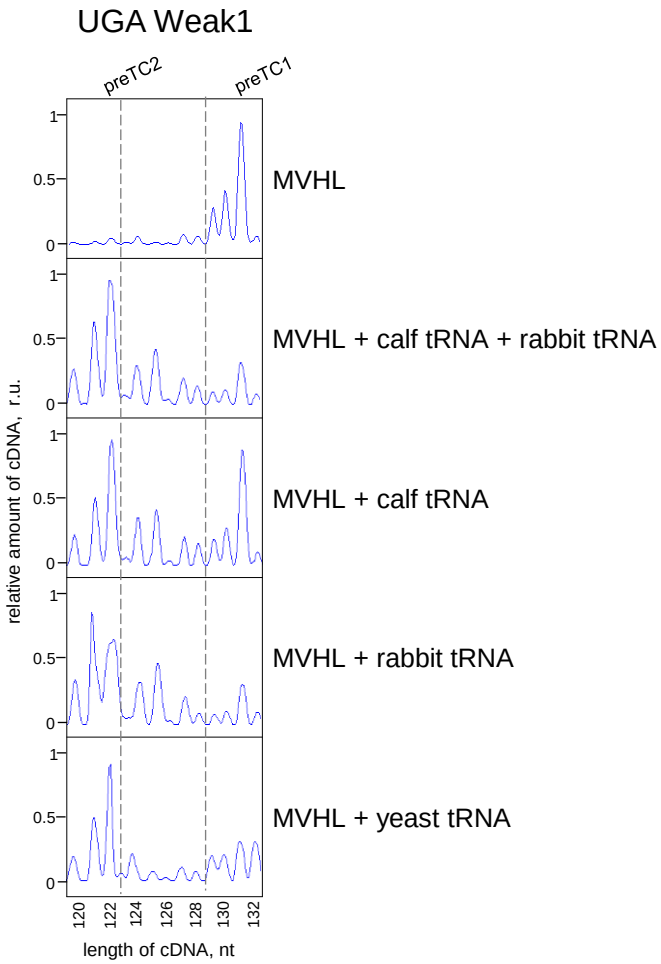


Figure S1. Stop codon readthrough on the UGA stop codon in the Weak1 context after addition of the aminoacylated tRNA from various sources: calf, rabbit, and yeast. Examples of toe-printing analysis of the ribosomal complexes. r.u., relative units.

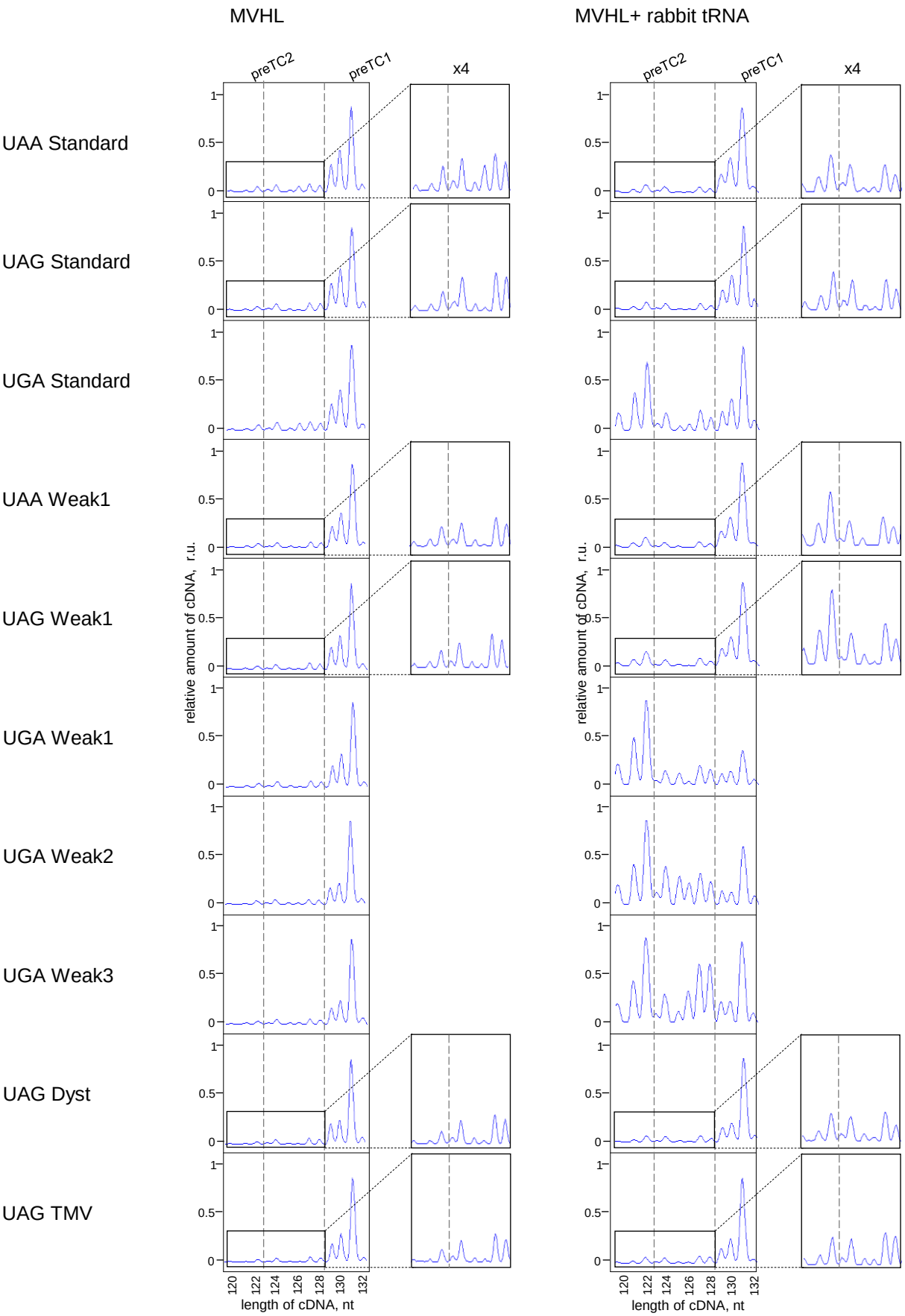


Figure S2. Examples of toe-printing analysis of stop codon readthrough on different stop codons and in different 3′ contexts. r.u., relative units.

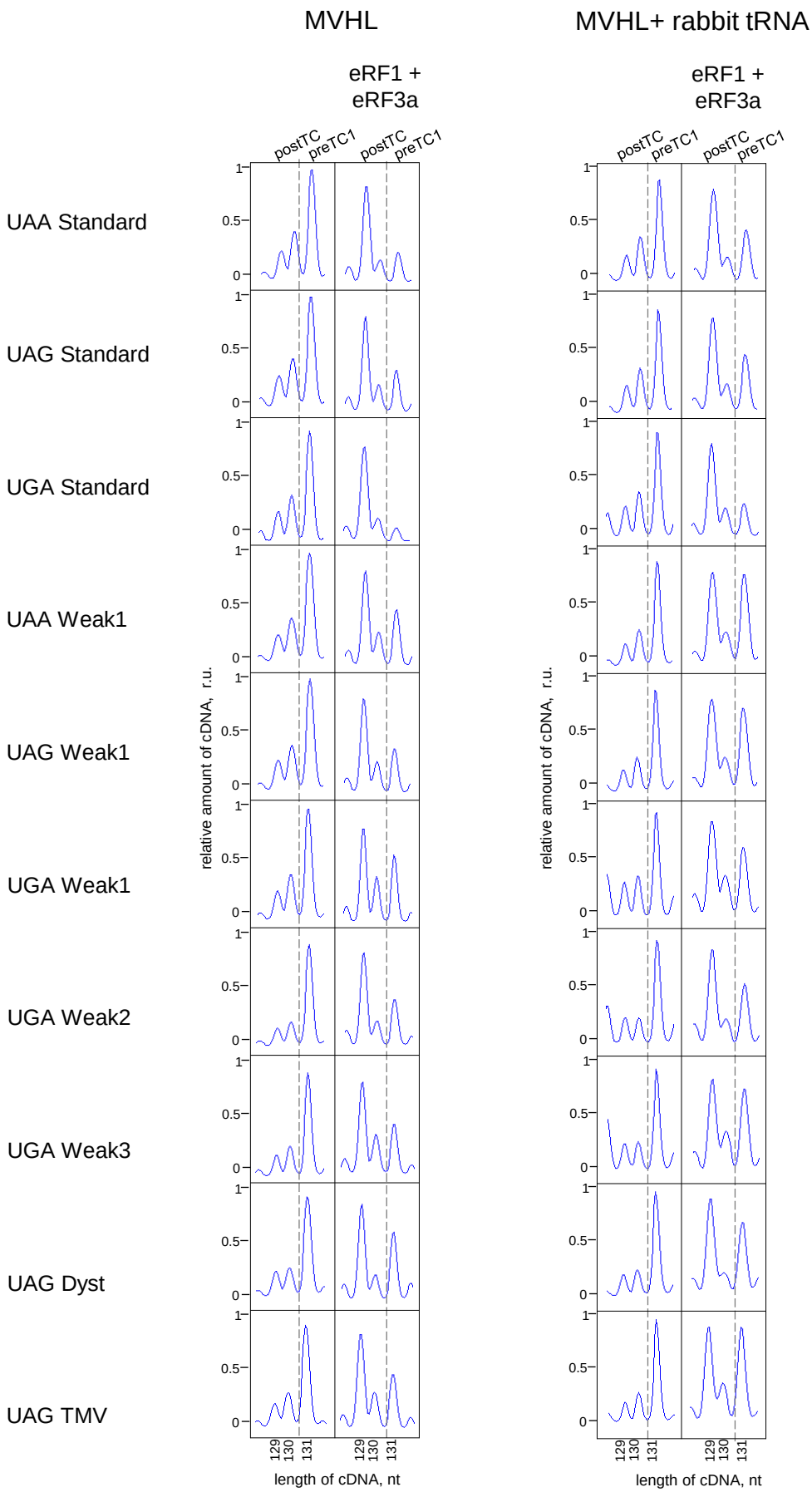


Figure S3. Examples of toe-printing analysis of translation termination on different stop codons and in different 3′ context. r.u., relative units.

Raw data for Fig 1C

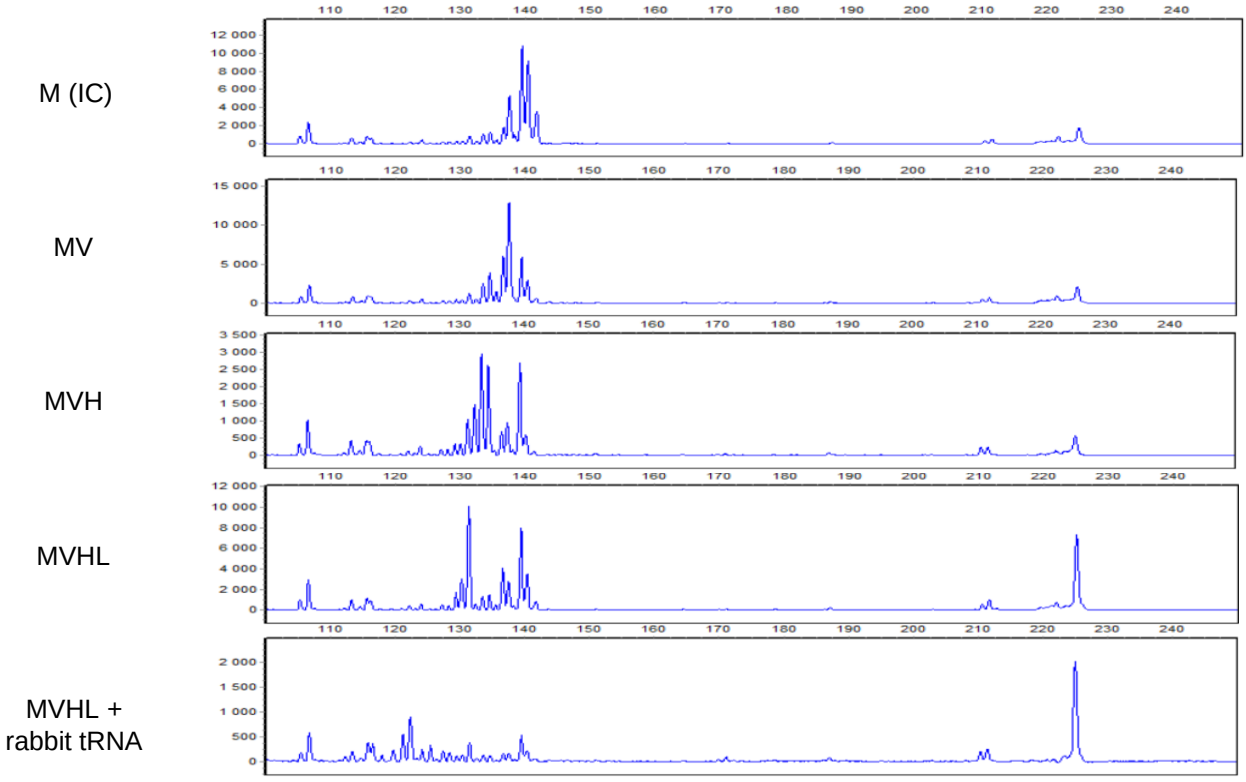


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig 4

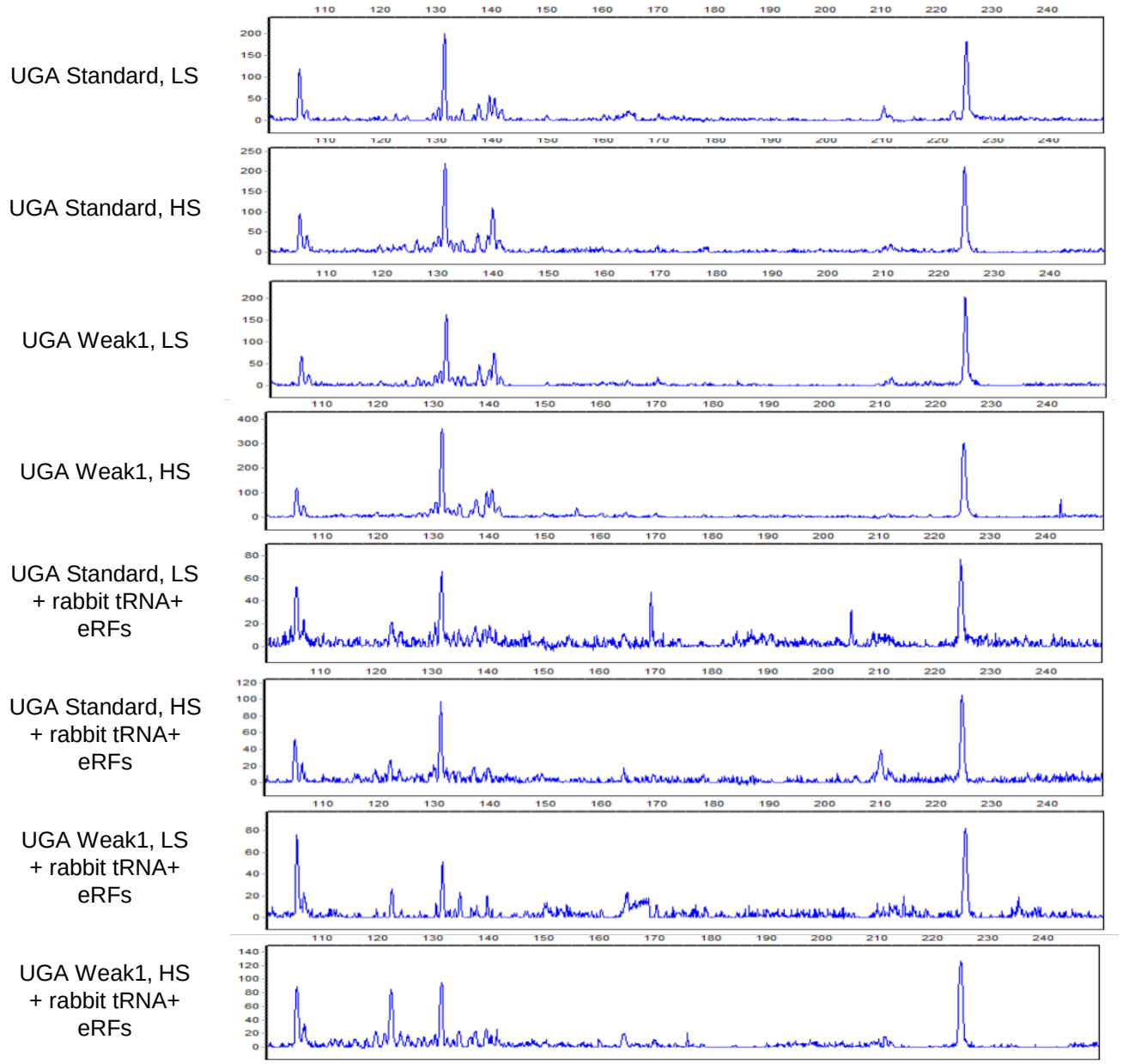


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig 5

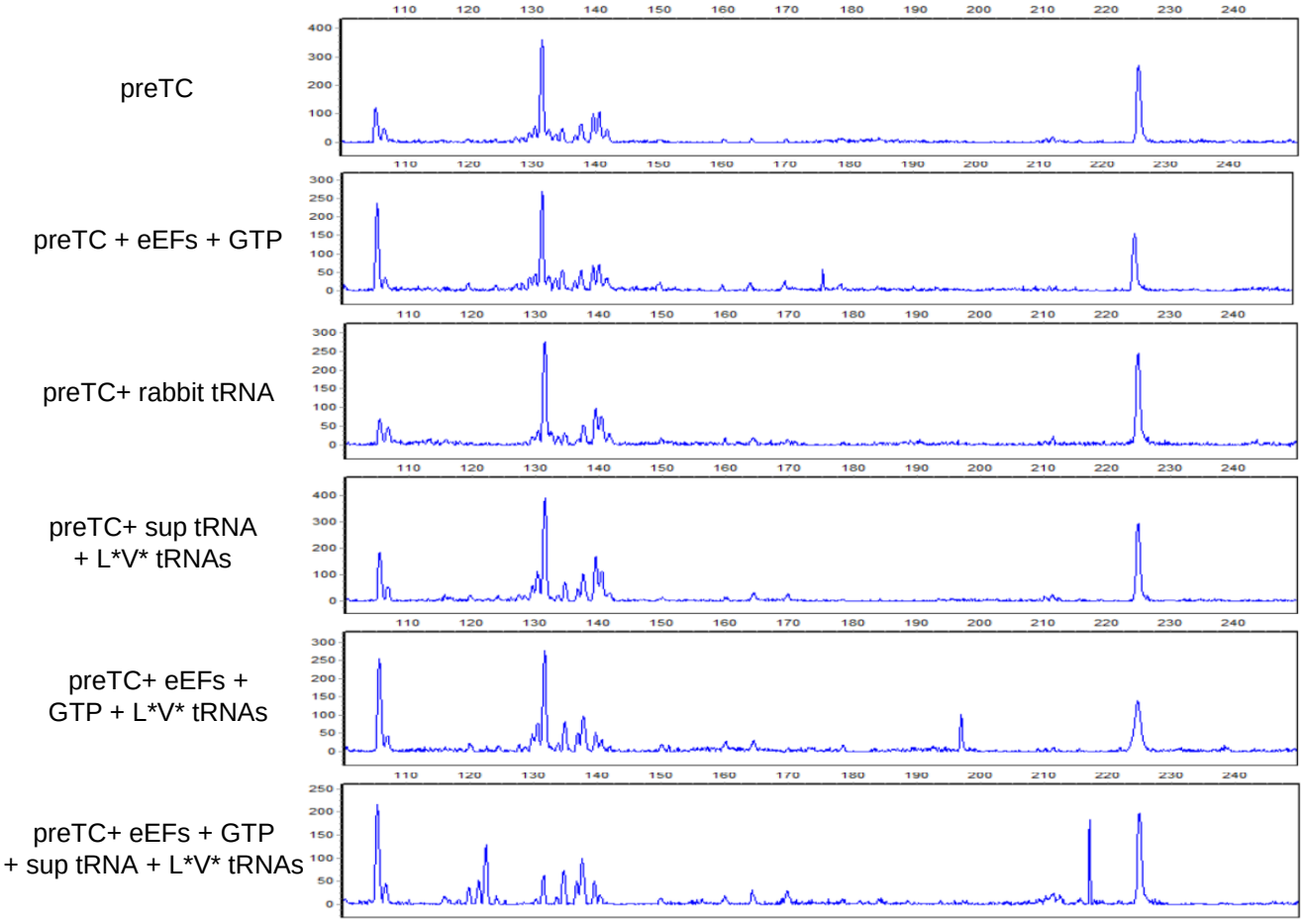


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S1

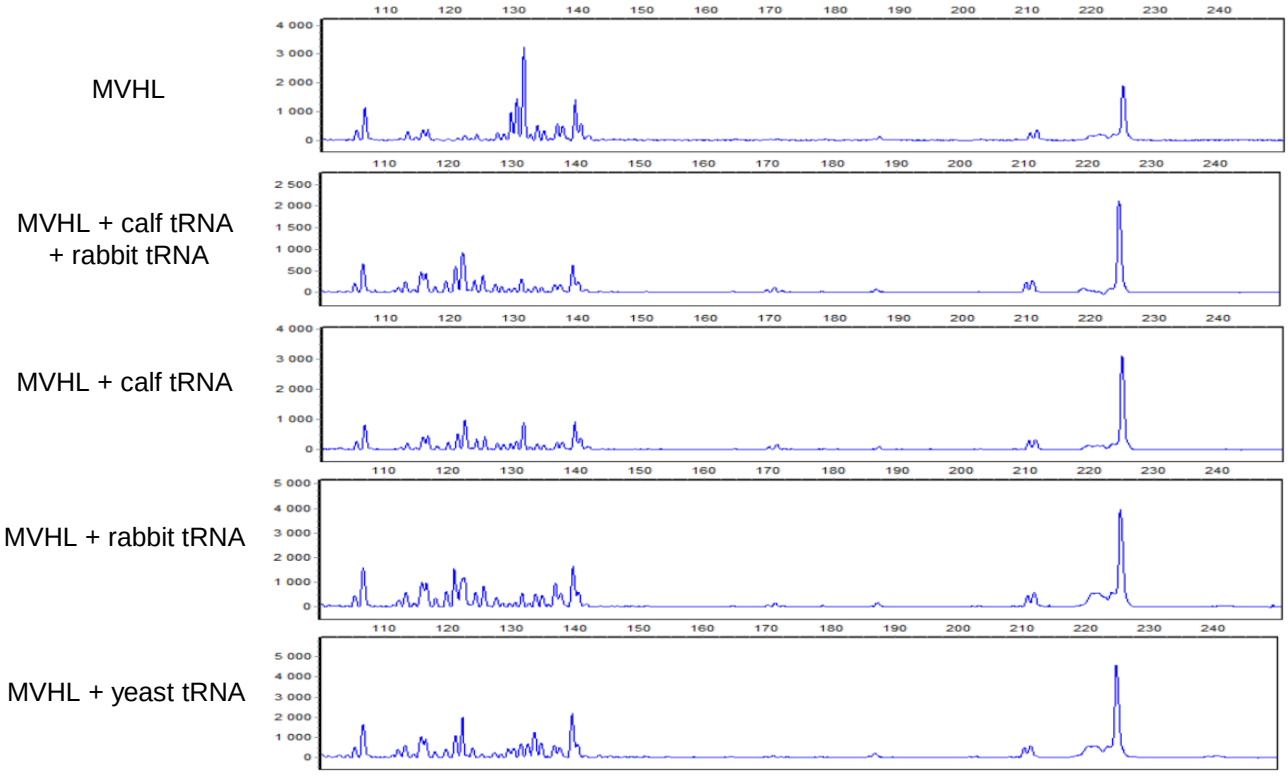


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S2 (MVHL)

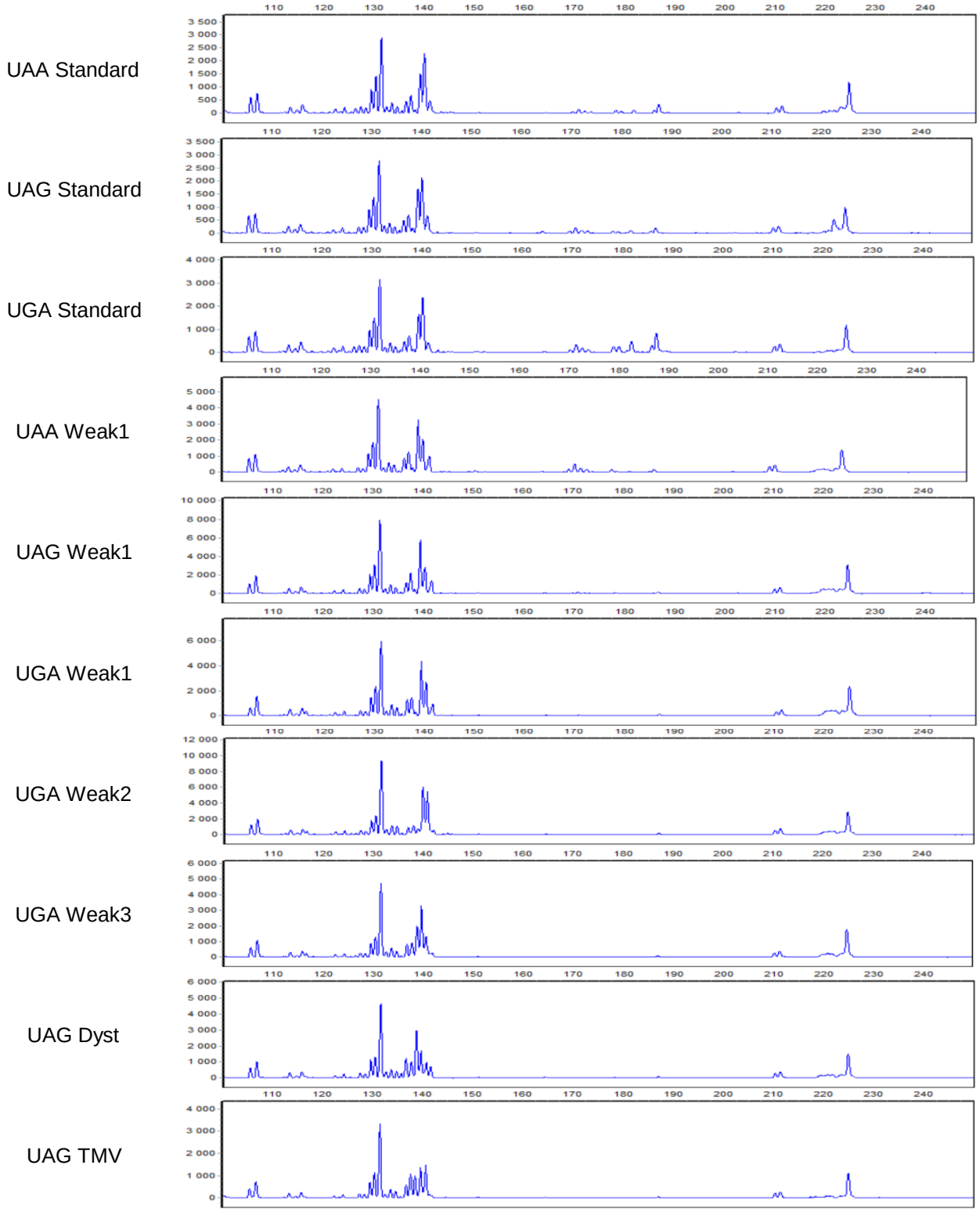


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S2 (MVHL+rabbit tRNA)

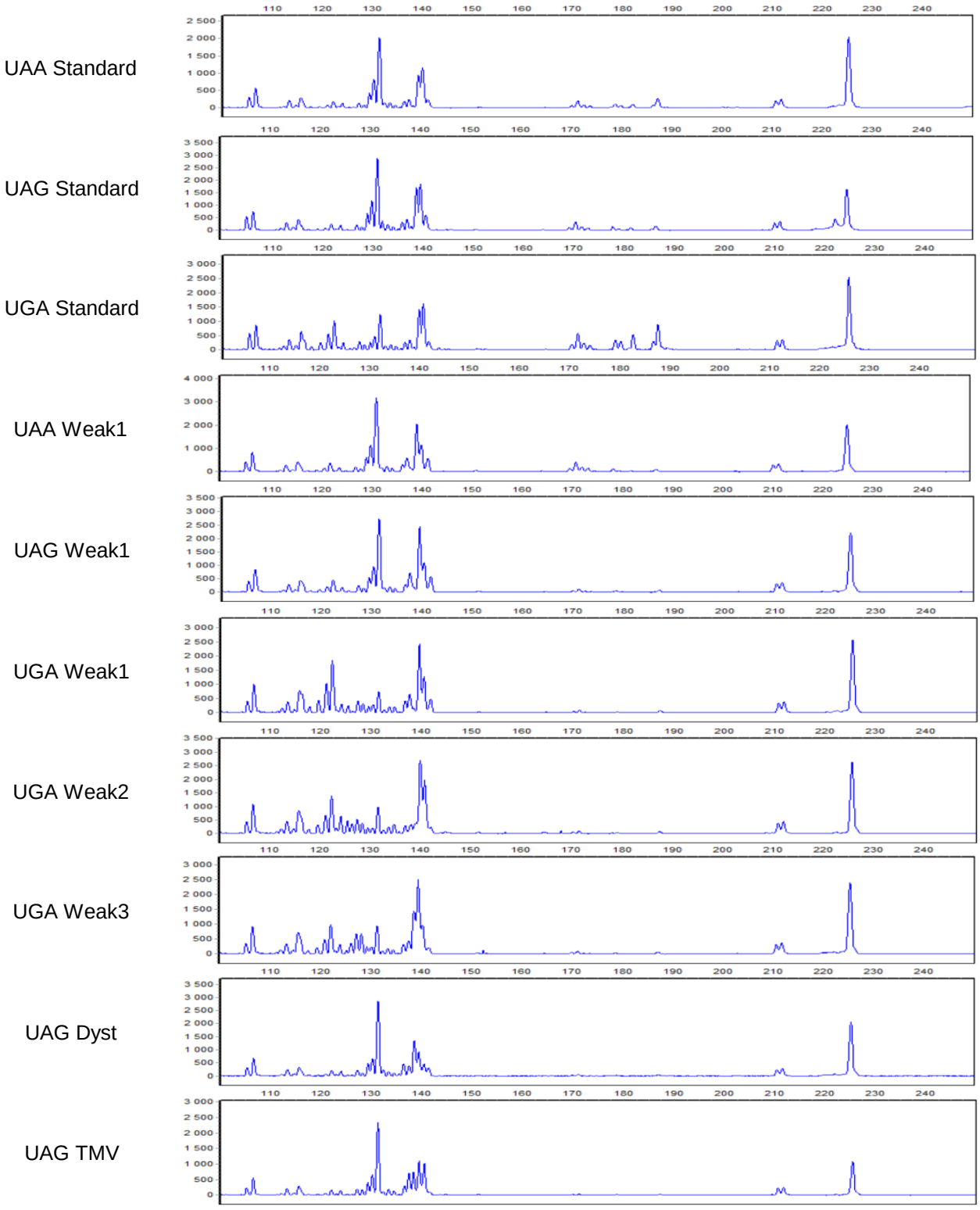


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S3 (MVHL)

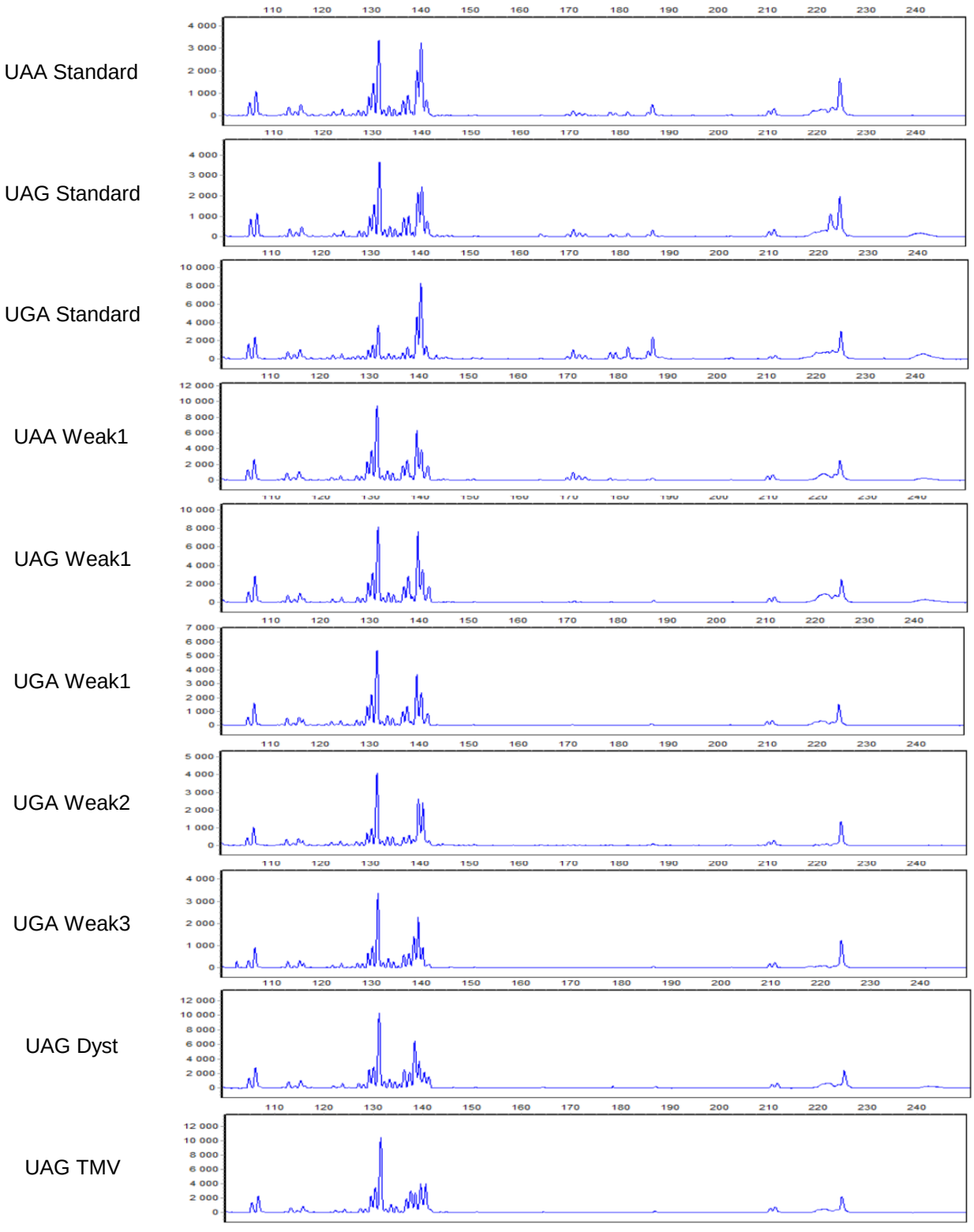


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S3 (MVHL+eRF1+eRF3)

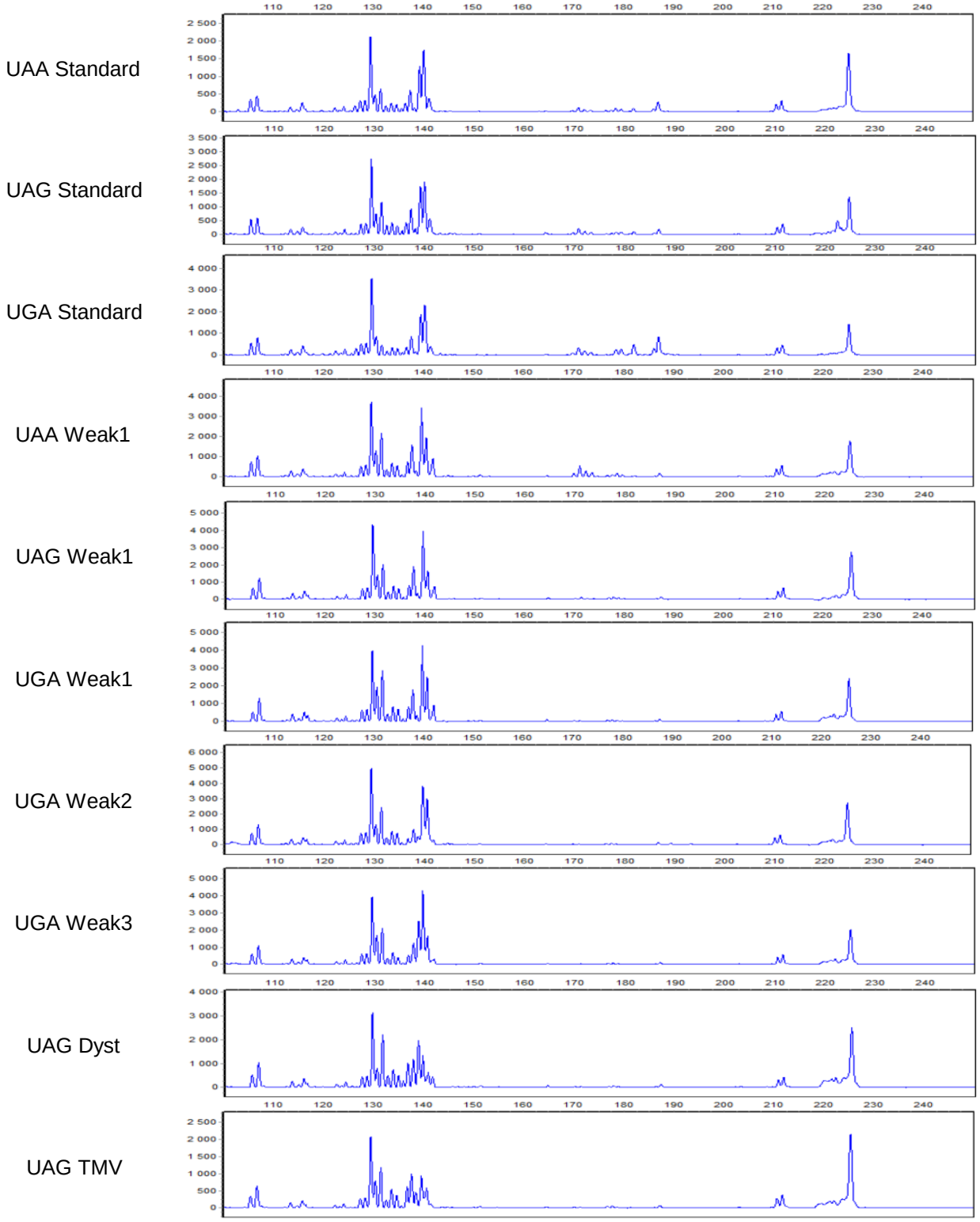


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S3 (MVHL+rabbit tRNA)

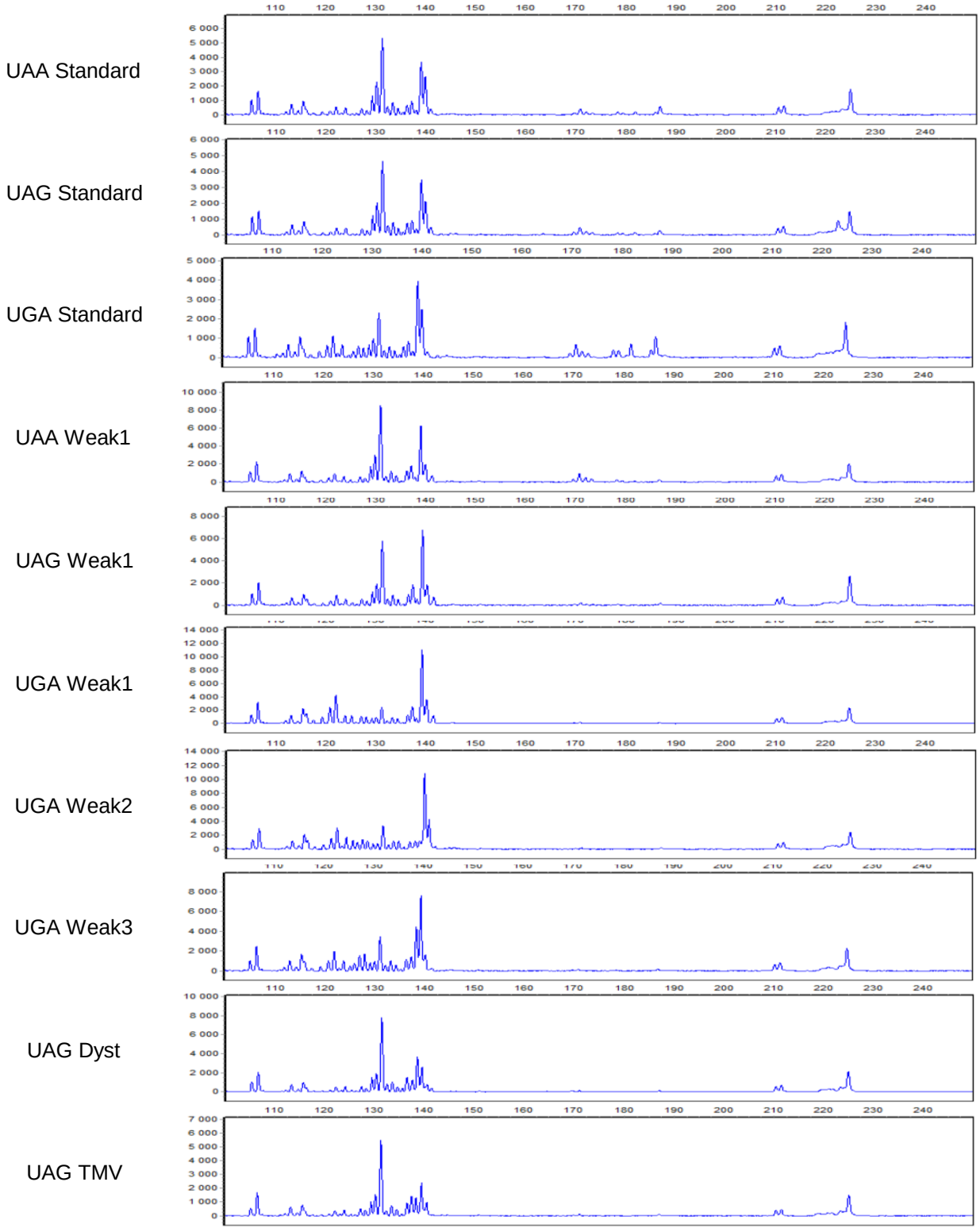


Figure S4. Examples of raw data for all toe-printing experiments.

Raw data for Fig S3 (MVHL+rabbit tRNA+eRF1+eRF3)

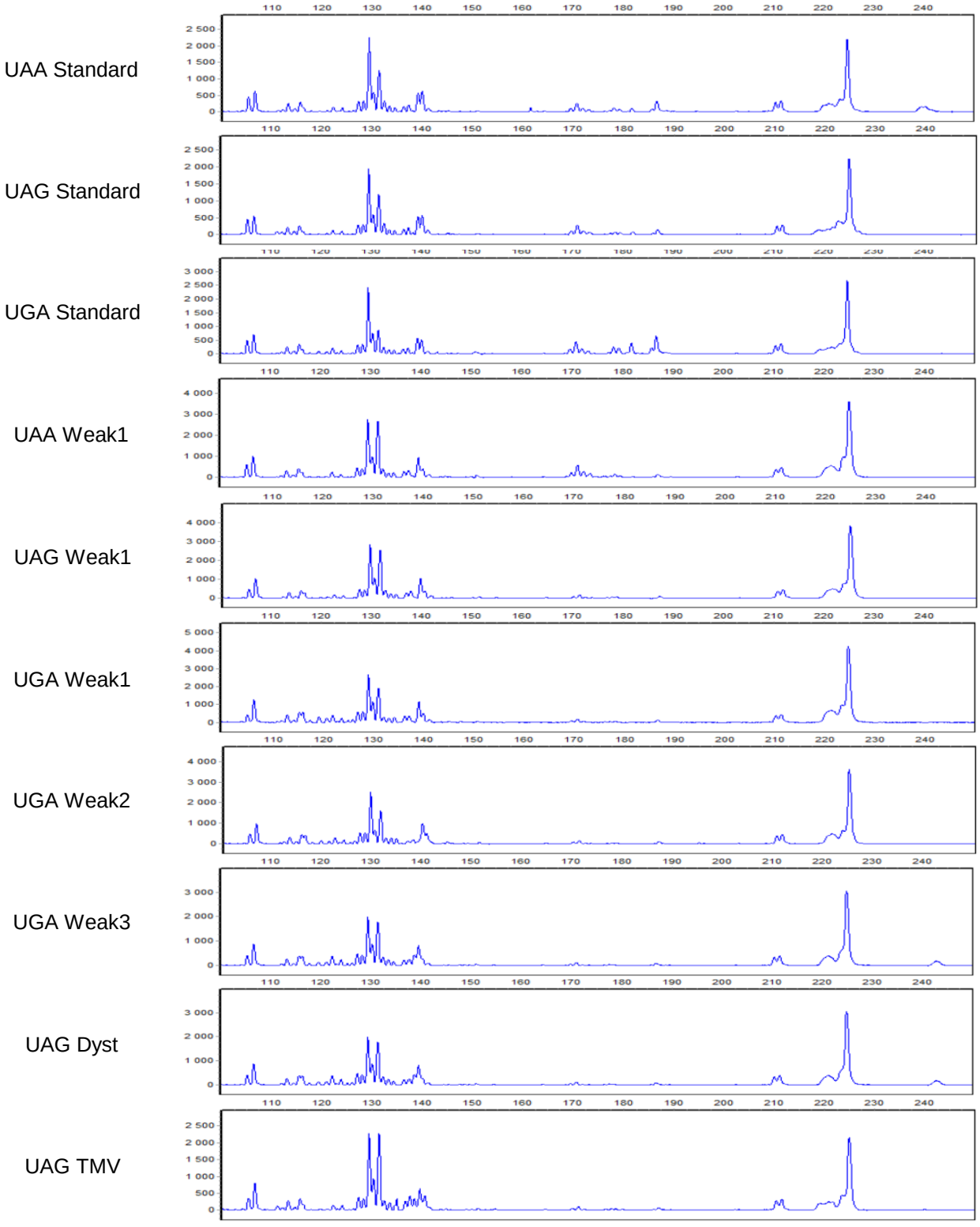


Figure S4. Examples of raw data for all toe-printing experiments.

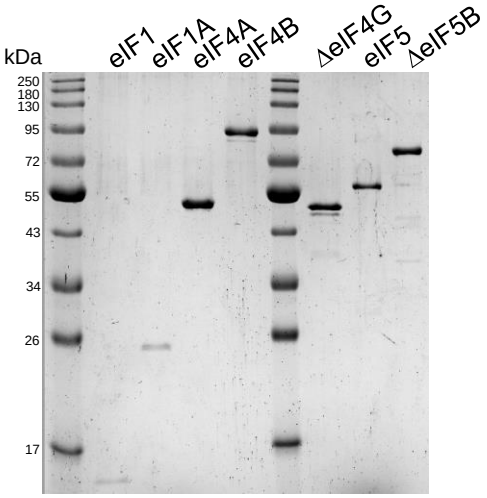
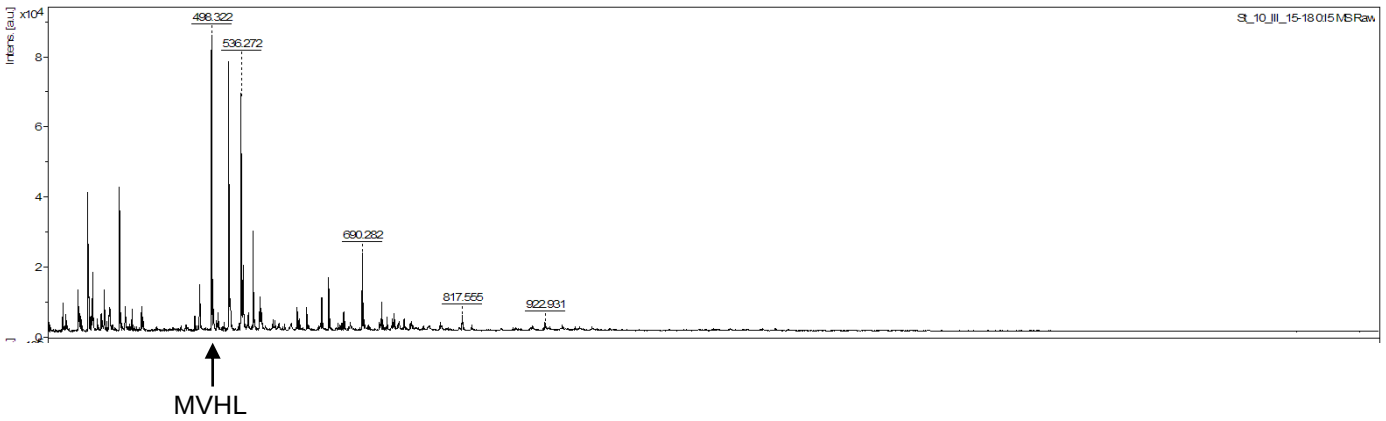
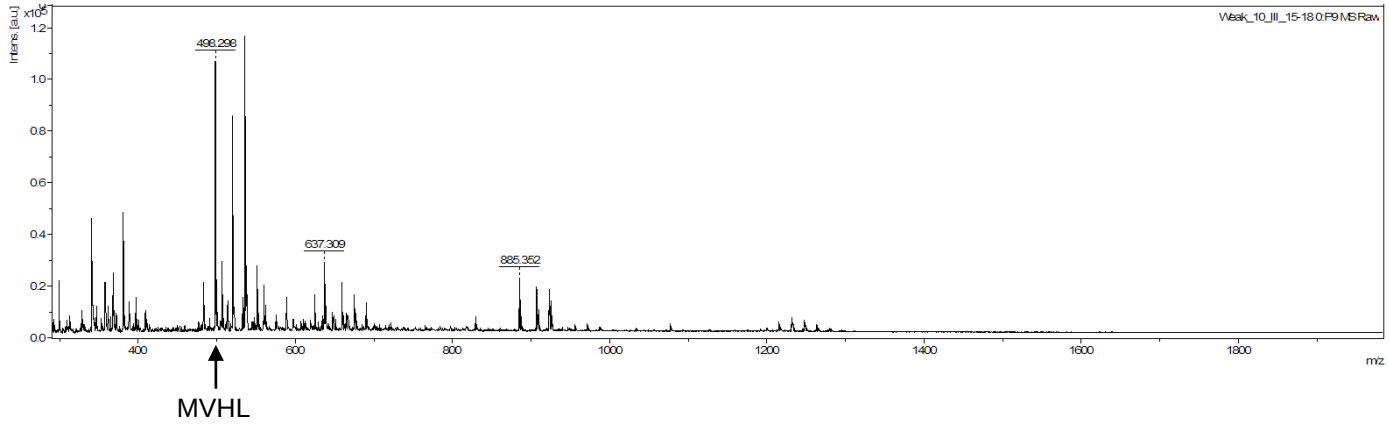


Figure S5. SDS-PAAG electrophoresis of recombinant eIFs used in the reconstituted eukaryotic translation system.

UAA Standard (peak 1)



UGA Weak1 (peak 1)



UGA Weak 1 (peak 2)

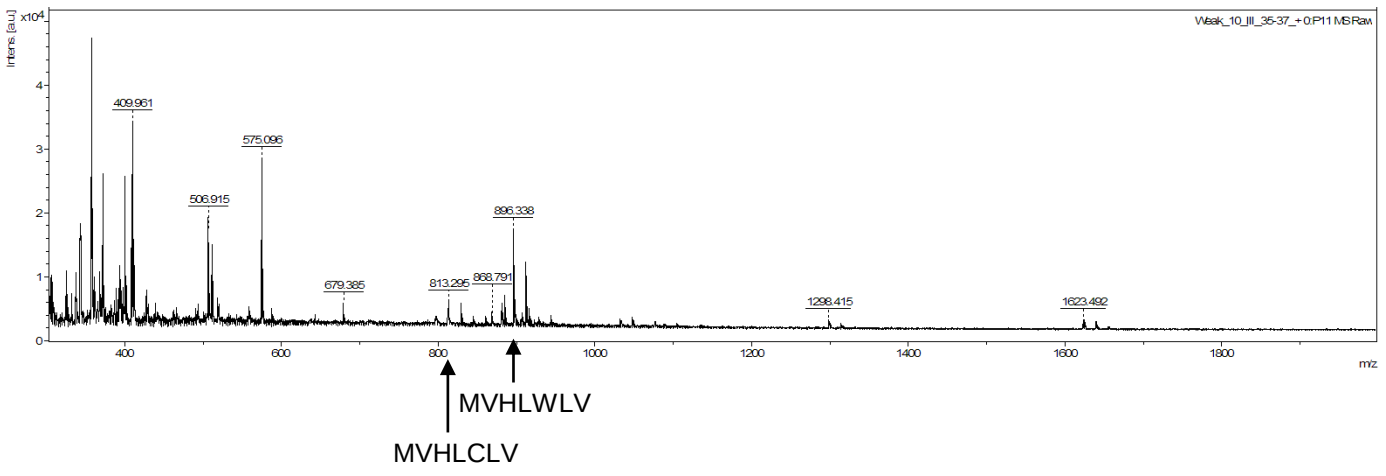
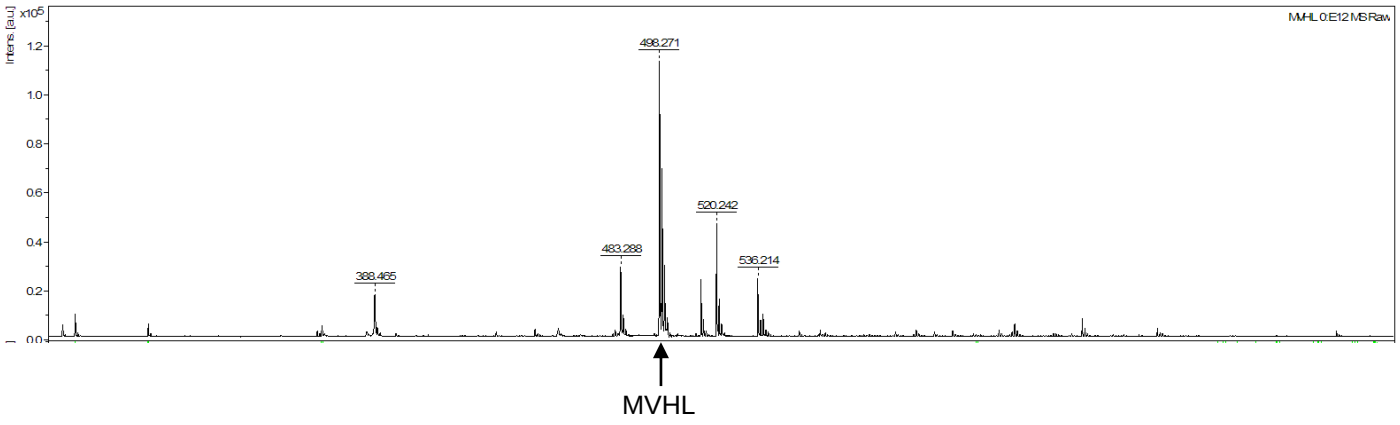
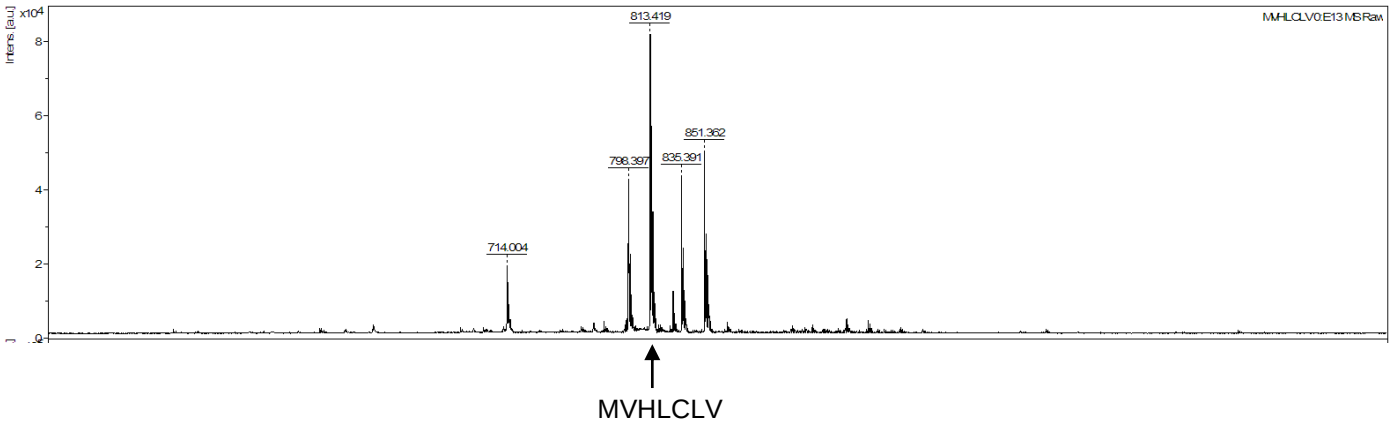


Figure S6. Raw data of MALDI-TOF MS of samples obtained in the radio RP-HPLC. The black arrows mark the peak corresponding to desired peptides.

MVHL peptide



MVHLCLV peptide



MVHLWLV peptide

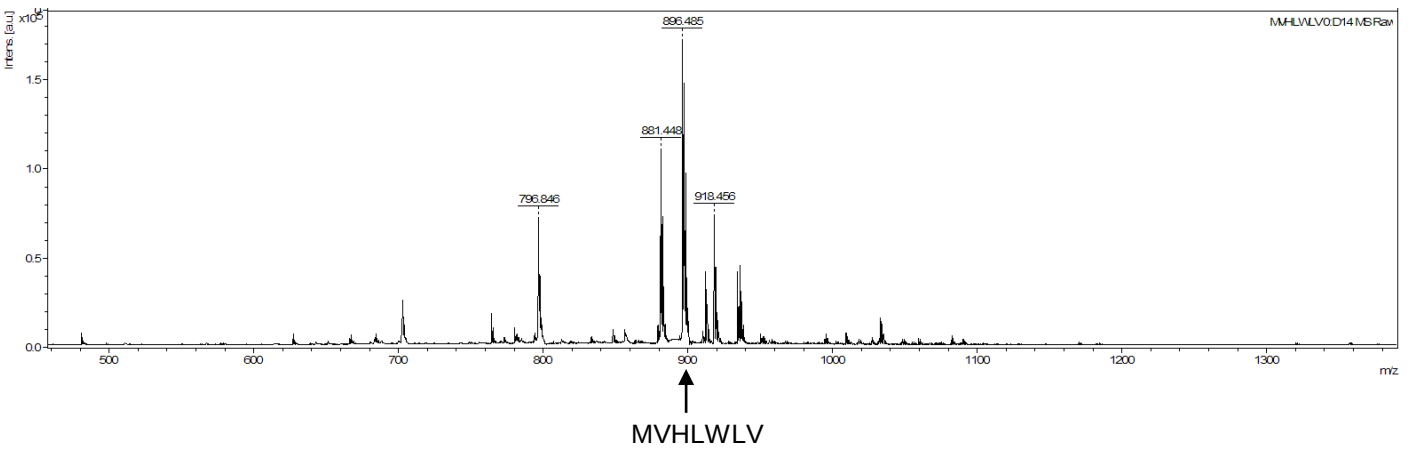


Figure S7. Raw data of MALDI-TOF MS of commercially synthesized MVHL, MVHLCLV and MVHLWLV tetra- and heptapepides. The black arrows mark the peak corresponding to desired peptide.