**1.RNA sequencing**

Samples had high quality which were proved by the RNA integrity testing with Agilent 5400 and were processed with further steps (Supplementary file 2). Total RNA was used as input material for the RNA sample preparations, and the RNA with polyA tail was enriched by Oligo(dT) magnetic beads. Then the RNA was amplified and subjected to 150 bp paired-end deep sequencing on the Illumina NovaSeq 6000 platform.

**2.Ribosome profiling**

Cells were lysed using 1 ml of mammalian lysis buffer (200 µI of 5 × Mammalian Polysome Buffer, 100 µI of 10% Triton X-100, 10 µI of DTT (100 mM), 10 µI of DNase I (1 U/µI), 2 µI of cycloheximide (50 mg/ml), 10 µI of 10% NP-40 and 668 µI of nuclease-free water). After incubation for 20 min on ice, the lysates were cleared by centrifugation at 10,000 × g and 4℃ for 3 min. For the 300-µI aliquots of clarified lysates per cell line, 5 units of ARTseq Nuclease were added to each A260 lysate, and the mixtures were incubated for 45 min at room temperature. Nuclease digestion was stopped by the addition of 15 µI of SUPERase In RNase Inhibitor (Ambion). Subsequently, the lysates were applied to Sephacryl S-400 HR spin columns (GE Healthcare Life Sciences), and ribosome-protected fragments were purified by the Zymo RNA Clean & Concentrator-25 kit (Zymo Research). Ribosomal RNA was depleted using the Ribo-Zero magnetic kit (Epi-centre). Sequencing libraries of ribosome-protected fragments (RPFs) were generated using the ARTseq™ Ribosome Profiling Kit (Epicentre, RPHMR12126), according to the manufacturer’s instructions. The libraries were sequenced using an Illumina HiSeq X Ten instrument in the 150bp paired-end mode.

**3.Liquid chromatography tandem mass spectrometry (LC-MS)**

Cells was homogenized in lysis buffer (8 M Urea, 100 mM TEAB, pH 8.5) with 1 × protease inhibitor (EDTA-free, Roche) by using sonication on ice. After centrifugation at 12000 g for 15 min at 4℃, the supernatant fraction was collected. About 500ug of each sample was aliquoted for subsequent protein digestion. Samples were reduced with 10 mM dithiothreitol at 56℃ for 1 h, then mixed with sufficient iodoacetamide alkylation in the dark for another 1 h. The samples were digested with trypsin at 37 °C for 16 h and stopped by adding formic acid (FA), then centrifuged at 12000 g for 5 min at room temperature. Next, the sample was desalted with a C18 Sep-Pak cartridge (Waters), dried by a vacuum centrifuge and then resuspended in 0.1% FA. The peptides were separated using high-pH reversed-phase chromatography (Hp-RP). The final ten fractions were collected and dried under vacuum, and then, reconstituted in 0.1% (v/v) formic acid (FA) in water.

The Q ExactiveTM HF-X mass spectrometer (Thermo Fisher), with ion source of Nanospray Flex™（ESI）were used to analyze the separated peptides by Novogene Bioinformatics Technology Co., Ltd (Beijing, China).