**Supplementary Table. 1. Data quality control.**

**Supplementary Table. 2. The Primers for RT-qPCR used in this study.**

**Supplementary Table. 3. The Antibodies for western blotting used in this study.**

**Supplementary Figure. 1. The co-location between METTL14 and DPAI.**

**Supplementary Figure. 2.** (A) The molecular function of the proteomics. (B) The cell viability (mean ± SD; n= 5/group; *P < 0.05, One-way ANOVA). (C) The ubiquitination of METTL14.

**Supplementary Figure. 3.** (A) The transduction efficiency of METTL14 lentivirus. (B) The mRNA knockdown efficiency of METTL14 (mean ± SD; n= 3/group; ***P < 0.001, One-way ANOVA). (C, D) The protein knockdown level of METTL14 (mean ± SD; n= 3/group; ***P < 0.001, One-way ANOVA). (E-H) The marker of M1-type and M2-type (mean ± SD; n= 3/group; ns > 0.05, unpaired Student's t-test). (I) Sample 2 (S2), S3, S4, S6, S7, S9, S10 were identified as homozygous $Mettl14^{fl/fl}$ mice, while S2, S5, S6, S7, S8 carried the Cx3cr1-Cre transgene. In summary, S2, S6, S7 were identified as homozygous Mettl14 cKO mice. (J-O) A wave and B wave of ERG between WT and Mettl14 cKO mice. (P) The H&E staining of WT and Mettl14 cKO mice. (Q) The immunofluorescent staining of TMEM119 and CD31 in OIR mice.

**Supplementary Figure. 4. The co-cultured system.**

**Supplementary Figure. 5. The m6A peak distribution.**

**Supplementary Table. 1 Data quality control**

| Samples | **Q20%** | Q30% | GC% |
|---|---|---|---|
| Sh-NC-1-IP | 98.17 | 94.62 | 51.14 |
| Sh-NC-2-IP | 98.13 | 94.50 | 50.91 |
| Sh-NC-3-IP | 98.19 | 94.68 | 51.08 |
| Sh-MET14-1-IP | 98.20 | 94.72 | 51.81 |
| Sh-MET14-2-IP | 98.11 | 94.47 | 50.95 |
| Sh-MET14-3-IP | 98.14 | 94.51 | 51.13 |
| Sh-NC-1-input | 98.36 | 94.96 | 49.18 |
| Sh-NC-2-input | 98.29 | 94.80 | 49.18 |
| Sh-NC-3-input | 98.36 | 94.98 | 49.29 |
| Sh-MET14-1-input | 98.37 | 95.03 | 49.93 |
| Sh-MET14-2-input | 98.31 | 94.82 | 49.39 |
| Sh-MET14-3-input | 98.31 | 94.81 | 49.46 |

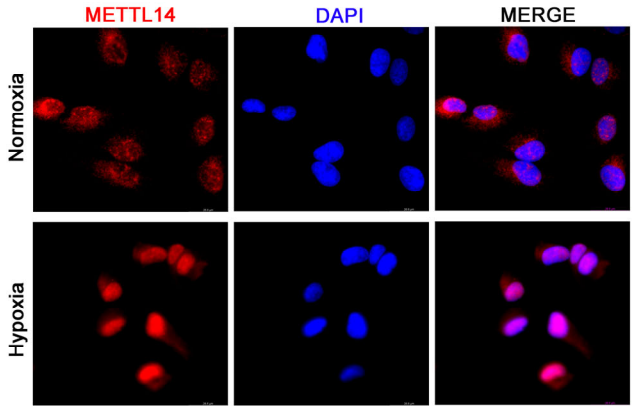
**Supplementary Table. 2 The Primers for RT-qPCR used in this study**

| Genes | Species | Sequences (5'-3') |
|---|---|---|
| METTL3 | Human | CATTGCCCACTGATGCTGTG |
| | | AGGCTTTCTACCCCATCTTGA |
| METTL14 | Human | AGTGCCGACAGCATTGGTG |
| | | GGAGCAGAGGTATCATAGGAAGC |
| FTO | Human | GCTGCTTATTTCGGGACCTG |
| | | AGCCTGGATTACCAATGAGGA |
| ALKBH5 | Human | CGGCGAAGGCTACACTTACG |
| | | CCACCAGCTTTTGGATCACCA |
| MXD1 | Human | TTTCCCTGTCAACCTAAG |
| | | GAAATAAGCCCACAAAAT |
| β-ACTIN | Human | CATGTACGTTGCTATCCAGGC |
| | | CTCCTTAATGTCACGCACGAT |
| Mxd1 | Mouse | AGATGCCTTCAAACGGAGGAA |
| | | CAAGCTCAGAGTGGTGTGTCG |
| β-actin | Mouse | GGCTGTATTCCCCTCCATCG |
| | | CCAGTTGGTAACAATGCCATGT |

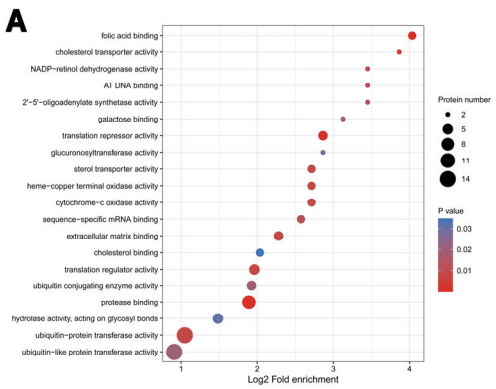
**Supplementary Table. 3 The Antibodies for western blotting used in this study**

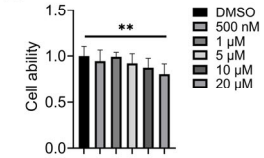
| Antibody | Host | Manufacturer | Application |
|---|---|---|---|
| β-actin | Mouse | Proteintech | 1:10,000 |
| METTL3 | Rabbit | Proteintech | 1:1,000 |
| METTL14 | Rabbit | NovusBio/Abclonal | 1:1,000/1:50 |
| FTO | Rabbit | Abcam | 1:2,000 |
| ALKBH5 | Rabbit | Abcam | 1:1,000 |
| Ubiquitination | Rabbit | HuaBio | 1:1,000 |
| BARD1 | Rabbit | Abclonal | 1:1,000 |
| Flag | Mouse | Origene | 1:1,000 |
| iNOS | Rabbit | Abcam | 1:1,000 |
| TNF-α | Rabbit | Proteintech | 1:1,000 |
| CD206 | Rabbit | Proteintech | 1:1,000 |
| ARG1 | Rabbit | Proteintech | 1:1,000 |
| VCAM1 | Rabbit | Proteintech | 1:1,000 |
| ICAM1 | Rabbit | Proteintech | 1:1,000 |
| YTHDF1 | Rabbit | Proteintech | 1:1,000 |
| YTHDF2 | Rabbit | Proteintech | 1:1,000 |
| YTHDF3 | Rabbit | Proteintech | 1:1000 |
| MXD1 | Rabbit | Affinity | 1:1,000 |
| VEGFA | Rabbit | Abcam | 1:800 |

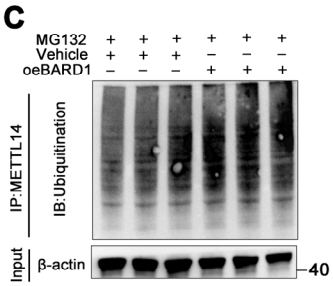
**Fig .S1**



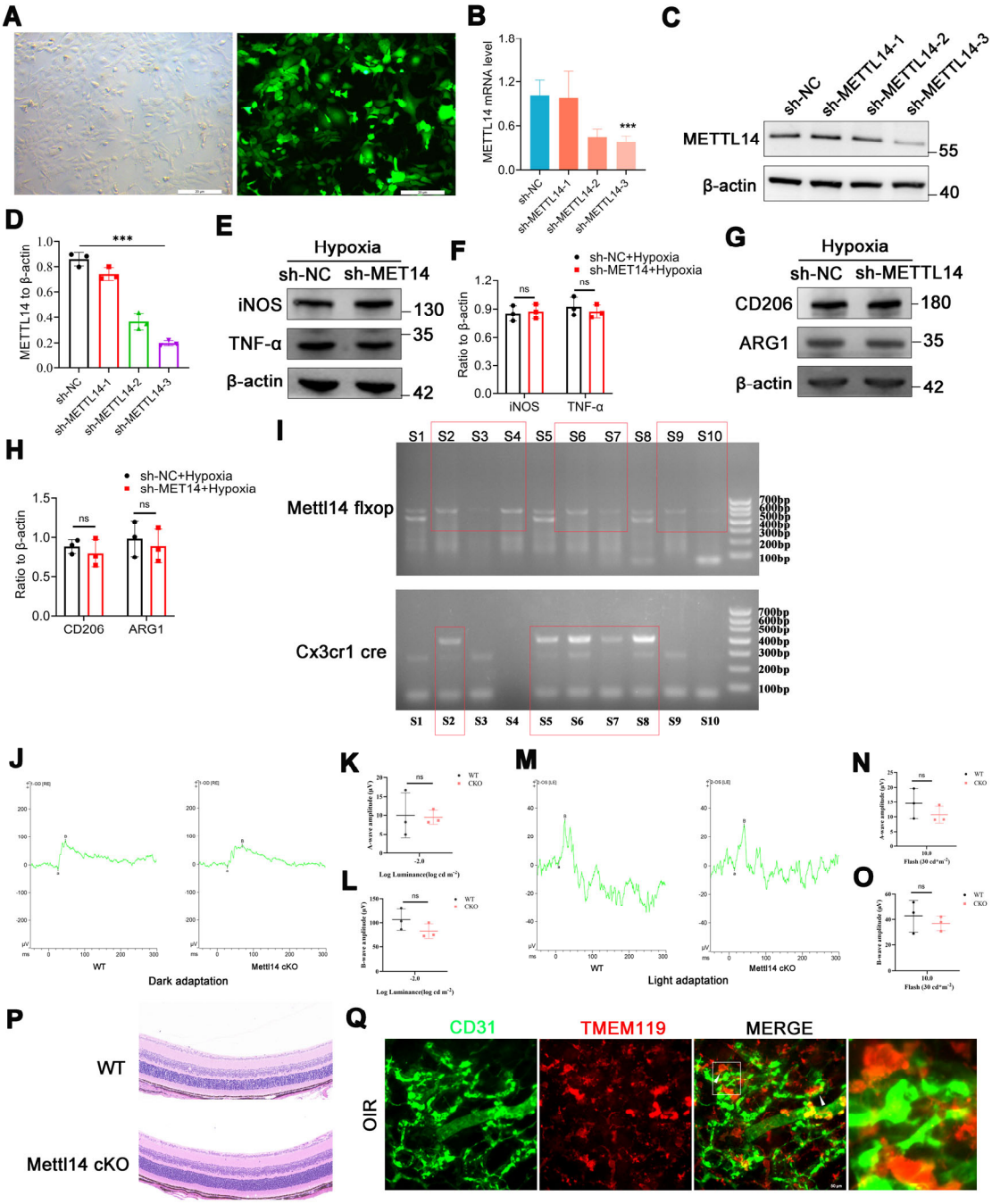
# Fig. S2


A
folic acid binding
cholesterol transporter activity
NADP−retinol dehydrogenase activity
AU RNA binding
2′−5′−oligoadenylate synthetase activity
galactose binding
translation repressor activity
glucuronosyltransferase activity
sterol transporter activity
heme−copper terminal oxidase activity
cytochrome−c oxidase activity
sequence−specific mRNA binding
extracellular matrix binding
cholesterol binding
translation regulator activity
ubiquitin conjugating enzyme activity
protease binding
hydrolase activity, acting on glycosyl bonds
ubiquitin−protein transferase activity
ubiquitin−like protein transferase activity
1
2
3
4
Log2 Fold enrichment
Protein number
2
5
8
11
14
P value
0.03
0.02
0.01

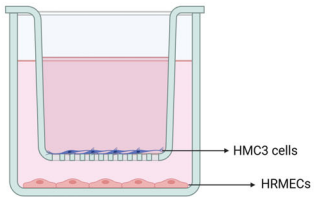

B
1.5
1.0
0.5
0.0
Cell ability
**
DMSO
500 nM
1 μM
5 μM
10 μM
20 μM


C
MG132 + + + + + +
Vehicle + + + − − −
oeBARD1 − − − + + +
IP:METTL14
IB:Ubiquitination
Input
β-actin
40

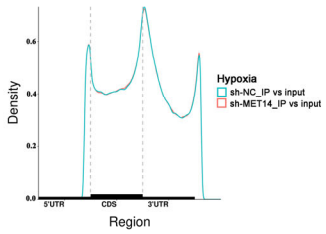
# Fig. S3


A
B
METTL14 mRNA level
sh-NC
sh-METTL14-1
sh-METTL14-2
sh-METTL14-3
C
METTL14
β-actin
55
40
D
METTL14 to β-actin
E
Hypoxia
iNOS
TNF-α
130
35
42
F
sh-NC+Hypoxia
sh-MET14+Hypoxia
Ratio to β-actin
G
CD206
ARG1
180
H
I
Mettl14 flxop
Cx3cr1 cre
700bp
600bp
500bp
400bp
300bp
200bp
100bp
J
Dark adaptation
Light adaptation
WT
Mettl14 cKO
K
L
M
N
O
P
Q
CD31
TMEM119
MERGE
OIR

# Fig. S4



# Fig. S5


Density
0.6
0.4
0.2
0.0
5'UTR
CDS
3'UTR
Region
Hypoxia
sh-NC_IP vs input
sh-MET14_IP vs input