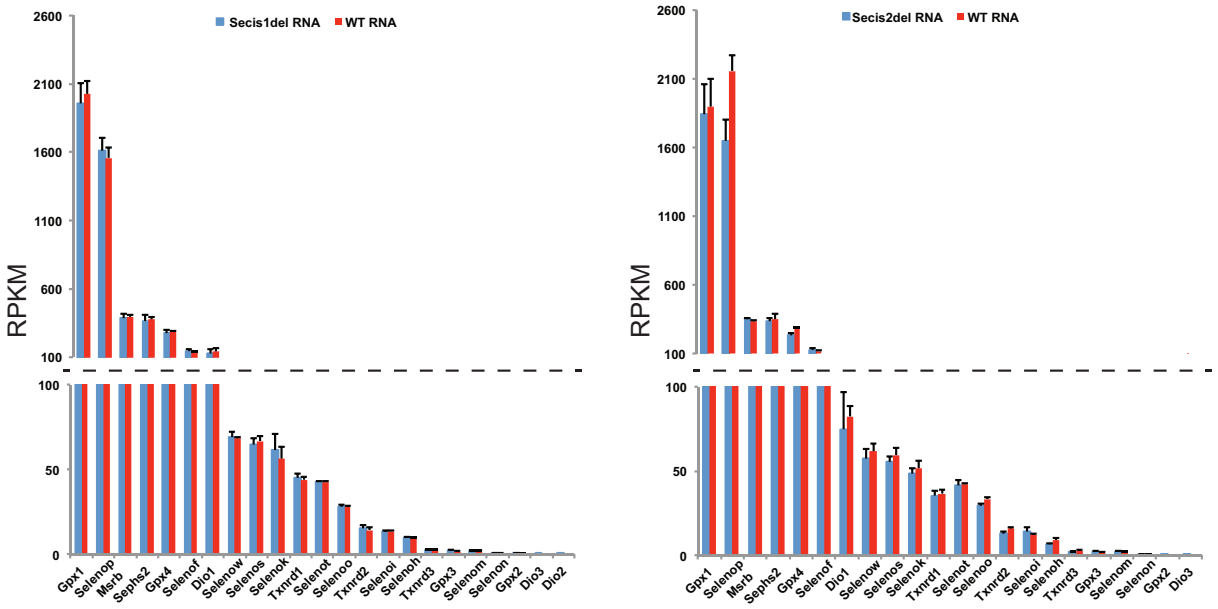
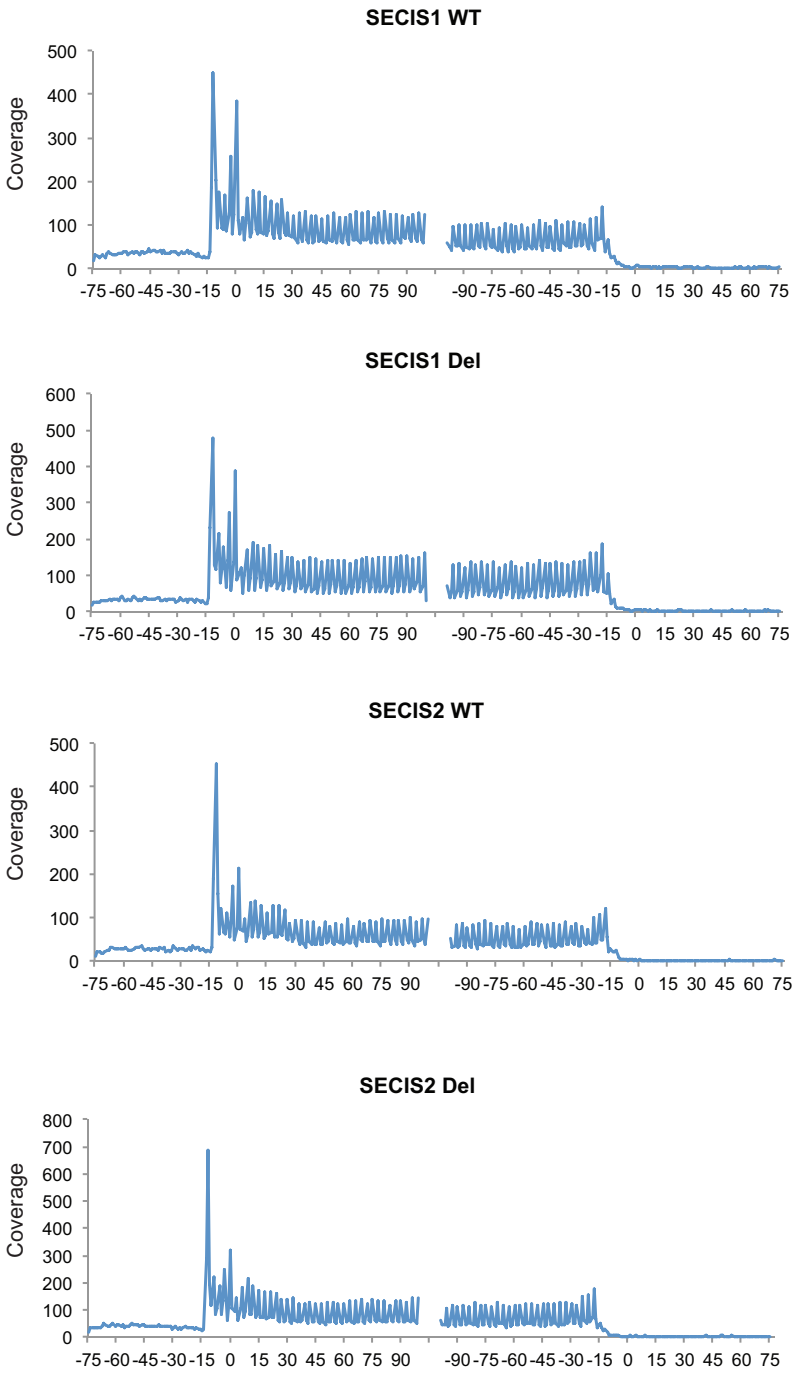
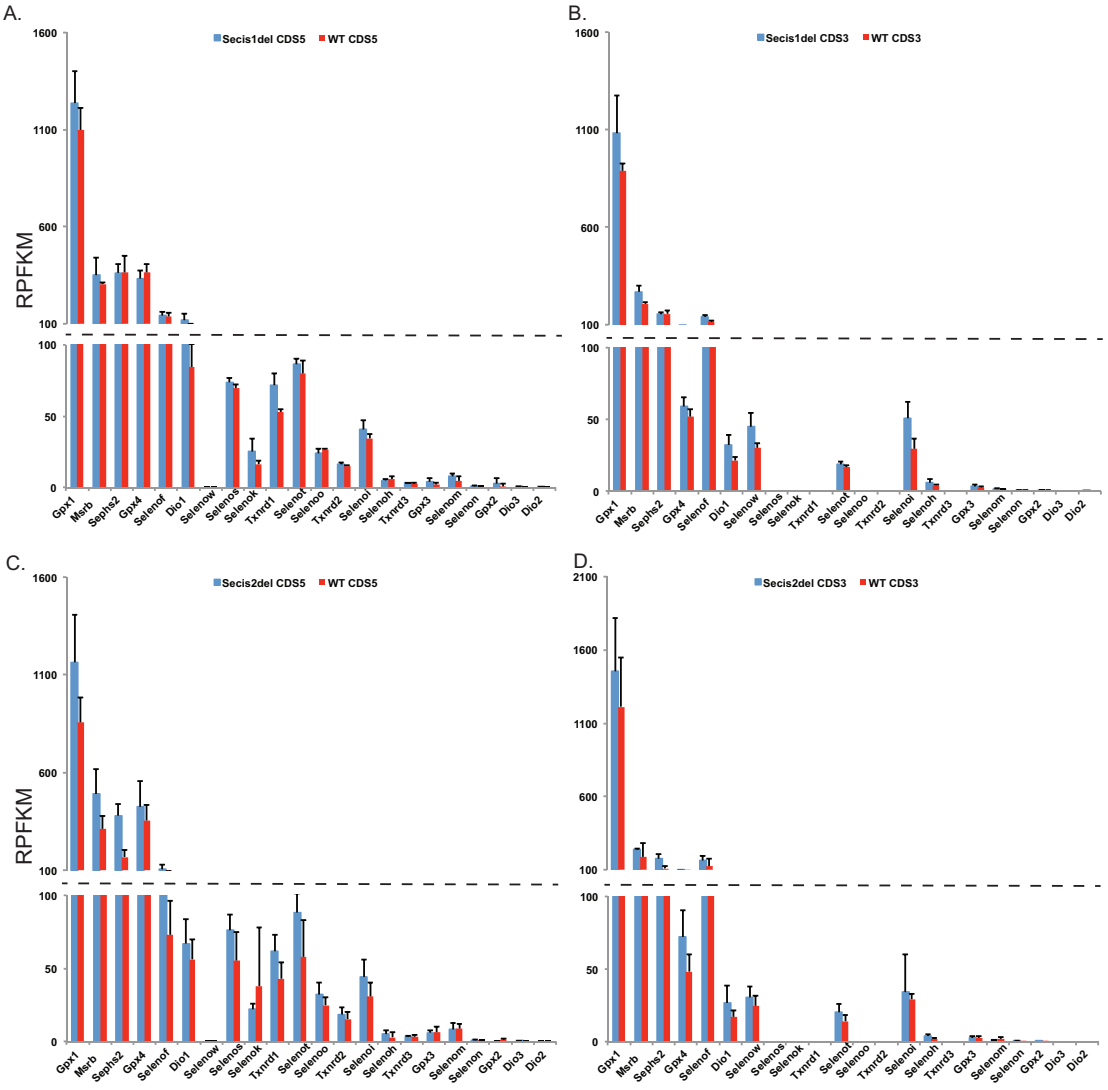


Supplementary Material S3. RNA-Seq data for all selenoproteins in wild type (WT) and SECIS deletion liver samples. RNA levels are expressed as reads per kilo base per million mapped reads (RPKM).



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 RPFKMs 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).