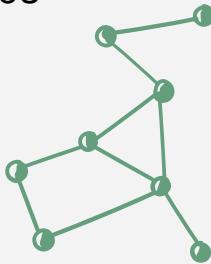




# DNA Pol 32 governs parental histone transfer to DNA replication lagging strand

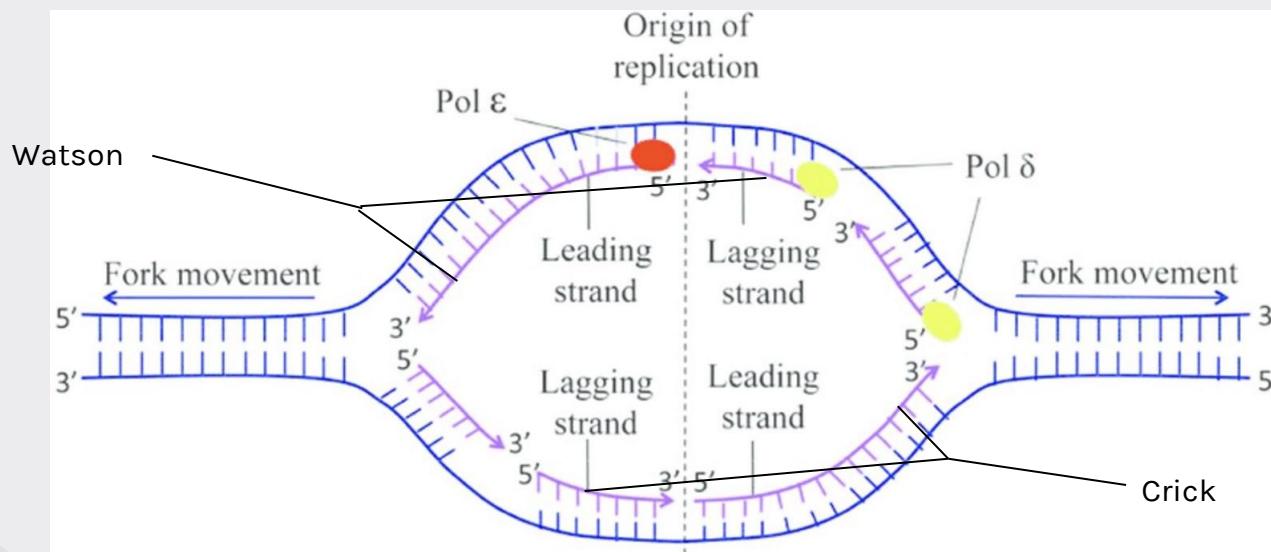
Kimin Nguyen, Jennifer Amador-Gonzalez,  
Meghana Nittala, Natalie Wang, James  
Mohn

$$A + B = C$$



# Intro

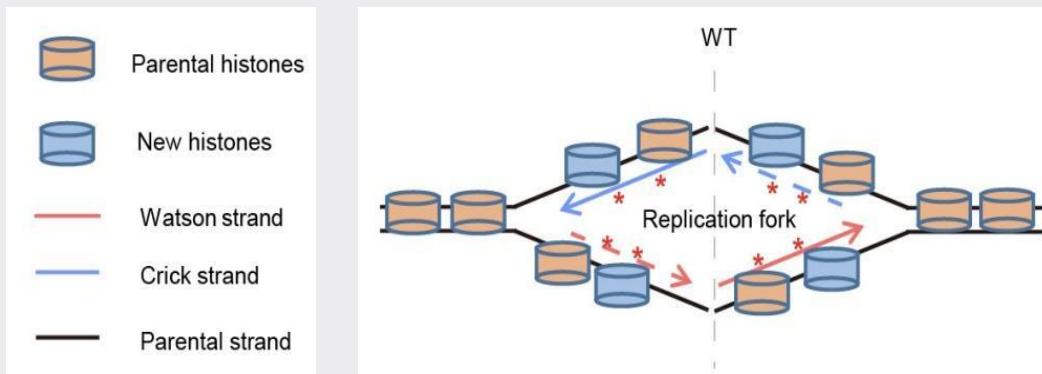
- Chromatin inheritance
  - Conservation of **cellular identity** during cell division
  - **chromatin replication** is linked with **DNA replication**





# System

- Nucleosome reassembly during replication
  - **Recycling of parental histones** + recruitment of **new histones** → restoration of chromatin in daughter strands
  - = **faithful epigenetic inheritance**



→ Daughter strands have **equal amounts of parental and new histones**



# Study

## Known

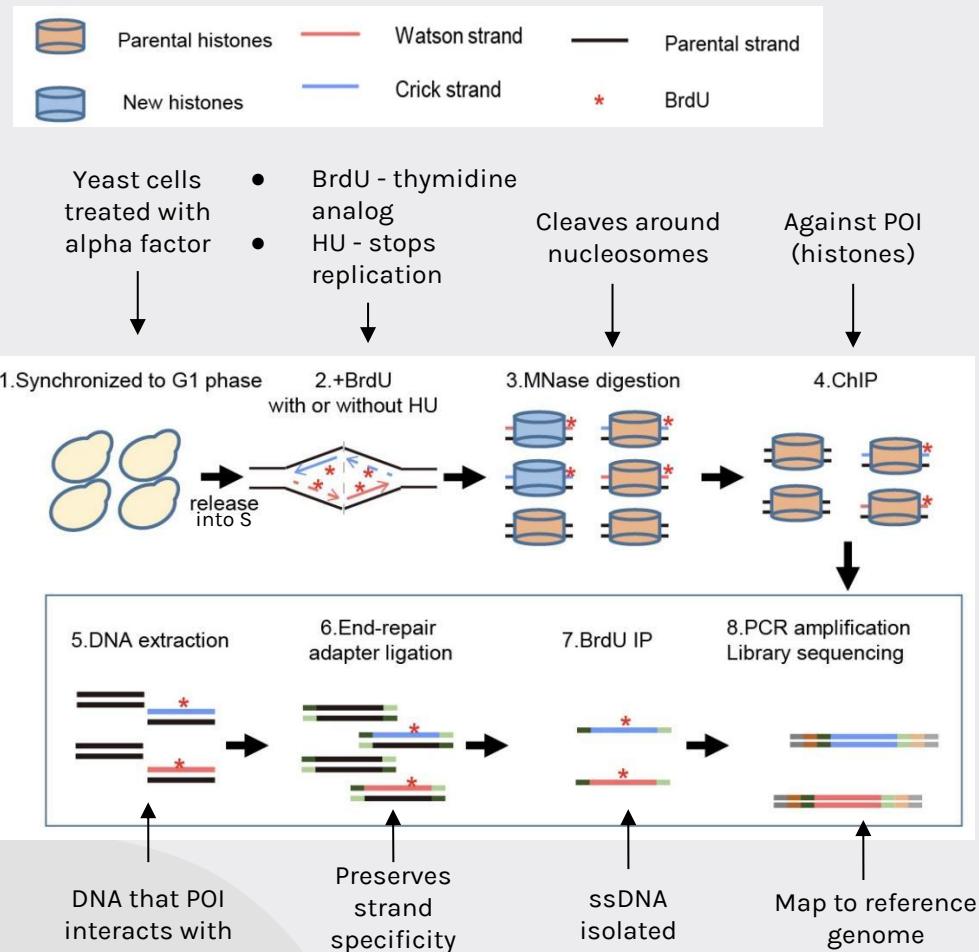
- In **yeast**, recycling of **parental histones** is mediated by...
  - DNA Pol  $\epsilon$  subunits **Dpb3/Dpb4**
    - Onto **leading strand**
  - MCM helicase subunit **Mcm2**
    - Onto **lagging strand**

Pathway?

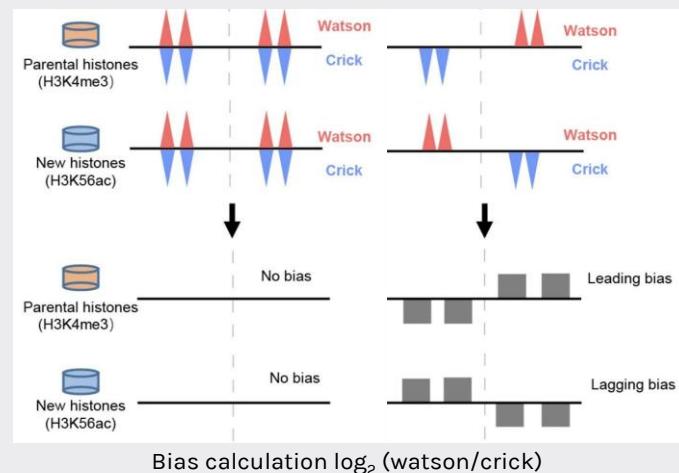
## Findings

- The researchers identified **Pol32...**
  - Non-essential subunit of DNA Pol  $\delta$
- Overall findings
  - Pol32 binds H3/H4 *in vitro* and *in vivo*
  - Is a critical **histone chaperone** acting downstream of Mcm2

# eSPAN



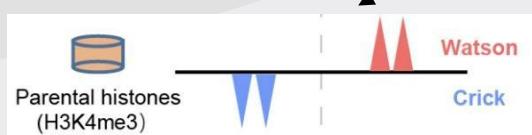
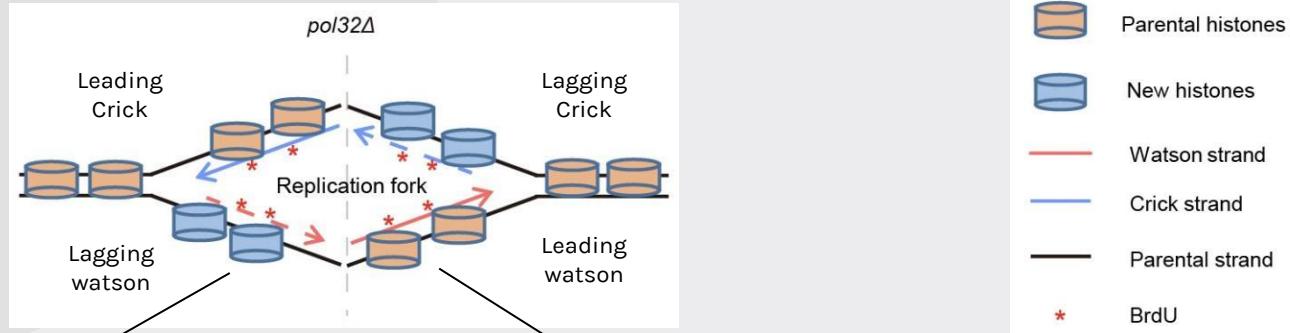
- Enrichment and sequencing of protein-associated nascent DNA
- Detects protein enrichment at replication forks w/ **strand specificity**
  - Leading vs. lagging strand



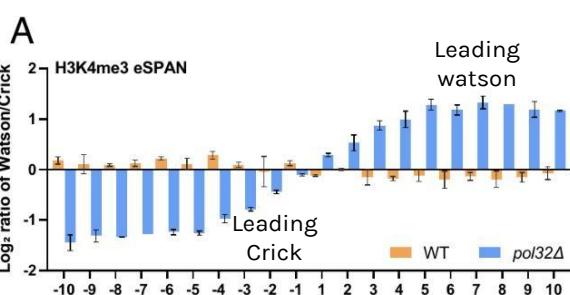
# **FIGURE 1**

# Pol32 Deposits Parental Histones - Histone Modifications

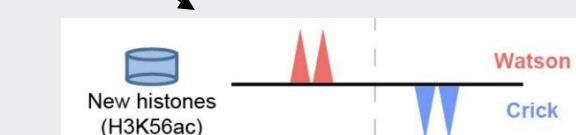
- H3K4me3 - marks **parental** histones
- H3K56ac - marks **new** histones



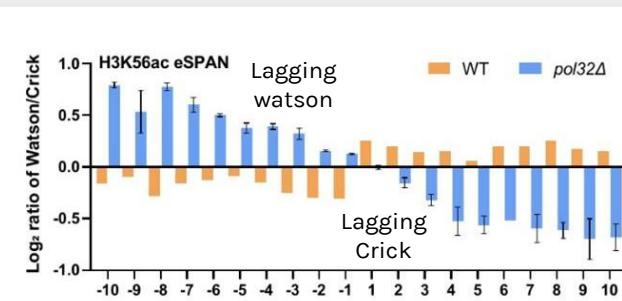
WT only shows slight bias



Parental histones show strong leading strand bias in *Pol32Δ*

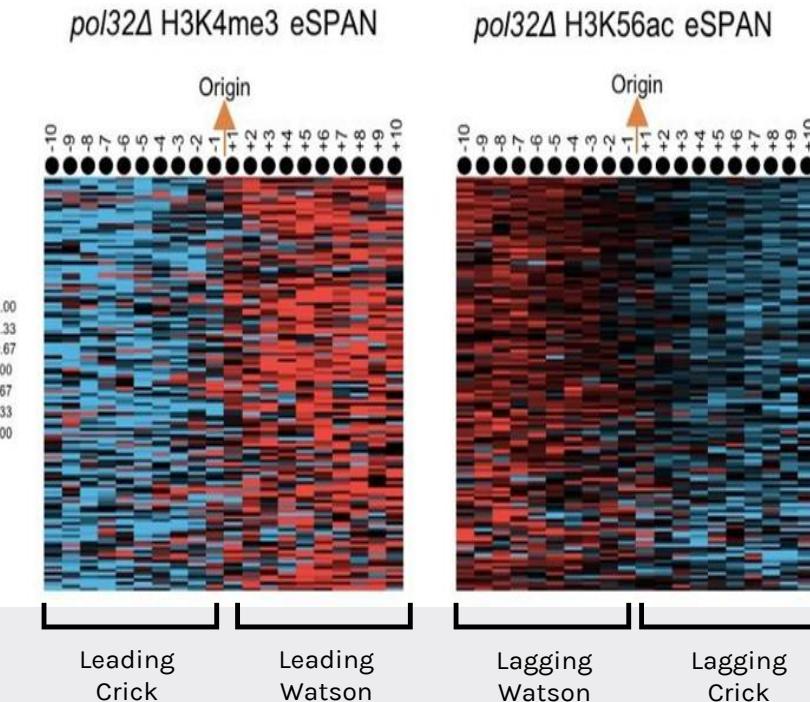


New histones show strong lagging strand bias in *Pol32Δ*



# Pol32 Deposits Parental Histones - Histone Modifications

B

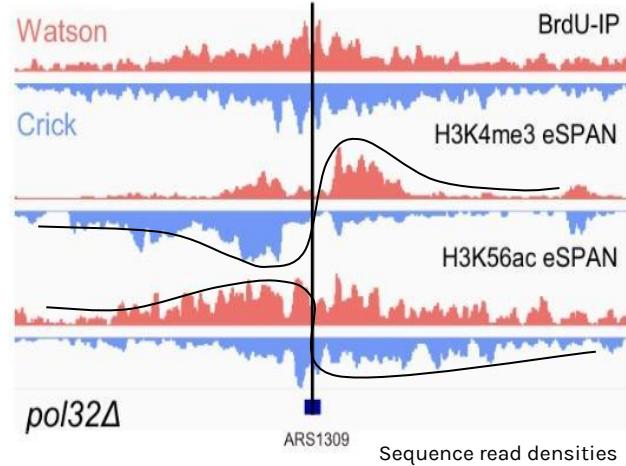


Clear color differences show Pol32 $\Delta$  have strong histone deposition biases

- Bias ratios of 10 flanking nucleosomes
- 134 early DNA replication origins

C

BrdU-IP-ssSeq control to normalize eSPAN data

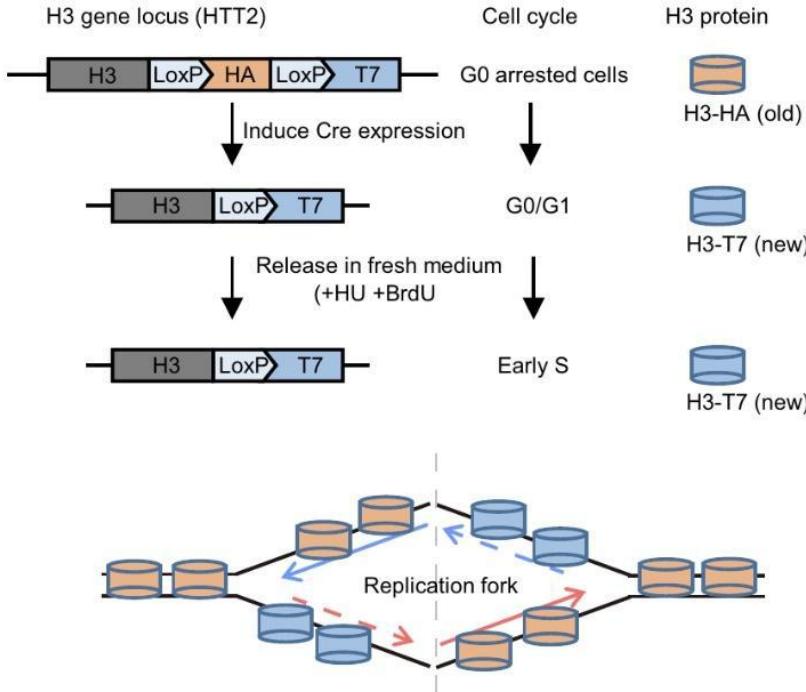


Pol32 participates in **parental** histone H3-H4 deposition onto the **lagging** strand



# Pol32 Deposits Parental Histones - Histone Subunits

D



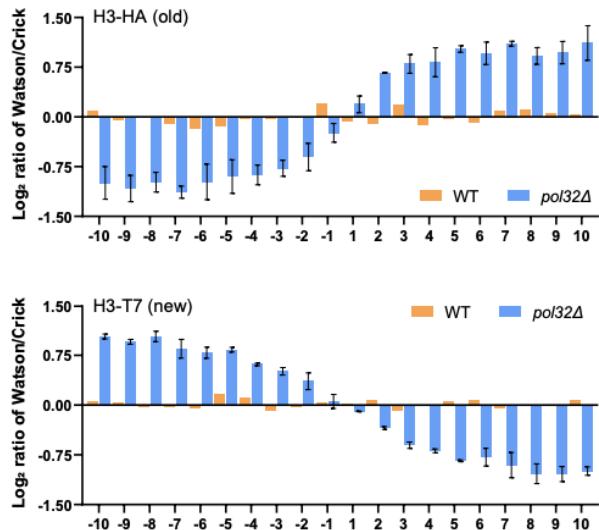
- Recombination-induced Tag Exchange System
  1. Integrate cassette w/ floxed HA
  2. Temporally control Cre expression
  3. Cre excises HA tag
  4. T7 tag now expressed
- H3-HA → **parental** histones
- H3-T7 → **new** histones



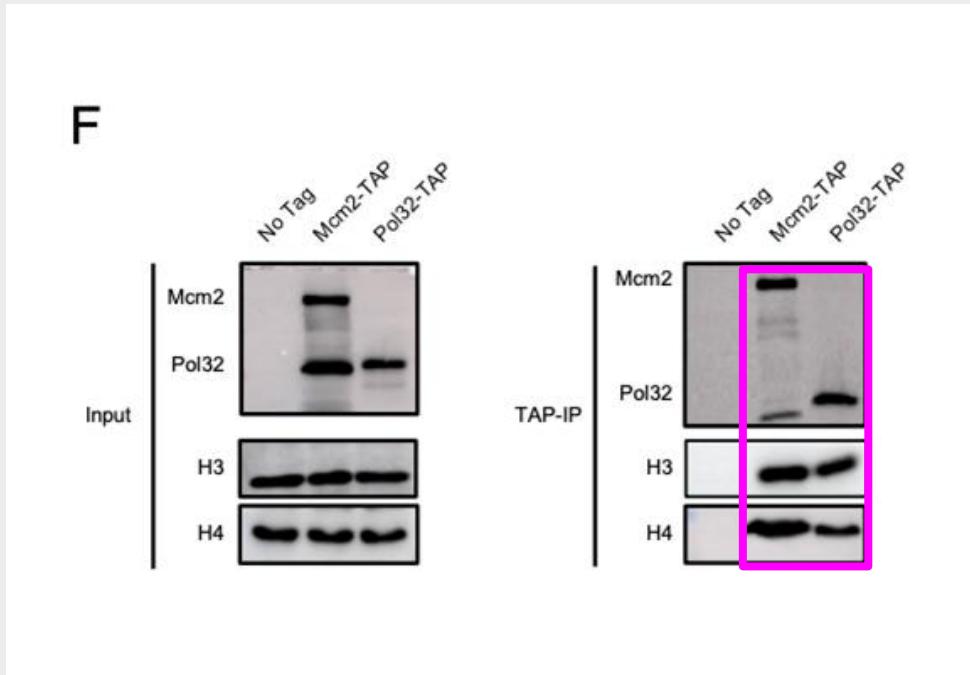


# Pol32's Role in Histone Transfer

E

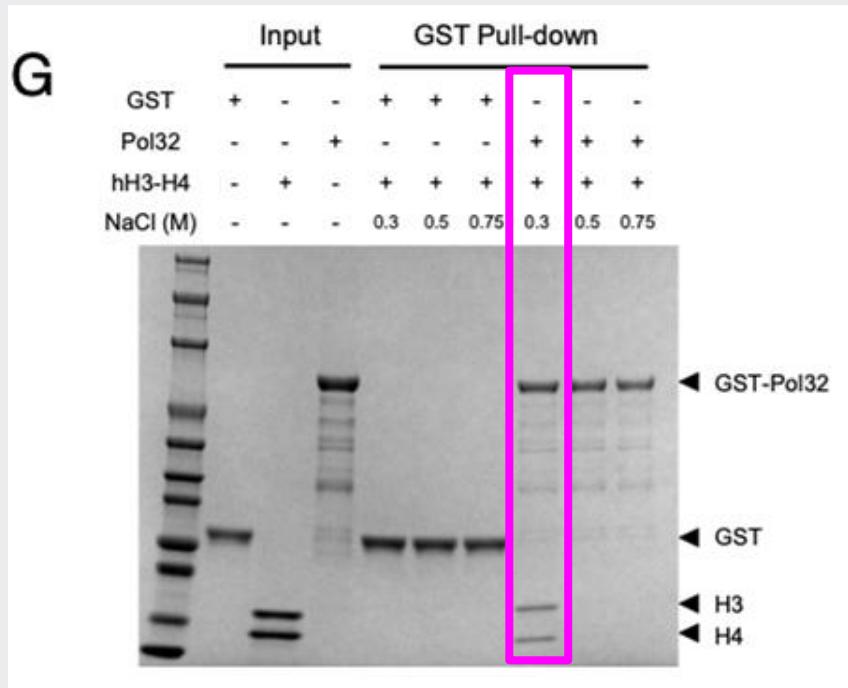


F





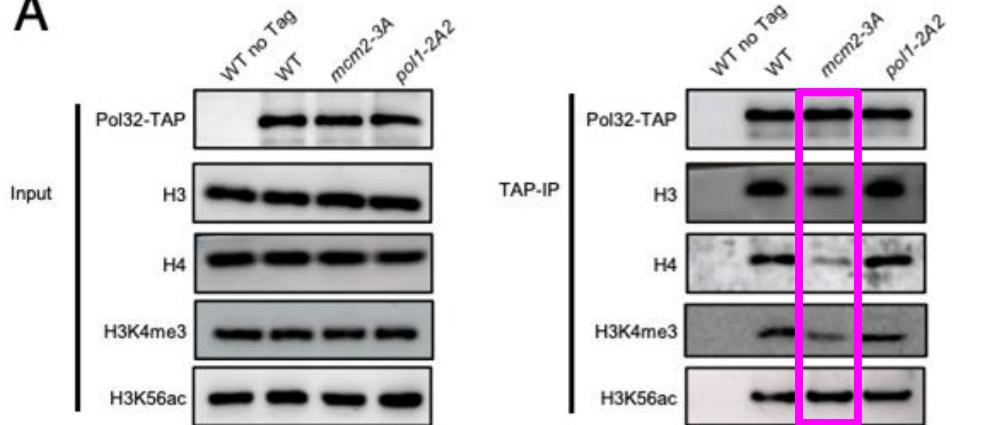
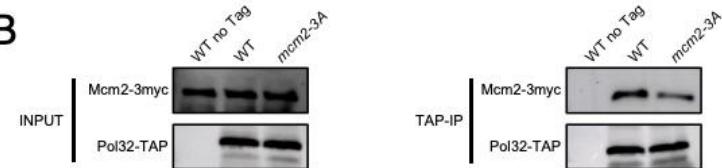
# Direct Interaction of Pol32 with Histones H3–H4 Confirmed by GST Pull-Down Assay



# **FIGURE 2**

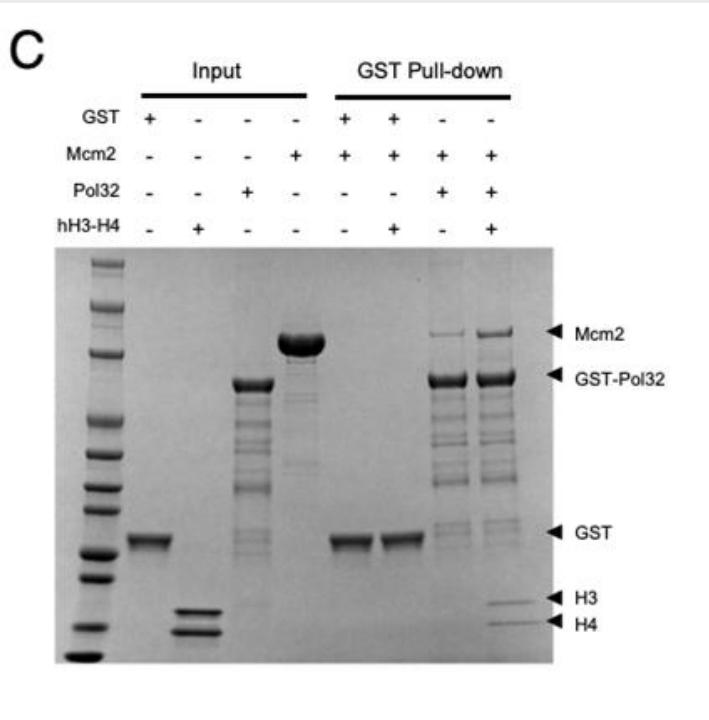


# Mcm2 Transfers Parental Histone to Pol32

**A****B**

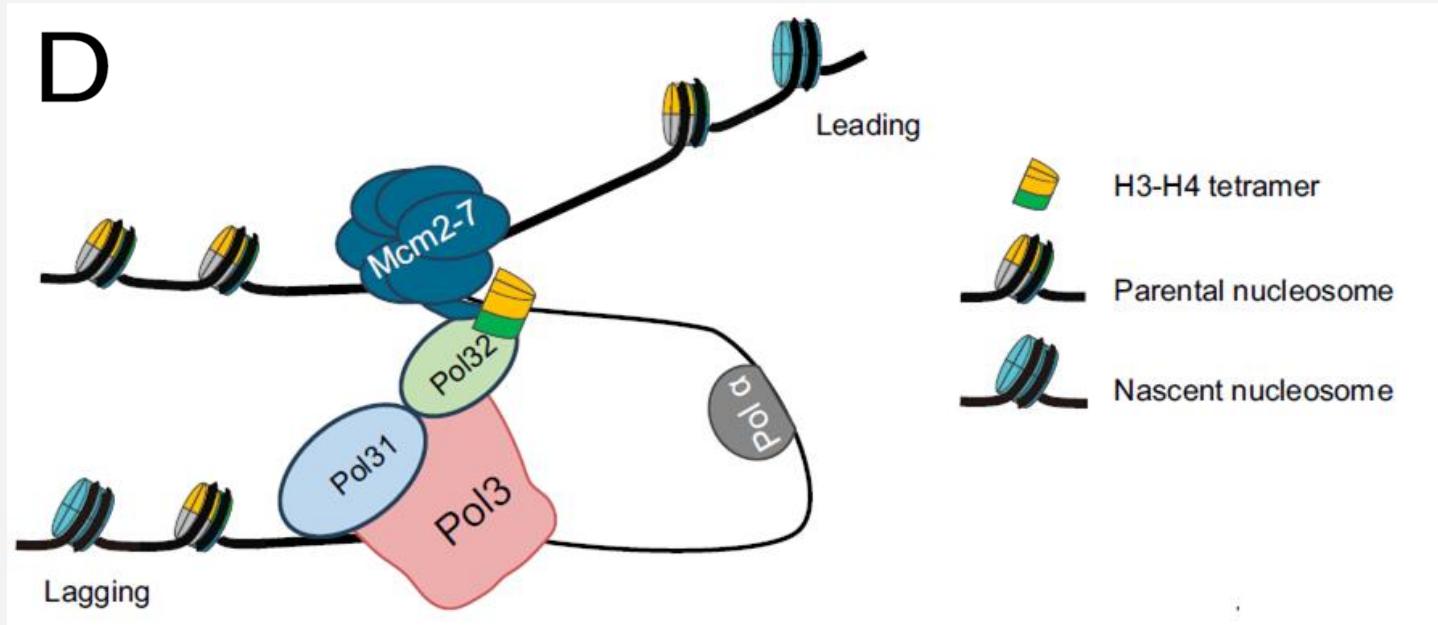


# Histone H3–H4 Enhances the Pol32–Mcm2 Interaction





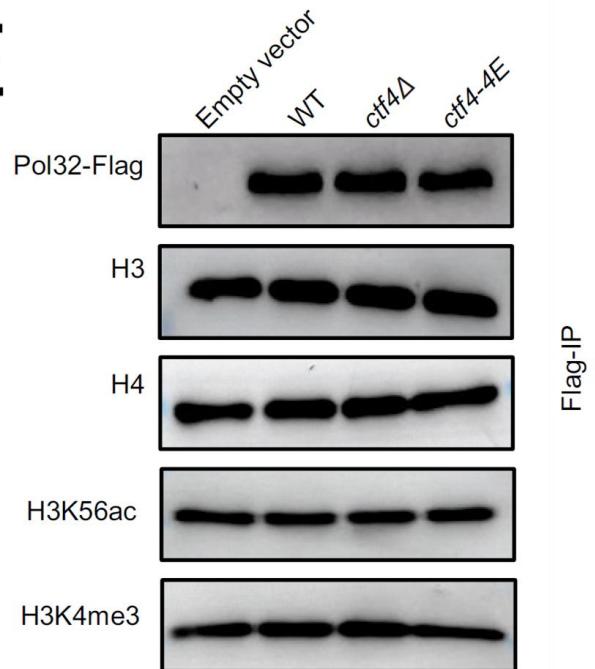
# A Model of MCM2-7 and Pol32 Interaction



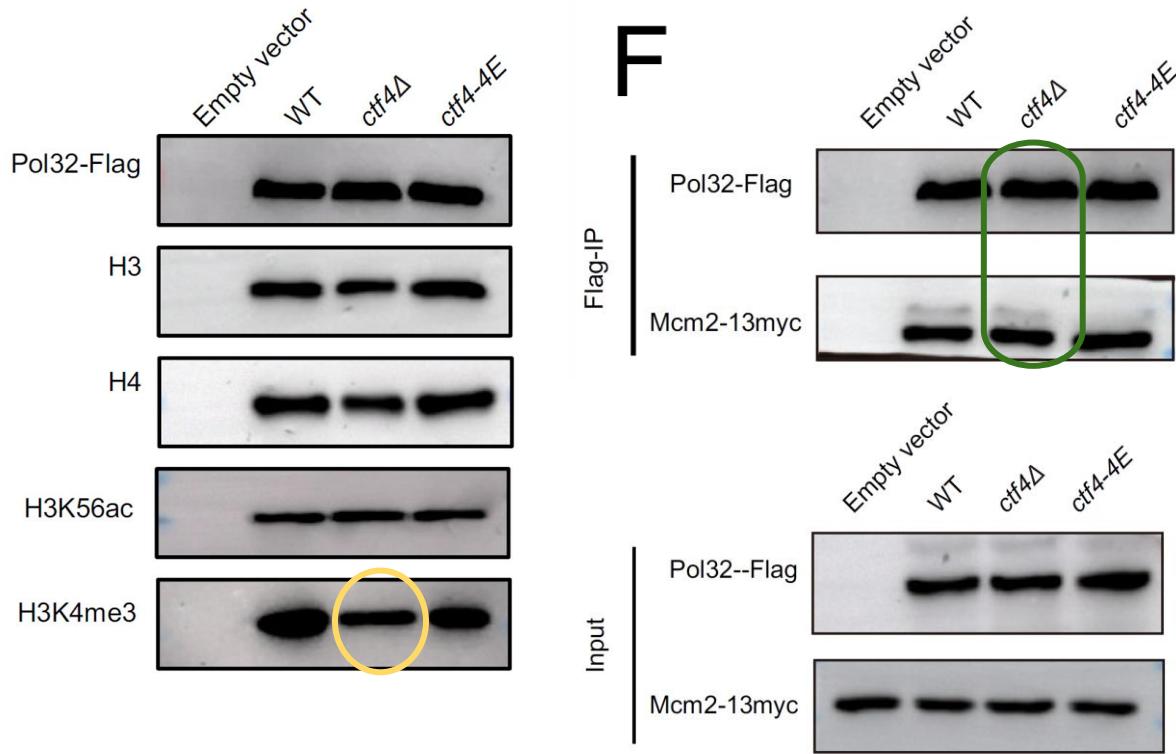


# Ctf4 is not critical to the Pol32-Mcm2 Interaction

E

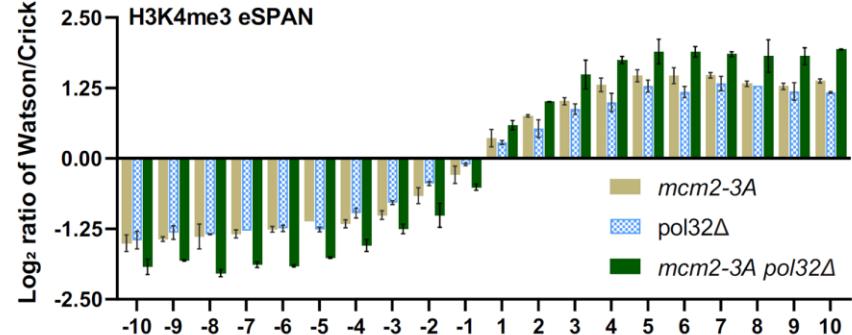


F

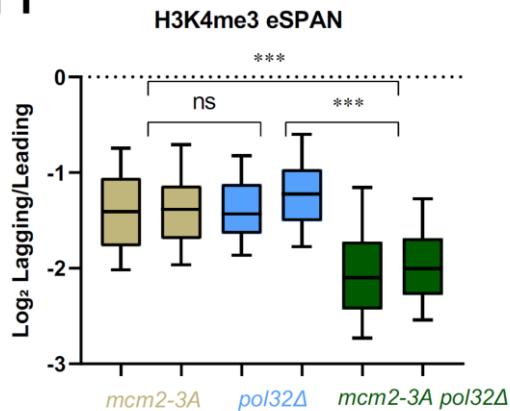


# eSPANs of Double Mutants Show Synergistic Effects

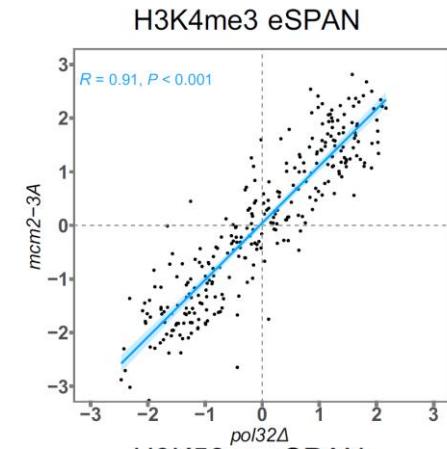
G



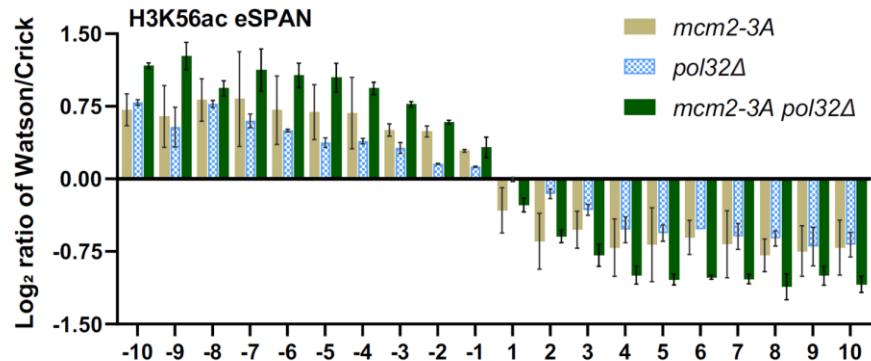
H



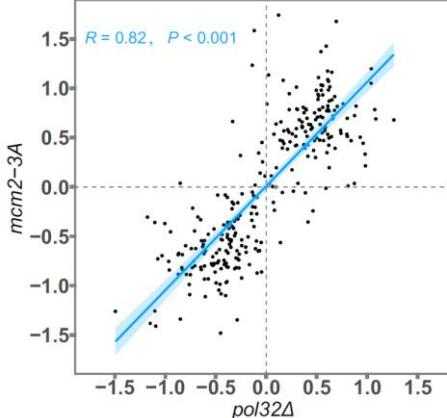
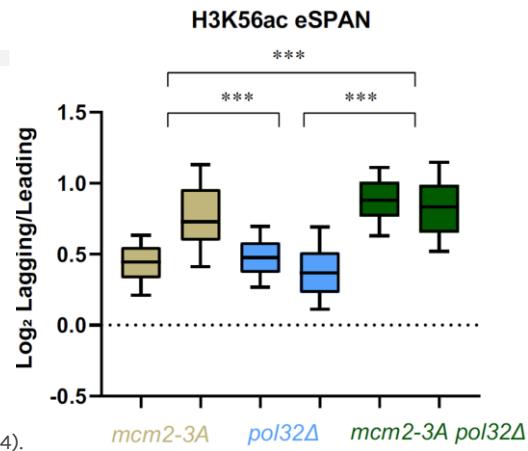
I



J



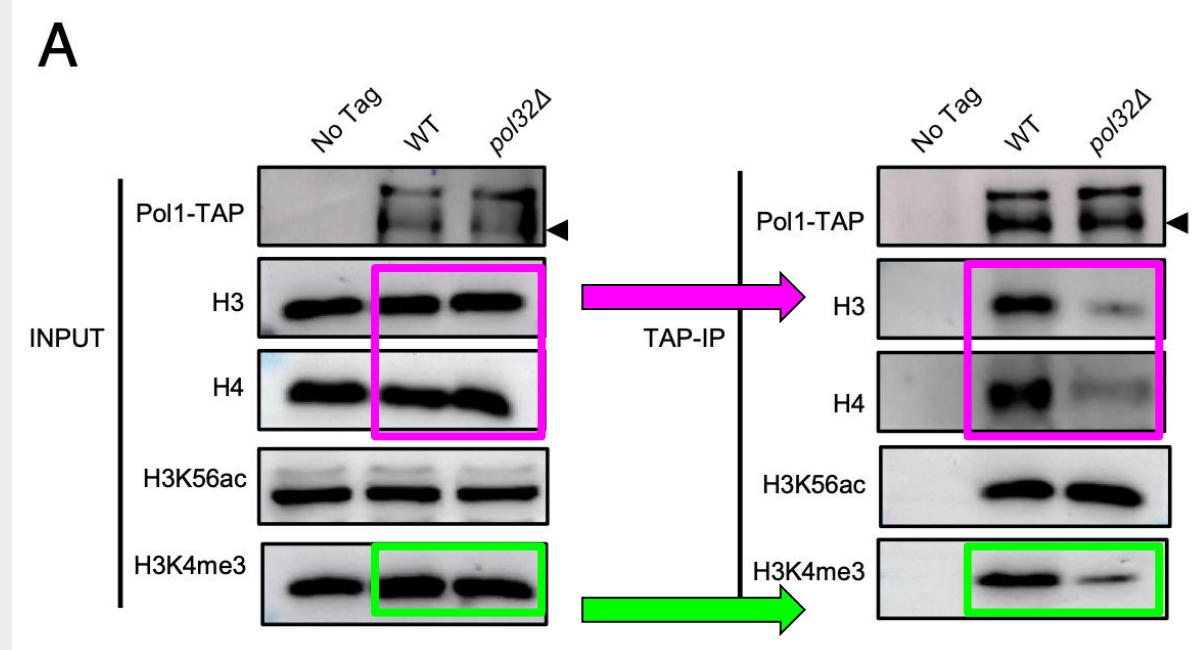
K



# **FIGURE 3**

# Pol1-TAP pull-down in WT vs. pol32 $\Delta$ cells

Observed association of histone H3, H4, H3K56ac, and H3K4me3 with Pol1 in both WT and pol32 $\Delta$  cells.



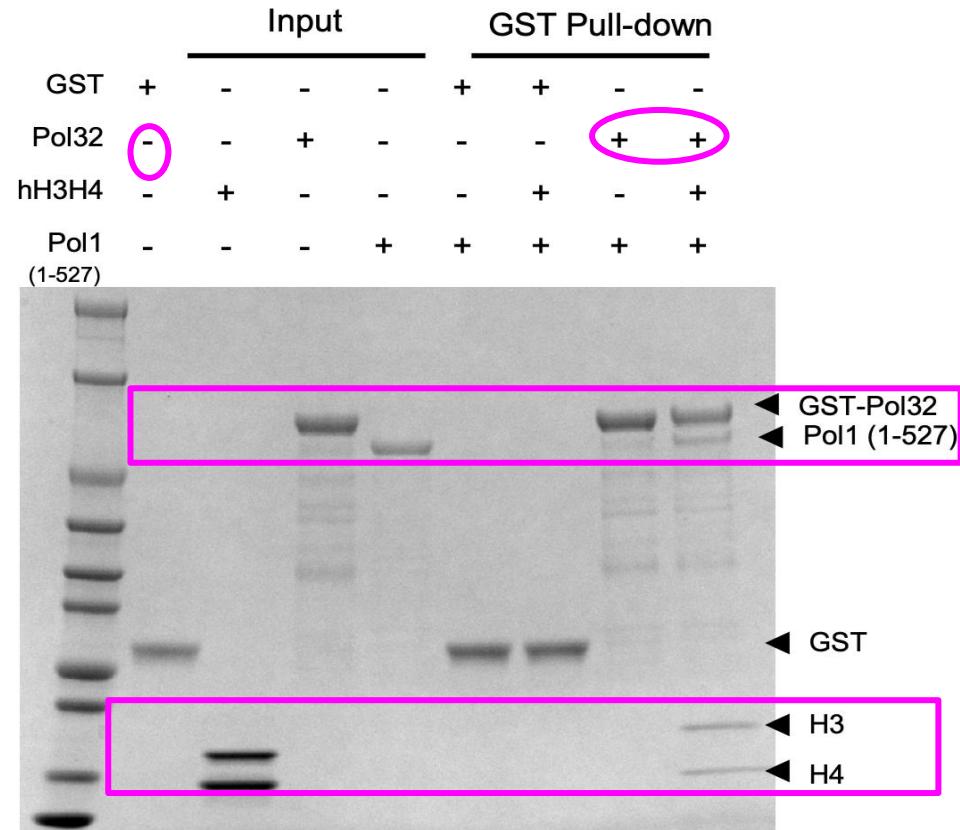
Indicating Pol32's essential role in facilitating Pol1's interaction with modified parental histones

# In vitro binding of Pol1 and Pol32 in presence of H3-H4 tetramers

**Increased Pol1-Pol32 interaction when H3-H4 tetramers are **present**.**

This supports the idea  
that Pol1 functions  
downstream of Pol32 in  
**histone transfer.**

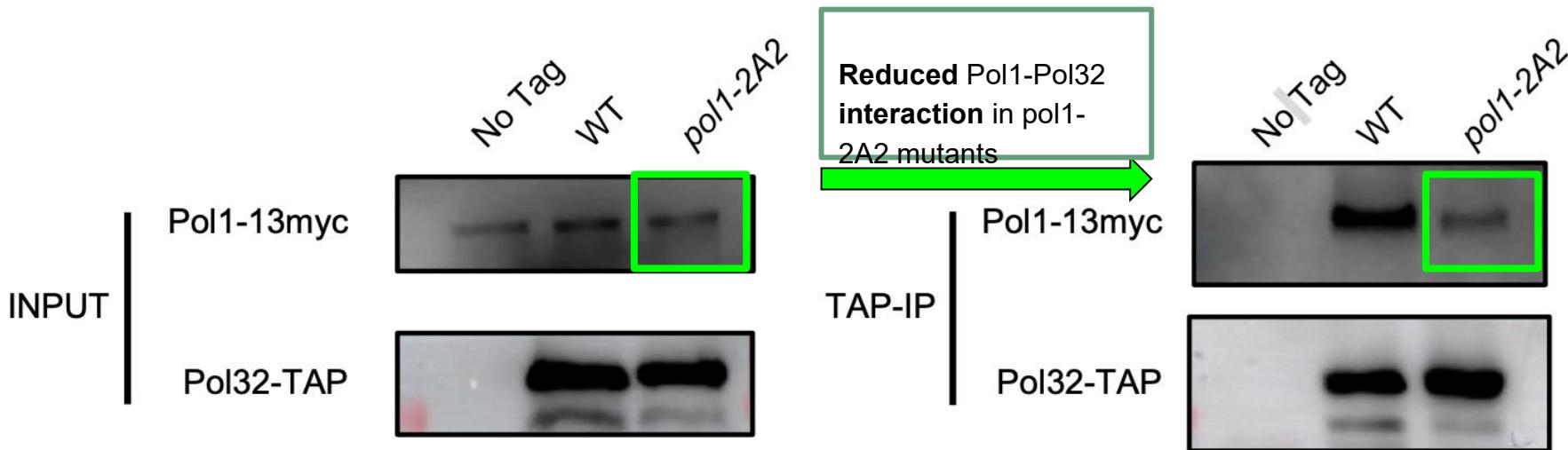
B



C

# Pol32-TAP purification and Pol1-13myc detection in WT and pol1-2A2

C



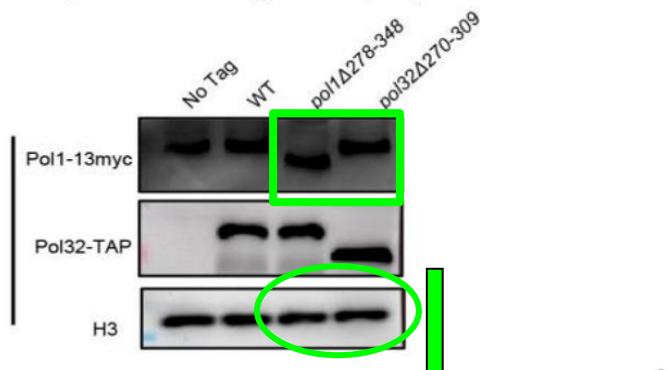
Suggesting that **specific amino acid changes in Pol1** (altered in the pol1-2A2 mutant) **impact its binding with Pol32**.

# Effect of Pol1 and Pol32 deletion mutants on interactions

Specific regions of Pol32 are crucial for Pol1-Pol32 interaction and for facilitating histone H3 transfer

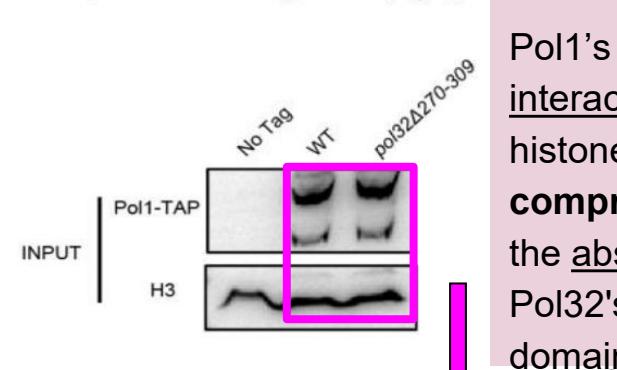
A

Input control for figure 3D (left)



B

Input control for figure 3D (right)

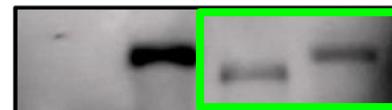


Pol1's ability to interact with histones is **compromised** in the absence of Pol32's C-terminal domain.

D

TAP-IP

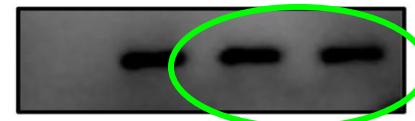
Pol1-13myc



Pol32-TAP

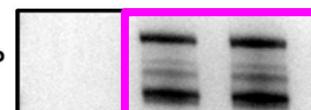


H3

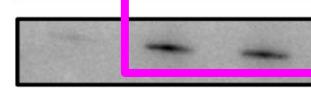


TAP-IP

Pol1-TAP

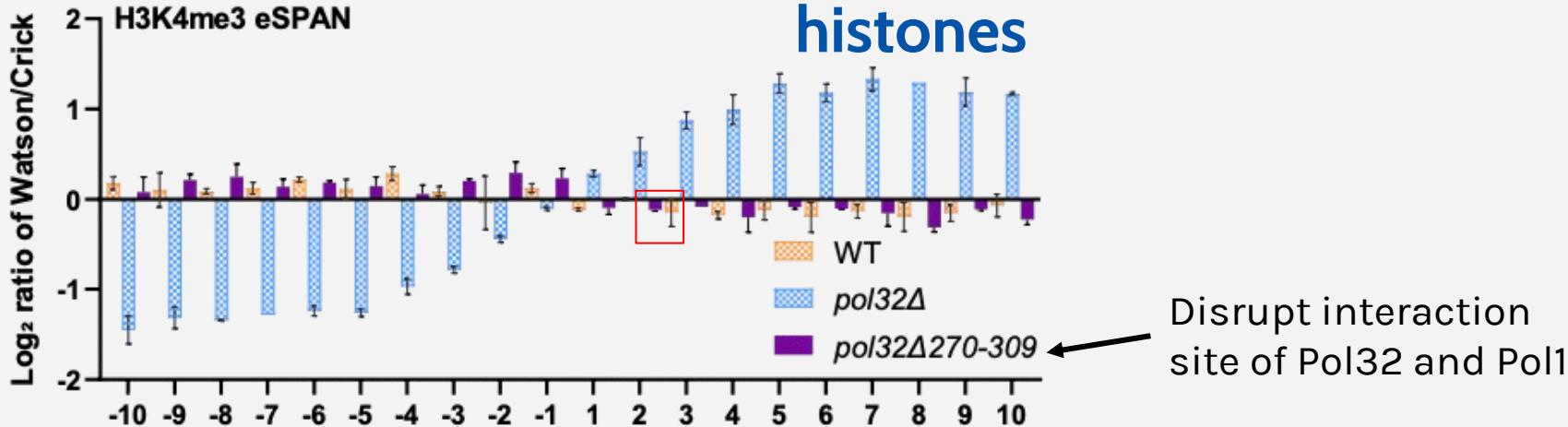


H3





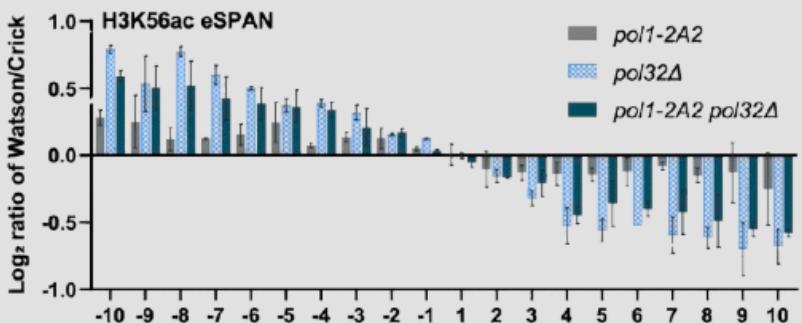
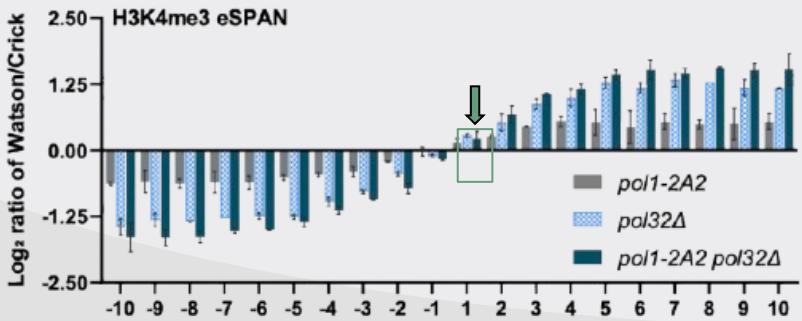
# Pol1 and Pol32 collaborate in the transfer of parental histones



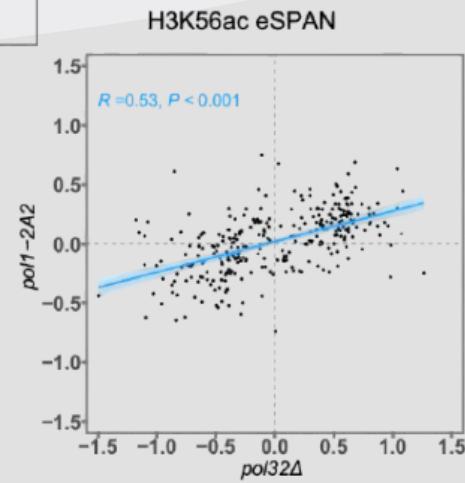
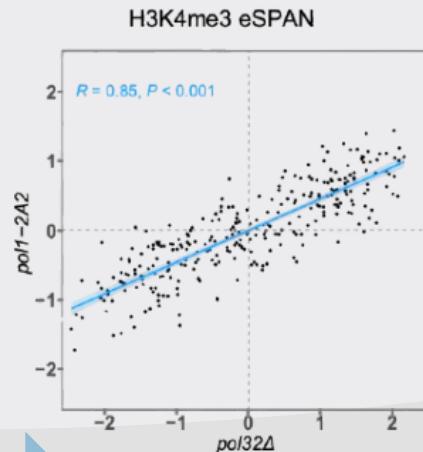
=> Pol32's interaction with the H3-H4 tetramer is more important for parental histone transfer than its direct interaction with Pol1.



# Strand Bias in Pol1 and Pol32 Mutants & Its correlation



Plotting the ratio of  
Watson/Crick between  
Pol $\Delta$ 32 and Pol1-2A2





## Limitation & Future change

- Model Organism Limitations
- Lack of Longitudinal Studies





## Key Findings

- The DNA polymerase δ subunit Pol32 is identified as a crucial regulator of parental histone H3-H4 transfer to the lagging strand during DNA replication.
- Pol32 directly binds to histone H3-H4 and functions downstream of Mcm2 and upstream of DNA Pol1 in the histone transfer pathway

=> opens new avenues for exploring the mechanisms of epigenetic inheritance.



H<sub>2</sub>CO<sub>2</sub>



# THANK YOU

IF YOU HAVE ANY QUESTIONS  
PLEASE ASK!

