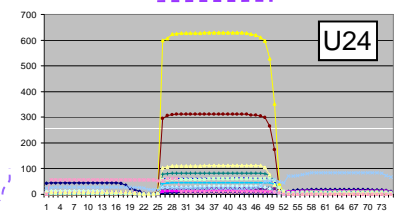
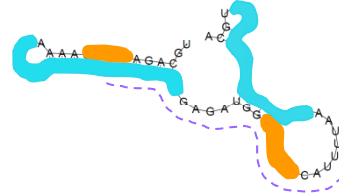
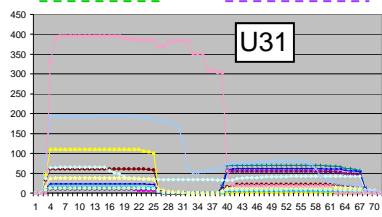
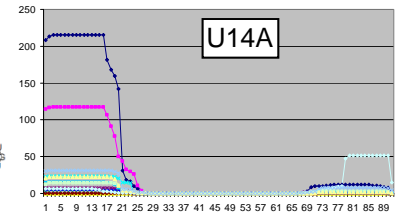
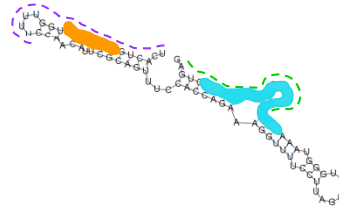
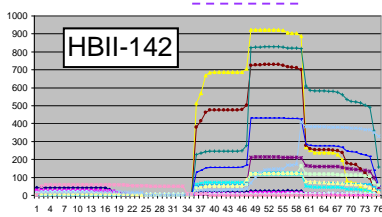
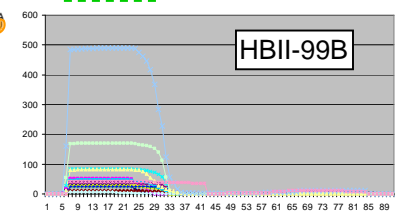
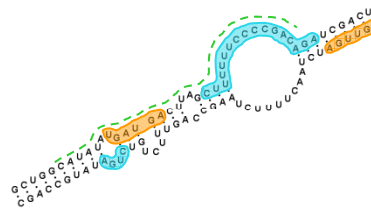
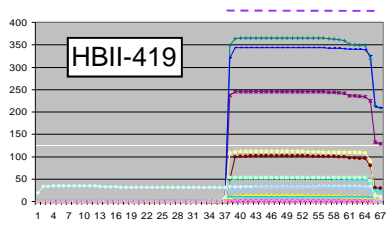


Supplementary Figure legends

Supplementary Figure 1: Accumulation profiles of snoRNAs and their predicted secondary structure. The accumulation profiles of a subset of box C/D snoRNAs from Figure 4A in the main text are shown again, but accompanied with predicted secondary structures of the full-length molecules. As in Figure 4 in the main text, the x axis on all graphs represents residue positions in the full-length (precursor) molecule. The y axis represents the number of smaller fragments detected, normalized by counts per million reads mapped, that contain a specific residue in the full-length molecule. The dashed lines above the graphs correspond to a dashed line of matching color in the predicted structure, indicating the position of the sdRNA in the structure.

Supplementary Figures 2-6: Detection of endogenous sdRNA fragments by RNase protection assays. The fragments processed from the box C/D snoRNAs U24 (Supp Figure 2), U31 (Supp Figure 3), HBII-142 (Supp Figure 4), HBII-419 (Supp Figure 5) and HBII-99B (Supp Figure 6) as identified by deep-sequencing were compared to endogenous sdRNAs detected by RNase A/T1 protection assays. In panel A of these figures, the distribution of fragment lengths obtained by deep sequencing in the HepG2 (when available), THP-1, HL60 and K562 cell lines is shown. In panel B of these figures, endogenous sdRNA fragments are detected by RNase A/T1 protection assay in the HepG2, THP-1, HL60 and K562 cell lines. As a control for the RNase protection assays, the diluted anti-sense probe against U14A was loaded without RNase digestion (Probe lane). For each cell line, the probes were incubated with increasing amounts of total RNA (0 μ g, 1 μ g, 5 μ g, 10 μ g respectively for lanes 2-5, and for lanes 6-9). Both the mature snoRNAs (arrow) and shorter fragments (arrow heads) were protected from RNase A/T1 digestion. Purple, blue and red arrow heads identify protected fragments found only in the HepG2, THP-1 and HL60 cell lines respectively.

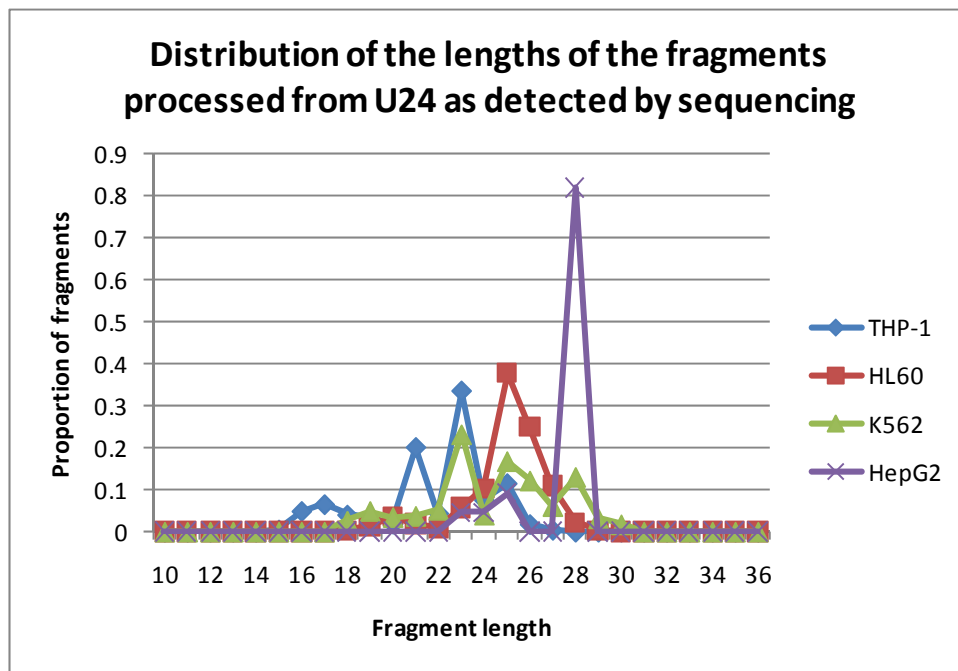
Supplementary Figure 1



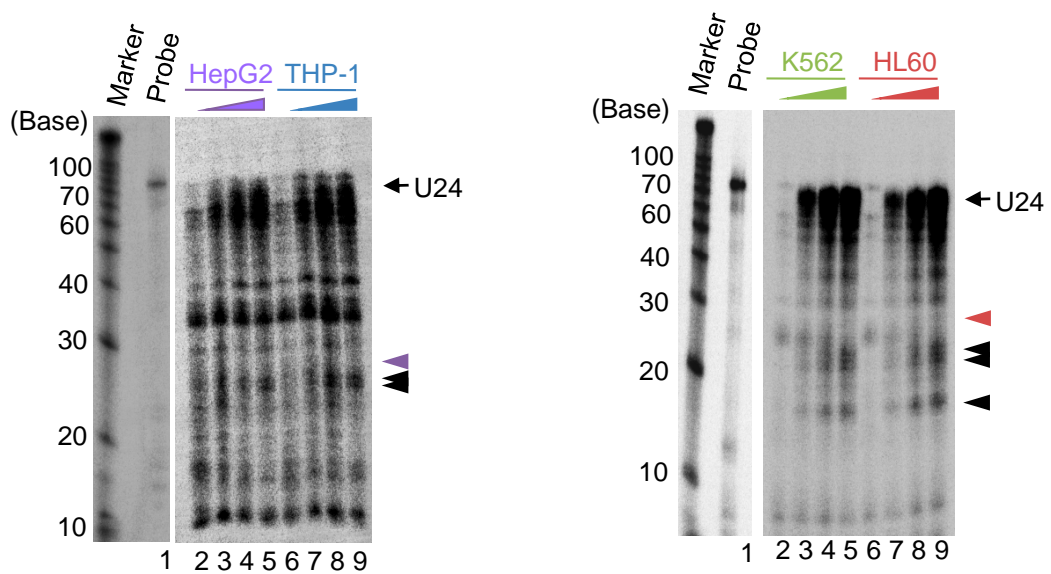
- ◆ hESC
- EB
- ▲ memory B cell
- × centroblast
- ✱ centrocyte
- naive B cell
- + plasma cell
- pre-germinal centre B cell
- NPC 5-8F
- ◆ THP-1
- ◆ HL60
- ◆ PBMC
- ◆ K562
- ✱ HepG2

Supplementary Figure 2

A

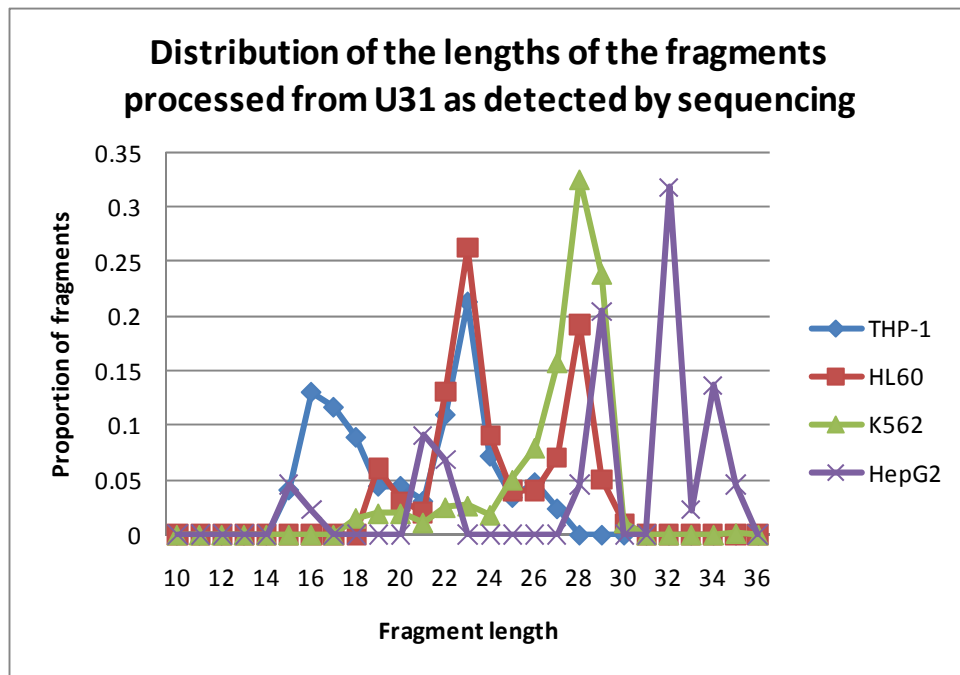


B

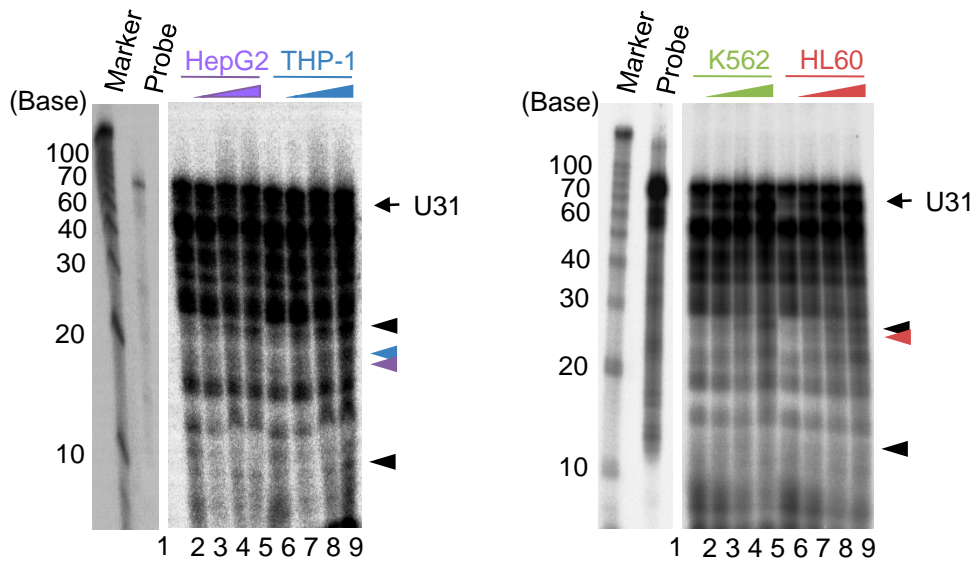


Supplementary Figure 3

A

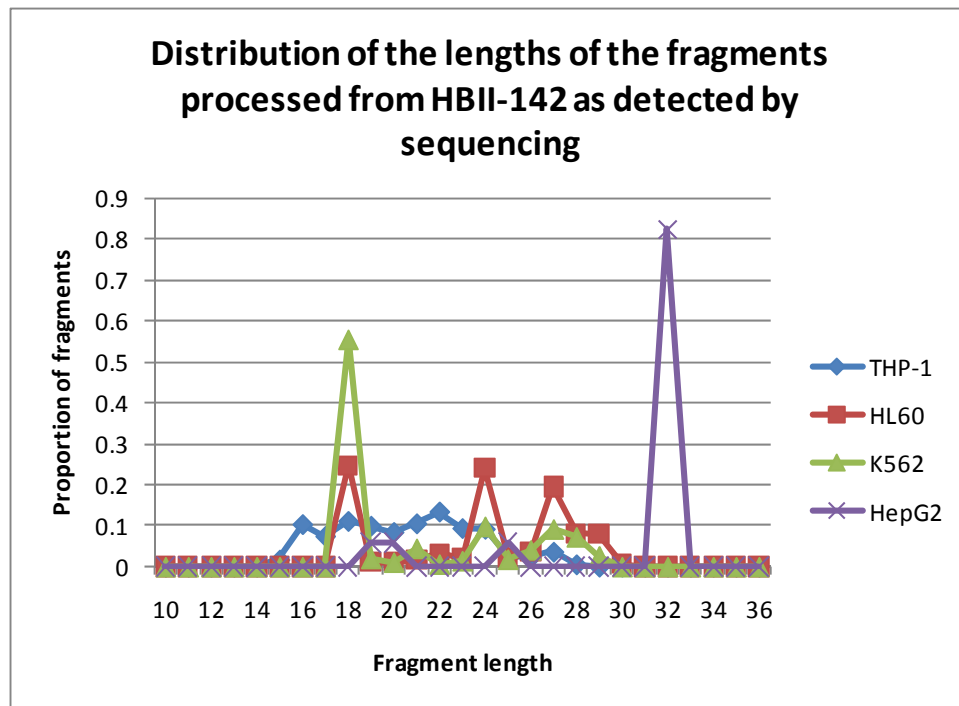


B

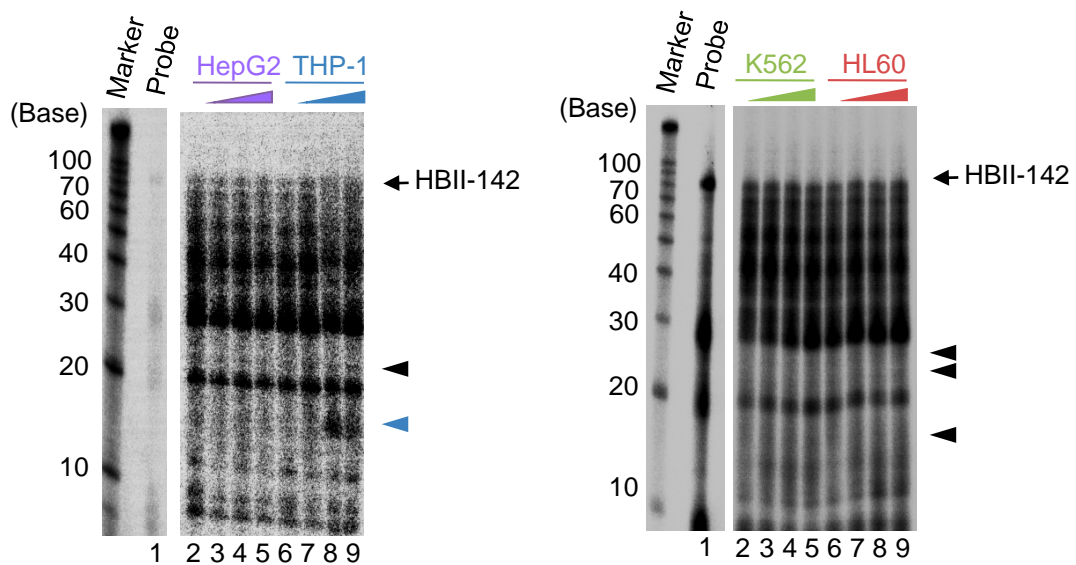


Supplementary Figure 4

A

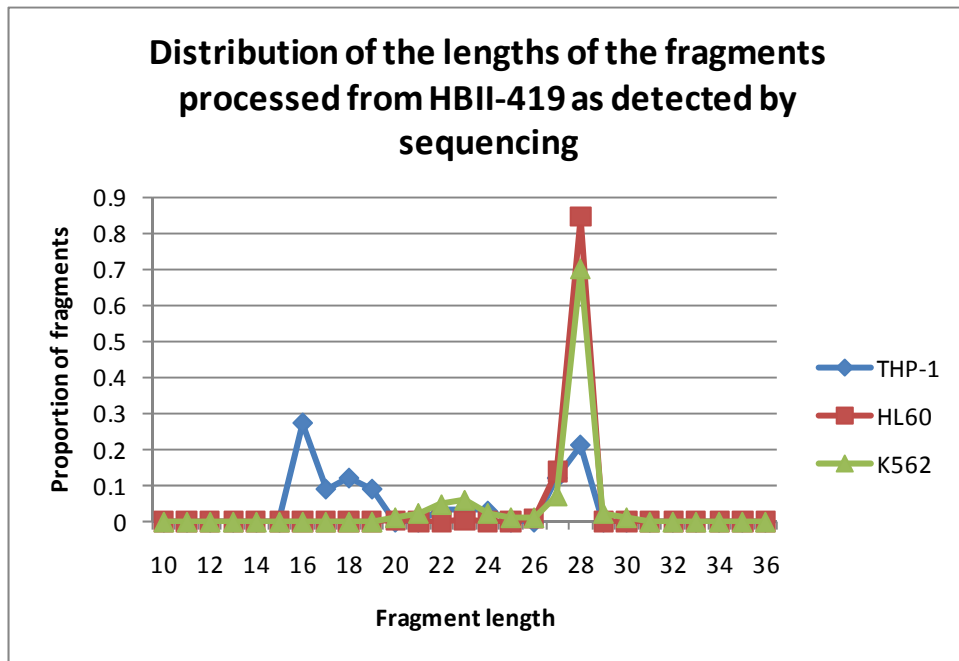


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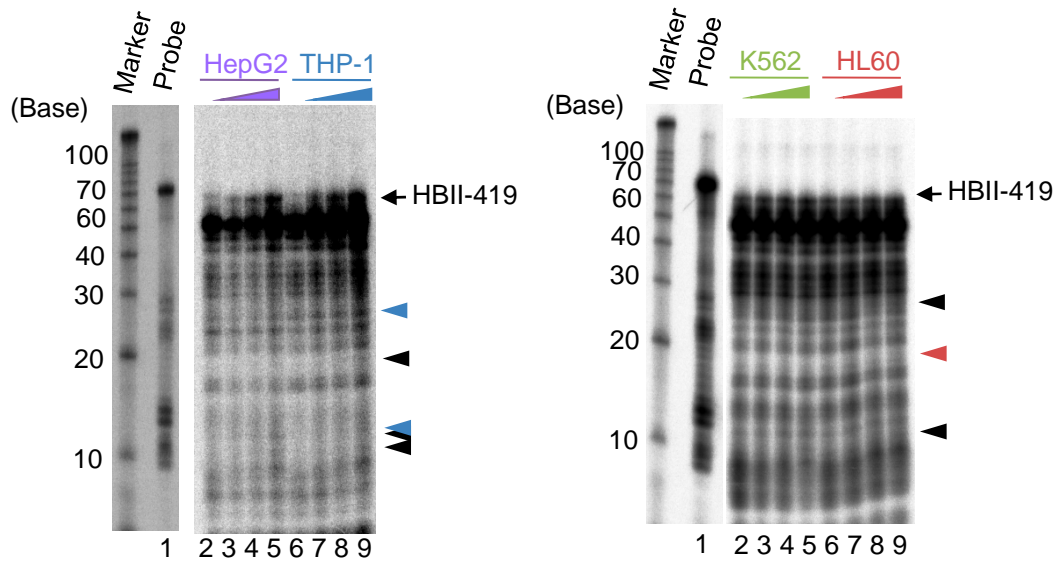


Supplementary Figure 5

A

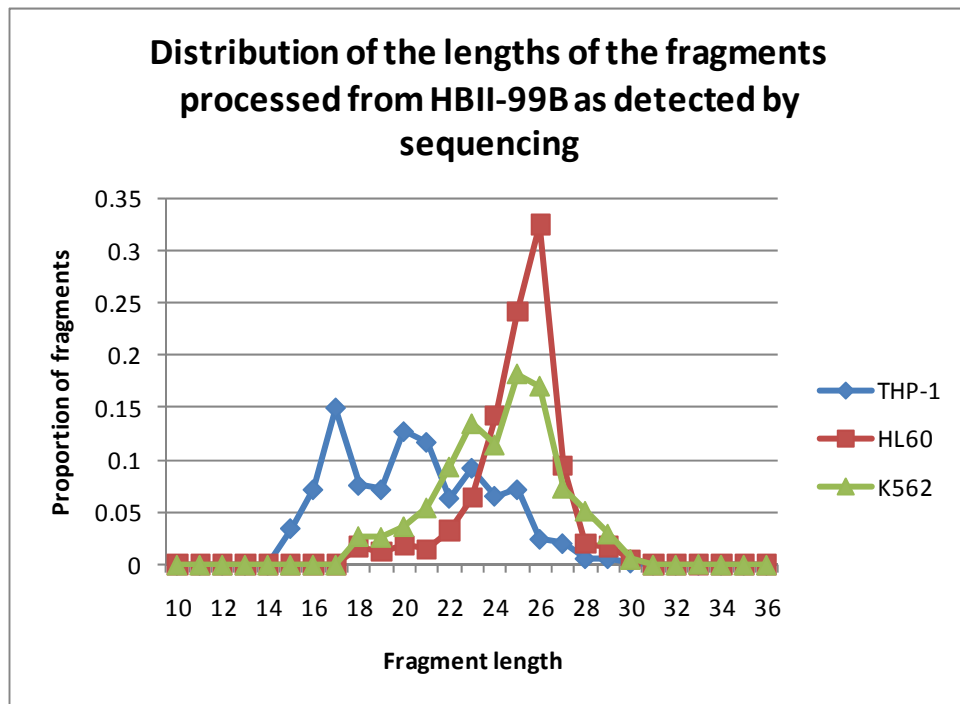


B



Supplementary Figure 6

A



B

