
| PLK1 | Polo Like Kinase 1 |
| MPG | N-Methylpurine DNA Glycosylase |
| BACH2 | BTB Domain And CNC Homolog 2 |
| GATA3 | GATA Binding Protein 3 |
| MYCN | MYCN Proto-Oncogene, BHLH Transcription Factor |
| ALK | ALK Receptor Tyrosine Kinase |
| ATRX | ATRX Chromatin Remodeler |
| TERT | Telomerase Reverse Transcriptase |
| SLC39A7 | Solute Carrier Family 39 Member 7 |
| SPATA2 | Spermatogenesis Associated 2 |
| RNF31 | Ring Finger Protein 31 |
| IDH1 | Isocitrate Dehydrogenase (NADP(+)) 1 |
| IDH2 | Isocitrate Dehydrogenase (NADP(+)) 2 |
| KLF9 | Kruppel Like Factor 9 |
| HDAC9 | Histone Deacetylase 9 |
| HSP90AA1 | Heat Shock Protein 90 Alpha Family Class A Member 1 |
| LEF1 | Lymphoid Enhancer Binding Factor 1 |
| BNIP3 | BCL2 Interacting Protein 3 |
| CD40 | CD40 Molecule |
| BCL2L11 | BCL2 Like 11 |
| EGFR | Epidermal Growth Factor Receptor |
| DDX58 | DExD/H-Box Helicase 58 |
| TARDBP | TAR DNA Binding Protein |
| APP | Amyloid Beta Precursor Protein |
| TNFRSF21 | TNF Receptor Superfamily Member 21 |

**Supplementary Table S3 Gene sets enriched in phenotype high**

|  |  |
| --- | --- |
| **GS follow link to MSigDB** | **RANK AT MAX** |
| ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY ARVC | 6971 |
| ALDOSTERONE REGULATED SODIUM REABSORPTION | 8475 |
| DILATED CARDIOMYOPATHY | 6414 |
| VASCULAR SMOOTH MUSCLE CONTRACTION | 7371 |
| LEUKOCYTE TRANSENDOTHELIAL MIGRATION | 7479 |
| CELL ADHESION MOLECULES CAMS | 12124 |
| ECM RECEPTOR INTERACTION | 6496 |
| HYPERTROPHIC CARDIOMYOPATHY HCM | 6435 |
| MELANOGENESIS | 6971 |
| NEUROACTIVE LIGAND RECEPTOR INTERACTION | 9864 |
| PRIMARY BILE ACID BIOSYNTHESIS | 5451 |
| TGF BETA SIGNALING PATHWAY | 8561 |
| HEDGEHOG SIGNALING PATHWAY | 8335 |
| CALCIUM SIGNALING PATHWAY | 6561 |
| T CELL RECEPTOR SIGNALING PATHWAY | 8475 |
| FOCAL ADHESION | 7564 |
| ABC TRANSPORTERS | 5289 |
| CYTOKINE CYTOKINE RECEPTOR INTERACTION | 8817 |
| JAK STAT SIGNALING PATHWAY | 10671 |
| CHEMOKINE SIGNALING PATHWAY | 8549 |
| ACUTE MYELOID LEUKEMIA | 7403 |
| MELANOMA | 8785 |
| TYPE II MELLITUS | 9773 |
| ENDOMETRIAL CANCER | 8544 |
| GNRH SIGNALING PATHWAY | 7304 |
| TIGHT JUNCTION | 7767 |
| LYSOSOME | 8839 |
| MAPK SIGNALING PATHWAY | 8714 |
| RENIN ANGIOTENSIN SYSTEM | 6250 |
| HEMATOPOIETIC CELL LINEAGE | 8086 |
| PHOSPHATIDYLINOSITOL SIGNALING SYSTEM | 9014 |
| GAP JUNCTION | 5389 |
| AXON GUIDANCE | 9290 |
| PATHWAYS IN CANCER | 8785 |
| GLIOMA | 8785 |
| FC GAMMA R MEDIATED PHAGOCYTOSIS | 7514 |
| BASAL CELL CARCINOMA | 8544 |
| INTESTINAL IMMUNE NETWORK FOR IGA PRODUCTION | 11792 |
| LONG TERM POTENTIATION | 6397 |
| REGULATION OF ACTIN CYTOSKELETON | 8666 |
| ASTHMA | 13179 |
| FC EPSILON RI SIGNALING PATHWAY | 8475 |
| GLYCOSPHINGOLIPID BIOSYNTHESIS GANGLIO SERIES | 8851 |
| B CELL RECEPTOR SIGNALING PATHWAY | 9290 |
| DORSO VENTRAL AXIS FORMATION | 5976 |
| TOLL LIKE RECEPTOR SIGNALING PATHWAY | 7403 |
| PROSTATE CANCER | 8785 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS CHONDROITIN SULFATE | 7495 |
| ENDOCYTOSIS | 11419 |
| LONG TERM DEPRESSION | 7335 |
| COLORECTAL CANCER | 8544 |
| NEUROTROPHIN SIGNALING PATHWAY | 8714 |
| PRIMARY IMMUNODEFICIENCY | 9243 |
| WNT SIGNALING PATHWAY | 8544 |
| LEISHMANIA INFECTION | 6787 |
| NATURAL KILLER CELL MEDIATED CYTOTOXICITY | 8792 |
| NON SMALL CELL LUNG CANCER | 8785 |
| ALLOGRAFT REJECTION | 13363 |
| VIRAL MYOCARDITIS | 6282 |
| INOSITOL PHOSPHATE METABOLISM | 9014 |
| AUTOIMMUNE THYROID DISEASE | 13363 |
| SMALL CELL LUNG CANCER | 10533 |
| VEGF SIGNALING PATHWAY | 8475 |
| ADHERENS JUNCTION | 8485 |
| O GLYCAN BIOSYNTHESIS | 8370 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS HEPARAN SULFATE | 5472 |
| INSULIN SIGNALING PATHWAY | 10417 |
| GLYCOSAMINOGLYCAN DEGRADATION | 11166 |
| PANCREATIC CANCER | 8785 |
| CHRONIC MYELOID LEUKEMIA | 8785 |
| RENAL CELL CARCINOMA | 5904 |
| APOPTOSIS | 8735 |
| ERBB SIGNALING PATHWAY | 8475 |
| VASOPRESSIN REGULATED WATER REABSORPTION | 6938 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS KERATAN SULFATE | 8020 |
| TASTE TRANSDUCTION | 7851 |
| OTHER GLYCAN DEGRADATION | 5226 |
| ARACHIDONIC ACID METABOLISM | 8309 |
| PPAR SIGNALING PATHWAY | 10307 |
| MTOR SIGNALING PATHWAY | 8646 |
| GRAFT VERSUS HOST DISEASE | 13381 |
| GLYCOSPHINGOLIPID BIOSYNTHESIS LACTO AND NEOLACTO SERIES | 8556 |
| ADIPOCYTOKINE SIGNALING PATHWAY | 12347 |
| RIBOFLAVIN METABOLISM | 10047 |
| NICOTINATE AND NICOTINAMIDE METABOLISM | 4252 |
| COMPLEMENT AND COAGULATION CASCDES | 9128 |
| ETHER LIPID METABOLISM | 9479 |
| NOTCH SIGNALING PATHWAY | 5976 |
| SPHINGOLIPID METABOLISM | 7660 |
| TYPE I MELLITUS | 13363 |
| BUTANOATE METABOLISM | 8274 |
| HISTIDINE METABOLISM | 8435 |
| BLADDER CANCER | 8785 |
| PROXIMAL TUBULE BICARBONATE RECLAMATION | 5308 |
| LINOLEIC ACID METABOLISM | 8309 |
| SELENOAMINO ACID METABOLISM | 3938 |
| EPITHELIAL CELL SIGNALING IN HELICOBACTER PYLORI INFECTION | 5652 |
| VALINE LEUCINE AND ISOLEUCINE DEGRADATION | 9317 |
| CARDIAC MUSCLE CONTRACTION | 6414 |
| VIBRIO CHOLERAE INFECTION | 8760 |
| FATTY ACID METABOLISM | 10307 |
| LYSINE DEGRADATION | 6544 |
| AMYOTROPHIC LATERAL SCLEROSIS ALS | 6769 |
| BETA ALANINE METABOLISM | 9160 |
| ALPHA LINOLENIC ACID METABOLISM | 8309 |
| PROPANOATE METABOLISM | 8917 |
| GLYCEROLIPID METABOLISM | 8884 |
| REGULATION OF AUTOPHAGY | 13236 |
| TRYPTOPHAN METABOLISM | 8699 |
| RIG I LIKE RECEPTOR SIGNALING PATHWAY | 3543 |
| PANTOTHENATE AND COA BIOSYNTHESIS | 9194 |
| SNARE INTERACTIONS IN VESICULAR TRANSPORT | 8367 |
| DRUG METABOLISM CYTOCHROME P450 | 6992 |
| PEROXISOME | 4856 |
| ANTIGEN PROCESSING AND PRESENTATION | 13381 |

**Supplementary Table S4 Gene sets enriched in phenotype low**

|  |  |
| --- | --- |
| **GS follow link to MSigDB** | **RANK AT MAX** |
| RNA POLYMERASE | 9676 |
| PYRIMIDINE METABOLISM | 7307 |
| SPLICEOSOME | 8640 |
| RIBOSOME | 5886 |
| RNA DEGRADATION | 7666 |
| PROTEASOME | 10177 |
| HOMOLOGOUS RECOMBINATION | 6124 |
| AMINOACYL TRNA BIOSYNTHESIS | 8245 |
| ONE CARBON POOL BY FOLATE | 4242 |
| HUNTINGTONS DISEASE | 11574 |
| BASE EXCISION REPAIR | 10118 |
| DRUG METABOLISM OTHER ENZYMES | 10425 |
| PROTEIN EXPORT | 5798 |
| CELL CYCLE | 4081 |
| OXIDATIVE PHOSPHORYLATION | 12231 |
| PARKINSONS DISEASE | 11364 |
| PURINE METABOLISM | 7307 |
| GLYOXYLATE AND DICARBOXYLATE METABOLISM | 6173 |
| BASAL TRANSCRIPTION FACTORS | 9280 |
| PORPHYRIN AND CHLOROPHYLL METABOLISM | 7878 |
| DNA REPLICATION | 10118 |
| NUCLEOTIDE EXCISION REPAIR | 8971 |
| ALZHEIMERS DISEASE | 8931 |
| PHENYLALANINE METABOLISM | 11661 |
| GLYCOLYSIS GLUCONEOGENESIS | 6587 |
| GLYCOSYLPHOSPHATIDYLINOSITOL GPI ANCHOR BIOSYNTHESIS | 8928 |
| ALANINE ASPARTATE AND GLUTAMATE METABOLISM | 8419 |
| PENTOSE PHOSPHATE PATHWAY | 16852 |
| CITRATE CYCLE TCA CYCLE | 17351 |
| MISMATCH REPAIR | 7889 |
| MATURITY ONSET DIABETES OF THE YOUNG | 6062 |
| CYSTEINE AND METHIONINE METABOLISM | 3484 |
| OOCYTE MEIOSIS | 5256 |
| PROGESTERONE MEDIATED OOCYTE MATURATION | 2744 |
| FRUCTOSE AND MANNOSE METABOLISM | 9222 |
| CYTOSOLIC DNA SENSING PATHWAY | 12709 |
| ARGININE AND PROLINE METABOLISM | 7436 |
| PATHOGENIC ESCHERICHIA COLI INFECTION | 4602 |
| STEROID BIOSYNTHESIS | 4998 |
| P53 SIGNALING PATHWAY | 2438 |
| BIOSYNTHESIS OF UNSATURATED FATTY ACIDS | 5426 |
| PENTOSE AND GLUCURONATE INTERCONVERSIONS | 17805 |
| NITROGEN METABOLISM | 6864 |
| GLUTATHIONE METABOLISM | 17520 |
| PYRUVATE METABOLISM | 6173 |
| AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM | 12545 |
| UBIQUITIN MEDIATED PROTEOLYSIS | 6883 |
| TYROSINE METABOLISM | 9585 |
| PRION DISEASES | 7920 |
| GLYCEROPHOSPHOLIPID METABOLISM | 9715 |
| GLYCINE SERINE AND THREONINE METABOLISM | 8064 |
| OLFACTORY TRANSDUCTION | 15003 |
| THYROID CANCER | 7748 |
| TERPENOID BACKBONE BIOSYNTHESIS | 10789 |
| GALACTOSE METABOLISM | 1117 |
| N GLYCAN BIOSYNTHESIS | 8458 |
| METABOLISM OF XENOBIOTICS BY CYTOCHROME P450 | 14996 |
| NOD LIKE RECEPTOR SIGNALING PATHWAY | 8821 |
| STEROID HORMONE BIOSYNTHESIS | 14996 |
| STARCH AND SUCROSE METABOLISM | 7878 |
| RETINOL METABOLISM | 14996 |
| ASCORBATE AND ALDARATE METABOLISM | 14996 |
| SYSTEMIC LUPUS ERYTHEMATOSUS | 5880 |

**Supplementary Table S5 The classification of each sample**

|  |  |  |
| --- | --- | --- |
| **ID** | **Risk** | **Cluster** |
| TCGA-CQ-A4C6 | high | C1 |
| TCGA-CV-7428 | high | C2 |
| TCGA-CR-6488 | low | C2 |
| TCGA-CV-5966 | high | C2 |
| TCGA-CR-7377 | low | C1 |
| TCGA-C9-A480 | high | C3 |
| TCGA-UF-A7JA | low | C2 |
| TCGA-CV-7411 | low | C3 |
| TCGA-CV-7091 | low | C1 |
| TCGA-CR-7379 | low | C1 |
| TCGA-CV-7100 | high | C2 |
| TCGA-CQ-5324 | low | C3 |
| TCGA-CQ-6222 | high | C3 |
| TCGA-CN-4736 | low | C3 |
| TCGA-D6-A6EN | high | C4 |
| TCGA-CV-A45R | low | C3 |
| TCGA-HD-8224 | low | C2 |
| TCGA-CV-7254 | low | C3 |
| TCGA-F7-A50J | low | C3 |
| TCGA-CV-5973 | low | C4 |
| TCGA-CV-6934 | low | C2 |
| TCGA-CV-6961 | high | C2 |
| TCGA-P3-A5QF | low | C2 |
| TCGA-IQ-7631 | low | C4 |
| TCGA-CQ-5332 | high | C2 |
| TCGA-CN-4734 | low | C1 |
| TCGA-BA-7269 | low | C4 |
| TCGA-H7-A6C4 | low | C3 |
| TCGA-CQ-6228 | high | C2 |
| TCGA-CN-6019 | low | C3 |
| TCGA-CV-A45P | low | C3 |
| TCGA-CX-A4AQ | high | C4 |
| TCGA-QK-A6II | high | C4 |
| TCGA-T2-A6WX | high | C2 |
| TCGA-CV-7090 | low | C1 |
| TCGA-CR-7391 | low | C3 |
| TCGA-CV-7180 | high | C2 |
| TCGA-CQ-5334 | high | C1 |
| TCGA-CV-A465 | high | C1 |
| TCGA-BA-A6DJ | low | C3 |
| TCGA-CV-6937 | high | C3 |
| TCGA-CQ-5329 | low | C1 |
| TCGA-CQ-5325 | low | C3 |
| TCGA-IQ-A61J | low | C3 |
| TCGA-BA-5558 | high | C1 |
| TCGA-CQ-A4CI | low | C3 |
| TCGA-T3-A92N | high | C2 |
| TCGA-CV-7253 | high | C3 |
| TCGA-CR-7367 | low | C2 |
| TCGA-CQ-6220 | high | C1 |
| TCGA-BA-6872 | high | C1 |
| TCGA-P3-A6T5 | high | C2 |
| TCGA-QK-AA3K | high | C2 |
| TCGA-CV-7102 | low | C1 |
| TCGA-BB-A5HZ | low | C3 |
| TCGA-CV-7406 | low | C2 |
| TCGA-D6-A6EO | low | C3 |
| TCGA-HL-7533 | low | C2 |
| TCGA-CN-4729 | low | C3 |
| TCGA-CN-6995 | low | C1 |
| TCGA-CN-5370 | low | C1 |
| TCGA-CV-7429 | high | C2 |
| TCGA-BA-A6DE | high | C2 |
| TCGA-CQ-6225 | high | C2 |
| TCGA-CV-6948 | high | C2 |
| TCGA-IQ-7632 | high | C1 |
| TCGA-BA-A6DD | high | C2 |
| TCGA-CR-6491 | high | C2 |
| TCGA-CV-A468 | low | C3 |
| TCGA-BA-6873 | low | C1 |
| TCGA-IQ-A61G | high | C3 |
| TCGA-HD-7831 | low | C3 |
| TCGA-P3-A6T0 | low | C3 |
| TCGA-F7-A61V | high | C3 |
| TCGA-UF-A71A | high | C2 |
| TCGA-BA-5557 | low | C3 |
| TCGA-MT-A7BN | high | C4 |
| TCGA-CX-7219 | high | C1 |
| TCGA-CV-7097 | high | C1 |
| TCGA-CX-7085 | low | C3 |
| TCGA-CR-7392 | low | C3 |
| TCGA-DQ-5631 | low | C2 |
| TCGA-UF-A7JT | high | C2 |
| TCGA-CR-6471 | low | C1 |
| TCGA-CV-6942 | low | C1 |
| TCGA-DQ-5625 | low | C3 |
| TCGA-DQ-7588 | high | C1 |
| TCGA-F7-A620 | low | C3 |
| TCGA-CV-6938 | high | C2 |
| TCGA-KU-A66T | high | C1 |
| TCGA-BB-A5HU | low | C1 |
| TCGA-CV-A45X | high | C2 |
| TCGA-CR-7386 | low | C3 |
| TCGA-4P-AA8J | high | C4 |
| TCGA-BB-8601 | low | C2 |
| TCGA-CN-6024 | high | C2 |
| TCGA-CV-6940 | high | C1 |
| TCGA-HD-8314 | low | C2 |
| TCGA-CV-6952 | high | C1 |
| TCGA-BA-6871 | high | C2 |
| TCGA-CR-7390 | high | C1 |
| TCGA-CX-7086 | high | C1 |
| TCGA-CQ-A4CG | high | C1 |
| TCGA-CV-A6JY | high | C3 |
| TCGA-CN-6018 | high | C1 |
| TCGA-CV-5971 | low | C3 |
| TCGA-QK-A6VB | low | C1 |
| TCGA-CV-A6K0 | low | C3 |
| TCGA-CV-7252 | high | C1 |
| TCGA-CV-5976 | high | C2 |
| TCGA-CV-A45U | low | C3 |
| TCGA-CV-7435 | low | C3 |
| TCGA-CQ-7063 | low | C3 |
| TCGA-CV-6003 | high | C2 |
| TCGA-BA-5556 | high | C2 |
| TCGA-BB-4228 | low | C2 |
| TCGA-CQ-6229 | low | C3 |
| TCGA-RS-A6TO | high | C2 |
| TCGA-CR-7380 | low | C1 |
| TCGA-CV-6933 | low | C1 |
| TCGA-T2-A6WZ | low | C4 |
| TCGA-IQ-A6SH | low | C3 |
| TCGA-CR-6484 | high | C2 |
| TCGA-CN-4741 | low | C2 |
| TCGA-CN-5358 | low | C1 |
| TCGA-BA-A6DG | low | C3 |
| TCGA-CN-4737 | high | C2 |
| TCGA-BA-5151 | high | C1 |
| TCGA-CV-7432 | high | C2 |
| TCGA-CR-7373 | low | C1 |
| TCGA-UF-A7JC | high | C2 |
| TCGA-CV-7255 | high | C2 |
| TCGA-QK-A6IG | high | C2 |
| TCGA-CR-7395 | high | C1 |
| TCGA-DQ-7591 | high | C2 |
| TCGA-CV-7236 | high | C2 |
| TCGA-CV-6945 | high | C1 |
| TCGA-CN-4742 | low | C1 |
| TCGA-CV-6441 | high | C2 |
| TCGA-CV-A6JO | high | C3 |
| TCGA-CR-7394 | low | C3 |
| TCGA-HD-A633 | high | C2 |
| TCGA-CV-5436 | high | C1 |
| TCGA-CV-7438 | high | C1 |
| TCGA-CN-4731 | high | C2 |
| TCGA-CV-6953 | low | C3 |
| TCGA-CR-6477 | high | C1 |
| TCGA-CR-7372 | low | C1 |
| TCGA-CN-5367 | high | C1 |
| TCGA-UF-A7JO | high | C3 |
| TCGA-CV-A45V | high | C2 |
| TCGA-CR-7376 | low | C3 |
| TCGA-CV-A464 | low | C3 |
| TCGA-CQ-5330 | low | C1 |
| TCGA-CV-7235 | low | C3 |
| TCGA-QK-A652 | low | C3 |
| TCGA-CN-6017 | low | C3 |
| TCGA-KU-A6H8 | low | C3 |
| TCGA-QK-A8Z7 | high | C2 |
| TCGA-CN-A6UY | low | C4 |
| TCGA-CN-6996 | high | C1 |
| TCGA-CV-6936 | high | C2 |
| TCGA-P3-A5QE | low | C3 |
| TCGA-CV-5970 | low | C3 |
| TCGA-CN-4728 | low | C3 |
| TCGA-CN-5373 | low | C3 |
| TCGA-CN-A49A | low | C2 |
| TCGA-HD-A6HZ | high | C1 |
| TCGA-CV-7103 | low | C3 |
| TCGA-CV-6956 | high | C2 |
| TCGA-BA-A6D8 | low | C4 |
| TCGA-F7-8489 | low | C3 |
| TCGA-CV-A45T | low | C3 |
| TCGA-CV-A45Q | low | C4 |
| TCGA-CV-7446 | high | C1 |
| TCGA-CQ-A4C9 | high | C2 |
| TCGA-P3-A5QA | low | C2 |
| TCGA-CQ-A4CE | high | C3 |
| TCGA-BA-4074 | high | C1 |
| TCGA-CV-6939 | low | C1 |
| TCGA-CN-A498 | low | C1 |
| TCGA-CV-7568 | low | C1 |
| TCGA-CQ-6219 | low | C1 |
| TCGA-CR-7369 | low | C1 |
| TCGA-CQ-7065 | high | C2 |
| TCGA-CV-6941 | high | C1 |
| TCGA-CN-4726 | low | C3 |
| TCGA-CQ-7069 | low | C3 |
| TCGA-CV-7238 | low | C3 |
| TCGA-MT-A67A | high | C4 |
| TCGA-CV-7416 | low | C1 |
| TCGA-UF-A71B | high | C1 |
| TCGA-D6-6823 | high | C1 |
| TCGA-CV-5442 | low | C2 |
| TCGA-F7-A61S | low | C3 |
| TCGA-CN-4733 | low | C3 |
| TCGA-CR-5250 | low | C1 |
| TCGA-CN-A6V6 | low | C2 |
| TCGA-CR-6492 | low | C1 |
| TCGA-P3-A6T8 | low | C2 |
| TCGA-P3-A6T3 | low | C3 |
| TCGA-CV-5977 | low | C1 |
| TCGA-CV-6951 | low | C3 |
| TCGA-UF-A71E | high | C4 |
| TCGA-CR-6493 | high | C2 |
| TCGA-MT-A67D | high | C1 |
| TCGA-CQ-7068 | high | C2 |
| TCGA-CR-6472 | low | C2 |
| TCGA-P3-A6T4 | low | C4 |
| TCGA-BA-A6DB | low | C3 |
| TCGA-CQ-6221 | high | C3 |
| TCGA-D6-6515 | low | C1 |
| TCGA-CR-7365 | high | C2 |
| TCGA-F7-A50G | high | C3 |
| TCGA-CQ-6224 | low | C3 |
| TCGA-UF-A719 | low | C2 |
| TCGA-CV-A6JN | low | C4 |
| TCGA-P3-A6T2 | high | C2 |
| TCGA-CN-4725 | high | C1 |
| TCGA-HD-8635 | low | C3 |
| TCGA-CN-6020 | high | C1 |
| TCGA-CV-6950 | high | C1 |
| TCGA-CV-6960 | high | C2 |
| TCGA-D6-8569 | low | C1 |
| TCGA-CR-7382 | low | C1 |
| TCGA-D6-A4ZB | high | C2 |
| TCGA-CQ-A4CH | high | C2 |
| TCGA-D6-6827 | low | C3 |
| TCGA-CV-7425 | low | C2 |
| TCGA-CV-7178 | low | C2 |
| TCGA-CV-6436 | high | C4 |
| TCGA-IQ-A61H | high | C2 |
| TCGA-BB-A6UO | high | C3 |
| TCGA-CQ-5327 | high | C2 |
| TCGA-CQ-5333 | high | C2 |
| TCGA-WA-A7H4 | low | C1 |
| TCGA-CN-A63V | high | C4 |
| TCGA-CN-6994 | high | C2 |
| TCGA-CQ-A4CB | high | C1 |
| TCGA-DQ-7592 | low | C1 |
| TCGA-CV-6954 | low | C3 |
| TCGA-CN-4730 | high | C1 |
| TCGA-CV-A6K2 | high | C2 |
| TCGA-BA-4077 | low | C2 |
| TCGA-CN-6013 | low | C3 |
| TCGA-HD-7832 | high | C2 |
| TCGA-DQ-5630 | low | C3 |
| TCGA-CV-7423 | high | C1 |
| TCGA-QK-A6IH | high | C3 |
| TCGA-CN-A642 | high | C4 |
| TCGA-UF-A7JD | low | C1 |
| TCGA-T2-A6X2 | low | C3 |
| TCGA-CN-6998 | high | C3 |
| TCGA-CV-A6JM | high | C4 |
| TCGA-CQ-6223 | high | C1 |
| TCGA-UF-A7JS | high | C4 |
| TCGA-CV-7183 | low | C3 |
| TCGA-F7-A624 | high | C1 |
| TCGA-HD-A6I0 | high | C4 |
| TCGA-MT-A51X | low | C1 |
| TCGA-CR-7393 | low | C3 |
| TCGA-QK-A64Z | low | C3 |
| TCGA-CQ-5323 | low | C2 |
| TCGA-CV-7263 | high | C3 |
| TCGA-CV-6955 | low | C3 |
| TCGA-MT-A67F | high | C3 |
| TCGA-D6-A4Z9 | high | C1 |
| TCGA-CN-5364 | high | C1 |
| TCGA-H7-7774 | low | C3 |
| TCGA-QK-A8Z9 | low | C3 |
| TCGA-CV-6433 | low | C2 |
| TCGA-CV-A6JU | low | C4 |
| TCGA-D6-A6EM | high | C2 |
| TCGA-P3-A6T7 | low | C1 |
| TCGA-CQ-7071 | low | C3 |
| TCGA-H7-8501 | high | C2 |
| TCGA-CQ-A4C7 | low | C1 |
| TCGA-CV-A6JZ | high | C1 |
| TCGA-CV-7104 | low | C3 |
| TCGA-CV-7407 | high | C2 |
| TCGA-CV-7434 | high | C1 |
| TCGA-CQ-6227 | high | C2 |
| TCGA-CN-4740 | low | C3 |
| TCGA-H7-8502 | high | C1 |
| TCGA-CV-7427 | high | C1 |
| TCGA-BA-5152 | high | C3 |
| TCGA-IQ-A6SG | high | C1 |
| TCGA-WA-A7GZ | high | C2 |
| TCGA-CV-5979 | high | C2 |
| TCGA-D6-6825 | low | C1 |
| TCGA-CV-A6JT | low | C4 |
| TCGA-CN-5359 | low | C2 |
| TCGA-CQ-7072 | low | C2 |
| TCGA-DQ-5624 | low | C2 |
| TCGA-CQ-6218 | low | C3 |
| TCGA-CV-5439 | high | C2 |
| TCGA-CV-7099 | high | C2 |
| TCGA-CR-7397 | low | C3 |
| TCGA-P3-A6T6 | low | C2 |
| TCGA-MZ-A7D7 | high | C3 |
| TCGA-CQ-5331 | low | C3 |
| TCGA-CV-A6JE | low | C3 |
| TCGA-HD-8634 | high | C2 |
| TCGA-CQ-5326 | high | C1 |
| TCGA-CN-6016 | low | C3 |
| TCGA-CV-7095 | high | C1 |
| TCGA-C9-A47Z | low | C3 |
| TCGA-QK-A6IJ | low | C4 |
| TCGA-CV-7413 | low | C3 |
| TCGA-CN-6011 | low | C2 |
| TCGA-BB-4224 | high | C2 |
| TCGA-CR-7368 | low | C2 |
| TCGA-CR-7401 | low | C3 |
| TCGA-CV-A45O | low | C3 |
| TCGA-D6-6516 | low | C2 |
| TCGA-CV-6959 | high | C1 |
| TCGA-CV-6943 | low | C3 |
| TCGA-UP-A6WW | low | C4 |
| TCGA-CV-A6JD | high | C4 |
| TCGA-BA-4075 | high | C2 |
| TCGA-IQ-A61E | low | C1 |
| TCGA-BB-4225 | low | C2 |

**Supplementary Table S6 93 antitomor drugs had significant differences among 4 clusters**

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| **antitumor drugs** |
| A.770041 |
| ABT.263 |
| AICAR |
| AKT.inhibitor.VIII |
| AMG.706 |
| AP.24534 |
| ATRA |
| Axitinib |
| AZD.0530 |
| AZD.2281 |
| AZD6244 |
| AZD6482 |
| AZD7762 |
| AZD8055 |
| BAY.61.3606 |
| Bexarotene |
| BI.2536 |
| BIRB.0796 |
| BMS.509744 |
| BMS.536924 |
| BMS.708163 |
| Bosutinib |
| Bryostatin.1 |
| BX.795 |
| Camptothecin |
| CCT007093 |
| CEP.701 |
| CGP.60474 |
| CI.1040 |
| CMK |
| Cyclopamine |
| Cytarabine |
| DMOG |
| Docetaxel |
| EHT.1864 |
| Elesclomol |
| Embelin |
| Epothilone.B |
| Etoposide |
| GDC.0449 |
| GDC0941 |
| Gemcitabine |
| GSK.650394 |
| GSK269962A |
| GW.441756 |
| GW843682X |
| Imatinib |
| JNJ.26854165 |
| JNK.9L |
| JNK.Inhibitor.VIII |
| JW.7.52.1 |
| KIN001.135 |
| KU.55933 |
| Lapatinib |
| LFM.A13 |
| Metformin |
| Methotrexate |
| MG.132 |
| Mitomycin.C |
| MK.2206 |
| MS.275 |
| NSC.87877 |
| NU.7441 |
| Nutlin.3a |
| NVP.BEZ235 |
| PAC.1 |
| Paclitaxel |
| Parthenolide |
| PD.0325901 |
| PD.0332991 |
| PF.562271 |
| PF.4708671 |
| QS11 |
| RDEA119 |
| RO.3306 |
| Roscovitine |
| S.Trityl.L.cysteine |
| Salubrinal |
| SB590885 |
| SL.0101.1 |
| Sorafenib |
| Sunitinib |
| Tipifarnib |
| TW.37 |
| Vinblastine |
| Vorinostat |
| VX.680 |
| VX.702 |
| WO2009093972 |
| WZ.1.84 |
| X17.AAG |
| Z.LLNle.CHO |
| ZM.447439 |