Supporting Information

Probing enzyme-dependent pseudouridylation using direct RNA sequencing to assess neuronal transcriptome plasticity

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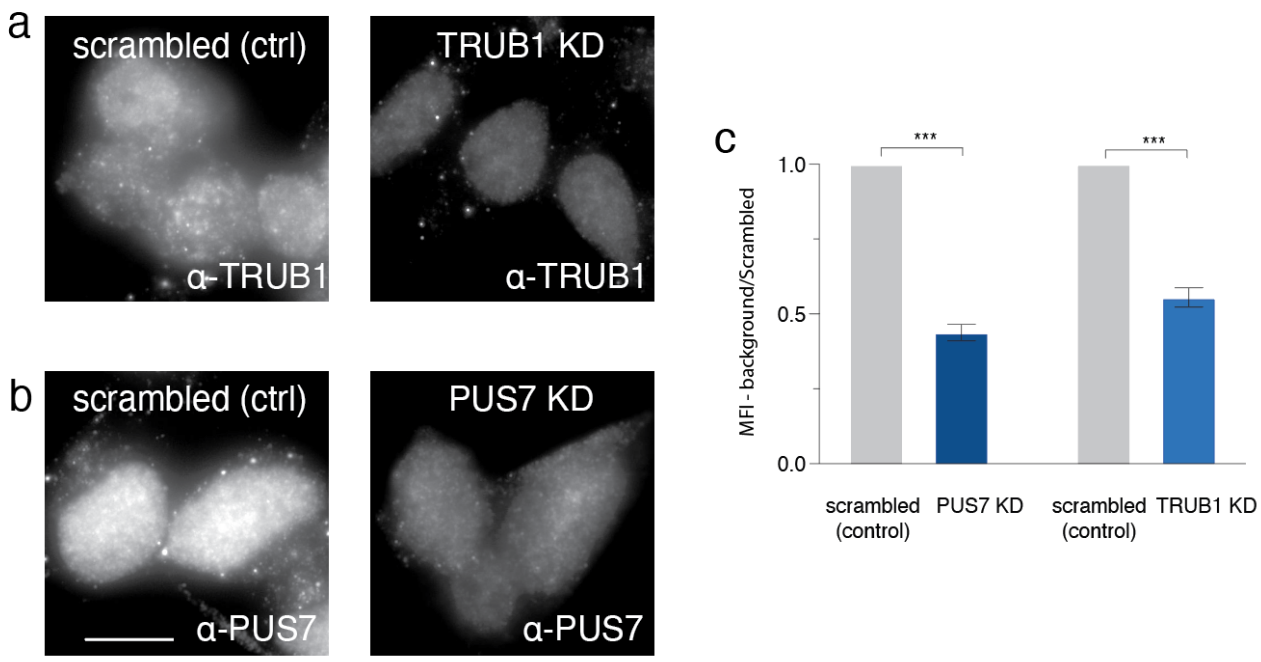
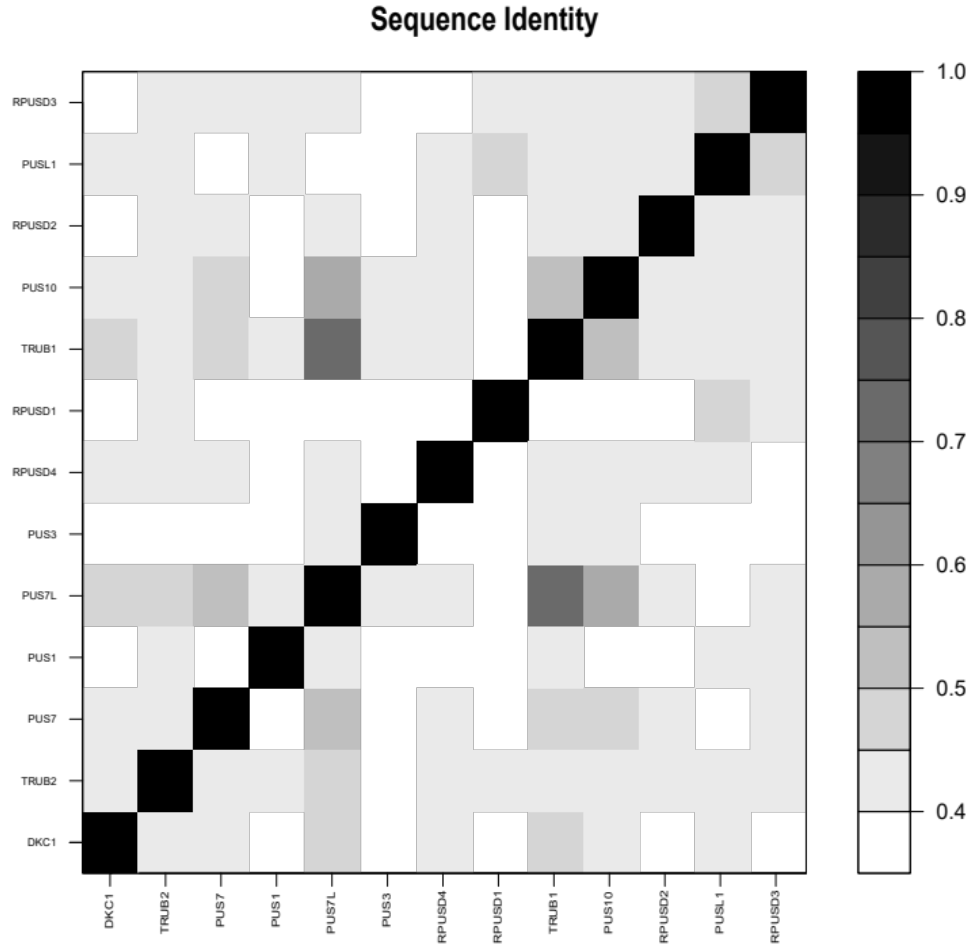
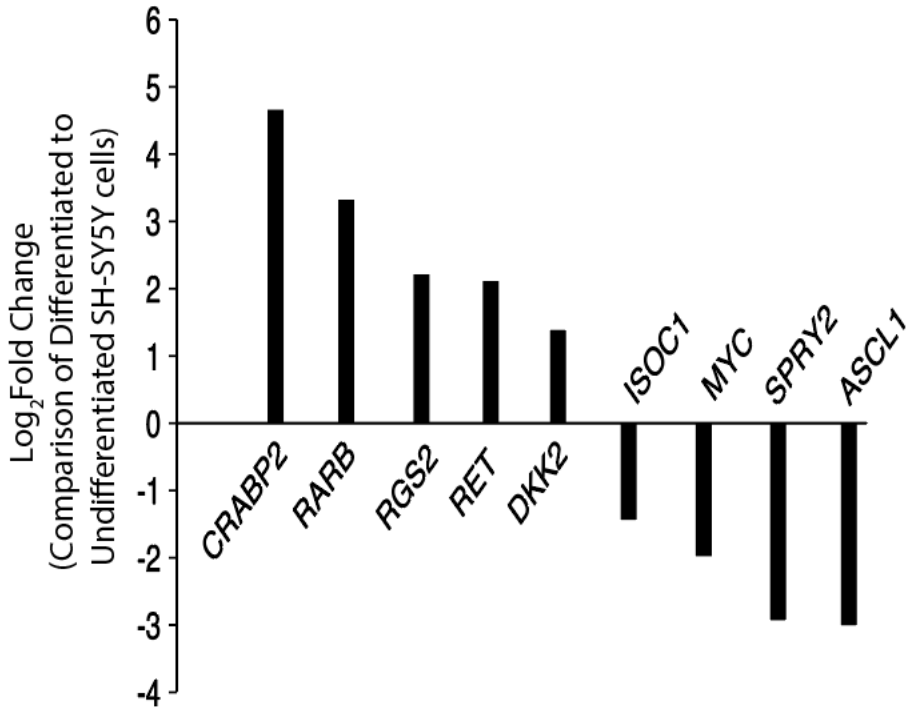
Table of Contents



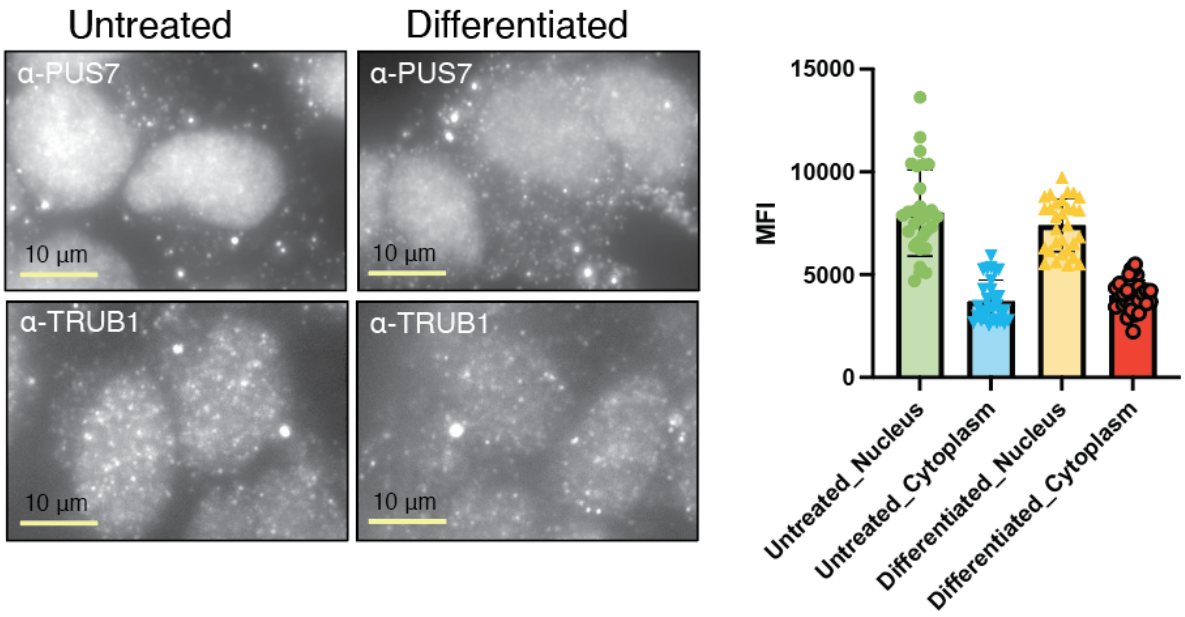
Supplementary Figure 1. a. Representative photomicrographs of a. TRUB1 knockdown (KD) and b. PUS7 KD vs Scrambled (control) cells show a substantial decrease in fluorescence in the KD library. c. Immunofluorescence (IF) of TRUB1 KD, PUS7 knockdown KD, and siRNA control show a decreased mean fluorescence intensity (MFI) in the KD cells compared to the control.



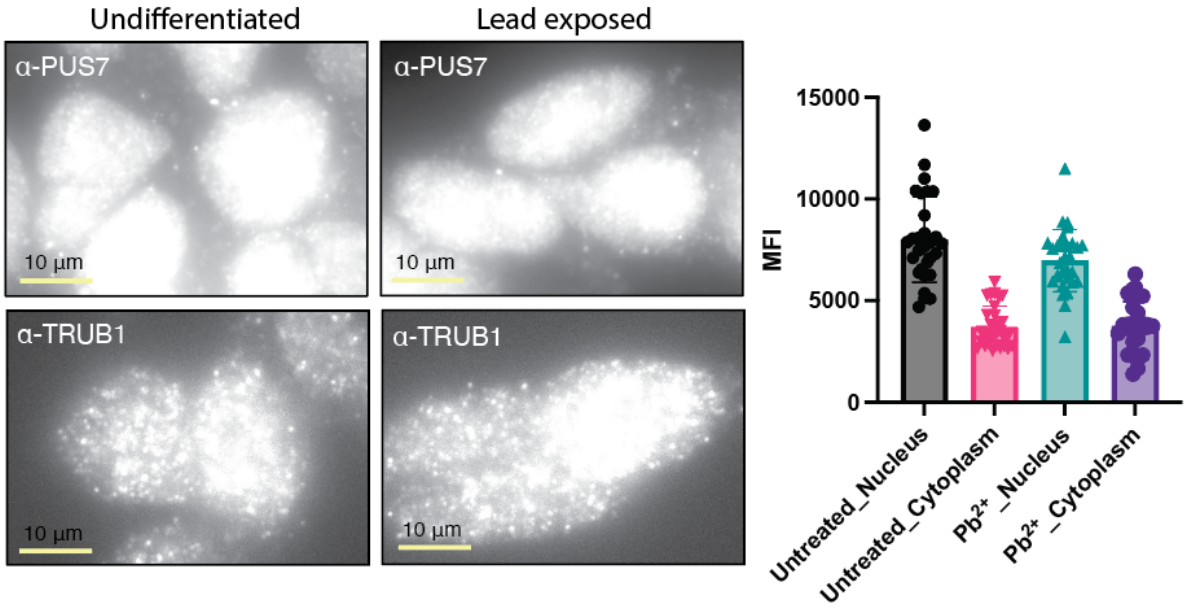
Supplementary Figure 2. Sequence identity matrix showing the sequence identity between each PUS enzyme nucleotide sequence in the multiple sequence alignment data (MSA).



Supplementary Figure 3. Differential mRNA expression of known differentiation markers supports a change in the SH-SY5Y cellular state after the retinoic acid-induced differentiation treatment.



Supplementary Figure 4. IF images of untreated and differentiated SH-SY5Y cells using a. PUS7 and b. TRUB1 antibodies. (right) Comparison of PUS7 and TRUB1 antibodies' fluorescence intensity in the nucleus and cytoplasm of untreated and differentiated SH-SY5Y cells.



Supplementary Figure 5. IF images of untreated and Lead exposed SH-SY5Y cells using PUS7 and TRUB1 antibodies. (right) Comparison of PUS7 and TRUB1 antibodies' fluorescence intensity in the nucleus and cytoplasm of untreated and lead treated SH-SY5Y cells.