**SLAM-seq Data Analysis**

To investigate the dynamics of transcriptional changes in our samples, we employed SLAM-seq and conducted a comprehensive bioinformatics analysis pipeline (<https://github.com/Liangyan-1996/BCL11A-paper>). The detailed workflow is described as follows:

1. Quality Control and Alignment

Raw sequencing reads were subjected to quality control using fastp (version: 0.23.2), with default parameters. High-quality reads were then aligned to the human genome (Ensembl GRCh38.110) using STAR (version: 2.7.11a) with stringent parameters: maximum mismatches (--outFilterMismatchNmax) allowed were set to 20, and the minimum alignment score (--outFilterScoreMinOverLread) and minimum match length (--outFilterMatchNminOverLread) was set to 0.4 of the read length. The resulting BAM files were sorted by coordinate and indexed using sambamba (version: 0.6.8).

1. 4sU Conversion Analysis

To assess the dynamics of 4sU-labeled transcripts, we utilized the GRAND-SLAM (version: 2.0.7b) to analyze the aligned BAM files and quantify 4sU conversion rates across the transcriptome. The parameters were set to trim 10 nucleotides from both the 5' and 3' ends (-trim5p 10 -trim5p 10) of the reads to minimize sequencing biases.

1. Differential Expression Analysis

Differential expression analysis was conducted using the DESeq2 package (version: 1.46.0) in R, combined with the grandR package (version: 0.2.6) for handling GRAND-SLAM output. Differential expression analysis was analyzed for both total transcripts (total) and newly synthesized transcripts (new). The analysis included normalization of counts, estimation of dispersion, and Wald testing to identify differentially expressed genes.

**Calculation of Sequence Charge Decoration Matrix (SCDM)**

To quantify the electrostatic interactions within the protein sequences and capture their conformational characteristics, we calculated the Sequence Charge Decoration Matrix (SCDM) using the method described by Huihui and Ghosh. The SCDM provides a detailed representation of the electrostatic interaction topology within the protein sequence, which is crucial for understanding the conformational behavior and functional properties of intrinsically disordered proteins (IDPs).

In this coarse-grained model, each amino acid residue is treated as a point charge. Specifically, Aspartic acid (Asp) and Glutamic acid (Glu) were assigned a charge of *q*=−1, Arginine (Arg) and Lysine (Lys) were assigned *q*=1, and all other amino acids were assigned *q*=0. For phosphorylation, the neutral charges of Serine (Ser) and Threonine (Thr) were replaced with *q*=−2 to mimic the double negative charge of phosphate groups.

The code used for SCDM calculation was slightly from the github (https://github.com/MaxCalLab/IDPTheory/tree/main) provided in the paper by Valverde et al. (2023).