**Supplementary data**

**Materials and methods**

**Cell transfection**

KGN cells were transfected with pCDNA3.1-PINK1, pCDNA3.1-METTL3, and pCDNA3.1-NC plasmids using Lipofectamine®2000 (Invitrogen, Carlsbad, CA, USA) at a final transfection concentration of 100 ng/μL. The plasmid pCDNA3.1(+) was purchased from GenePharma Co., Ltd. (Shanghai, China), and HindIII and XhoI double enzyme sites were used. The overexpression primers are listed in Supplementary table 1. Transfection efficiency was determined by RT-qPCR 24 h post-transfection.

**Supplementary table 1** PINK1 and METTL3 overexpression primer sequences

|  |  |  |
| --- | --- | --- |
| Gene | Forward 5’-3’ | Reverse 5’-3’ |
| oe-PINK1 | GACT-AAGCTT-ATGGCGGTGCGACAGGCG | GACC-CTCGAG-TCATGCCTGGCAGAGCGTTTC |
| oe-METTL3 | GACT-AAGCTT-ATGTCGGACACGTGGAGCTC | GACC-CTCGAG-CTAACCATCTGGGTACCTTTG |

**RT-****qPCR**

Cells were subjected to total RNA extraction using Trizol reagent (Thermo Fisher Scientific). RNA concentrations were ascertained using a spectrophotometer (Thermo Fisher Scientific). The synthesis of cDNA was performed by reverse transcribing 1 μg total RNA using the PrimeScriptTM RT Reagent Kit (Invitrogen). RT-qPCR analysis was carried out using an ABI ViiA7DX system (Foster City, CA, USA). With GAPDH as an internal reference, data analysis was conducted using the 2-ΔΔCt method. The primers are illustrated in Supplementary table 2.

**Supplementary table 2** Primer sequences

|  |  |  |
| --- | --- | --- |
| Gene | Forward 5’-3’ | Reverse 5’-3’ |
| PINK1 | GCCTCATCGAGGAAAAACAGG | GTCTCGTGTCCAACGGGTC |
| METTL3 | AGCCTTCTGAACCAACAGTCC | CCGACCTCGAGAGCGAAAT |
| GAPDH | CAATGACCCCTTCATTGACC | GACAAGCTTCCCGTTCTCAG |

**Results**

**Detection of transfection efficiency of PINK1 and METTL3 overexpression**

Transfection efficiency of pCDNA3.1-PINK1, pCDNA3.1-METTL3, and pCDNA3.1-NC into KGN cells was assessed by RT-qPCR 24 h post-transfection. The results showed that, compared to the negative control group, the expression levels of PINK1 and METTL3 mRNA were significantly increased, indicating that the overexpression vectors effectively enhanced the transcriptional activities of PINK1 and METTL3 genes (*p* < 0.001, Supplementary figure 1A-B).

**Supplementary figure 1** Detection of transfection efficiency of PINK1 and METTL3 overexpression. Transfection of pCDNA3.1-PINK1 and pCDNA3.1-METTL3 overexpression plasmids into KGN cells could efficiently increase the transcriptional activities of PINK1 and METTL3 genes. (A) (B) RT-qPCR to determine the mRNA expression levels of PINK1 and METTL3 in KGN cells. The KGN cells used were the third passage cells. Cell experiments were independently repeated three times, and data were presented as mean ± SD. Comparisons among multiple groups were performed using one-way ANOVA, followed by Tukey's multiple comparison test. \*\*\* *p* < 0.001. PINK1, PTEN-induced kinase 1; METTL3, methyltransferase-like 3; oe-NC, overexpression negative control; oe-PINK1, overexpression of PINK1; oe-METTL3, overexpression of METTL3.