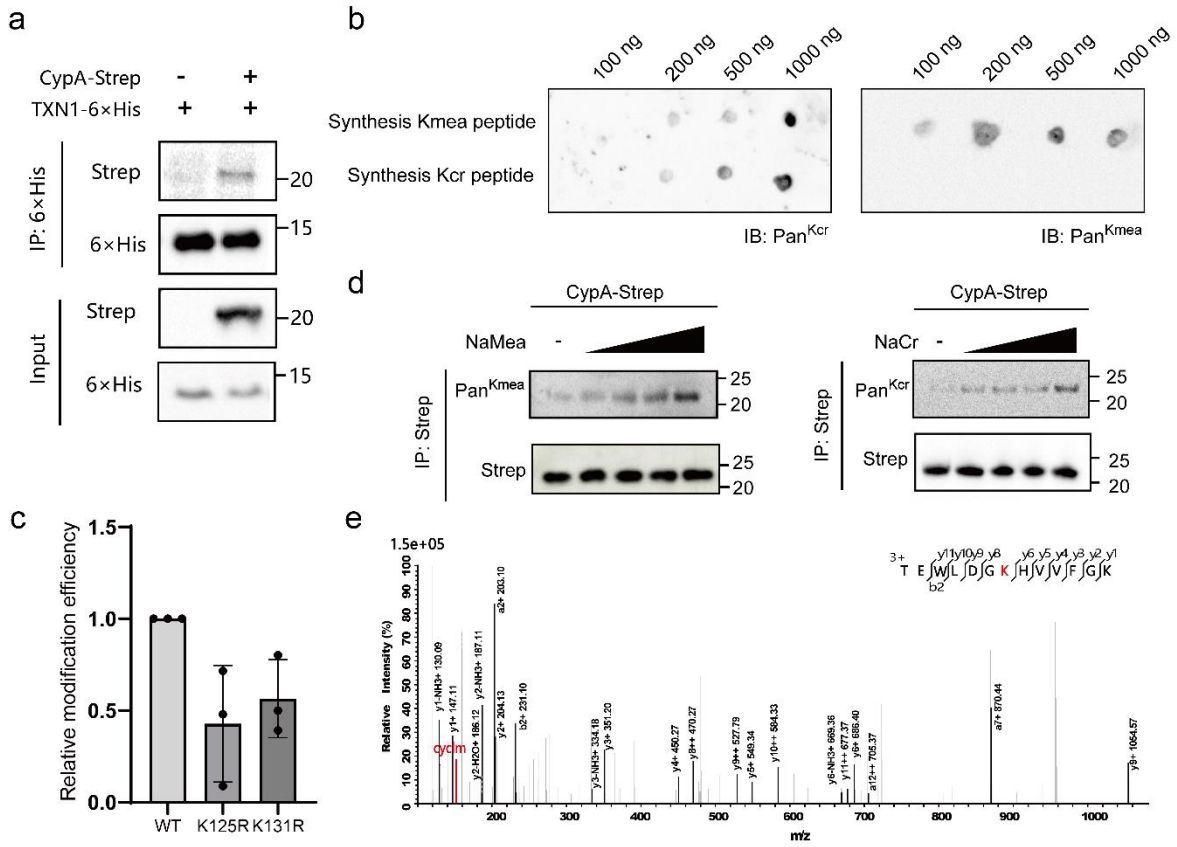
Supporting Information

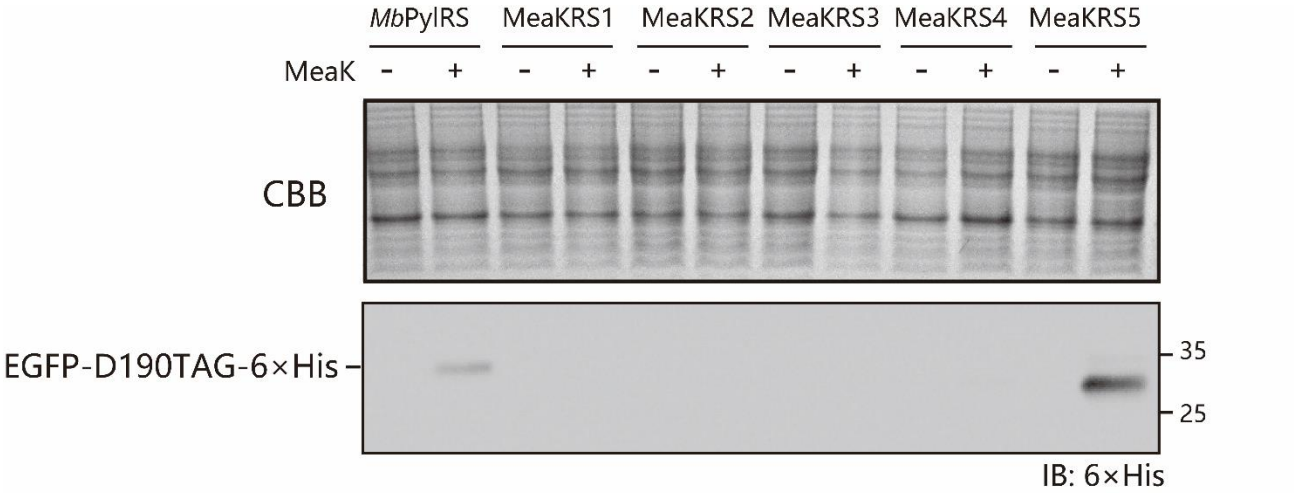
Genetically encoding *ε*-*N*-methacryllysine into proteins in live cells

Tian-Yi Zhu, Shi-Yi Chen, Mengdi Zhang, Heyu Li, Ting Wu, Emmanuel Ajiboye, Jia Wen Wang, Bi-Kun Jin, Dan-Dan Liu, Xintong Zhou, He Huang, Xiaobo Wan, Ke Sun, Peilong Lu, Yaxin Fu,Ying Yuan, Hai Song, Anna A. Sablina, Chao Tong, Long Zhang, Ming Wu, Haifan Wu, Bing Yang

Supplementary Figures

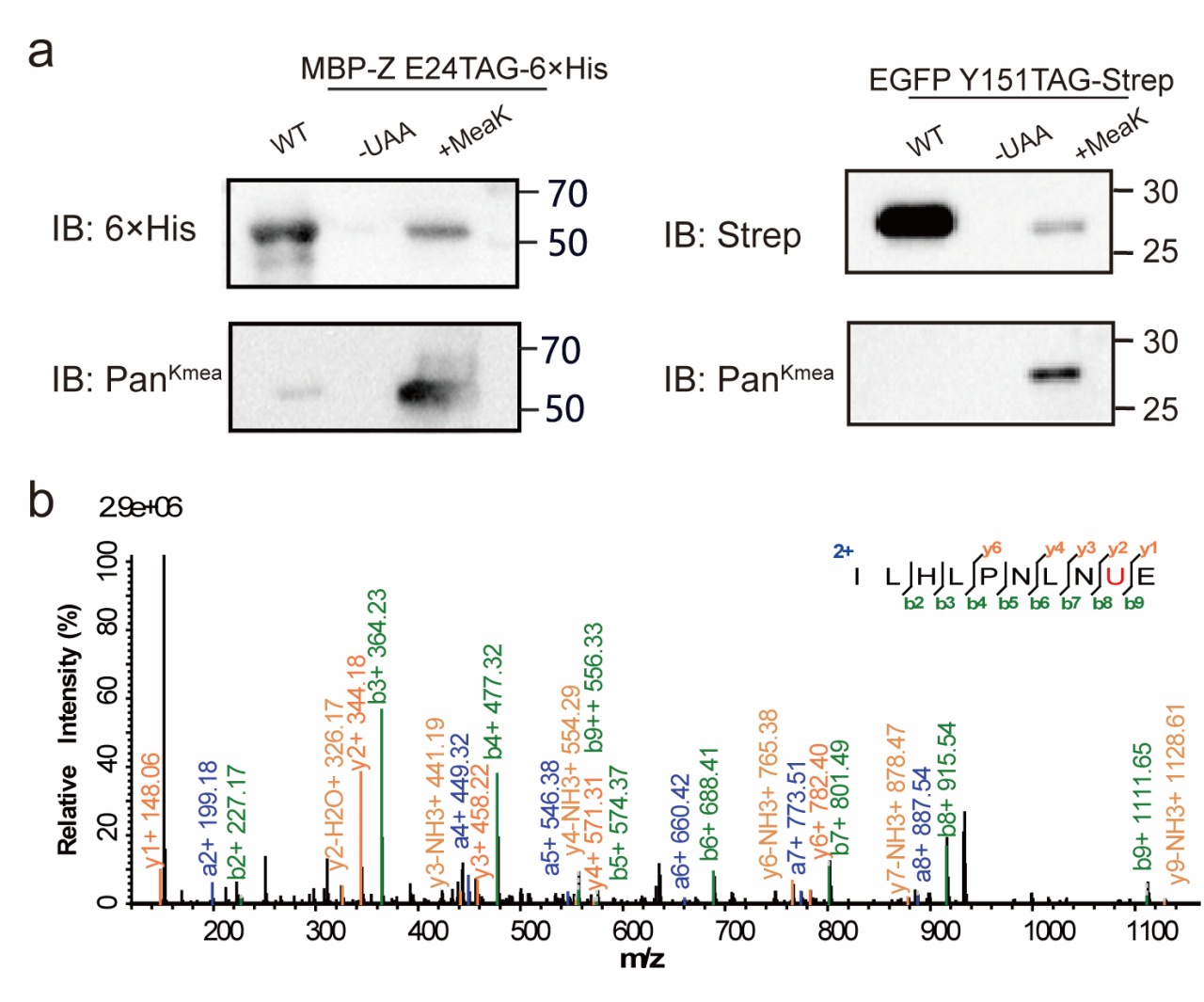


Supplementary Figure 1. Kmea modification on CypA (a) Co-IP experiment for validation protein interaction between TXN1 and CypA. (b) Synthesized peptides HVVFGKmeaVK and HVVFGKcrVK were used to assess the specificity of pan anti-Kmea and anti-Kcr antibody in Dot blot assay. The amounts of peptides spotted in each column of the membrane were labeled on the top of figures. (c) Methacrylation levels of CypA and its K125R/K131R mutants (n = 3). Data are normalized by intensity of CypA, and methacrylation levels were shown as ratios to intensity of methacylated CypA WT. Data are presented as mean ± SD. (d) HEK293T cells were treated with 1, 3, 5 and 10 mM sodium methacrylate or sodium crotonate for 24h, respectively. Kmea and Kcr signal of CypA increased with the increasing doses of sodium methacrylate or sodium crotonate in HEK293T cells transfected with CypA-Strep. (e) CycIm ion were mapped on MS/MS spectrum of methacrylated peptide (Kmea on CypA Lys 125).

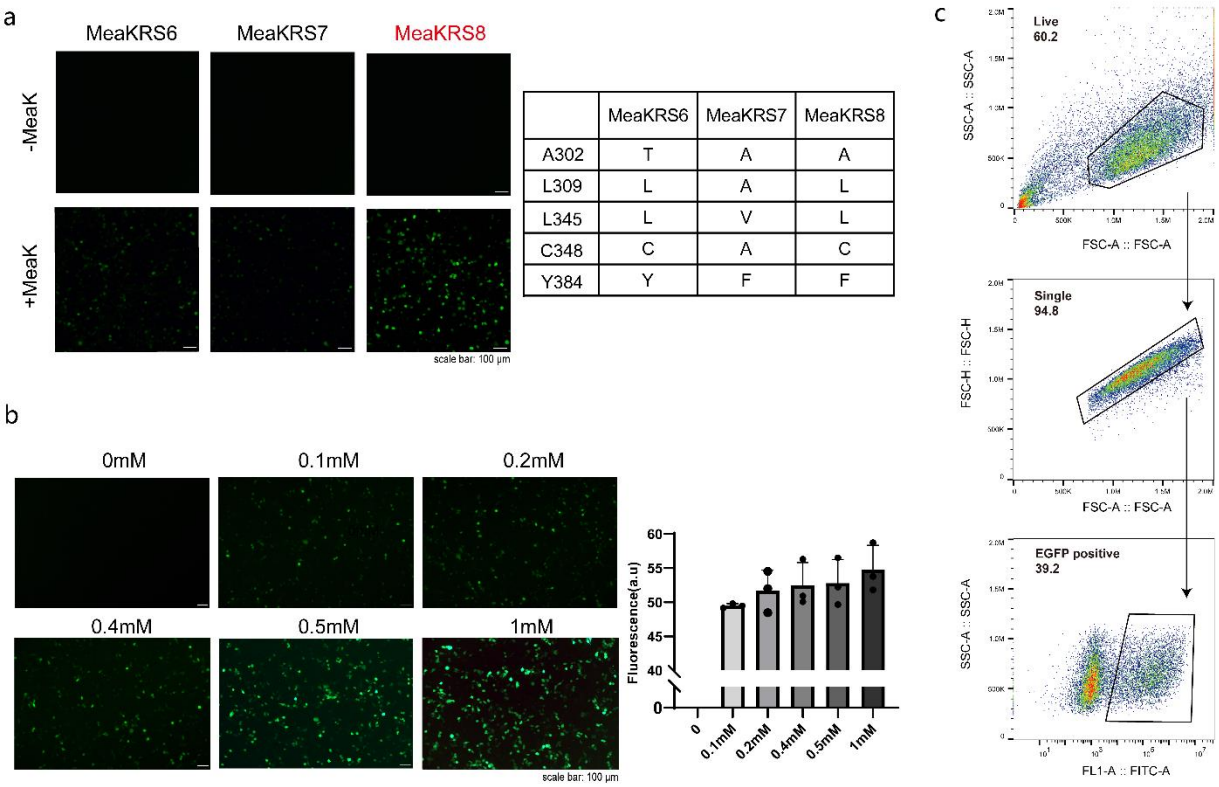


*Mm*PylRS	*Mb*PylRS	MeaKRS1	MeaKRS2	MeaKRS3	MeaKRS4	MeaKRS5
A302	A267	T	A	A	A	A
L309	L274	L	A	A	L	L
L345	V310	L	V	V	L	V
N346	N311	A	N	N	N	N
C348	C313	A	C	A	C	C
Y384	Y349	F	F	F	Y	F
W417	W382	T	W	W	W	W

Supplementary Figure 2. Western blot of cell lysates from *E. coli* cells co-expressing EGFP D190TAG and *Mb*PylRS mutants showing that *Mb*PylRS and *Mb*PylRS Y349F can recognize MeaK. SDS-PAGE gel of cell lysates was used as a loading control, the SDS-PAGE gel was running parallel with Western blot.

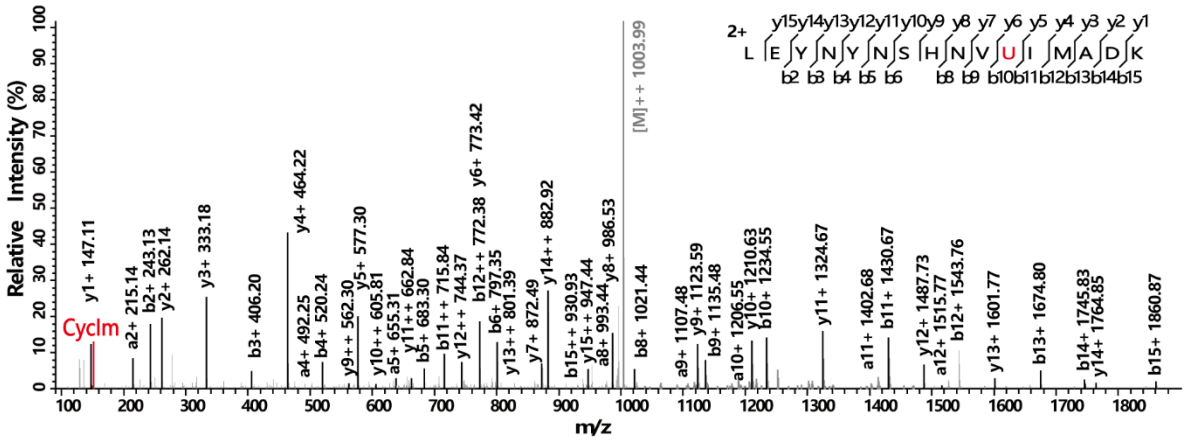


Supplementary Figure 3. (a). Western blot of purified wild type MBP-Z and EGFP or mutant proteins with or without MeaK incorporated. MBP-Z was purified from *E. coli* thought 6 ×His tag and EGFP was purified in HEK293T cells by Strep tag. (b). Tandem mass spectrum of MeaK incorporated peptide of MBP-Z E24MeaK. The red U represents MeaK incorporation site.

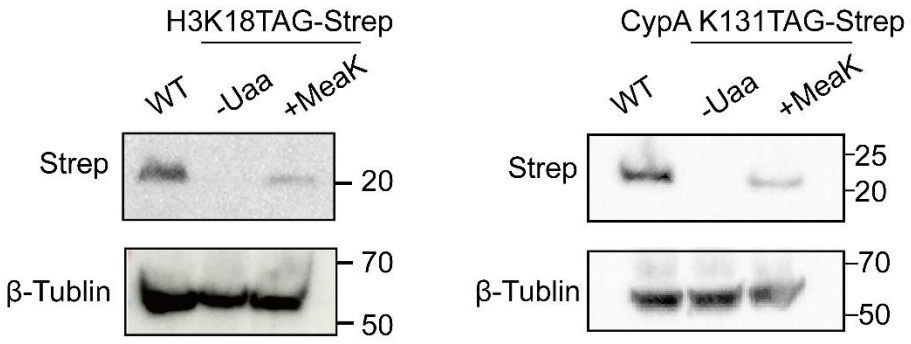


	MeaKRS6	MeaKRS7	MeaKRS8
A302	T	A	A
L309	L	A	L
L345	L	V	L
C348	C	A	C
Y384	Y	F	F

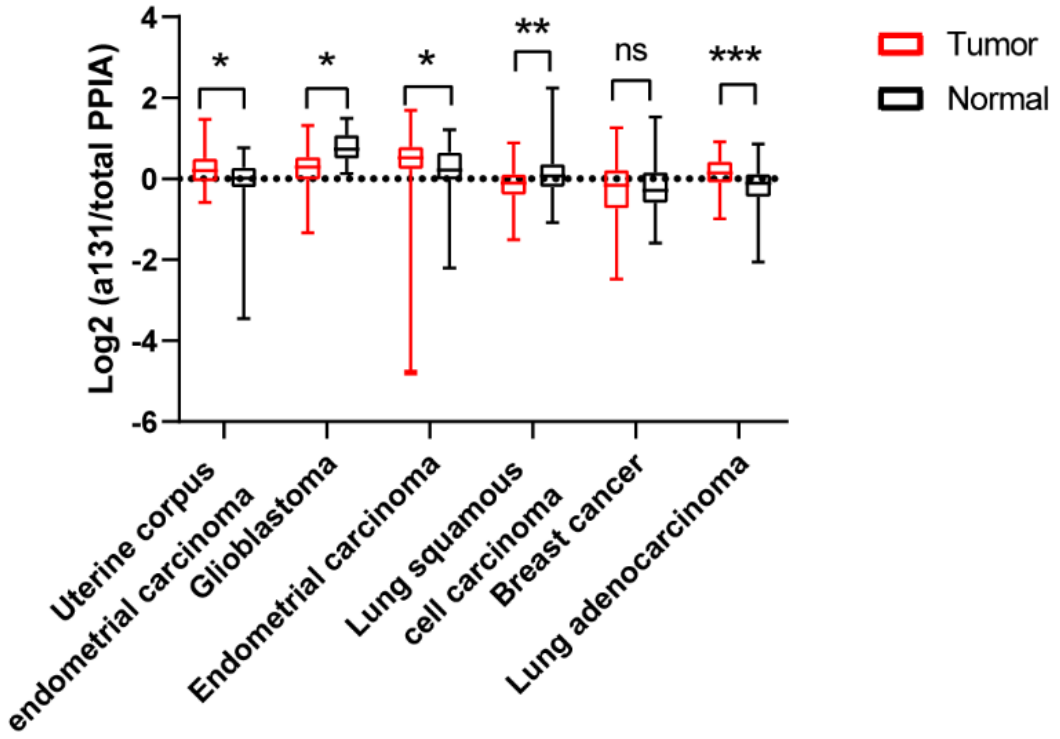
Supplementary Figure 4. Screen MeaK synthetase in mammalian cells. (a) co-expressing EGFP Y151TAG with different chPylRS mutants. Residue numbering is based on *Mm*PylRS. (b) Optimizing MeaK concentration for incorporation MeaK in HEK293T cells co-expressing EGFP Y151TAG with $tRNA^{pyl}_{CUA}$/chPylRS Y384F. Statistics by mean fluorescence intensity (n=3 biological replicates). Error bar represents +/- one standard deviation (SD). (c) Gating strategy in FlowJo. HEK 293T cells trasfected with EGFP were used to set appropriate forward scatter (FSC) and side scatter (SSC) gains. HEK 293T cells without transfection were used as negative control to set FITC gate. Each gate was highlighted by black boxes.



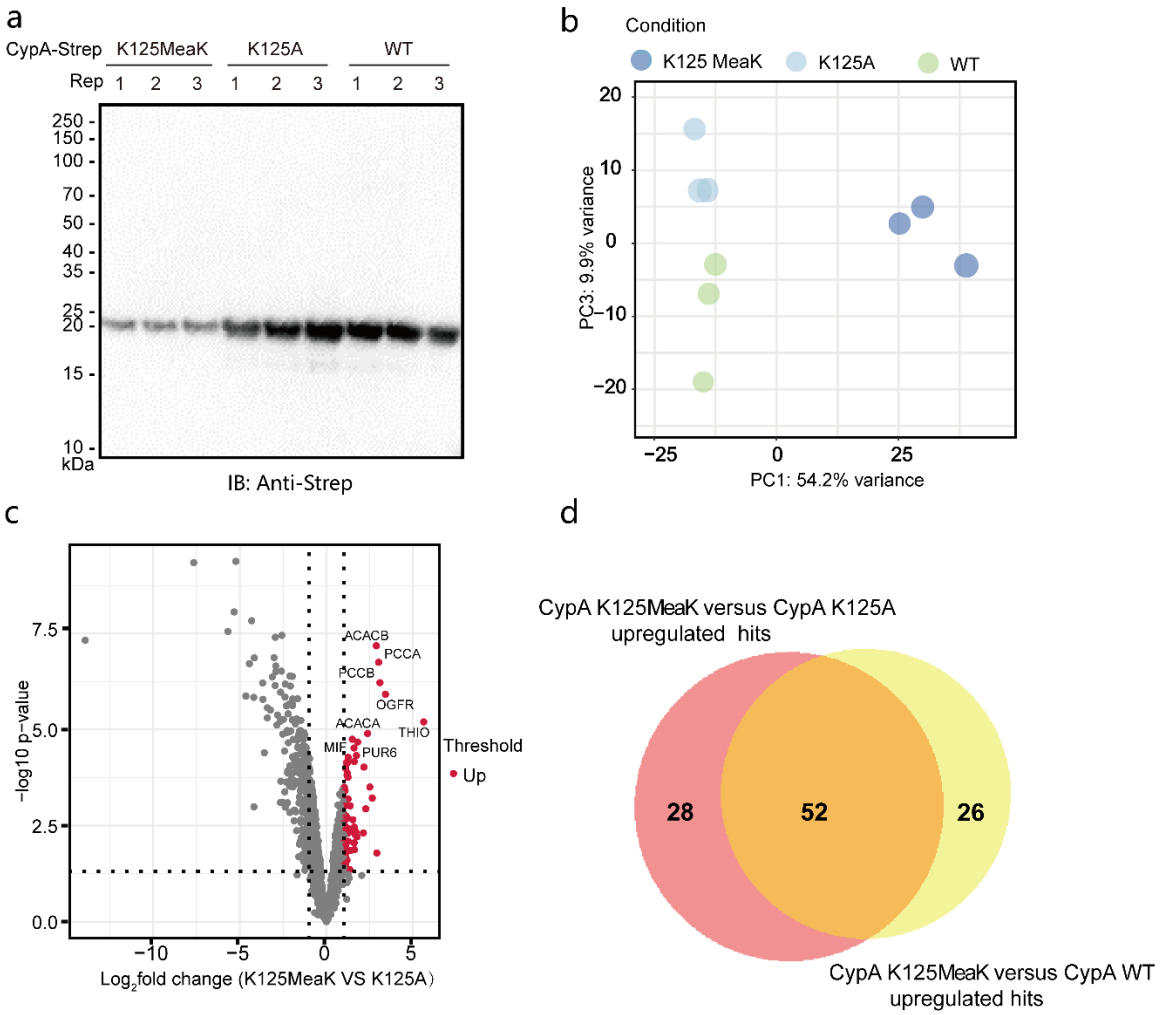
Supplementary Figure 5. CycIm ion on tandem mass spectrum of MeaK incorporated peptide from EGFP site 151 incorporation.



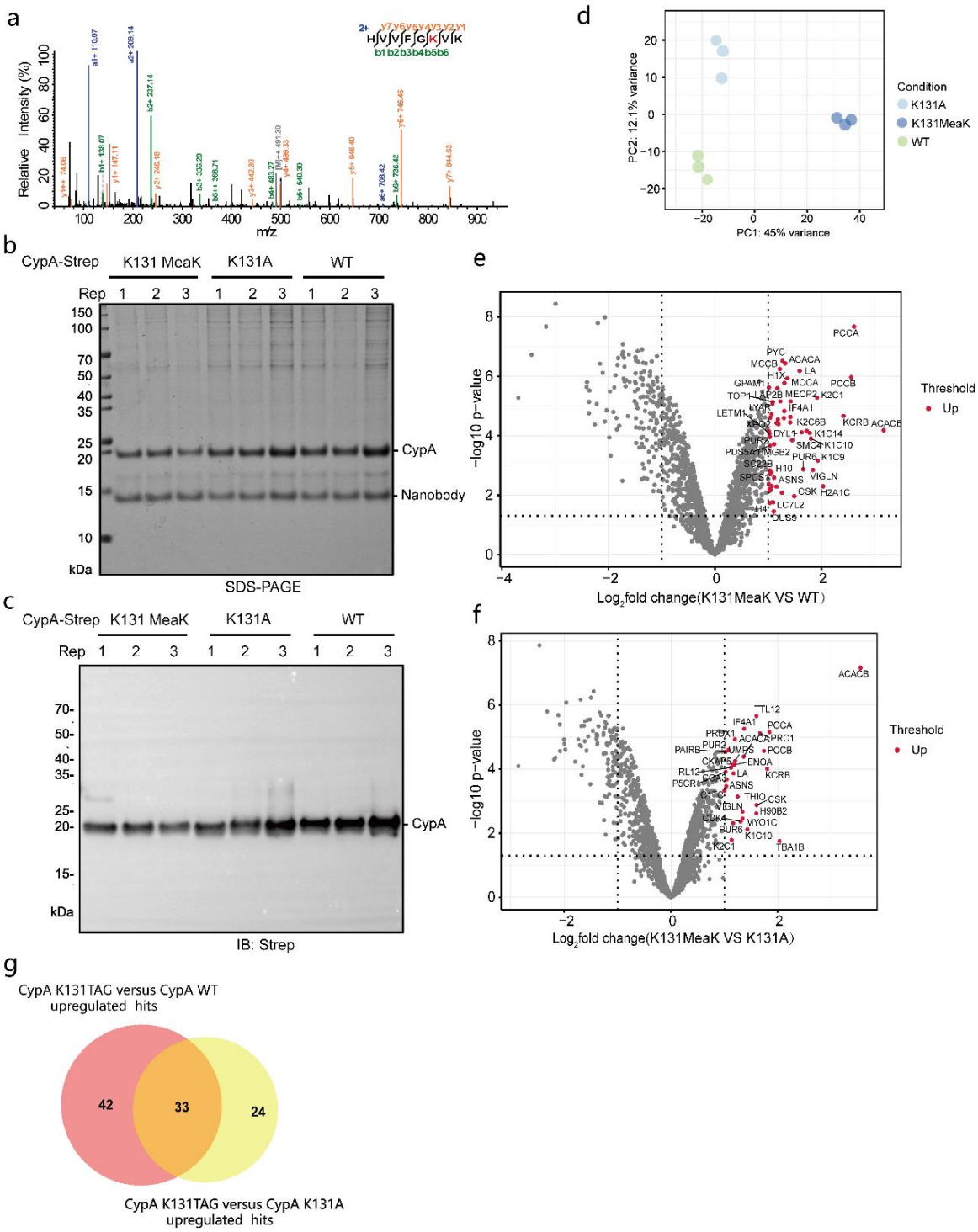
Supplementary Figure 6. Western blot of cell lysates from HEK293T cells expressing CypA K131TAG and H3 K18TAG with MeaK incorporated.



Supplementary Figure 7. Comparison of CypA acetylated K131 levels between tumor and adjacent tissues from different cancer types. Raw data were obtained from six acylated proteomes of CPTAC (Clinical Proteomic Tumor Analysis Consortium) database. *, P < 0. 5; **, P < 0.01; ***, P < 0.001 (two-tailed t-test). The centre line denotes the median value, the box contains the 25th to 75th percentiles. The whiskers mark the minima and maxima. Sample numbers are provided in the Source Data file.

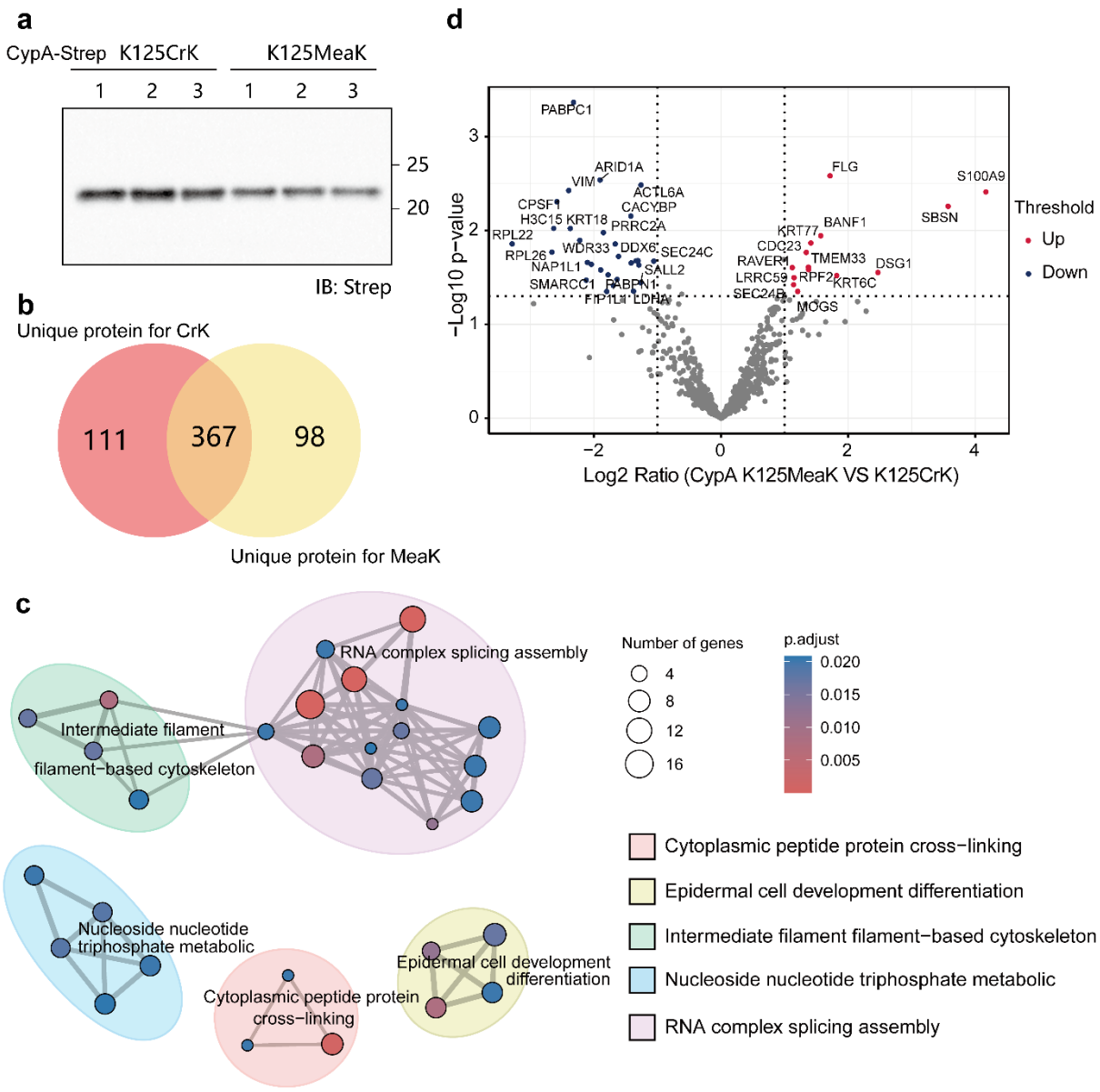


Supplementary Figure 8. Identify interacting proteins of CypA (K125MeaK, K125A and WT). (a) Western blot of CypA (K125MeaK, K125A and WT) Strep-IP with three biological replicates. (b) PCA analysis proved repeatable for CypA (K125MeaK, K125A and WT) IP. (c) Volcano plot of semi-quantitation on CypA K125MeaK and CypA WT IP samples. Red dots, significantly upregulated hits. Grey dots, downregulated hits or non-differentially expressed proteins. (Fold Change $\geqslant$ 2, *p*-value < 0.05). Data quantified with Empirical Bayes test two-sided. (d) Overlap of interaction enhanced and unique proteins in CypA K125MeaK IP in comparison with CypA K125A IP and CypA WT IP. Unique proteins mean that unique peptides appear in all three replicates in the MS analysis.

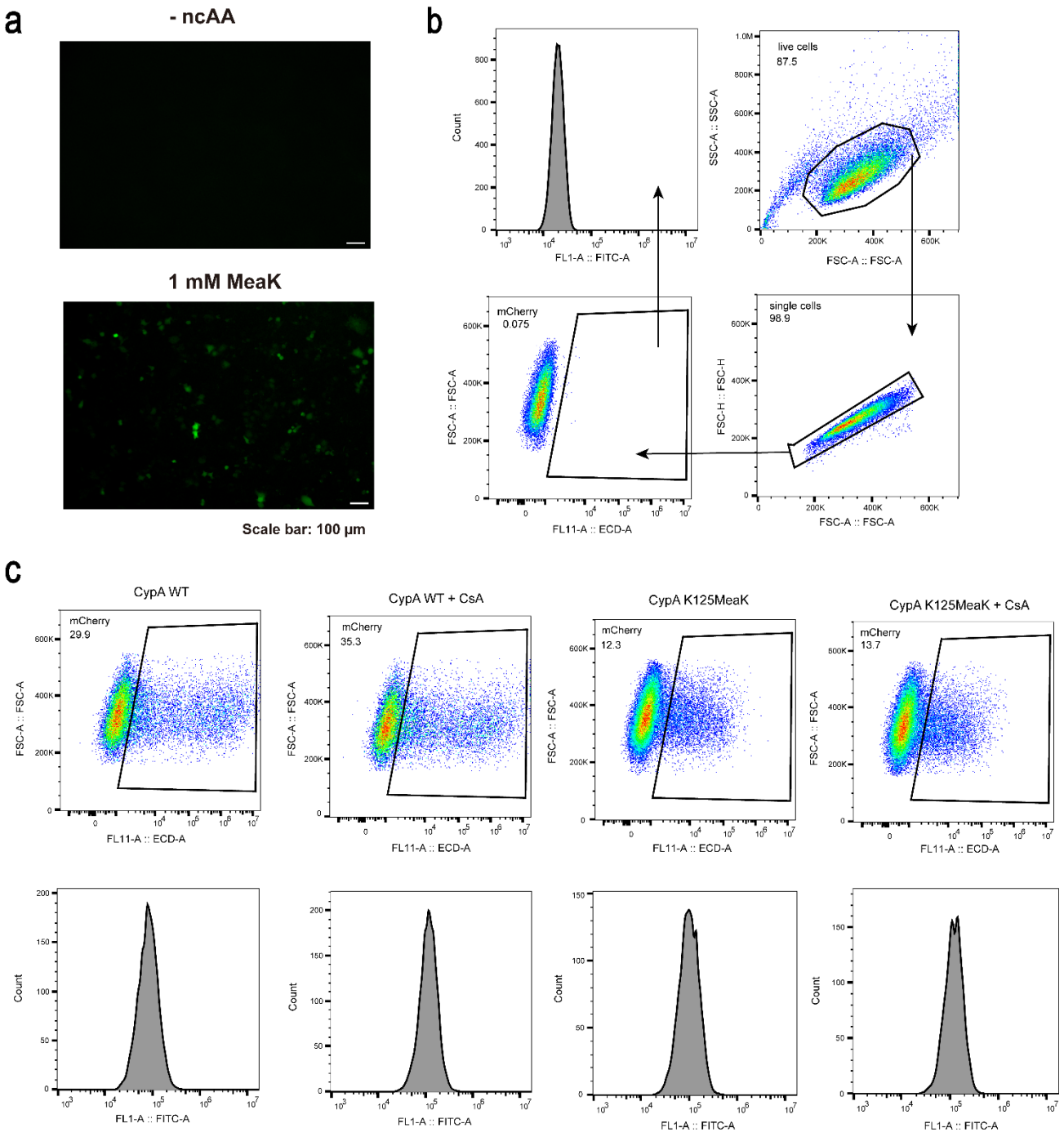


Supplementary Figure 9. Identify interacting proteins of CypA (K131MeaK, K131A and WT). (a) Tandem spectra of MeaK incorporated peptide from CypA K131MeaK. The K in red represents the Kmea modification.(b) SDS-PAGE gel of CypA (K131MeaK, K131A and WT) Strep-IP with three biological replicates. Nanobody comes from alpaca-derived heavy VHH carried by strep beads. (c)

Western blot of CypA (K131MeaK, K131A and WT) Strep-IP. (d) PCA analysis proved repeatable for CypA (K131MeaK, K131A and WT) IP. (e) Volcano plot of semi-quantitation on CypA K131MeaK and CypA WT IP samples. Red dots, significantly upregulated hits. Grey dots, downregulated hits or non-differentially expressed proteins. (Fold Change ≥ 2, *p*-value < 0.05). Data quantified with Empirical Bayes test two-sided. (f) Overlap of interaction enhanced proteins in CypA K131MeaK IP in comparison with CypA K131A IP and CypA WT IP. Red dots, significantly upregulated hits; Grey dots, downregulated hits or non-differentially expressed proteins. (Fold Change ⩾ 2, *p*-value < 0.05). (g) Overlap of interaction enhanced proteins and unique in CypA K131MeaK IP in comparison with CypA K131A IP and CypA WT IP. Unique proteins mean that unique peptides appear in all three replicates in the MS analysis.

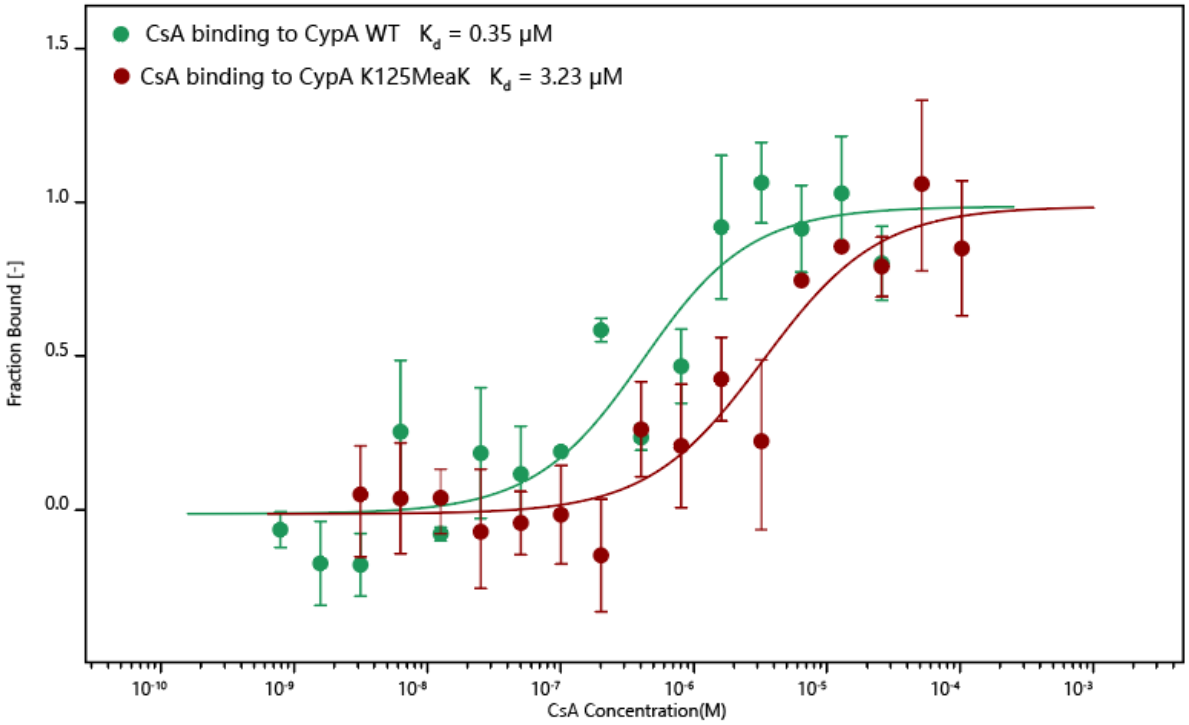


Supplementary Figure 10. Identify interacting proteins of CypA (K125MeaK, K125CrK). (a) Western blot of CypA (K125MeaK, K125CrK) Strep-IP (three biological replicates). (b) Venn diagram showing the interactome of CypA K125MeaK and CypA K125CrK. (c) Biological process analysis of the unique proteins identified in CypA K125MeaK in Strep-IP. (d) Volcano plot of semi-quantitation on CypA K125MeaK and CypA K125CrK IP samples. Red dots, significantly upregulated hits; Blue dots, significantly downregulated hits; Grey dots, non-differentially hits. (Fold Change $\geqslant$ 2, *p*-value < 0.05). Data quantified with Empirical Bayes test two-sided.

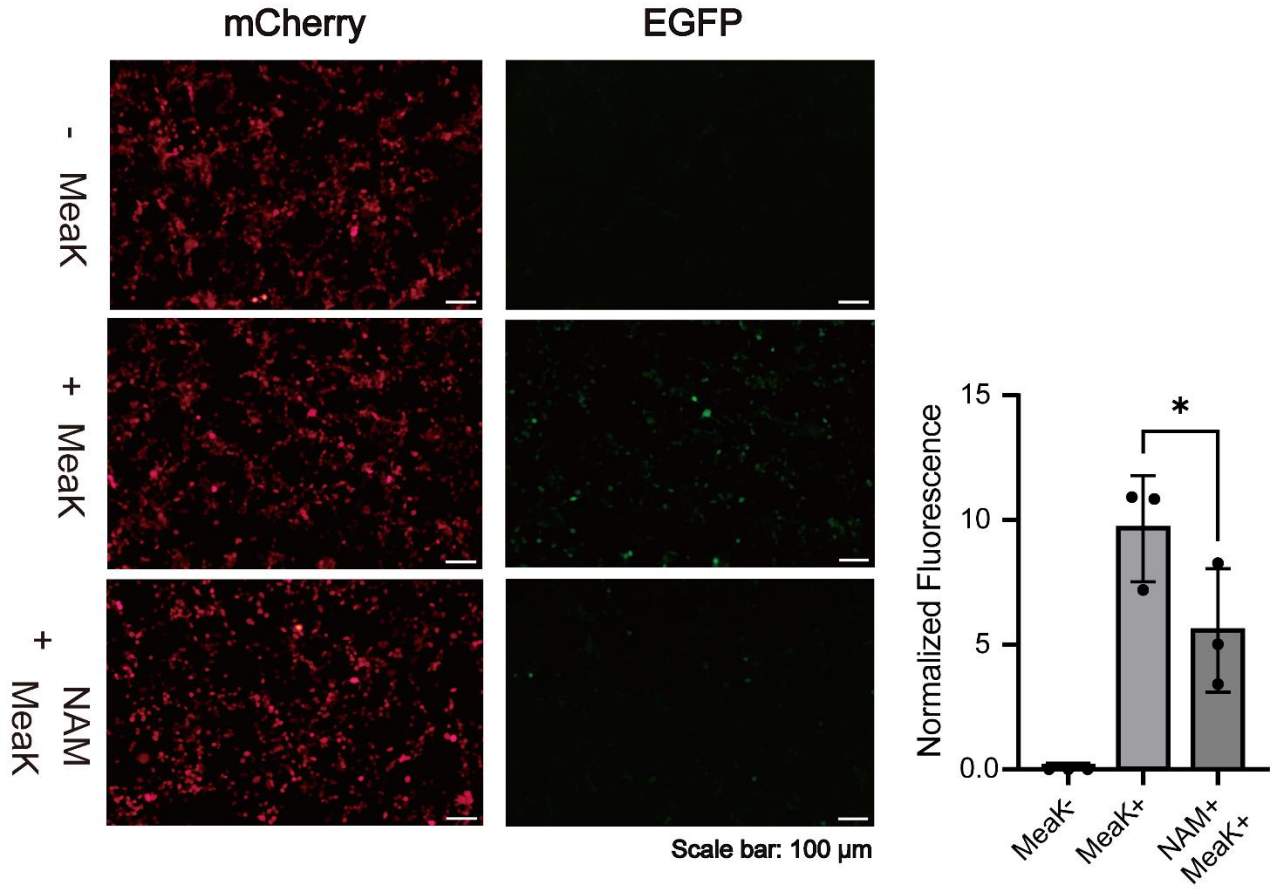


Supplementary Figure 11. (a) Fluorescence imaging of HeLa cells co-expressing $tRNA^{pyl}_{CUA}$/ chPylRS Y384F and EGFP Y151TAG in the presence or absence of 1 mM MeaK showing that MeaK can be successfully incorporated in HeLa cells. (b) Control gating strategy in FlowJo. Cells were first gated based on their size (FSC-A) and granularity (SSC-A). Further gating is done in an FSC-H and FSC-A dot plot to eliminate doublets. Then target cell population for further analysis

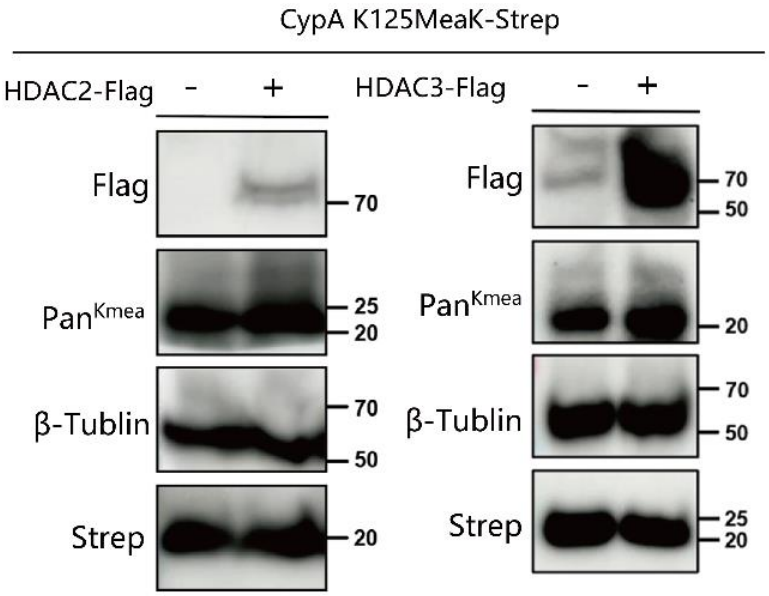
were gated by mCherry (ECD-A). (c) The mCherry (ECD-A) gate obtained cells to detect their fluorescent signal in the FTIC channel.



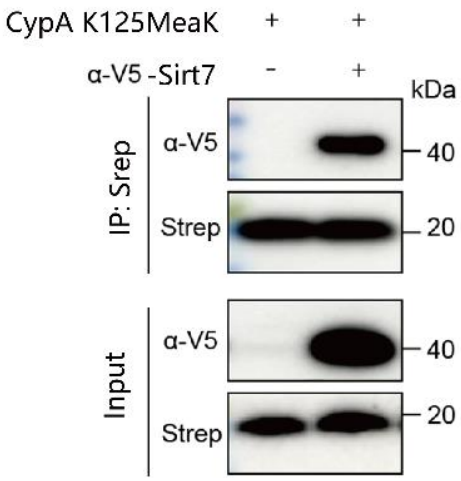
Supplementary Figure 12. C-terminal of CypA WT and CypA K125MeaK were fused with GFP. Binding affinity of CsA and GFP fused proteins were measure by MST binding affinity analysis. Data are presented as mean ± SD. Kd values are shown. CypA WT exhibited stronger binding to CsA than K125MeaK mutations. Technical replicates of the MST measurements were performed (n = 3).



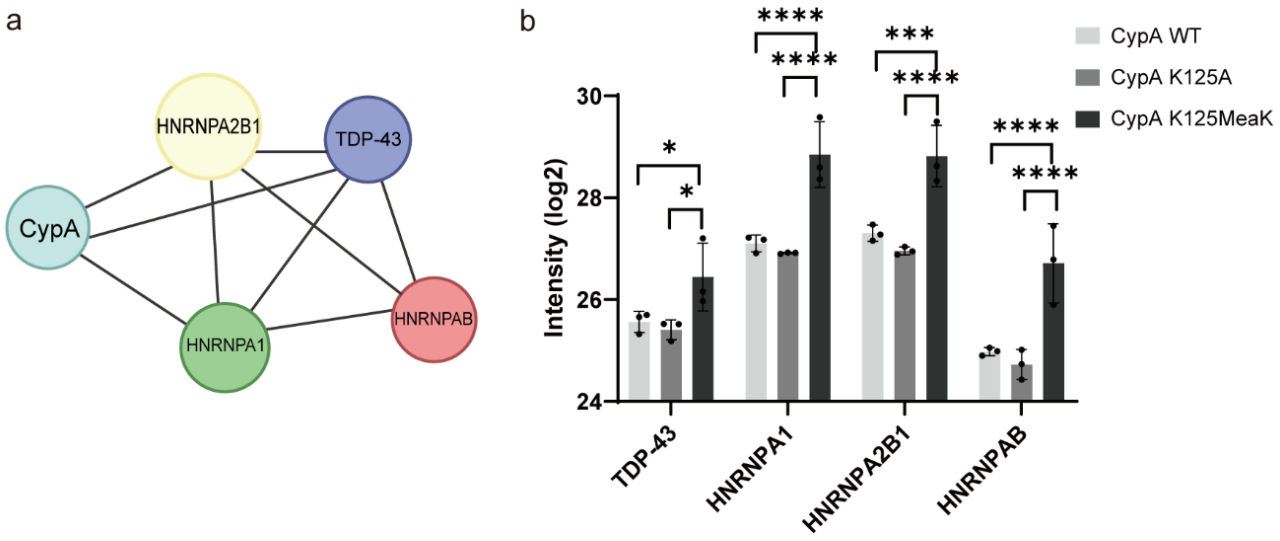
Supplementary Figure 13. Gentically encoded Kmea can be removed by endogenous Sirtuins in live cells which was detected by EGFP K85MeaK fluorogenic probe. Left: Fluorescence imaging of sirtuin de-methacrylation activity in HEK293T cells. The cells were cotransfected with two plasmids: one containing chPylRS Y384F/tRNA$^{Pyl}_{CUA}$ and another containing mCherry-EGFP-K85TAG with addition of different modulators; MeaK (final concentration 1 mM) and NAM (final concentration 10 mM) were added after transfection 6 h. Imaging was carried out after 36 h. Scale bars, 100 μm. Right: Normalizing signal of EGFP with mCherry. The error bars represent standard deviation from the mean (n = 3). *, P < 0.1 (two-tailed t-test), p = 0.0481.



Supplementary Figure 14. CypA K125TAG-Strep and chPylRS Y384F/tRNA$^{Pyl}_{CUA}$ were co-transfected with or without HDAC2-Flag (a)/HDAC3-Flag (b). Whole cell lysates were prepared 48h post-transfection and then subjected to Western blot analysis with the indicated antibodies. There were no changes of CypA Kmea, it showing that HDAC 2 and 3 may not remove Kmea modification on CypA site 125.



Supplementary Figure 15. HEK293T cells were co-transfected with CypA-K125MeaK-Strep and Sirt7-V5, separately. Test interactions between CypA K125MeaK and Sirtuins with Co-IP experiment.



Supplementary Figure 16. (a). Protein-protein interaction network analysis based on STRING database. (b). Intensities of CypA (K125MeaK, K125A and WT) interacting proteins were detected by mass spectrometry after streptavidin IP. Normalization by CypA (132-148) peptide. *, $P < 0.05$; ****, $P < 0.0001$(Two-Way ANOVA, n = 3).

Supplementary Tables

Supplementary Table 1. The table of PCR primers for DNA constructions and mutations

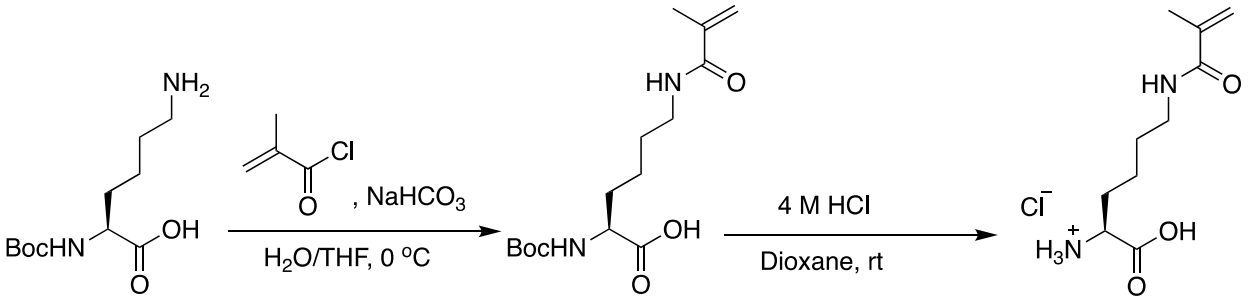
Primer name	Sequence	Clone
GFP_Y151TAG_F	CCACAACGTCTAGATCATGGCCG	pRK5M-GFP-Y151TAG-Strep
GFP_Y151TAG_R	CGGCCATGATCTAGACGTTGTGG	
flag pRK5M_SIRT2_F	TTAAGCTTGGTGGATCCATGGATTACAAGGATGACGATGACAAGGACTTCCTGCGGAAC	pRK5M-SIRT2-Flag
flag pRK5M_SIRT2_R	GGGTGGCTCCATGCGGCCGCCTGGGGTTTCTCCCTCTCTG	
pRK5M_H3_F	ATTAAGCTTGGTGGATCCATGGCCCGTACTAAGCAGACTG	pRK5M_H3-K18TAG_Strep
pRK5M_H3_R	CGGGTGGCTCCATGCGGCCGCAGCCCGCTCTCCACGG	
H3K18TAG_F	GGCCCCGAGGTAGCAGCTGGC	
H3K18TAG_R	GCCAGCTGCTACCTCGGGGCC	
pRK5M_PPIA_F	AATTAAGCTTGGTGGATCCATGGTCAACCCCACCGTGT	pRK5M_PPIA-K125WT/TAG/R_Strep
pRK5M_PPIA_R	GGGTGGCTCCATGCGGCCGCTTCGAGTTGTCCACAGTCAGCA	
PPIA_K125TAG_F	GTTGGATGGCTAGCATGTGGT	
PPIA_K125TAG_R	ACCACATGCTAGCCATCCAAC	
PPIA_K125R_F	TTGGATGGCAGGCATGTGGTG	
PPIA_K125R_R	CACCACATGCCTGCCATCCAA	
pRK5M_PPIA_K131R_F	TGTTTGGCAGAGTGAAAGAAG	

pRK5M_PPIA_K131R_R	CTTCTTTCACTCTGCCAAACA	pRK5M_PPIA-K131R_Strep
pRK5M_HDAC1_flag_F	AATTAAGCTTGGTGGATCCATGGCGCAGACGCAGG	pRK5M-HDAC1-Flag
pRK5M_HDAC1_flag_R	GTCTTTGTAGTCTGCGGCCGCGGCCAACTTGACCTCCTCC	
pRK5M_HDAC2_flag_F	GAATTAAGCTTGGTGGATCCATGGCGTACAGTCAAGGAGG	pRK5M-HDAC2-Flag
pRK5M_HDAC2_flag_R	GTCTTTGTAGTCTGCGGCCGCGGGGTTGCTGAGCTGTTC	
pRK5M_HDAC3_flag_F	GAATTAAGCTTGGTGGATCCATGGCCAAGACCGTGGC	pRK5M-HDAC3-Flag
pRK5M_HDAC3_flag_R	GTCTTTGTAGTCTGCGGCCGCAATCTCCACATCGCTTTCCTTG	
pRK5M_PPIA_gfp_F	TCTATCGATTGAATTAAGCTATGGTCAACCCCACCGTG	pRK5M-PPIA-WT/K125TAG-EGFP-Strep
pRK5M_PPIA_gfp_R	CCCTTGCTCACCATGGATCCTTCGAGTTGTCCACAGTCAGC	
GFP_Strep-F	GCTGTACAAGGCAGCGGCCGCA	
GFP_Strep-R	TGCGGCCGCTGCCTTGTACAGC	
EGFP_K85TAG_F	CGACTTCTTCTAGTCCGCCAT	pRK5M-mCherry-P2A-EGFP-K85TAG
EGFP_K85TAG_R	ATGGCGGACTAGAAGAAGTCG	
MBPZ_E24TAG_F	TAACCTGAATTAGGAGCAGCG	pBAD-MBPZ-6×His
MBPZ_E24TAG_R	CGCTGCTCCTAATTCAGGTTA	
pBAD-HDAC1-STREP-F	AGAAGGAGATATACATATGGCGCAGACGC	pBAD-HDAC1-Strep

pBAD-HDAC1-STREP-R	TGCGGGTGGCTCCAAAGCTTGGCCAACTTGACCTCCT	
PPIA_P2A_R	ACTTCCTCTGCCCTCTTCGAGTTGTCCACAGTCAG	pRK5M-PPIA-WT/K125TAG-mCherry
PPIA_P2A_F	TGTGGACAACTCGAAGAGGGCAGAGGAAGTCTGC	
pRK5M_mcherry_R	CGGGTGGCTCCATGCGGCCGCCTTGTACAGCTCGTCCATGC	
The plasmids and primers not mentioned are lab stored		

Supplementary Note

Supplementary Note 1. Synthesis of MeaK.



N^2-(tert-butoxycarbonyl)-N^6-methacryloyl-L-lysine. A 100 mL round-bottomed flask with a magnetic stir bar was charged with Boc-Lys-OH (1 g, 1 equiv), sodium bicarbonate (0.853 g, 2.5 equiv), and H_2O/THF (3:1, 20 mL). The mixture was cooled on ice. A solution of methacryloyl chloride (436 μL, 1.1 equiv) in 1 mL THF was added dropwise to the reaction mixture. The reaction was stirred on ice for 4 h. The progress of the reaction was monitored with TLC. After completion, 20 mL 0.5 M HCl was added to adjust the pH to ~3. The aqueous layer was extracted with 30 mL EtOAc three times. The combined organic layers were washed once with 50 mL brine, dried over Na_2SO_4, and filtered. The solution was concentrated by rotary evaporation to afford the crude product as a white solid, which was purified by flash column chromatography using DCM and methanol. Fractions containing the product were combined and evaporated to dryness to afford the product as a white solid (760 mg, 60%). ^{1}H NMR ($CDCl_3$, 500 MHz) δ 5.70 (s, 1H), 5.33 (s, 1H), 4.28 (m 1H), 3.31 (m, 2H), 1.95 (s, 3H), 1.72 (m, 2H), 1.56 (m, 2H), 1.43 (s, 9H), 1.42 (m, 2H) ppm. ^{13}C NMR ($CDCl_3$, 125 MHz) δ 175.3, 169.1, 155.9, 139.7, 120.1, 80.1, 53.1, 39.4, 31.9, 29.0, 28.3, 22.4, 18.7 ppm. MS (ESI): Calcd. for $C_{15}H_{27}N_2O_5^+$ $[M+H]^+$ m/z 315.19, found 315.30.

ncAA MeaK. 4 M HCl/dioxane (5 mL) was added to a 50 mL falcon tube containing 760mg of N^2-(tert-butoxycarbonyl)-N^6-methacryloyl-L-lysine. The reaction mixture was kept at ambient temperature for 15 min. The falcon tube was spun at 6k rpm for 5 min to collect the pellet, which was washed with 20 mL diethyl ether. After drying, 10 mL water was added to dissolve the pellet. The suspension was spun at 6k rpm for 5 min, and the supernatant was collect and freeze dryed to obtain white powder (410 mg, 79%). ^{1}H NMR (D_2O, 500 MHz) δ 5.64 (s, 1H), 5.41 (s, 1H), 4.07 (t, J = 6.3

Hz, 1H), 3.25 (t, *J* = 6.9 Hz, 2H), 1.96 (m, 2H), 1.89 (s, 3H), 1.59 (m, 2H), 1.45 (m, 2H) ppm. ^{13}C NMR (D_2O, 125 MHz) δ 172.6, 172.5, 139.9, 121.5, 53.3, 39.5, 30.0, 28.5, 22.2, 18.3 ppm. MS (ESI): Calcd. for $C_{10}H_{19}N_2O_3^+$ $[M+H]^+$ m/z 215.14, found 215.10.

Supplementary Note 2. Sequence of the recombinant protein

Sequence of EGFP for incorporation MeaK in mammalian cells (U=MeaK residue)

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
VTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
NRIELKGIDFKEDGNILGHKLEYNYNSHNVUIMADKQKNGIKVNFKIRHNIEDGSVQLADH
YQQNTPIGDGPVLLPDNHYLSTQSKLSKDPNEKRDHMVLLEFVTAAGITLGMDELYKAAA
WSHPQFEKGGGSGGGSGGSAWSHPQFEK

Sequence of EGFP for incorporation MeaK in *E. coli* (U=MeaK residue)

MGKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
TTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLVN
RIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ
QNTPIGUGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYKGPHHH
HHH

Sequence of MBP-Z for incorporation MeaK in *E. coli* (U=MeaK residue)

MMKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPD
IIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKD
LLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDV
GVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKV
NYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGA
VALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEAL
KDAQTNSSSNNNNNNNNNNLGSSGLVPRGSHGTSVDNKFNKEQQNAFYEILHLPNLNEUQ
RNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKHHHHHH

Sequence of recombinant CypA with Strep tag

MVNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFGYKGSCFHRIIPGFMC
QGGDFTRHNGTGGKSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLD
GKHVVFGKVKEGMNIVEAMERFGSRNGKTSKKITIADCGQLEAAAWSHPQFEKGGGSGGG
SGGSAWSHPQFEK

Sequence of recombinant H3 with Strep tag for incorporation MeaK in mammalian cells (U=MeaK residue)

MARTKQTARKSTGGKAPUAQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTE
LLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMP
KDIQLARRIRGERAAAAWSHPQFEKGGGSGGGSGGSAWSHPQFEK

Sequence of recombinant TXN1 with 6 × His tag

MVKQIESKTAFQEALDAAGDKLVVVDFSATWCGPCKMIKPFFHSLSEKYSNVIFLEVDVDD
CQDVASECEVKCMPTFQFFKKGQKVGEFSGANKEKLEATINELVAAAHHHHHH

Sequence of recombinant HDAC1 with Flag tag

MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHK
ANAEEMTKYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVA
SAVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHG
DGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIF
KPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGG
GYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
QRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEE
GEGGRKNSSNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLAAAAD
YKDDDDK

Sequence of recombinant HDAC2 with Flag tag

MAYSQGGGKKKVCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPH
KATAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSV
AGAVKLNRQQTDMAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIH
HGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNFPMRDGIDDESY
GQIFKPIISKVMEMYQPSAVVLQCGADSLSGDRLGCFNLTVKGHAKCVEVVKTFNLPLLML
GGGGYTIRNVARCWTYETAVALDCEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTPEYM
EKIKQRLFENLRMLPHAPGVQMQAIPEDAVHEDSGDEDGEDPDKRISIRASDKRIACDEEFS
DSEDEGEGGRRNVADHKKGAKKARIEEDKKETEDKKTDVKEEDKSKDNSGEKTDTKGTK
SEQLSNPAAADYKDDDDK

Sequence of recombinant HDAC3 with Flag tag

MAKTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDM
CRFHSEDYIDFLQRVSPTNMQGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLN
NKICDIAINWAGGLHHAKKFEASGFCYVNDIVIGILELLKYHPRVLYIDIDIHHGDGVQEAFY
LTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVINQ
VVDFYQPTCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLGGGGYTVRNV
ARCWTYETSLLVEEAISEELPYSEYFEYFAPDFTLHPDVSTRIENQNSRQYLDQIRQTIFENL
KMLNHAPSVQIHDVPADLLTYDRTDEADAEERGPEENYSRPEAPNEFYDGDHDNDKESDV
EI AAADYKDDDDK