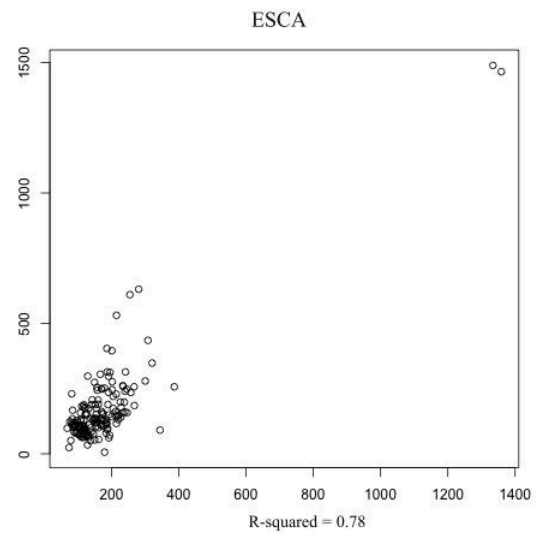
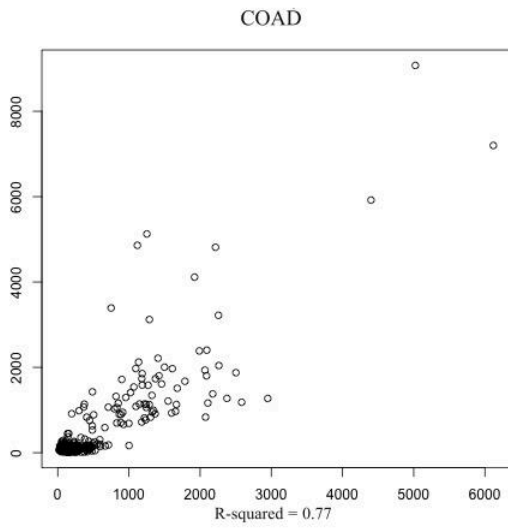
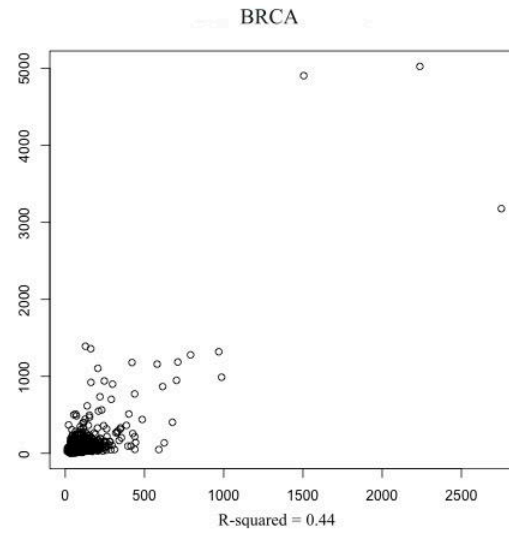
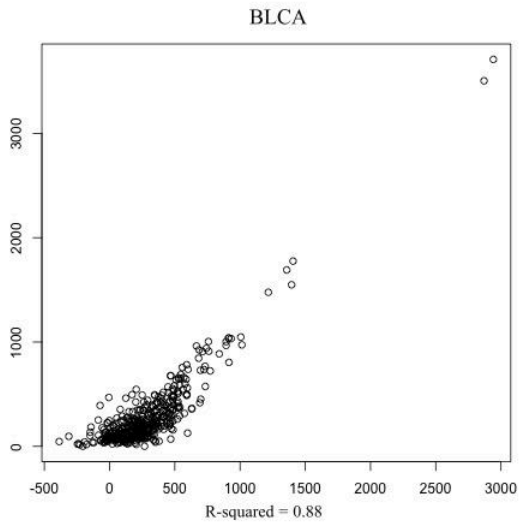
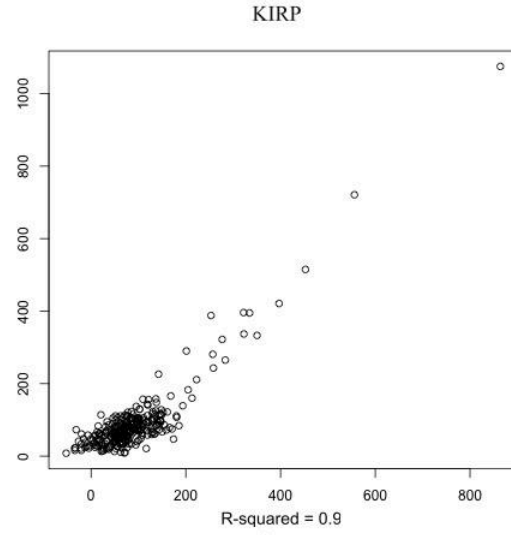
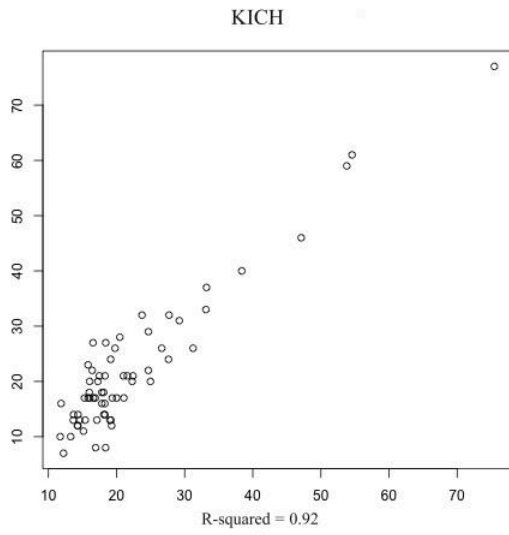
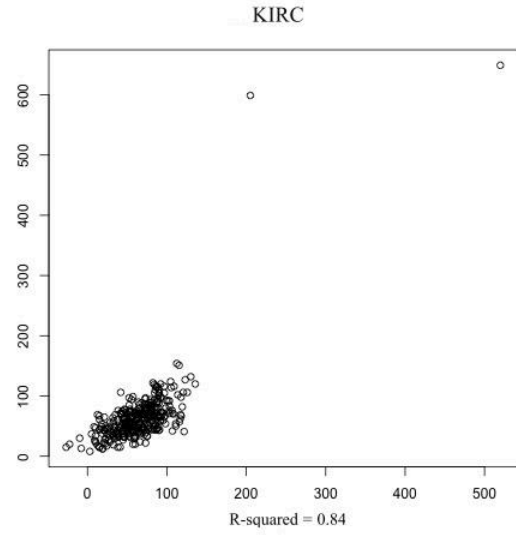
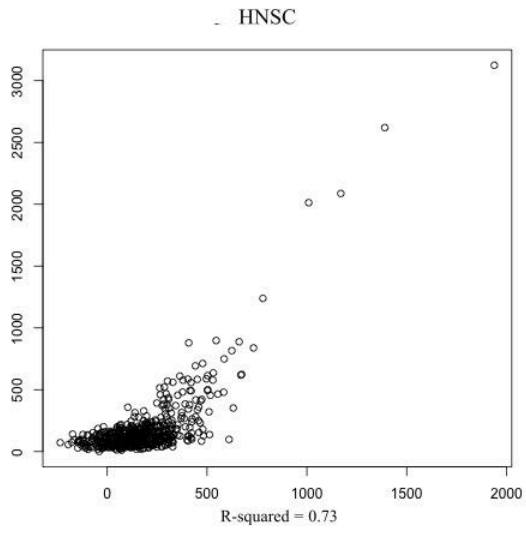
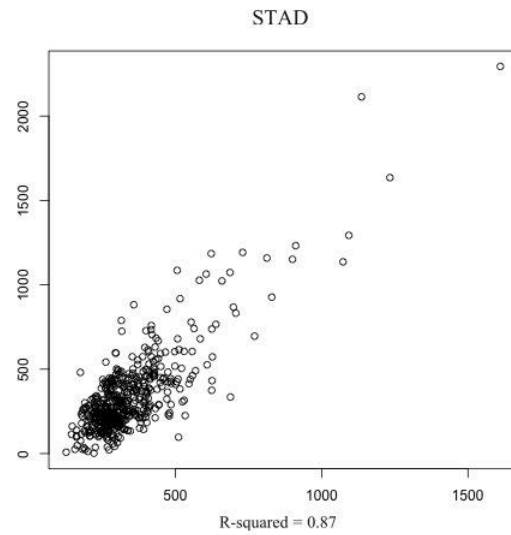
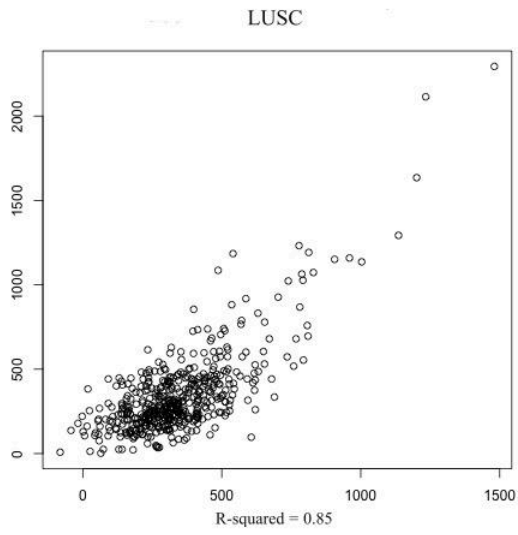
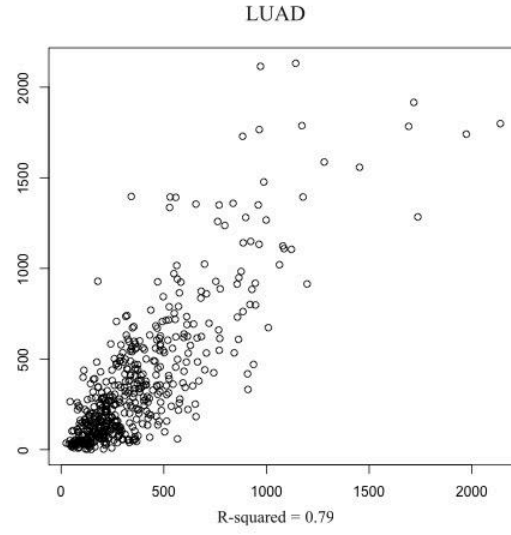
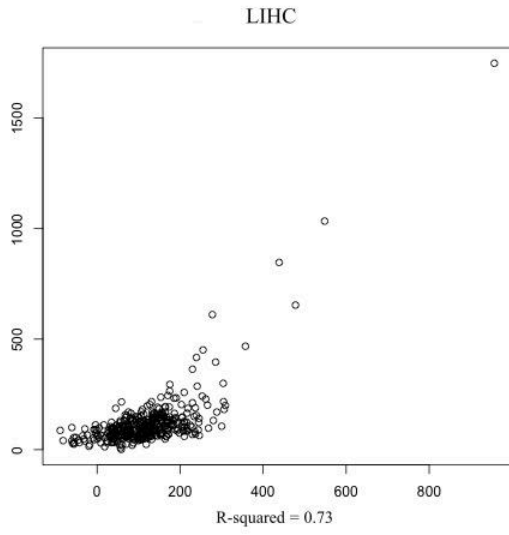


Supplementary Material







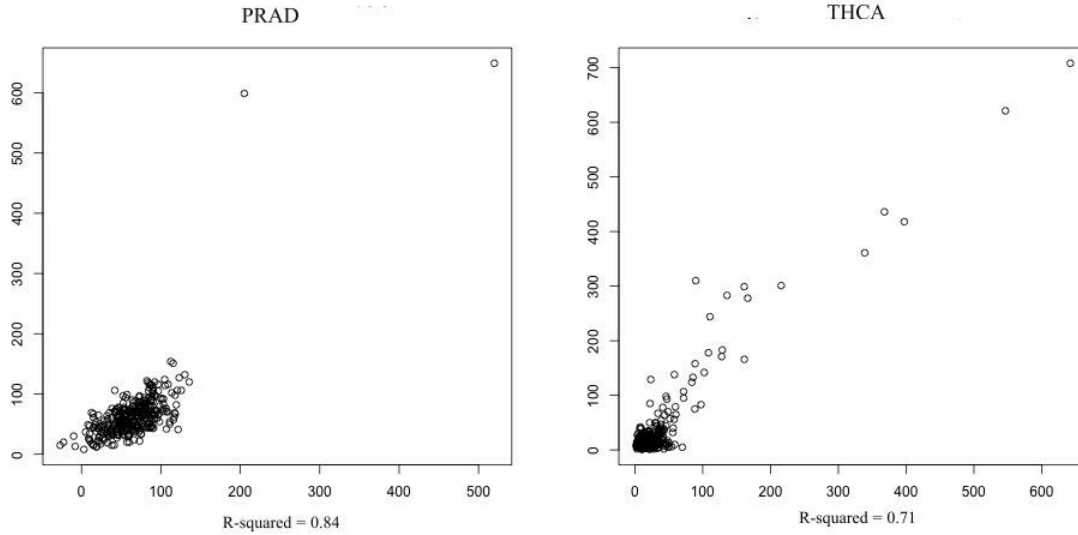


Figure S1: Scatter plots for predicted oxidative stress level vs. mutation rates in the test samples in 14 cancer types. For each panel, the x-axis represents the predicted oxidative stress level and the y-axis denotes the actual mutation rate.

Table S1: Genes selected from each regression model for each of the 14 cancer types, based on their level of contribution to the regression result as measured using p-values.

| Cancer | Gene names |
|-------------|---|
| BLCA | ACPI, AGK, B3GALT2, B4GALT2, B4GALT3, B4GALT4, BPGM, C1R, C1S, C2, CDC14A, CDC14B, CELA3A, CFB, CFD, CFI, CHPF, CLP1, CMA1, CTRB1, CTSG, DCK, DUSP1, DUSP14, DUSP6, ELANE, ETNK1, ETNK2, EXT1, EXT2, F10, F11, F12, F2, F7F9, FUK, FUT8, GALK1, GALK2, GNE, GZMA, GZMB, HTRA2, IMPA1, IMPA2, INPP5A, INPP5B, INPPL1, KLK3, KLKB1, LHPP, MASP2, MBTPS1, NAGK, PGP, PHPT1, PLAT, PLAU, PLG, PLPP1, PLPP2, PLPP3, PPM1D, PPP1CA, PPP3CA, PPP3CB, PPP5C, PROC, PRSS1, PRSS2, PRSS3, PTPN5, PTPRJ, PTPRM, PTPRN, RELN, RNGTT, SGPP1, SGPP2, TIGAR, UGT8 |
| BRCA | ACAA2, ADK, ADPGK, AGK, B3GNT2, B4GALT1, B4GALT2, B4GALT3, B4GALT4, B4GALT7, B4GAT1, CHPF, CHSY1, CLP1, CMAS, CPT1B, DBT, DCK, DGKA, DGUOK, DLAT, DOLK, ETNK1, ETNK2, EXT1, EXT2, EXTL1, EXTL2, EXTL3, FPGT, FUT8, GALT, GCAT, GCK, GNE, HK1, HK3, IPPK, ITPK1, ITPKB, LIPT2, NAGS, PDXK, PFKM, PGM2L1, POLR3D, PSTK, RFK, TKFC |
| COAD | ACPI, ALPL, LPPL2, B3GNT2, B4GALT1, B4GALT7, B4GAT1, BPGM, BPNT1, C1R, C1S, C2, CELA2A, CELA2B, CELA3A, CFB, CFD, CFI, CMA1, CSGALNACT1, CSGALNACT2, CTRB1, CTRL, CTSG, DGKD, ELANE, ENOPH1, EXT1, EXT2, EXTL1, EXTL2, F12, F2, FUT8, FUT9, G6PC, G6PC2, GBE1, GZMA, GZMB, HTRA2, INPP1, ITPK1, KLK3, KLKB1, MASP1, MASP2, MBTPS1, MINPP1, NADK, NT5C, NT5C2, NT5E, PFKFB1, PFKFB2, PFKFB4, PHOSPHO1, PHOSPHO2, PHPT1, PLAT, PLAU, PLG, PROC, PTEN, PTPN11, PTPN5, PTPRJ, PTPRM, RELN, SGPP1, SGPP2, TIGAR |
| ESCA | ALG2, B3GALT1, B3GALT2, B3GNT4, B3GNT7, B4GALT1, B4GALT2, B4GALT3, B4GALT4, CHPF, CHSY3, COQ3, CPT1A, CPT1B, ELOVL2, EXTL1, EXTL2, EXTL3, FUT8, GAMT, GCNT1, GNMT, LIPT2, MGAT5B, MTR, NAT10, OXSM, PEMT, PRMT5, SCP2, TAT |
| HNSC | A4GALT, ABO, ACPI, ADK, ADPGK, B3GALT2, B4GALT2, B4GALT3, B4GALT4, BPGM, C2, CELA2B, CELA3A, CERK, CFB, CMA1, COASY, CSGALNACT1, CSGALNACT2, CTRB1, CTRL, CTSG, DGKA, DGUOK, DOLK, ELANE, F10, F2, FBP1, FBP2, FUK, GCK, GK, GK2, GLYCTK, GNE, GZMA, GZMB, HKDC1, HTRA2, IMPA1, IMPA2, IPMK, IPPK, KHK, KLK3, KLKB1, LHPP, MASP1, MASP2, MBTPS1, MVK, NADK, NAGK, NMRK1, NT5C2, NT5E, OCRL, PDXP, PFKL, PFKM, PFKP, PGM2L1, PGP, PHPT1, PIK3C2A, PIK3C2B, PIK3C3, PIK3CA, PIK3CD, PIKFYVE, PIP4K2A, PIP4K2C, PKM, PLAT, PLAU, PPM1D, PPP5C, PROC, PSPH, PSTK, PTPN1, PTPN5, PTPN7, RBKS, RELN, RFK, SGPP1, SGPP2, SYNJ1, SYNJ2, TIGAR, TK1, TK2, TKFC, UGT8, XYLB |
| KICH | CHST1, CMAS, COQ3, DNMT1, DNMT3A, DNMT3B, FDPS, FLAD1, FPGT, SMS, SRM, UAP1, UAP1L1 |

| | |
|-------------|--|
| KIRC | ACHE, ACP1, ACPP, AGL, BPGM, BPNT1, CEL, CES2, CES5A, CFD, CFI, CHI3L1, CHIA, CMA1, CMBL, CTSG, DUSP10, ENGASE, FBP1, FBP2, FUCA1, FUCA2, GAA, GALC, GANAB, GBA, GBA3, GLA, GZMA, GZMB, H6PD, HPSE, HPSE2, HYAL1, IDUA, IMPA1, IMPA2, INPP1, INPP4A, INPP4B, INPP5B, KLK3, LCT, LHPP, LIPA, LIPE, MAN2A2, MAN2B1, MANBA, MASP1, MBTPS1, MGAM, MGLL, MOGS, NAGA, NAGLU, NANP, NCEH1, NEU1, NEU3, NT5M, PAFAH2, PDXP, PGLS, PGP, PHPT1, PLA2G4B, PLA2G4E, PLAT, PLAU, PLB1, PLG, PNLIP, PPM1D, PPP5C, PROC, PSPH, PTEN, PTPN1, PTPN5, PTPN6, PTPRB, RELN, SGPP1, SGPP2, SI, SPAM1, SYNJ1, SYNJ2, TIGAR, TREH |
| KIRP | CES1, CES2m, CES5A, CEL, LIPA, MGLL, LIPF, LIPG, PNLIP, PNLIPRP1, PNLIPRP2, H6PD, PGLS, LPL, PLA2G1B, PLA2G3, PLA2G4B, CMBL, PAFAH1B2, PAFAH1B3, LYPLA1, LYPLA2, PLB1, ACHE, PHPT1, LHPP, SGPP1, SGPP2, ALPI, ALPPL2, FBP1, FBP2, BPGM, PPM1A, ACP2, ACP5, PSPH, RNGTT, OCRL, INPP5E, TIGAR, ACP1, CTRL, RELN, CTRB1, MASP2, HTRA2, KLKB1, ELANE, F12, PRSS1, PRSS2, C1S, CFI, CFD, CFB, F2, F10, PLAT, PLG, CELA3B, PLAU, KLK3, ATP4B, ATP5A1, ATP5O, ATP6V0A2, ATP6V0D2, DHX58, TCIRG1, CFTR, ATP2B2, ATP2B4, ATP1A1, ATP1A2 |
| LIHC | TA, SLC33A1, ELOVL2, NAT10, LPCAT4, NAGS, HADHB, ACAA2, DBT, FUT4, FUT7, B4GALT1, OGT, B4GALT4, B4GALT3, B4GALT2, B3GALT2, B3GALT1, CSGALNACT2, CSGALNACT1, EXTL2, EXTL1, EXTL3, CHSY1, CHPF2, ABO, PLOD3, FUT8, SGPP1, SGPP2, FBP1, FBP2, BPGM, PPP5C, PGP, PLPP1, PLPP2, PLPP3, TIGAR, ACP1, PTPRF, PTPRJ, DUSP16, PTPN5, NT5E, NT5M, NT5C1, INPP5J, INPP1, PTEN, BPNT1, PDXP, PHOSPHO2, PHOSPHO1, ENOPH1, MBTPS1, CTSG, F7, CMA1, C1S, CFB, PROC, CELA3A, PLAU, KLK3 |
| LUAD | PGP, IMPA, PSPH, RNGTT, INPP5B, INPP5E, TIGAR, DUSP16, PTPN5, ENPP6, PLCB2, PLCB3, SMPD, SMPD3, PDE1A, PDE1C, PDE1B, PDE7B, PDE9A, ENPP2, PLD2, NAGPA, CTRL, MASP1, RELN, CTRB1, MASP2, HTRA2, MBTPS1, CTSG, F9, KLKB1, ELANE, F12, PRSS1, PRSS2, C1R, C1S, C2, CFI, CFD, CFB, F2, F10, PLAT, PROC, PLG, CELA2B, CELA2A, PLAU, KLK3, GZMB, ATP4A, ATP4B, ATP5B, ATP5C1, ATP5D, ATP5E, ATP5F, ATP5G2, ATP5I, ATP5J, ATP6V1B1, ATP6V1C1, ATP6V1E1, ATP6API, ATP5O, MT-ATP8, ATP6V1F, TCIRG1, ATP5H, DDX58, ATP6V1H, DHX58, ATP6V1G3, CFTR, ATP2A1, ATP2A2, ATP2B1, ATP2B4, ATP1A1, ATP1A3 |
| LUSC | PGLS, LPL, CMBL, LYPLA1, LYPLA2, PLA2G15, PLB1, ACHE, LIPE, PHPT1, LHPP, SGPP1, SGPP2, ALPPL2, BPGM, PPM1B, PPP2CA, PPP3CB, ACP2, ACP4, NANP, PSPH, RNGTT, INPP5B, TIGAR, ACP1, CDC25B, PTPN6, PTPRR, NT5M, INPP1, PTEN, BPNT1, RELN, MASP2, HTRA2, MBTPS1, F9, KLKB1, ELANE, F12, C1R, C2, CFB, F2, PLAT, PROC, PLG, ATP4B, ATP5A1, ATP5B, ATP5, ATP6V0A1, ATP6API, MT-ATP6, MT-ATP8, TCIRG1, ATP5, ATP5L, CFTR, ATP2A1, ATP2B3, ATP1A1 |
| PRAD | B4GALT1, OGT, B4GALT4, B4GALT3, B4GALT2, B3GALT2, EXTL1, EXTL3, EXT1, EXT2, CHPF, UGT8, FUT5, FUT8, B3GALNT1, DPM1, GBTG1, HKDC1, PGM2L1, DGKH, DOLK, PFKM, ITPKA, ITPKB, CER, IPPK, PSTK, XYLB, GCK, PHPT1, LHPP, SGPP1, SGPP2, ALPI, FBP1, FBP2, BPG, PPP5, PPM1D, PGP, ACPP, ACP6, NANP, PSPH, RNGTT, OCRL, SYNJ1, SYNJ2, INPP5, TIGA, ACP1, PTPN1, PTPN, CTRL, MASP1, REL, CTRB1, MASP2, HTRA2, MBTPS1, CTSG, F7, F9, F11, KLKB1, ELANE, F1, CMA1, PRSS1, C1R, C1S, C2, CFI, CFD, CFB, F2, F10, PLAT, PROC, PLG, CELA3A, CELA3, CELA2B, CELA2A, PLAU, KLK3, GZMA, GZMB |
| STAD | ABO, ACP, ACP2, ACPP, ADK, ADPGK, BPGM, C1R, C1, CERK, CHPF2, CHSY, CMA1, COASY, CTSG, DGKA, DGKB, DGKH, DGKI, DGUOK, DOLK, DPM1, DUSP1, ELANE, EXT1, EXT2, EXTL1, EXTL3, FBP1, F2, GBTG1, GCK, GK, GK2, GLYCTK, HK, HKDC1, IMPA1, IMPA, INPP5B, INPP5E, IPMK, IPPK, ITPK1, KHK, KL, LHPP, MVK, NADK, NANP, NMRK1, NT5C2, NT5E, NT5M, OCRL, PAPS1, PAPS2, PFKL, PGM2L1, PGP, PHPT1, PIK3C3, PIKFYVE, PIP4K2C, PKM, PPM1D, PRSS1, PRSS2, PRSS3, PSPH, PSTK, PTPN5, PTPRJ, PTPRN, RBKS, RNGTT, SGPP1, SGPP2, SYNJ2, TIGAR, TK1, TK2, TKFC, XYLB |
| THCA | ACP1, AGK, B3GALT2, B4GALT2, B4GALT3, B4GALT4, BPGM, C1R, C1S, C2, CDC14A, CDC14B, CELA3A, CFB, CFD, CFI, CHPF, CLP1, CMA1, CTRB1, CTSG, DCK, DUSP1, DUSP14, DUSP6, ELANE, ETNK1, ETNK2, EXT1, EXT2, F10, F11, F12, F2, F7, F9, FUK, FUT8, GALK1, GALK2, GNE, GZMA, GZMB, HTRA2, IMPA1, IMPA2, INPP5A, INPP5B, INPPL1, KLK3, KLKB1, LHPP, MASP2, MBTPS1, NAGK, PGP, PHPT1, PLAT, PLAU, PLG, PLPP1, PLPP2, PLPP3, PPM1D, PPP1CA, PPP3CA, PPP3CB, PPP5C, PROC, PRSS1, PRSS2, PRSS3, PTPN5, PTPRJ, PTPRM, PTPRN, RELN, RNGTT, SGPP1, SGPP2, TIGAR, UGT8 |

Table S2: Enzymes used in our linear regression analysis with gene number in each enzyme class.

| Cancer | EC classes used | Number of genes used |
|--------|-----------------|----------------------|
| BLCA | 3.1.1 | 20 |

| | | |
|-------------|--------|----|
| | 3.1.4 | 12 |
| | 3.4.21 | 32 |
| | 3.2.1 | 17 |
| BRCA | 2.3.1 | 7 |
| | 2.4.1 | 15 |
| COAD | 2.7.1 | 24 |
| | 2.7.7 | 4 |
| | 2.7.1 | 3 |
| | 2.4.1 | 13 |
| | 3.1.3 | 27 |
| | 3.4.21 | 29 |
| ESCA | 2.1.1 | 6 |
| | 2.3.1 | 7 |
| | 2.4.1 | 17 |
| HNSC | 2.6.1 | 1 |
| | 2.7.1 | 41 |
| | 2.4.1 | 9 |
| | 3.1.3 | 24 |
| | 3.4.21 | 23 |
| KICH | 2.7.7 | 5 |
| | 2.1.1 | 4 |
| | 2.5.1 | 3 |
| | 2.8.2 | 1 |
| KIRC | 3.1.1 | 16 |
| | 3.1.3 | 32 |
| KIRP | 3.2.1 | 29 |
| | 3.4.21 | 14 |
| | 3.1.1 | 24 |
| | 3.1.3 | 18 |
| | 3.4.21 | 21 |
| | 3.6.3 | 12 |
| LIHC | 2.4.1 | 19 |
| | 3.1.3 | 27 |
| | 3.4.21 | 10 |

| | | |
|-------------|--------|----|
| | 2.3.1 | 9 |
| LUAD | 3.1.3 | 10 |
| | 3.1.4 | 13 |
| | 3.4.21 | 30 |
| LUSC | 3.6.3 | 30 |
| | 3.1.1 | 9 |
| | 3.1.3 | 24 |
| | 3.4.21 | 15 |
| | 3.6.3 | 15 |
| PRAD | 2.7.1 | 12 |
| | 2.4.1 | 18 |
| | 3.4.21 | 35 |
| STAD | 3.1.3 | 24 |
| | 2.7.1 | 37 |
| | 2.4.1 | 9 |
| | 3.1.3 | 29 |
| | 3.4.21 | 9 |
| THCA | 2.7.1 | 10 |
| | 2.4.1 | 9 |
| | 3.1.3 | 31 |
| | 3.4.21 | 32 |

Table S3: The statistical significance for correlations between our predictor and the mucin gene across 14 cancer types.

| Cancer | MUC12 | MUCL1 | MUC5B | MUC1 | MUC5AC | MUC22 | MUC15 | MUC21 | MUC16 | MUC17 | MUC13 | MUC7 | MUC3A | MUC20 | MUC6 |
|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| BLCA | 3.19E-01 | 1.65E-02 | 8.45E-01 | 2.40E-13 | 1.00E+00 | 4.96E-01 | 1.50E-02 | 2.47E-01 | 2.29E-01 | 6.18E-01 | 1.83E-01 | 1.42E-01 | 3.22E-02 | 1.59E-03 | 2.45E-01 |
| BRCA | 5.03E-01 | 3.00E-01 | 2.54E-02 | 9.52E-07 | 3.21E-01 | 1.81E-03 | 6.60E-03 | 8.24E-01 | 6.92E-01 | 1.46E-01 | 8.54E-05 | 1.94E-05 | 4.01E-11 | 7.14E-06 | 2.45E-01 |
| COAD | 2.39E-08 | 4.19E-02 | 5.05E-01 | 1.91E-02 | 2.15E-02 | 6.47E-01 | 4.90E-01 | 9.89E-02 | 4.95E-02 | 1.98E-01 | 2.04E-12 | 9.11E-01 | 1.11E-01 | 2.13E-08 | 1.37E-03 |
| ESCA | 1.51E-01 | 4.89E-01 | 4.09E-01 | 8.74E-07 | 1.51E-01 | 7.43E-01 | 4.48E-02 | 3.78E-02 | 1.02E-01 | 3.33E-01 | 5.20E-01 | 3.24E-01 | 9.23E-01 | 3.10E-01 | 7.37E-01 |
| HNSC | 1.19E-01 | 6.66E-01 | 2.80E-04 | 1.55E-22 | 2.29E-01 | 3.01E-02 | 3.90E-03 | 1.93E-04 | 3.02E-03 | 3.50E-03 | 3.57E-01 | 7.95E-02 | 2.30E-01 | 3.36E-01 | 8.72E-01 |
| KICH | 4.45E-02 | 8.65E-01 | 6.26E-01 | 1.10E-04 | 5.01E-01 | 9.99E-01 | 6.86E-01 | 3.44E-01 | 3.86E-01 | 2.97E-01 | 3.40E-01 | 4.15E-01 | 6.18E-01 | 2.51E-01 | 8.61E-02 |
| KIRC | 6.89E-02 | 8.91E-01 | 3.00E-01 | 4.50E-04 | 2.61E-01 | 4.25E-01 | 4.05E-04 | 1.94E-01 | 5.43E-01 | 2.54E-02 | 5.99E-05 | 9.64E-01 | 3.95E-07 | 5.66E-02 | 1.56E-01 |
| KIRP | 1.66E-01 | 1.76E-01 | 6.91E-01 | 5.88E-01 | 1.89E-01 | 7.73E-01 | 4.02E-01 | 8.91E-01 | 5.80E-01 | 8.19E-02 | 2.49E-02 | 8.06E-01 | 9.38E-06 | 5.55E-03 | 2.60E-01 |
| LIHC | 7.24E-01 | 3.52E-02 | 6.47E-01 | 2.96E-08 | 1.52E-01 | 7.84E-01 | 2.39E-04 | 6.97E-02 | 4.16E-01 | 6.59E-01 | 3.92E-03 | 1.22E-01 | 9.79E-01 | 2.19E-06 | 7.45E-03 |
| LUAD | 1.40E-01 | 5.59E-04 | 1.22E-03 | 6.28E-07 | 3.49E-01 | 9.22E-05 | 5.81E-01 | 1.33E-05 | 1.76E-02 | 7.61E-02 | 2.01E-02 | 1.16E-01 | 5.62E-01 | 1.62E-02 | 6.26E-02 |
| LUSC | 1.76E-02 | 5.98E-01 | 7.84E-02 | 8.48E-11 | 7.91E-01 | 1.72E-01 | 2.78E-05 | 4.12E-04 | 7.65E-03 | 5.24E-01 | 8.66E-01 | 1.17E-01 | 3.31E-03 | 2.58E-02 | 2.02E-01 |
| PRAD | 3.04E-01 | 1.27E-01 | 3.89E-01 | 9.33E-04 | 3.05E-01 | 1.04E-01 | 3.87E-02 | 1.08E-01 | 6.00E-02 | 2.23E-02 | 1.12E-03 | 1.41E-01 | 8.91E-03 | 7.21E-04 | 6.09E-02 |
| STAD | 6.48E-01 | 2.62E-02 | 2.01E-01 | 8.31E-04 | 1.09E-01 | 1.17E-02 | 5.35E-05 | 4.11E-02 | 4.84E-01 | 2.75E-01 | 3.40E-07 | 4.57E-01 | 4.64E-01 | 1.76E-02 | 4.99E-01 |
| THCA | 5.25E-01 | 4.27E-01 | 3.94E-01 | 2.27E-03 | 3.36E-01 | 7.42E-01 | 2.00E-01 | 5.73E-02 | 4.95E-01 | 1.54E-01 | 3.38E-01 | 5.71E-01 | 2.56E-01 | 3.42E-01 | 8.93E-01 |

Table S4: Pathways enriched for each of the 14 cancer types (p-value cutoff is 0.05), where pathway names in bold denote those known to be related to oxidative stress.

| Database | Enriched pathways in BLCA | P-Value |
|------------------|---|----------|
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 2.38E-19 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 2.86E-09 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 7.99E-09 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 3.13E-07 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 5.19E-07 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 5.19E-07 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 1.62E-06 |
| BIOCARTA | h_intrinsicPathway:Intrinsic Prothrombin Activation Pathway | 1.90E-06 |
| BIOCARTA | h_plateletAppPathway:Platelet Amyloid Precursor Protein Pathway | 4.01E-06 |
| BIOCARTA | h_compPathway:Complement Pathway | 1.94E-05 |
| BIOCARTA | h_amiPathway:Acute Myocardial Infarction | 2.51E-05 |
| REACTOME_PATHWAY | Synthesis of IP2, IP, and Ins in the cytosol | 5.82E-05 |
| KEGG_PATHWAY | hsa00600:Sphingolipid metabolism | 1.45E-04 |
| REACTOME_PATHWAY | Sphingolipid de novo biosynthesis | 2.11E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4.45E-04 |
| REACTOME_PATHWAY | Extrinsic Pathway of Fibrin Clot Formation | 5.14E-04 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 5.16E-04 |
| BIOCARTA | h_extrinsicPathway:Extrinsic Prothrombin Activation Pathway | 1.43E-03 |
| BIOCARTA | h_fibrinolysisPathway:Fibrinolysis Pathway | 1.43E-03 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 2.70E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 3.86E-03 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 4.19E-03 |
| REACTOME_PATHWAY | N-Glycan antennae elongation | 5.15E-03 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 7.30E-03 |
| REACTOME_PATHWAY | Cobalamin (Cbl, vitamin B12) transport and metabolism | 1.00E-02 |
| REACTOME_PATHWAY | Common Pathway of Fibrin Clot Formation | 1.10E-02 |
| KEGG_PATHWAY | hsa00565:Ether lipid metabolism | 1.27E-02 |
| REACTOME_PATHWAY | DARPP-32 events | 1.51E-02 |
| KEGG_PATHWAY | hsa00520:Amino sugar and nucleotide sugar metabolism | 1.52E-02 |
| REACTOME_PATHWAY | Initial triggering of complement | 1.71E-02 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 1.74E-02 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.74E-02 |
| KEGG_PATHWAY | hsa00564:Glycerophospholipid metabolism | 1.97E-02 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 2.18E-02 |
| BIOCARTA | h_classicPathway:Classical Complement Pathway | 2.98E-02 |
| REACTOME_PATHWAY | Negative regulation of MAPK pathway | 3.10E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 3.58E-02 |

| Database | Enriched pathways in BRCA | P-Value |
|------------------|---|----------|
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 1.01E-22 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 1.27E-19 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 1.64E-15 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.10E-08 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 3.85E-08 |
| GOTERM_BP_DIRECT | GO:0006003~fructose 2,6-bisphosphate metabolic process | 6.90E-07 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.29E-06 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 1.63E-06 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 3.25E-06 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 1.60E-05 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 2.75E-05 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 4.52E-05 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 5.75E-05 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 7.54E-05 |
| GOTERM_BP_DIRECT | GO:0015014~heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.02E-04 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 1.02E-04 |
| GOTERM_BP_DIRECT | GO:0048008~platelet-derived growth factor receptor signaling pathway | 2.35E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 2.46E-04 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 2.83E-04 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 3.70E-04 |
| GOTERM_BP_DIRECT | GO:0006487~protein N-linked glycosylation | 5.69E-04 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 7.54E-04 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 7.74E-04 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 8.13E-04 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 9.86E-04 |
| REACTOME_PATHWAY | Initial triggering of complement | 9.96E-04 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 1.02E-03 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 1.27E-03 |
| GOTERM_BP_DIRECT | GO:0006195~purine nucleotide catabolic process | 1.30E-03 |
| REACTOME_PATHWAY | Purine catabolism | 1.85E-03 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 1.96E-03 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 2.51E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 2.60E-03 |
| KEGG_PATHWAY | hsa00760:Nicotinate and nicotinamide metabolism | 2.69E-03 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 3.37E-03 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 3.58E-03 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 4.10E-03 |
| GOTERM_BP_DIRECT | GO:0001958~endochondral ossification | 5.22E-03 |
| GOTERM_BP_DIRECT | GO:0061621~canonical glycolysis | 5.22E-03 |

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| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 6.04E-03 |
| GOTERM_BP_DIRECT | GO:0030449~regulation of complement activation | 6.91E-03 |
| GOTERM_BP_DIRECT | GO:0050653~chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0033692~cellular polysaccharide biosynthetic process | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process | 8.82E-03 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.19E-02 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 1.19E-02 |
| GOTERM_BP_DIRECT | GO:0050651~dermatan sulfate proteoglycan biosynthetic process | 1.25E-02 |
| GOTERM_BP_DIRECT | GO:0019276~UDP-N-acetylgalactosamine metabolic process | 1.25E-02 |
| GOTERM_BP_DIRECT | GO:0044267~cellular protein metabolic process | 1.32E-02 |
| GOTERM_BP_DIRECT | GO:0050900~leukocyte migration | 1.44E-02 |
| REACTOME_PATHWAY | Glycolysis | 1.54E-02 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 1.57E-02 |
| KEGG_PATHWAY | hsa00532:Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate | 1.59E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.66E-02 |
| GOTERM_BP_DIRECT | GO:0033133~positive regulation of glucokinase activity | 2.07E-02 |
| GOTERM_BP_DIRECT | GO:0030311~poly-N-acetylactosamine biosynthetic process | 2.07E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.07E-02 |
| KEGG_PATHWAY | hsa00010:Glycolysis / Gluconeogenesis | 2.72E-02 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 2.84E-02 |
| GOTERM_BP_DIRECT | GO:0007411~axon guidance | 2.87E-02 |
| GOTERM_BP_DIRECT | GO:0001867~complement activation, lectin pathway | 2.88E-02 |
| REACTOME_PATHWAY | Ficolins bind to repetitive carbohydrate structures on the target cell surface | 2.94E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 2.94E-02 |
| KEGG_PATHWAY | hsa04152:AMPK signaling pathway | 3.14E-02 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 3.15E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.29E-02 |
| GOTERM_BP_DIRECT | GO:0050650~chondroitin sulfate proteoglycan biosynthetic process | 3.29E-02 |
| KEGG_PATHWAY | hsa00052:Galactose metabolism | 3.41E-02 |
| REACTOME_PATHWAY | Lectin pathway of complement activation | 3.52E-02 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 3.61E-02 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 3.69E-02 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 3.69E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 3.69E-02 |
| KEGG_PATHWAY | hsa00500:Starch and sucrose metabolism | 4.06E-02 |
| GOTERM_BP_DIRECT | GO:0042355~L-fucose catabolic process | 4.09E-02 |
| GOTERM_BP_DIRECT | GO:0051156~glucose 6-phosphate metabolic process | 4.09E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.09E-02 |
| KEGG_PATHWAY | hsa05322:Systemic lupus erythematosus | 4.11E-02 |
| GOTERM_BP_DIRECT | GO:0050728~negative regulation of inflammatory response | 4.30E-02 |

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| GOTERM_BP_DIRECT | GO:0001503~ossification | 4.39E-02 |
| GOTERM_BP_DIRECT | GO:0002003~angiotensin maturation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0009312~oligosaccharide biosynthetic process | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0046135~pyrimidine nucleoside catabolic process | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0033628~regulation of cell adhesion mediated by integrin | 4.49E-02 |
| REACTOME_PATHWAY | Activation of C3 and C5 | 4.66E-02 |
| GOTERM_BP_DIRECT | GO:0030166~proteoglycan biosynthetic process | 4.89E-02 |

| Database | Enriched pathways in COAD | P-Value |
|------------------|---|----------|
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 1.01E-22 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 1.27E-19 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 1.64E-15 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.10E-08 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 3.85E-08 |
| GOTERM_BP_DIRECT | GO:0006003~fructose 2,6-bisphosphate metabolic process | 6.90E-07 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.29E-06 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 1.63E-06 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 3.25E-06 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 1.60E-05 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 2.75E-05 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 4.52E-05 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 5.75E-05 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 7.54E-05 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 1.02E-04 |
| GOTERM_BP_DIRECT | GO:0015014~heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.02E-04 |
| GOTERM_BP_DIRECT | GO:0048008~platelet-derived growth factor receptor signaling pathway | 2.35E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 2.46E-04 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 2.83E-04 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 3.70E-04 |
| GOTERM_BP_DIRECT | GO:0006487~protein N-linked glycosylation | 5.69E-04 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 7.54E-04 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 7.74E-04 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 8.13E-04 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 9.86E-04 |
| REACTOME_PATHWAY | Initial triggering of complement | 9.96E-04 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 1.02E-03 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 1.27E-03 |
| GOTERM_BP_DIRECT | GO:0006195~purine nucleotide catabolic process | 1.30E-03 |
| REACTOME_PATHWAY | R-HSA-74259:R-HSA-74259 | 1.85E-03 |

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| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 1.96E-03 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 2.51E-03 |
| REACTOME_PATHWAY | Purine catabolism | 2.60E-03 |
| KEGG_PATHWAY | hsa00760:Nicotinate and nicotinamide metabolism | 2.69E-03 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 3.37E-03 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 3.58E-03 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 4.10E-03 |
| GOTERM_BP_DIRECT | GO:0061621~canonical glycolysis | 5.22E-03 |
| GOTERM_BP_DIRECT | GO:0001958~endochondral ossification | 5.22E-03 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 6.04E-03 |
| GOTERM_BP_DIRECT | GO:0030449~regulation of complement activation | 6.91E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0050653~chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0033692~cellular polysaccharide biosynthetic process | 8.32E-03 |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process | 8.82E-03 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 1.19E-02 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.19E-02 |
| GOTERM_BP_DIRECT | GO:0050651~dermatan sulfate proteoglycan biosynthetic process | 1.25E-02 |
| GOTERM_BP_DIRECT | GO:0019276~UDP-N-acetylgalactosamine metabolic process | 1.25E-02 |
| GOTERM_BP_DIRECT | GO:0044267~cellular protein metabolic process | 1.32E-02 |
| GOTERM_BP_DIRECT | GO:0050900~leukocyte migration | 1.44E-02 |
| REACTOME_PATHWAY | Glycolysis | 1.54E-02 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 1.57E-02 |
| KEGG_PATHWAY | hsa00532:Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate | 1.59E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.66E-02 |
| GOTERM_BP_DIRECT | GO:0033133~positive regulation of glucokinase activity | 2.07E-02 |
| GOTERM_BP_DIRECT | GO:0030311~poly-N-acetyllactosamine biosynthetic process | 2.07E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.07E-02 |
| KEGG_PATHWAY | hsa00010:Glycolysis / Gluconeogenesis | 2.72E-02 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 2.84E-02 |
| GOTERM_BP_DIRECT | GO:0007411~axon guidance | 2.87E-02 |
| GOTERM_BP_DIRECT | GO:0001867~complement activation, lectin pathway | 2.88E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 2.94E-02 |
| REACTOME_PATHWAY | Ficolins bind to repetitive carbohydrate structures on the target cell surface | 2.94E-02 |
| KEGG_PATHWAY | hsa04152:AMPK signaling pathway | 3.14E-02 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 3.15E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.29E-02 |
| GOTERM_BP_DIRECT | GO:0050650~chondroitin sulfate proteoglycan biosynthetic process | 3.29E-02 |
| KEGG_PATHWAY | hsa00052:Galactose metabolism | 3.41E-02 |
| REACTOME_PATHWAY | Lectin pathway of complement activation | 3.52E-02 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 3.61E-02 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 3.69E-02 |

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| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 3.69E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 3.69E-02 |
| KEGG_PATHWAY | hsa00500:Starch and sucrose metabolism | 4.06E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.09E-02 |
| GOTERM_BP_DIRECT | GO:0042355~L-fucose catabolic process | 4.09E-02 |
| GOTERM_BP_DIRECT | GO:0051156~glucose 6-phosphate metabolic process | 4.09E-02 |
| KEGG_PATHWAY | hsa05322:Systemic lupus erythematosus | 4.11E-02 |
| GOTERM_BP_DIRECT | GO:0050728~negative regulation of inflammatory response | 4.30E-02 |
| GOTERM_BP_DIRECT | GO:0001503~ossification | 4.39E-02 |
| GOTERM_BP_DIRECT | GO:0046135~pyrimidine nucleoside catabolic process | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0033628~regulation of cell adhesion mediated by integrin | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0002003~angiotensin maturation | 4.49E-02 |
| GOTERM_BP_DIRECT | GO:0009312~oligosaccharide biosynthetic process | 4.49E-02 |
| REACTOME_PATHWAY | Activation of C3 and C5 | 4.66E-02 |
| GOTERM_BP_DIRECT | GO:0030166~proteoglycan biosynthetic process | 4.89E-02 |

| Database | Enriched pathways in ESCA | P-Value |
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| KEGG_PATHWAY | hsa01100:Metabolic pathways | 2.47E-12 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 8.77E-10 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 1.22E-09 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 3.24E-09 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 6.21E-09 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 4.23E-08 |
| GOTERM_BP_DIRECT | GO:0009312~oligosaccharide biosynthetic process | 8.41E-07 |
| KEGG_PATHWAY | hsa00510:N-Glycan biosynthesis | 1.85E-06 |
| REACTOME_PATHWAY | N-Glycan antennae elongation | 6.34E-06 |
| GOTERM_BP_DIRECT | GO:0032259~methylation | 8.27E-06 |
| GOTERM_BP_DIRECT | GO:0046500~S-adenosylmethionine metabolic process | 6.44E-05 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 4.13E-04 |
| KEGG_PATHWAY | hsa01212:Fatty acid metabolism | 1.13E-03 |
| GOTERM_BP_DIRECT | GO:0006487~protein N-linked glycosylation | 2.19E-03 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 2.54E-03 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 3.61E-03 |
| KEGG_PATHWAY | hsa00514:Other types of O-glycan biosynthesis | 4.02E-03 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 4.78E-03 |
| GOTERM_BP_DIRECT | GO:0016266~O-glycan processing | 5.12E-03 |
| GOTERM_BP_DIRECT | GO:0046498~S-adenosylhomocysteine metabolic process | 7.13E-03 |
| REACTOME_PATHWAY | O-linked glycosylation of mucins | 9.63E-03 |
| GOTERM_BP_DIRECT | GO:0006853~carnitine shuttle | 1.60E-02 |
| GOTERM_BP_DIRECT | GO:0036109~alpha-linolenic acid metabolic process | 2.30E-02 |
| REACTOME_PATHWAY | Import of palmitoyl-CoA into the mitochondrial matrix | 2.75E-02 |
| REACTOME_PATHWAY | alpha-linolenic acid (ALA) metabolism | 3.25E-02 |
| KEGG_PATHWAY | hsa03320:PPAR signaling pathway | 3.41E-02 |
| GOTERM_BP_DIRECT | GO:0030206~chondroitin sulfate biosynthetic process | 4.38E-02 |
| GOTERM_BP_DIRECT | GO:0046487~glyoxylate metabolic process | 4.55E-02 |
| KEGG_PATHWAY | hsa00130:Ubiquinone and other terpenoid-quinone biosynthesis | 4.70E-02 |
| REACTOME_PATHWAY | Signaling by Retinoic Acid | 4.95E-02 |
| REACTOME_PATHWAY | Chondroitin sulfate biosynthesis | 4.95E-02 |

| Database | Enriched pathways in HNSC | P-Value |
|------------------|---|----------|
| GOTERM_BP_DIRECT | GO:0016310~phosphorylation | 1.21E-17 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 2.46E-17 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 2.09E-16 |
| GOTERM_BP_DIRECT | GO:0006661~phosphatidylinositol biosynthetic process | 2.16E-14 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 2.74E-13 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 1.80E-12 |
| REACTOME_PATHWAY | Synthesis of PIPs at the plasma membrane | 3.26E-10 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 3.99E-10 |
| GOTERM_BP_DIRECT | GO:0046854~phosphatidylinositol phosphorylation | 3.17E-09 |

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| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 6.08E-09 |
| GOTERM_BP_DIRECT | GO:0036092~phosphatidylinositol-3-phosphate biosynthetic process | 1.13E-08 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 3.12E-08 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 6.90E-08 |
| KEGG_PATHWAY | hsa00010:Glycolysis / Gluconeogenesis | 2.08E-07 |
| KEGG_PATHWAY | hsa01200:Carbon metabolism | 2.53E-07 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 2.70E-07 |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process | 1.34E-06 |
| KEGG_PATHWAY | hsa05230:Central carbon metabolism in cancer | 1.80E-06 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 6.23E-06 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 6.91E-06 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 6.97E-06 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 7.76E-06 |
| GOTERM_BP_DIRECT | GO:0061621~canonical glycolysis | 1.36E-05 |
| KEGG_PATHWAY | hsa01130:Biosynthesis of antibiotics | 2.22E-05 |
| KEGG_PATHWAY | hsa00030:Pentose phosphate pathway | 3.53E-05 |
| KEGG_PATHWAY | hsa00052:Galactose metabolism | 4.20E-05 |
| REACTOME_PATHWAY | Synthesis of IP2, IP, and Ins in the cytosol | 8.88E-05 |
| REACTOME_PATHWAY | Glycolysis | 1.37E-04 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.55E-04 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.23E-04 |
| GOTERM_BP_DIRECT | GO:0061624~fructose catabolic process to hydroxyacetone phosphate and glyceraldehyde-3-phosphate | 3.20E-04 |
| GOTERM_BP_DIRECT | GO:0009157~deoxyribonucleoside monophosphate biosynthetic process | 3.20E-04 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 3.58E-04 |
| REACTOME_PATHWAY | Synthesis of PIPs at the Golgi membrane | 4.21E-04 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 4.74E-04 |
| REACTOME_PATHWAY | Fructose catabolism | 6.81E-04 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 7.75E-04 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 9.39E-04 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 1.41E-03 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 1.72E-03 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 1.72E-03 |
| GOTERM_BP_DIRECT | GO:0006071~glycerol metabolic process | 1.72E-03 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 2.40E-03 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 2.49E-03 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 2.98E-03 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 2.98E-03 |
| REACTOME_PATHWAY | Synthesis of PIPs at the late endosome membrane | 2.98E-03 |
| GOTERM_BP_DIRECT | GO:0048015~phosphatidylinositol-mediated signaling | 3.19E-03 |
| GOTERM_BP_DIRECT | GO:0009165~nucleotide biosynthetic process | 3.24E-03 |
| KEGG_PATHWAY | hsa00520:Amino sugar and nucleotide sugar metabolism | 3.72E-03 |
| KEGG_PATHWAY | hsa04930:Type II diabetes mellitus | 3.72E-03 |

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| GOTERM_BP_DIRECT | GO:0006796~phosphate-containing compound metabolic process | 4.66E-03 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 4.66E-03 |
| KEGG_PATHWAY | hsa04152:AMPK signaling pathway | 5.90E-03 |
| REACTOME_PATHWAY | Synthesis of PIPs at the early endosome membrane | 5.90E-03 |
| KEGG_PATHWAY | hsa00760:Nicotinate and nicotinamide metabolism | 6.58E-03 |
| GOTERM_BP_DIRECT | GO:0006006~glucose metabolic process | 6.66E-03 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 8.12E-03 |
| GOTERM_BP_DIRECT | GO:0046856~phosphatidylinositol dephosphorylation | 8.23E-03 |
| GOTERM_BP_DIRECT | GO:0006465~signal peptide processing | 8.91E-03 |
| GOTERM_BP_DIRECT | GO:0014066~regulation of phosphatidylinositol 3-kinase signaling | 1.01E-02 |
| KEGG_PATHWAY | hsa04910:Insulin signaling pathway | 1.02E-02 |
| GOTERM_BP_DIRECT | GO:0050728~negative regulation of inflammatory response | 1.05E-02 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 1.11E-02 |
| GOTERM_BP_DIRECT | GO:0050653~chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.14E-02 |
| GOTERM_BP_DIRECT | GO:0046104~thymidine metabolic process | 1.14E-02 |
| GOTERM_BP_DIRECT | GO:0006001~fructose catabolic process | 1.14E-02 |
| GOTERM_BP_DIRECT | GO:0005986~sucrose biosynthetic process | 1.14E-02 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 1.31E-02 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 1.36E-02 |
| REACTOME_PATHWAY | Common Pathway of Fibrin Clot Formation | 1.43E-02 |
| KEGG_PATHWAY | hsa01230:Biosynthesis of amino acids | 1.54E-02 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 1.66E-02 |
| GOTERM_BP_DIRECT | GO:0050651~dermatan sulfate proteoglycan biosynthetic process | 1.71E-02 |
| GOTERM_BP_DIRECT | GO:0046167~glycerol-3-phosphate biosynthetic process | 1.71E-02 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 2.12E-02 |
| GOTERM_BP_DIRECT | GO:1901215~negative regulation of neuron death | 2.19E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 2.27E-02 |
| GOTERM_BP_DIRECT | GO:0006021~inositol biosynthetic process | 2.27E-02 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 2.27E-02 |
| KEGG_PATHWAY | hsa00600:Sphingolipid metabolism | 2.46E-02 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 2.62E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.83E-02 |
| REACTOME_PATHWAY | Synthesis of IPs in the nucleus | 3.31E-02 |
| GOTERM_BP_DIRECT | GO:0032958~inositol phosphate biosynthetic process | 3.38E-02 |
| GOTERM_BP_DIRECT | GO:0019563~glycerol catabolic process | 3.38E-02 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 3.52E-02 |
| GOTERM_BP_DIRECT | GO:0001867~complement activation, lectin pathway | 3.93E-02 |
| GOTERM_BP_DIRECT | GO:0006020~inositol metabolic process | 3.93E-02 |
| REACTOME_PATHWAY | Ficolins bind to repetitive carbohydrate structures on the target cell surface | 4.12E-02 |
| REACTOME_PATHWAY | Glucose metabolism | 4.12E-02 |
| KEGG_PATHWAY | hsa00561:Glycerolipid metabolism | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 4.48E-02 |

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| GOTERM_BP_DIRECT | GO:0050650~chondroitin sulfate proteoglycan biosynthetic process | 4.48E-02 |
| GOTERM_BP_DIRECT | GO:0051289~protein homotetramerization | 4.62E-02 |
| REACTOME_PATHWAY | Lectin pathway of complement activation | 4.92E-02 |

| Database | Enriched pathways in KICH | P-Value |
|------------------|--|----------------|
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 5.25E-08 |
| KEGG_PATHWAY | hsa00270:Cysteine and methionine metabolism | 3.80E-07 |
| GOTERM_BP_DIRECT | GO:0090116~C-5 methylation of cytosine | 1.40E-06 |
| KEGG_PATHWAY | hsa00520:Amino sugar and nucleotide sugar metabolism | 6.71E-05 |
| GOTERM_BP_DIRECT | GO:0006306~DNA methylation | 1.39E-04 |
| GOTERM_BP_DIRECT | GO:0045814~negative regulation of gene expression, epigenetic | 5.63E-04 |
| GOTERM_BP_DIRECT | GO:0046499~S-adenosylmethioninamine metabolic process | 1.43E-03 |
| GOTERM_BP_DIRECT | GO:0010424~DNA methylation on cytosine within a CG sequence | 2.14E-03 |
| REACTOME_PATHWAY | DNA methylation | 2.67E-03 |
| GOTERM_BP_DIRECT | GO:0046498~S-adenosylhomocysteine metabolic process | 2.86E-03 |
| REACTOME_PATHWAY | PRC2 methylates histones and DNA | 3.35E-03 |
| GOTERM_BP_DIRECT | GO:0043045~DNA methylation involved in embryo development | 3.57E-03 |
| GOTERM_BP_DIRECT | GO:0051573~negative regulation of histone H3-K9 methylation | 4.28E-03 |
| REACTOME_PATHWAY | Metabolism of polyamines | 4.84E-03 |
| GOTERM_BP_DIRECT | GO:0006595~polyamine metabolic process | 4.99E-03 |
| GOTERM_BP_DIRECT | GO:0006048~UDP-N-acetylglucosamine biosynthetic process | 7.84E-03 |
| GOTERM_BP_DIRECT | GO:0051571~positive regulation of histone H3-K4 methylation | 1.21E-02 |
| GOTERM_BP_DIRECT | GO:0033189~response to vitamin A | 1.28E-02 |
| GOTERM_BP_DIRECT | GO:0042220~response to cocaine | 2.26E-02 |
| GOTERM_BP_DIRECT | GO:0071230~cellular response to amino acid stimulus | 3.31E-02 |
| GOTERM_BP_DIRECT | GO:0010212~response to ionizing radiation | 3.45E-02 |

| database | Enriched pathways in KIRC | P-Value |
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| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 8.13E-28 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 1.55E-17 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 7.47E-13 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 6.07E-11 |
| REACTOME_PATHWAY | Synthesis of IP2, IP, and Ins in the cytosol | 8.28E-11 |
| KEGG_PATHWAY | hsa00511:Other glycan degradation | 9.76E-10 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 4.89E-09 |
| KEGG_PATHWAY | hsa04142:Lysosome | 2.25E-07 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 2.36E-07 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 9.27E-07 |
| GOTERM_BP_DIRECT | GO:0016139~glycoside catabolic process | 1.43E-06 |
| GOTERM_BP_DIRECT | GO:0006796~phosphate-containing compound metabolic process | 2.13E-06 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 2.20E-06 |
| KEGG_PATHWAY | hsa00531:Glycosaminoglycan degradation | 2.60E-06 |

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| GOTERM_BP_DIRECT | GO:0006687~glycosphingolipid metabolic process | 3.86E-06 |
| GOTERM_BP_DIRECT | GO:0006027~glycosaminoglycan catabolic process | 1.01E-05 |
| GOTERM_BP_DIRECT | GO:0006661~phosphatidylinositol biosynthetic process | 1.37E-05 |
| KEGG_PATHWAY | hsa00600:Sphingolipid metabolism | 2.13E-05 |
| GOTERM_BP_DIRECT | GO:0009313~oligosaccharide catabolic process | 2.30E-05 |
| REACTOME_PATHWAY | Glycosphingolipid metabolism | 2.44E-05 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 2.48E-05 |
| REACTOME_PATHWAY | Digestion of dietary carbohydrate | 3.73E-05 |
| KEGG_PATHWAY | hsa00500:Starch and sucrose metabolism | 4.63E-05 |
| GOTERM_BP_DIRECT | GO:0016042~lipid catabolic process | 8.77E-05 |
| REACTOME_PATHWAY | Synthesis of PIPs at the plasma membrane | 1.50E-04 |
| GOTERM_BP_DIRECT | GO:0044245~polysaccharide digestion | 1.66E-04 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 1.92E-04 |
| GOTERM_BP_DIRECT | GO:0046856~phosphatidylinositol dephosphorylation | 2.69E-04 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 3.10E-04 |
| KEGG_PATHWAY | hsa00052:Galactose metabolism | 4.66E-04 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 5.73E-04 |
| REACTOME_PATHWAY | HS-GAG degradation | 6.35E-04 |
| GOTERM_BP_DIRECT | GO:0006517~protein deglycosylation | 1.22E-03 |
| GOTERM_BP_DIRECT | GO:0036092~phosphatidylinositol-3-phosphate biosynthetic process | 2.22E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 4.45E-03 |
| KEGG_PATHWAY | hsa01130:Biosynthesis of antibiotics | 4.48E-03 |
| KEGG_PATHWAY | hsa00030:Pentose phosphate pathway | 5.28E-03 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 5.46E-03 |
| REACTOME_PATHWAY | N-glycan trimming in the ER and Calnexin/Calreticulin cycle | 6.75E-03 |
| GOTERM_BP_DIRECT | GO:0036151~phosphatidylcholine acyl-chain remodeling | 8.95E-03 |
| GOTERM_BP_DIRECT | GO:0006629~lipid metabolic process | 9.71E-03 |
| GOTERM_BP_DIRECT | GO:0046477~glycosylceramide catabolic process | 1.06E-02 |
| GOTERM_BP_DIRECT | GO:0005986~sucrose biosynthetic process | 1.06E-02 |
| GOTERM_BP_DIRECT | GO:0006001~fructose catabolic process | 1.06E-02 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 1.15E-02 |
| KEGG_PATHWAY | hsa01200:Carbon metabolism | 1.27E-02 |
| GOTERM_BP_DIRECT | GO:0046854~phosphatidylinositol phosphorylation | 1.36E-02 |
| GOTERM_BP_DIRECT | GO:0043407~negative regulation of MAP kinase activity | 1.56E-02 |
| GOTERM_BP_DIRECT | GO:0007040~lysosome organization | 1.56E-02 |
| REACTOME_PATHWAY | Intestinal saccharidase deficiencies | 1.56E-02 |
| GOTERM_BP_DIRECT | GO:0000023~maltose metabolic process | 1.58E-02 |
| KEGG_PATHWAY | hsa00565:Ether lipid metabolism | 1.78E-02 |
| REACTOME_PATHWAY | Acyl chain remodelling of PC | 1.87E-02 |
| GOTERM_BP_DIRECT | GO:1901215~negative regulation of neuron death | 1.90E-02 |
| REACTOME_PATHWAY | Synthesis of IP3 and IP4 in the cytosol | 2.00E-02 |
| GOTERM_BP_DIRECT | GO:0030200~heparan sulfate proteoglycan catabolic process | 2.10E-02 |

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| GOTERM_BP_DIRECT | GO:0006021~inositol biosynthetic process | 2.10E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 2.10E-02 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 2.27E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.62E-02 |
| REACTOME_PATHWAY | Sialic acid metabolism | 2.73E-02 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 2.73E-02 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 2.87E-02 |
| GOTERM_BP_DIRECT | GO:0006689~ganglioside catabolic process | 3.14E-02 |
| KEGG_PATHWAY | hsa00561:Glycerolipid metabolism | 3.45E-02 |
| GOTERM_BP_DIRECT | GO:0009056~catabolic process | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0006013~mannose metabolic process | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0006020~inositol metabolic process | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0006004~fucose metabolic process | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0006032~chitin catabolic process | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0048771~tissue remodeling | 3.65E-02 |
| KEGG_PATHWAY | hsa00592:alpha-Linolenic acid metabolism | 3.77E-02 |
| GOTERM_BP_DIRECT | GO:0007416~synapse assembly | 4.15E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0030299~intestinal cholesterol absorption | 4.67E-02 |
| GOTERM_BP_DIRECT | GO:0006006~glucose metabolic process | 4.92E-02 |
| KEGG_PATHWAY | hsa00591:Linoleic acid metabolism | 4.94E-02 |

| Database | Enriched pathways in KIRP | P-Value |
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| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 7.70E-14 |
| KEGG_PATHWAY | hsa04972:Pancreatic secretion | 2.10E-13 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 2.34E-12 |
| GOTERM_BP_DIRECT | GO:0016042~lipid catabolic process | 2.66E-12 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 5.22E-11 |
| GOTERM_BP_DIRECT | GO:0006629~lipid metabolic process | 1.25E-09 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.43E-08 |
| REACTOME_PATHWAY | Digestion of dietary lipid | 5.22E-08 |
| GOTERM_BP_DIRECT | GO:0015991~ATP hydrolysis coupled proton transport | 2.32E-07 |
| KEGG_PATHWAY | hsa00561:Glycerolipid metabolism | 1.50E-06 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.85E-06 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 1.89E-06 |
| KEGG_PATHWAY | hsa04975:Fat digestion and absorption | 2.05E-06 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 1.84E-05 |
| GOTERM_BP_DIRECT | GO:0044241~lipid digestion | 2.10E-05 |
| GOTERM_BP_DIRECT | GO:0034220~ion transmembrane transport | 3.20E-05 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 5.89E-05 |
| KEGG_PATHWAY | hsa00565:Ether lipid metabolism | 7.85E-05 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 1.08E-04 |

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| GOTERM_BP_DIRECT | GO:0015986~ATP synthesis coupled proton transport | 1.10E-04 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 1.53E-04 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 1.89E-04 |
| GOTERM_BP_DIRECT | GO:0036151~phosphatidylcholine acyl-chain remodeling | 2.05E-04 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 3.50E-04 |
| KEGG_PATHWAY | hsa00564:Glycerophospholipid metabolism | 3.52E-04 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 3.75E-04 |
| GOTERM_BP_DIRECT | GO:0006641~triglyceride metabolic process | 4.48E-04 |
| REACTOME_PATHWAY | Ion transport by P-type ATPases | 4.61E-04 |
| REACTOME_PATHWAY | Acyl chain remodelling of PC | 6.50E-04 |
| GOTERM_BP_DIRECT | GO:0007035~vacuolar acidification | 1.60E-03 |
| GOTERM_BP_DIRECT | GO:0006644~phospholipid metabolic process | 1.60E-03 |
| GOTERM_BP_DIRECT | GO:1903779~regulation of cardiac conduction | 1.78E-03 |
| KEGG_PATHWAY | hsa04974:Protein digestion and absorption | 1.80E-03 |
| KEGG_PATHWAY | hsa00592:alpha-Linolenic acid metabolism | 1.90E-03 |
| KEGG_PATHWAY | hsa00190:Oxidative phosphorylation | 2.06E-03 |
| KEGG_PATHWAY | hsa04966:Collecting duct acid secretion | 2.38E-03 |
| GOTERM_BP_DIRECT | GO:0036148~phosphatidylglycerol acyl-chain remodeling | 2.65E-03 |
| KEGG_PATHWAY | hsa00030:Pentose phosphate pathway | 2.93E-03 |
| KEGG_PATHWAY | hsa00591:Linoleic acid metabolism | 2.93E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 2.99E-03 |
| GOTERM_BP_DIRECT | GO:0036152~phosphatidylethanolamine acyl-chain remodeling | 4.71E-03 |
| REACTOME_PATHWAY | Ion homeostasis | 5.40E-03 |
| GOTERM_BP_DIRECT | GO:0090383~phagosome acidification | 5.94E-03 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 6.19E-03 |
| REACTOME_PATHWAY | Acyl chain remodelling of PG | 6.40E-03 |
| KEGG_PATHWAY | hsa04142:Lysosome | 7.11E-03 |
| REACTOME_PATHWAY | Acyl chain remodelling of PG | 7.80E-03 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 8.04E-03 |
| GOTERM_BP_DIRECT | GO:0005986~sucrose biosynthetic process | 8.56E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 8.56E-03 |
| GOTERM_BP_DIRECT | GO:0006001~fructose catabolic process | 8.56E-03 |
| GOTERM_BP_DIRECT | GO:0033572~transferrin transport | 9.85E-03 |
| REACTOME_PATHWAY | Ion channel transport | 1.01E-02 |
| REACTOME_PATHWAY | Insulin receptor recycling | 1.18E-02 |
| GOTERM_BP_DIRECT | GO:1903416~response to glycoside | 1.28E-02 |
| REACTOME_PATHWAY | Transferrin endocytosis and recycling | 1.46E-02 |
| KEGG_PATHWAY | hsa05110:Vibrio cholerae infection | 1.50E-02 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 1.53E-02 |
| REACTOME_PATHWAY | Acyl chain remodelling of PE | 1.56E-02 |
| GOTERM_BP_DIRECT | GO:0002084~protein depalmitoylation | 1.70E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.70E-02 |
| REACTOME_PATHWAY | ROS, RNS production in phagocytes | 1.98E-02 |

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| GOTERM_BP_DIRECT | GO:0006633~fatty acid biosynthetic process | 2.09E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.13E-02 |
| KEGG_PATHWAY | hsa00590:Arachidonic acid metabolism | 2.30E-02 |
| KEGG_PATHWAY | hsa01200:Carbon metabolism | 2.64E-02 |
| GOTERM_BP_DIRECT | GO:0001523~retinoid metabolic process | 2.82E-02 |
| GOTERM_BP_DIRECT | GO:0045822~negative regulation of heart contraction | 2.96E-02 |
| GOTERM_BP_DIRECT | GO:0048771~tissue remodeling | 2.96E-02 |
| REACTOME_PATHWAY | Retinoid metabolism and transport | 3.07E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 3.16E-02 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 3.38E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.38E-02 |
| KEGG_PATHWAY | hsa04971:Gastric acid secretion | 3.65E-02 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 3.79E-02 |
| GOTERM_BP_DIRECT | GO:1990573~potassium ion import across plasma membrane | 3.79E-02 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 3.79E-02 |
| GOTERM_BP_DIRECT | GO:0086009~membrane repolarization | 3.79E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 3.79E-02 |
| GOTERM_BP_DIRECT | GO:0030299~intestinal cholesterol absorption | 3.79E-02 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 4.05E-02 |
| GOTERM_BP_DIRECT | GO:0070072~vacuolar proton-transporting V-type ATPase complex assembly | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0036376~sodium ion export from cell | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0071383~cellular response to steroid hormone stimulus | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0040011~locomotion | 4.21E-02 |
| GOTERM_BP_DIRECT | GO:0008286~insulin receptor signaling pathway | 4.42E-02 |
| GOTERM_BP_DIRECT | GO:0045820~negative regulation of glycolytic process | 4.62E-02 |
| GOTERM_BP_DIRECT | GO:0006098~pentose-phosphate shunt | 4.62E-02 |
| GOTERM_BP_DIRECT | GO:0060081~membrane hyperpolarization | 4.62E-02 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 4.62E-02 |

| Database | Enriched pathways in LIHC | P-Value |
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| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 2.53E-16 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 9.27E-15 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 3.28E-11 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 8.18E-09 |
| GOTERM_BP_DIRECT | GO:0030148~sphingolipid biosynthetic process | 8.82E-07 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 1.70E-06 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 6.90E-06 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 7.10E-06 |
| GOTERM_BP_DIRECT | GO:0009312~oligosaccharide biosynthetic process | 7.74E-06 |
| KEGG_PATHWAY | hsa00514:Other types of O-glycan biosynthesis | 3.63E-05 |

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| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 4.32E-05 |
| REACTOME_PATHWAY | Sphingolipid de novo biosynthesis | 5.10E-05 |
| REACTOME_PATHWAY | N-Glycan antennae elongation | 5.31E-05 |
| GOTERM_BP_DIRECT | GO:0030206~chondroitin sulfate biosynthetic process | 1.04E-04 |
| REACTOME_PATHWAY | Chondroitin sulfate biosynthesis | 1.31E-04 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 1.47E-04 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 2.78E-04 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 3.65E-04 |
| GOTERM_BP_DIRECT | GO:0006487~protein N-linked glycosylation | 3.98E-04 |
| GOTERM_BP_DIRECT | GO:0042355~L-fucose catabolic process | 5.92E-04 |
| KEGG_PATHWAY | hsa00532:Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate | 6.79E-04 |
| GOTERM_BP_DIRECT | GO:0046839~phospholipid dephosphorylation | 7.22E-04 |
| KEGG_PATHWAY | hsa00600:Sphingolipid metabolism | 7.51E-04 |
| GOTERM_BP_DIRECT | GO:0006644~phospholipid metabolic process | 1.04E-03 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 1.76E-03 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 2.38E-03 |
| KEGG_PATHWAY | hsa01130:Biosynthesis of antibiotics | 2.54E-03 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 3.15E-03 |
| KEGG_PATHWAY | hsa00565:Ether lipid metabolism | 7.23E-03 |
| GOTERM_BP_DIRECT | GO:0050653~chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 7.37E-03 |
| GOTERM_BP_DIRECT | GO:0006001~fructose catabolic process | 7.37E-03 |
| GOTERM_BP_DIRECT | GO:0005986~sucrose biosynthetic process | 7.37E-03 |
| KEGG_PATHWAY | hsa00510:N-Glycan biosynthesis | 9.15E-03 |
| KEGG_PATHWAY | hsa00564:Glycerophospholipid metabolism | 9.77E-03 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 1.05E-02 |
| GOTERM_BP_DIRECT | GO:0019276~UDP-N-acetylgalactosamine metabolic process | 1.10E-02 |
| GOTERM_BP_DIRECT | GO:0050651~dermatan sulfate proteoglycan biosynthetic process | 1.10E-02 |
| GOTERM_BP_DIRECT | GO:0006094~gluconeogenesis | 1.15E-02 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 1.30E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.47E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 1.83E-02 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 1.88E-02 |
| KEGG_PATHWAY | hsa00062:Fatty acid elongation | 2.04E-02 |
| GOTERM_BP_DIRECT | GO:0001933~negative regulation of protein phosphorylation | 2.13E-02 |
| GOTERM_BP_DIRECT | GO:0008152~metabolic process | 2.42E-02 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 2.91E-02 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 2.92E-02 |
| GOTERM_BP_DIRECT | GO:0050650~chondroitin sulfate proteoglycan biosynthetic process | 2.92E-02 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 3.24E-02 |
| GOTERM_BP_DIRECT | GO:0008354~germ cell migration | 3.28E-02 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 3.63E-02 |

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| GOTERM_BP_DIRECT | GO:0036065~fucosylation | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0046135~pyrimidine nucleoside catabolic process | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0002003~angiotensin maturation | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0045820~negative regulation of glycolytic process | 3.99E-02 |
| GOTERM_BP_DIRECT | GO:0030166~proteoglycan biosynthetic process | 4.34E-02 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 4.47E-02 |
| KEGG_PATHWAY | hsa04975:Fat digestion and absorption | 4.65E-02 |
| GOTERM_BP_DIRECT | GO:0071456~cellular response to hypoxia | 4.90E-02 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 4.96E-02 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 4.96E-02 |

| Database | Enriched pathways in LUAD | P-Value |
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| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 2.73E-21 |
| GOTERM_BP_DIRECT | GO:0015991~ATP hydrolysis coupled proton transport | 7.80E-19 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 6.94E-18 |
| KEGG_PATHWAY | hsa00190:Oxidative phosphorylation | 1.34E-15 |
| GOTERM_BP_DIRECT | GO:0034220~ion transmembrane transport | 2.04E-14 |
| GOTERM_BP_DIRECT | GO:0042776~mitochondrial ATP synthesis coupled proton transport | 2.09E-14 |
| REACTOME_PATHWAY | Formation of ATP by chemiosmotic coupling | 1.84E-13 |
| GOTERM_BP_DIRECT | GO:0006754~ATP biosynthetic process | 4.29E-13 |
| GOTERM_BP_DIRECT | GO:0015986~ATP synthesis coupled proton transport | 4.30E-12 |
| KEGG_PATHWAY | hsa04972:Pancreatic secretion | 1.14E-11 |
| GOTERM_BP_DIRECT | GO:0033572~transferrin transport | 1.62E-10 |
| REACTOME_PATHWAY | Ion channel transport | 2.18E-10 |
| REACTOME_PATHWAY | Insulin receptor recycling | 4.10E-10 |
| REACTOME_PATHWAY | Transferrin endocytosis and recycling | 9.57E-10 |
| GOTERM_BP_DIRECT | GO:0090383~phagosome acidification | 1.78E-09 |
| GOTERM_BP_DIRECT | GO:0015992~proton transport | 1.97E-09 |
| KEGG_PATHWAY | hsa04966:Collecting duct acid secretion | 9.34E-09 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.99E-08 |
| GOTERM_BP_DIRECT | GO:0008286~insulin receptor signaling pathway | 5.46E-08 |
| KEGG_PATHWAY | hsa05110:Vibrio cholerae infection | 6.28E-08 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 8.53E-08 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.02E-07 |
| REACTOME_PATHWAY | ROS, RNS production in phagocytes | 1.23E-07 |
| REACTOME_PATHWAY | Ion transport by P-type ATPases | 1.39E-07 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 3.86E-07 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 1.07E-06 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 1.11E-06 |
| KEGG_PATHWAY | hsa05010:Alzheimer's disease | 1.47E-06 |

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| GOTERM_BP_DIRECT | GO:0006956~complement activation | 2.46E-06 |
| GOTERM_BP_DIRECT | GO:1903779~regulation of cardiac conduction | 4.97E-06 |
| KEGG_PATHWAY | hsa05120:Epithelial cell signaling in Helicobacter pylori infection | 6.49E-06 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 1.38E-05 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 2.86E-05 |
| KEGG_PATHWAY | hsa05323:Rheumatoid arthritis | 3.96E-05 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 4.06E-05 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 4.06E-05 |
| REACTOME_PATHWAY | Ion homeostasis | 4.65E-05 |
| KEGG_PATHWAY | hsa04721:Synaptic vesicle cycle | 5.28E-05 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 1.17E-04 |
| REACTOME_PATHWAY | Reduction of cytosolic Ca⁺⁺ levels | 1.21E-04 |
| KEGG_PATHWAY | hsa04971:Gastric acid secretion | 1.22E-04 |
| KEGG_PATHWAY | hsa05012:Parkinson's disease | 1.29E-04 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 1.72E-04 |
| GOTERM_BP_DIRECT | GO:0006465~signal peptide processing | 1.83E-04 |
| KEGG_PATHWAY | hsa04145:Phagosome | 1.89E-04 |
| KEGG_PATHWAY | hsa05016:Huntington's disease | 1.96E-04 |
| KEGG_PATHWAY | hsa04974:Protein digestion and absorption | 3.41E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4.25E-04 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 5.91E-04 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 6.94E-04 |
| GOTERM_BP_DIRECT | GO:0036376~sodium ion export from cell | 8.65E-04 |
| GOTERM_BP_DIRECT | GO:0016241~regulation of macroautophagy | 9.94E-04 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 1.00E-03 |
| GOTERM_BP_DIRECT | GO:0030007~cellular potassium ion homeostasis | 1.26E-03 |
| KEGG_PATHWAY | hsa04022:cGMP-PKG signaling pathway | 1.46E-03 |
| GOTERM_BP_DIRECT | GO:0010248~establishment or maintenance of transmembrane electrochemical gradient | 1.49E-03 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 1.51E-03 |
| REACTOME_PATHWAY | Initial triggering of complement | 1.99E-03 |
| KEGG_PATHWAY | hsa04970:Salivary secretion | 2.22E-03 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 2.80E-03 |
| GOTERM_BP_DIRECT | GO:0006883~cellular sodium ion homeostasis | 3.20E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 3.74E-03 |
| GOTERM_BP_DIRECT | GO:0010107~potassium ion import | 6.90E-03 |
| GOTERM_BP_DIRECT | GO:0030449~regulation of complement activation | 7.90E-03 |
| GOTERM_BP_DIRECT | GO:0006874~cellular calcium ion homeostasis | 8.33E-03 |
| GOTERM_BP_DIRECT | GO:0032470~positive regulation of endoplasmic reticulum calcium ion concentration | 8.91E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 8.91E-03 |
| GOTERM_BP_DIRECT | GO:0045851~pH reduction | 8.91E-03 |

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| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 9.88E-03 |
| REACTOME_PATHWAY | Common Pathway of Fibrin Clot Formation | 1.06E-02 |
| KEGG_PATHWAY | hsa04020:Calcium signaling pathway | 1.22E-02 |
| KEGG_PATHWAY | hsa04961:Endocrine and other factor-regulated calcium reabsorption | 1.23E-02 |
| GOTERM_BP_DIRECT | GO:0045087~innate immune response | 1.24E-02 |
| GOTERM_BP_DIRECT | GO:1903416~response to glycoside | 1.33E-02 |
| GOTERM_BP_DIRECT | GO:1901660~calcium ion export | 1.33E-02 |
| GOTERM_BP_DIRECT | GO:0044267~cellular protein metabolic process | 1.58E-02 |
| KEGG_PATHWAY | hsa04261:Adrenergic signaling in cardiomyocytes | 1.61E-02 |
| GOTERM_BP_DIRECT | GO:0070588~calcium ion transmembrane transport | 1.62E-02 |
| REACTOME_PATHWAY | Synthesis of IP3 and IP4 in the cytosol | 1.69E-02 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.69E-02 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 1.87E-02 |
| GOTERM_BP_DIRECT | GO:0007598~blood coagulation, extrinsic pathway | 2.21E-02 |
| GOTERM_BP_DIRECT | GO:0045822~negative regulation of heart contraction | 3.09E-02 |
| GOTERM_BP_DIRECT | GO:0046069~cGMP catabolic process | 3.09E-02 |
| GOTERM_BP_DIRECT | GO:0001867~complement activation, lectin pathway | 3.09E-02 |
| GOTERM_BP_DIRECT | GO:0006888~ER to Golgi vesicle-mediated transport | 3.48E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.52E-02 |
| GOTERM_BP_DIRECT | GO:0086036~regulation of cardiac muscle cell membrane potential | 3.52E-02 |
| REACTOME_PATHWAY | Ficolins bind to repetitive carbohydrate structures on the target cell surface | 3.53E-02 |
| REACTOME_PATHWAY | Extrinsic Pathway of Fibrin Clot Formation | 3.53E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 3.53E-02 |
| KEGG_PATHWAY | hsa04918:Thyroid hormone synthesis | 3.92E-02 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 3.95E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 3.95E-02 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 4.06E-02 |
| KEGG_PATHWAY | hsa04142:Lysosome | 4.08E-02 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 4.12E-02 |
| REACTOME_PATHWAY | Lectin pathway of complement activation | 4.22E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.38E-02 |
| GOTERM_BP_DIRECT | GO:0071383~cellular response to steroid hormone stimulus | 4.38E-02 |

| Database | Enriched pathways in LUSC | P-Value |
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| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 2.57E-13 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 1.08E-10 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 9.16E-09 |
| GOTERM_BP_DIRECT | GO:0015991~ATP hydrolysis coupled proton transport | 7.07E-08 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 2.19E-07 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 6.84E-07 |
| GOTERM_BP_DIRECT | GO:0015986~ATP synthesis coupled proton transport | 8.34E-07 |

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| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 4.70E-06 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 2.11E-05 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 2.92E-05 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 6.76E-05 |
| GOTERM_BP_DIRECT | GO:0034220~ion transmembrane transport | 7.60E-05 |
| KEGG_PATHWAY | hsa00190:Oxidative phosphorylation | 8.08E-05 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 4.01E-04 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 6.11E-04 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 8.60E-04 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 9.63E-04 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 1.20E-03 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 1.20E-03 |
| GOTERM_BP_DIRECT | GO:0006672~ceramide metabolic process | 1.49E-03 |
| GOTERM_BP_DIRECT | GO:0006629~lipid metabolic process | 1.98E-03 |
| GOTERM_BP_DIRECT | GO:0042776~mitochondrial ATP synthesis coupled proton transport | 2.28E-03 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 3.21E-03 |
| GOTERM_BP_DIRECT | GO:0006465~signal peptide processing | 3.23E-03 |
| REACTOME_PATHWAY | Ion transport by P-type ATPases | 3.33E-03 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 3.51E-03 |
| REACTOME_PATHWAY | Formation of ATP by chemiosmotic coupling | 3.97E-03 |
| GOTERM_BP_DIRECT | GO:0006754~ATP biosynthetic process | 4.33E-03 |
| GOTERM_BP_DIRECT | GO:0035774~positive regulation of insulin secretion involved in cellular response to glucose stimulus | 4.33E-03 |
| GOTERM_BP_DIRECT | GO:0033572~transferrin transport | 6.27E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 6.78E-03 |
| KEGG_PATHWAY | hsa00564:Glycerophospholipid metabolism | 6.80E-03 |
| REACTOME_PATHWAY | Ion channel transport | 7.02E-03 |
| KEGG_PATHWAY | hsa05110:Vibrio cholerae infection | 8.11E-03 |
| REACTOME_PATHWAY | Insulin receptor recycling | 8.21E-03 |
| REACTOME_PATHWAY | Transferrin endocytosis and recycling | 1.02E-02 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 1.11E-02 |
| GOTERM_BP_DIRECT | GO:0015992~proton transport | 1.20E-02 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 1.30E-02 |
| GOTERM_BP_DIRECT | GO:0002084~protein depalmitoylation | 1.35E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.35E-02 |
| GOTERM_BP_DIRECT | GO:1903779~regulation of cardiac conduction | 1.55E-02 |
| KEGG_PATHWAY | hsa04142:Lysosome | 1.56E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 1.69E-02 |
| KEGG_PATHWAY | hsa04966:Collecting duct acid secretion | 1.94E-02 |
| GOTERM_BP_DIRECT | GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling | 2.05E-02 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 2.56E-02 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 2.75E-02 |

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| GOTERM_BP_DIRECT | GO:0008286~insulin receptor signaling pathway | 2.88E-02 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 3.01E-02 |
| GOTERM_BP_DIRECT | GO:0070072~vacuolar proton-transporting V-type ATPase complex assembly | 3.34E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 3.34E-02 |
| GOTERM_BP_DIRECT | GO:0016042~lipid catabolic process | 3.38E-02 |
| REACTOME_PATHWAY | Ion homeostasis | 3.52E-02 |
| GOTERM_BP_DIRECT | GO:0060081~membrane hyperpolarization | 3.67E-02 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 3.67E-02 |
| KEGG_PATHWAY | hsa04972:Pancreatic secretion | 3.79E-02 |
| REACTOME_PATHWAY | Activation of C3 and C5 | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0016540~protein autoprocessing | 4.33E-02 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 4.45E-02 |
| KEGG_PATHWAY | hsa05010:Alzheimer's disease | 4.47E-02 |
| GOTERM_BP_DIRECT | GO:0007035~vacuolar acidification | 4.65E-02 |
| GOTERM_BP_DIRECT | GO:0030194~positive regulation of blood coagulation | 4.65E-02 |

| Database | Enriched pathways in PRAD | P-Value |
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| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 1.25E-20 |
| KEGG_PATHWAY | hsa04610:Complement and coagulation cascades | 1.86E-19 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 2.43E-10 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 2.85E-09 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 5.63E-08 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 6.71E-08 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 8.53E-08 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 1.46E-07 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 1.98E-07 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 2.36E-07 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 3.29E-07 |
| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 3.29E-07 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 1.32E-06 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 1.50E-06 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 2.40E-06 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 2.56E-06 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 3.34E-06 |
| GOTERM_BP_DIRECT | GO:0006465~signal peptide processing | 5.32E-06 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 6.93E-06 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 1.54E-05 |
| GOTERM_BP_DIRECT | GO:0009312~oligosaccharide biosynthetic process | 1.61E-05 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 1.76E-05 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 6.50E-05 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 6.94E-05 |

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| REACTOME_PATHWAY | N-Glycan antennae elongation | 1.12E-04 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 1.30E-04 |
| KEGG_PATHWAY | hsa00510:N-Glycan biosynthesis | 1.66E-04 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 1.66E-04 |
| GOTERM_BP_DIRECT | GO:0007598~blood coagulation, extrinsic pathway | 2.17E-04 |
| KEGG_PATHWAY | hsa00052:Galactose metabolism | 2.74E-04 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 3.02E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 3.19E-04 |
| REACTOME_PATHWAY | Extrinsic Pathway of Fibrin Clot Formation | 4.10E-04 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 6.01E-04 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 6.08E-04 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 7.62E-04 |
| REACTOME_PATHWAY | Synthesis of IP3 and IP4 in the cytosol | 7.62E-04 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 7.70E-04 |
| GOTERM_BP_DIRECT | GO:0006487~protein N-linked glycosylation | 8.11E-04 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 9.42E-04 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 1.01E-03 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 1.22E-03 |
| KEGG_PATHWAY | hsa01200:Carbon metabolism | 1.29E-03 |
| REACTOME_PATHWAY | Initial triggering of complement | 1.39E-03 |
| KEGG_PATHWAY | hsa00514:Other types of O-glycan biosynthesis | 1.59E-03 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 2.06E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 3.10E-03 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 3.25E-03 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 4.73E-03 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 4.74E-03 |
| GOTERM_BP_DIRECT | GO:0046856~phosphatidylinositol dephosphorylation | 5.64E-03 |
| KEGG_PATHWAY | hsa00010:Glycolysis / Gluconeogenesis | 5.67E-03 |
| GOTERM_BP_DIRECT | GO:0006888~ER to Golgi vesicle-mediated transport | 6.86E-03 |
| GOTERM_BP_DIRECT | GO:0030449~regulation of complement activation | 8.73E-03 |
| REACTOME_PATHWAY | Common Pathway of Fibrin Clot Formation | 8.83E-03 |
| GOTERM_BP_DIRECT | GO:0006001~fructose catabolic process | 9.39E-03 |
| GOTERM_BP_DIRECT | GO:0005986~sucrose biosynthetic process | 9.39E-03 |
| GOTERM_BP_DIRECT | GO:0033692~cellular polysaccharide biosynthetic process | 9.39E-03 |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process | 1.11E-02 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 1.14E-02 |
| GOTERM_BP_DIRECT | GO:0016310~phosphorylation | 1.17E-02 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.41E-02 |
| KEGG_PATHWAY | hsa04974:Protein digestion and absorption | 1.46E-02 |
| KEGG_PATHWAY | hsa04972:Pancreatic secretion | 1.75E-02 |
| GOTERM_BP_DIRECT | GO:0044267~cellular protein metabolic process | 1.82E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.87E-02 |

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| GOTERM_BP_DIRECT | GO:0015014~heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.87E-02 |
| REACTOME_PATHWAY | Synthesis of PIPs at the plasma membrane | 2.15E-02 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 2.16E-02 |
| KEGG_PATHWAY | hsa01130:Biosynthesis of antibiotics | 2.60E-02 |
| GOTERM_BP_DIRECT | GO:0006661~phosphatidylinositol biosynthetic process | 3.05E-02 |
| REACTOME_PATHWAY | Ficolins bind to repetitive carbohydrate structures on the target cell surface | 3.21E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 3.21E-02 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 3.25E-02 |
| GOTERM_BP_DIRECT | GO:0001867~complement activation, lectin pathway | 3.25E-02 |
| GOTERM_BP_DIRECT | GO:0006110~regulation of glycolytic process | 3.25E-02 |
| KEGG_PATHWAY | hsa05202:Transcriptional misregulation in cancer | 3.34E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.70E-02 |
| GOTERM_BP_DIRECT | GO:0046626~regulation of insulin receptor signaling pathway | 3.70E-02 |
| REACTOME_PATHWAY | Lectin pathway of complement activation | 3.84E-02 |
| KEGG_PATHWAY | hsa00030:Pentose phosphate pathway | 3.84E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0042355~L-fucose catabolic process | 4.61E-02 |
| GOTERM_BP_DIRECT | GO:0051156~glucose 6-phosphate metabolic process | 4.61E-02 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 4.61E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.61E-02 |
| KEGG_PATHWAY | hsa00500:Starch and sucrose metabolism | 4.86E-02 |

| Database | Enriched pathways in STAD | P-Value |
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| KEGG_PATHWAY | hsa01100:Metabolic pathways | 2.20E-21 |
| GOTERM_BP_DIRECT | GO:0016310~phosphorylation | 5.68E-21 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 1.24E-12 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 5.25E-12 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 6.68E-10 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 3.04E-09 |
| GOTERM_BP_DIRECT | GO:0006661~phosphatidylinositol biosynthetic process | 2.36E-07 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 1.17E-06 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 2.20E-06 |
| KEGG_PATHWAY | hsa01130:Biosynthesis of antibiotics | 1.40E-05 |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process | 1.62E-05 |
| GOTERM_BP_DIRECT | GO:0046834~lipid phosphorylation | 1.90E-05 |
| KEGG_PATHWAY | hsa01200:Carbon metabolism | 2.53E-05 |
| KEGG_PATHWAY | hsa00561:Glycerolipid metabolism | 3.28E-05 |
| GOTERM_BP_DIRECT | GO:0015012~heparan sulfate proteoglycan biosynthetic process | 5.79E-05 |
| KEGG_PATHWAY | hsa00010:Glycolysis / Gluconeogenesis | 7.50E-05 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 7.90E-05 |
| GOTERM_BP_DIRECT | GO:0046856~phosphatidylinositol dephosphorylation | 1.68E-04 |

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| GOTERM_BP_DIRECT | GO:0009157~deoxyribonucleoside monophosphate biosynthetic process | 2.00E-04 |
| GOTERM_BP_DIRECT | GO:0061624~fructose catabolic process to hydroxyacetone phosphate and glyceraldehyde-3-phosphate | 2.00E-04 |
| KEGG_PATHWAY | hsa00760:Nicotinate and nicotinamide metabolism | 2.39E-04 |
| REACTOME_PATHWAY | Synthesis of PIPs at the Golgi membrane | 2.53E-04 |
| KEGG_PATHWAY | hsa00051:Fructose and mannose metabolism | 3.53E-04 |
| GOTERM_BP_DIRECT | GO:0007205~protein kinase C-activating G-protein coupled receptor signaling pathway | 3.66E-04 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 3.88E-04 |
| GOTERM_BP_DIRECT | GO:0030388~fructose 1,6-bisphosphate metabolic process | 4.18E-04 |
| REACTOME_PATHWAY | Effects of PIP2 hydrolysis | 4.68E-04 |
| REACTOME_PATHWAY | Fructose catabolism | 4.83E-04 |
| GOTERM_BP_DIRECT | GO:0046854~phosphatidylinositol phosphorylation | 8.68E-04 |
| GOTERM_BP_DIRECT | GO:0006024~glycosaminoglycan biosynthetic process | 9.01E-04 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 1.05E-03 |
| GOTERM_BP_DIRECT | GO:0006071~glycerol metabolic process | 1.08E-03 |
| GOTERM_BP_DIRECT | GO:0036092~phosphatidylinositol-3-phosphate biosynthetic process | 1.41E-03 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 1.72E-03 |
| GOTERM_BP_DIRECT | GO:0030168~platelet activation | 1.83E-03 |
| GOTERM_BP_DIRECT | GO:0009165~nucleotide biosynthetic process | 2.04E-03 |
| KEGG_PATHWAY | hsa00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin | 2.06E-03 |
| REACTOME_PATHWAY | Synthesis of IP2, IP, and Ins in the cytosol | 2.58E-03 |
| KEGG_PATHWAY | hsa00230:Purine metabolism | 2.71E-03 |
| KEGG_PATHWAY | hsa05230:Central carbon metabolism in cancer | 4.82E-03 |
| GOTERM_BP_DIRECT | GO:0061621~canonical glycolysis | 6.12E-03 |
| GOTERM_BP_DIRECT | GO:0033692~cellular polysaccharide biosynthetic process | 9.03E-03 |
| GOTERM_BP_DIRECT | GO:0046104~thymidine metabolic process | 9.03E-03 |
| GOTERM_BP_DIRECT | GO:0046167~glycerol-3-phosphate biosynthetic process | 1.35E-02 |
| KEGG_PATHWAY | hsa00450:Selenocompound metabolism | 1.40E-02 |
| REACTOME_PATHWAY | Synthesis of IP3 and IP4 in the cytosol | 1.64E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.80E-02 |
| GOTERM_BP_DIRECT | GO:0015014~heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.80E-02 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 1.95E-02 |
| REACTOME_PATHWAY | Glycolysis | 2.12E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.24E-02 |
| KEGG_PATHWAY | hsa00240:Pyrimidine metabolism | 2.30E-02 |
| GOTERM_BP_DIRECT | GO:0001501~skeletal system development | 2.42E-02 |
| REACTOME_PATHWAY | Synthesis of PIPs at the plasma membrane | 2.51E-02 |
| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 2.56E-02 |
| GOTERM_BP_DIRECT | GO:0050428~3'-phosphoadenosine 5'-phosphosulfate biosynthetic process | 2.69E-02 |
| GOTERM_BP_DIRECT | GO:0032958~inositol phosphate biosynthetic process | 2.69E-02 |
| GOTERM_BP_DIRECT | GO:0019563~glycerol catabolic process | 2.69E-02 |

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| REACTOME_PATHWAY | Metabolism of ingested H ₂ SeO ₄ and H ₂ SeO ₃ into H ₂ Se | 2.79E-02 |
| REACTOME_PATHWAY | Synthesis of IPs in the nucleus | 2.79E-02 |
| GOTERM_BP_DIRECT | GO:0051289~protein homotetramerization | 3.02E-02 |
| GOTERM_BP_DIRECT | GO:0030259~lipid glycosylation | 3.13E-02 |
| GOTERM_BP_DIRECT | GO:0046486~glycerolipid metabolic process | 3.13E-02 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 3.31E-02 |
| REACTOME_PATHWAY | Glucose metabolism | 3.48E-02 |
| GOTERM_BP_DIRECT | GO:0006002~fructose 6-phosphate metabolic process | 3.56E-02 |
| GOTERM_BP_DIRECT | GO:0000103~sulfate assimilation | 3.56E-02 |
| GOTERM_BP_DIRECT | GO:0035556~intracellular signal transduction | 3.58E-02 |
| GOTERM_BP_DIRECT | GO:0032868~response to insulin | 3.70E-02 |
| GOTERM_BP_DIRECT | GO:0006006~glucose metabolic process | 3.70E-02 |
| KEGG_PATHWAY | hsa00030: Pentose phosphate pathway | 3.84E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 4.00E-02 |
| KEGG_PATHWAY | hsa00052: Galactose metabolism | 4.09E-02 |
| REACTOME_PATHWAY | Transport and synthesis of PAPS | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 4.22E-02 |
| GOTERM_BP_DIRECT | GO:0006000~fructose metabolic process | 4.44E-02 |
| GOTERM_BP_DIRECT | GO:0051156~glucose 6-phosphate metabolic process | 4.44E-02 |
| GOTERM_BP_DIRECT | GO:0009247~glycolipid biosynthetic process | 4.44E-02 |
| KEGG_PATHWAY | hsa00500: Starch and sucrose metabolism | 4.86E-02 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 4.87E-02 |
| GOTERM_BP_DIRECT | GO:0035970~peptidyl-threonine dephosphorylation | 4.87E-02 |
| GOTERM_BP_DIRECT | GO:0045820~negative regulation of glycolytic process | 4.87E-02 |
| GOTERM_BP_DIRECT | GO:0002003~angiotensin maturation | 4.87E-02 |
| GOTERM_BP_DIRECT | GO:0046135~pyrimidine nucleoside catabolic process | 4.87E-02 |
| GOTERM_BP_DIRECT | GO:0050728~negative regulation of inflammatory response | 4.98E-02 |

| Database | Enriched pathways in THCA | P-Value |
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| GOTERM_BP_DIRECT | GO:0006508~proteolysis | 2.05E-19 |
| KEGG_PATHWAY | hsa04610: Complement and coagulation cascades | 2.38E-19 |
| GOTERM_BP_DIRECT | GO:0006470~protein dephosphorylation | 6.26E-13 |
| GOTERM_BP_DIRECT | GO:0035335~peptidyl-tyrosine dephosphorylation | 8.70E-10 |
| REACTOME_PATHWAY | Activation of Matrix Metalloproteinases | 2.86E-09 |
| REACTOME_PATHWAY | Intrinsic Pathway of Fibrin Clot Formation | 7.99E-09 |
| GOTERM_BP_DIRECT | GO:0007597~blood coagulation, intrinsic pathway | 1.66E-08 |
| GOTERM_BP_DIRECT | GO:0042730~fibrinolysis | 3.89E-08 |
| GOTERM_BP_DIRECT | GO:0022617~extracellular matrix disassembly | 6.55E-08 |
| GOTERM_BP_DIRECT | GO:0017187~peptidyl-glutamic acid carboxylation | 1.46E-07 |
| REACTOME_PATHWAY | Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | 3.13E-07 |
| GOTERM_BP_DIRECT | GO:0051919~positive regulation of fibrinolysis | 4.00E-07 |
| REACTOME_PATHWAY | Gamma-carboxylation of protein precursors | 5.19E-07 |

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| REACTOME_PATHWAY | Removal of aminoterminal propeptides from gamma-carboxylated proteins | 5.19E-07 |
| KEGG_PATHWAY | hsa05150:Staphylococcus aureus infection | 1.62E-06 |
| GOTERM_BP_DIRECT | GO:0007596~blood coagulation | 2.40E-06 |
| GOTERM_BP_DIRECT | GO:0016311~dephosphorylation | 3.12E-06 |
| GOTERM_BP_DIRECT | GO:0046835~carbohydrate phosphorylation | 3.75E-06 |
| GOTERM_BP_DIRECT | GO:0006465~signal peptide processing | 5.32E-06 |
| GOTERM_BP_DIRECT | GO:0031638~zymogen activation | 8.25E-06 |
| GOTERM_BP_DIRECT | GO:0006956~complement activation | 5.54E-05 |
| REACTOME_PATHWAY | Synthesis of IP2, IP, and Ins in the cytosol | 5.82E-05 |
| GOTERM_BP_DIRECT | GO:0043647~inositol phosphate metabolic process | 6.94E-05 |
| GOTERM_BP_DIRECT | GO:0030148~sphingolipid biosynthetic process | 7.54E-05 |
| KEGG_PATHWAY | hsa00600:Sphingolipid metabolism | 1.45E-04 |
| GOTERM_BP_DIRECT | GO:0006486~protein glycosylation | 1.91E-04 |
| REACTOME_PATHWAY | Sphingolipid de novo biosynthesis | 2.11E-04 |
| GOTERM_BP_DIRECT | GO:0007598~blood coagulation, extrinsic pathway | 2.17E-04 |
| GOTERM_BP_DIRECT | GO:0007586~digestion | 2.19E-04 |
| GOTERM_BP_DIRECT | GO:0016485~protein processing | 3.66E-04 |
| REACTOME_PATHWAY | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4.45E-04 |
| REACTOME_PATHWAY | Extrinsic Pathway of Fibrin Clot Formation | 5.14E-04 |
| KEGG_PATHWAY | hsa00533:Glycosaminoglycan biosynthesis - keratan sulfate | 5.16E-04 |
| GOTERM_BP_DIRECT | GO:0031639~plasminogen activation | 7.70E-04 |
| GOTERM_BP_DIRECT | GO:0046855~inositol phosphate dephosphorylation | 1.17E-03 |
| GOTERM_BP_DIRECT | GO:0046839~phospholipid dephosphorylation | 1.17E-03 |
| GOTERM_BP_DIRECT | GO:0006958~complement activation, classical pathway | 1.22E-03 |
| GOTERM_BP_DIRECT | GO:0030194~positive regulation of blood coagulation | 1.92E-03 |
| KEGG_PATHWAY | hsa00601:Glycosphingolipid biosynthesis - lacto and neolacto series | 2.70E-03 |
| GOTERM_BP_DIRECT | GO:0006796~phosphate-containing compound metabolic process | 3.18E-03 |
| REACTOME_PATHWAY | Dissolution of Fibrin Clot | 3.86E-03 |
| KEGG_PATHWAY | hsa01100:Metabolic pathways | 4.19E-03 |
| GOTERM_BP_DIRECT | GO:0009235~cobalamin metabolic process | 4.33E-03 |
| REACTOME_PATHWAY | N-Glycan antennae elongation | 5.15E-03 |
| GOTERM_BP_DIRECT | GO:0046856~phosphatidylinositol dephosphorylation | 5.64E-03 |
| GOTERM_BP_DIRECT | GO:0000188~inactivation of MAPK activity | 6.11E-03 |
| GOTERM_BP_DIRECT | GO:0006888~ER to Golgi vesicle-mediated transport | 6.86E-03 |
| KEGG_PATHWAY | hsa00562:Inositol phosphate metabolism | 7.30E-03 |
| GOTERM_BP_DIRECT | GO:0018146~keratan sulfate biosynthetic process | 7.63E-03 |
| GOTERM_BP_DIRECT | GO:0030449~regulation of complement activation | 8.73E-03 |
| GOTERM_BP_DIRECT | GO:0005975~carbohydrate metabolic process | 9.16E-03 |
| GOTERM_BP_DIRECT | GO:0002542~Factor XII activation | 9.39E-03 |
| GOTERM_BP_DIRECT | GO:0033692~cellular polysaccharide biosynthetic process | 9.39E-03 |
| REACTOME_PATHWAY | Cobalamin (Cbl, vitamin B12) transport and metabolism | 1.00E-02 |
| REACTOME_PATHWAY | Common Pathway of Fibrin Clot Formation | 1.10E-02 |

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| GOTERM_BP_DIRECT | GO:0016310~phosphorylation | 1.17E-02 |
| KEGG_PATHWAY | hsa00565:Ether lipid metabolism | 1.27E-02 |
| REACTOME_PATHWAY | DARPP-32 events | 1.51E-02 |
| KEGG_PATHWAY | hsa00520:Amino sugar and nucleotide sugar metabolism | 1.52E-02 |
| GOTERM_BP_DIRECT | GO:1901215~negative regulation of neuron death | 1.52E-02 |
| REACTOME_PATHWAY | Initial triggering of complement | 1.71E-02 |
| REACTOME_PATHWAY | Keratan sulfate biosynthesis | 1.74E-02 |
| REACTOME_PATHWAY | Regulation of Complement cascade | 1.74E-02 |
| GOTERM_BP_DIRECT | GO:0044267~cellular protein metabolic process | 1.82E-02 |
| GOTERM_BP_DIRECT | GO:0006670~sphingosine metabolic process | 1.87E-02 |
| GOTERM_BP_DIRECT | GO:0006021~inositol biosynthetic process | 1.87E-02 |
| GOTERM_BP_DIRECT | GO:0015014~heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process | 1.87E-02 |
| KEGG_PATHWAY | hsa00564:Glycerophospholipid metabolism | 1.97E-02 |
| KEGG_PATHWAY | hsa04070:Phosphatidylinositol signaling system | 2.18E-02 |
| GOTERM_BP_DIRECT | GO:0043456~regulation of pentose-phosphate shunt | 2.33E-02 |
| GOTERM_BP_DIRECT | GO:0006644~phospholipid metabolic process | 2.67E-02 |
| REACTOME_PATHWAY | Negative regulation of MAPK pathway | 3.10E-02 |
| GOTERM_BP_DIRECT | GO:0006020~inositol metabolic process | 3.25E-02 |
| REACTOME_PATHWAY | Alternative complement activation | 3.58E-02 |
| GOTERM_BP_DIRECT | GO:0033173~calcineurin-NFAT signaling cascade | 3.70E-02 |
| GOTERM_BP_DIRECT | GO:0014909~smooth muscle cell migration | 3.70E-02 |
| GOTERM_BP_DIRECT | GO:0008354~germ cell migration | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0006012~galactose metabolic process | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0050778~positive regulation of immune response | 4.16E-02 |
| GOTERM_BP_DIRECT | GO:0051918~negative regulation of fibrinolysis | 4.61E-02 |
| GOTERM_BP_DIRECT | GO:0051533~positive regulation of NFAT protein import into nucleus | 4.61E-02 |