Organic & Biomolecular Chemistry Supporting Information Oligonucleotide modifications enhance probe stability for single cell transcriptome in vivo analysis (TIVA) S. B. Yeldell^a, B. K. Ruble^a, and I. J. Dmochowski^a ^aDepartment of Chemistry, University of Pennsylvania, 231 South 34th Street, Philadelphia, PA 19104-6323, USA. E-mail: ivandmo@sas.upenn.edu Tel: +1 215-898-6459 **Contents:** Figure S1 S2 RP-HPLC purification of crude 22/9/9 GC probe after cleavage Figure S2 **S3** AX-HPLC purification of 22/9/9 GC probe after conjugation to (D-Arg)₉ cell-penetrating peptide S4 Figure S3 RP-HPLC purification of crude PS-22/9/9 probe after solid-phase synthesis and cleavage **Figure S4 S5** FRET efficiencies of 18/7/7 and 22/9/9 TIVA probes in buffer, pre-photolysis Figure S5 **S6** RP-HPLC purification of crude 22/9/9 GC probe after solid-phase synthesis and cleavage **Figure S6 S7** AX-HPLC purification of 22/9/9 probe after conjugation to (D-Arg)₉ cell-penetrating peptide **S8** Figure S5 RP-HPLC purification of cleaved 18/7/7 TIVA syntheses before and after protocol improvements **Figure S8 S9** ESI-MS analysis of 22/9/9 +(D-Arg)₉ TIVA

Figure S1. RP-HPLC purification of crude 22/9/9 GC probe after solid-phase synthesis and cleavage



Separation was performed on C-18 column under a gradient of increasing acetonitrile in 0.5 M TEAA, with the product eluting at roughly 28 min.

Figure S2. AX-HPLC purification of 22/9/9 GC probe after conjugation to $(D-Arg)_9$ cell-penetrating peptide



Separation was performed on Source 15q ion-exchange column under a gradient of increasing $NaClO_4$ in 1:1 formamide: Tris-HCl buffer, with the product eluting at roughly 24 min.

Figure S3. RP-HPLC purification of crude PS-22/9/9 probe after solid-phase synthesis and cleavage



Separation was performed on C-18 column under a gradient of increasing acetonitrile in 0.5 M TEAA, with the product eluting at roughly 27 min.

Figure S4. FRET efficiencies of 18/7/7 and 22/9/9 TIVA probes in buffer, pre-photolysis



FRET efficiencies were measured for both probes at 1.0 μ M in 1x STE buffer. 18/7/7 and 22/9/9 TIVA probes were synthesized according to [19].

Figure S5. RP-HPLC purification of crude 22/9/9 GC probe after solid-phase synthesis and cleavage



Separation was performed on C-18 column under a gradient of increasing acetonitrile in 0.5 M TEAA, with the product eluting at roughly 50 min.

Figure S6. AX-HPLC purification of 22/9/9 probe after conjugation to $(D-Arg)_9$ cell-penetrating peptide



Separation was performed on Source 15q ion-exchange column under a gradient of increasing NaClO₄ in 1:1 formamide: Tris-HCl buffer, with the product eluting at roughly 24 min.





RP-HPLC purification of six different 18/7/7 TIVA probe syntheses, three before (A) and three after (B) protocol improvements, resulting in more consistent syntheses with higher yield. Separation was performed on a C-18 column under a gradient of increasing acetonitrile in 0.5 M.

Figure S8. ESI-MS analysis of 22/9/9 +(D-Arg)₉ TIVA



ESI-MS verified the product mass (16,913 Da predicted, 16,912 Da observed). The principal impurity corresponded to TIVA product with one missing 2'F-U (-307 Da), which is not expected to significantly impact probe performance.