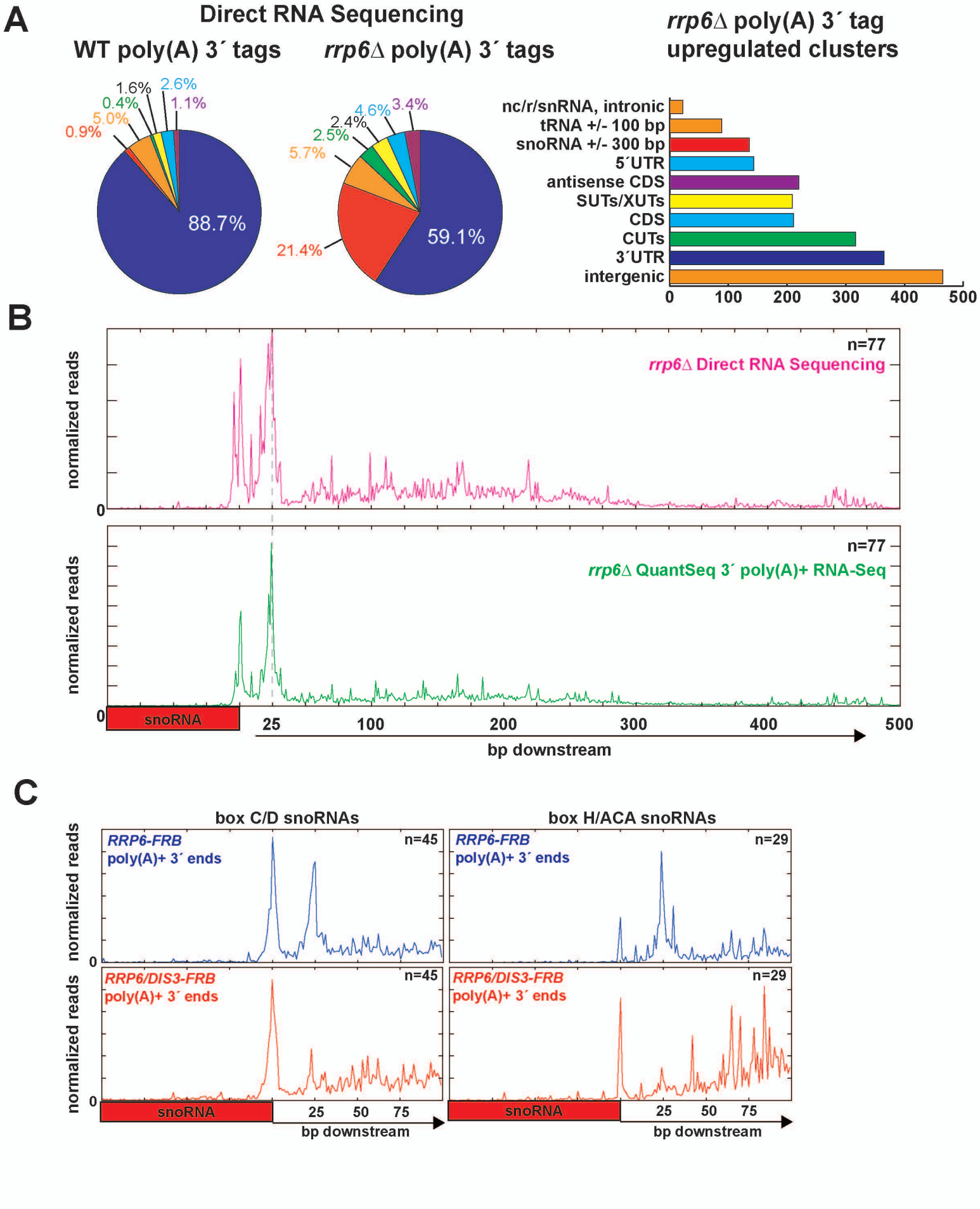
Roy_et_al_Supplemental_Fig.S1



Supplemental Figure S1. Comparison of different poly(A)+ 3´-end (PAT) sequencing methods for mapping snoRNA termination products and processing intermediates, Related to Figure 1

(A) Global distribution of poly(A)+ 3´-ends (PATs) in WT and *rrp6Δ* as profiled by direct RNA sequencing. 3´-ends were grouped by mass into the indicated regions (left pie charts). Genomic distribution of PAT clusters upregulated in *rrp6Δ* over WT cells (right panel). Upregulated PATs situated within 20 base pairs of one another were clustered together and grouped into the indicated regions according to the chromosomal coordinate of the cluster peak (see Methods).

(B) Meta-gene analysis for snoRNA downstream regions (as in Figure 2) on PATs in *rrp6Δ* as determined by Direct RNA Sequencing (Heliscope single-molecule sequencing, SeqLL, LLC) and with Illumina-based 3´-end poly(A)+ RNA sequencing (QuantSeq library prep kit, Lexogen GmbH).

(C) Meta-gene analysis for PATs in a 200 bp window centered on the mature 3´-ends of all snoRNAs. The top panels show PATs accumulating upon nuclear depletion of Rrp6p (*RRP6-FRB*), while the bottom panel shows PATs accumulating after nuclear depletion of both Rrp6p and Dis3p (*RRP6/DIS3-FRB*). The panels are further grouped into box C/D snoRNAs (left) and box H/ACA snoRNAs (right). Note that these panels show all snoRNAs, including those not terminated by the NNS pathway, while Figure 2 is restricted to those snoRNAs undergoing NNS termination (see Methods).