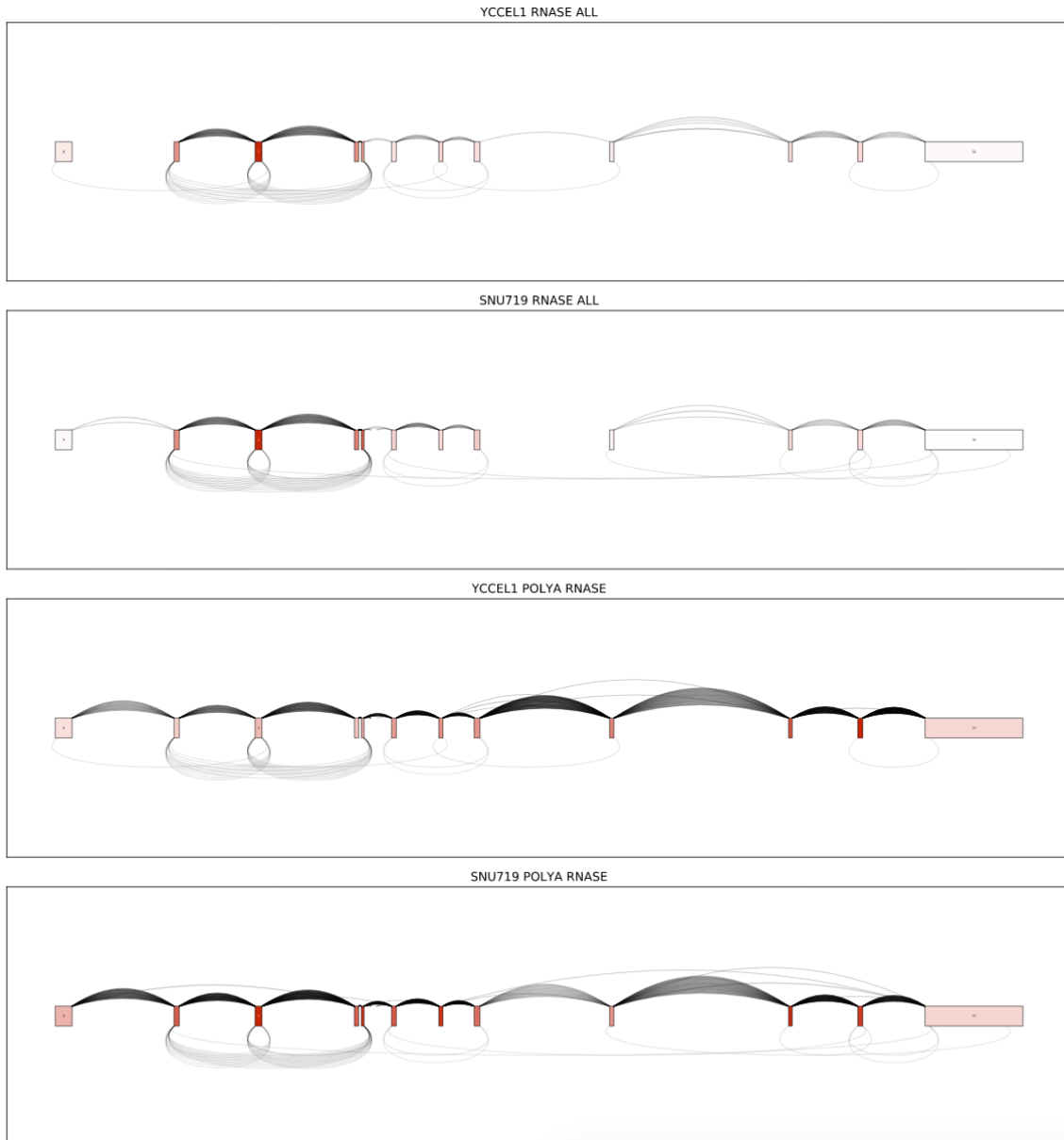


plotcirc

Minimum arguments: `-db -g/-t`

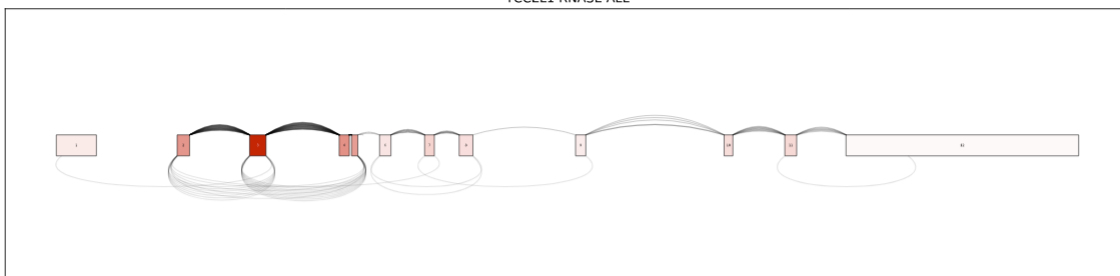


`cirplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17`

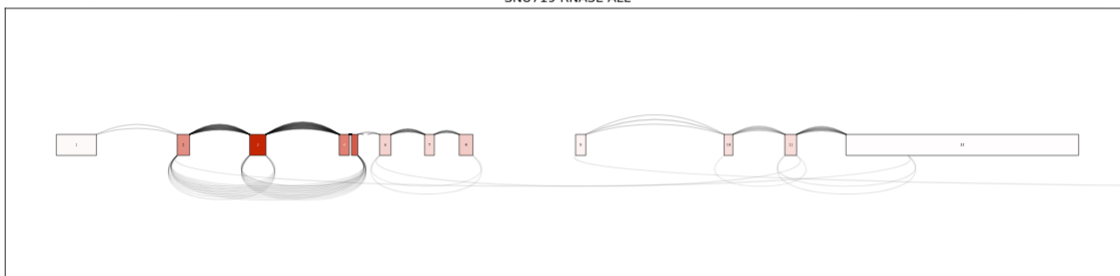
RNASE ALL: coverage, canonical and backsplice junctions from RNase R treated samples
POLYA RNASE: coverage and canonical junctions from Poly-A selected and backsplice junctions from RNase R treated samples

Scale introns: -is

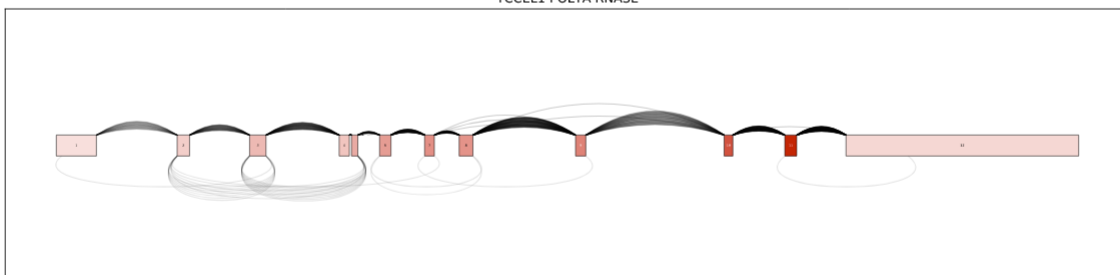
YCCEL1 RNASE ALL



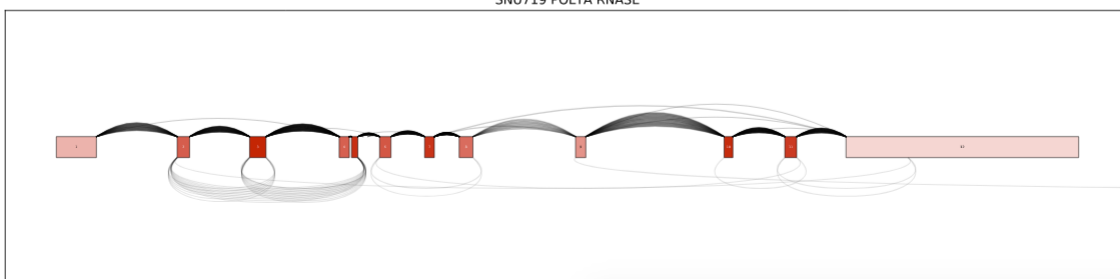
SNU719 RNASE ALL



YCCEL1 POLYA RNASE



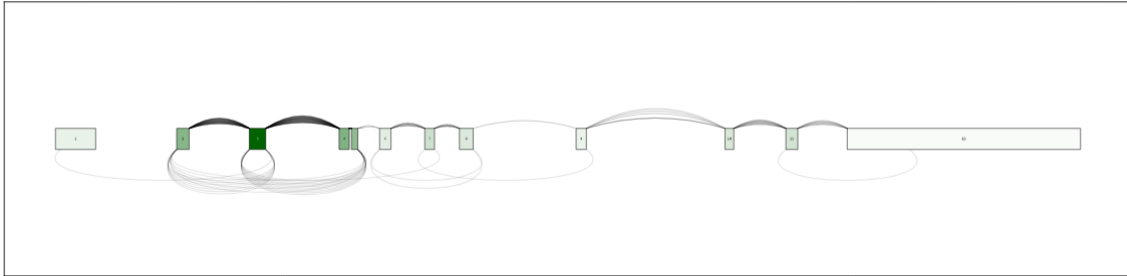
SNU719 POLYA RNASE



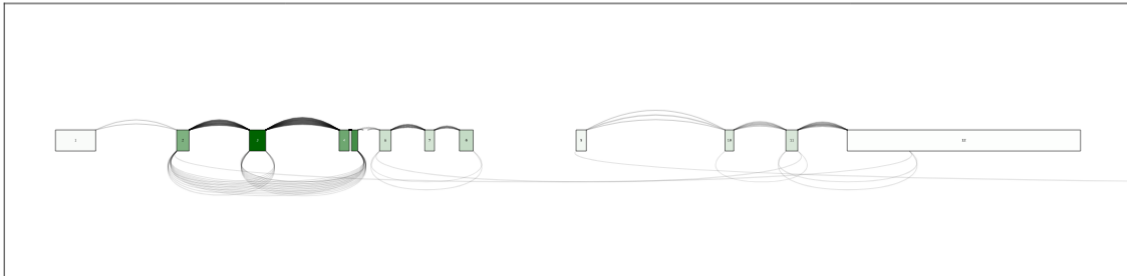
cirplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17 -is 3

Specify color: -c

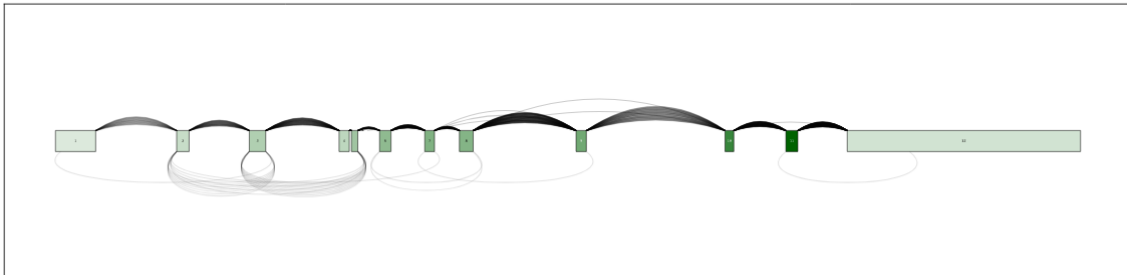
YCCEL1 RNASE ALL



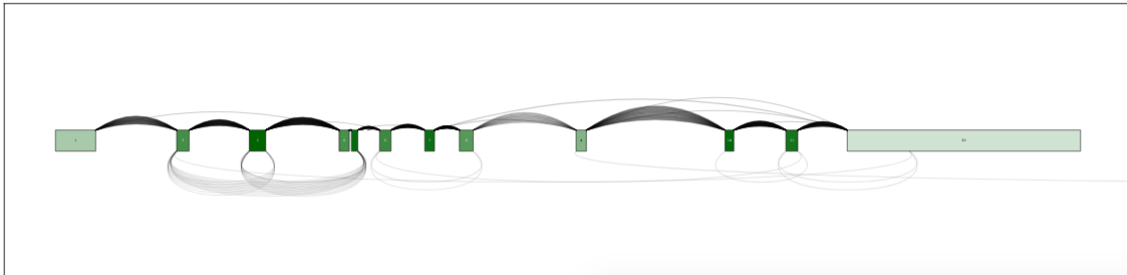
SNU719 RNASE ALL



YCCEL1 POLYA RNASE

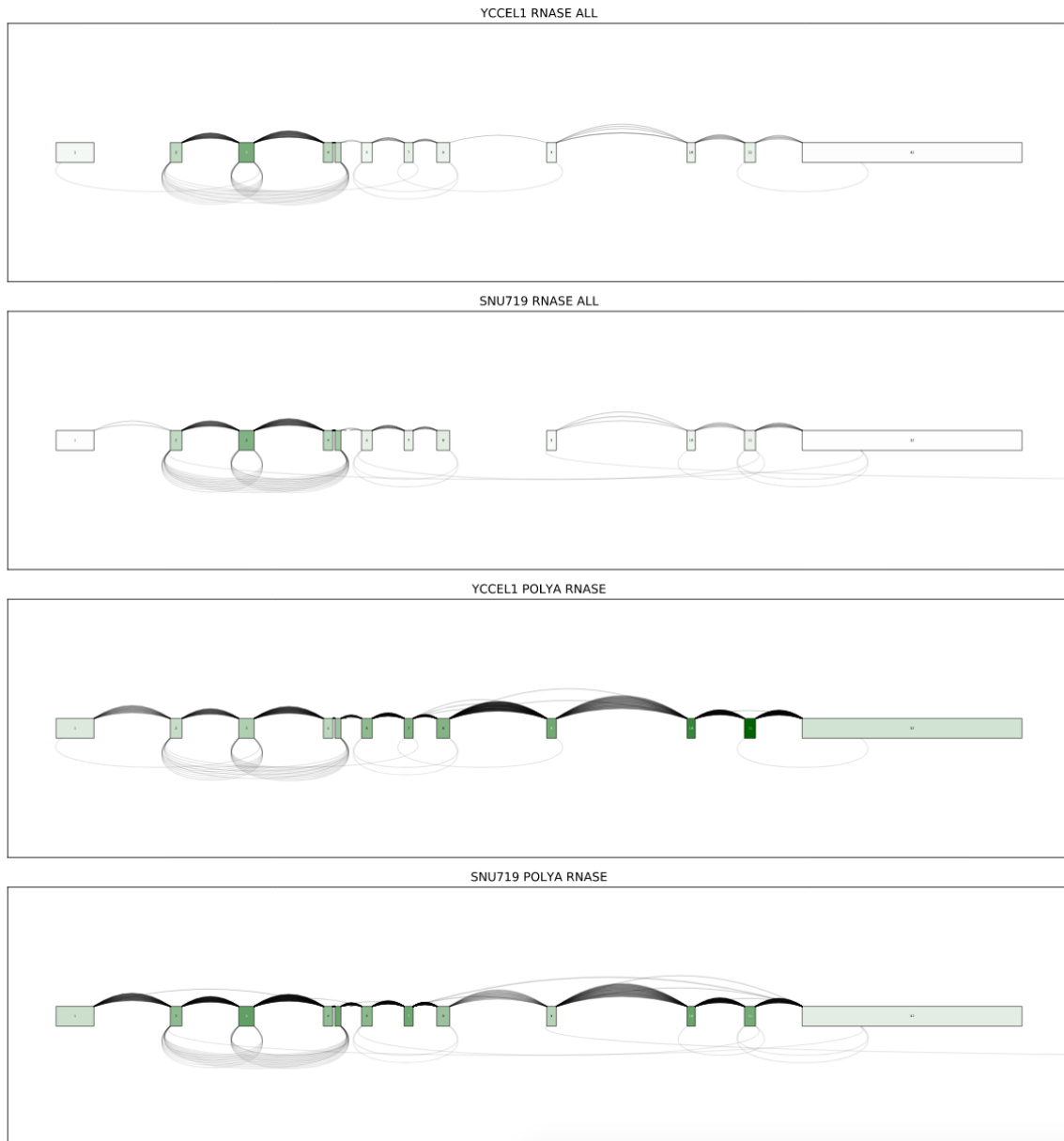


SNU719 POLYA RNASE



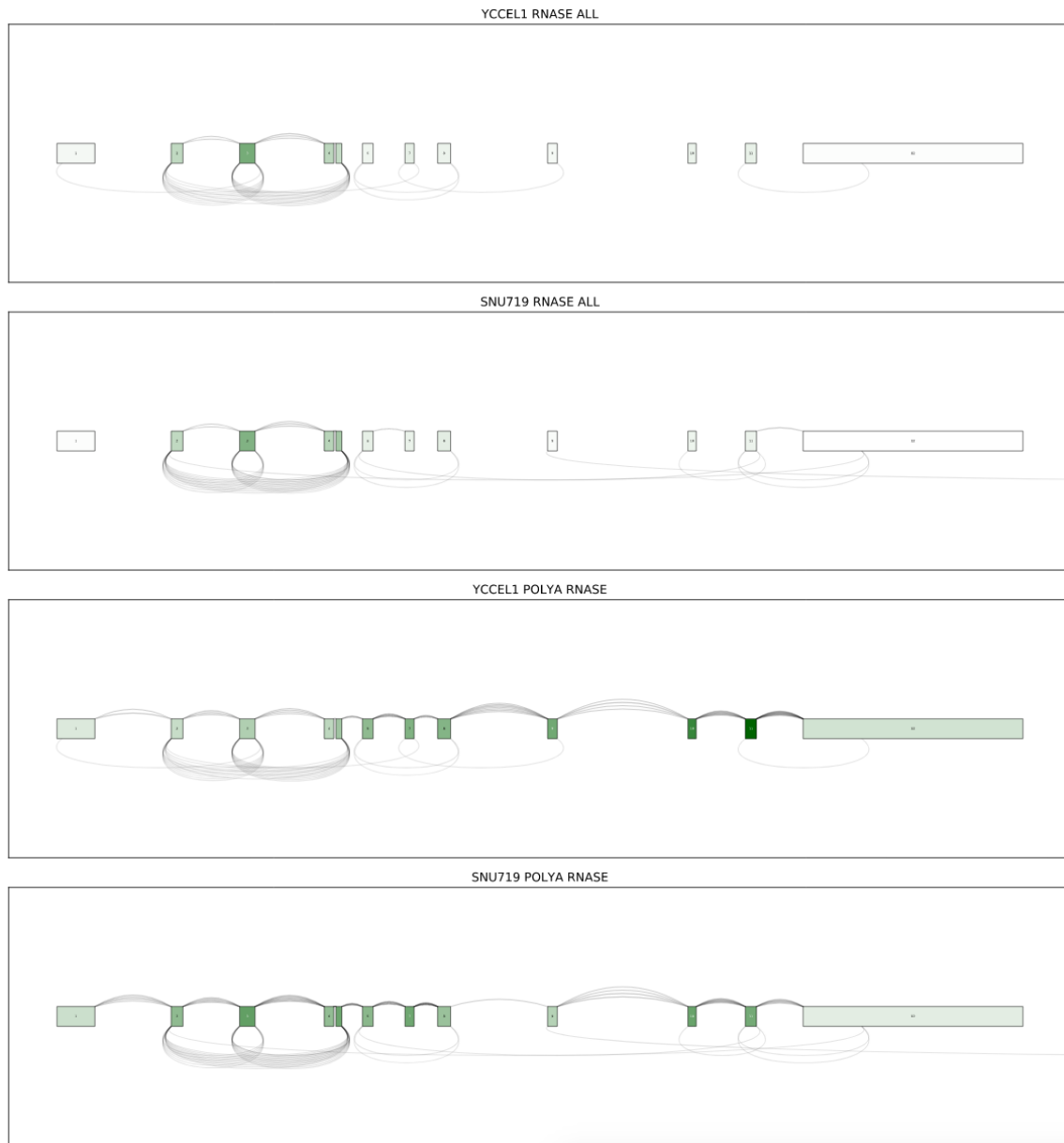
cirplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17 -is 3 -c green

Compare expression between samples: -n



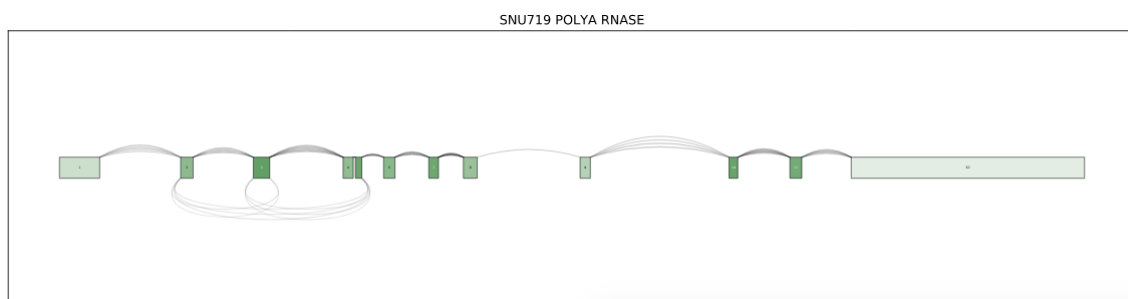
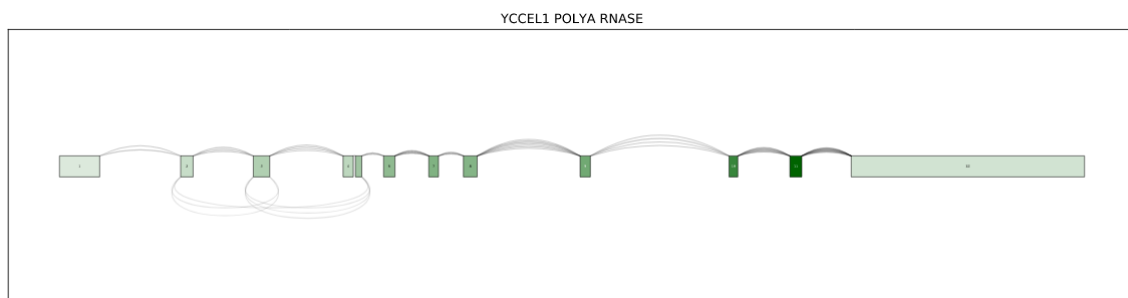
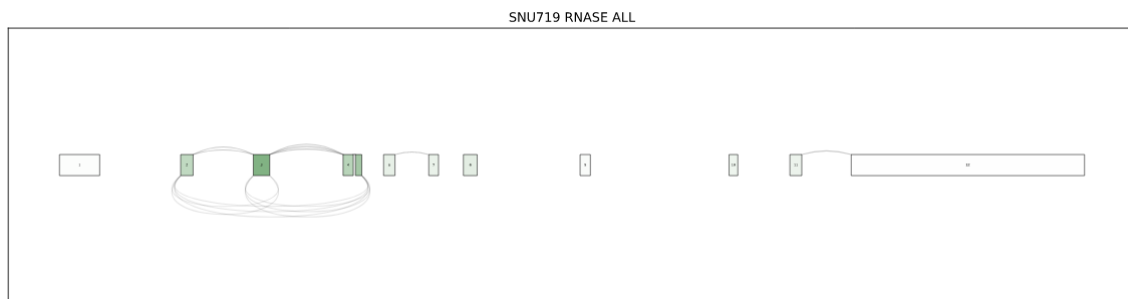
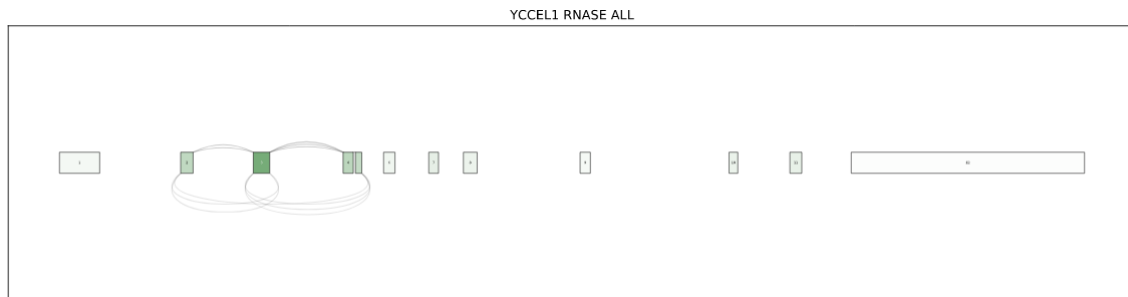
cirplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17 -is 3 -c green -n

Reduce number of canonical splice junctions plotted: -rc



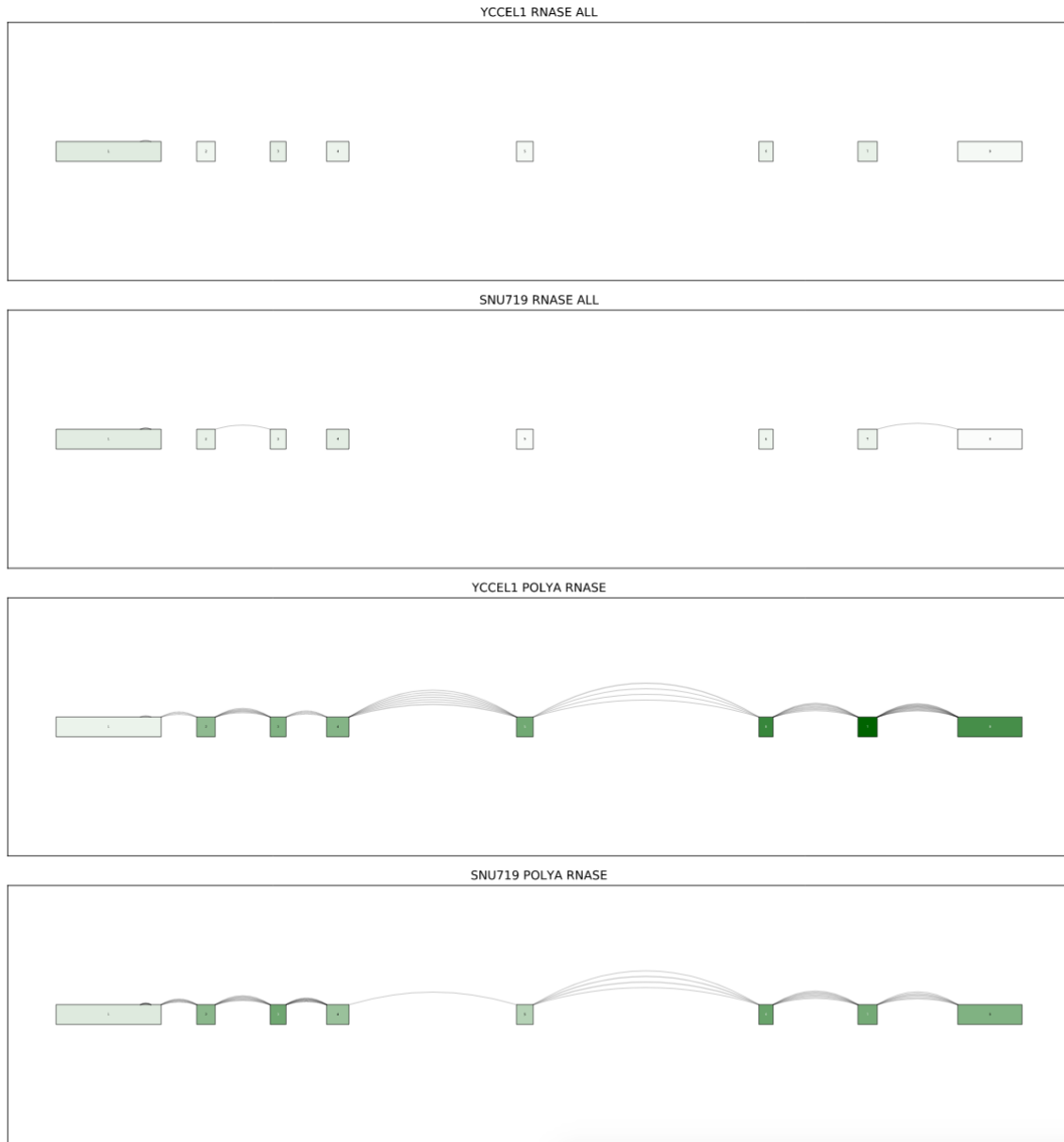
circplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17 -is 3 -c green -n -rc 10

Reduce backsplice junctions plotted: -rbs



```
circplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -g MED17 -is 3 -c green -n -rc 10 -rbs 3
```

Plot specific transcript: -t



cirplot -db yccel1_rnase_all.db snu719_rnase_all.db yccel1_polya_rnase.db snu719_polya_rnase.db -t ENST00000529626 -is 3 -c green
-n -rc 10 -rbs 3