

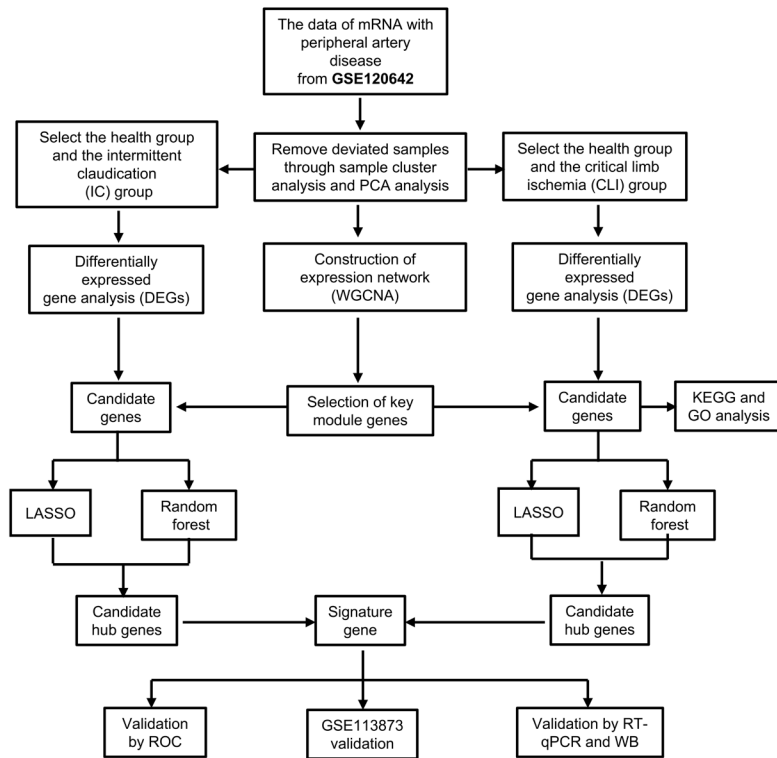


Figure S1 Flow chart of data preparation, processing, analysis, and validation.

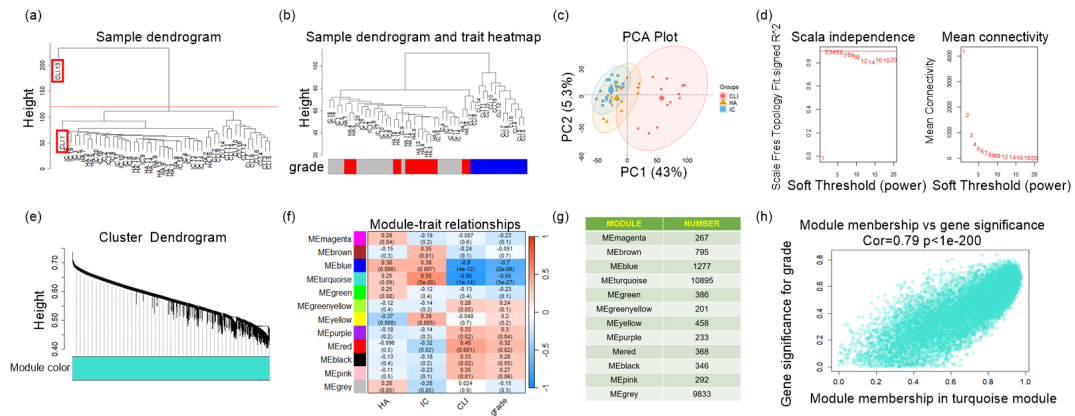


Figure S2 WGCNA bioinformatics analysis.

(a) Sample clustering of skeletal muscle samples of 15 health older adults, 20 IC patients and 16 CLI patients to detect outliers. (b) Sample clustering of skeletal muscle samples of 15 health older adults, 20 IC patients and 14 CLI patients to detect outliers. (c) PCA plot of HA group, IC group and CLI group. (d) Soft-thresholding power analysis was used to obtain the scale-free fit index of network topology. (e) Hierarchical cluster analysis was conducted to detect co-expression clusters with corresponding color assignments. Each color represents a module in the constructed gene co-expression network by WGCNA. (f) Heatmap plot of module-trait relationships. Row corresponds to modules, column corresponds to PAD traits. Each square contains the corresponding correlation in the first line and the p-value in the second line. Red represents a positive correlation, and the blue represents a negative correlation. (g) The number of genes in the 12 modules. (h) Correlation between the Module Membership and Gene significance in the turquoise module. HA, healthy; IC, intermittent claudication, CLI: critical limb ischemia. PAD, peripheral arterial disease. WGCNA, weighted gene co-expression network analysis.

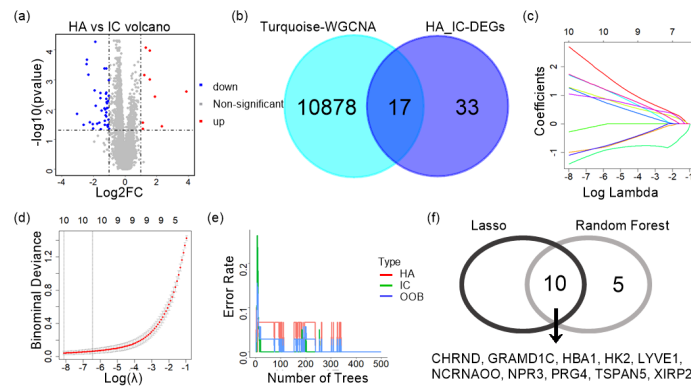


Figure S3 Screening for hub genes in HA and IC groups.

(a) Volcano plot of DEGs between HA group and IC group. X-axis represents $\log_2$ fold-changes and Y-axis represents negative logarithm to the base 10 of the p-values. (b) Venn diagram shows common 17 DEGs between DEGs and turquoise module genes. (c) LASSO plot showed the variations in the size of coefficients for parameters shrunk as the value of k penalty increased. (d) Penalty plot of the LASSO model with error bars denoting standard errors. (e) The error rate confidence intervals for random forest model. (f) The intersection of the LASSO and random forest algorithms. HA, healthy; IC, intermittent claudication, CLI: critical limb ischemia. DEGs, differential expressed gene. LASSO, least absolute shrinkage and selection operator.

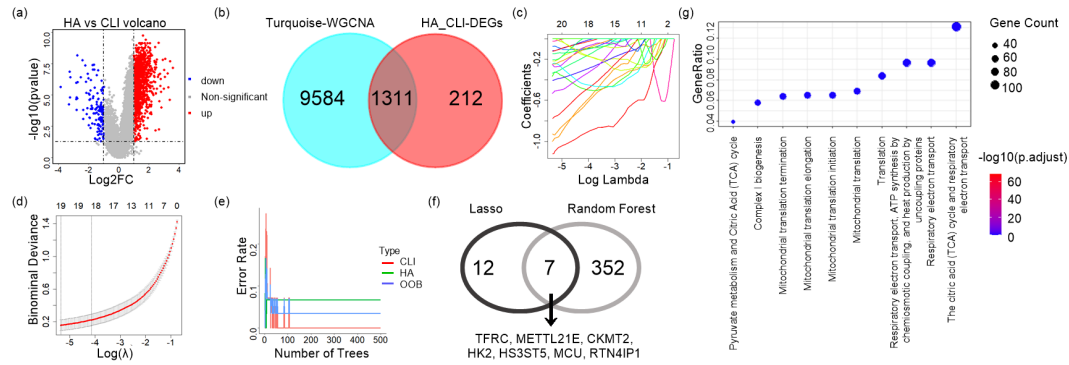


Figure S4 Screening for hub genes in HA and CLI groups.

(a) Volcano plot of DEGs between HA group and CLI group. X-axis represents log2 fold-changes and Y-axis represents negative logarithm to the base 10 of the p-values. (b) Venn diagram shows common 1311 DEGs between DEGs and turquoise module genes. (c) LASSO plot showed the variations in the size of coefficients for parameters shrank as the value of k penalty increased. (d) Penalty plot of the LASSO model with error bars denoting standard errors. (e) The error rate confidence intervals for random forest model. (f) The intersection of the LASSO and random forest algorithms. (g) Pathway and process enrichment analysis of 1311 DEGs by Rectom pathway. HA, healthy; IC, intermittent claudication, CLI: critical limb ischemia. DEGs, differential expressed gene. LASSO, least absolute shrinkage and selection operator.

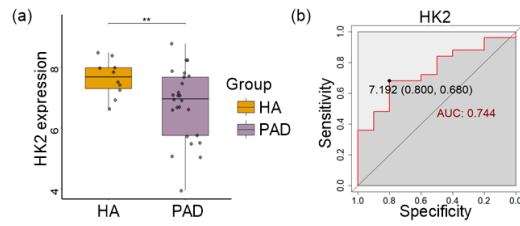


Figure S5 Expression level of HK2.

(a) The expression of HK2 between the PAD and HA group. The data was sourced from the GSE113873 dataset. (b) ROC showed the diagnostic performance of HK2. HA, healthy; PAD, peripheral arterial disease.

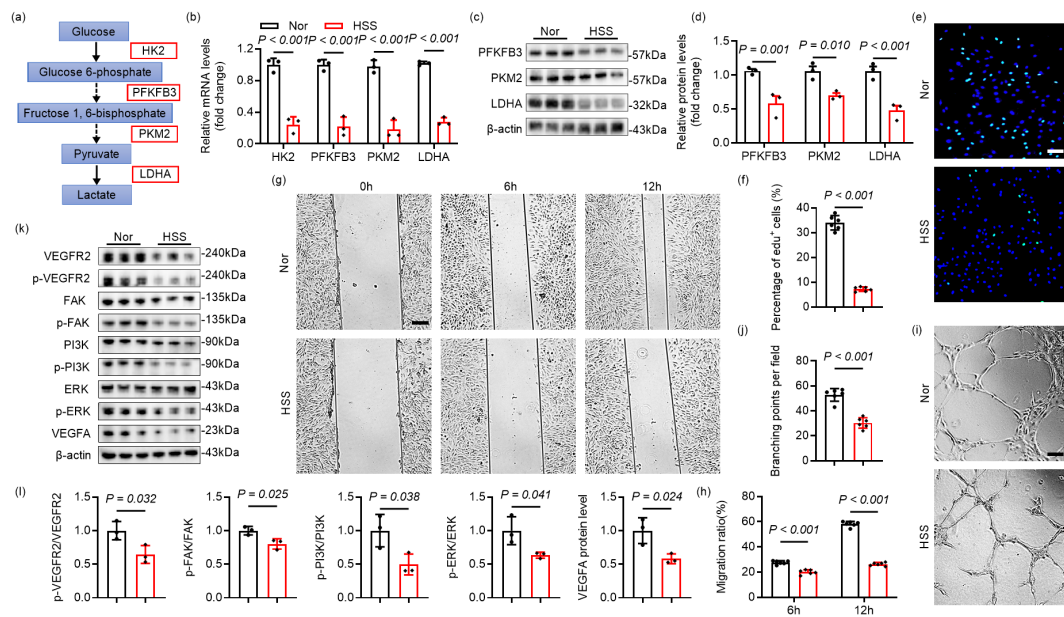


Figure S6 Angiogenesis was inhibited in HSS-treated HUVECs.

(a) Schematic flowchart illustrating key regulatory enzymes in glucose metabolism. (b) Quantitative RT-PCR analysis of *HK2*, fructose-2,6-bisphosphatase 3 (*PFKFB3*), pyruvate kinase M2 (*PKM2*), and lactate dehydrogenase A (*LDHA*) mRNA levels in HUVECs under normoxia or HSS. $n = 3$. (c-d) Western blot and densitometry analysis of PFKFB3, PKM2, and LDHA expression levels in HUVECs under normoxia or HSS. $n = 3$. (e-f) EdU proliferation assay with statistical analysis of HUVEC growth under normoxia versus HSS. $n = 6$. Scale bars, 100 μm . (g-h) Scratch wound healing assay and migration rate quantification of HUVECs exposed to normoxia or HSS at 0, 6, and 12 hours. $n = 6$. Scale bars, 100 μm . (i-j) Tube formation assay and quantitative assessment of angiogenic capacity in HUVECs under normoxia or HSS. $n = 6$. Scale bars, 100 μm . (k-l) Western blot and densitometry of angiogenesis-associated proteins (VEGFA, VEGFR2, p-VEGFR2, FAK, p-FAK, PI3K, p-PI3K, ERK, p-ERK) in HUVECs treated with normoxia or HSS. $n = 3$. (f, j, l) Two-tailed unpaired Student's *t* test. (d, h) Two-way ANOVA followed by Bonferroni's multiple comparisons test. Nor, normoxia. HSS, hypoxia/serum starvation.

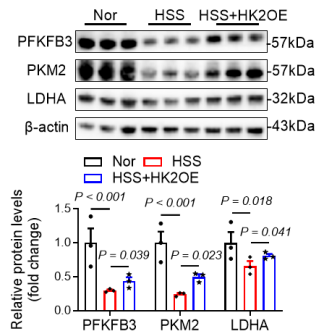


Figure S7 The expression of the series of enzymes involved in glycolysis in HUVECs under HSS and HSS-induced HK2 overexpression.

Western blot and densitometry of glycolytic enzymes (PFKFB3, PKM2, LDHA) in HUVECs under normoxia, HSS, and HSS+HK2OE. $n = 3$. Two-way ANOVA followed by Bonferroni's multiple comparisons test. Nor, normoxia. HSS, hypoxia/serum starvation. HK2OE, HK2 overexpression.

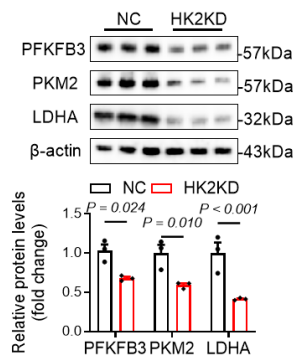


Figure S8 The expression of glycolysis-related enzymes in HK2-knockdown HUVECs.

Western blot and densitometry of glycolytic enzymes (PFKFB3, PKM2, LDHA) in HUVECs under NC and HK2KD. $n = 3$. Two-way ANOVA followed by Bonferroni's multiple comparisons test. Nor, normoxia. HK2KD, HK2-knockdown.

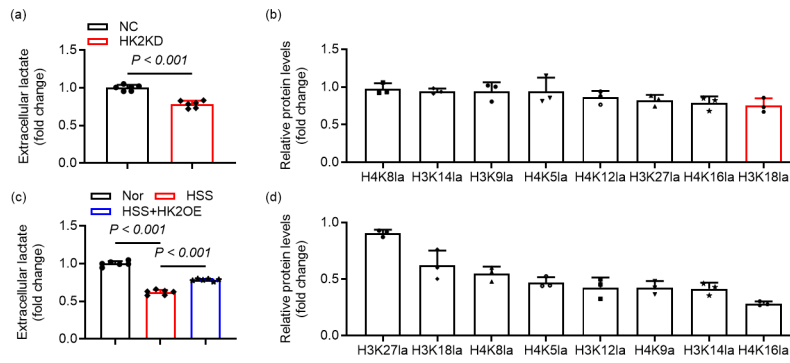


Figure S9. Quantitative analysis of lactate dynamics and histone lactylation in HUVECs.

(a) Extracellular lactate levels in control (NC) versus HK2-knockdown (HK2KD) HUVECs. $n = 6$. (b) Site-specific histone lactylation levels in HK2KD HUVECs, normalized to histone H3/H4 levels. $n = 3$. (c) Extracellular lactate concentrations in HUVECs under normoxia (Nor), HSS, and HSS with HK2 overexpression (HSS+HK2OE). $n = 6$. (d) Site-specific histone lactylation levels in HSS-treated HUVECs. $n = 3$. (a) Two-tailed unpaired Student's t test. (c) One-way ANOVA followed by Tukey's multiple comparisons test. Nor, normoxia. HSS, hypoxia/serum starvation. HK2OE, HK2 overexpression. HK2KD, HK2-knockdown.

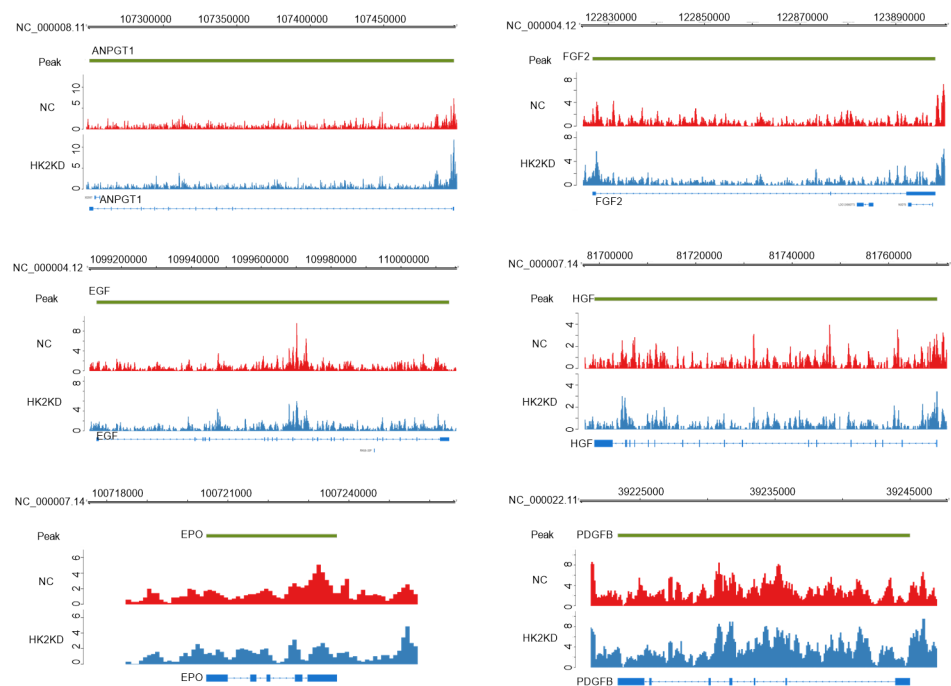


Figure S10 H3K18la enrichment profiles at additional angiogenic gene loci

Genome browser tracks of CUT& Tag signal at the ANGPT1, FGF2, EGF, HGF, EPO and PDGFB loci.

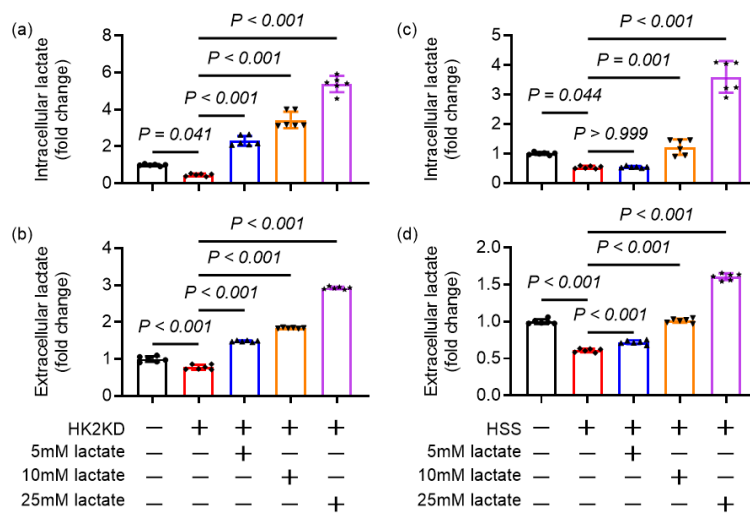


Figure S11 HK2 knockdown and HSS regulate intra- and extracellular lactate dynamics in HUVECs.

(a) Intracellular lactate levels in NC, HK2KD, and HK2KD HUVECs supplemented with 5, 10, or 25mM exogenous lactate. n = 6. (b) Extracellular lactate levels in NC, HK2KD, and HK2KD HUVECs treated with 5, 10, or 25mM exogenous lactate. n = 6. (c) Intracellular lactate levels in normoxia, HSS and HSS-treated HUVECs supplemented with 5, 10, or 25mM exogenous lactate. n = 6. (d) Extracellular lactate levels in normoxia, HSS and HSS-treated HUVECs supplemented with 5, 10, or 25mM exogenous lactate. n = 6. (a-c) One-way ANOVA with Dunnett's T3 multiple comparisons test. (d) One-way ANOVA followed by Dunnett's multiple comparisons test. Nor, normoxia. HSS, hypoxia/serum starvation. Lac, lactate. HK2KD, HK2-knockdown.

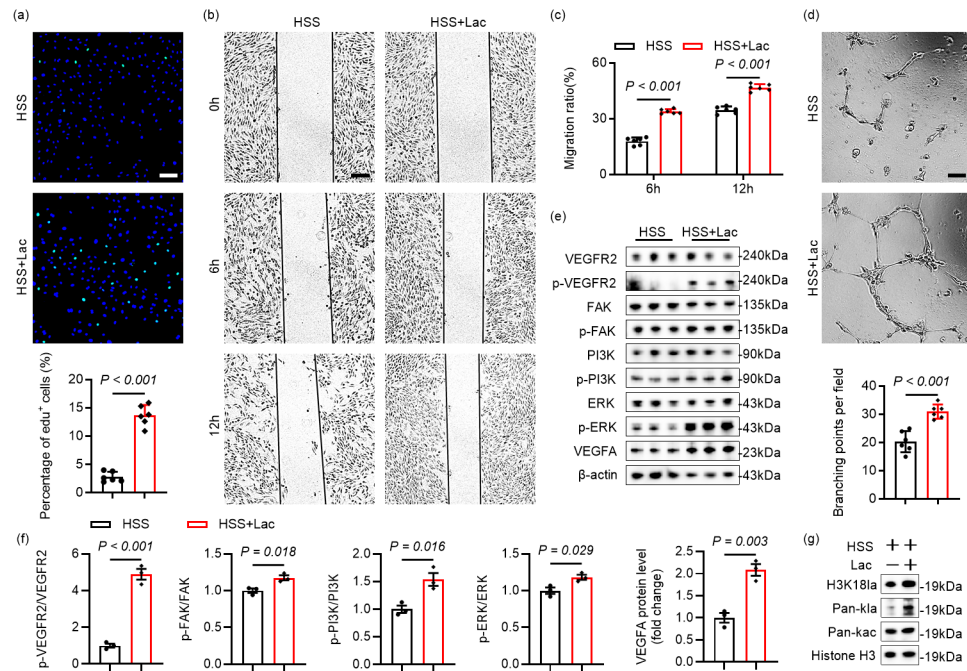


Figure S12 Lactate rescued angiogenic dysfunction in HSS-treated HUVECs.

(a) EdU proliferation assay with statistical analysis of HUVECs under HSS with or without 10 mM lactate for 24 hours. $n = 6$. Scale bars, 100 μm . (b-c) Scratch wound healing assay and migration rate quantification of HUVECs under HSS with or without 10 mM lactate at 0, 6, and 12 hours. $n = 6$. Scale bars, 100 μm . (d) Tube formation assay and angiogenic capacity quantification of HUVECs under HSS with or without 10 mM lactate. $n = 6$. Scale bars, 100 μm . (e-f) Western blot and densitometry of angiogenesis-related proteins (VEGFA, VEGFR2, p-VEGFR2, FAK, p-FAK, PI3K, p-PI3K, ERK, p-ERK) in HUVECs under HSS with or without 10 mM lactate. $n = 3$. (g) Western blot analysis of histone pan-lactylation, pan-acetylation, and H3K18 lactylation (H3K18la) in HUVECs treated with HSS with or without 10 mM lactate. $n = 3$. Scale bars, 100 μm . (B) Two-way ANOVA followed by Bonferroni's multiple comparisons test. (a, d, f) Two-tailed unpaired Student's t test. Lac, lactate. HSS, hypoxia/serum starvation.

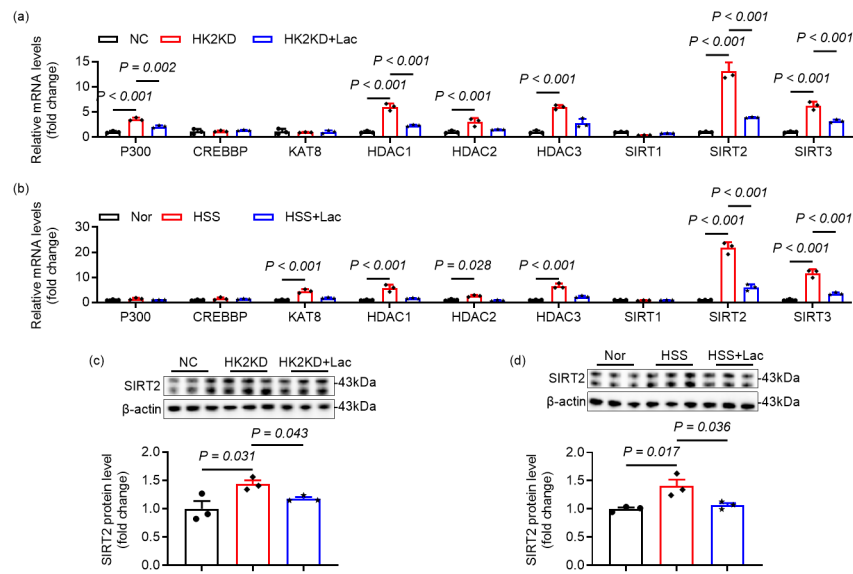


Figure S13 The HK2-lactate-SIRT2 axis regulates histone lactylation in HUVECs.

(a) qPCR analysis of 9 genes (P300, CREBBP, KAT8, HDAC1-3, SIRT1-3) in NC, HK2KD, and HK2KD HUVECs supplemented with 5 mM exogenous lactate. $n = 3$. (b) qPCR analysis of the same 9 genes in normoxia, HSS-treated, and HSS-treated HUVECs supplemented with 10 mM exogenous lactate. $n = 3$. (c) Western blot and quantification of SIRT2 expression in NC, HK2KD, and HK2KD HUVECs with 5 mM lactate supplementation. $n = 3$. (d) Western blot and quantification analysis of SIRT2 expression in normoxia, HSS, and HSS-treated HUVECs supplemented with 10 mM exogenous lactate. $n = 3$. (a-b) Two-way ANOVA followed by Tukey's multiple comparisons test. (c-d) One-way ANOVA followed by Tukey's multiple comparisons test. Nor, normoxia. HSS, hypoxia/serum starvation. HK2KD, HK2-knockdown. Lac, lactate.

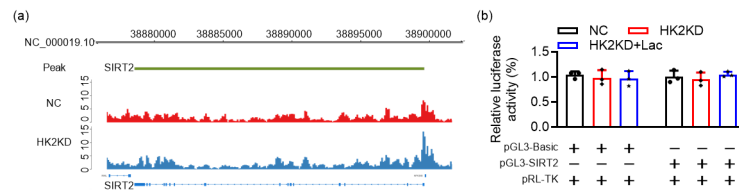


Figure S14 SIRT2 transcription is not directly regulated by lactate via promoter lactylation
 (a) Genome browser tracks of CUT& Tag signal at the SIRT2 loci. (b) Luciferase reporter assay assessing SIRT2 promoter activity in HUVECs under control (NC), HK2-knockdown (HK2KD), and HK2-knockdown with 10 mM lactate rescue (HK2KD + Lac) conditions.

Supplementary Table 1 Genes of turquoise module

Gene symbol
A2M-AS1, AAAS, AACS, AADAT, AAGAB, AAMDC, AAMP, AAR2, AARS, AARS2,
AARSD1, AASDH, AASDHPPT, AASS, AATF, ABCA10, ABCA11P, ABCA17P, ABCA2,
ABCA3, ABCA5, ABCA7, ABCB10, ABCB11, ABCB4, ABCB6, ABCB7, ABCC1, ABCC10,
ABCC5, ABCC6, ABCC6P2, ABCC9, ABCD1, ABCD3, ABCD4, ABCE1, ABCF1, ABCF2,
ABCF3, ABHD10, ABHD11, ABHD12, ABHD13, ABHD14A, ABHD14B, ABHD16A,
ABHD16B, ABHD17A, ABHD17B, ABHD4, ABHD5, ABHD8, ABI1, ABI3BP, ABL1
ABL2, ABLIM2, ABO, ABRA, ABT1, ABTB1, ABTB2, ACAA1, ACAD10, ACAD8,
ACAD9, ACADL, ACADM, ACADS, ACADSB, ACAP1, ACAP2, ACAP3, ACAT1, ACAT2,
ACBD3, ACBD4, ACBD5, ACBD6, ACBD7, ACD, ACER3, ACHE, ACIN1, ACKR1,
ACKR2, ACKR4, ACN9, ACO1, ACO2, ACOT1, ACOT13, ACOT2, ACOT6, ACOT8,
ACOT9, ACOX1, ACOX3, ACP1, ACP5, ACP6, ACPP, ACR, ACRBP, ACSBG1, ACSF2,
ACSF3, ACSL3, ACSL6, ACSM5, ACSS2, ACSS3, ACTA1, ACTC1, ACTG1, ACTG1P4,
ACTL6A, ACTL6B, ACTN1, ACTN2, ACTN3, ACTR10, ACTR1A, ACTR1B, ACTR2,
ACTR3, ACTR3B, ACTR3C, ACTR5, ACTR6, ACTR8, ACVR1, ACVR1B, ACVR2A,
ACY1, ACYP1, ACYP2, ADA, ADAL, ADAM10, ADAM12, ADAM19, ADAM1A,
ADAM20P1, ADAM23, ADAM28, ADAM9, ADAMDEC1, ADAMTS1, ADAMTS13,
ADAMTS17, ADAMTS2, ADAMTSL2, ADAMTSL4, ADAMTSL5, ADAP1, ADAP2,
ADARB1, ADAT1, ADCK1, ADCK2, ADCK3, ADCK4, ADCK5, ADCY1, ADCY2, ADCY9,
ADD1, ADD3, ADH5, ADHFE1, ADI1, ADIPOR1, ADIPOR2, ADK, ADM5, ADNP, ADO,
ADORA1, ADORA2B, ADORA3, ADPGK, ADPRH, ADPRHL1, ADPRHL2, ADPRM,
ADRA1B, ADRA2C, ADRB2, ADRBK1, ADRM1, ADSL, ADSS, ADSSL1, AEBP1, AEBP2,
AES, AFAP1L1, AFF1, AFF2, AFF4, AFG3L1P, AFG3L2, AFMID, AFTPH, AGA, AGAP1,
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AGPAT9, AGPS, AGT, AGTPBP1, AHCTF1, AHCTF1P1, AHCY, AHCYL1, AHCYL2, AHR,
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Supplementary Table 2 Differentially expressed genes between HA and IC

Gene symbol
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Supplementary Table 3 Differentially expressed genes between HA and CLI

Gene symbol
SDHC, TMEM161B-AS1, CKMT2, IQCH-AS1, ETFA, TMEM108, NDUFS1, RTN4IP1, COQ6, C1orf192, ACADM, NMNAT1, ETFDH, COQ2, MTIF2, ARHGAP21, FAM96A, NDUFA9, TP53INP2, IMMT, ALAS1, PTCDD3, COA1, MCU, LYRM7, DLD, DECR1, ACAT1, HIBADH, ADAL, PDHB, MTO1, C10orf76, SIAE, ENDOG, NDUFB3, UBE2T, SDHB, NDUFAF7, ARHGEF6, RIC8B, ATP5G1, HERC1, LACTB2, GBAS, MIR22HG, MRPL35, NDUFAF5, TIMM21, C9orf3, NDUFA8, ZNF252P, GOT2, MRPL34, CECR5, NDUFB8, NIPSNAP3B, DBI, MRPL13, ATP5J, PPP1R1C, SUCLG1, MTRF1, PAQR9, ATPAF1, MRPL33, APOO, UQCRC2, SMIM4, SIRT5, FUNDC2, RUNX1, MDH1, HSDL2, IDH3B, CALU, MPC2, EGFLAM, CCDC69, PCCB, SUPV3L1, COX5B, ATP5A1, UQCC1, PCBD2, HNRNPA2B1, C21orf33, SLC16A1, VDAC1, NDUFA6, MUT, APPL1, KIAA0232, DUSP3, RASL12, FAM26E, COX7B, DLAT, NXPE3, COA7, HMGCL, WIP1, PDHA1, ITGB6, PTGR2, HSPA9, ECI2, COX8A, ACADSB, C7orf55, PDSS1, COQ3, FABP3, NUDT9, VWA8, CYC1, SDHA, CLPX, NDUFB2, ASB14, OXSM, SLC25A12, NDUFA10, BOLA3, COQ9, NDUFAF6, PARP1, TIMM23, NDUFV2, HMBS, NEDD9, ATP5F1, METTL21EP, ACO2, MRS2, ING2, GADD45A, DCUN1D2, MAD2L1BP, TMX2, PRKAG1, SLC25A4, KCNS3, ATP5G3, COQ7, NDUFB10, IDH2, SLC16A3, GTPBP8, FH, FAM210A, LACTB, FKBP3, C12orf73, MKKS, MTRNR2L2, NNT-AS1, TFRC, COQ5, DHRS4, COX6C, SUCLA2, MRPS31, TECRL, MRPL11, NDUFS2, NDUFV1, C14orf2, MRPS22, UQCR11, TMTC4, RNF34, NNT, MB, GSTK1, NDUFS6, NDUFAF1, UQCR10, APOOL, MTRNR2L1, C1orf43, CD9, PDE7A, TIMMDC1, ATP5B, TMEM261, PDHX, SYNGR1, AUH, GOT1, CHCHD4, MRPL46, ISCU, MTRR, PDK1, LDLRAD4, SYNJ2BP, MRPL50, TACO1, ZFYVE9, RNF7, ELP5, ACOT2, TOMM40L, C15orf61, VEGFA, PPM1B, CYCS, VTI1B, AAMDC, CUTC, NRG4, ACN9, MTRF1L, MRPL47, RIN1, NDUFB4, NDUFB1, NDUFA12, BBC3, NDUFB5, ASB12, KIF22, TRMT2B, PHF10, TIMM8A, FST, CTAGE5, TATDN3, PMEPA1, RET, TXN2, MRPL39, FASTKD5, DNAJC19, CISD1, SMIM12, IDI1, FHL1, SOX9-AS1, SNRPG, LOC150381, MRPS33, ANAPC1, CD59, ANXA3, LINC00888, UQCRC1, MAP6D1, DHRS4L2, NDUFA1, UQCRFS1, NDUFS3, AFG3L2, PPARA, ALDH5A1, SDHD, CAMTA1, ATP5C1, DTNA, NDUFA4, GLTPD1, ATP5H, ATP1B1, MCRS1, HCCS, RGS9BP, ATP5O, MRPL44, ZNF32, POLR2M, COX6B1, UQCRCQ, CCRN4L, VDAC3, ATAD1, FNDC5, MAP2K6, ATP5SL, PPIF, CHCHD3, NDUFA13, GNG5, COX4I1, ARV1, MINOS1, HK2, ZDHHC3, BZW2, SPAG7, C3orf43, MRPS11, ANK2, DNMI1L, MRPL15, EIF2B3, PLA2G12A, HADHB, HS3ST5, AP5M1, ZNF511, PLN, MGST2, LSM1, TMEM11, TSFM, NETO2, INO80C, PET112, TIMM17A, DNAJB5,

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FAM78A, TPM3, MRPL14, EML1, DANCER, PPP1CB, PRKG1, FDX1, PCYOX1, MOB3C, NNMT, MTRNR2L10, COPS5, TMEM126A, PPAPDC3, LRRC2, PPTC7, GCSHP3, GTF2F2, PHKB, FBXO6, ITGAE, MRPS36, APOBEC2, C2orf47, DGCR6L, LOC101927755, GYS1, GRHPR, IDO1, MALSU1, TMEM88, FILIP1L, UTP11L, GCAT, NAA38, SLC30A9, PDCL3, ALDH1L1-AS2, EIF3K, ETFB, ALDH6A1, CBWD2, HIBCH, MS4A8, MYOZ3, LSM3, GYPC, SMAD7, LMO1, NUDT3, MRPL4, CTNNA3, NFU1, RTN4, RAB3A, FOXO4, KTN1, SYNPO, BPGM, MTRNR2L3, DNAJC12, NCOA3, DMRT2, MASP1, PET100, 2-Mar, PAIP1, RGS3, SLC6A1, MECR, WARS, LIAS, ANO5, PDLIM2, ABCB4, FARP1, DOPEY2, TRAK1, ORAI1, NARF, UGP2, OSBPL1, COX6A2, ATP5E, SUCLG2, RAB10, ATF4, C14orf159, FXVD6, COX16, EXTL1, EPS15, TRIL, PDGFB, EMC4, PLIN2, AURKA, PHYH, C12orf5, ACKR3, PPM1J, SNAI3, BCO2, HINT2, PTPRB, FITM1, TAL2, UBB, SLC25A30, ACTA2, OXA1L, NDUFB1, LIPT2, TGFB3, FOSB, ASB8, HIGD2A, ACAA2, EIF1B, FASTK, SNHG16, RGMA, PERM1, ZDHHC14, PLEKHN1, ZCRB1, KIF1C, ECHDC2, NMNAT3, MAPK12, DLEU2L, TXNL4A, TRIM52-AS1, ADCY2, RWDD1, KALRN, VIPR2, GCSH, LTBP4, SUOX, CAPRIN2, SCCPDH, COMMD7, DNAH3, HSPB7, CWC15, MRPL23-AS1, GSDMC, HIPK3, OSGIN2, DCAF6, C6orf106, PPP2R3A, MID1IP1, CNST, SLC25A25, FGF1, APIP, SLC25A26, HSPA8, RP9, RAB4A, ANGPTL1, ENO3, MYL3, USP2, UFSP2, KBTBD12, EFR3B, FAM46C, CCDC58, PDP1, MYLK4, KLF9, SLC35B1, TMEM38B, LIMS2, GPR116, OR51E1, RPPH1, MYEOV2, NDRG4, ITIH6, CACNA2D1, NHP2L1, USMG5, TBC1D8, PLCL1, SPSB1, C20orf24, SAA1, MRPS9, ANKRD9, SGK223, PRKCQ-AS1, PARK2, PRSS56, DPF3, SLC6A8, TTL, PEX2, BAI2, CENPV, GDNF-AS1, TMEM159, DEXI, PDE4A, CCNB1IP1, FAM107A, SAR1B, TAZ, ABHD14A, FIS1, SLC4A7, F13A1, INPP5A, PKIA, BCKDK, FRAS1, CCDC28B, SNRNP25, SFXN4, CEP70, TOMM7, LMOD3, MAF1, HINT3, VDR, FLT1, LMOD2, ZCWPW2, PECR, ABCC6, ASB11, PDE4DIP, EEF1G, GADL1, TRMT10C, TUBB2B, NDUFS5, LBX1, CTDNEP1, BAG1, RBM24, ALDOA, TMEM120A, AKR1B1, ATG4D, SBDS, MPP7, FASTKD1, LOC100131138, PDK2, LRRC14B, SBK1, TAPT1, RGN, PAM16, APOPT1, CAMK2G, ARAF, ACOT1, GSTA4, CARS2, MSRB3, SLC20A2, RFTN1, EMC9, TWF2, MRPL1, CKB, LINC00312, ECH1, LRRC20, ANKRD1, SCN2B, FAM174B, NUDT16L1, ANK1, C3AR1, IDI2, DGCR6, TRO, MRPL21, LINC00998, PAIP2B, KCNT1, CHRND, THAP11, SMYD1, ALKBH7, ACSS1, NMRK2, FRMD3, PTP4A1, GRB10, CHRA1, LOC101927100, PPP3CC, ART1, UBL5, SIVA1, C7, ECI1, MRPS10, NEK10, TNNI1, ACTN2, PTGES3L-AARSD1, SPRY4, MN1, NPHP1, KLHL38, HES1, IER3IP1, RTN2, OXCT1, SLC2A4, GLUL, LINC00493, LAPTM4B, TNNT1, DUSP28, AKAP7, AMHR2, CCND1, SLC29A2, RHOQ, POLR2I, RASGRP3, CA8, TECR, HMCN2, PGP, TUBA8, IZUMO4, CMYA5, PPA2, GOLGA4, MACROD1, CLEC3B, XPO4, MUSK, C15orf27, CHRNA10, P2RY2, LDB3, CFL2, RANBP6, TINAGL1, TPM2, MTFP1, UBE2D1, CCR3, TST, RRAGD, LINC00693, P4HA1, HOXA10, HOXB2, MAPKAPK2, FAM220A, PLEKHF1, SMDT1, PITX3, FOS, FYCO1, SGCG, HIST1H2BD, CHI3L1, ASB10, PANK1, JPH2, RELT, ECSIT, LOC100996255, NOS1, TMEM150A, PHKG1, SLC29A1, C2orf88, CDH13, ACADS, ADSL, SATB1, G0S2, DVL1, GMPR, PRR16, COLQ, CP, VDACC2, ATP5D, RASSF3, LOC100288911, MIEF2, COX14, CCDC106, LOC100506476, DHRS7B, NDUFA2, LINC00310, MYH7, INPP5J, THSD4, VEGFB, SFRP2, RXRG, HDAC11, UBE2B, FADS2, CKM, CLYBL, MYC, PTGDR2, GAPDH, RPL3L, MBP, DDX59, CITED4, CD68,

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Supplementary Table 4 Overlapping genes between turquoise module and HA_IC_DEG

Gene symbol
CHRND, EIF1AY, GRAMD1C, GSDMC, HBA1, HBA2, HBB, HK2, LYVE1, NCRNA00185, NPR3, PRG4, SAA1, SAA2, TSPAN5, XIRP2, ZFY

Supplementary Table 5 Overlapping genes between turquoise module and HA_CLI_DEG

Gene symbol
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Supplementary Table 6 Genes identified by multiple machine-Learning Strategies RF and LASSO

Strategy	Gene symbol
RF	CHRND, EIF1AY, GRAMD1C, HBA1, HBA2, HBB, HK2, LYVE1, NCRNA00185, NPR3, PRG4, SAA1, TSPAN5, XIRP2, ZFY
LASSO	CHRND, GRAMD1C, HBA1, HK2, LYVE1, NCRNA00185, NPR3, PRG4, TSPAN5, XIRP2

Supplementary Table 7 Genes identified by multiple machine-Learning Strategies RF and LASSO

Strategy	Gene symbol
RF	DNAJC19, CYR61, OXSM, ANXA3, FOSB, COL19A1, FLAD1, PRKG1, RASL12, TFRC, DBI, FUNDC2, PTPN3, ABCA7, EFCAB7, C21orf33, FAM96A, MAP2K6, LYRM7, NDUFC1, ATPAF1, TMEM261, MRPS33, ITGB6, EIF5, UQCR10, ANKH, MCRS1, NUDT6, PPP1R12B, ZMAT5, ZNF511, VCAM1, ARHGAP44, CEP85, COX7B, DPP8, MRPL34, MRS2, MTRNR2L1, NDUFAF6, NMNAT1, SBK1,

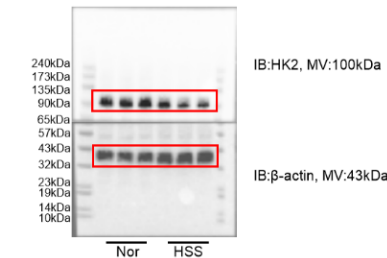
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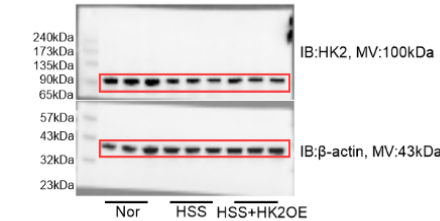
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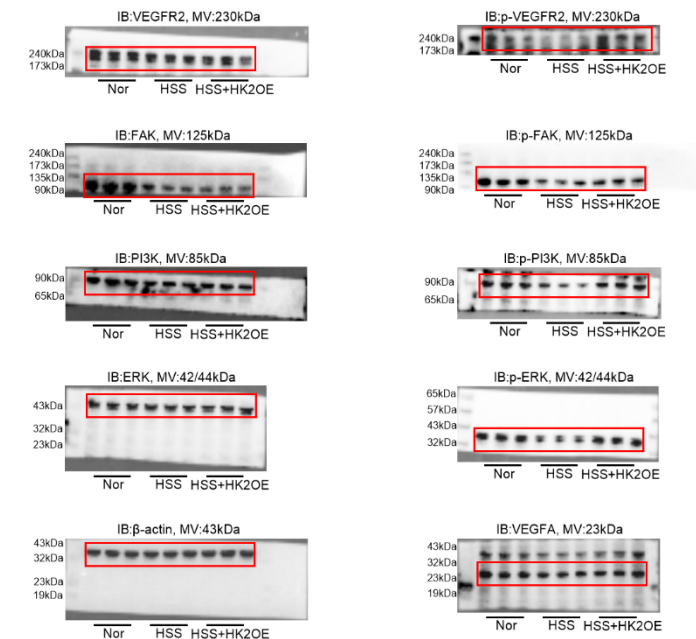
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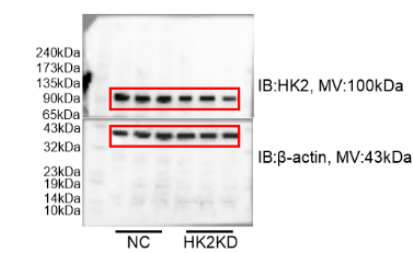
Full unedited gel for Figure 2(e)



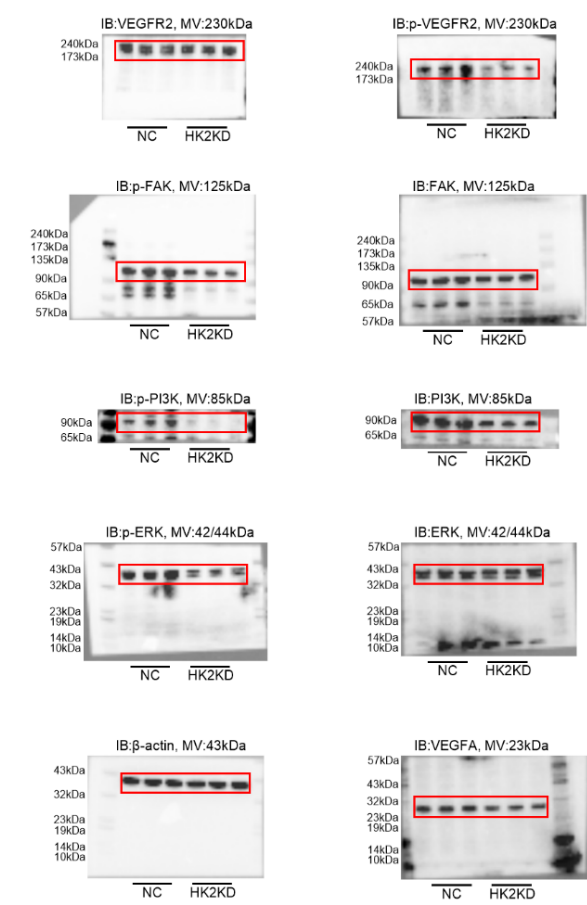
Full unedited gel for Figure 2(k)



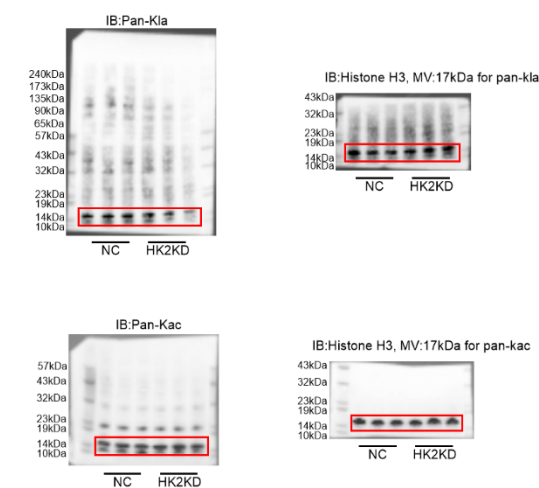
Full unedited gel for Figure 3(a)



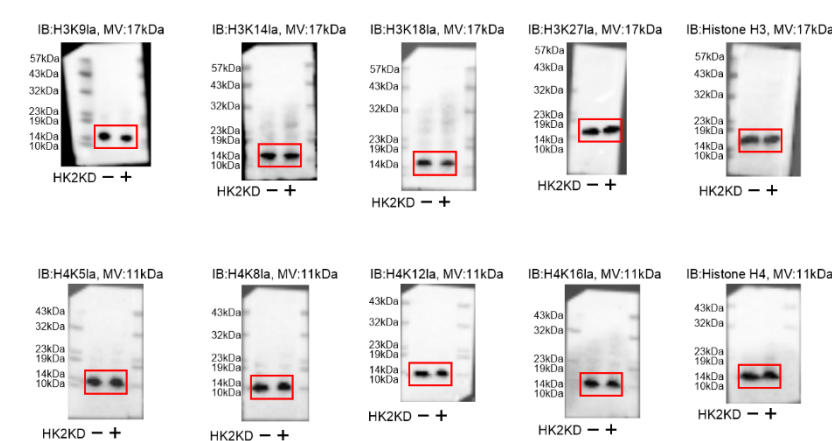
Full unedited gel for Figure 3(f)



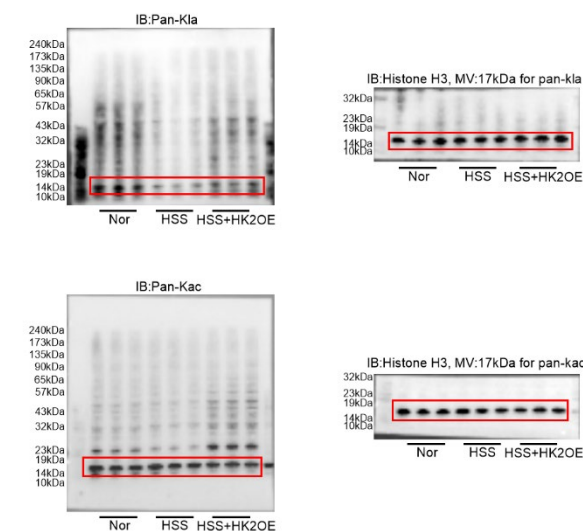
Full unedited gel for Figure 4(b)



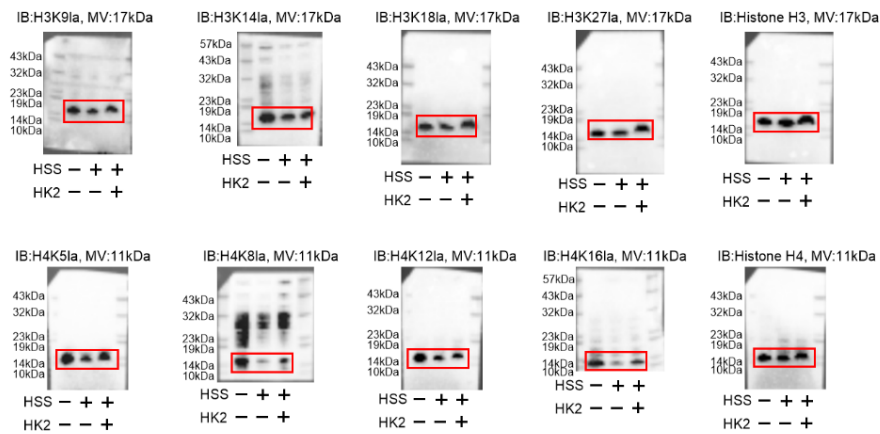
Full unedited gel for Figure 4(c)



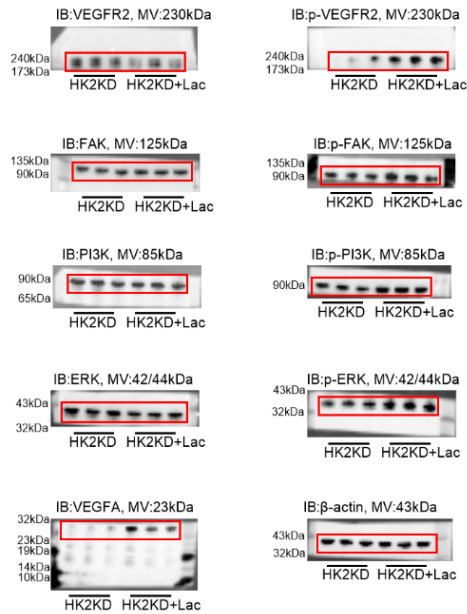
Full unedited gel for Figure 4(f)



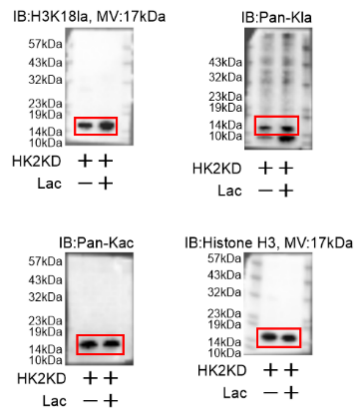
Full unedited gel for Figure 4(g)



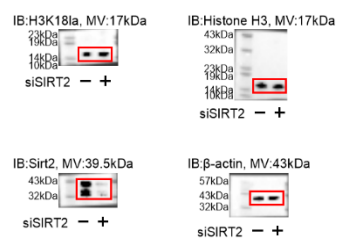
Full unedited gel for Figure 6(e)



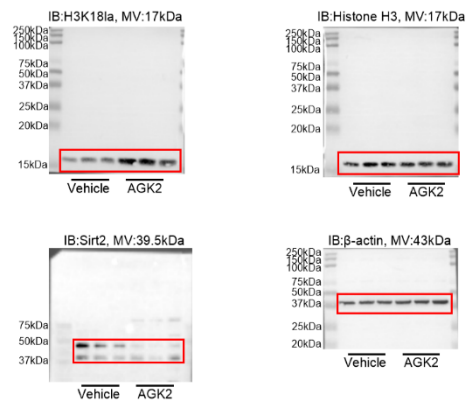
Full unedited gel for Figure 6(g)



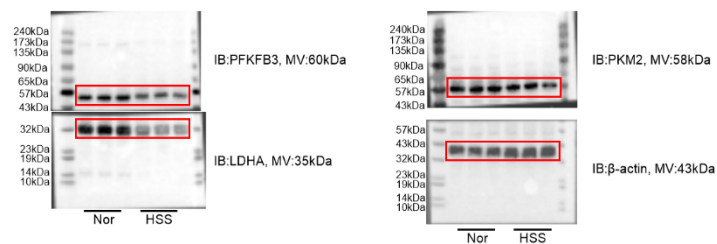
Full unedited gel for Figure 7(a)



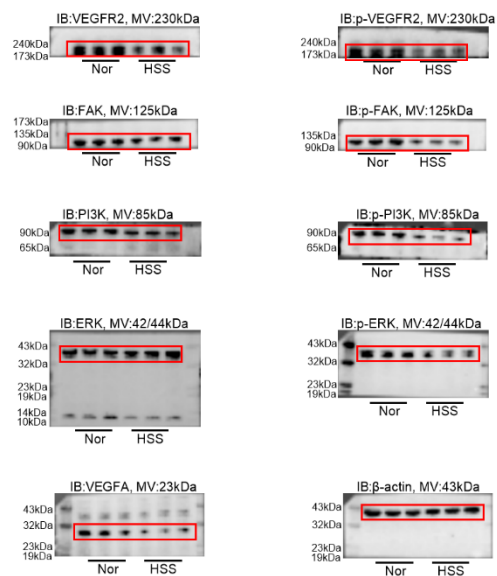
Full unedited gel for Figure 7(l)



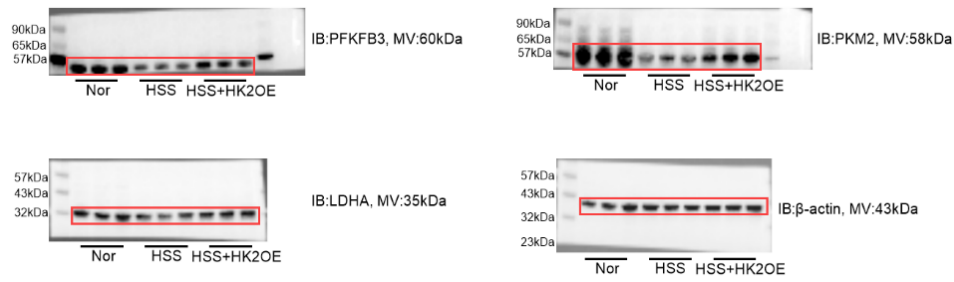
Full unedited gel for Figure S6(c)



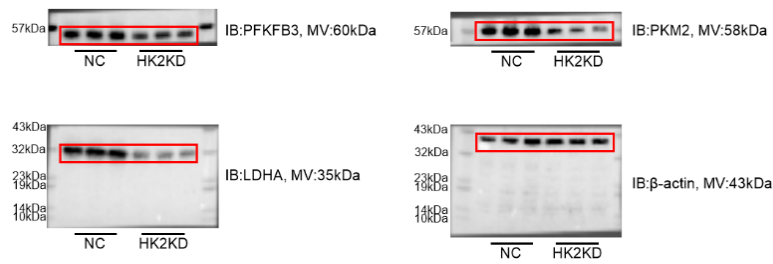
Full unedited gel for Figure S6(k)



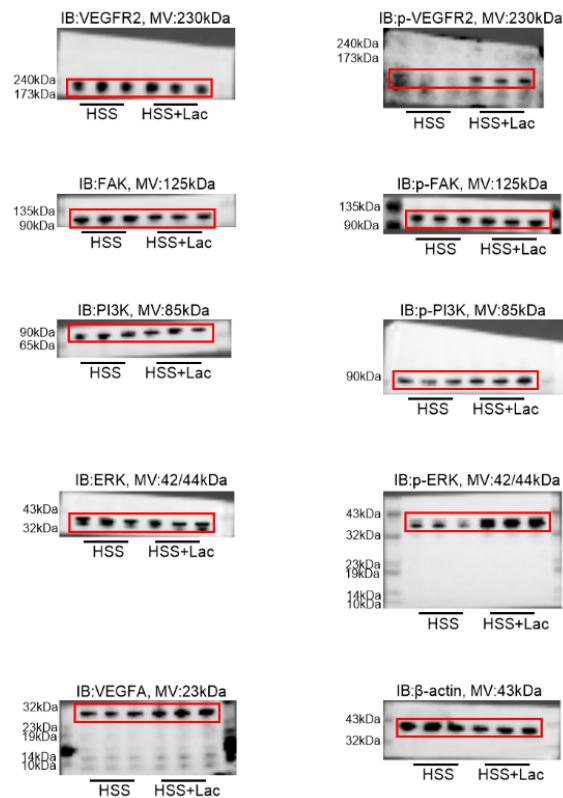
Full unedited gel for Figure S7



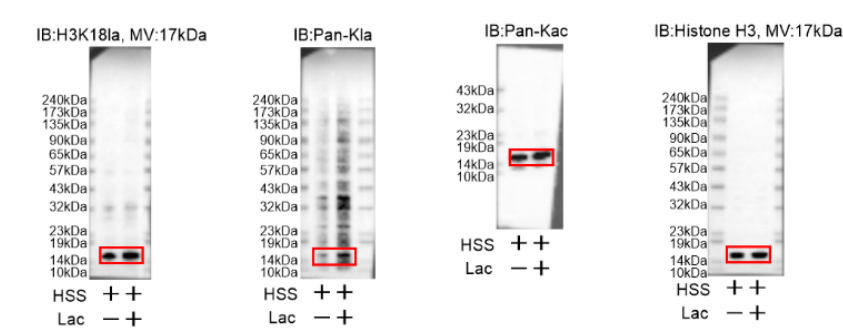
Full unedited gel for Figure S8



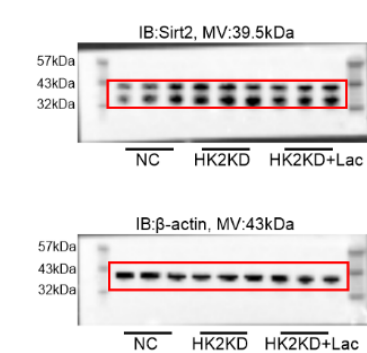
Full unedited gel for Figure S12(e)



Full unedited gel for Figure S12(g)



Full unedited gel for Figure S13(c)



Full unedited gel for Figure S13(d)

