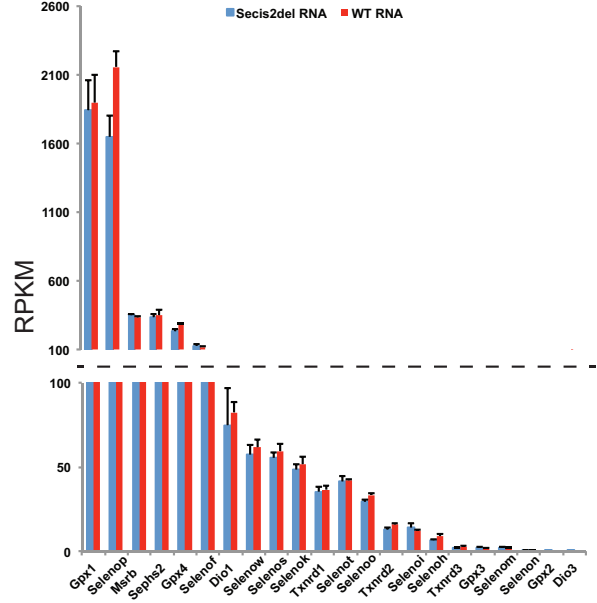
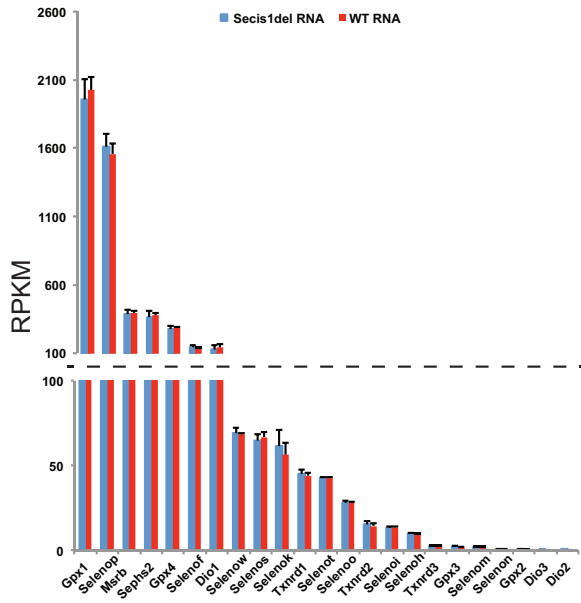


Title	Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P
Authors	Mariotti, Marco;Shetty, Sumangala;Baird, Lisa;Wu, Sen;Loughran, Gary;Copeland, Paul R.;Atkins, John F.;Howard, Michael T.
Publication date	2017
Original Citation	Mariotti, M., Shetty, S., Baird, L., Wu, S., Loughran, G., Copeland, P. R., Atkins, J. F. and Howard, M. T. (2017) 'Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P', Nucleic Acids Research, 45(22), pp. 13004-13015. doi: 10.1093/nar/gkx982
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://academic.oup.com/nar/article/45/22/13004/4561653 - 10.1093/nar/gkx982
Rights	© 2017, the authors . Published by Oxford University Press on behalf of Nucleic Acids Research. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by-nc/4.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com - http://creativecommons.org/licenses/by-nc/4.0/
Download date	2023-10-02 07:31:57
Item downloaded from	https://hdl.handle.net/10468/5387

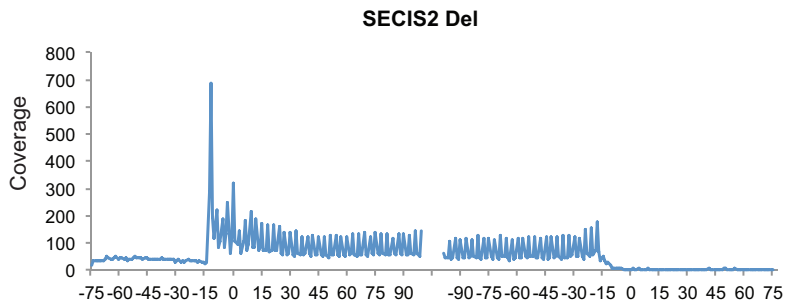
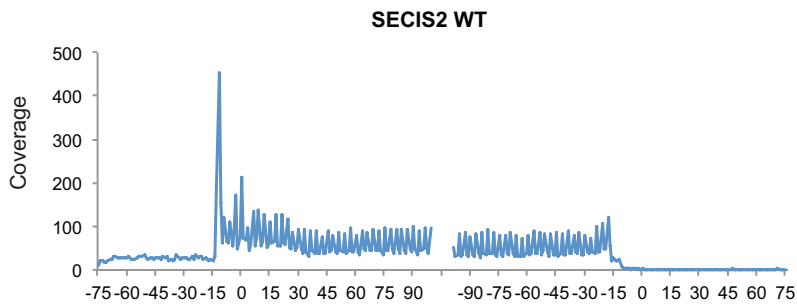
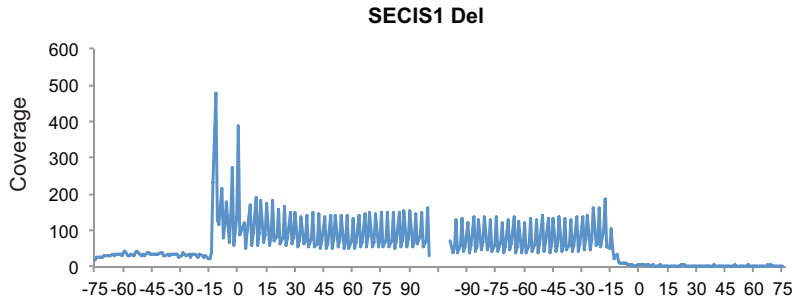
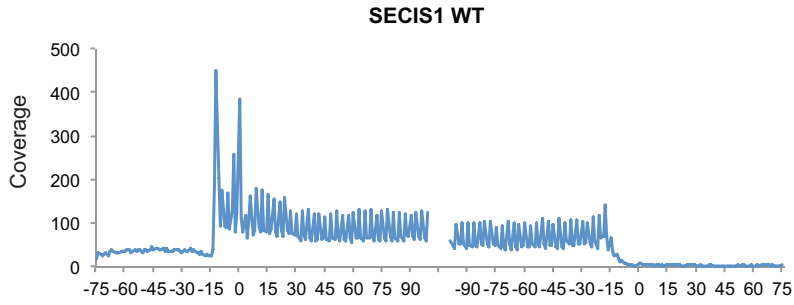


UCC

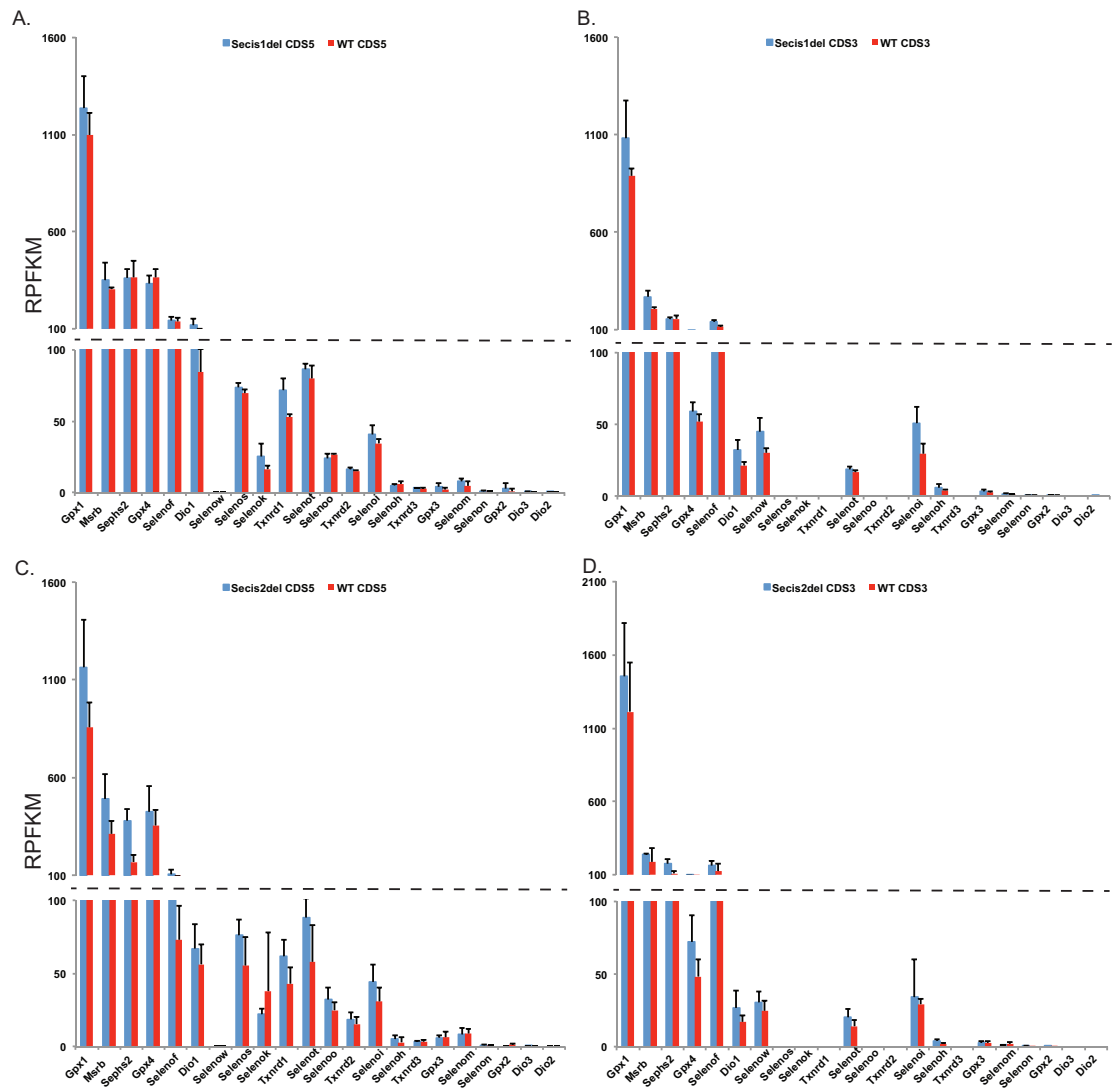
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh



Supplementary Material S3. RNA-Seq data for all selenoproteins in wild type (WT) and SECIS deletion liver samples. RNA levels are expressed as reads per kilo base per million mapped reads (RPKM).



Supplementary Material S4. Ribosome profiling coverage (5' ends) mapped across RefSeq mRNAs from -75 to +90 relative to the annotated start codons (position 0 left) and stop codons (position 0 right). Peaks across the coding sequence are 3 nts apart indicating footprints reflect the 1 codon step size of translating ribosomes.



Supplementary Material S5. Ribosome profiling of liver selenoproteins excluding *Selenop*. A) Ribosome footprint (RPF) reads per kilo base per million mapped reads (RPFKM) for each selenoprotein upstream (CDS5) is shown for wild type (WT) and SECIS1 deleted (Secis1del) samples are shown. B) Same as A for RPKMs downstream of the UGA codon (CDS3). C) Same as A for wild type (WT) and SECIS2 deleted samples (Secis2del). D) Same as B for wild type (WT) and SECIS2 deleted samples (Secis2del).