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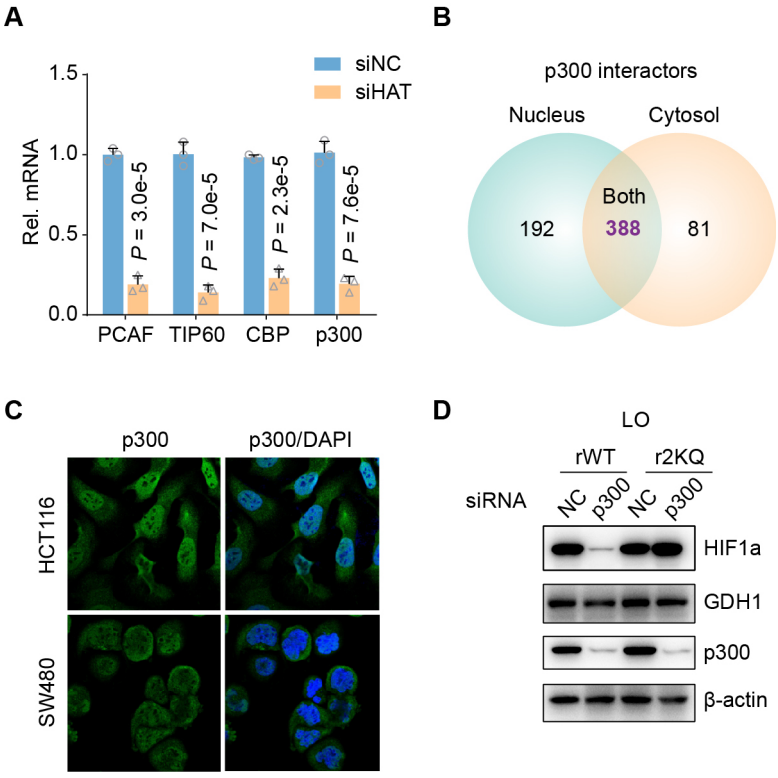


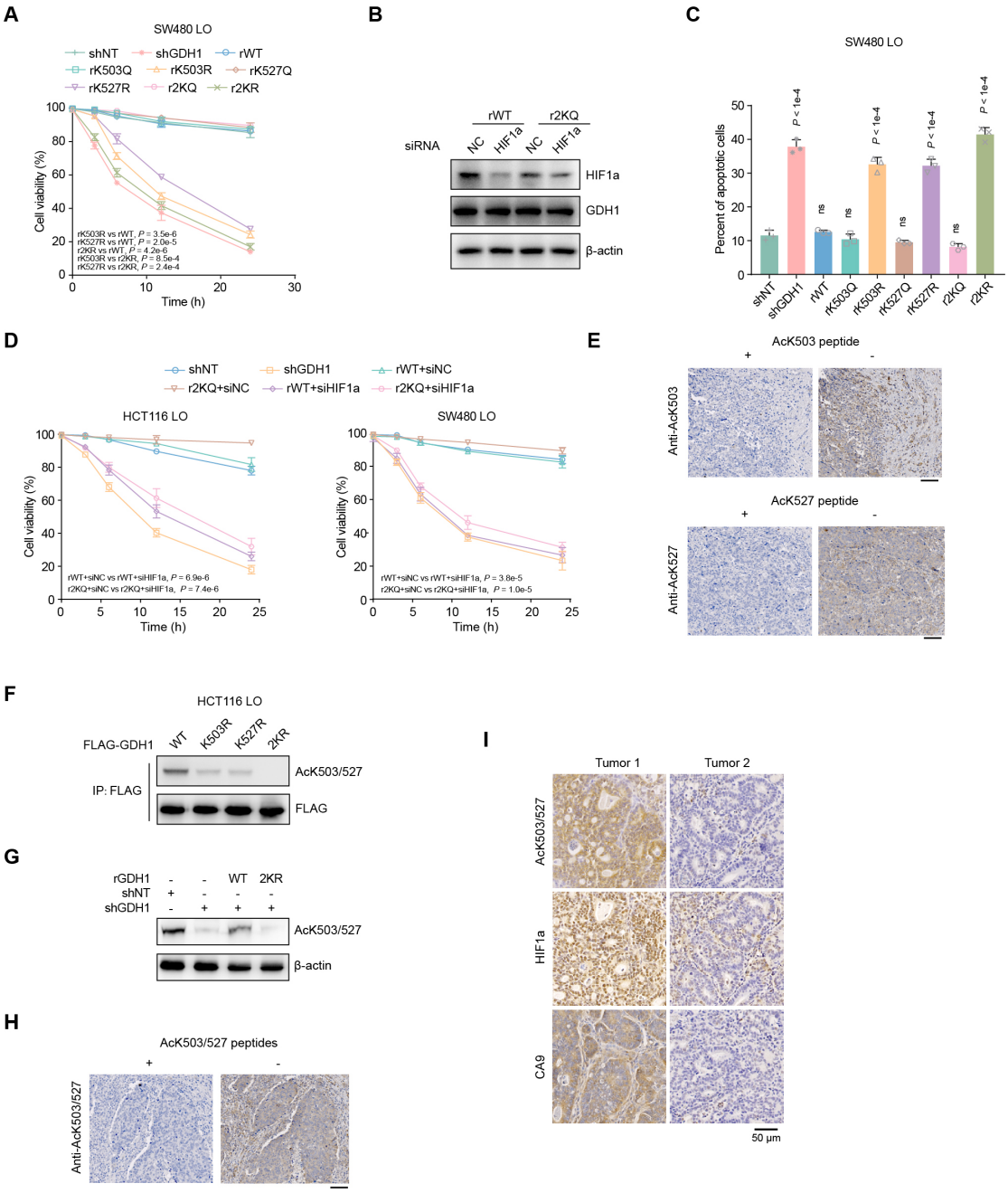
Appendix Figure S1. p300 is localized in both the cytosol and nucleus.

(A) The knockdown efficiency of siRNA targeting PCAF, TIP60, CBP and p300 in HCT116 cells was analyzed by qRT-PCR. Data represent the mean ± SD (unpaired two-tailed student's t-test, n=3).

(B) The cellular localization of the interactors of p300 from Biogrid database.

(C) Immunofluorescence of p300 in HCT116 and SW480 cells was performed to analyze p300 localization. DAPI indicates nuclei location.

(D) Immunoblot of HIF1α protein level in the NC or siP300 groups when overexpressing WT- or 2KQ-GDH1.



Appendix Figure S2. GDH1 acetylation at both K503 and K527 increased resistance of CRC cell to hypoxia

(A) Cell viability percent of indicated cell lines under hypoxia was analyzed by trypan blue and PI/Annexing V double staining, respectively. Mean ± SD, two-way ANOVA with Tukey's HSD post hoc test, n=3.

(B) Immunoblot of HIF1α protein level in the NC or siHIF1α groups when overexpressing WT- or 2KQ-GDH1.

(C) Cell apoptotic percent of indicated cell lines under hypoxia was analyzed by trypan blue and

PI/Annexing V double staining, respectively. Mean ± SD, one-way ANOVA with Tukey's HSD post hoc test, n=3.

(D) Cell viability of indicated cell lines under hypoxia was analyzed by trypan blue and PI/Annexing V double staining, respectively. Mean ± SD, two-way ANOVA with Tukey's HSD post hoc test.

(E) Validation of the specificity of antibodies against AcK503 and AcK507 in IHC. IHC analyses of human CRC tissues were performed with the indicated antibodies in the presence (+) or absence (-) of specific blocking peptides.

(F-G) Western blot analysis of the specificity of antibody against GDH1-AcK503/527.

(H) Validation of the specificity of antibody against AcK503/527 in IHC. IHC analyses of human CRC tissues were performed with the indicated antibodies in the presence (+) or absence (-) of specific blocking peptides.

(I) The representative images were shown after antibodies against GDH1-AcK503/527 and HIF1α were stained in the tumor tissues from AOM/DSS CRC samples.

Appendix Tables and Table legends

Appendix Table S1. siRNA sequence used in this study. Related to Methods.

Human Gene	siRNA sequences (5'-3', sense)	siRNA sequences (5'-3', anti-sense)
siRNA sequences against 163 dehydrogenases		
AASDH-1	UUAAUGCUGCUUCUGAAUUAU	AUAAUUCAGAAGCAGCAUUAA
AASDH-2	UGUGCAGUUACAUGGUAUAAU	AUUAUACCAUGUAACUGCACA
AASDH-3	GGUCACCUGCAGUGGAAAUUU	AAAUUUCCACUGCAGGUGACC
AASDHPPT-1	CGUCUGAUGAUAAGGAAAUUA	UAAUUUCCUUAUCAUCAGACG
AASDHPPT-2	GCAAGUUGGAAUUGAUAUAAU	AUUAUAUCAAUUCCAACUUGC
AASDHPPT-3	GAUAUAGGCCAAGUUUAUAAA	UUUAUAAACUUGGCCUAUAUC
ACAD10-1	UAUCCCUUCUGGAACUAUAUU	AAUAUAGUUCCAGAAGGGAUA
ACAD10-2	UGCAGUCUUGAGCAAUAAUUU	AAAUUAUUGCUCAAGACUGCA
ACAD10-3	UUGGAUAUAGCCAUGAUUAAA	UUUAAUCAUGGCUAUAUCCAA
ACAD11-1	GUCGAAUCUUCCGUGAUUUAA	UUAAAUCACGGAAGAUUCGAC
ACAD11-2	GAUAUCUUCUGGGAAAUAAUU	AAUUAUUUCCCAGAAGAUAUC
ACAD11-3	AGACUGACAGCCAAGAUAUAA	UUAUAUCUUGGCUGUCAGUCU
ACAD8-1	CCGAGAGAUGGCUCCAAAUAU	AUAUUUGGAGCCAUCUCUCGG
ACAD8-2	ACCAGCACCACAGCCUAUAUA	UAUAUAGGCUGUGGUGCUGGU
ACAD8-3	GAGGAACAGAGGCACAAAUUU	AAAUUUGUGCCUCUGUUCCUC
ACAD9-1	AUGGAGGACUGGCCAAUAUUU	AAAUAUUGGCCAGUCCUCCAU
ACAD9-2	GGGAAACCCGAAGAUAAAUUA	UAAUUUAUCUUCGGGUUUCCC
ACAD9-3	GGAUUGAUUCAGGAGAAAUUU	AAAUUUCUCCUGAAUCAAUCC
ACADL-1	GGACUGCUUGGUGUCAAUAUU	AAUAUUGACACCAAGCAGUCC
ACADL-2	CAGACAGUGCAACAUAAAUUA	UAAUUUAUGUUGCACUGUCUG
ACADL-3	UGGUGGUACAAAUGAAAUAAU	AUUAUUUCAUUUGUACCACCA
ACADM-1	UCAAGCUACUGCUCGUAAAUU	AAUUUACGAGCAGUAGCUUGA
ACADM-2	AGAUUGGGAGAAAGGAAUUAA	UUAAUUCCUUUCUCCCAAUCU
ACADM-3	UUGGAGGCAAUGGAUUUAAUA	UAUUAAAUCCAUUGCCUCCAA
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ACADSB-3	GACUACACUAUUCCAUAUAUU	AAUAUAUGGAAUAGUGUAGUC
ACADVL-1	AGAGCAGACACAGUUUCUUAA	UUAAGAAACUGUGUCUGCUCU
ACADVL-2	GCGGUAGAUCAUGCCACUAAU	AUUAGUGGCAUGAUCUACCGC
ACADVL-3	GGUGGAGGCCAAGCUGAUAAA	UUUAUCAGCUUGGCCUCCACC
ADH1A-1	GGCCCAUGAAGUUCGUAUUAA	UUAAUACGAACUUCAUGGGCC
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ADH1B-1	GACAUCAACAAGGACAAAUUU	AAAUUUGUCCUUGUUGAUGUC
ADH1B-2	UUCCCAGAACCUCUCAAUAAA	UUUAUUGAGAGGUUCUGGGAA

ADH1B-3	UUUCACUGGAUGCGUUAAUAA	UUAUUAACGCAUCCAGUGAAA
ADH1C-1	GACAUCAACAAGGACAAAUUU	AAAUUUGUCCUUGUUGAUGUC
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ADH5-1	CAGUGUGGAGAAUGCAAAUUU	AAAUUUGCAUUCUCCACACUG
ADH5-2	UGGAGCCACUGAAUGUAUUAA	UUAAUACAUUCAGUGGCUCCA
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BCKDHA-3	AGGUCAAUUACUGGGAUAAAC	GUUUAUCCCAGUAAUUGACCU
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BCKDHB-2	GUUGGCUUGCGAGACAAAUAU	AUAUUUGUCUCGCAAGCCAAC
BCKDHB-3	AUUGAUCUGAGGACUAUAAAUA	UAUUAUAGUCCUCAGAUCAAU
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DHDH-2	CGAAGGAGUUUGCACAGAAAC	GUUUCUGUGCAAACUCCUUCG
DHDH-3	AUCCCGAGCCCUCUUCCUUAU	AUAAGGAAGAGGGCUCGGGAU
DHODH-1	UGAGAGUUCUGGGCCAUAAAU	AUUUAUGGCCCAGAACUCUCA
DHODH-2	CAUUAACAGGUAUGGAUUUAA	UUAAAUCCAUACCUGUUAAUG
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DHRS1-1	CGUGUGCCCAAGUGGAUUAUU	AAUAAUCCACUUGGGCACACG
DHRS11-1	UACAGAUGUGACCUAUCAAAU	AUUUGAUAGGUCACAUCUGUA
DHRS11-2	UGGACGAUGGGCACAUCAUUA	UAAUGAUGUGCCCAUCGUCCA
DHRS11-3	AGGUGUGGUGGAGACACAAUU	AAUUGUGUCUCCACCACACCU
DHRS1-2	CAAAGCAGGCGCCACAGUUUA	UAAACUGUGGCGCCUGCUUUG
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DHRS3-3	ACUUUCAAAGGGCGGACAUAG	CUAUGUCCGCCCUUUGAAAGU
DHRS4-1	GACAAGACUCUGGACAUUAAU	AUUAAUGUCCAGAGUCUUGUC
DHRS4-2	CCUUUCUUUGGAAGCAUAAUG	CAUUAUGCUUCCAAAGAAAGG
DHRS4-3	CUGCCUAGCACCUGGACUUAU	AUAAGUCCAGGUGCUAGGCAG
DHRS4L2-1	GACAAGACUCUGGACAUUAAU	AUUAAUGUCCAGAGUCUUGUC
DHRS4L2-2	AGUCCUUACAAUGUCAGUAAA	UUUACUGACAUUGUAAGGACU
DHRS4L2-3	ACUGCCUGCACCUGGACUUAU	AUAAGUCCAGGUGCAGGCAGU
DHRS7-1	UGCCUAGAGAAUGGCAAUUUA	UAAAUUGCCAUUCUCUAGGCA
DHRS7-2	UGCCACAUACCCAGGUAUAAU	AUUAUACCUGGGUAUGUGGCA

DHRS7-3	GGAUGCAGACUCUUCUUAUUU	AAAUAAGAAGAGUCUGCAUCC
DHRS7B-1	CGAGAUGGAACAGUAUGAAAU	AUUUCAUACUGUUCCAUCUCG
DHRS7B-2	CACACCAACCUCUCUGUAAAU	AUUUACAGAGAGGUUGGUGUG
DHRS7B-3	UGCCUUCCUUGGCUGUUUAUC	GAUAAACAGCCAAGGAAGGCA
DHRS7C-1	CAAAUCGUGUUAGUGAAUAAU	AUUAUUCACUAACACGAUUUG
DHRS7C-2	CAGCGGCCUCCUCUUCAUUUA	UAAAUGAAGAGGAGGCCGCUG
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DHRS9-1	AUCAGGAUCAACAGCUUUAAA	UUUAAAGCUGUUGAUCCUGAU
DHRS9-2	AGCUCAAGGGAGAGUUAUUAA	UUAAUAACUCUCCCUUGAGCU
DHRS9-3	ACAAACUGAAAGGCAAUAAAU	AUUUAUUGCCUUUCAGUUUGU
DHRSX-1	UGUUAUCAUAGCUGGAAAUAA	UUAUUUCCAGCUAUGAUAACA
DHRSX-2	GAGACUUGGCAUGCAUGUUAU	AUAACAUGCAUGCCAAGUCUC
DHRSX-3	AGAUGGAUUCGAAGAACAUUU	AAAUGUUCUUCGAAUCCAUCU
DHTKD1-1	CCAGGUUGGUGACAGUAUAUU	AAUAUACUGUCACCAACCUGG
DHTKD1-2	AUAGAGGGAGGCUGAAUUUAU	AUAAAUUCAGCCUCCCUCUAU
DHTKD1-3	GGAGGAGGUGUCUGAAAUAAA	UUUAUUUCAGACACCUCCUCC
DLD-1	GGAUAUGUUGCUGCUAUUAAA	UUUAAUAGCAGCAACAUAUCC
DLD-2	UCCGAAGUUCGCUUGAAUUUA	UAAAUUCAAGCGAACUUCGGA
DLD-3	UACAGGUGCUUUAUCUUUAAA	UUUAAAGAUAAAGCACCUGUA
DMGDH-1	AGAGCAGAAACAGUGAUAAUU	AAUUAUCACUGUUUCUGCUCU
DMGDH-2	GACCUGGAAGGAUCAUAUUAU	AUAAUAUGAUCCUUCCAGGUC
DMGDH-3	GGAAGCUGGACUGGAAUAUUU	AAAUAUUCCAGUCCAGCUUCC
DPYD-1	CCUGAUAAGAACUGCUUUAAU	AUUAAAGCAGUUCUUAUCAGG
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EHHADH-2	CGCUGAAAGGAAAGCAAAUAA	UUAUUUGCUUUCCUUUCAGCG
EHHADH-3	UCCUUGAACGCUGCUUAUAUU	AAUAUAAGCAGCGUUCAAGGA
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GAPDHS-2	CUGCAUGGAGAAGGGUGUUAA	UUAACACCCUUCUCCAUGCAG
GAPDHS-3	ACAAUUUCGUGAAGCUCAUUU	AAAUGAGCUUCACGAAAUUGU
GCDH-1	CAGACAUGCUCACUGAGAUUA	UAAUCUCAGUGAGCAUGUCUG
GCDH-2	UUCUCUGCUGAAGAGGAAUAA	UUAUUCCUCUUCAGCAGAGAA
GCDH-3	UCGUCAUGCACCCUAUCUAUG	CAUAGAUAGGGUGCAUGACGA

GLUD1-1	AUAGGGCACUAUGAUAUUAAU	AUUAAUAUCAUAGUGCCCUAU
GLUD1-2	CCUACACUCUAUGAGAUAUUU	AAAUAUCUCAUAGAGUGUAGG
GLUD1-3	AGCGUUCUGCCAGGCAAAUUA	UAAUUUGCCUGGCAGAACGCU
GPD1-1	CCACUGGCAUAUCUCUUAUUA	UAAUAAGAGAUAUGCCAGUGG
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GPD1L-2	ACUGACAGACAUCAUAAAUAA	UUAUUUAUGAUGUCUGUCAGU
GPD1L-3	ACUUCUGCAGACUCCAAAUUU	AAAUUUGGAGUCUGCAGAAGU
GPD2-1	CAGCAGCAGAAGCACUAAAUU	AAUUUAGUGCUUCUGCUGCUG
GPD2-2	UCAGUGAGAGUGGCCUUAUUA	UAAUAAGGCCACUCUCACUGA
GPD2-3	GCAGACCAGAAAGGCUUUAUU	AAUAAAGCCUUUCUGGUCUGC
H6PD-1	GCACCCAGGCAUGUGGAAUAU	AUAUUCCACAUGCCUGGGUGC
H6PD-2	ACCUGGCUAAGAAGUACUUAU	AUAAGUACUUCUUAGCCAGGU
H6PD-3	UUCCAUGGCCGGAAGAAUUUC	GAAAUUCUUCCGGCCAUGGAA
HADH-1	AUUGACACUGCUAUGAAAUUA	UAAUUUCAUAGCAGUGUCAAU
HADH-2	GCCCAGCCCAUCCUUAAAUAA	UUAUUUAAGGAUGGGCUGGGC
HADH-3	GCCUCGGCCAAGAAGAUAAUC	GAUUAUCUUCUUGGCCGAGGC
HADHA-1	UCCGCUCCCGAGGUUAUAUAU	AUAUAUAACCUCGGGAGCGGA
HADHA-2	CUCUGUGAAUCUCAGAAAUUU	AAAUUUCUGAGAUUCACAGAG
HADHA-3	GUGGACCGGCUCAAGAAAUAU	AUAUUUCUUGAGCCGGUCCAC
HADHB-1	ACGUUAGCCAAACCCAAUAUA	UAUAUUGGGUUUGGCUAACGU
HADHB-2	GGGCCAGCGACUGUCUUUAAU	AUUAAAGACAGUCGCUGGCCC
HADHB-3	UCCUUUGGAGAAGUUUAAUAA	UUAUUAAACUUCUCCAAAGGA
HIBADH-1	ACAUGGCUAUCCACUUAUUAU	AUAAUAAGUGGAUAGCCAUGU
HIBADH-2	GUGAAGAAGGGCUCAUUAUUA	UAAUAAUGAGCCCUUCUUCAC
HIBADH-3	UGGCGUUCCCUCGGCUAAUAA	UUAUUAGCCGAGGGAACGCCA
HPGD-1	UUGCACAGCAGCCGGUUUAUU	AAUAAACCGGCUGCUGUGCAA
HPGD-2	CAUUGAAGAUGAUGCUUUAAA	UUUAAAGCAUCAUCUUCAAUG
HPGD-3	UGCUUUAAAUGGUGCUAUUAU	AUAAUAGCACCAUUUAAAGCA
HSD11B1-1	CCUCCAUCAGAAAGGAAUAUU	AAUAUUCCUUUCUGAUGGAGG
HSD11B1-2	CGCCAAGAAGAAGUGUAUUAU	AUAAUACACUUCUUCUUGGCG
HSD11B1-3	CUACUCAACGAGCUAUAAUAU	AUAUUAUAGCUCGUUGAGUAG
HSD11B1L-1	GCCCUGUUCUUCGCCUAUUAU	AUAAUAGGCGAAGAACAGGGC
HSD11B1L-2	GGCCCUGUUCUUCGCCUAUUA	UAAUAGGCGAAGAACAGGGCC
HSD11B1L-3	GGCUCAUGCAGGUAAACUUUG	CAAAGUUUACCUGCAUGAGCC
HSD11B2-1	UGACCAAACCAGGAGACAUUA	UAAUGUCUCCUGGUUUGGUCA
HSD11B2-2	UAGCUGCAUGGAGGUGAAUUU	AAAUUCACCUCCAUGCAGCUA
HSD11B2-3	AGCUGCAUGGAGGUGAAUUUC	GAAAUUCACCUCCAUGCAGCU
HSD17B10-1	CUAGCAAGACGUACAACUUAA	UUAAGUUGUACGUCUUGCUAG
HSD17B10-2	UAGCAAGACGUACAACUUAAA	UUUAAGUUGUACGUCUUGCUA
HSD17B10-3	AGCAAGACGUACAACUUAAAG	CUUUAAGUUGUACGUCUUGCU
HSD17B1-1	AUCCAUCCCAGAGCUUCAAAG	CUUUGAAGCUCUGGGAUGGAU

HSD17B11-1	GCUGCCUUUCAAUGACGUUUA	UAAACGUCAUUGAAAGGCAGC
HSD17B11-2	CCCACAGCAAGCAAGUCUUUC	GAAAGACUUGCUUGCUGUGGG
HSD17B11-3	AGCUGGUUCUCUGGGAUAUAA	UUAUAUCCCAGAGAACCAGCU
HSD17B1-2	GCAGCAACCGAGAAGAUAUUU	AAAUAUCUUCUCGGUUGCUGC
HSD17B12-1	GAUGCAGUUAUUGGAUAUAAA	UUUAUAUCCAAUAACUGCAUC
HSD17B12-2	ACCAGGUUUCCAGUGAAAUAA	UUAUUUCACUGGAAACCUGGU
HSD17B12-3	CUUUGCAUCAGAAGAUAUUUA	UAAAUAUCUUCUGAUGCAAAG
HSD17B1-3	ACCUGCCUUCUUGGAUUUAUU	AAUAAAUCCAAGAAGGCAGGU
HSD17B13-1	UAUUGGUUCUGUGGGAUAUUA	UAAUAUCCCACAGAACCAAUA
HSD17B13-2	GUAACAAUCGUGGUGAAUAAU	AUUAUUCACCACGAUUGUUAC
HSD17B13-3	CCAUAUUGUUCCAGCAAAUUU	AAAUUUGCUGGAACAAUAUGG
HSD17B14-1	GCUCCCUGGAGCUGUCUUUAU	AUAAAGACAGCUCCAGGGAGC
HSD17B14-2	UCUGAGACCAUCCGCCGAUUU	AAAUCGGCGGAUGGUCUCAGA
HSD17B14-3	AGCUUUGGCCCUGGAUGAAAG	CUUUCAUCCAGGGCCAAAGCU
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HSD17B2-2	UAUUUGCCUAUUGGCAUAUAU	AUAUAUGCCAAUAGGCAAAUA
HSD17B2-3	AGUACUAUGUGGGACAGUAUU	AAUACUGUCCCACAUAGUACU
HSD17B3-1	GACUCAAUGUUGUCCUUAUUA	UAAUAAGGACAACAUUGAGUC
HSD17B3-2	GACAUCUACGAGCAUAUUAAA	UUUAAUAUGCUCGUAGAUGUC
HSD17B3-3	GCCCUGCAAGAGGAAUAUAAA	UUUAUAUUCCUCUUGCAGGGC
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HSD17B4-2	UACGGAACUGGAAGCUAUUAU	AUAAUAGCUUCCAGUUCCGUA
HSD17B4-3	UAUAACCAAAGGCGGAAAUAU	AUAUUUCCGCCUUUGGUUAUA
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HSD17B6-2	GCUGGCUGGGAUGCUAAAUUU	AAAUUUAGCAUCCCAGCCAGC
HSD17B6-3	UUCAUCCCUCUAUCUUAUUUA	UAAAUAAGAUAGAGGGAUGAA
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HSD17B7-2	CCCUACAGCUCUUCCAAAUAU	AUAUUUGGAAGAGCUGUAGGG
HSD17B7-3	CUCAAUCCUCUGAUCAAAUAU	AUAUUUGAUCAGAGGAUUGAG
HSD17B8-1	AGAAAGUGGUGGACAAGAUUA	UAAUCUUGUCCACCACUUUCU
HSD17B8-2	GGUGGACAAGAUUACUGAAAU	AUUUCAGUAAUCUUGUCCACC
HSD17B8-3	CUGAGGAUGACUGGGACAAAG	CUUUGUCCCAGUCAUCCUCAG
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HSD3B1-3	CGUAUUCACCUUCUCUUAUAA	UUAUAAGAGAAGGUGAAUACG
HSD3B2-1	UGCGUUAAGACCCACAUAUAU	AUAUAUGUGGGUCUUAACGCA
HSD3B2-2	UUCCUUUCUGCCAGUAUAAAU	AUUUAUACUGGCAGAAAGGAA
HSD3B2-3	CUUCCUACUCAGCCCAAUUUA	UAAAUUGGGCUGAGUAGGAAG
HSD3B7-1	CUACAGGAGCUACGAGGAUUU	AAAUCCUCGUAGCUCCUGUAG
HSD3B7-2	CGGGUCUAUGUGGGCAAUGUU	AACAUUGCCCACAUAGACCCG
HSD3B7-3	UACAGGAGCUACGAGGAUUUC	GAAAUCCUCGUAGCUCCUGUA
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HSDL1-2	ACGUUGGCAUCUUGGUAAAUA	UAUUUACCAAGAUGCCAACGU

HSDL1-3	UCUGCUUCUAAGGCUUAUUUA	UAAAUAAGCCUUAGAAGCAGA
HSDL2-1	AGCAAAGGAUGGAGCAAAUAU	AUAUUUGCUCCAUCCUUUGCU
HSDL2-2	UUGGAAUGGCAGAAGAAUUUA	UAAAUUCUUCUGCCAUUCCAA
HSDL2-3	UCAGGGAAAUUGAAGAUUAAA	UUUAAUCUUCAAUUUCCCUGA
IDH1-1	GGAUGCUGCAGAAGCUAUAAA	UUUAUAGCUUCUGCAGCAUCC
IDH1-2	GACAUCUUUCAGGAGAUAUAU	AUAUAUCUCCUGAAAGAUGUC
IDH1-3	GCAAAGCUUGAUAACAAUAAA	UUUAUUGUUAUCAAGCUUUGC
IDH2-1	UGAUGAGAUGACCCGUAUUAU	AUAAUACGGGUCAUCUCAUCA
IDH2-2	GGACAUCCAGCUAAAGUAUUU	AAAUACUUUAGCUGGAUGUCC
IDH2-3	AUCUUUGACAAGCACUAUAAG	CUUAUAGUGCUUGUCAAAGAU
IDH3A-1	UGUUCAGACAGUAACUUUAAU	AUUAAAGUUACUGUCUGAACA
IDH3A-2	GGUCACCCAUCUAUGAAUUUA	UAAAUUCAUAGAUGGGUGACC
IDH3A-3	CAGAAAGCUGUAAAGAUAUUA	UAAUAUCUUUACAGCUUUCUG
IDH3B-1	AGGCGUAAGUUGGACUUAUUU	AAAUAAGUCCAACUUACGCCU
IDH3B-2	CAGGCAGUGGGCAGGAAUAUA	UAUAUUCCUGCCCACUGCCUG
IDH3B-3	ACCUGAGUGAGGUGCAGAAUA	UAUUCUGCACCUCACUCAGGU
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IDH3G-2	CAUCCAUGGACAAUGAGAAUA	UAUUCUCAUUGUCCAUGGAUG
IDH3G-3	UCCAUGGACAAUGAGAAUAUG	CAUAUUCUCAUUGUCCAUGGA
IMPDH1-1	GCACCCGUGAGGAUGACAAAU	AUUUGUCAUCCUCACGGGUGC
IMPDH1-2	CACCCGUGAGGAUGACAAAUA	UAUUUGUCAUCCUCACGGGUG
IMPDH1-3	ACCCGUGAGGAUGACAAAUAC	GUAUUUGUCAUCCUCACGGGU
IMPDH2-1	GUUCGGAAAGUGAAGAAAUAU	AUAUUUCUUCACUUUCCGAAC
IMPDH2-2	GGGAUCCGGCUAAAGAAAUAU	AUAUUUCUUUAGCCGGAUCCC
IMPDH2-3	CAGCAGCCAGAACAGAUAUUU	AAAUAUCUGUUCUGGCUGCUG
IVD-1	UUCAAGAACCUGCGAGAAUUU	AAAUUCUCGCAGGUUCUUGAA
IVD-2	ACAUCCUGGGCCAUGAGAAUA	UAUUCUCAUGGCCCAGGAUGU
IVD-3	CUGUGCAGGUGUGAUUCUUUA	UAAAGAAUCACACCUGCACAG
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L2HGDH-2	AGUCUCUGAAAGCCAAAUUAU	AUAAUUUGGCUUUCAGAGACU
L2HGDH-3	CCACAGAUGUUAUGGAUAUAA	UUAUAUCCAUAACAUCUGUGG
LDHA-1	UAAAGGAUCAGCUGAUUUAUA	UAUAAAUCAGCUGAUCCUUUA
LDHA-2	GGGAGAAAGCCGUCUUAAUUU	AAAUUAAGACGGCUUUCUCCC
LDHA-3	UAAGGGUCUUUACGGAAUAAA	UUUAUUCCGUAAAGACCCUUA
LDHAL6A-1	UGUGCUAUCAGCAUCUUAUUA	UAAUAAGAUGCUGAUAGCACA
LDHAL6A-2	CGAAAUGUAUCCAUCUUUAAA	UUUAAAGAUGGAUACAUUUCG
LDHAL6A-3	UAAGGGCCUCUAUGGAAUAAA	UUUAUUCCAUAGAGGCCCUUA
LDHAL6B-1	GCGCUAUCAGCAUCUUAUUAA	UUAAUAAGAUGCUGAUAGCGC
LDHAL6B-2	GGAGAAACGCGCCUUAAUUUA	UAAAUUAAGGCGCGUUUCUCC
LDHAL6B-3	UCCAGUUUCCACCAUAAUUAA	UUAAUUAUGGUGGAAACUGGA
LDHB-1	CUGCAGCAUGGGAGCUUAUUU	AAAUAAGCUCCCAUGCUGCAG
LDHB-2	UUGUGGCAGAUAAAGAUUAUU	AAUAAUCUUUAUCUGCCACAA
LDHB-3	AGUCCUGAUUGCAUCAUAAUU	AAUUAUGAUGCAAUCAGGACU

LDHC-1	CCAACGUAAUGUGGCUAUAAU	AUUAUAGCCACAUUACGUUGG
LDHC-2	AGCUGCCAUGGUUGGAUUAUU	AAUAAUCCAACCAUGGCAGCU
LDHC-3	CACCAUGGUUAAGGGAUUAUA	UAUAAUCCCUUAACCAUGGUG
LDHD-1	CUUCGGCUUCUGGCCAGAAAU	AUUUCUGGCCAGAAGCCGAAG
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MDH1-2	AGGGUGCAGCCUUAGAUAAAU	AUUUAUCUAAGGCUGCACCCU
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MDH2-1	UCAUUGCCAAUCCGGUUAAUU	AAUUAACCGGAUUGGCAAUGA
MDH2-2	AGGUUGUGAUGUGGUAGUUAU	AUAACUACCACAUCACAACCU
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MTHFD1-1	CACACCACGCCUGGCAAUAUU	AAUAUUGCCAGGCGUGGUGUG
MTHFD1-2	UCUGGAUGAGGAGGUAAAUAA	UUAUUUACCUCCUCAUCCAGA
MTHFD1-3	UGUCUGAAGAGGUAGAAUUAU	AUAAUUCUACCUCUUCAGACA
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MTHFD2-3	UCAUUGAUGUGGGAAUAAAUA	UAUUUAUUCCCACAUCAAUGA
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MTHFD2L-2	CCAAGAGUCAGCGGUAUAUUA	UAAUAUACCGCUGACUCUUGG
MTHFD2L-3	AUACGCAGCUGGCAGAUAUUA	UAAUAUCUGCCAGCUGCGUAU
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NQO1-2	GAGUCUGUUCUGGCUUAUAAA	UUUAUAAGCCAGAACAGACUC
NQO1-3	AGAAACGCCUGGAGAAUAUUU	AAAUAUUCUCCAGGCGUUUCU
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NSDHL-2	AGGAUAUGCUGUCAAUGUAUU	AAUACAUUGACAGCAUAUCCU
NSDHL-3	CCCAGCUCUGAAAGGUGUAAA	UUUACACCUUUCAGAGCUGGG
OGDH-1	CUGAGUAUGAGGAGGAAAUUU	AAAUUUCCUCCUCAUACUCAG
OGDH-2	CAUUCCGGAAGCCGUUAAUUA	UAAUUAACGGCUUCCGGAAUG
OGDH-3	UGCACCGGCAAAGUGUAUUAU	AUAAUACACUUUGCCGGUGCA
OGDHL-1	GACCCAGAGGCUGUGAUAUAU	AUAUAUCACAGCCUCUGGGUC
OGDHL-2	CGGACCAAGACCAGCAAAUUG	CAAUUUGCUGGUCUUGGUCCG
OGDHL-3	UGAUCACAACCAUUGAUAAAC	GUUUAUCAAUGGUUGUGAUCA
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PDHA1-2	UGAGGUCUGCCUGACUUUAUA	UAUAAAGUCAGGCAGACCUCA
PDHA1-3	AUGGCAGCUUUGUGGAAAUUA	UAAUUUCCACAAAGCUGCCAU
PDHA2-1	UGACGCUACAUUUGAAAUUAA	UUAAUUUCAAAUGUAGCGUCA
PDHA2-2	GCUCUGGCCUGUAAAUAUAAA	UUUAUAUUUACAGGCCAGAGC
PDHA2-3	GUAAGAGGGAUCCUAUAAUAA	UUAUUAUAGGAUCCCUCUUAC
PDHB-1	ACAGUUCGUGAUGCUAUAAAU	AUUUAUAGCAUCACGAACUGU

PDHB-2	AGGAUGCUAAAGGACUUAUUA	UAAUAAGUCCUUUAGCAUCCU
PDHB-3	UGAAUGUGAGGUGAUAAAUAU	AUAUUUAUCACCUCACAUUCA
PDHX-1	AGUCCAGCUGCCCGCAAUAUU	AAUAUUGCGGGCAGCUGGACU
PDHX-2	CUGGUCAAAGAUGACAUUAAA	UUUAAUGUCAUCUUUGACCAG
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PDK1-2	UGAGGAUGCUAAAGCUAUUUA	UAAAUAGCUUUAGCAUCCUCA
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PDK2-2	GCUCCUGUGUGACAAGUAUUA	UAAUACUUGUCACACAGGAGC
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PDK4-1	UCCCGACCCAAUUAGUAAAUA	UAUUUACUAAUUGGGUCGGGA
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PDPR-1	GGAUGCUGAUGGAAGAAUUUA	UAAAUUCUUCCAUCAGCAUCC
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PDPR-3	CGAGAGUCUCGGGUGAAAUUA	UAAUUUCACCCGAGACUCUCG
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PHGDH-2	UCUGGACCAGCUUUGUUUAAA	UUUAAACAAAGCUGGUCCAGA
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RDH10-2	CCUACGAUGCUGGAGAUUAAU	AUUAAUCUCCAGCAUCGUAGG
RDH10-3	UGGGAAUGGUGAGGAAGAAAU	AUUUCUUCCUCACCAUUCCCA
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RDH11-2	CUGUCUGAUACUAAGUCUAUU	AAUAGACUUAGUAUCAGACAG
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RDH8-3	CUGCCAUGCAGAAUGUCUUUG	CAAAGACAUUCUGCAUGGCAG
SARDH-1	UCGUGUGUGGACGGAUGAUUU	AAAUCAUCCGUCCACACACGA
SARDH-2	CCGAGAAGAGUGUGCCAUAUC	GAUAUGGCACACUCUUCUCGG
SARDH-3	AGGAGGUGUCAGACAAGUUUG	CAAACUUGUCUGACACCUCCU
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SDHA-2	UCGCUAUUGCACACCUUAUAU	AUAUAAGGUGUGCAAUAGCGA
SDHA-3	AGAUAAAGUCCCUCCAAUUAA	UUAAUUGGAGGGACUUUAUCU
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SDHAF1-2	UCUGAGCCUGUACCGCGAUCU	AGAUCGCGGUACAGGCUCAGA
SDHAF1-3	CUGCGCAUCGAGUACCUGUAC	GUACAGGUACUCGAUGCGCAG
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SDHAF2-2	CCUCUAUGACCGCCUGAUUAA	UUAAUCAGGCGGUCAUAGAGG
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SDHAF4-3	ACCUACCCGAUAUGGAGAUUG	CAAUCUCCAUAUCGGGUAGGU
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SDHB-2	CAUGGUAUUGGAUGCUUUAAU	AUUAAAGCAUCCAAUACCAUG
SDHB-3	CAAAUCCAUUGAGCCUUAUUU	AAAUAAGGCUCAAUGGAUUUG
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SDHC-2	UGGGAACUUUGAGUCUUAUUU	AAAUAAGACUCAAAGUUCCCA
SDHC-3	CCUCAGCUCUGUAUCAGAAAU	AUUUCUGAUACAGAGCUGAGG
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SDHD-2	AGUGGUCAGACCUGCUCAUAU	AUAUGAGCAGGUCUGACCACU
SDHD-3	CUUGCUCUGCGAUGGACUAUU	AAUAGUCCAUCGCAGAGCAAG
SDR16C5-1	AGCACAUUUAUGGACUUAUAA	UUAUAAGUCCAUAAAUGUGCU
SDR16C5-2	GUCUUCUGGAGGCUAUGAUUU	AAAUCAUAGCCUCCAGAAGAC
SDR16C5-3	AGAACGUUGCUGGUGAAAUAG	CUAUUUCACCAGCAACGUUCU

SDR42E1-1	CCAGAAGGAAUCAAGUUUAUA	UAUAAACUUGAUUCCUUCUGG
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SDR42E1-3	GAAGCAGUGGAAUGGUUUAAA	UUUAAACCAUUCCACUGCUUC
SDR9C7-1	CCUCACAGACCUCUCAUUUAU	AUAAAUGAGAGGUCUGUGAGG
SDR9C7-2	GACUUUGUGAAGGUGAUUAAU	AUUAAUCACCUUCACAAAGUC
SDR9C7-3	ACAGCUACGGAGAGGAUUAUU	AAUAAUCCUCUCCGUAGCUGU
SORD-1	GGAGGCCUUUGAAACAUUUAA	UUAAAUGUUUCAAAGGCCUCC
SORD-2	GUAUGGUCGAAUUGGGAAUUU	AAAUUCCCAAUUCGACCAUAC
SORD-3	GUCCAAGUCUGUGAAUGUAAA	UUUACAUUCACAGACUUGGAC
TDH-1	GACCAUCCACGAGUCUUAAUU	AAUUAAGACUCGUGGAUGGUC
TDH-2	CACAGUGGUCCAUUCAUUUAU	AUAAAUGAAUGGACCACUGUG
TDH-3	CUGGCGAGAGCAGUGAAUAUA	UAUAUUCACUGCUCUCGCCAG
UGDH-1	UUCUCCUACACUUCCUAUUUA	UAAAUAGGAAGUGUAGGAGAA
UGDH-2	AGAAGCUGAUCUUGUAUUUAU	AUAAAUACAAGAUCAGCUUCU
UGDH-3	GCAGCAGAUCUGAAGUAUAUU	AAUAUACUUCAGAUCUGCUGC
XDH-1	UGUGGAGGAGAUGGGAAUAAU	AUUAUUCCCAUCUCCUCCACA
XDH-2	CAGCCUCUCGCCAUCUUUAUU	AAUAAAGAUGGCGAGAGGCUG
XDH-3	GGAUCUCUCUCAGAGUAUUAU	AUAAUACUCUGAGAGAGAUCC
ZADH2-1	GAUCGUCCUAUCAACUAUAAA	UUUAUAGUUGAUAGGACGAUC
ZADH2-2	AUAUUCCGUGCUGUCAAUUAU	AUAAUUGACAGCACGGAAUAU
ZADH2-3	UAUUCCGUGCUGUCAAUUAUA	UAUAAUUGACAGCACGGAAUA
siRNA sequences against four acetyltransferases and HIF1A		
PCAF	GUUGGCUAUAUCAAGGAUUAU	AUAAUCCUUGAUAUAGCCAAC
TIP60	GGACGUAAGAACAAGAGUUAU	AUAACUCUUGUUCUUACGUCC
CBP	AUCGCCACGUCCCUUAGUAAC	GUUACUAAGGGACGUGGCGAU
p300	UAACCAAUGGUGGUGAUAUUA	UAAUAUCACCACCAUUGGUUA
HIF1A	CCGCUGGAGACACAAUCAUAU	AUAUGAUUGUGUCUCCAGCGG

Appendix Table S2. RT-qPCR primer sequences used in this study. Related to Methods.

RT-qPCR primer sequences (5'-3')		
Homo Target	Forward primer	Reverse primer
PCAF	AGGAAAACCTGTGGTTGAAGG	CAGTCTTCGTTGAGATGGTGC
TIP60	AACAAACGTCTGGATGAATGGG	AGGAAGTCCGTTCTTAGTGGG
CBP	CCTGCCACGTCACAGACTG	GGCCAGAGTTACTATTGAGGAGG
p300	GCTTCAGACAAGTCTTGGCAT	ACTACCAGATCGCAGCAATTC
HIF1A	ATCCATGTGACCATGAGGAAATG	TCGGCTAGTTAGGGTACACTTC
GLUT1	GGCCAAGAGTGTGCTAAAGAA	ACAGCGTTGATGCCAGACAG
HK1	CCAACATTCGTAAGGTCCATTCC	CCTCGGACTCCATGTGAACATT
PGK1	GAACAAGGTTAAAGCCGAGCC	GTGGCAGATTGACTCCTACCA
CCND1	TGGAGCCCGTGAAAAAGAGC	TCTCCTTCATCTTAGAGGCCAC
β-ACTIN	CACCATTGGCAATGAGCGGTTC	AGGTCTTTGCGGATGTCCACGT
Murine Target	Forward primer	Reverse primer
Tnfα	CCCTCACACTCAGATCATCT	GCTACGACGTGGGCTACAG
Ifng	ATGAACGCTACACACTGCATC	CCATCCTTTTGCCAGTTCCTC
Il6	TAGTCCTTCCTACCCCAATTTC	TTGGTCCTTAGCCACTCCTTC
Hif1a	GATGACGGCGACATGGTTTAC	CTCACTGGGCCATTTCTGTGT
β-Actin	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT