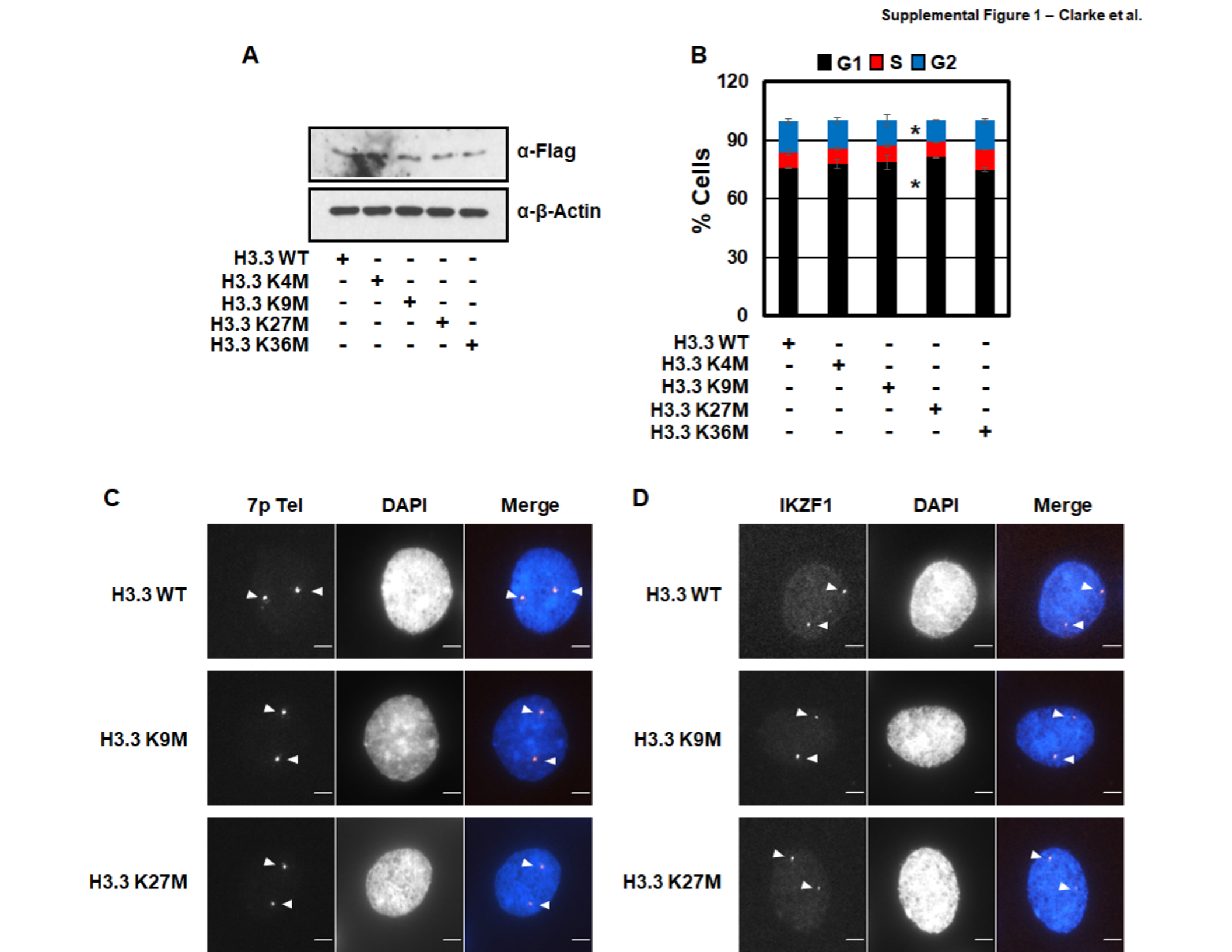

A
α-Flag
α-β-Actin
H3.3 WT + - - - -
H3.3 K4M - + - - -
H3.3 K9M - - + - -
H3.3 K27M - - - + -
H3.3 K36M - - - - +
B
G1 S G2
% Cells
120
90
60
30
0
*
*
H3.3 WT + - - - -
H3.3 K4M - + - - -
H3.3 K9M - - + - -
H3.3 K27M - - - + -
H3.3 K36M - - - - +
C
7p Tel
DAPI
Merge
H3.3 WT
H3.3 K9M
H3.3 K27M
D
IKZF1
DAPI
Merge
H3.3 WT
H3.3 K9M
H3.3 K27M

Supplementary Figure 1. H3K9/27 methylation controls *EGFR* amplification.

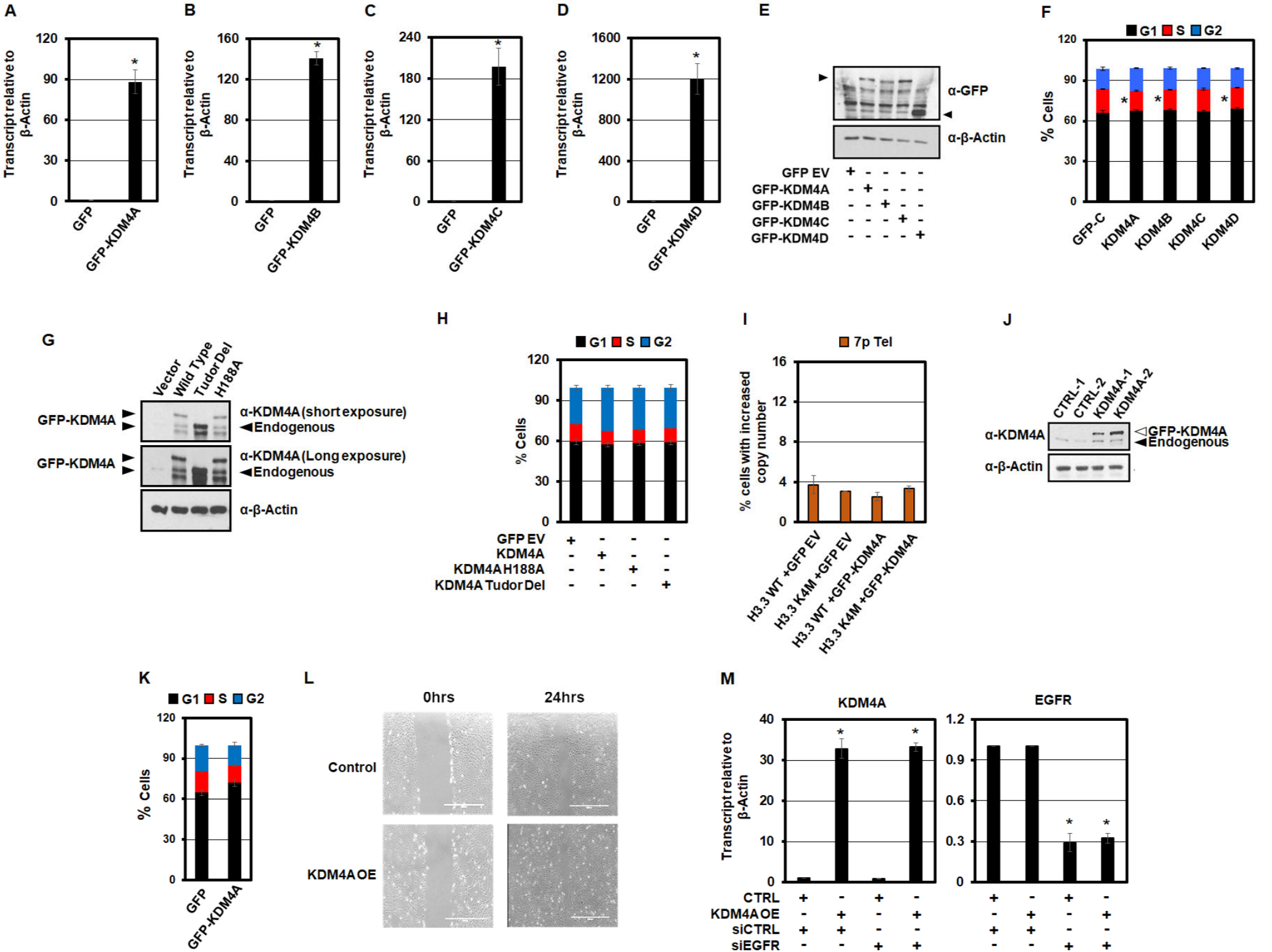
A) Immunoblots for RPE whole cell extracts (WCEs) verifying expression of flag-tagged histone H3.3 constructs.

B) Cell cycle analysis of RPE cells expressing histone H3.3 variants 48 hours after virus transduction.

C) Representative DNA FISH images of RPE nuclei from cells transduced with H3.3 Wild Type (H3.3 WT), K9M or K27M variants. 7p Tel (red) and DAPI (blue) are shown in the merge.

D) Representative DNA FISH images of RPE nuclei from cells transduced with H3.3 Wild Type (H3.3 WT), K9M or K27M variants. *IKZF1* (red) and DAPI (blue) are shown in the merge.

Error bars represents S.E.M. The * represents p=≤0.05 by two-tailed Student's t-test.



Supplemental Figure 2 – Clarke et al.

Supplementary Figure 2. KDM4A overexpression promotes *EGFR* copy gains.

A-D) qRT-PCR validating expression of KDM4 family members normalized to β-Actin.

E) Immunoblots for RPE WCE verifying GFP-tagged KDM4 family members expression 24 hours post DNA transfection. β-Actin immunoblot was performed as a loading control.

F) Cell cycle analysis of RPE cells expressing different GFP-tagged KDM4 family members from panel E.

G) α-KDM4A immunoblot analysis validating protein expression of GFP-tagged KDM4A wild type or mutant constructs after 24 hours of DNA transfection. β-Actin immunoblot was performed as a loading control.

H) Cell cycle analysis of RPE cells expressing GFP-tagged KDM4A wild type or KDM4A mutant constructs from panel G.

I) Neither transient over expression of GFP-tagged KDM4A nor does H3.3 K-M transduction promote 7p Tel copy number gains in RPE cells.

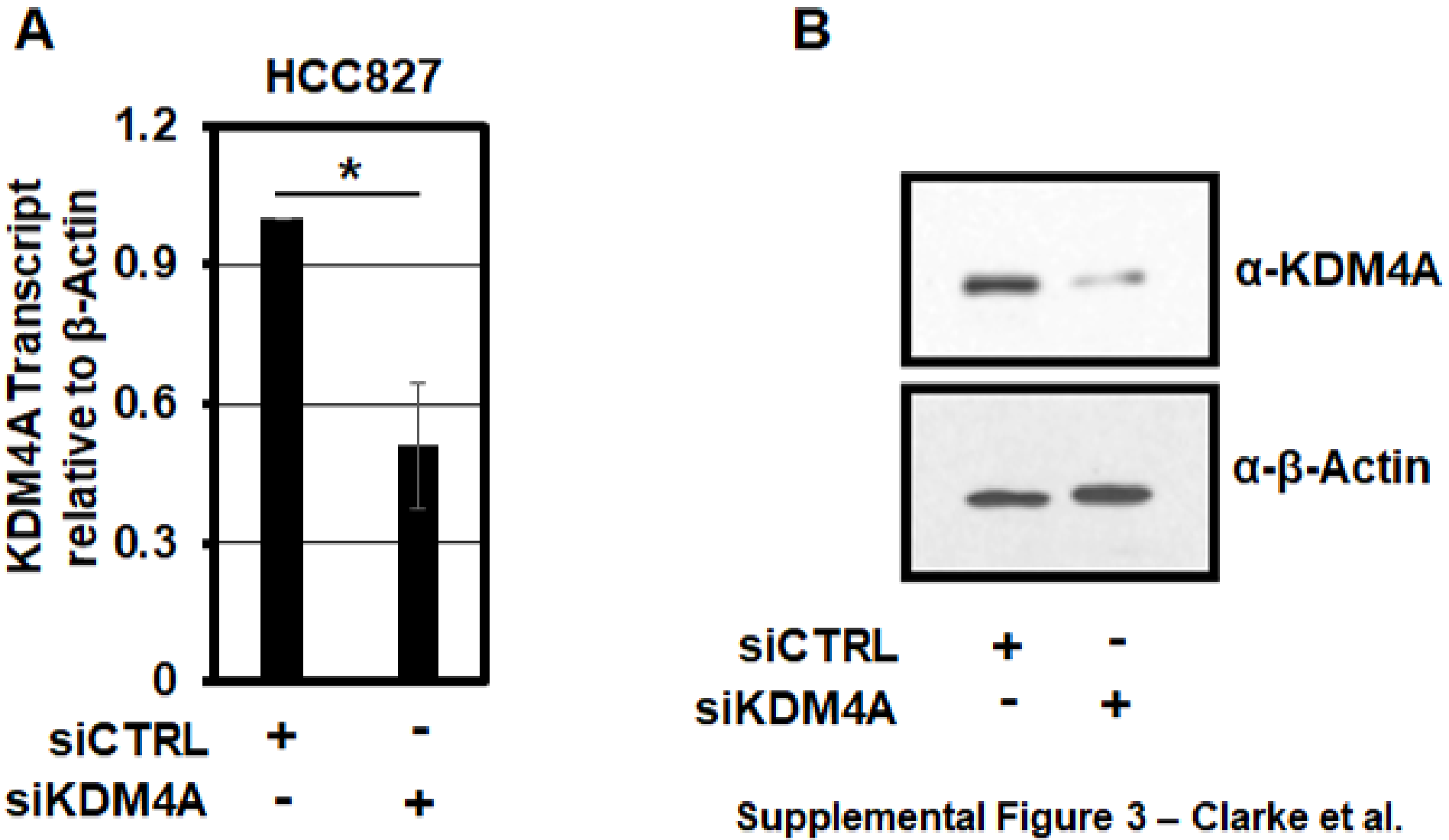
J) α-KDM4A immunoblot demonstrating stable overexpression of KDM4A in RPE cells. β-Actin immunoblot was performed as a loading control.

K) Cell cycle analysis of control and stable GFP-KDM4A-overexpressing RPE cells.

L) Representative bright field microscopy images of scratch assays performed in control or KDM4A over-expressing RPE cells. Cells were treated with 50ng/ml EGF immediately after the scratch. 0hr and 24hr time points are shown. Images taken at 4x magnification on the EVOS microscope. Scale bar represents 500um.

M) qRT-PCR analysis of control or stable KDM4A expressing RPE cells treated with non-targeted siRNA (siCTRL) or *EGFR* siRNA (siEGFR). Cells were harvested 48 hours post siRNA transfection. Knockdown represents the relative knockdown of cells upon EGF treatment (**Figure 2K**).

Error bars represents S.E.M. The * represents p=≤0.05 by two-tailed Student's t-test.



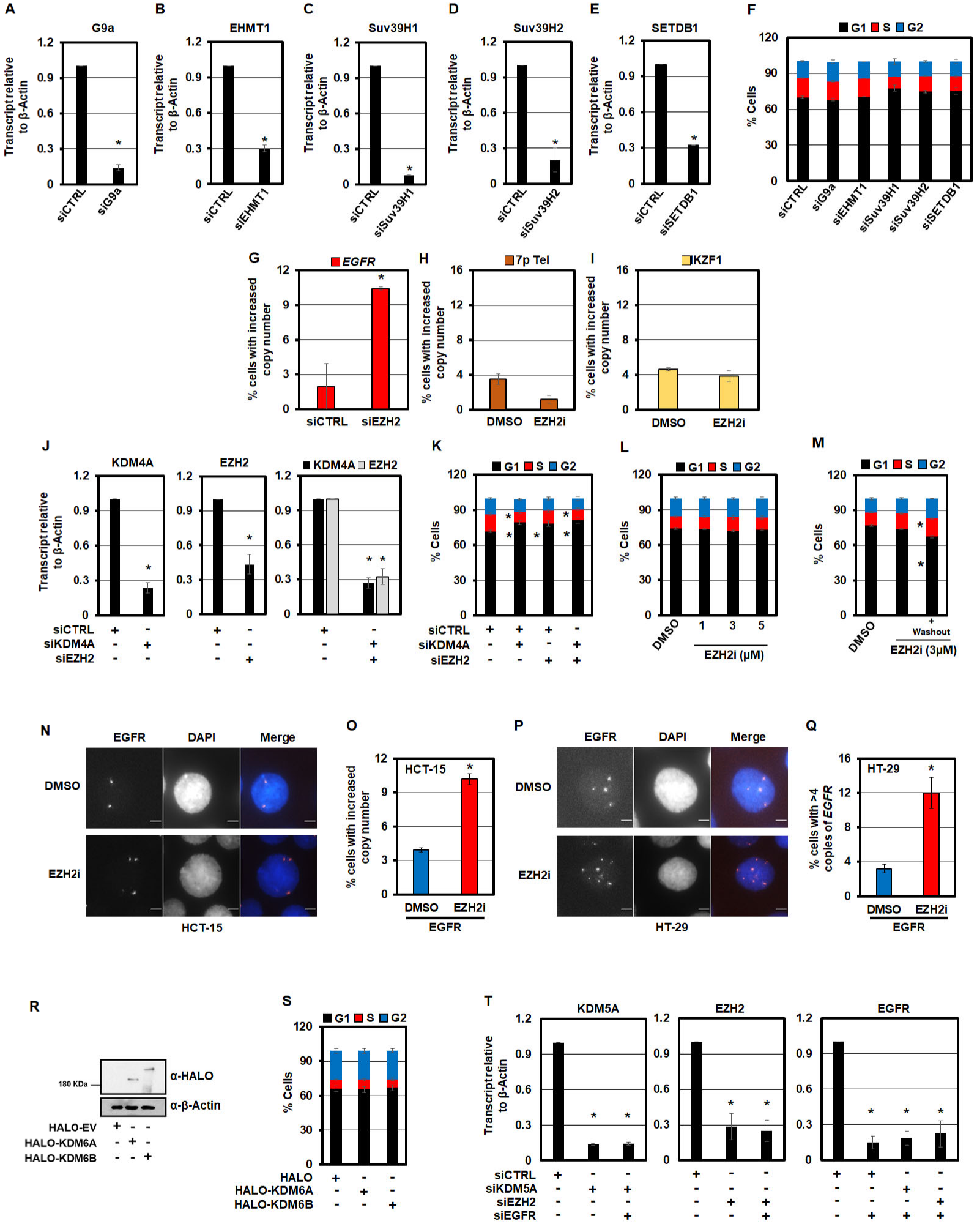
Supplemental Figure 3 – Clarke et al.

Supplementary Figure 3. KDM4A controls *EGFR* amplification in HCC827 cells.

A) qRT-PCR analysis of HCC827 lung cancer cells treated with siControl or siKDM4A. Cells were harvested 72 hours post siRNA transfection. KDM4A transcript levels are normalized to β-Actin.

B) Representative α-KDM4A immunoblot of HCC827 lung cancer cells treated with siControl or siKDM4A. Cells were harvested 72 hours post siRNA transfection. β-Actin immunoblot was performed as a loading control.

Error bars represents S.E.M. The * represents p=≤0.05 by two-tailed Student's t-test.


A
G9a
Transcript relative to β-Actin
siCTRL
siG9a
B
EHMT1
siEHMT1
C
Suv39H1
siSuv39H1
D
Suv39H2
siSuv39H2
E
SETDB1
siSETDB1
F
G1 S G2
% Cells
siCTRL
siG9a
siEHMT1
siSuv39H1
siSuv39H2
siSETDB1
G
EGFR
% cells with increased copy number
siCTRL
siEZH2
H
7p Tel
DMSO
EZH2i
I
IKZF1
J
KDM4A
EZH2
KDM4A EZH2
siCTRL
siKDM4A
siEZH2
K
L
EZH2i (μM)
M
Washout
EZH2i (3μM)
N
EGFR
DAPI
Merge
DMSO
EZH2i
HCT-15
O
HCT-15
EGFR
P
HT-29
Q
HT-29
% cells with >4 copies of EGFR
R
180 KDa
α-HALO
α-β-Actin
HALO-EV
HALO-KDM6A
HALO-KDM6B
S
HALO
T
KDM5A
siKDM5A
siEZH2
siEGFR

Supplementary Figure 4. H3K9/27 KMTs regulate *EGFR* amplification.

A-E) qRT-PCR analysis of H3K9 KMT transcripts in RPE cells treated with siControl or siRNAs targeting the indicated H3K9 KMT. Cells were harvested 72 hours post siRNA transfection. Transcript levels are normalized to β-Actin.

F) Cell cycle analysis of RPE cells treated with siRNAs targeting the H3K9 KMT family. Cells were harvested 72 hours post transfection.

G) siEZH2 treated RPE cells have significantly increased *EGFR* copy gains.

H) siEZH2 treated RPE cells do not have significantly altered 7ptel DNA copy levels.

I) siEZH2 treated RPE cells do not have significantly altered *IKZF1* DNA copy levels.

J) qRT-PCR analysis of RPE cells treated with siRNAs targeting KDM4A and EZH2 either alone or in combination. Cells were harvested 72 hours post siRNA transfection.

K) Cell cycle analysis of RPE cells treated with siRNAs targeting KDM4A and EZH2 either alone or in combination. Cells were harvested 72 hours post siRNA transfection.

L) Cell cycle analysis of RPE cells treated with 1μM, 3μM or 5μM of EZH2i for 72 hours.

M) Cell cycle analysis of RPE cells treated with continuous 3μM EZH2i or after washout and replacement with drug-free DMEM.

N) Representative DNA FISH images of HCT-15 nuclei from cells treated with EZH2i. *EGFR* (red) and DAPI (blue) are shown in the merge.

O) EZH2i promotes significant *EGFR* DNA copy gains in HCT-15 cells.

P) Representative DNA FISH images of HT-29 nuclei from cells treated with EZH2i. *EGFR* (red) and DAPI (blue) are shown in the merge.

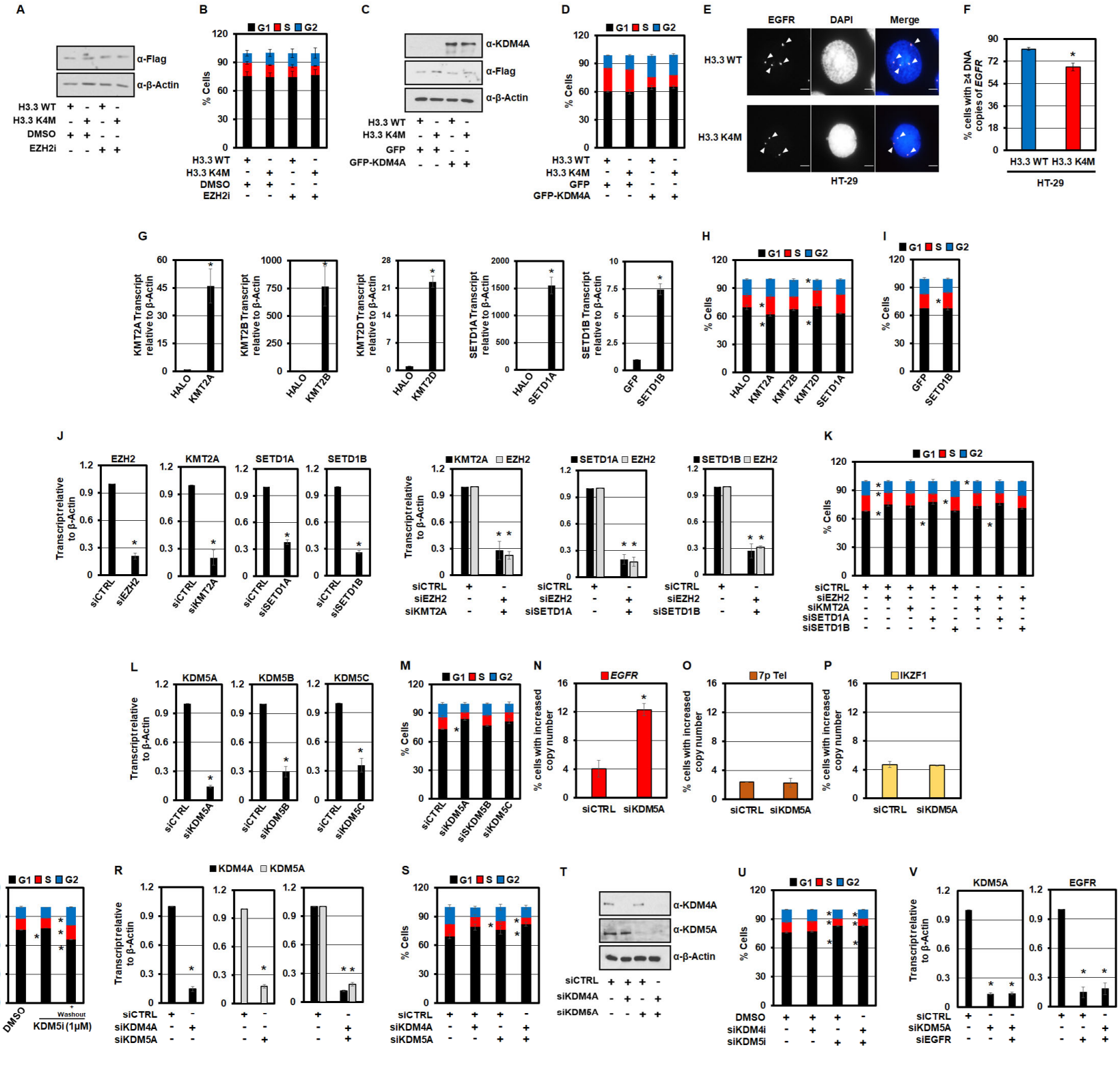
Q) EZH2i promotes significant *EGFR* DNA copy gains in HT-29 cells.

R) Representative α-HALO immunoblot analysis verifying expression of HALO-tagged KDM6A or KDM6B constructs in RPE cells. Cells were harvested 24 hours post DNA transfection.

S) Cell cycle analysis of RPE cells expressing HALO-tagged KDM6A or KDM6B constructs. Cells were harvested 24 hours post DNA transfection.

T) Quantitative real time PCR analysis of RPE cells treated with siKDM5A, siEZH2 or siEGFR. Cells were treated with individual siRNAs or siRNAs targeting KDM5A or EZH2 with EGFR. Cells were harvested 48 hours post siRNA transfection and transcript levels reflect the relative siRNA-mediated knockdowns upon EGF treatment (Figure 4K and 5T).

Error bars represents S.E.M. The * represents $p=\leq 0.05$ by two-tailed Student's t-test.



Supplemental Figure 5 – Clarke et al.

Supplementary Figure 5. H3K4/K27 methylation control *EGFR* amplification.

A) Immunoblot analysis of whole cell extracts from RPE cells treated with EZH2i that verify expression of flag-tagged histone H3.3 wild type of K4M constructs. β-Actin was used as a loading control.

B) Cell cycle analysis of RPE cells in panel A.

C) Immunoblot analysis of whole cell extracts from RPE cells validating expression of flag-tagged histone H3.3 wild type or K4M constructs and GFP-tagged KDM4A. β-Actin was used as a loading control.

D) Cell cycle analysis of RPE cells in panel C.

E) Representative DNA FISH images of HT-29 nuclei from cells transduced with H3.3 WT or H3.3 K4M. *EGFR* (red) and DAPI (blue) are shown in the merge.

F) H3.3 K4M transduction significantly reduces *EGFR* DNA copy number in HT-29 when compared to H3.3 WT transduced HT-29 cells.

G) qRT-PCR analysis of H3K4 methyltransferase family transcripts in RPE cells transiently transfected with HALO-tagged KMT2A, KMT2B, KMT2D, SETD1A or GFP-tagged SETD1B. Cells were harvested 24 hours post DNA transfection.

H,I) Cell cycle analysis of RPE cells in panel G.

J) qRT-PCR analysis of RPE cells treated with siRNAs to EZH2, KMT2A, SETD1A and SETD1B, alone or in combination. Cells were harvested 72 hours post siRNA transfection.

K) Cell cycle analysis of RPE cells in panel J.

L) qRT-PCR analysis of RPE cells treated with siRNAs targeting the KDM5 family. Cells were harvested 72 hours post siRNA transfection.

M) Cell cycle analysis of RPE cells in panel L.

N) siKDM5A treated RPE cells have a significant increase in *EGFR* copy number.

O) siKDM5A treated RPE cells do not have a significant change in 7p tel copy number.

P) siKDM5A treated RPE cells do not have a significant change in *IKZF1* copy number.

Q) Cell cycle analysis of RPE cells treated with KDM5i (1μM) and following drug removal and replenishment with complete DMEM.

R) qRT-PCR analysis of RPE cells treated with siRNAs targeted to KDM4A or KDM5A, alone or in combination. Cells were harvested 72 hours post siRNA transfection.

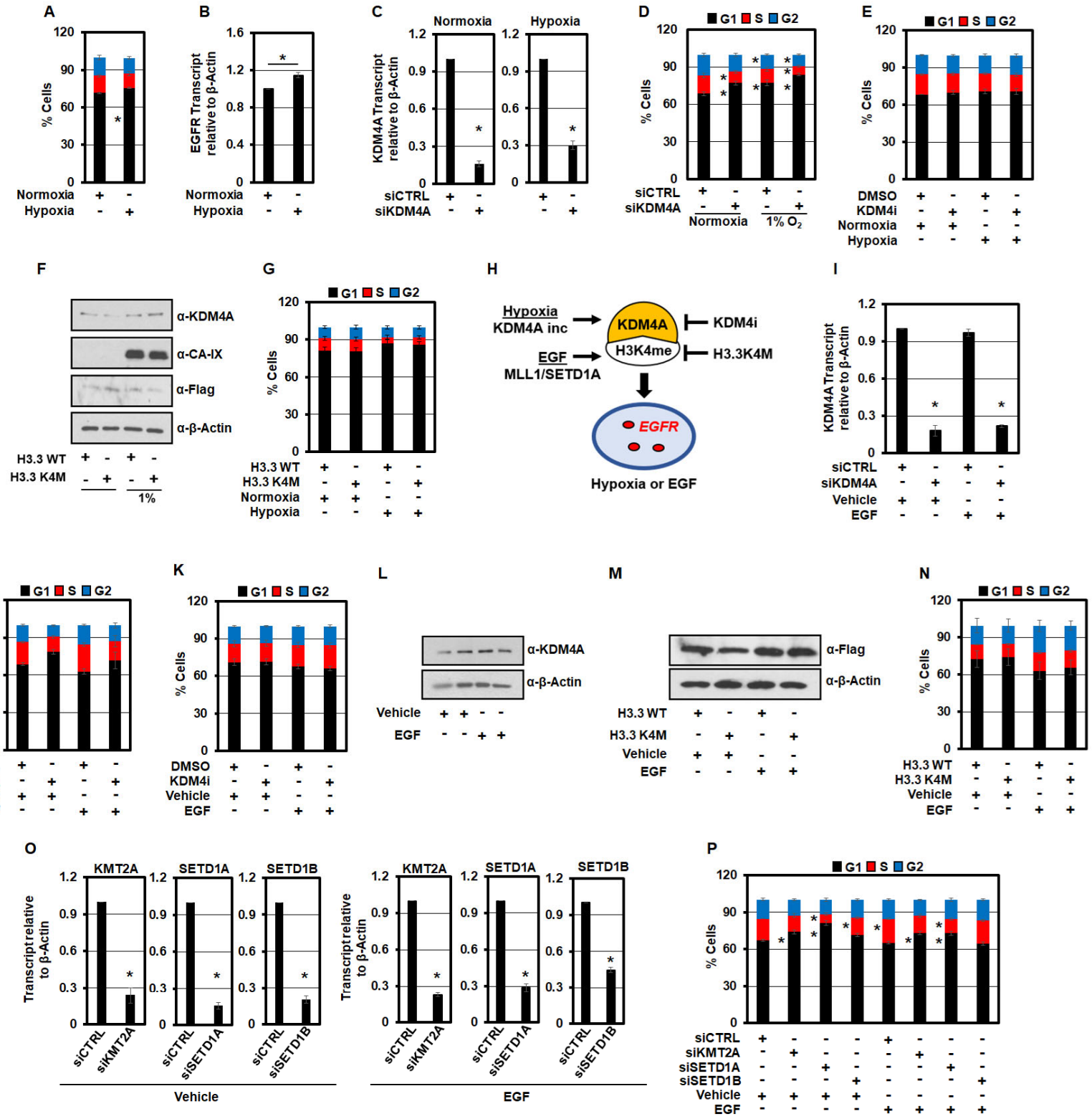
S) Cell cycle analysis of RPE cells in panel R.

T) α-KDM4A and α-KDM5A immunoblot analysis of siRNA treated RPE cells from panel R. β-Actin was used as a loading control.

U) Cell cycle analysis of RPE cells treated with KDM4i (1nM) and KDM5i (1μM) alone or in combination. Cells were pre-treated with KDM4i for 24 hours followed by a second treatment in combination with KDM5i (24 hours later). Cells were harvested 48 hours after combination treatment.

V) qRT-PCR analysis of RPE cells treated with siRNAs targeted to KDM5A or EGFR, alone or in combination prior to EGF treatment (Figure 5K). Cells were harvested 48 hours post siRNA transfection; therefore, the data reflects the relative gene knockdown upon EGF treatment.

Error bars represents S.E.M. The * represents $p=\leq 0.05$ by two-tailed Student's t-test.



S Figure 6 –Clarke et al

Supplementary Figure 6. Hypoxia and EGF induce *EGFR* amplification.

A) Cell cycle analysis of RPE cells cultured in normoxia or hypoxia (1% O_2) for 24 hours.

B) qRT-PCR analysis for *EGFR* transcript levels in RPE cells cultured in normoxia or hypoxia (1% O_2) for 24 hours.

C) qRT-PCR analysis of RPE cells treated with siRNA targeted to KDM4A. 48 hours post siRNA transfection, cells were transferred to hypoxic culture conditions (1% O_2) for 24 hours.

D) Cell cycle analysis of RPE cells in panel C.

E) Cell cycle analysis of RPE cells pre-treated with KDM4i (1nM) for 24 hours, before a second treatment (1nM) followed by immediate transfer to hypoxic culture conditions (1% O_2) for 24 hours.

F) Immunoblot analysis of α-KDM4A, α-Flag, α-CA-IX and α-β-Actin, validating expression of histone H3.3 wild type or K4M constructs from whole cell extract in RPE cells. KDM4A and CA-IX immunoblot analysis is used to validate hypoxic culture conditions and β-Actin is used as a loading control.

G) Cell cycle analysis of RPE cells in panel F.

H) A model depicting the impact hypoxia/KDM4A and EGF/KMT2 (MLL1/SETD1A,B) have on promoting *EGFR* copy gains through KDM4A and H3K4 methylation. The suppression of hypoxia and EGF promoted *EGFR* copy gains are noted with KDM4i and H3.3 K4M transduction. The model is based on the genetic experiments in Figure 6.

I) qRT-PCR analysis of RPE cells treated with siRNAs targeted to KDM4A. 48 hours post siRNA transfection, cells were treated with 50ng/ml EGF for 24 hours.

J) Cell cycle analysis of RPE cells in panel I.

K) Cell cycle analysis of RPE cells pre-treated with KDM4i (1nM) for 24 hours, followed by a second 1nM treatment and EGF treatment (50ng/ml) for 24 hours.

L) Immunoblot analysis of KDM4A protein levels in RPE cells from two independent experiments following EGF treatment (50ng/ml) for 24 hours.

M) Immunoblot analysis verifying expression of histone H3.3 wild type and K4M constructs from whole cell extracts of RPE cells. 24 hours after viral transduction, cells were treated with 50ng/ml EGF. β-Actin is used as a loading control.

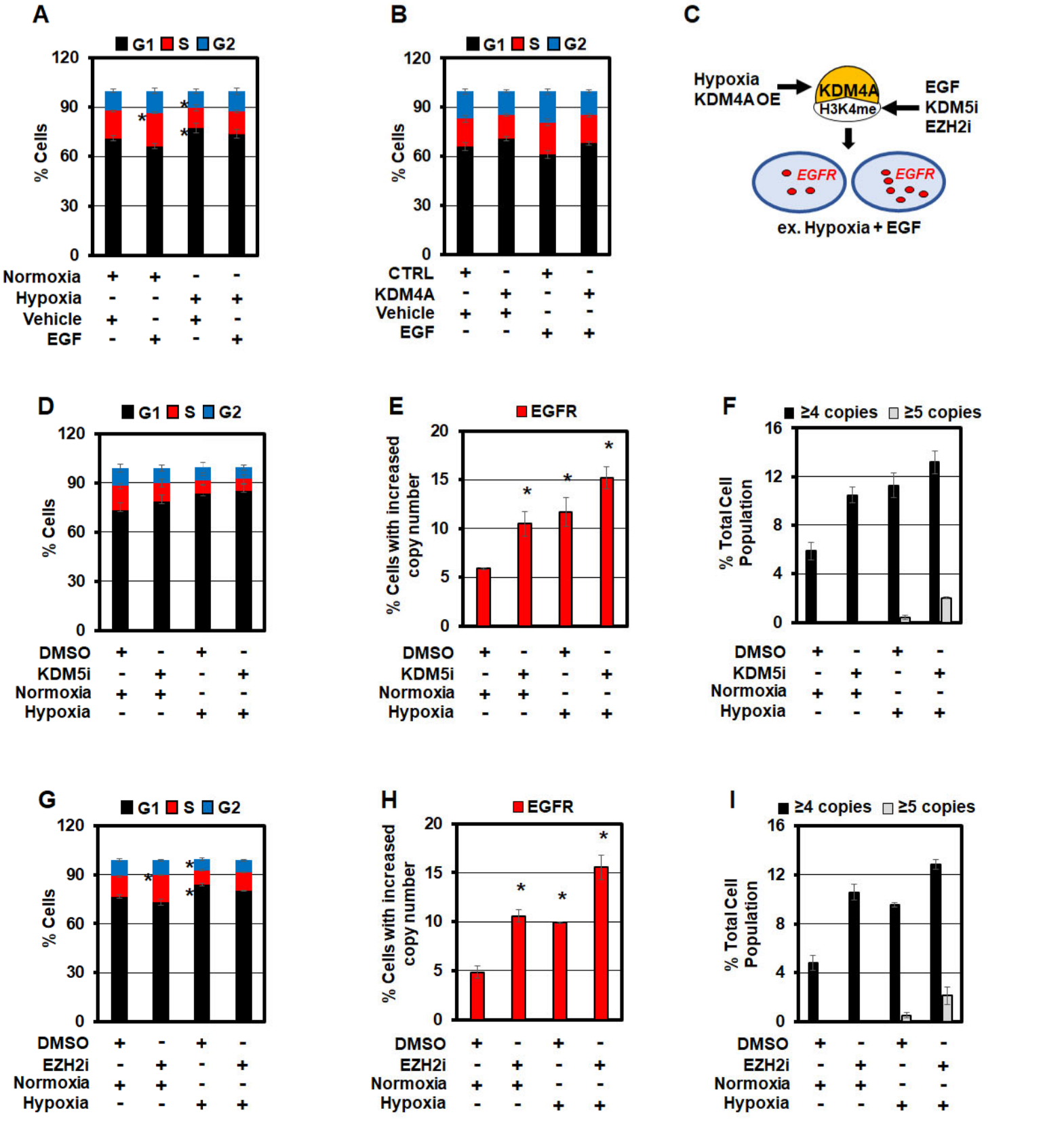
N) Cell cycle analysis of RPE cells in panel M.

O) qRT-PCR analysis of RPE cells treated with siRNAs targeted to KMT2A, SETD1A or SETD1B. 48 hours post siRNA transfection cells were treated with 50ng/ml EGF or DMSO as a vehicle control, for 24 hours.

P) Cell cycle analysis of RPE cells in panel O.

Error bars represents S.E.M. The * represents $p=\leq 0.05$ by two-tailed Student's t-test.

Supplemental Figure 7 – Clarke et al.



Supplementary Figure 7. Combining epigenetic dysregulation, hypoxia and EGF increases *EGFR* amplification.

A) Cell cycle analysis of RPE cells treated with 50ng/ml EGF for 24 hours, followed by transfer to hypoxic culture conditions (1% O_2) for an additional 24 hours.

B) Cell cycle analysis of KDM4A stable overexpression RPE cells treated with 50ng/ml EGF for 48 hours.

C) A model depicting the increased DNA copy number per nucleus observed when combining either hypoxia/KDM4A with EGF or other factors impacting H3K4/27 methylation with hypoxia. The model is based on the genetic experiments in Figure 7 and Figure S7D-I.

D) Cell cycle analysis of RPE cells pre-treated with a KDM5i (1μM) for 24 hours followed by transfer to hypoxic culture conditions (1% O_2) for an additional 24 hours.

E) DNA FISH analysis of cells in panel D.

F) Graph illustrating the percentage of the total cell population with >4 and >5 *EGFR* DNA copies from panel E.

G) Cell cycle analysis of RPE cells pre-treated with a EZH2i (3μM) for 24 hours followed by transfer to hypoxic culture conditions (1% O_2) for an additional 24 hours.

H) DNA FISH analysis for cells in panel G.

I) Graph illustrating the percentage of the total cell population with >4 and >5 *EGFR* DNA copies from panel H.

Error bars represents S.E.M. The * represents p=≤0.05 by two-tailed Student's t-test.

Histone Lysine Methylation Dynamics Control *EGFR* DNA Copy Number Amplification
Clarke *et al.*
Supplementary Table 1. siRNA Oligos

siRNA Name	siRNA Sequence	Unique Identifier
EGFR	GAAUAGGUAUUGGUGAAUUtt	s563
EGFR	CCAUAAAUGCUACGAAUAUtt	s564
KDM4A	CUAUGGAAGAGUUCCGAAAtt	s18635
KDM4A	GCGACAAUCUUUAUCCUGAtt	s18637
G9A	GCUCUAACUGAACAACUAAtt	s21469
G9A	CGCUGAUUUUCGAGUGUAAtt	s21470
EHMT1	CAGCUGCAGUAUCUCGGAAtt	s36390
EHMT1	CUCUCACCGUUUCCACAAAtt	s36391
Suv39H1	AGAACAGCUUCGUCAUGGAtt	s13658
Suv39H1	CAAAUCGUGUGGUACAGAAtt	s13660
Suv39H2	GAAUGAGUUUUGUCAUGGAtt	s36183
Suv39H2	GUAUUCGCUUUGCAUCUUUtt	s36184
SETDB1	GGACAAUGCAGGAGAUAGAtt	s19110
SETDB1	CAACCAGACAUAUAGAUCAtt	s19111
EZH2	GCUGACCAUUGGGACAGUAtt	s4916
EZH2	GUGUAUGAGUUUAGAGUCAtt	s4917
KDM5A	GGACCGACAUUGGUGUAUAtt	s11834
KDM5A	GCGAGUUUGUUGUGACAUUtt	s11836
KDM5B	GGCAGUAAAGGAAAUCGAAtt	s21145
KDM5B	GGAAGAUCUUGGACUUAUUtt	s21146
KDM5C	CAGACGAGAGUGAAACUGAtt	s15748
KDM5C	GGAGUUACUCCAUUAACUAtt	s15749
KDM5C	CAGAGAAGCUAGACCUGAAtt	s15750
KMT2A	GGAGUGUAAUAAGUGCCGAtt	s8817
KMT2A	GGUUGCUAUAUGUUCCGAAtt	s8818
SETD1A	CAACGACUCAAAGUAUAUAtt	s18789
SETD1A	CGCAGUGAGUUUGAACAGAtt	s18790
SETD1B	CGUUCAAGGCUCAACCACAtt	s22960
SETD1B	CGGUGGAAAUUGUCGAAGAtt	s22961

Histone Lysine Methylation Dynamics Control *EGFR* DNA Copy Number Amplification
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Supplementary Table 2. qPCR Primer Sequences:

Primer Identifier	Primer Sequence
KDM4A Forward	5'-GCCTCCCACCCTATCCAA-3'
KDM4A Reverse	5'-TCATCCAGTGTGTATACATCATCTCTC-3'
KDM4B Forward	5'-GGCCTCAAGTGACGAGGA-3'
KDM4B Reverse	5'-CTTCCACTGCAGAGACAGCA-3'
KDM4C Forward	5'-AGCAGCAGTGAAGCTGAGG-3'
KDM4C Reverse	5'-TGTACTTAAGCAGCTGTTTCCTGA-3'
KDM4D Forward	5'-AATGGCAGACGTGGTCGT-3'
KDM4D Reverse	5'-TCTTGGCTGGAGTCTGGAG-3'
KDM5A Forward	5'-TCAGCACTGATACCCAAACTTC-3'
KDM5A Reverse	5'-TCACATCTCCAGATTCTGACTGA-3'
KDM5B Forward	5'-AGCAGACTGGCATCTGTAAGG-3'
KDM5B Reverse	5'-GAAGTTTATCAACATCACATGCAA-3'
KDM5C Forward	5'-CGAACGCATTGTTTATCCCTA-3'
KDM5C Reverse	5'-CGTGTGTTACACTGCACAAGG-3'
KDM6A Forward	5'-CTGCACAAGTAAAAGCAACTGTC-3'
KDM6A Reverse	5'-CTTTTGGAGATACTGAATAGCATAGC-3'
KDM6B Forward	5'-ACCCTCGAAATCCCATCAC-3'
KDM6B Reverse	5'-GTGTTCGCCACTCGCTTC-3'
KMT2A Forward	5'-GACAGTGTGCGTTATGTTTGACT-3'
KMT2A Reverse	5'-TGGCCAATATATATAGTAAACGACCA-3'
KMT2B Forward	5'-GGAGGAAGCAGCAAGCAGTA-3'
KMT2B Reverse	5'-GCTCAGGTTTGGGGATTGT-3'
KMT2C Forward	5'-CCACGAAAACAAAGAGGACAG-3'
KMT2C Reverse	5'-TGGGTGCTTACACTTACACAAGAT-3'
KMT2D Forward	5'-ATCCTGGAGACACCCATCAG-3'
KMT2D Reverse	5'-GACAGGCTCAGGGTCAGTG-3'
SETD1A Forward	5'-GCGGTCAGAGAACAGCTACC-3'
SETD1A Reverse	5'-GGAGGCTGAAGATGCAGAGA-3'
SETD1B Forward	5'-CAAGTTCACGGACGCCTAC-3'
SETD1B Reverse	5'-CCGCGGGAGAATTGTGTA-3'
G9A Forward	5'-TGGGAAAGGTGACCTCAGAT-3'
G9A Reverse	5'-GGGCAGAACCTAACTCCTCTG-3'
EHMT1 Forward	5'-GCCAAAGAGGTGACGATAGC-3'
EHMT1 Reverse	5'-ACTGCCCGTTGTGGTGTC-3'
Suv39H1 Forward	5'-GTCATGGAGTACGTGGGAGAG-3'
Suv39H1 Reverse	5'-CCTGACGGTCGTAGATCTGG-3'

Suv39H2 Forward	5’-TCTTTCAAAAATGTTGTCCTGCT-3’
Suv39H2 Reverse	5’-AGGTGGGATTTTAATTTGTTGG-3’
SETDB1 Forward	5’-GCTTCCCCTTCCCTCTTTC-3’
SETDB1 Reverse	5’-GGGAAGACATGCTTTTGTCCT-3’
EZH2 Forward	5’-TGGGACCAAAACATGTAGACAG-3’
EZH2 Reverse	5’-TTCCTTGGAGGAGTATCCACA-3’
EGFR Forward	5’-GATACAGCTCAGACCCCACAG-3’
EGFR Reverse	5’-TTTTGGGAACGGACTGGTT-3’
Actin Forward	5'-AGGCCAACCGCGAGAAG-3'
Actin Reverse	5'-ACAGCCTGGATAGCAACGTACAT-3'

Histone Lysine Methylation Dynamics Control *EGFR* DNA Copy Number Amplification
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Supplementary Table 3. Key Resources Table

Reagent or Resource	Source	Identifier
miRNeasy Mini Kit	Qiagen	Cat# 217004
Superscript IV 1st Strand System	Life Technologies	Cat# 18091050
Lumi-Light Western Blotting Substrate	Roche	Cat# 12015200001
Super Signal West Pico Plus Chemiluminescent Substrate	Thermo Scientific	Cat# 32477
Pierce BCA Protein Assay	Thermo Scientific	Cat# 23223 and 23224
FISH Wash Buffer(s)	DAKO-Agilent	Cat# G9401A and G9402A
Trypan Blue Solution	Sigma Aldrich	Cat# T8154

Antibodies	Source	Identifier
Anti-KDM4A, clone N154/21	UC Davis/NIH Neuro mAb	Cat# 75-189; RRID:AB10671303
Anti-KDM5A	Abcam	Cat# ab70892; RRID:AB2280628
Anti-Flag	Sigma Aldrich	Cat# A8592; RRID:AB439702
Anti-beta Actin	Millipore	Cat# MAB1501; RRID:AB626633
Anti-GFP	Neuro mAb	Cat# 73-131 RRID: AB10671444
Anti-HALO	Promega	Cat# G9211
Anti-Carbonic Anhydrase IX	Abcam	Cat# Ab108351
Goat anti-mouse HRP	Biorad	Cat# 170-6516; RRID: AB11125547
Goat anti-rabbit HRP	GenScript	Cat# A00167

Experimental Models: Cell Lines		
RPE-hTERT1	Nick Dyson	N/A
293T	ATCC	CRL-1573
HCC827	Cyril Benes	N/A
HCT-15	Cyril Benes	N/A
HT-29	Cyril Benes	N/A

Recombinant DNA	Source	Identifier
pCDH-H3.3-Flag-HA-Puro	Peter Lewis	N/A
pCDH-H3.3-Flag-HA-Puro K4M	Peter Lewis	N/A
pCDH-H3.3-Flag-HA-Puro K9M	Peter Lewis	N/A
pCDH-H3.3-Flag-HA-Puro K27M	Peter Lewis	N/A
pCDH-H3.3-Flag-HA-Puro K36M	Peter Lewis	N/A
GFP-KDM4A	Mishra *et al* (2018)	N/A
GFP-KDM4A H188A	Whetstine *et al.* (2006)	N/A
GFP-KDM4A Tudor Del	Black *et al.* (2013)	N/A
GFP-KDM4A N940R	This Study	
GFP-KDM4B	Mishra *et al* (2018)	N/A
GFP-KDM4C	Mishra *et al* (2018)	N/A
HALO-KMT2A (HALO-MLL1)	Promega	N/A
HALO-KMT2B (Gene ID: 9757)	Promega	N/A
HALO-KMT2D (Gene ID: 8085)	Promega	N/A
HALO-SETD1A	Promega	N/A
GFP-SETD1B	GeneCopoeia	Cat# GC-H3298-GS
HALO-Tag Alone	Promega	Cat# G6591
HALO-KDM6A	Promega	Cat# FHC00327
HALO-KDM6B	Promega	Cat# FHC00511
psPAX2	Nick Dyson	N/A
VSVG	Nick Dyson	N/A
SureFISH 7p11.2 EGFR 188kb Rd	Agilent	Cat# G101155R
SureFISH Chr7 CEP	Agilent	Cat# G101099R
Chromosome 8 Centromere Red	Rainbow – Oxford	Cat# LPE008R-A

Chemicals, Peptides and Recombinant Proteins	Source	Identifier
Propidium Iodide Solution	Sigma Aldrich	Cat# P4864
Xcess Bio KDM5-C70	Fisher Scientific	Cat# NC0732032
C24 – EZH2 inhibitor	Jian Jin	N/A
KDM4 Family inhibitor	Jian Jin	N/A
Lapatinib	Abcam	ab219408
Geftinib	Abcam	ab142052
Recombinant Human EGF	Abcam	Cat# ab9697
Dulbecco's Modified Eagles Medium – High Glucose	Sigma Aldrich	Cat# D5648
Roswell Park Memorial Institute Medium (RPMI)1640	Sigma Aldrich	Cat# R6504
RPMI Glutamax Supp, HEPES	Thermo Fisher	Cat# 724000-047
Sodium Pyruvate (100mM)	Thermo Fisher	Cat # 11360070
Glucose Solution	Thermo Fisher	Cat # A2494001
Opti-Mem	Life Technologies	Cat# 31985070Life
Trypsin (0.25%) EDTA	Life Technologies	Cat# 2520056
L-Glutamine	Life Technologies	Cat# 25030-081
Penicillin and Streptomycin	Life Technologies	Cat# 15140122
Fetal Bovine Serum (FBS)	Gibco	Cat# 26140-079

Lipofectamine 3000	Life Technologies	Cat# L30000015

Software and Algorithms	Source	
Scaffold 6.0	3i-intelligent imaging Innovations	https://www.intelligent-imaging.com/slidebook