

# RNA-mediated trans-generational inheritance in ciliates

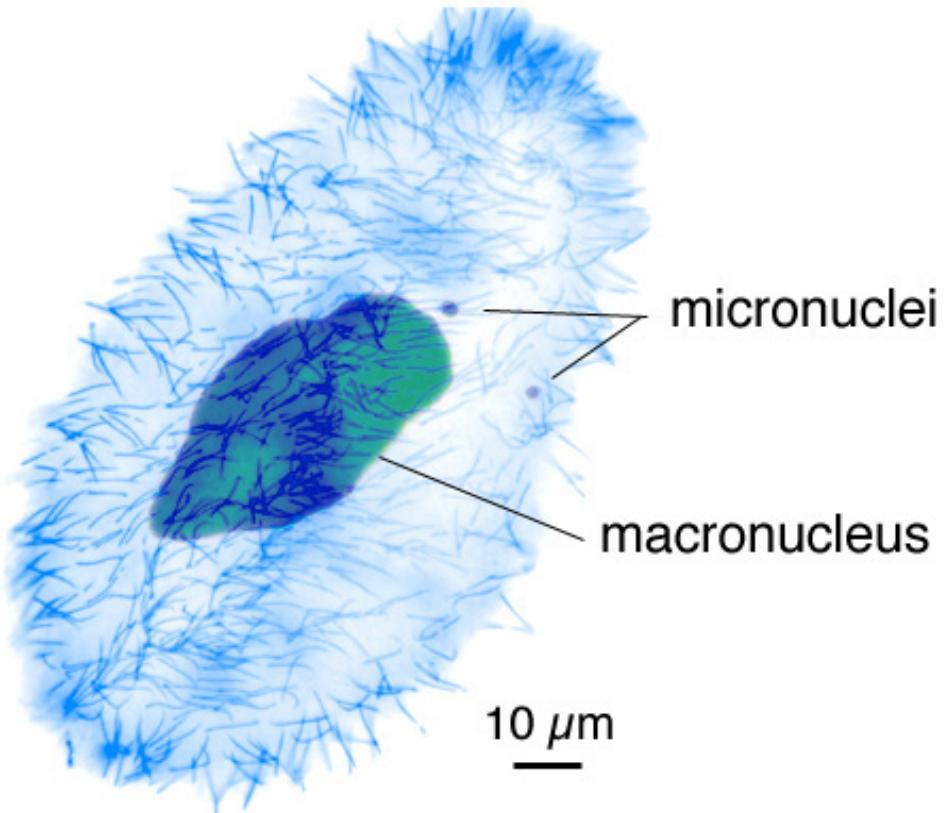
Mariusz Nowacki



**University of Bern  
Institute of Cell Biology  
Switzerland**



# Nuclear dimorphism in ciliates



*Paramecium* cell

## MICRONUCLEUS:

- germline
- transcriptionally silent
- diploid
- contains transposons and other germline-limited DNA

## MACRONUCLEUS:

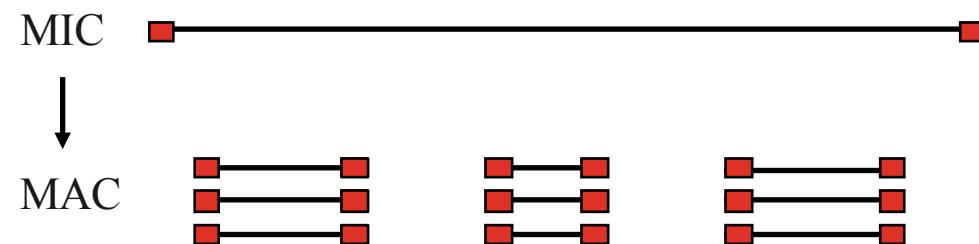
- somatic
- transcriptionally active
- highly polypliod
- short chromosomes
- replaced at each sexual process

# Macronuclear development

A. Genome amplification

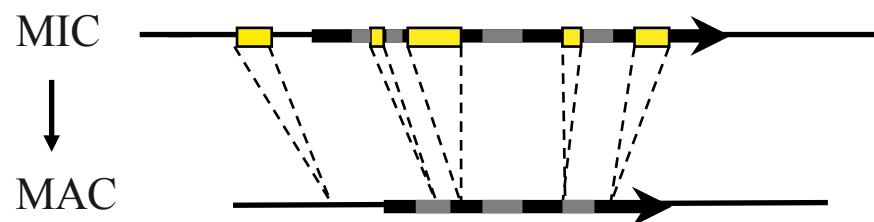
MIC 2n → MAC **800n**

B. Genome reduction by **20%**



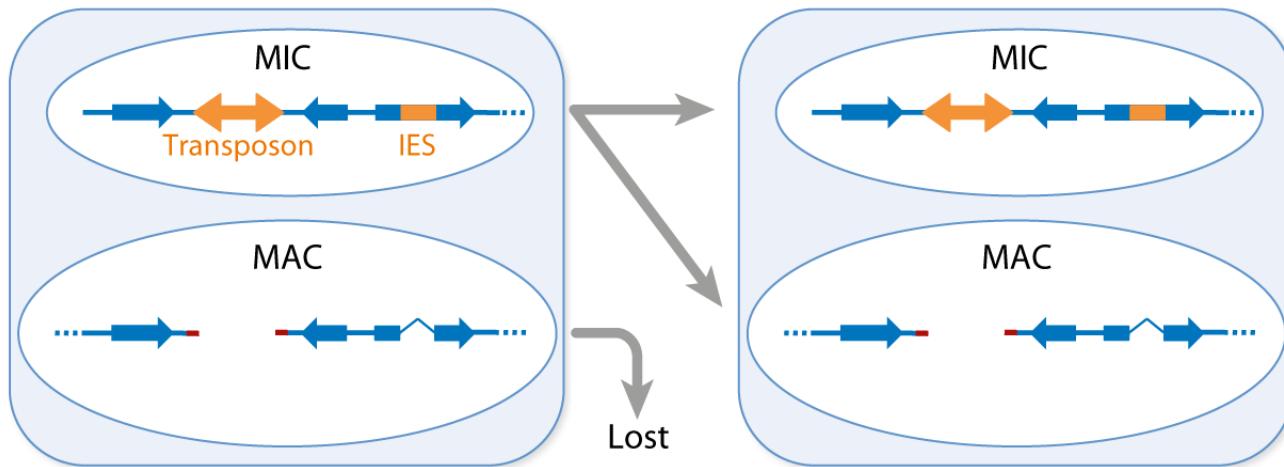
C. Chromosome fragmentation

D. Precise excision of short  
Internal Eliminated Sequences  
(IES)



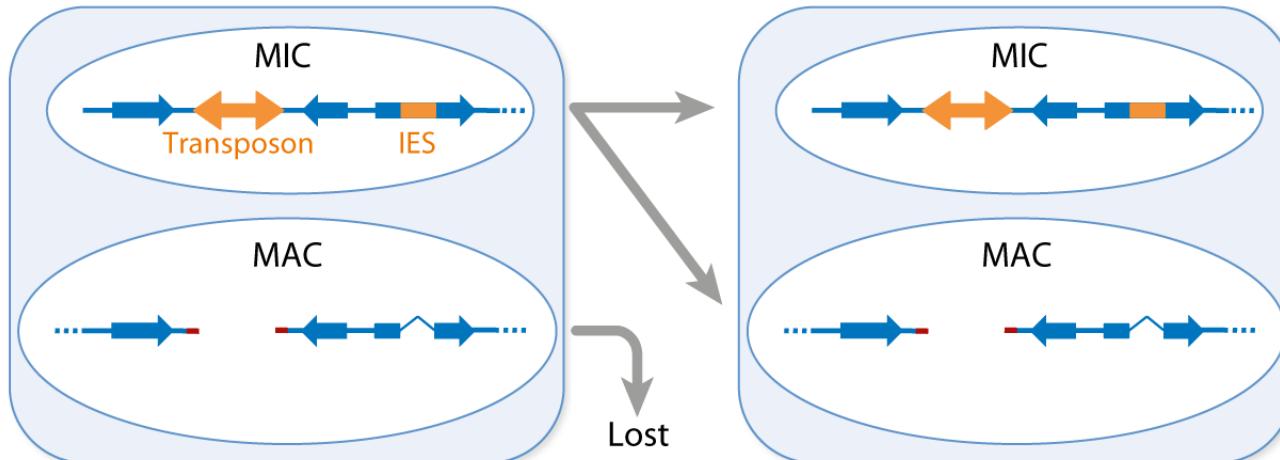
# Epigenetic inhibition of DNA excision.

a

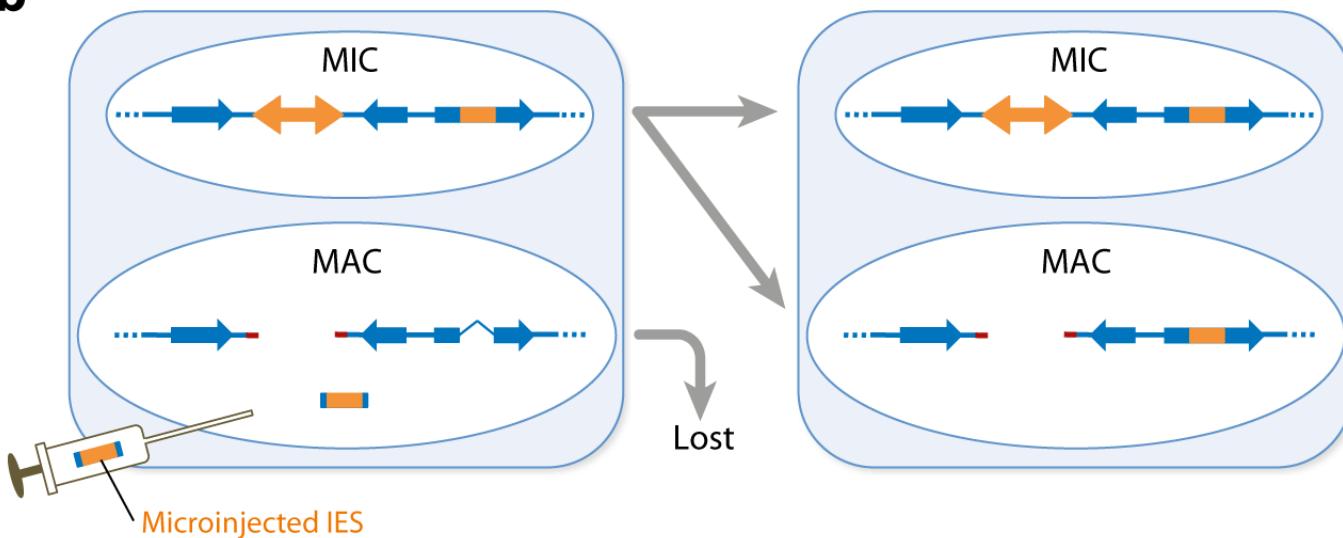


# Epigenetic inhibition of DNA excision.

a



b

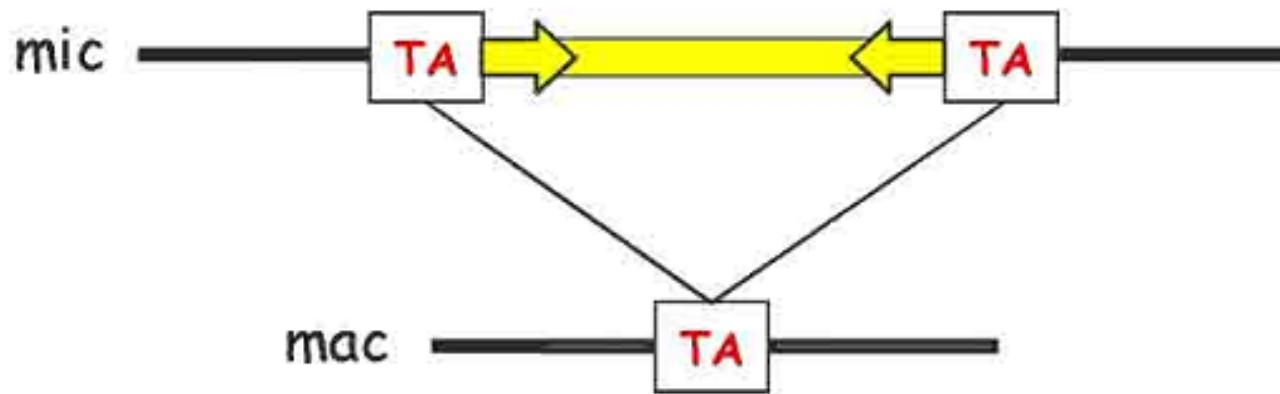


Nowacki M, et al. 2011.

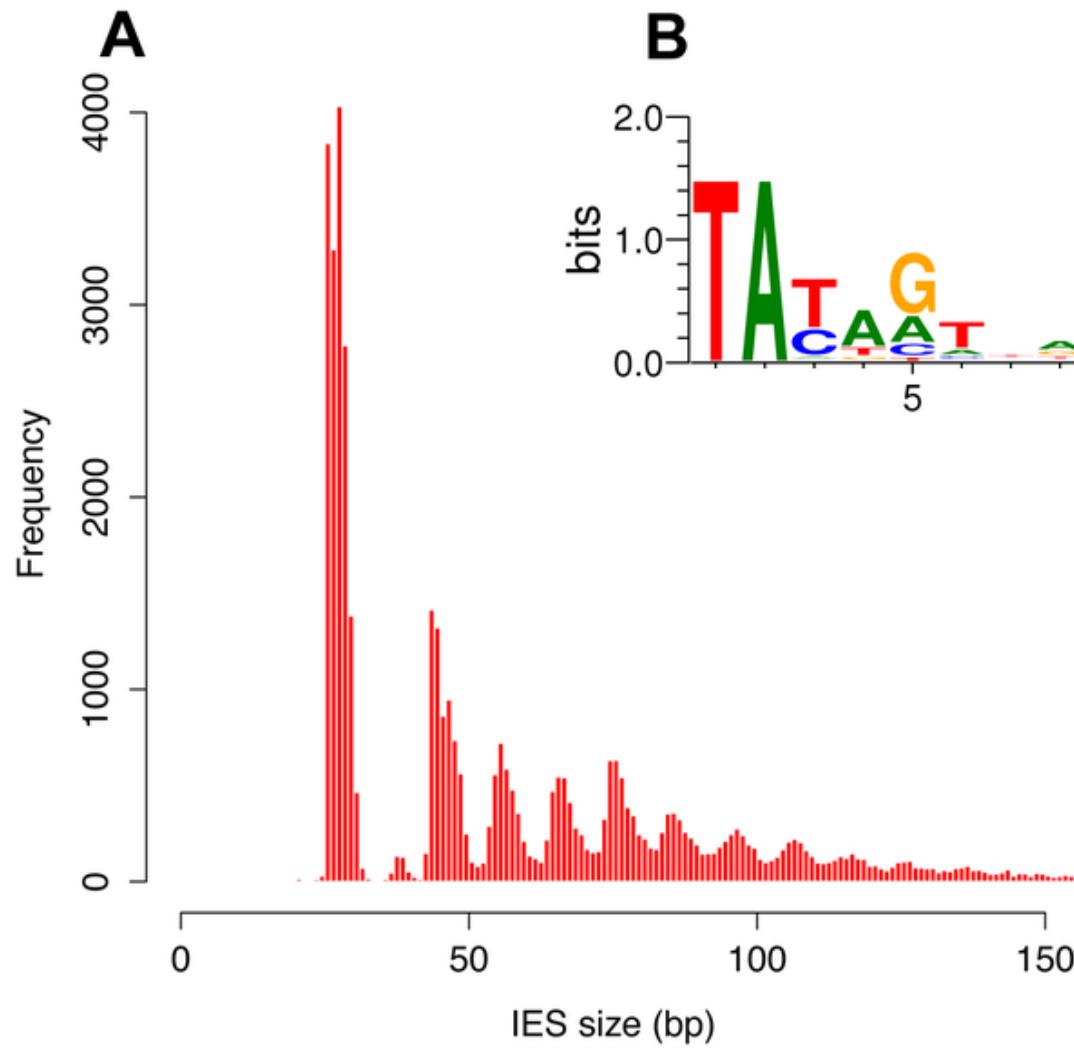
Annu. Rev. Genomics Hum. Genet. 12:367–89

## *Paramecium* Internal Eliminated Sequences (IES)

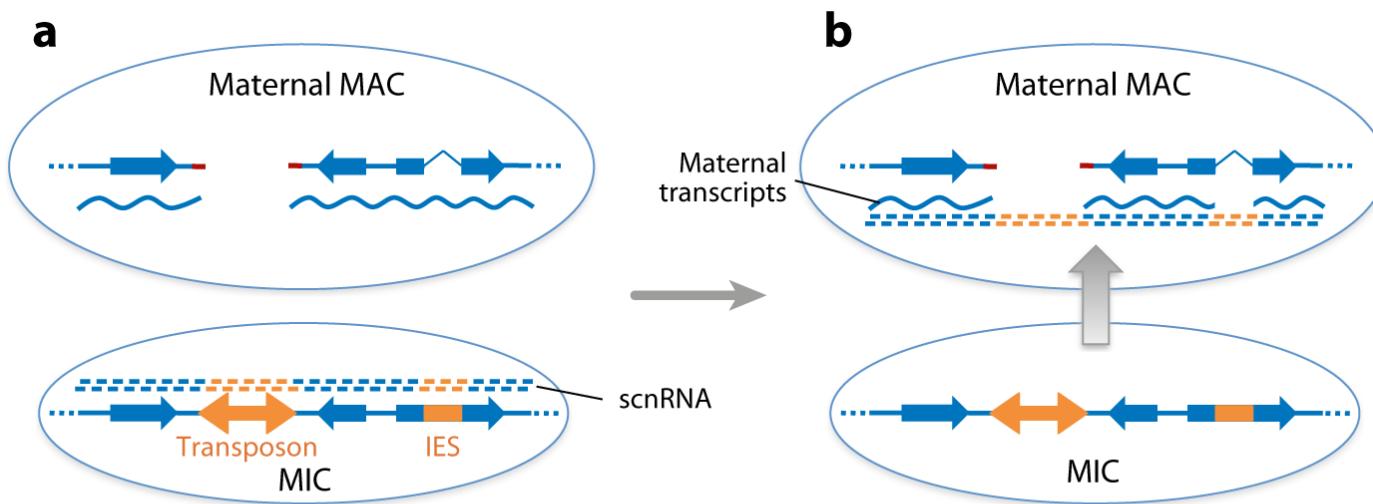
- $\approx 45\,000$  per haploid genome
- present in genic and intergenic regions
- Short (28 bp length mode), single-copy, non-coding sequences
- 5'-TAYAGYNR-3' consensus sequence extending into IES resembles that of Tc1/Mariner transposons



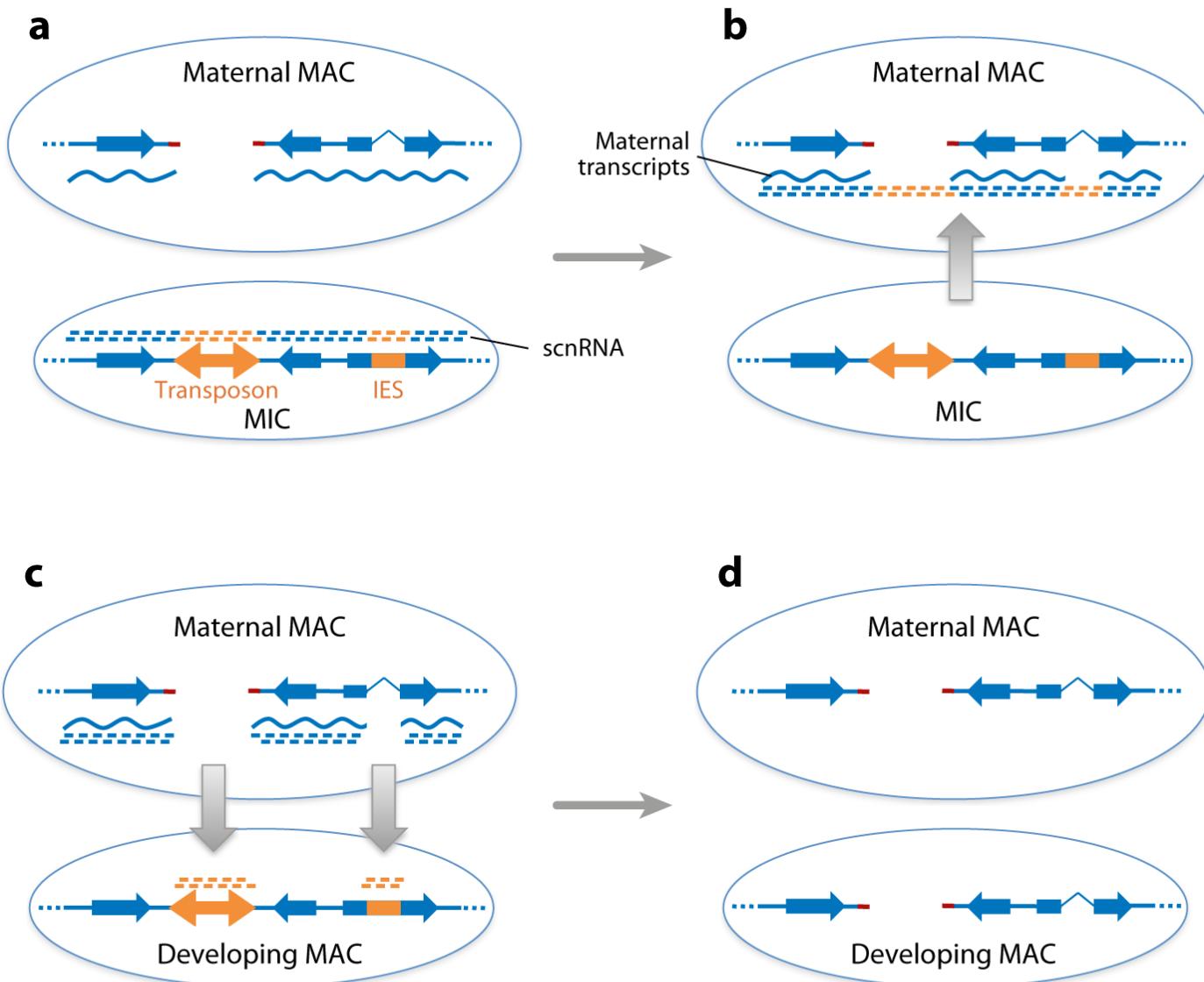
# *Paramecium* Internal Eliminated Sequences (IES)



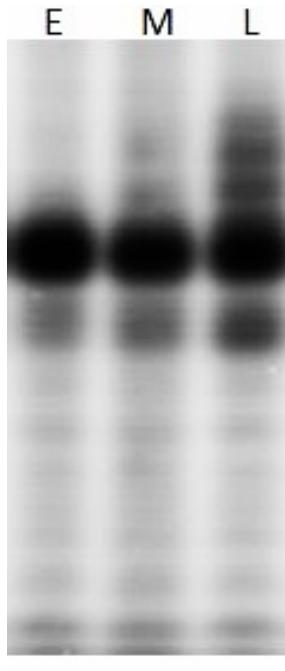
# The scan RNA model for programmed genome rearrangements.



# The scan RNA model for programmed genome rearrangements.



# New class of small RNAs in *Paramecium*?



???

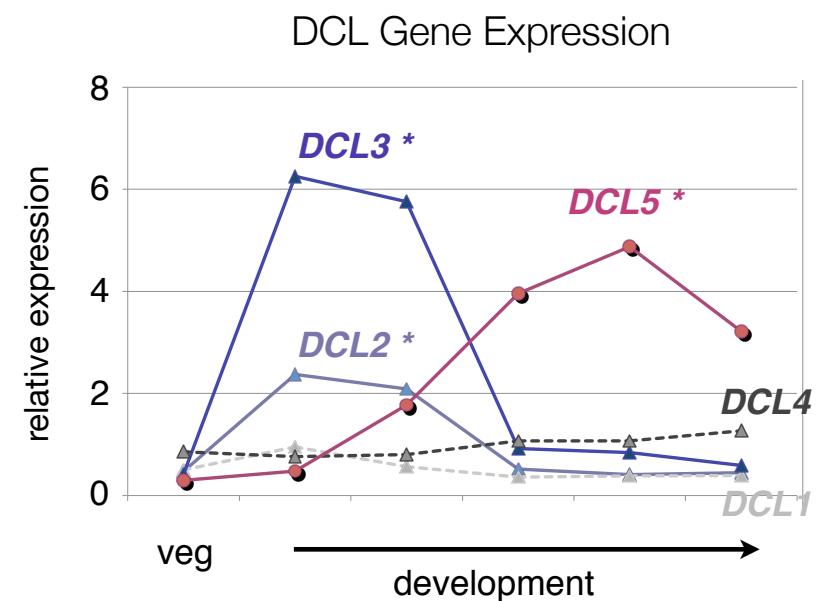
25 nt scnRNA

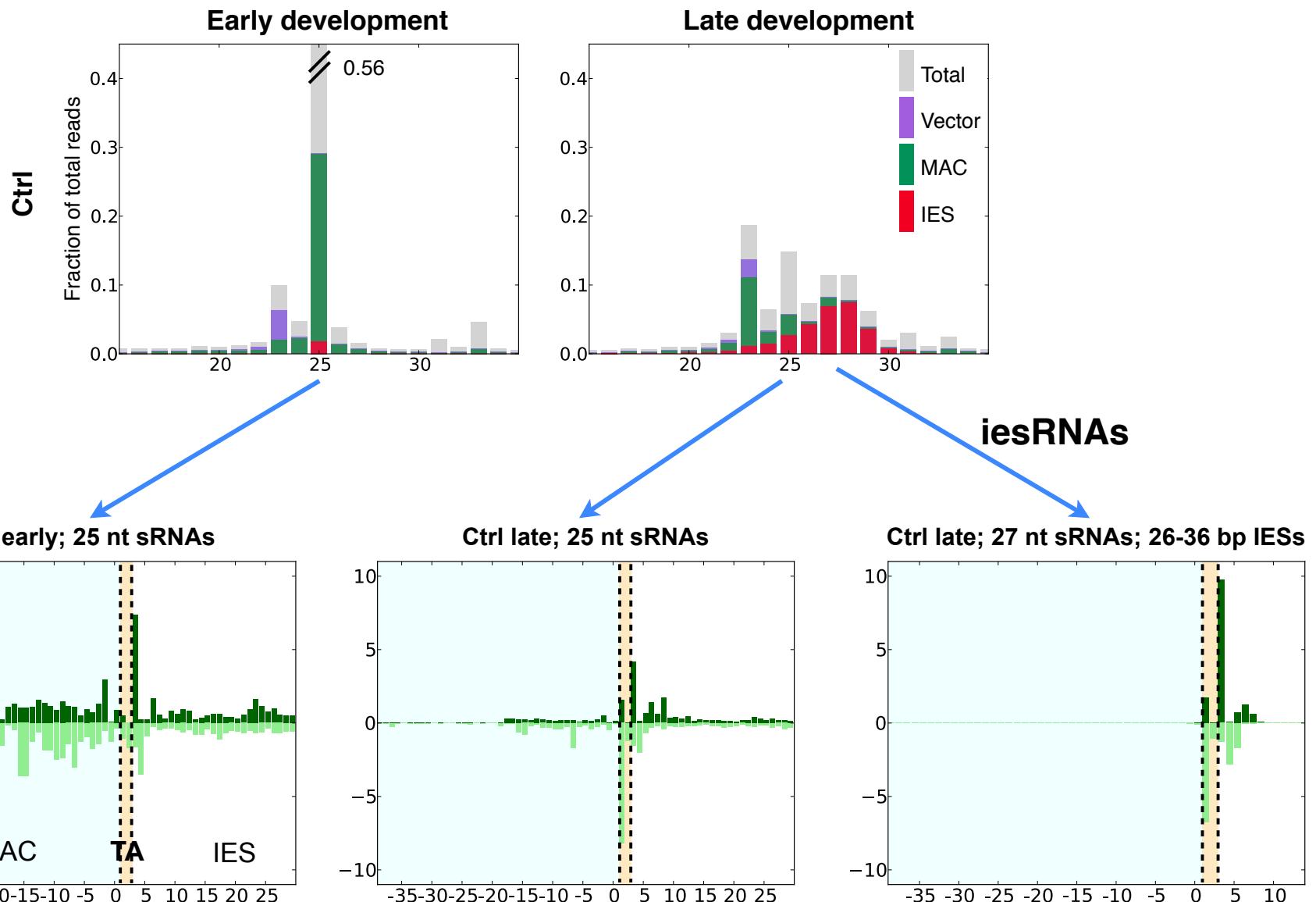
23 nt siRNA



Pamela  
Sandoval

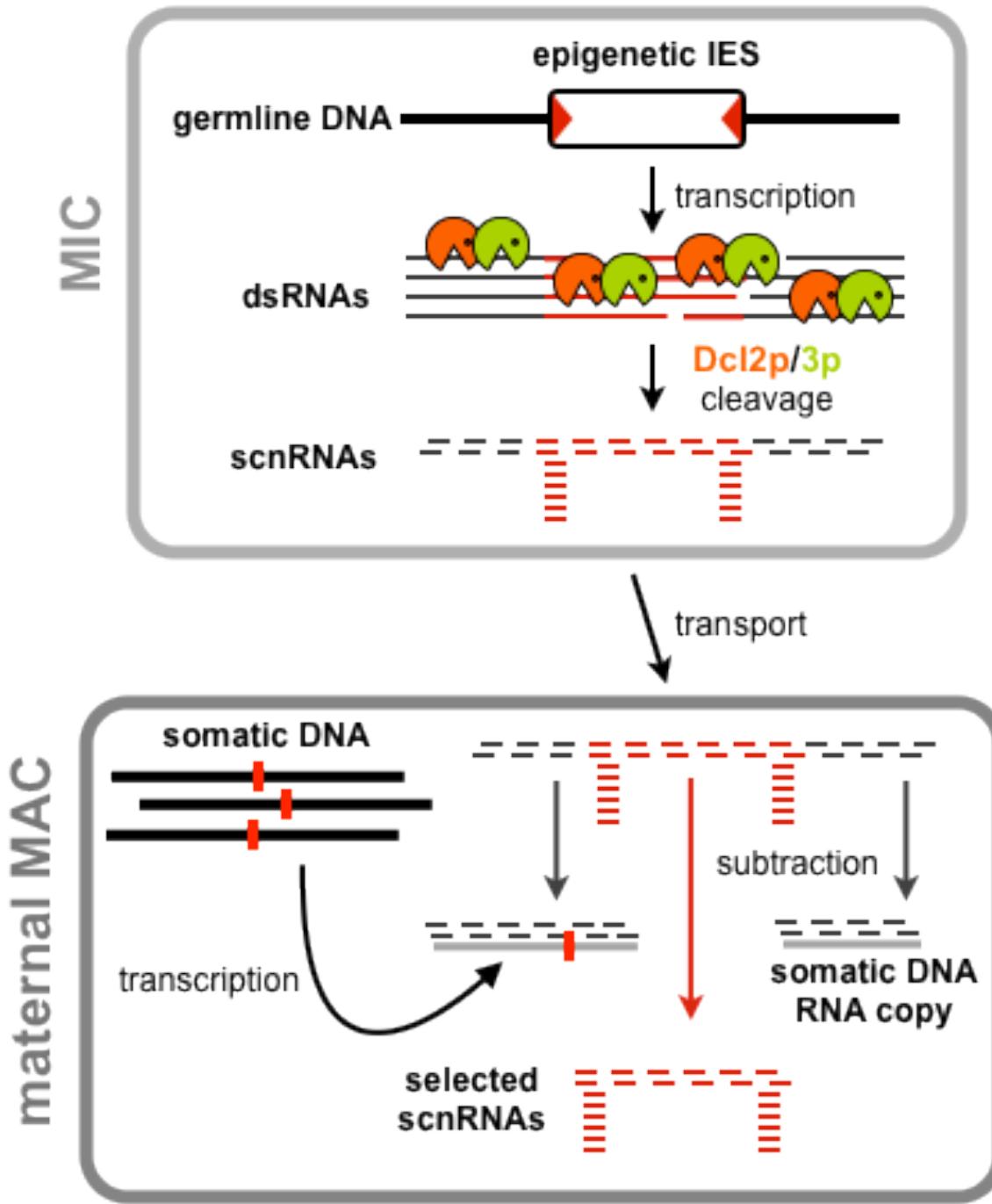
Estienne  
Swart





- scnRNAs overlap MAC/IES junctions and concentrate at IES ends
- iesRNAs map exclusively to IESs and concentrate at IES ends

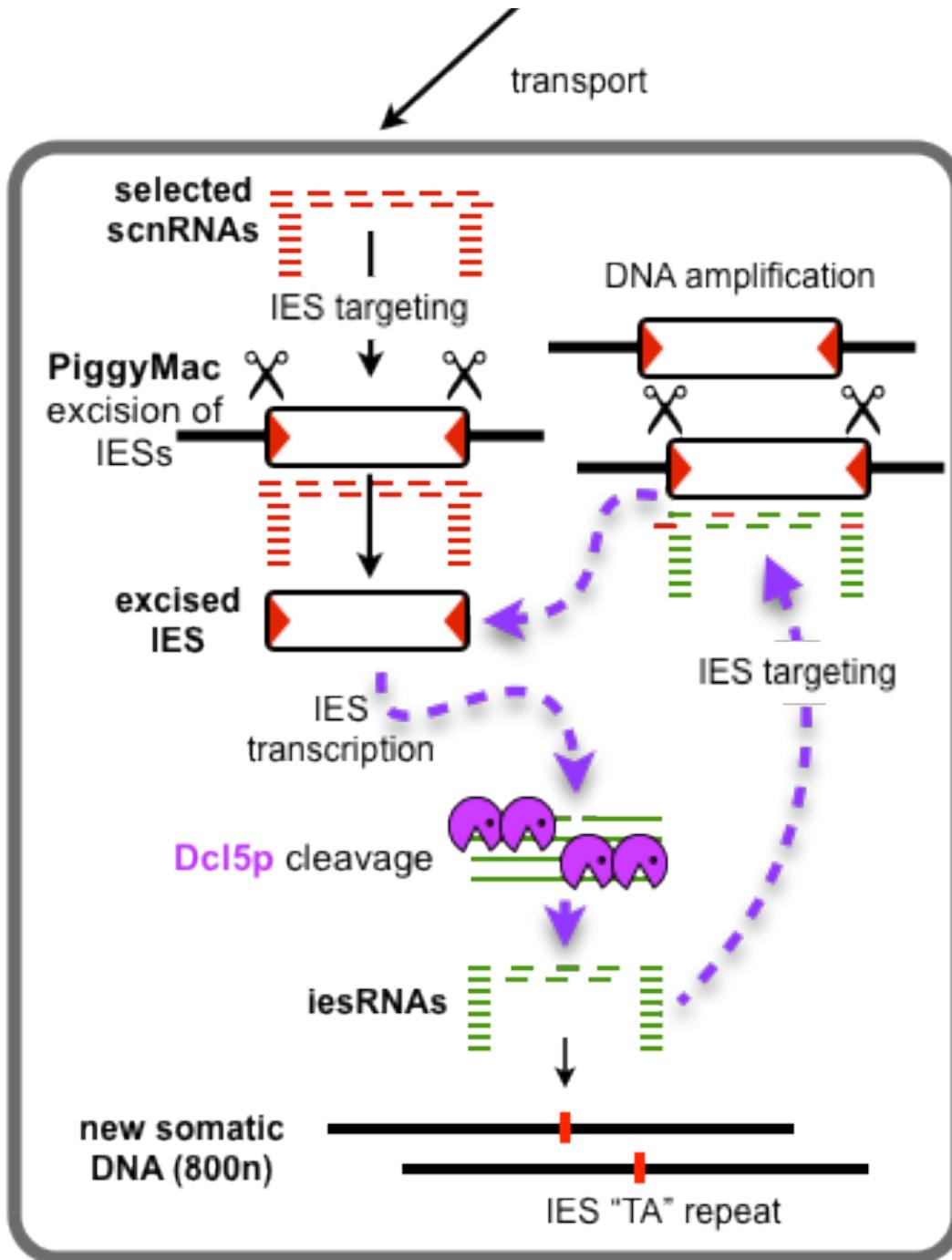
### i. scnRNA production



### ii. RNA scanning

iii. Genome whittling

developing MAC



# How to transcribe ultrashort DNA segments?

Cell

Article

## Circular Concatemers of Ultra-Short DNA Segments Produce Regulatory RNAs

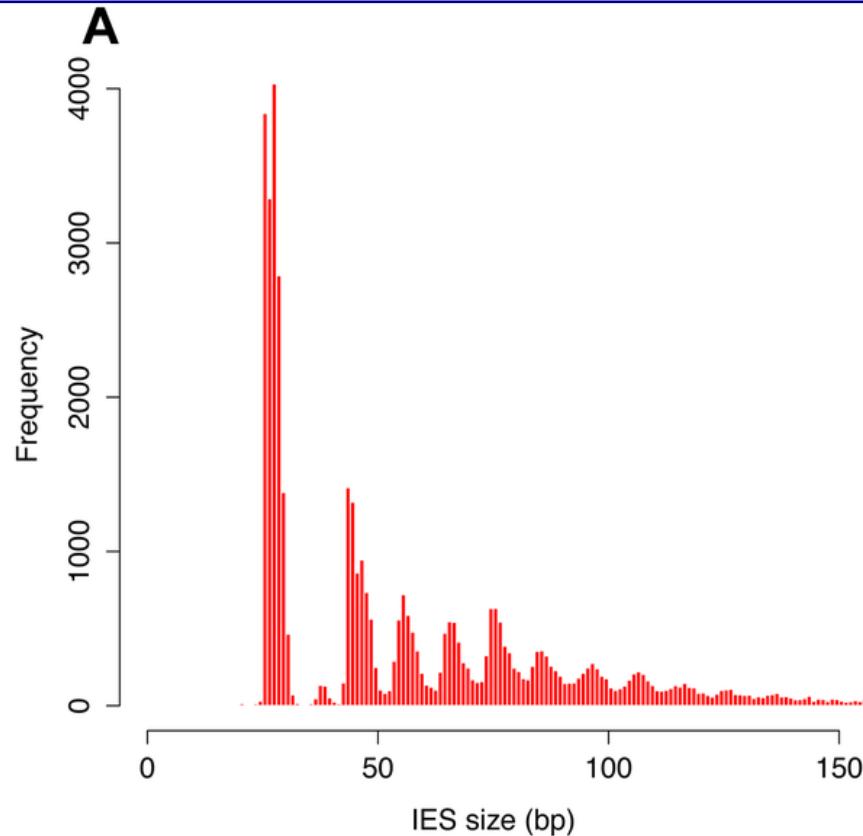
Sarah E. Allen,<sup>1</sup> Iris Hug,<sup>1</sup> Sylwia Pabian,<sup>1</sup> Iwona Rzeszutek,<sup>1</sup> Cristina Hoehener,<sup>1</sup> and Mariusz Nowacki<sup>1,2,\*</sup>

<sup>1</sup>Institute of Cell Biology, University of Bern, Baltzerstrasse 4, 3012 Bern, Switzerland

<sup>2</sup>Lead Contact

\*Correspondence: mariusz.nowacki@izb.unibe.ch

<http://dx.doi.org/10.1016/j.cell.2017.02.020>

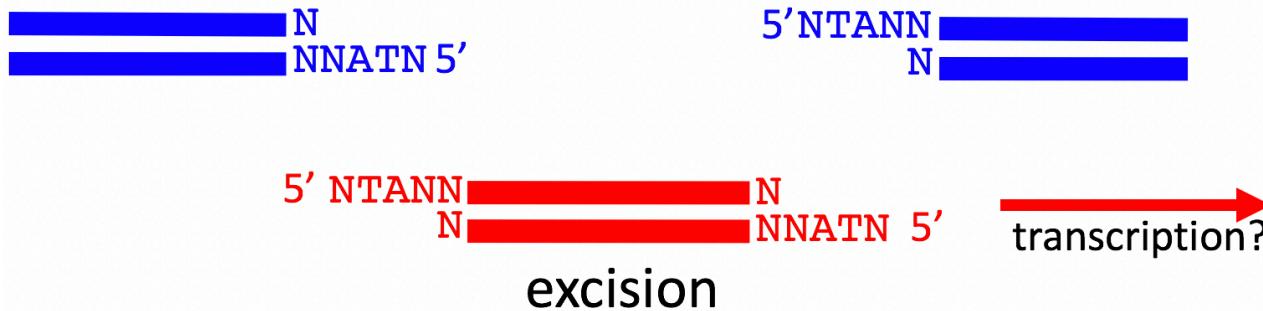


Sarah Allen



Allen et al. 2017, *Cell*.

# Are iesRNAs formed from excised IESs?



Assembly of RNA polymerase complex on a 27 bp excised IES poses problems

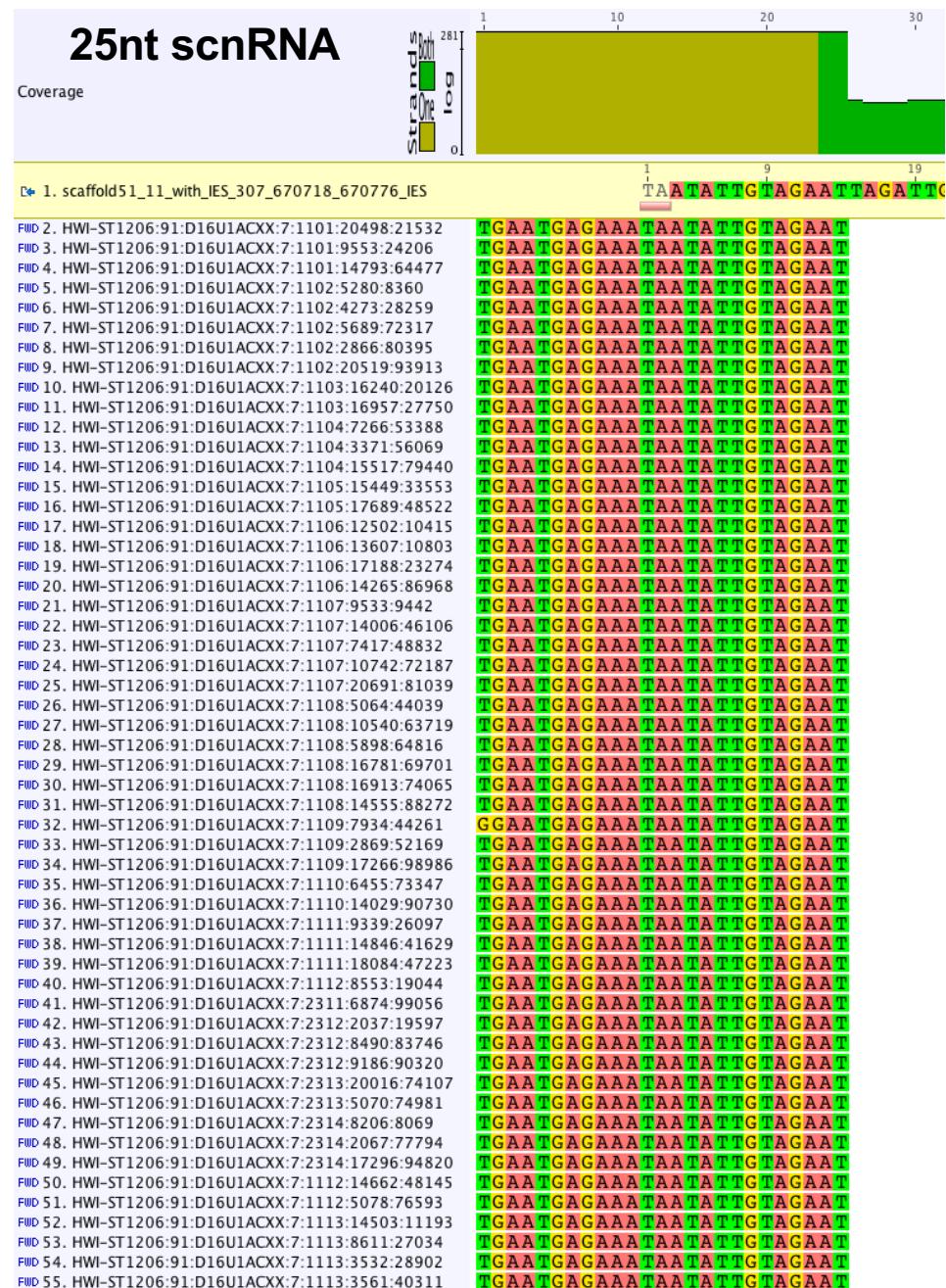
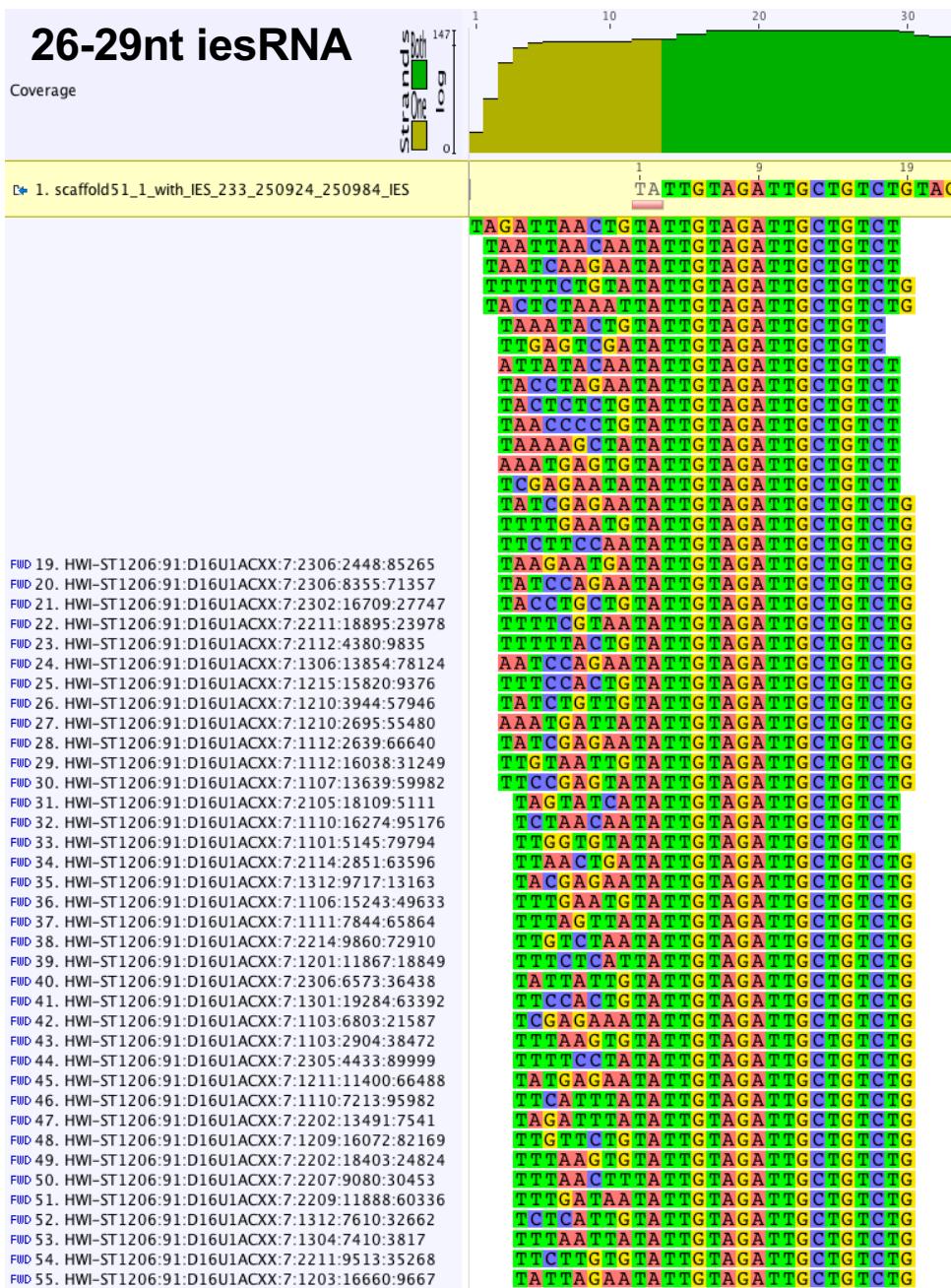
# The concatemer model

- Most IESs are too short to form circles individually

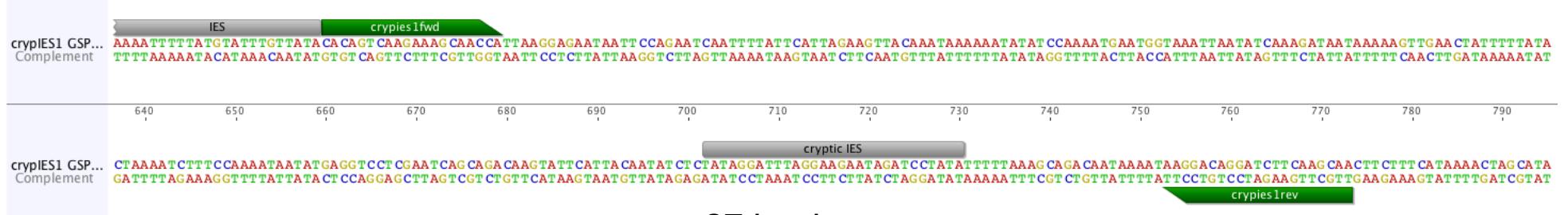


Long IES (>200 bp)

Some iesRNAs map to IES-IES junctions

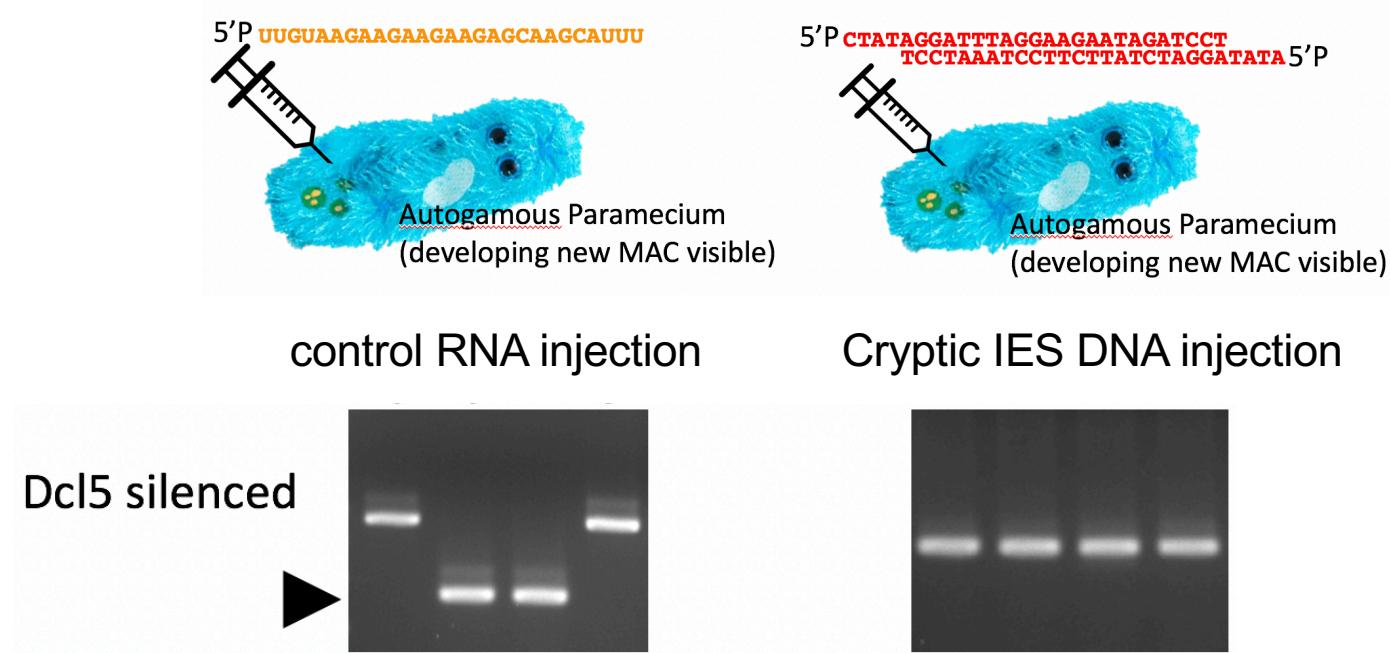


# Experimental approach: ‘cryptic’ IES excision



- 27 bp long
- ‘consensus’ 5’TATAG
- Located in unknown genes

# Is cryptic IES excision dependent on iesRNAs? Dcl5 silencing



# Dependence of iesRNA production on 5' overhangs

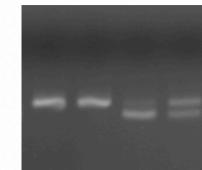
Injection of cryptic IESs with 3' overhangs does not induce excision



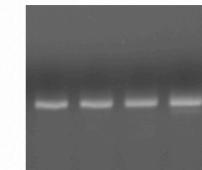
3' overhangs



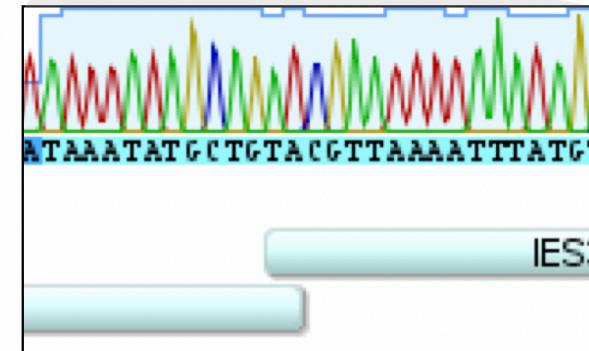
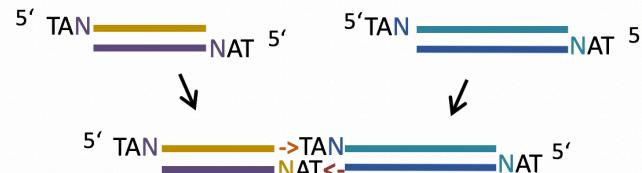
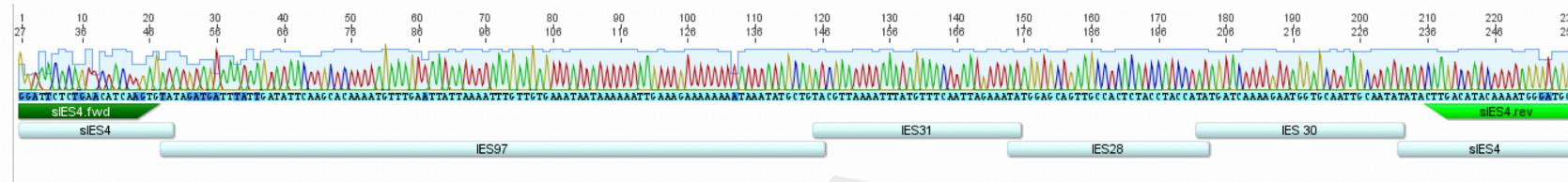
ctrl (cryp4)



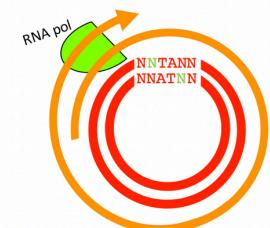
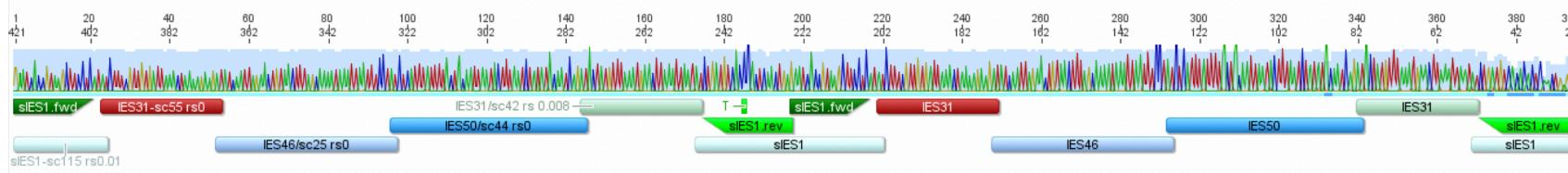
cryp2 3' overhangs



# Sequencing identifies RNA corresponding to concatemers of IESs



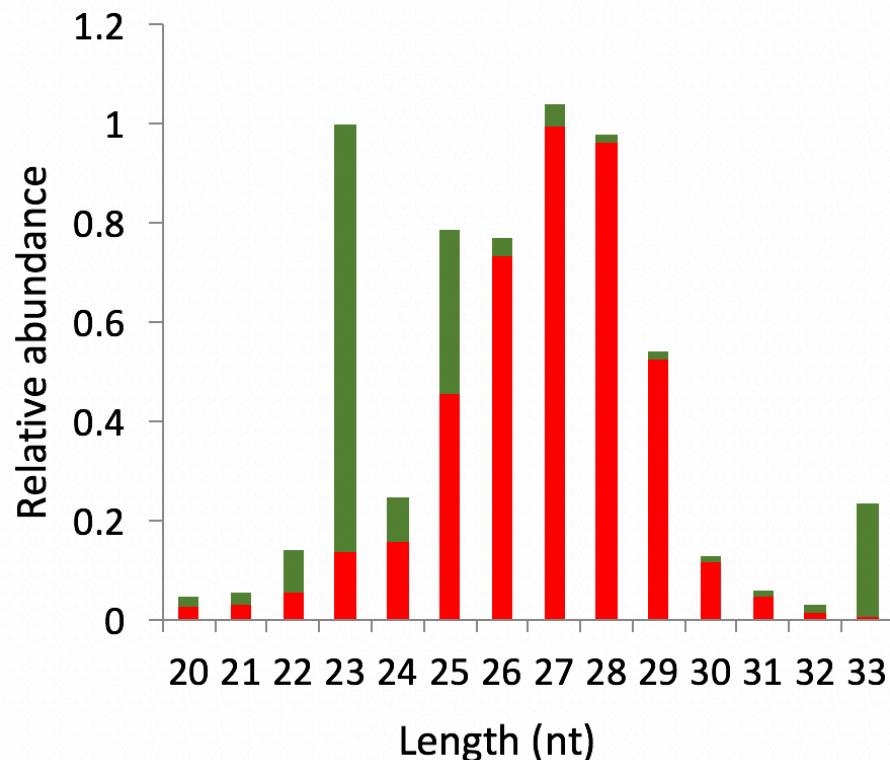
## Concatemer repeat



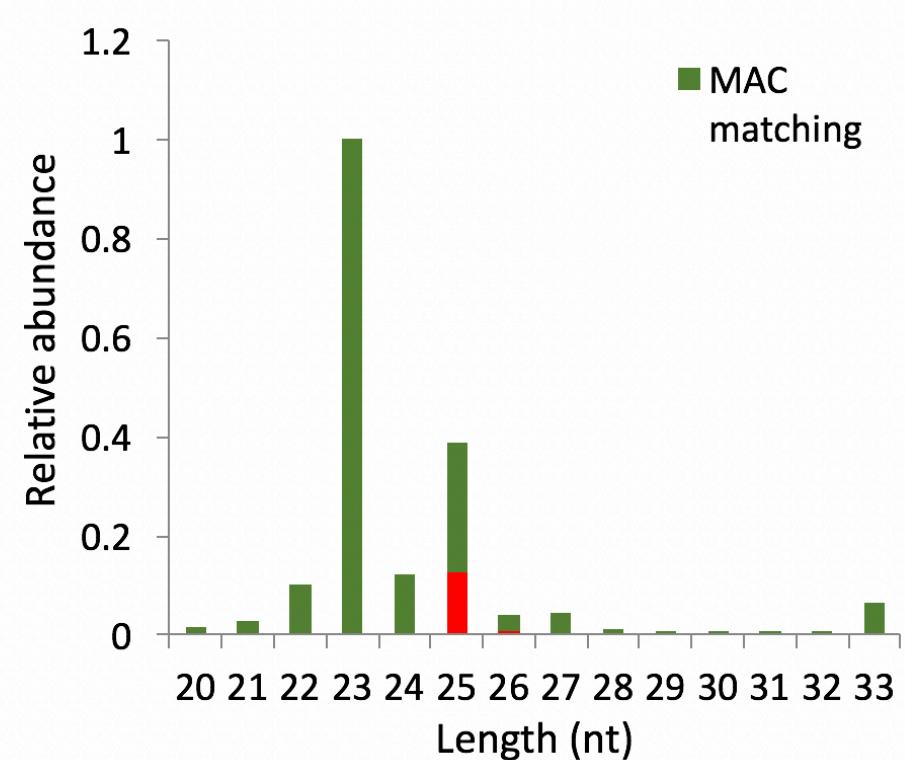
# How are putative concatemers formed? Ligase IV?

Silencing of Ligase IV by RNAi feeding

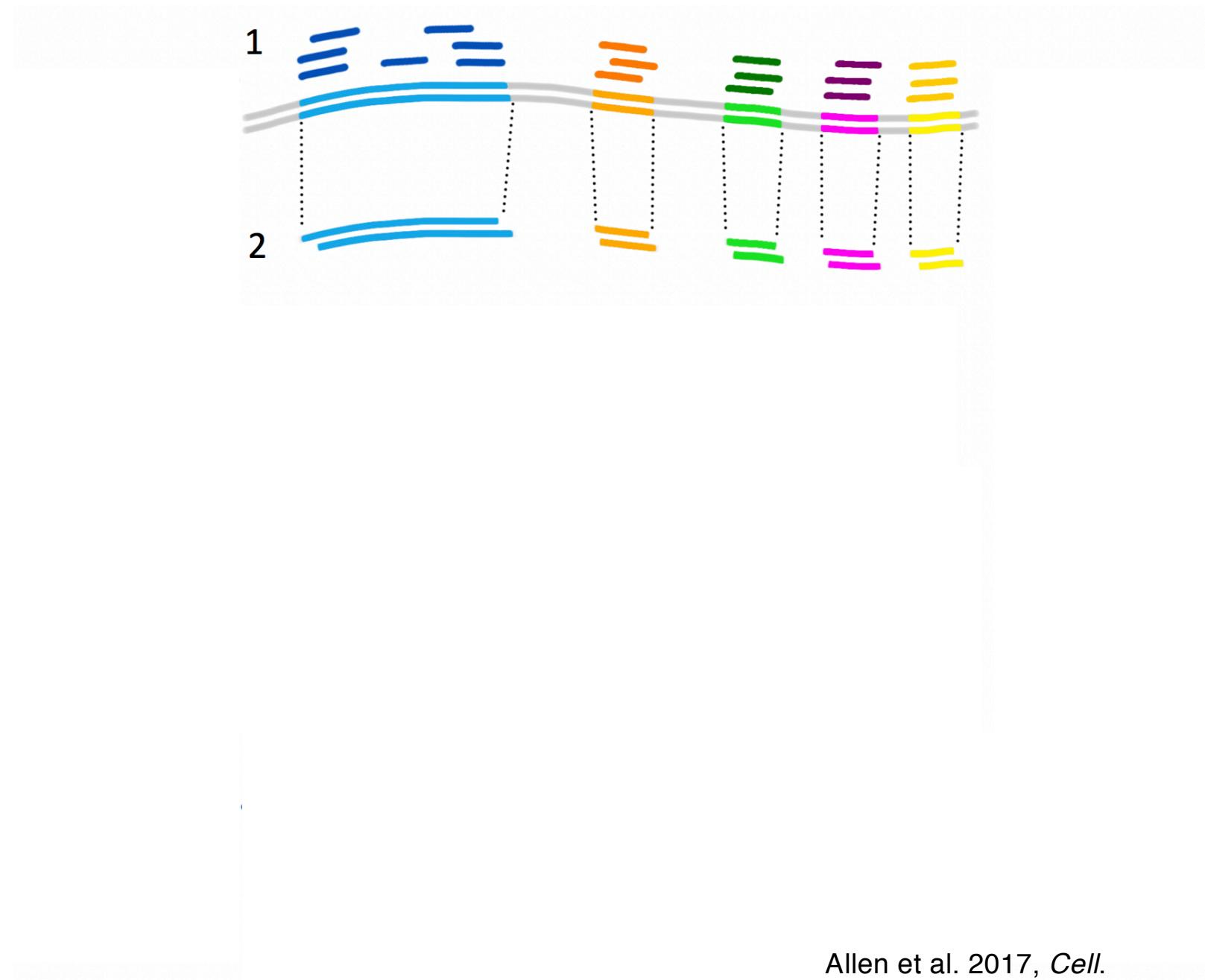
Control (empty vector)



Ligase IV silencing



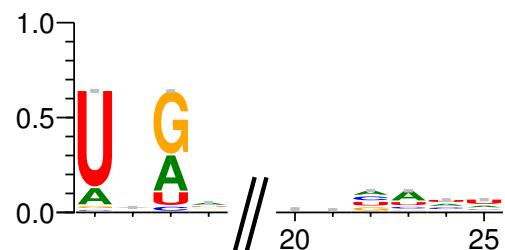
# A model for small RNA production from short DNA fragments in *Paramecium*



# Dicer-like enzymes with sequence cleavage preferences

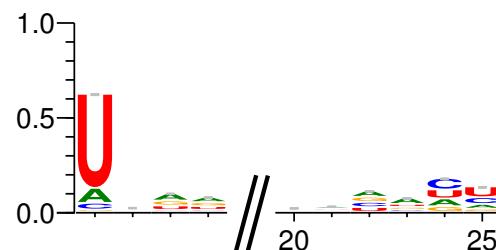


Dcl3



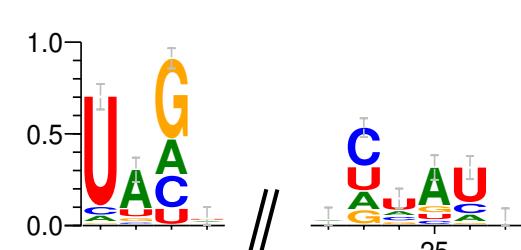
size 22-32 nt

Dcl2

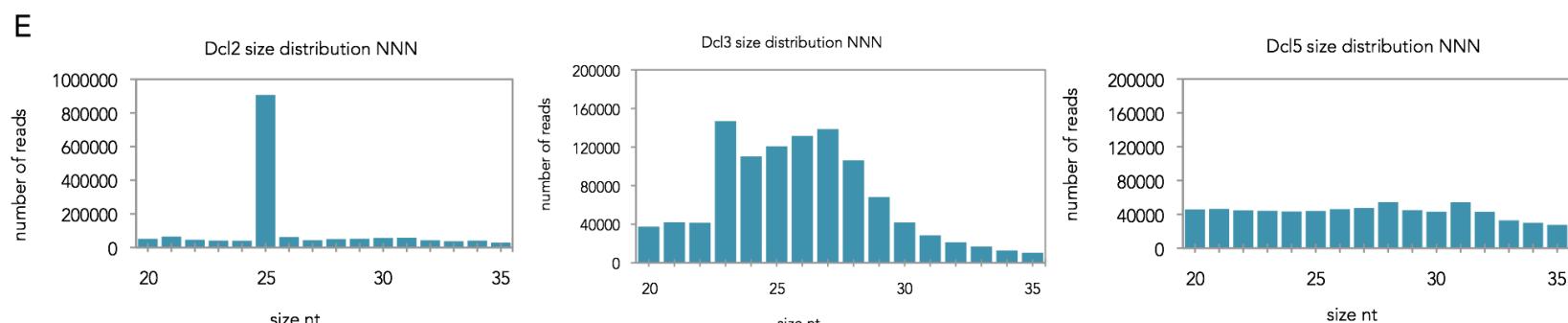
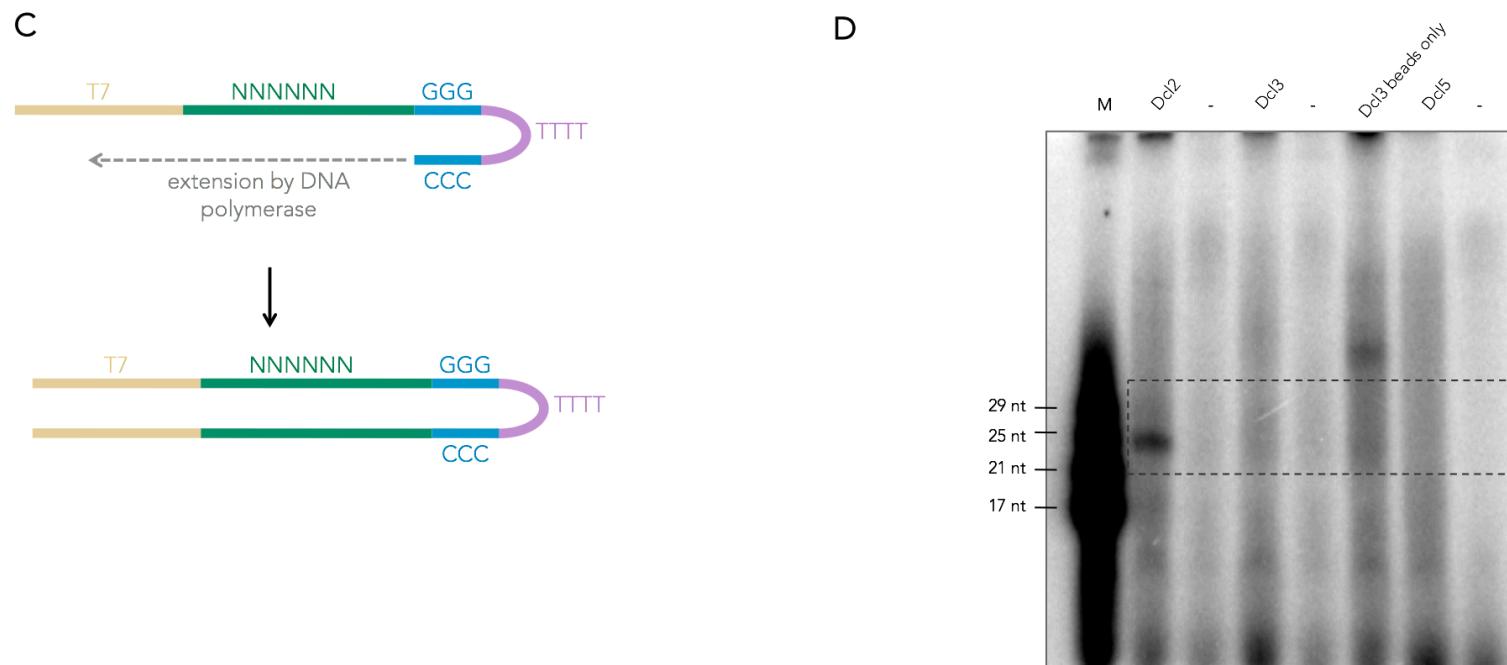
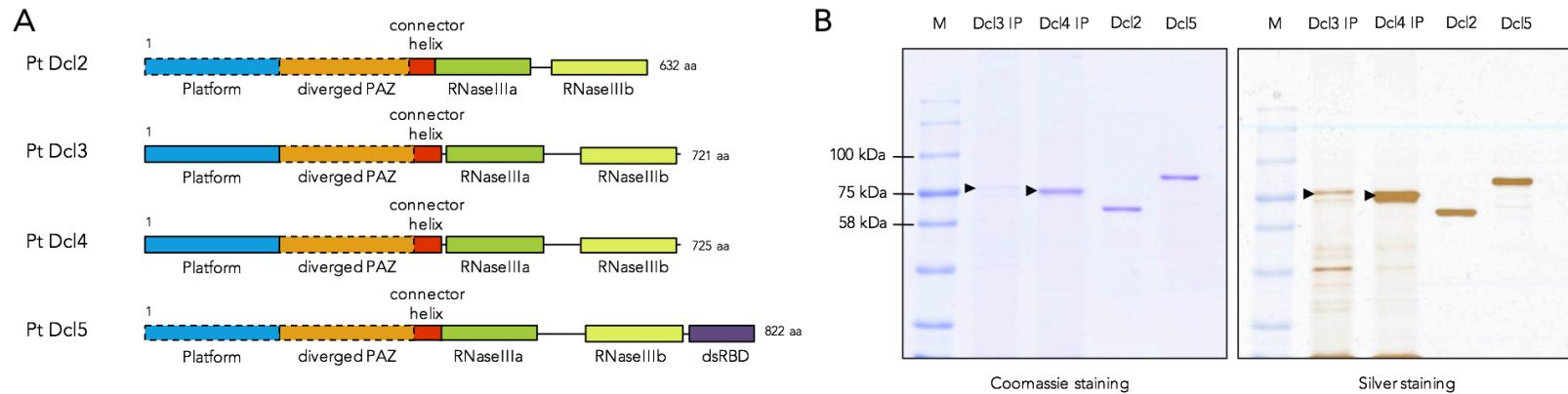


size 25 nt

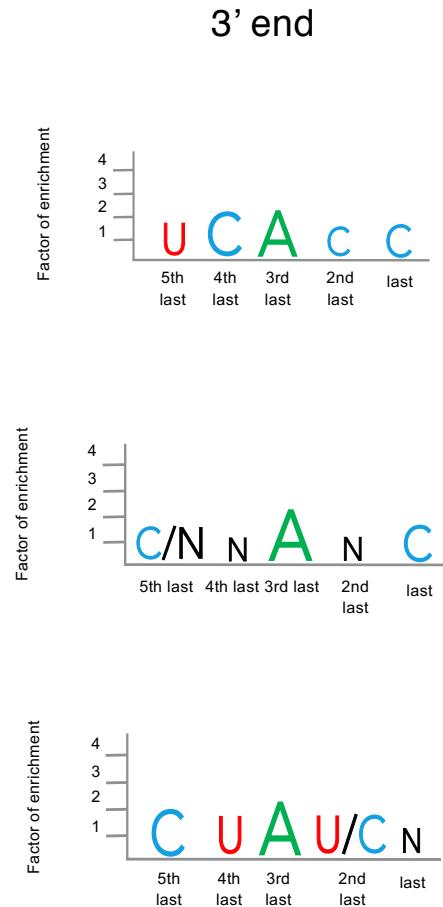
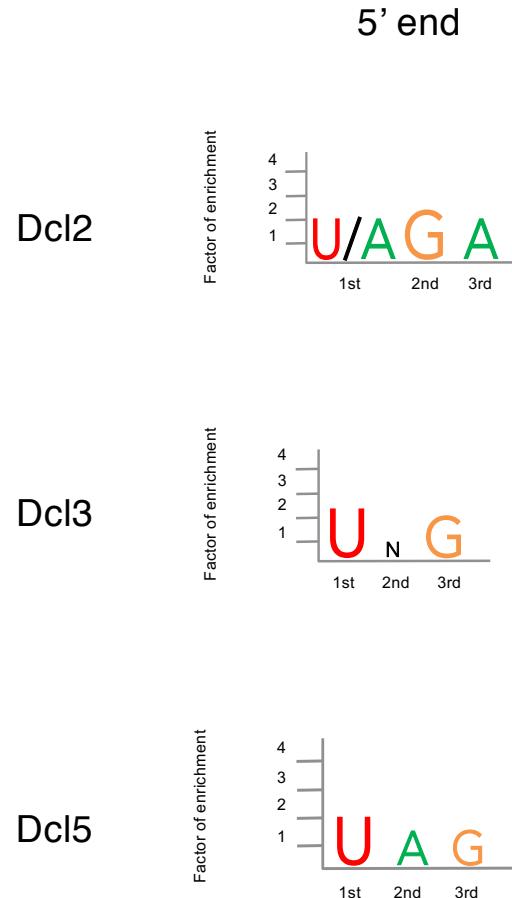
Dcl5



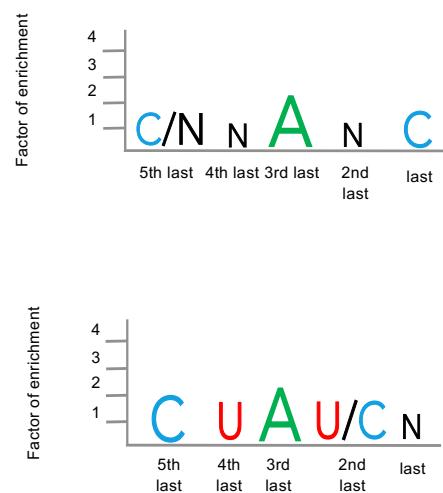
size 22-31 nt



# Dicer-like enzymes with sequence cleavage preferences

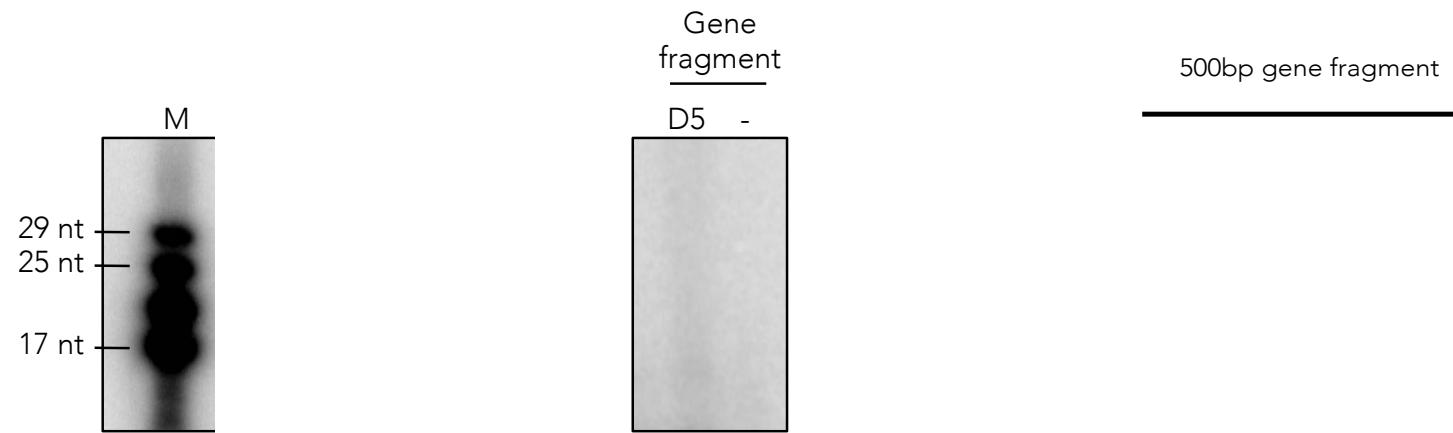
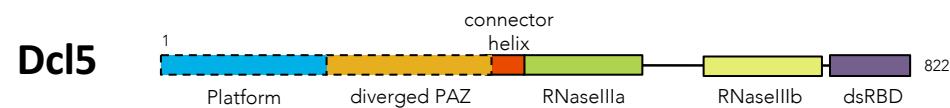


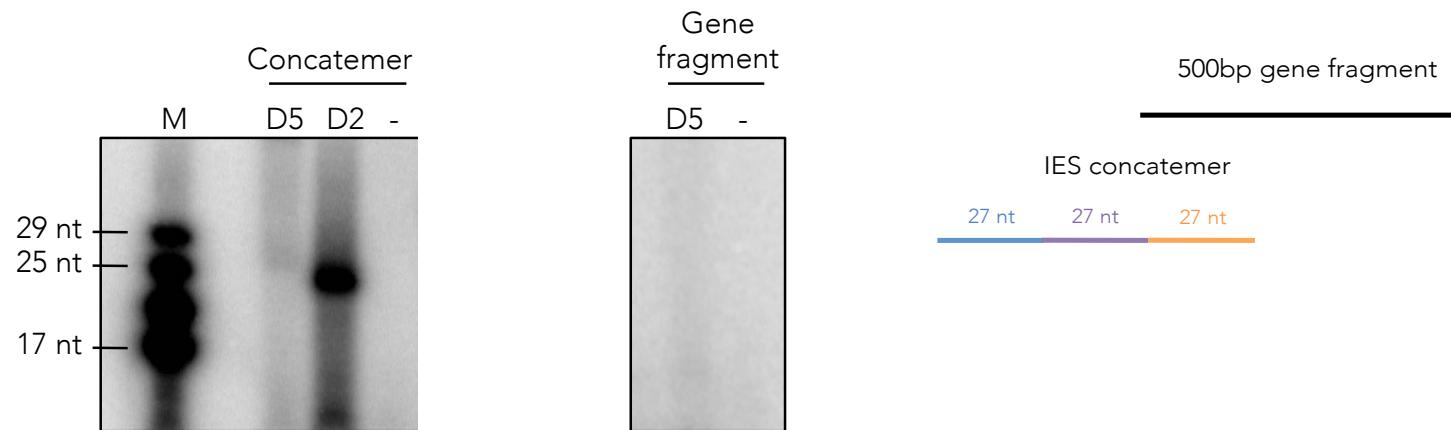
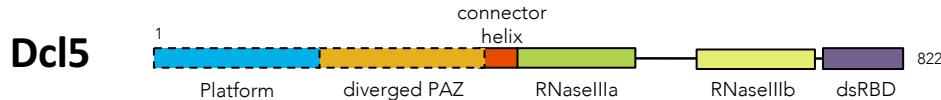
5'-UNNNNNNNNNNNNNNNNNUCUNN-3'  
3'-NNANNNNNNNNNNNNNNAGA-5'



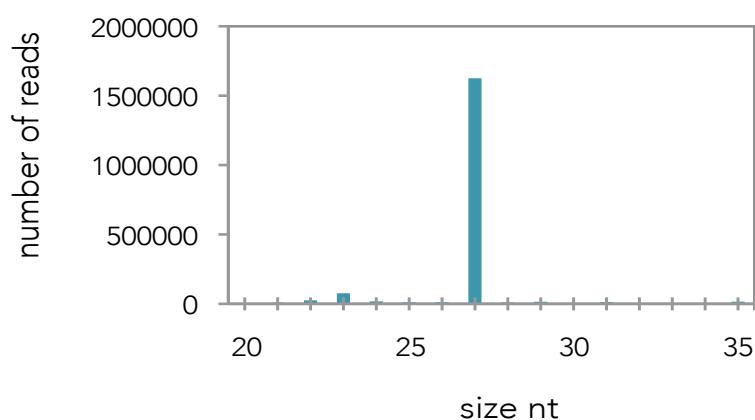
5'-UNGNNNNNNNNNNNNNNCNANN-3'  
3'-NNANCNNNNNNNNNNNNNGNU-5'

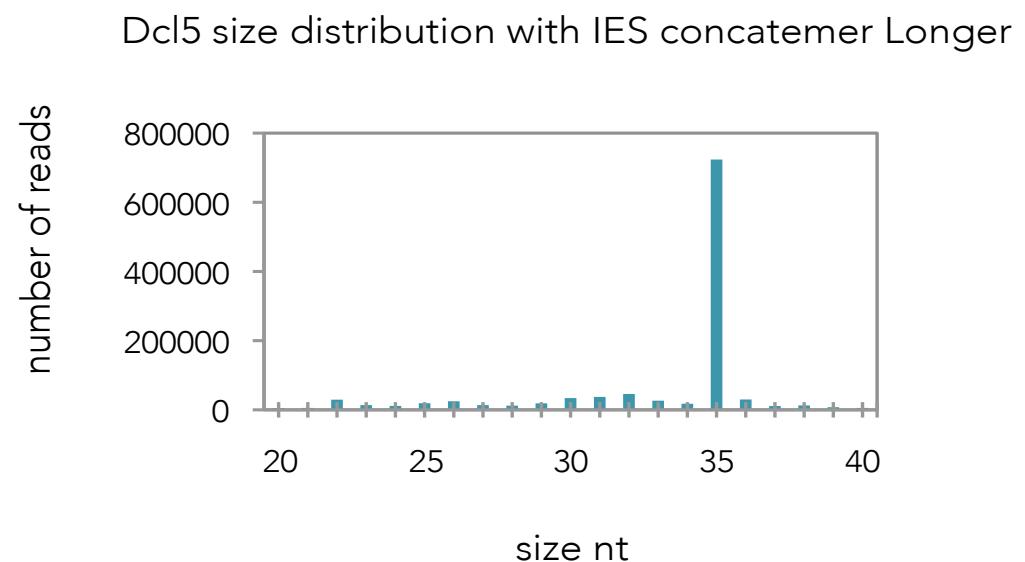
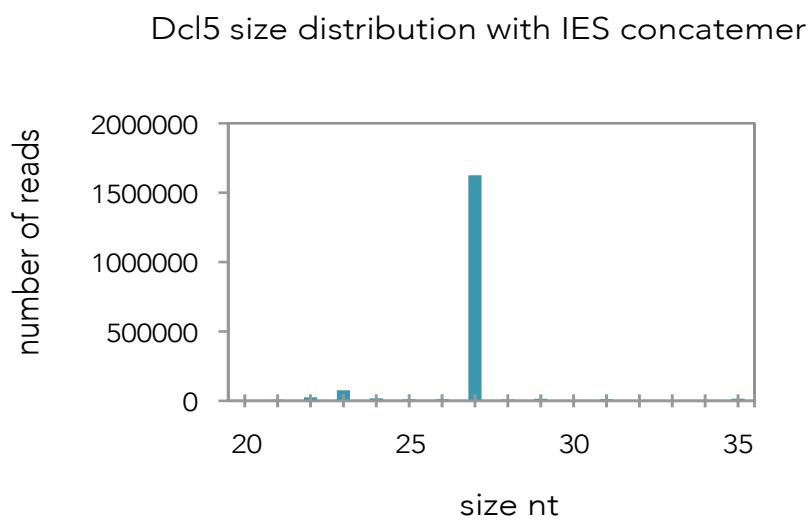
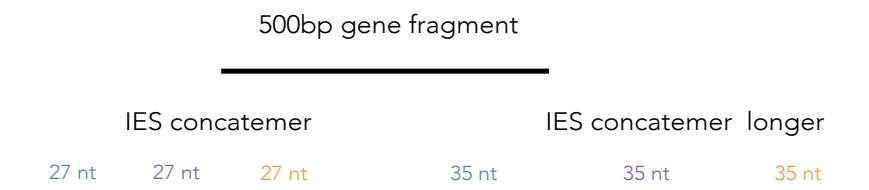
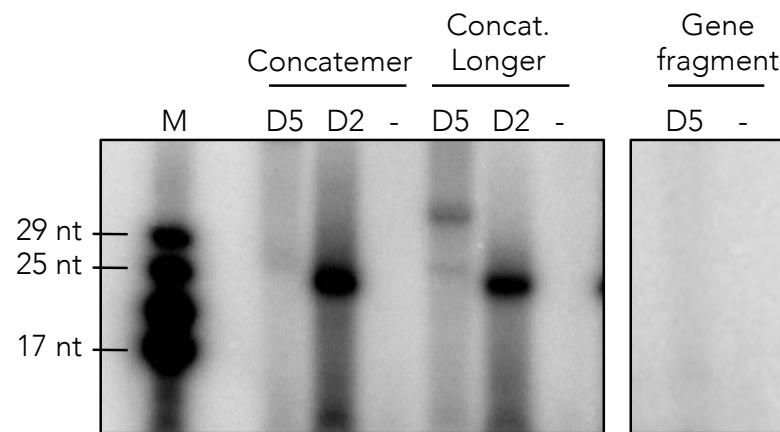
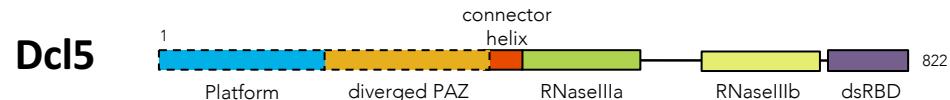
5'-UAGNNNNNNNNNNNNNNCUAU-3'  
3'-NUAUCNNNNNNNNNNNNNGAU-5'



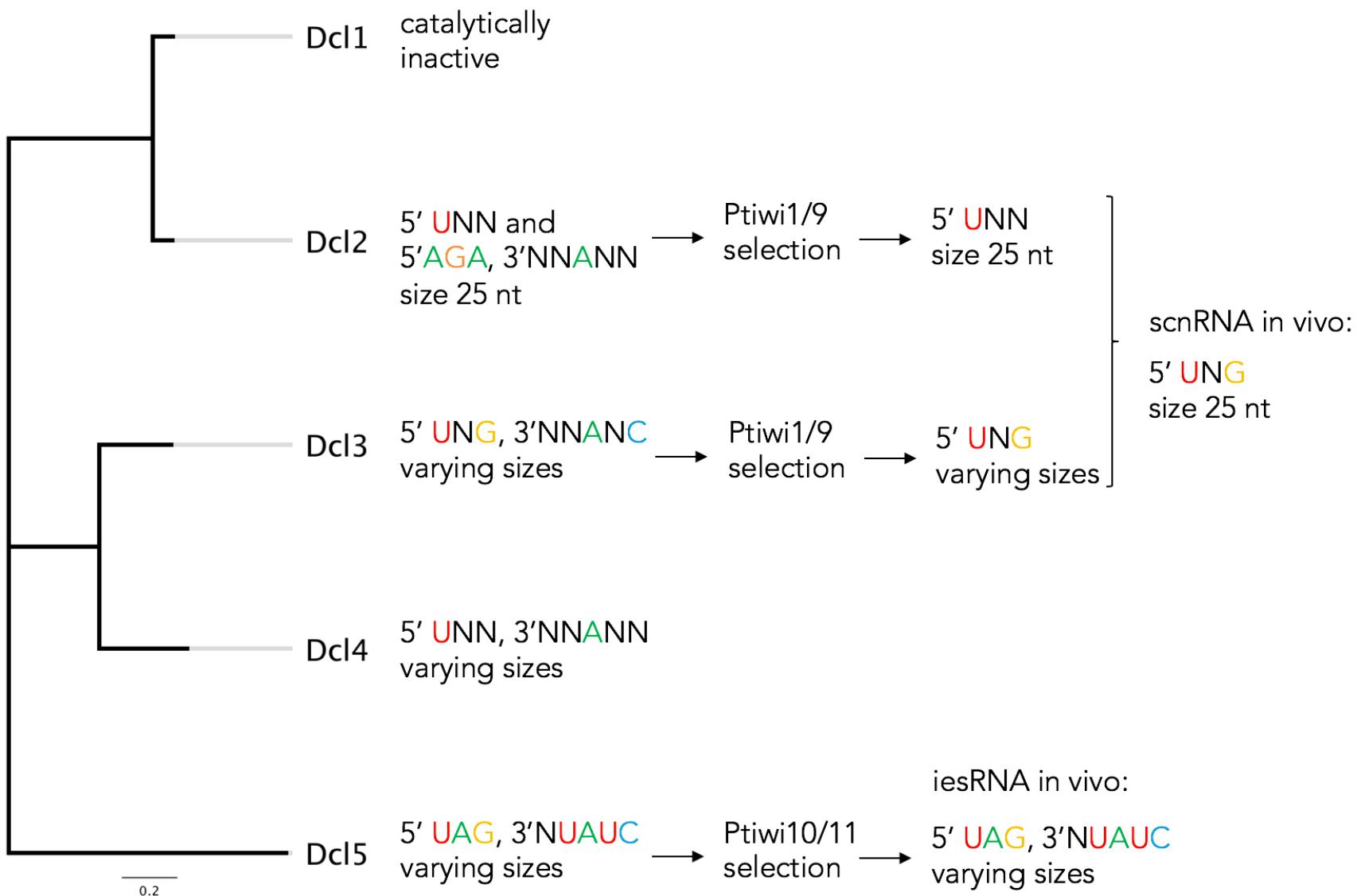


Dcl5 size distribution with IES concatemer

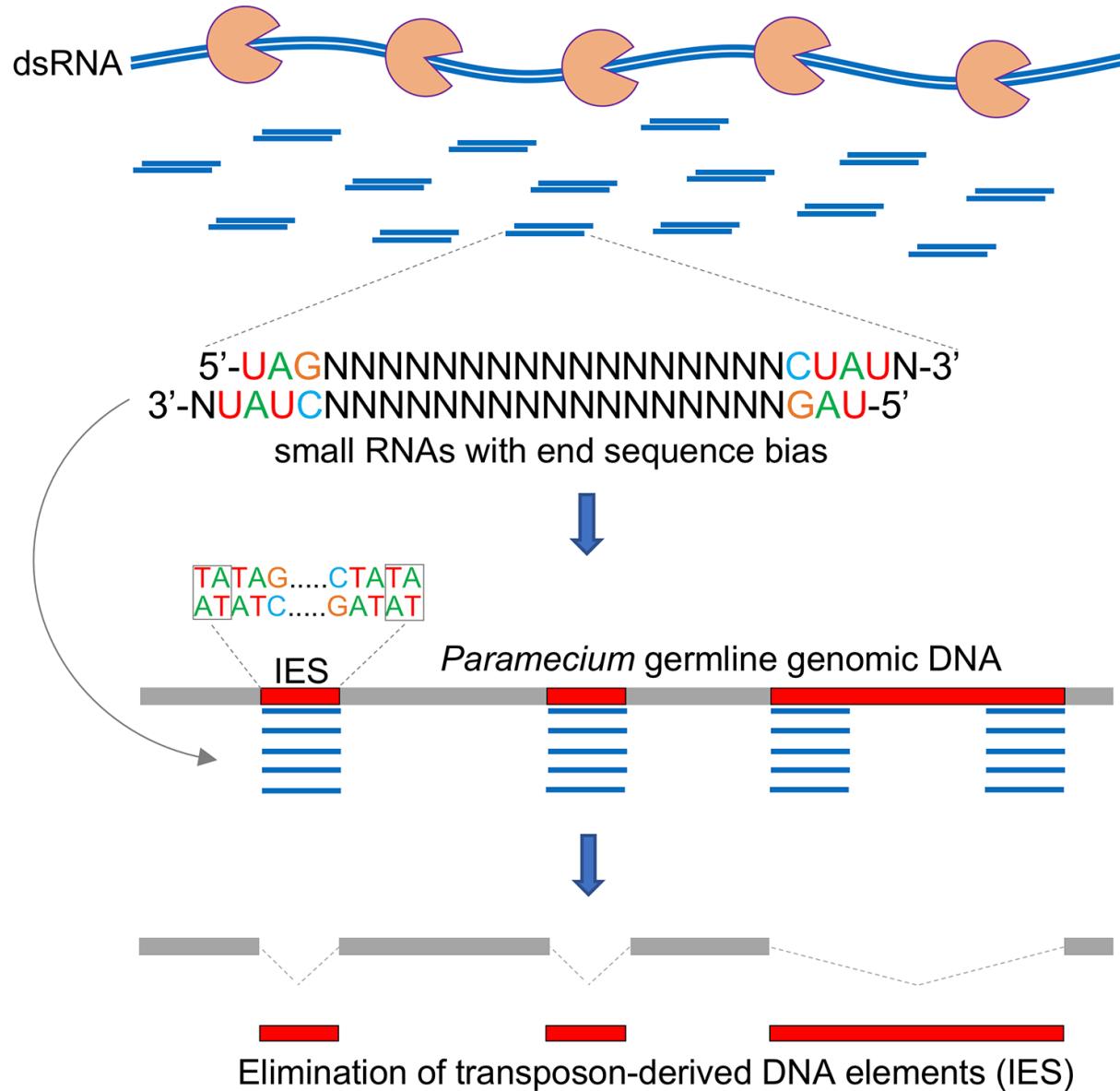




# Summary of Dcl cleavage preferences



Dicer-like proteins with sequence cleavage preferences



# Acknowledgments

## Nowacki lab:

Sarah Allen, PhD  
Estienne Swart, PhD  
Michael Brauchle, PhD  
Zachary Neeb, PhD  
Xyrus Maurer-Alcalá, PhD  
Ryuma Matsubara, PhD  
Nasikhat Stahlberger, PhD  
Elvis Tasih Ajuh, PhD  
Aditi Singh, PhD  
Cristina Hoehener  
Iwona Rzeszutek  
Iris Hug  
Sebastian Bechara  
Therese Solberg  
Lyna Kabbani  
Flurin Caviezel



## Funding:



FONDS NATIONAL SUISSE  
SCHWEIZERISCHER NATIONALFONDS  
FONDO NAZIONALE SVIZZERO  
SWISS NATIONAL SCIENCE FOUNDATION

