

Paul Nurse
KITP Evo Cell, Feb 25, 2010



Overview: The Cell-Cycle Control System 3-0

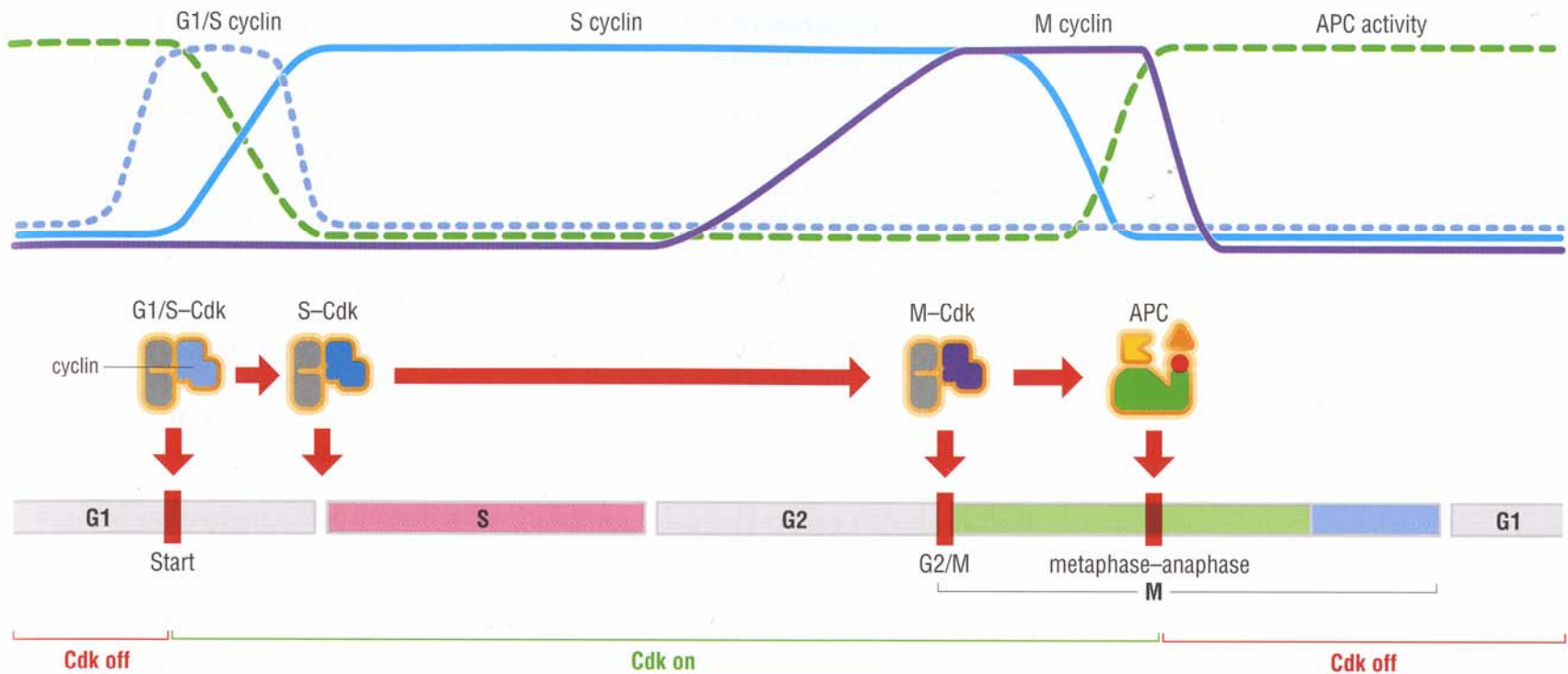
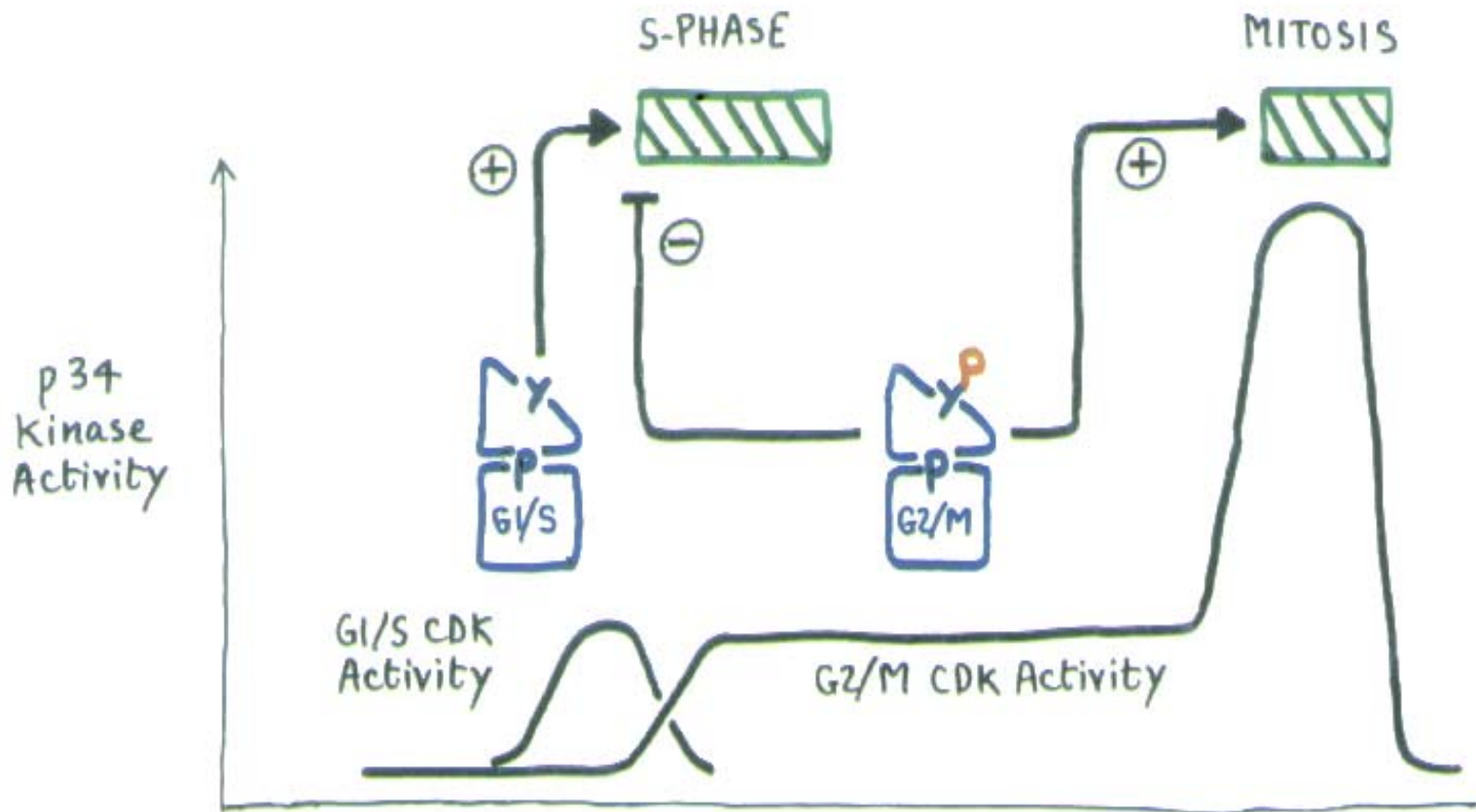
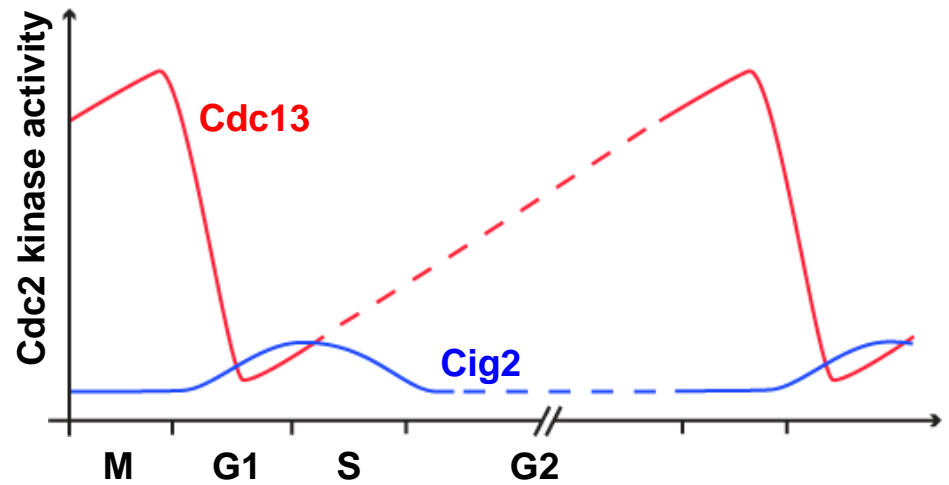
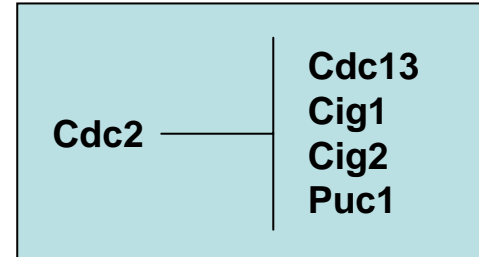
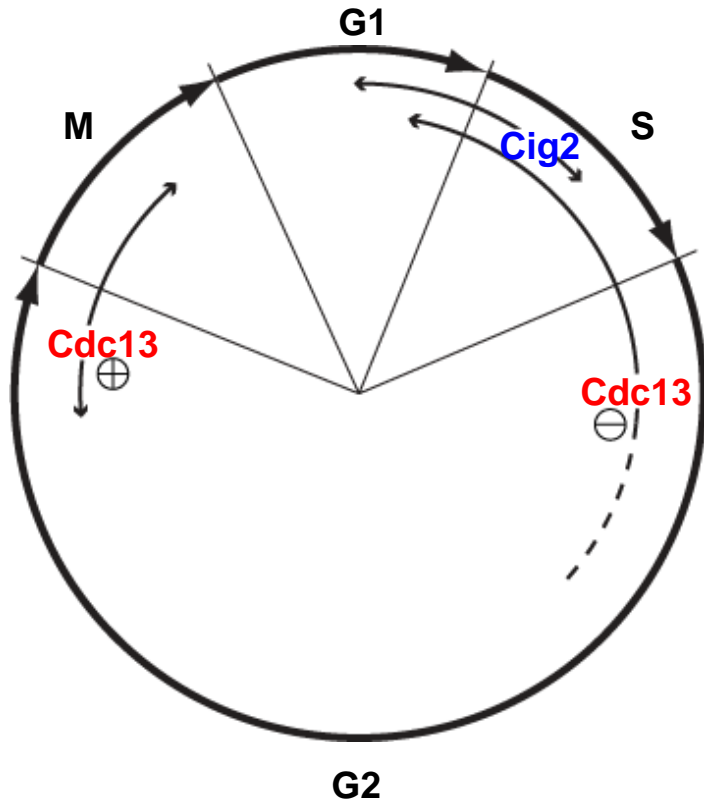


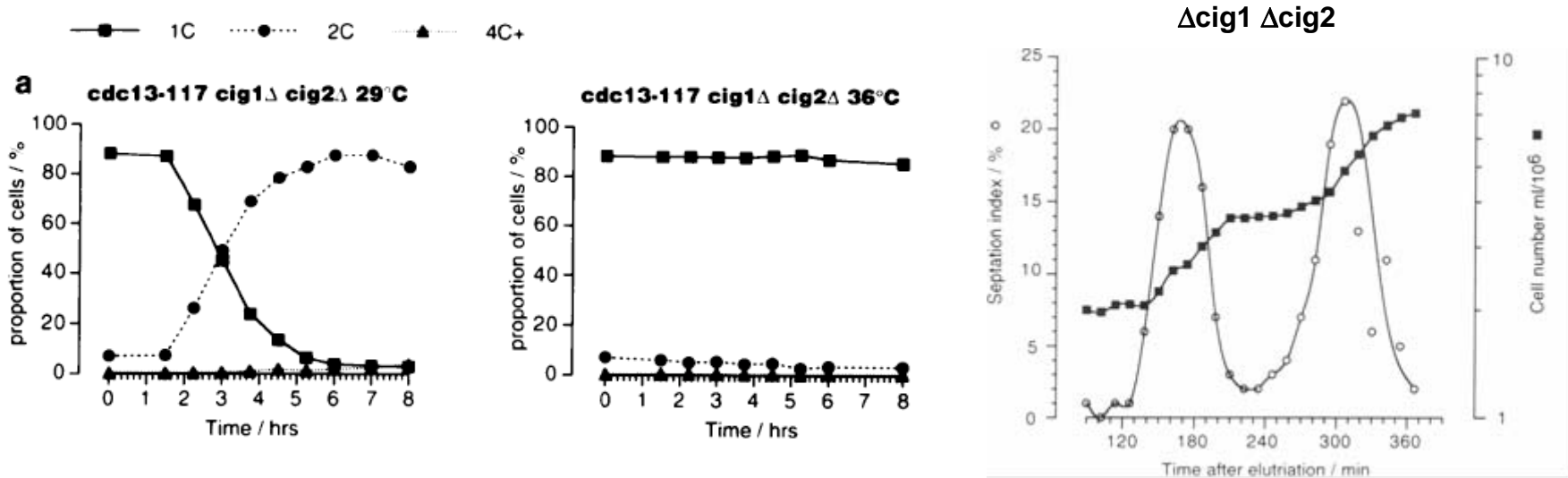
Figure 3-1 A simplified view of the cell-cycle control system Levels of the three major cyclin types oscillate during the cell cycle (top), providing the basis for oscillations in the cyclin–Cdk complexes that drive cell-cycle events (bottom). In general, Cdk levels are constant and in large excess over cyclin levels; thus, cyclin–Cdk complexes form in parallel with cyclin levels. The enzymatic activities of cyclin–Cdk complexes also tend to rise and fall in parallel with cyclin levels, although in some cases Cdk inhibitor proteins or phosphorylation introduce a delay between the formation and activation of cyclin–Cdk complexes. Formation of active G1/S–Cdk complexes commits the cell to a new division cycle at the Start checkpoint in late G1. G1/S–Cdks then activate the S–Cdk complexes that initiate DNA replication at the beginning of S phase. M–Cdk activation occurs after the completion of S phase, resulting in progression through the G2/M checkpoint and assembly of the mitotic spindle. APC activation then triggers sister-chromatid separation at the metaphase-to-anaphase transition. APC activity also causes the destruction of S and M cyclins and thus the inactivation of Cdks, which promotes the completion of mitosis and cytokinesis. APC activity is maintained in G1 until G1/S–Cdk activity rises again and commits the cell to the next cycle. This scheme serves only as a general guide and does not apply to all cell types.



Different cyclins control different phases of the cell cycle



Questioning the dogma of cyclin mediated cdk specificity



(Fisher and Nurse, 1996)

Cdk1 is sufficient to drive the mammalian cell cycle

David Santamaría^{1*}, Cédric Barrière^{1,2*†}, Antonio Cerqueira¹, Sarah Hunt^{1†}, Claudine Tardy¹, Kathryn Newton³, Javier F. Cáceres³, Pierre Dubus², Marcos Malumbres¹ & Mariano Barbacid¹

Nature 2007

- Is a single cdk-cyclin oscillator sufficient and flexible enough to drive dramatically different events?
- What constitutes the minimal machinery that supports the cell cycle?

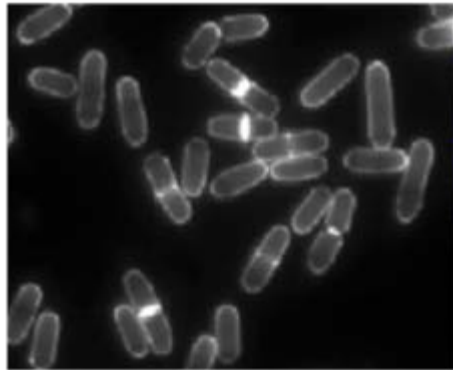


Damien Coudreuse

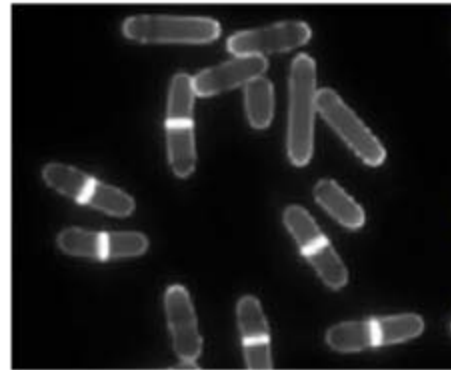
Reduction of the fission yeast Cdk oscillator to a single fusion protein



Wild type

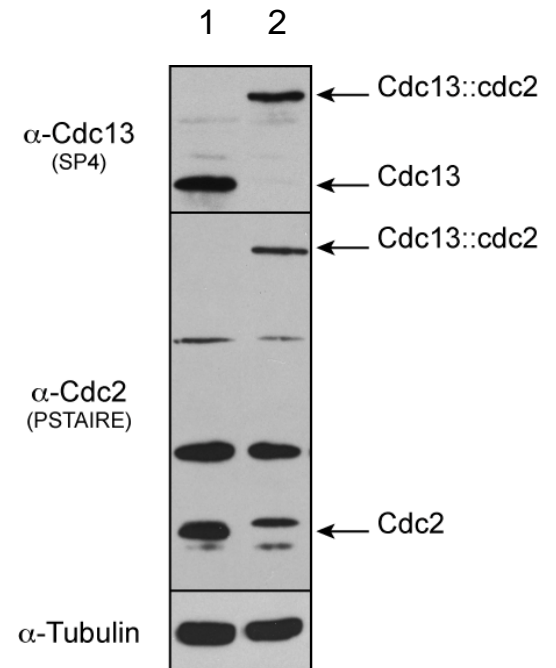
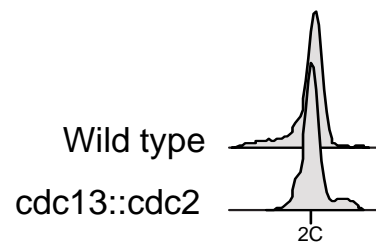


**cdc13::cdc2 Δcdc2
Δcdc13 Δcig1 Δcig2 Δpuc1**



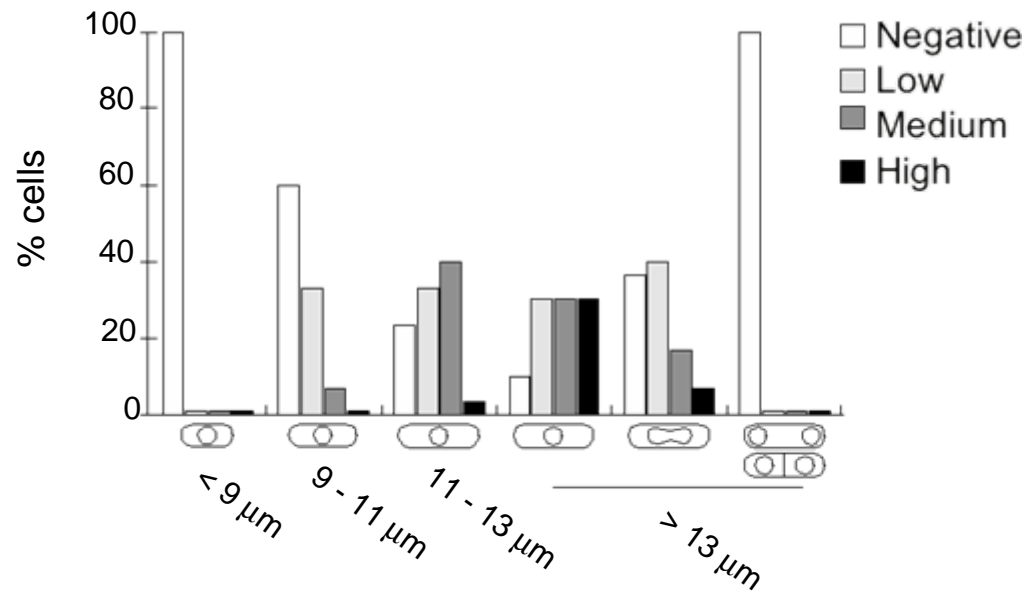
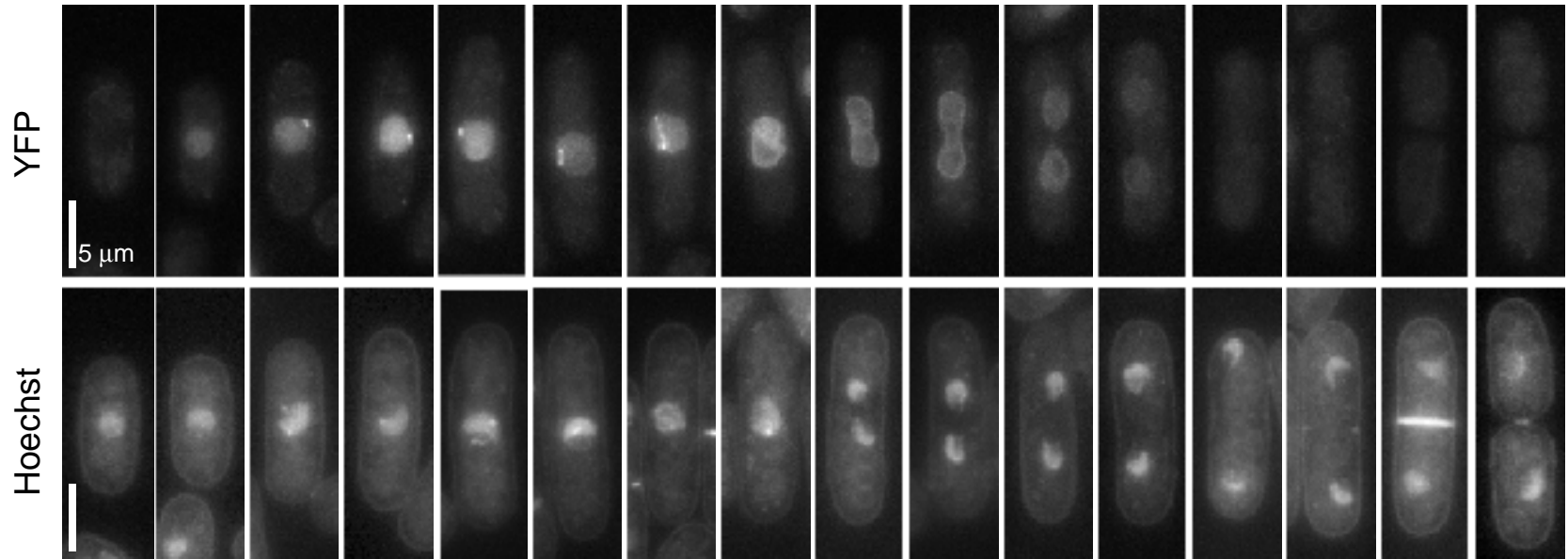
Size at division (μm)	13.7 ± 0.2	15.9 ± 0.2
Generation time (min)	163 ± 2.3	162 ± 5.5
Septation index (%)	11.7 ± 0.7	13.4 ± 0.1

DNA content



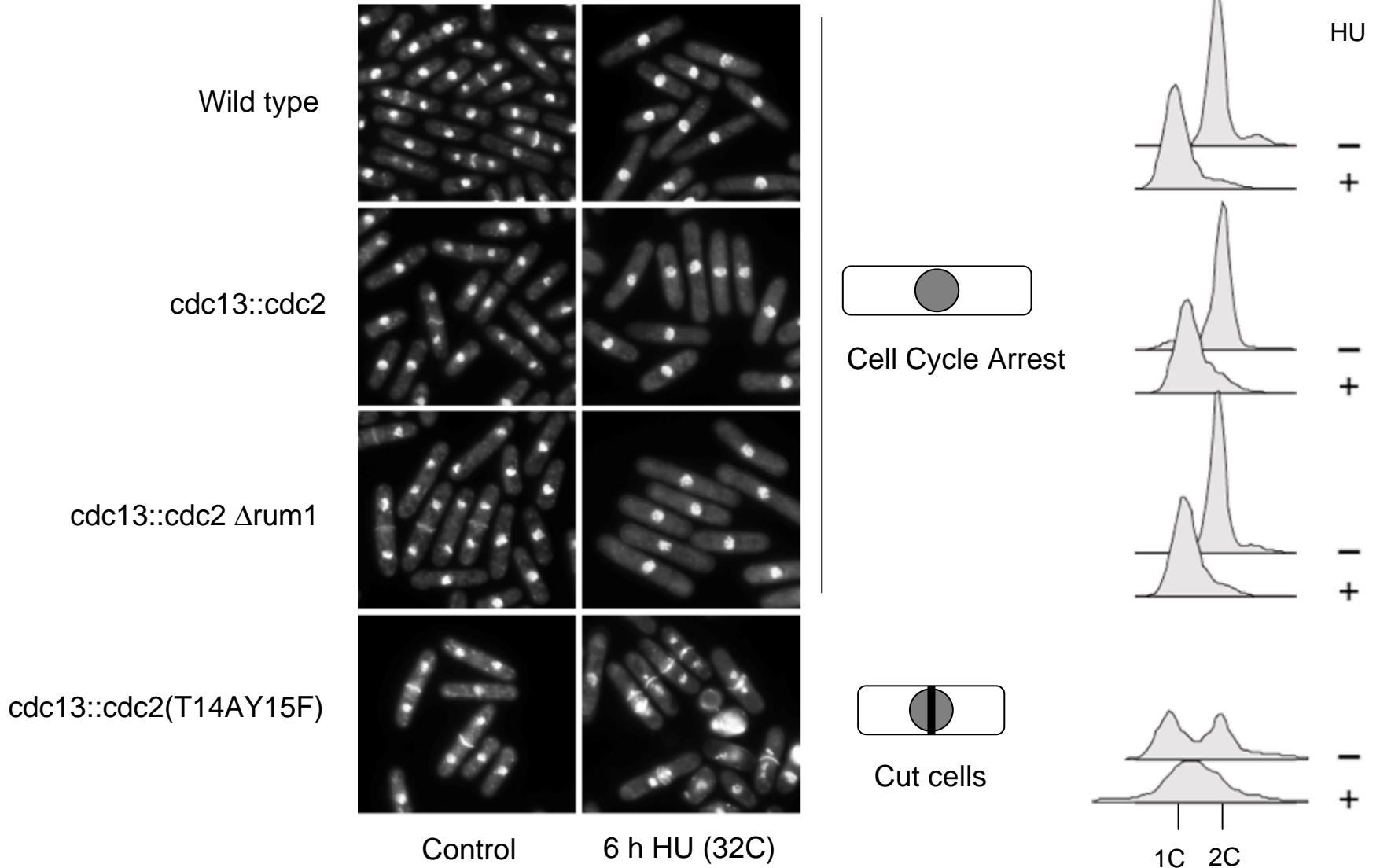
Reduction of the fission yeast Cdk oscillator to a single fusion protein

cdc13::cdc2::YFP $\Delta cdc2$ $\Delta cdc13\Delta cig1$ $\Delta cig2$ $\Delta puc1$



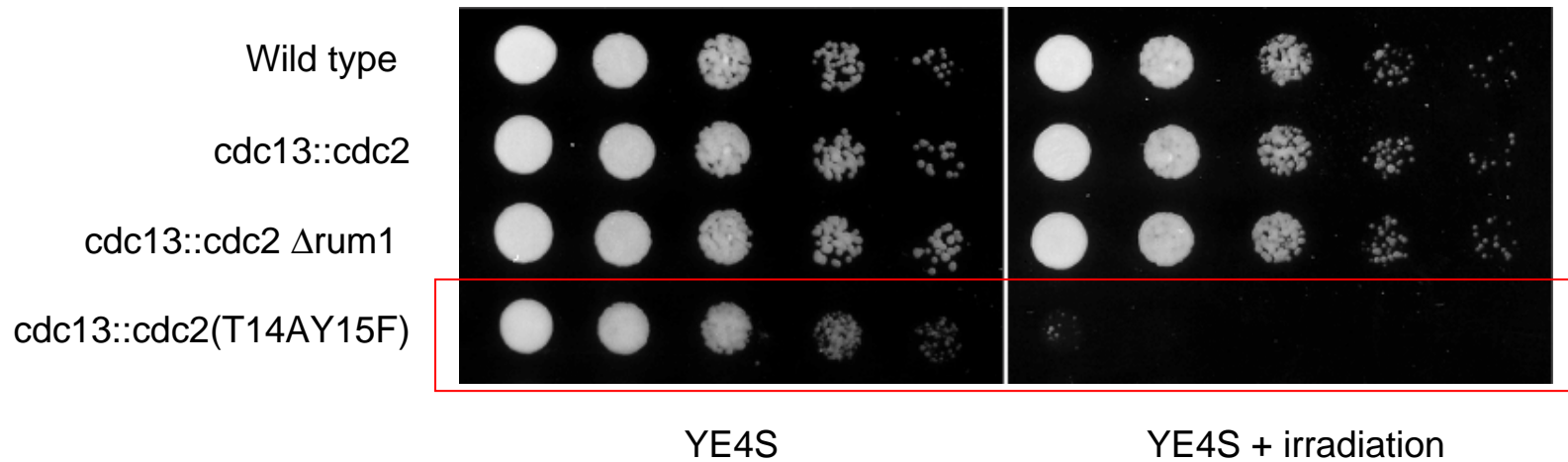
The Wee1 and Cdc25 network is essential for checkpoint activation

S phase checkpoint

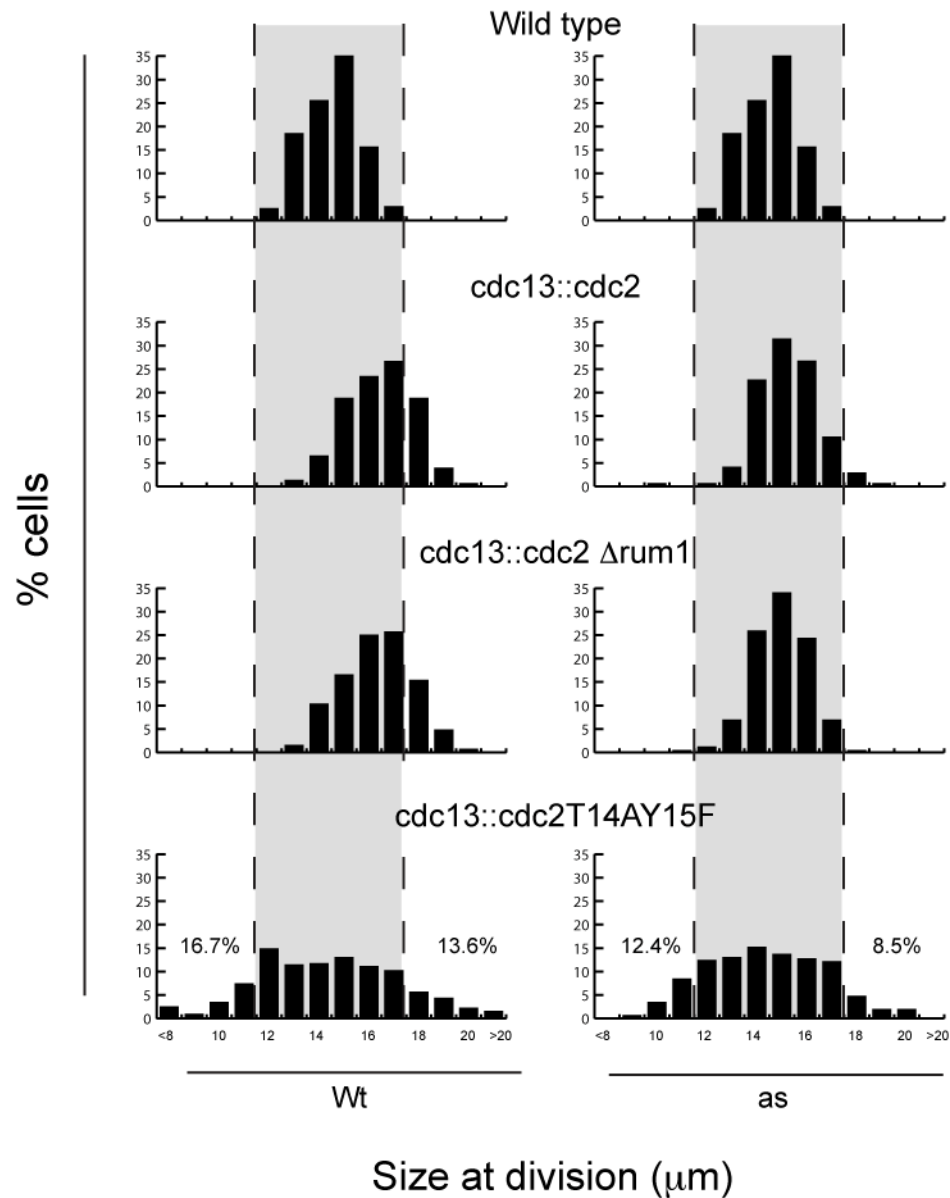


The Wee1 and Cdc25 network is essential for checkpoint activation

DNA damage checkpoint

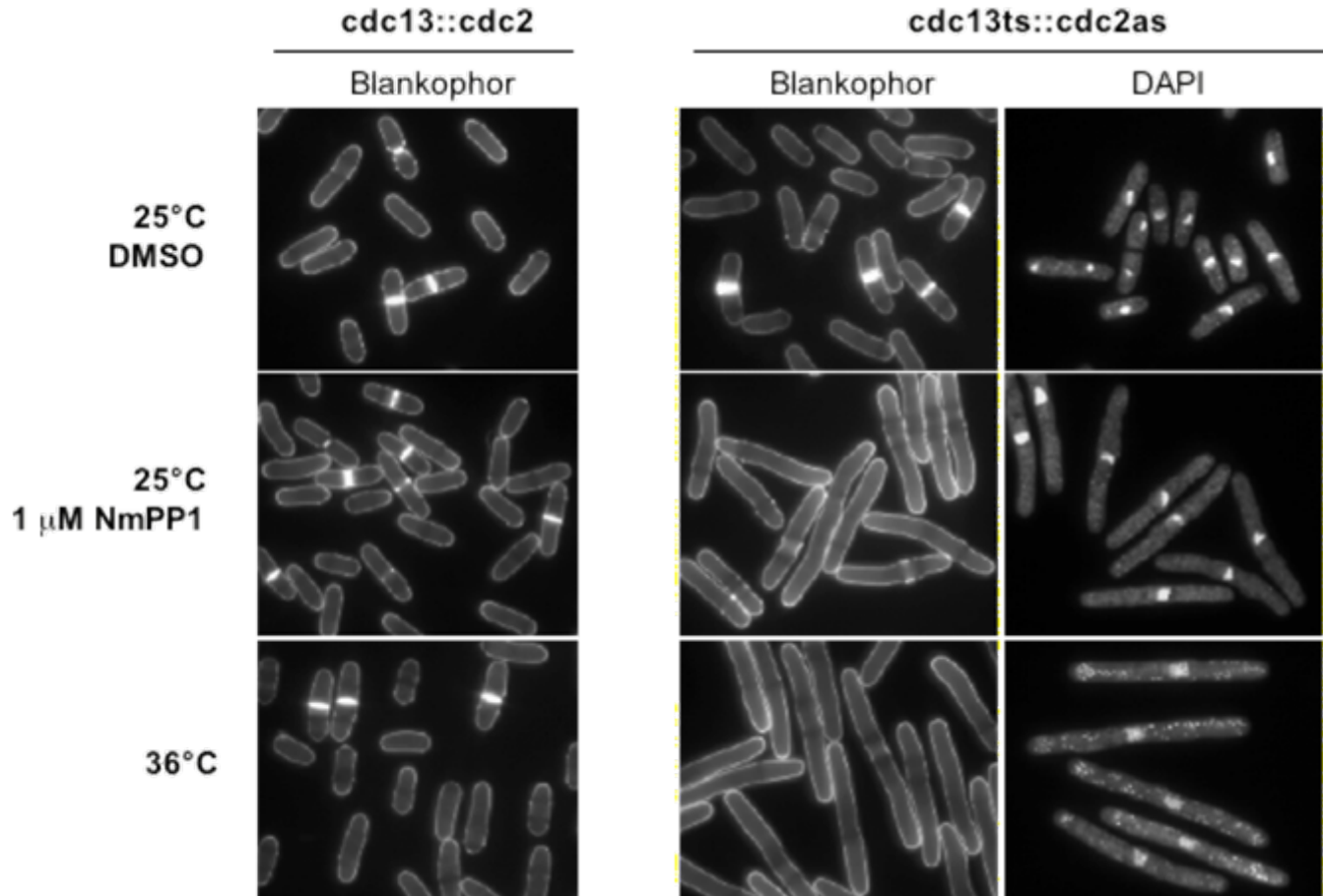
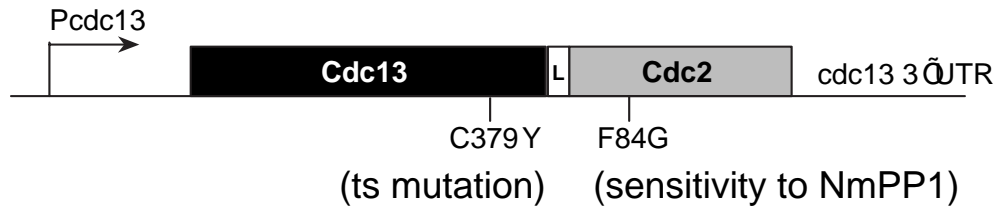


The Wee1/Cdc25 loop is essential for the homogeneity of the population



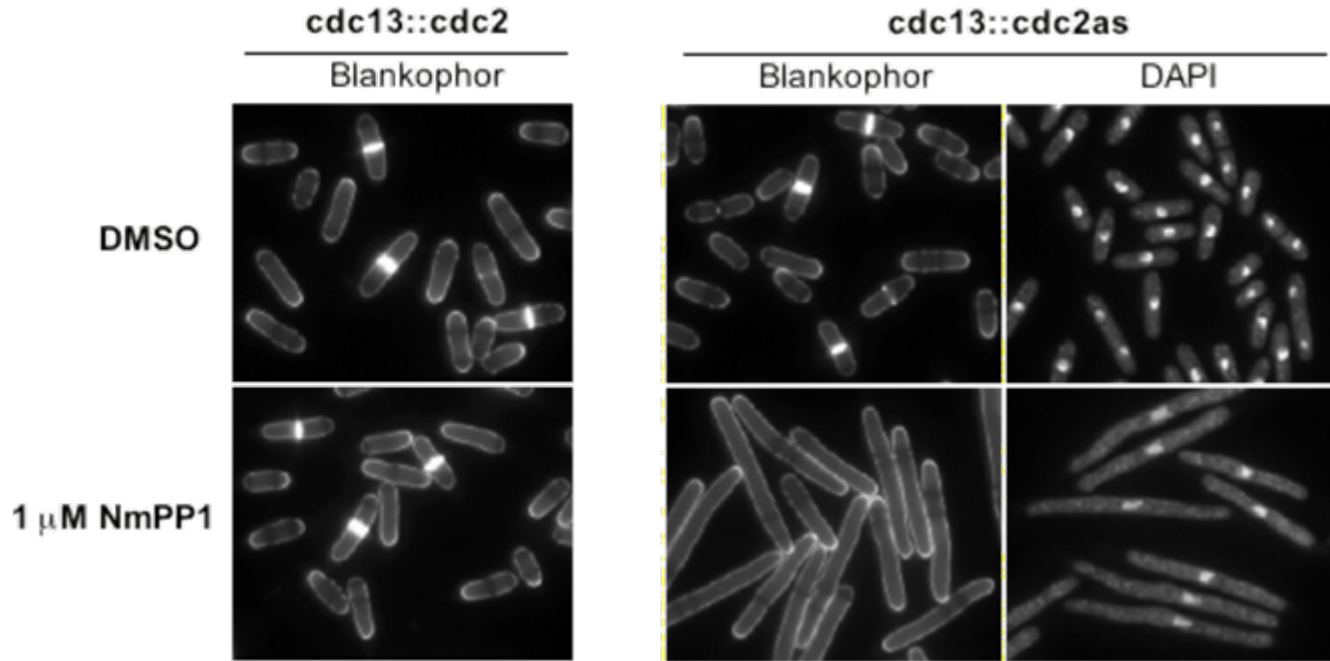
The Cdc13::cdc2 fusion protein drives the cell cycle autonomously

cdc13C379Y::cdc2as Δcdc2 Δcdc13



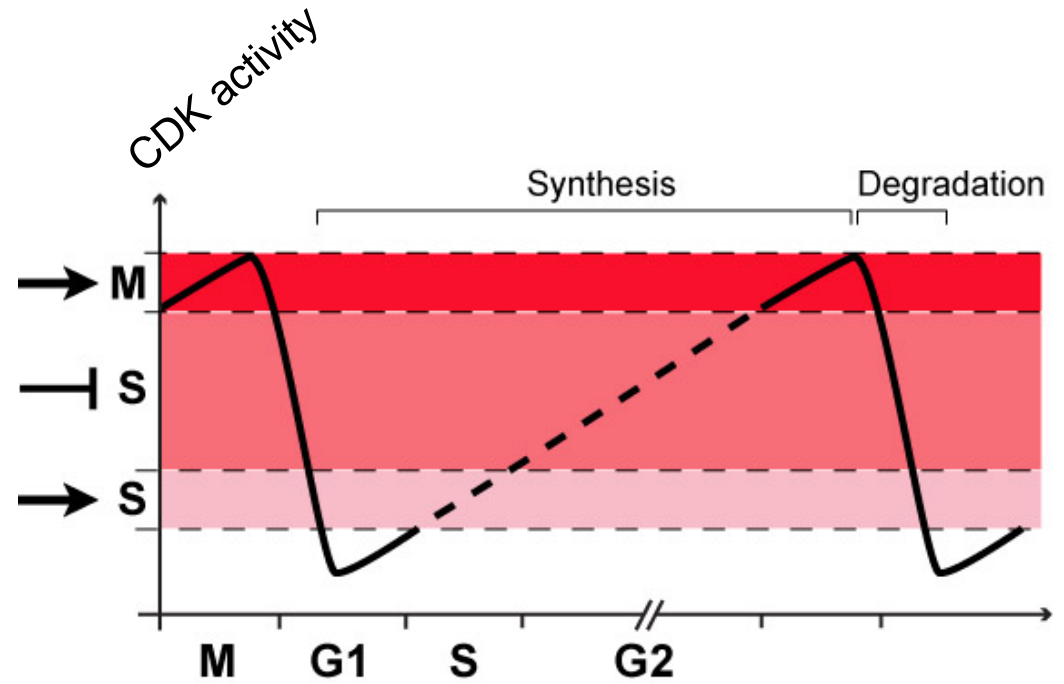
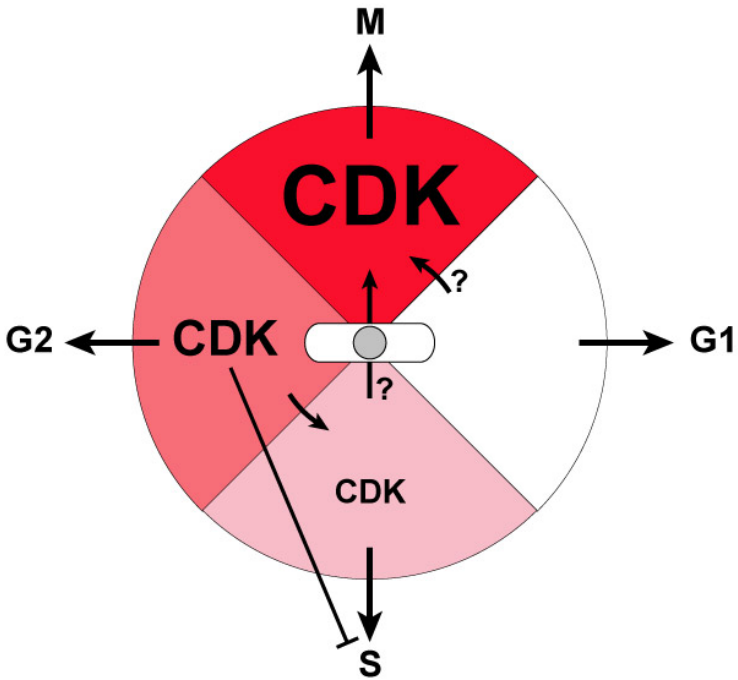
A tunable and minimal cell cycle

cdc13::cdc2as Δcdc2 Δcdc13 Δcig1 Δcig2 Δpuc1

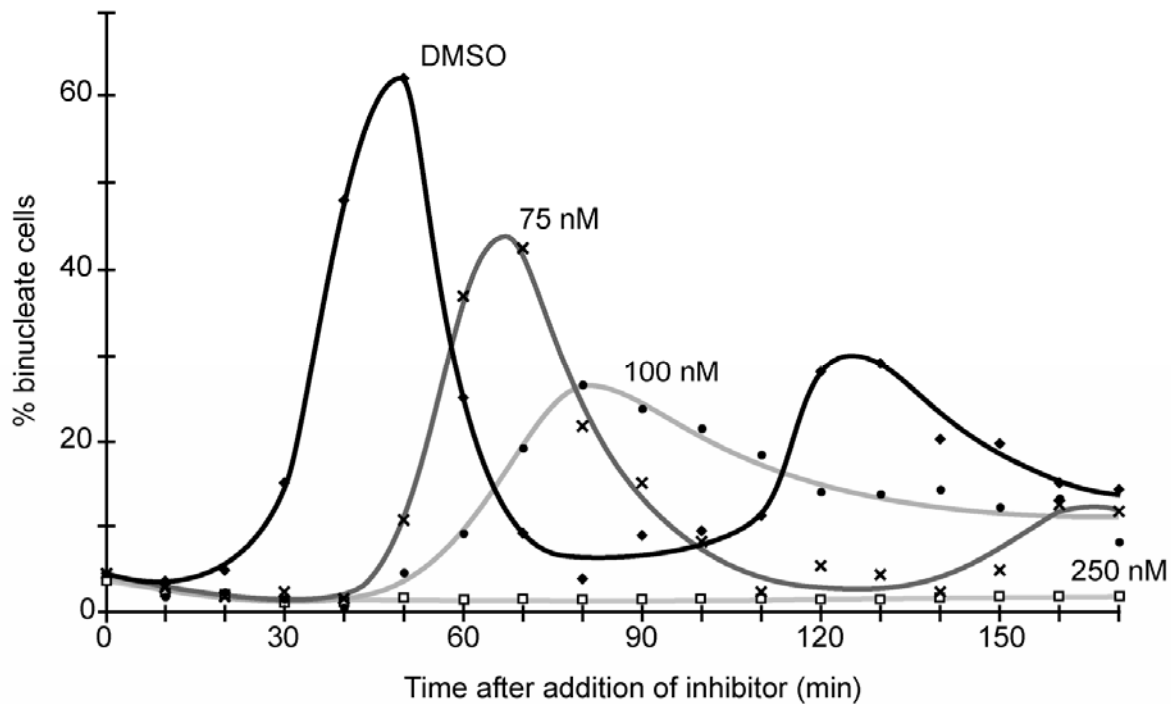


	Wt	as
Size at division (μm)	15.9 ± 0.2	14.7 ± 0.3
Generation time (min)	162 ± 5.5	158 ± 5.5
Septation index (%)	13.4 ± 0.1	13.7 ± 0.6

The minimal cell cycle is dependant upon changes in a single CDK activity



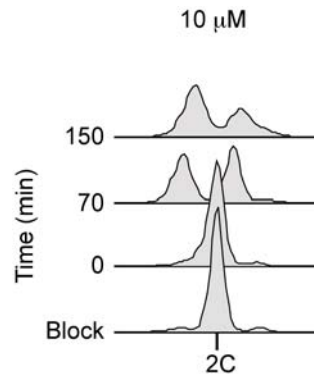
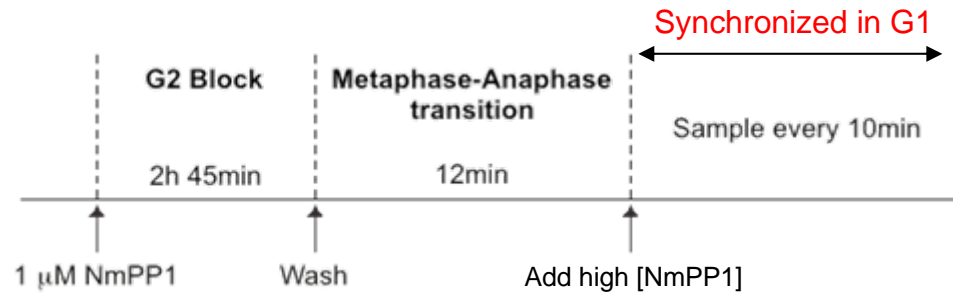
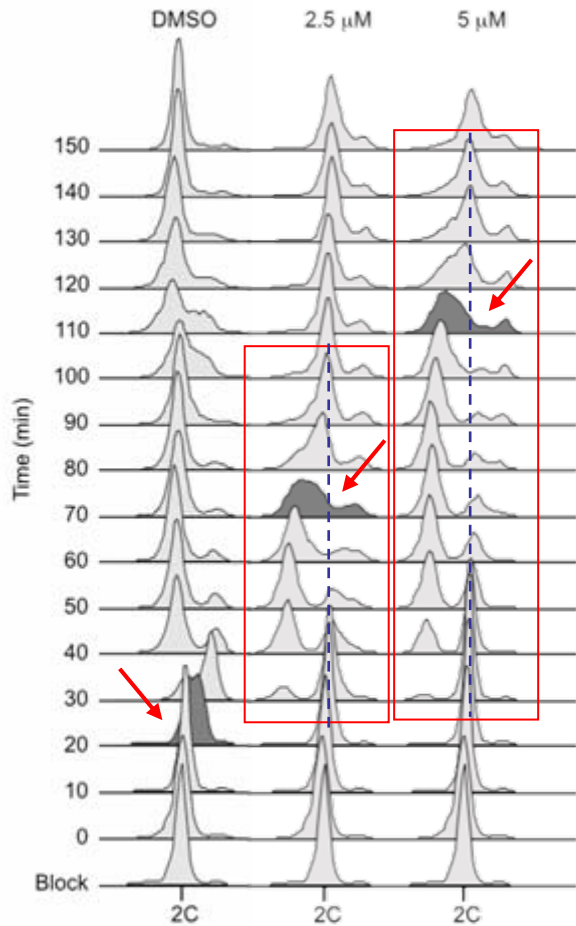
Entry into M depends upon a high activity threshold



0.25 μM NmPP1 prevents mitotic entry

Entry into S depends upon a low activity threshold

cdc13::cdc2as Δcdc2 Δcdc13Δcig1 Δcig2 Δpuc1



10 μM NmPP1 prevents S phase for 2.5 hours

The M or S decision depends on CDK activity level

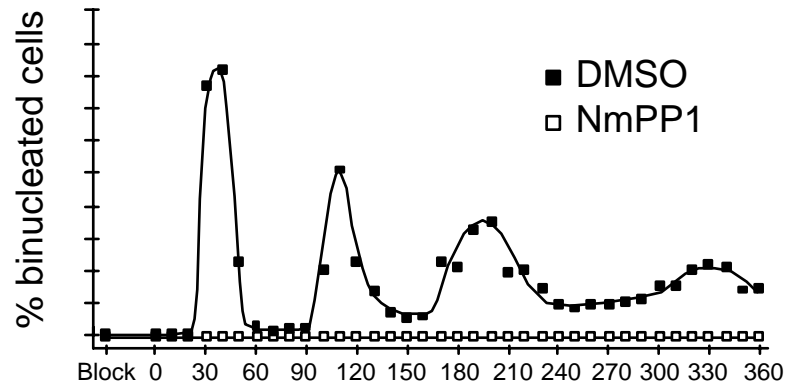
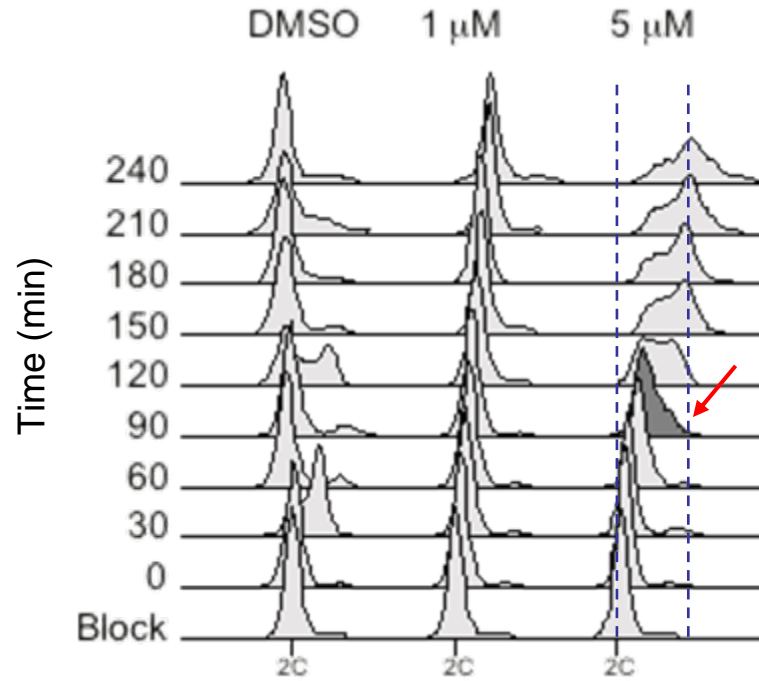
cdc13::cdc2as Δcdc2 Δcdc13Δcig1 Δcig2 Δpuc1

G2 Block (1 μ M NmPP1)

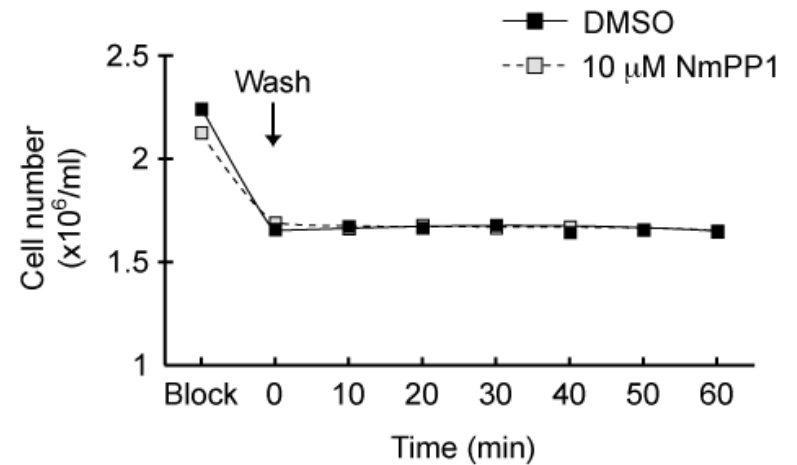
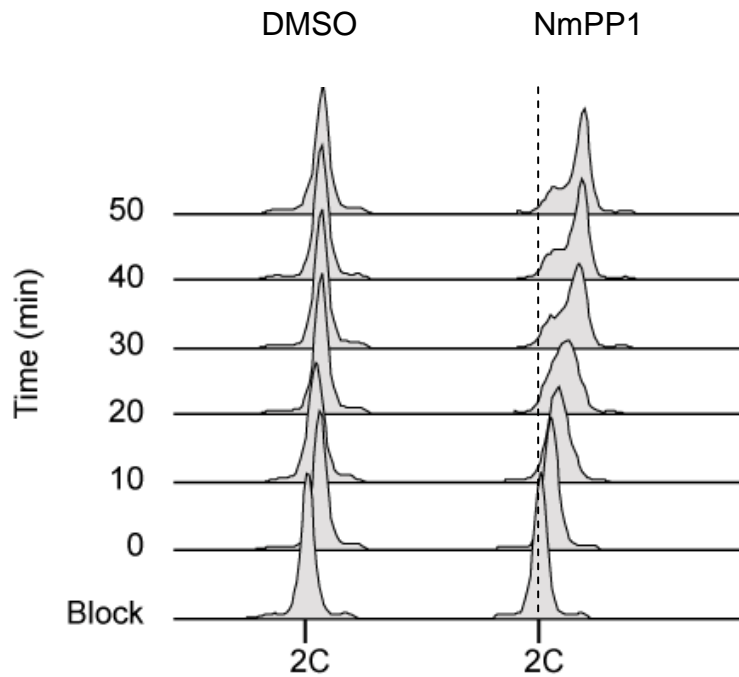
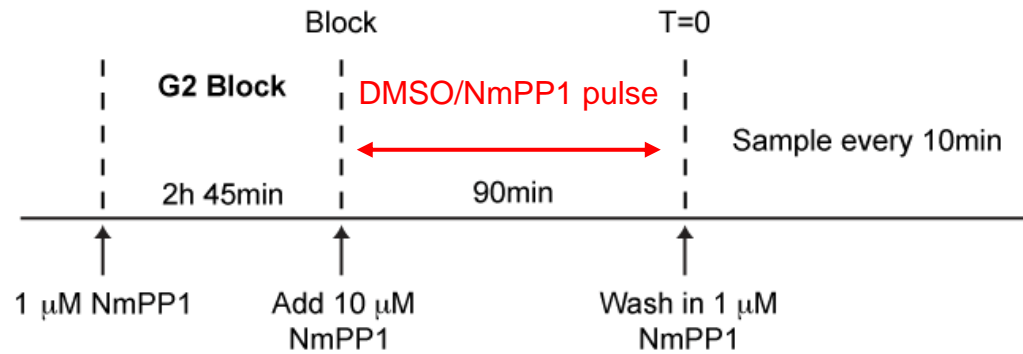
Release
(DMSO)

Add NmPP1

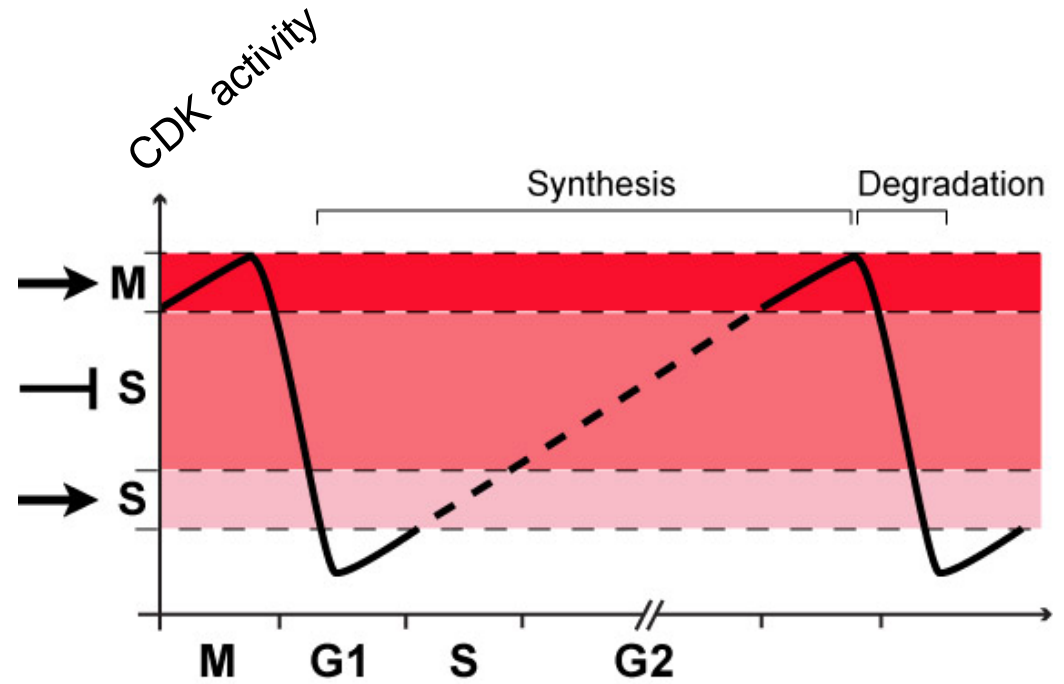
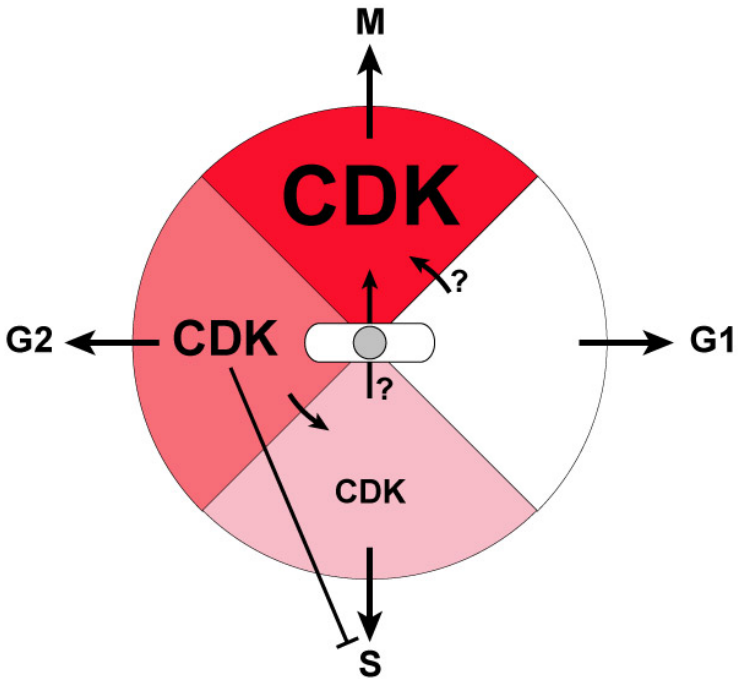
Samples for DNA content
And binucleated cells



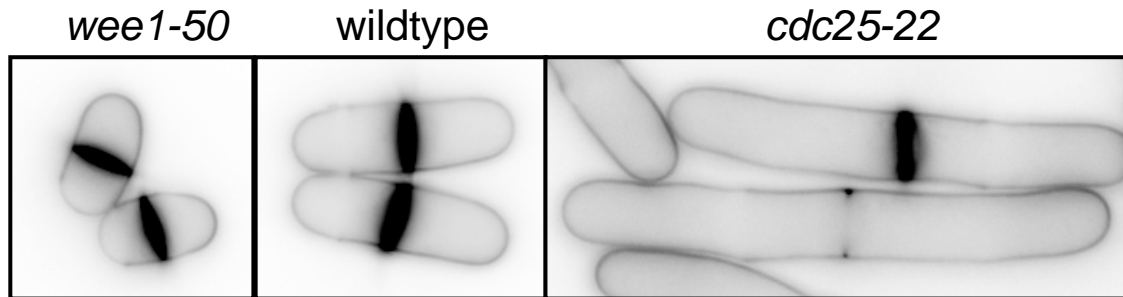
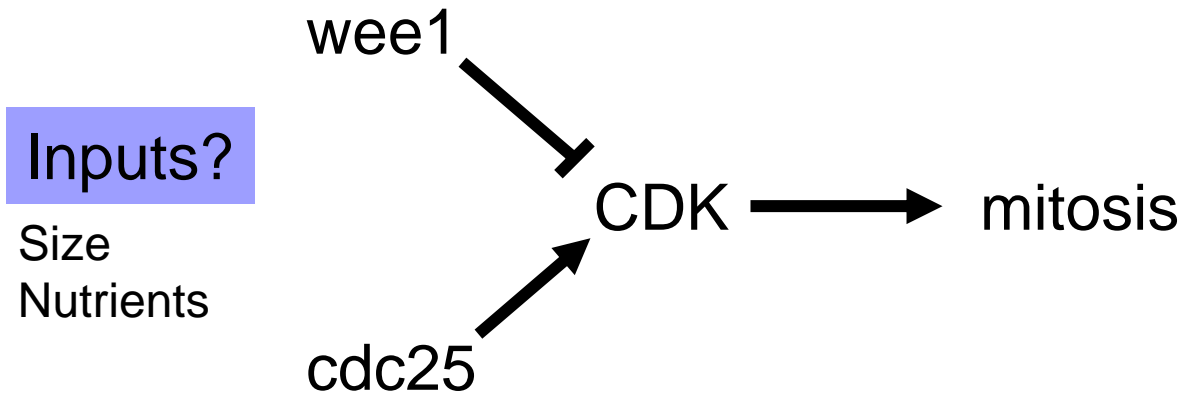
Transient inhibition of CDK activity in G2 allows resetting in G1



The minimal cell cycle is dependant upon changes in a single CDK activity



Regulation of the G2/M transition



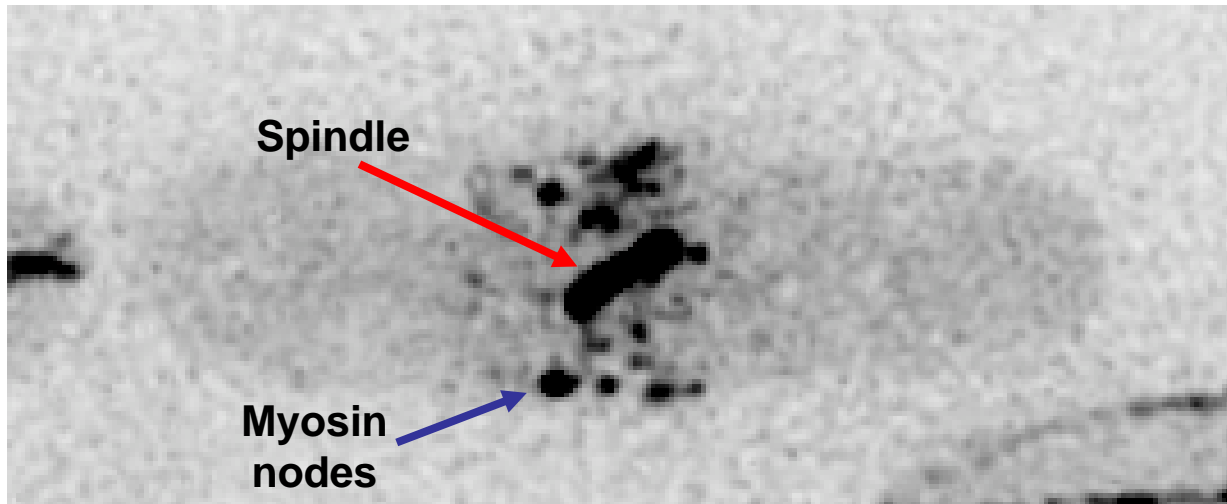


Jamie Moseley

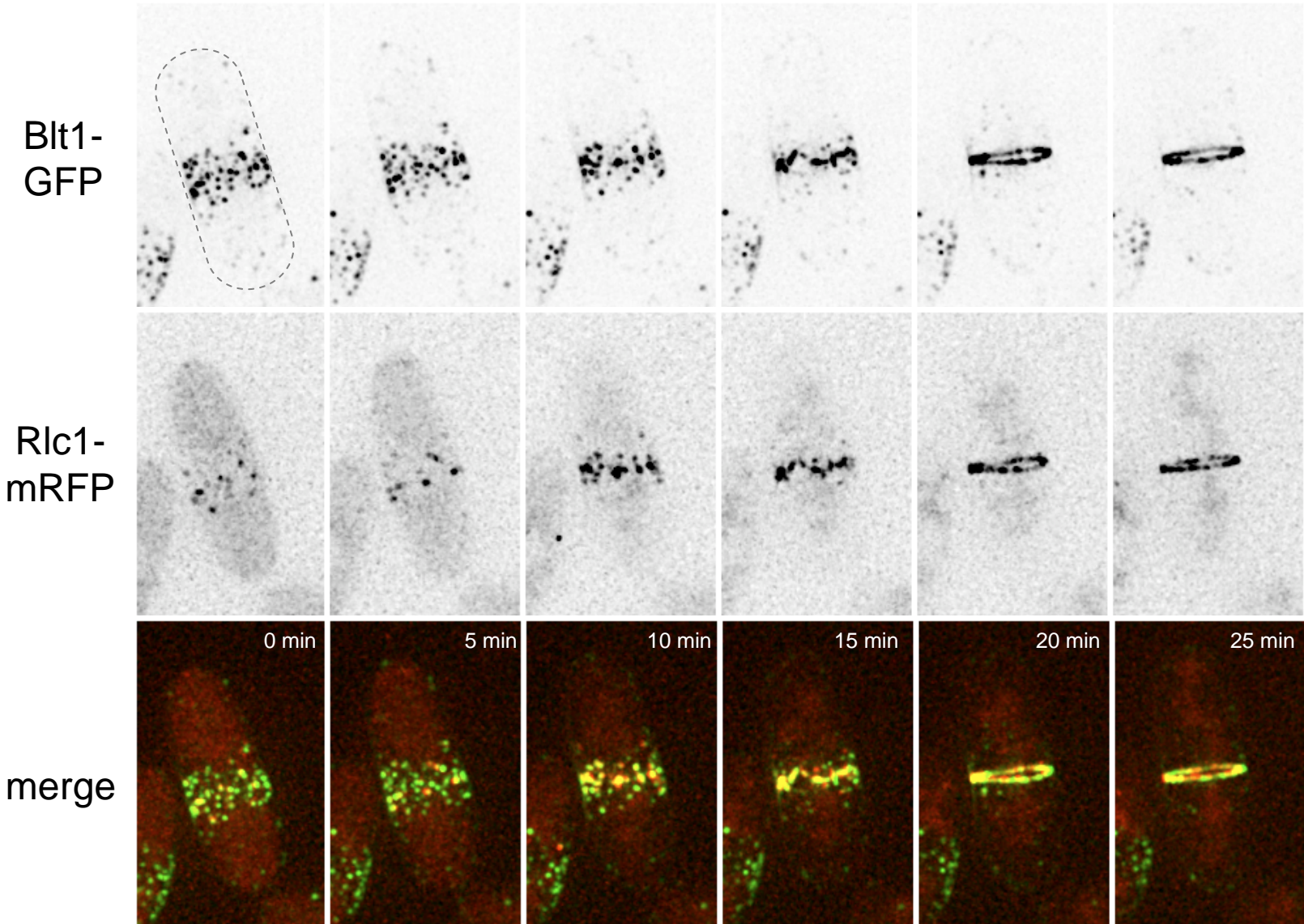
in collaboration with Anne Paoletti's group
at Institut Curie



Cytokinesis myosin cortical nodes

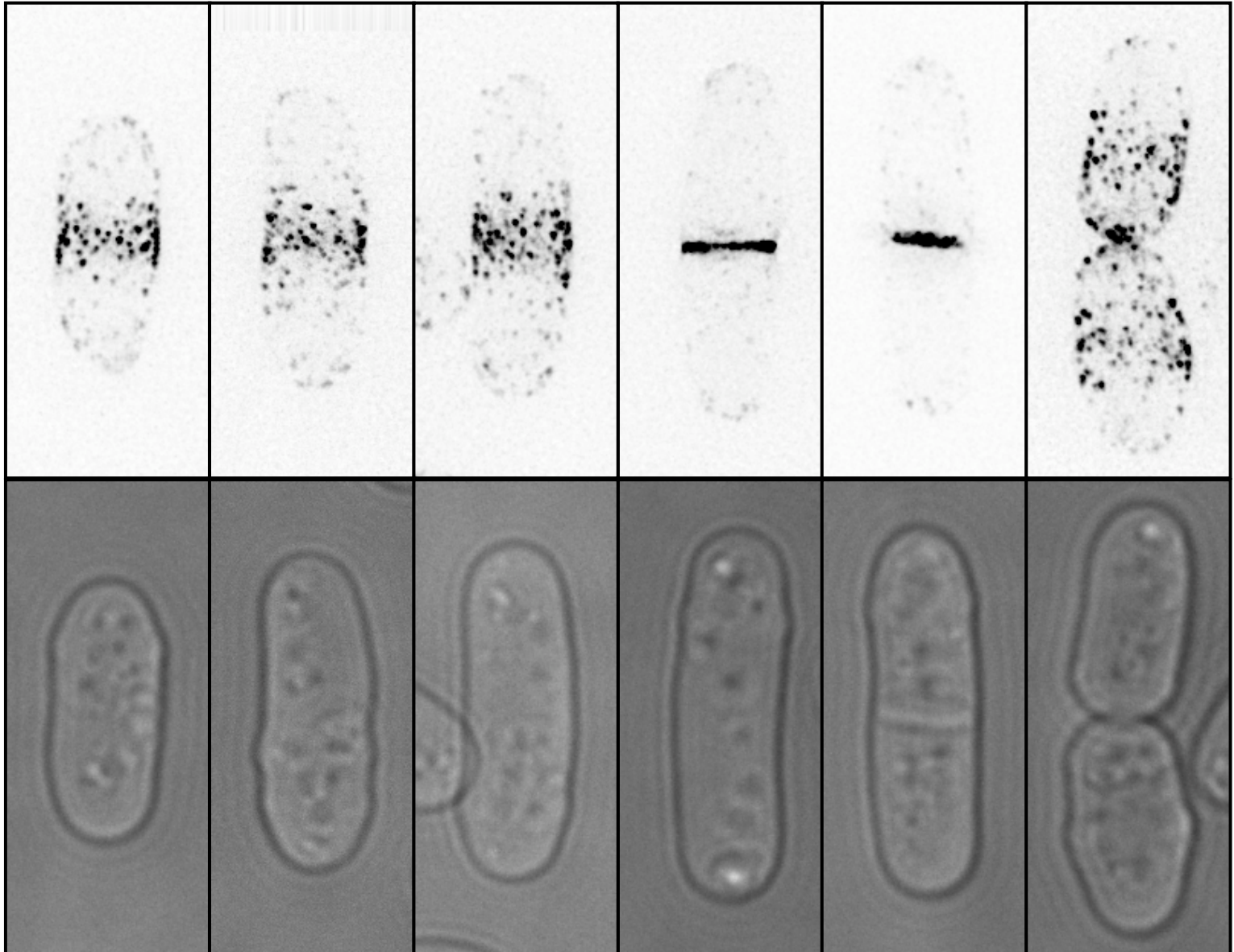


Blt1 is at myosin cortical nodes and actomyosin ring

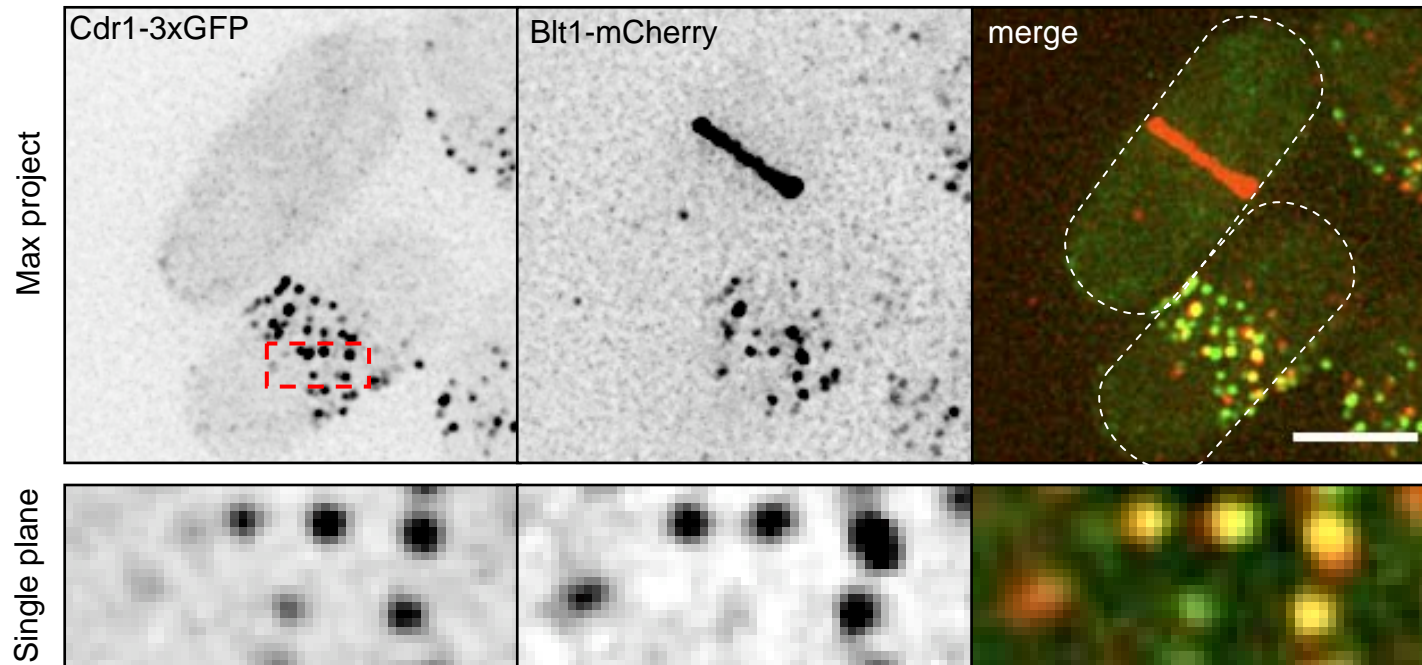
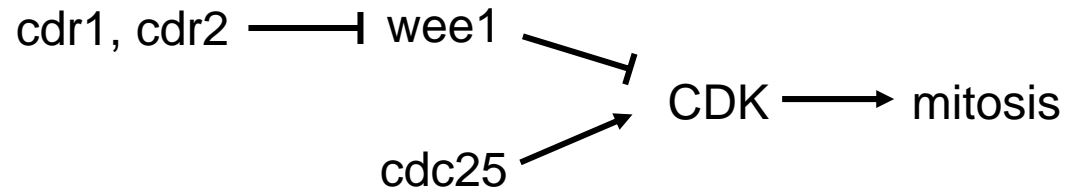


Unlike actomyosin, Blt1 localizes to cortical nodes throughout G2

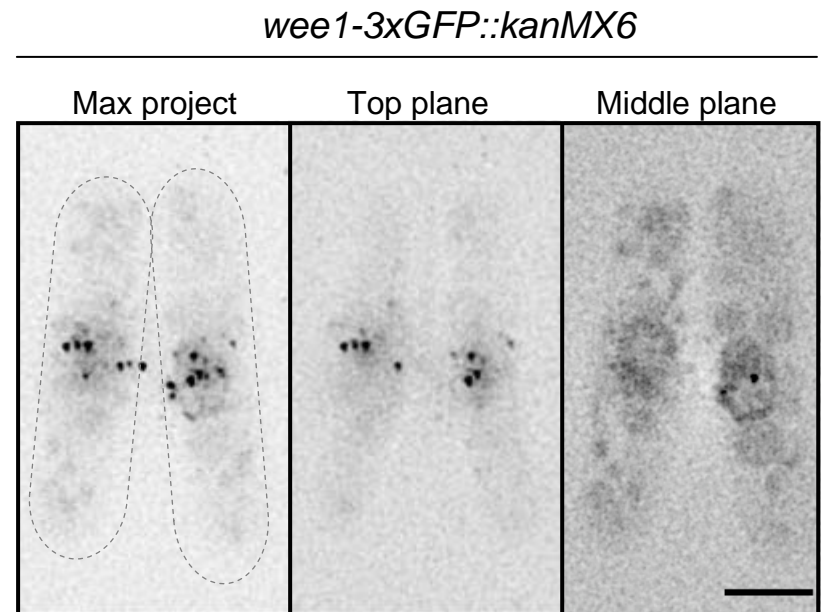
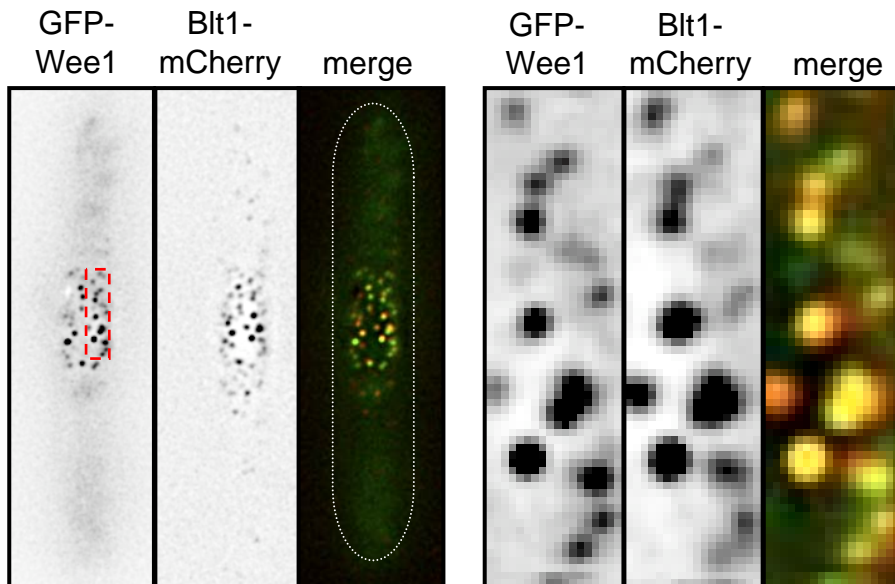
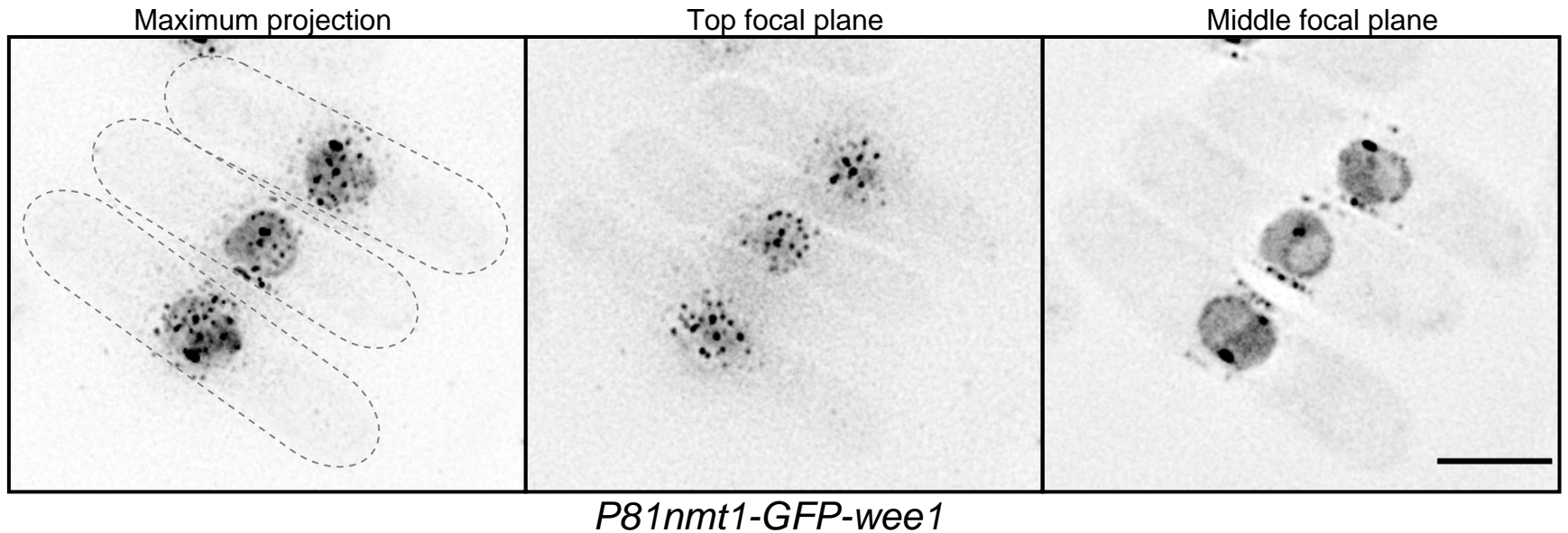
Blt1-
mEGFP



Both Wee1 inhibitory kinases associate with interphase nodes

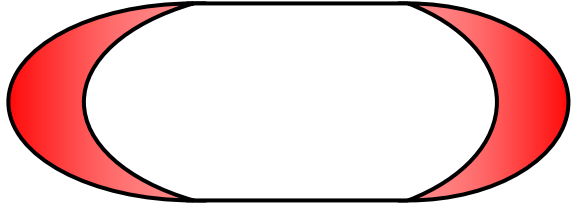


Wee1 localizes to nodes



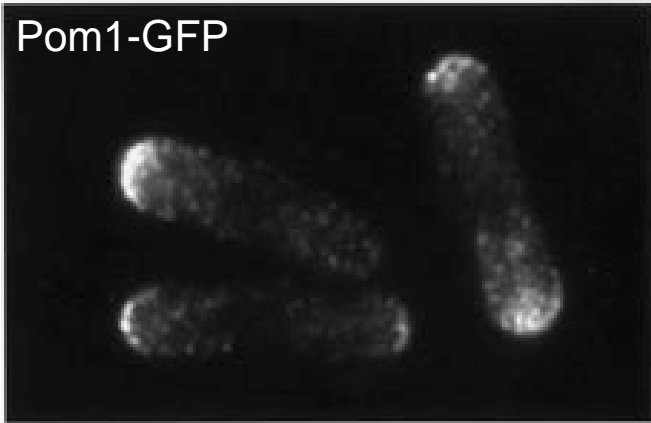
A

Negative cell tip signals



B

Pom1-GFP



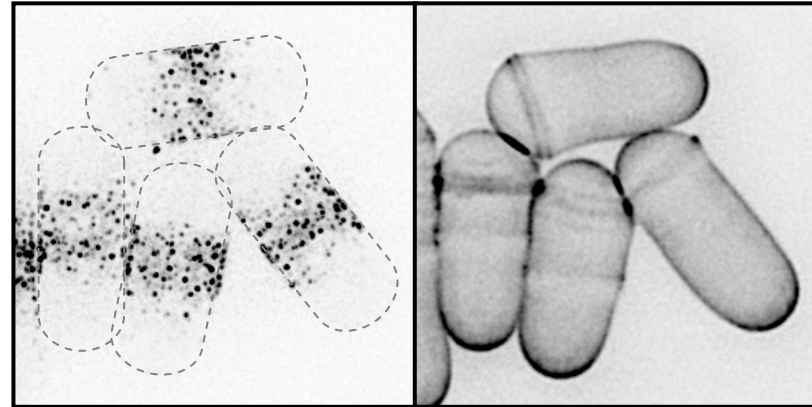
Bähler and Pringle, 1998
Bähler and Nurse, 2001

C

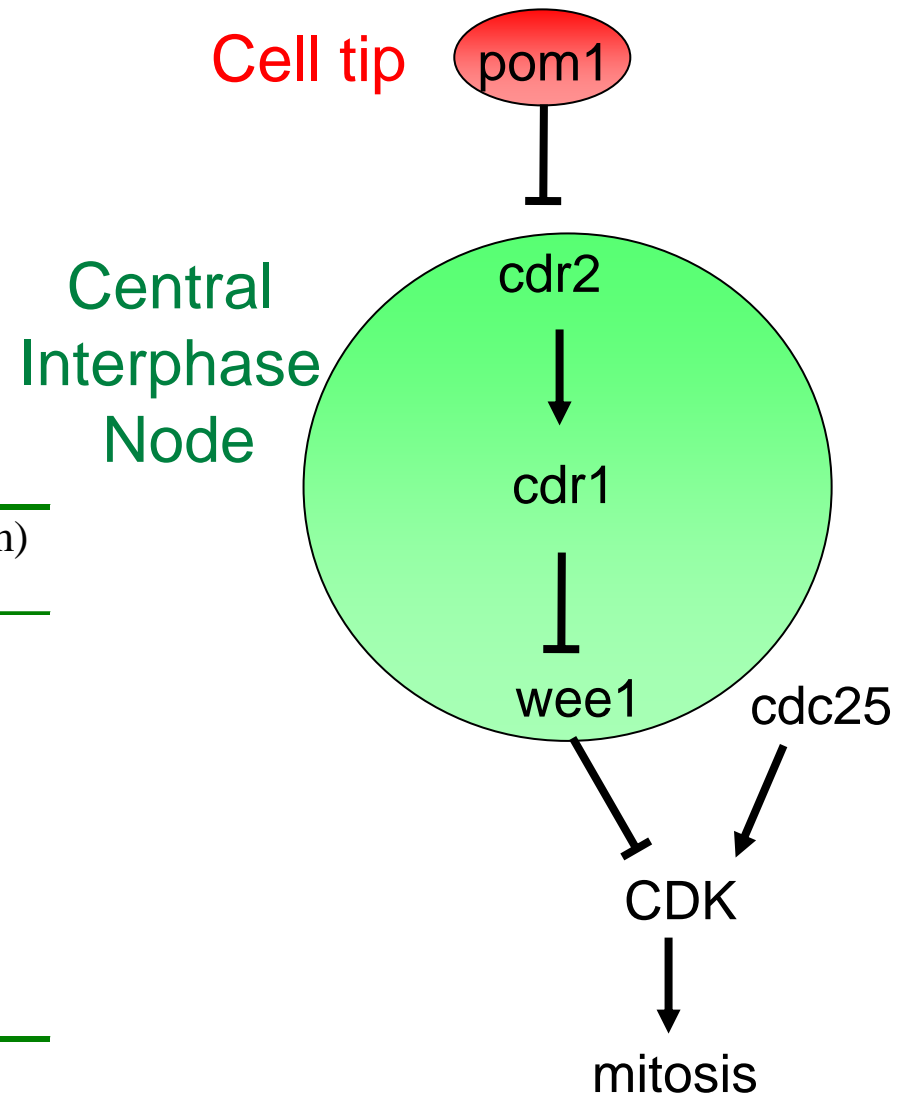
Cdr2-GFP

Calcofluor

wt

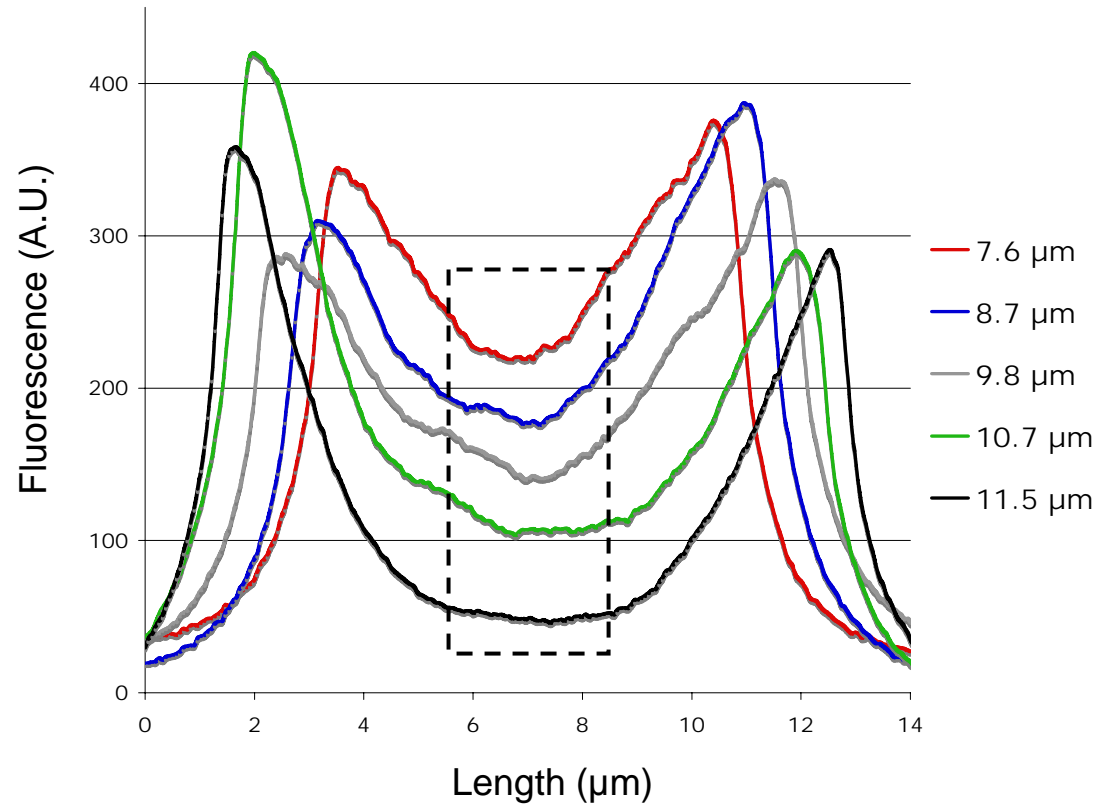
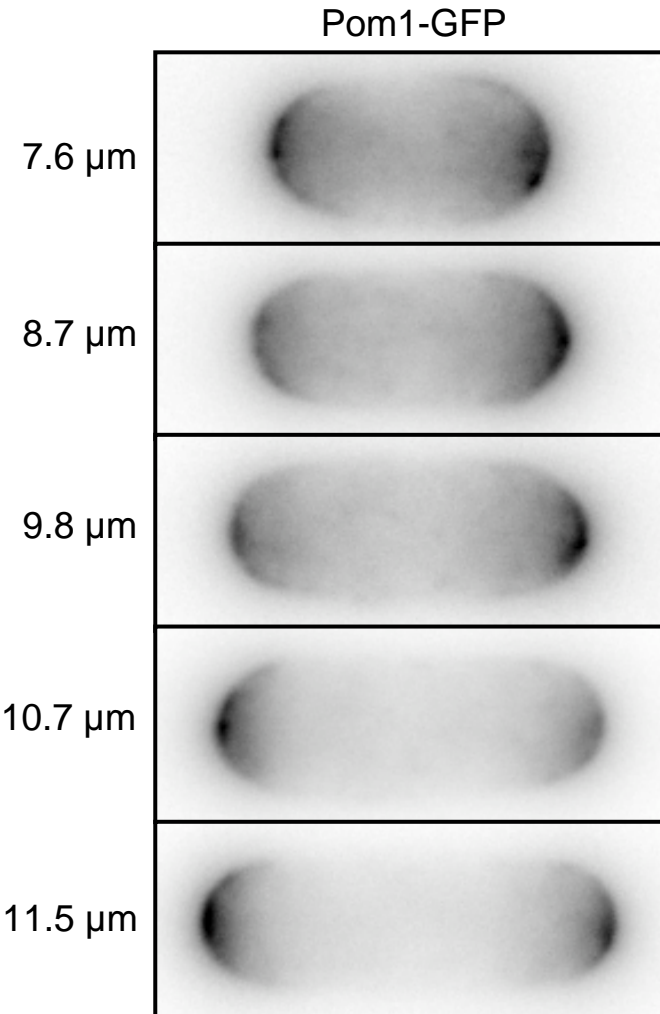


pom1 inhibits mitosis through cdr2 and wee1

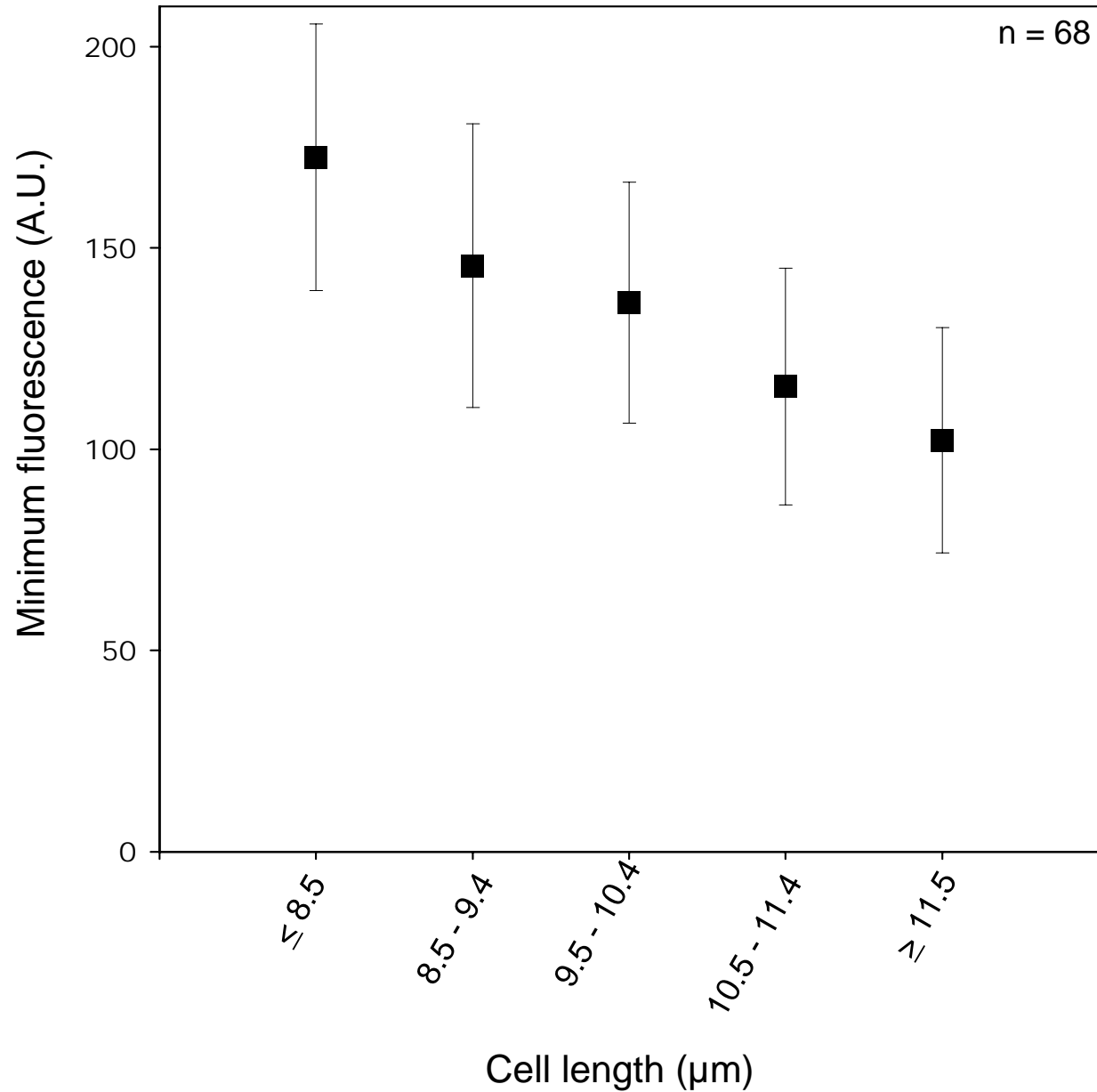


Strain	Length at division (μm)
wildtype	13.7 ± 1.0
<i>pom1E_q</i>	11.7 ± 1.8
<i>cdr1E_q</i>	17.8 ± 1.4
<i>pom1E_q cdr1E_q</i>	17.2 ± 1.4

Pom1 polar gradient through the cell cycle

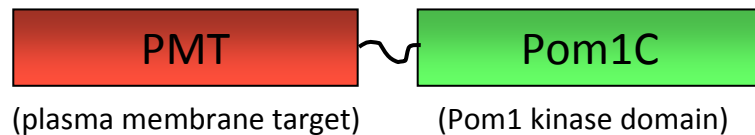


Pom1 levels at cell center decrease during G2

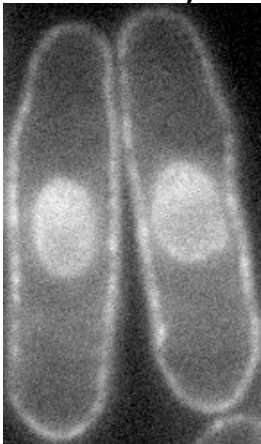


Ectopic targeting of Pom1 to cell middle disrupts Cdr2 localization and cell cycle

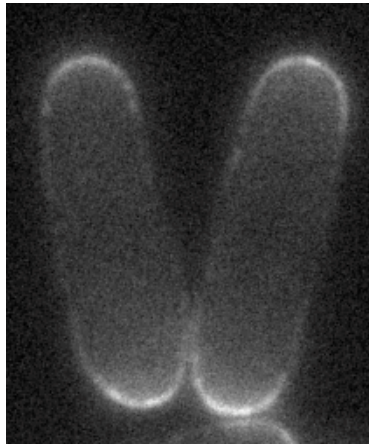
Chimera



Chimera-
mCherry

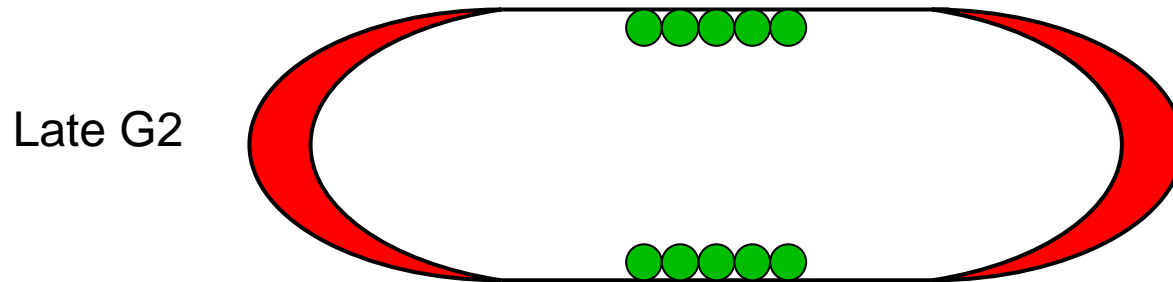
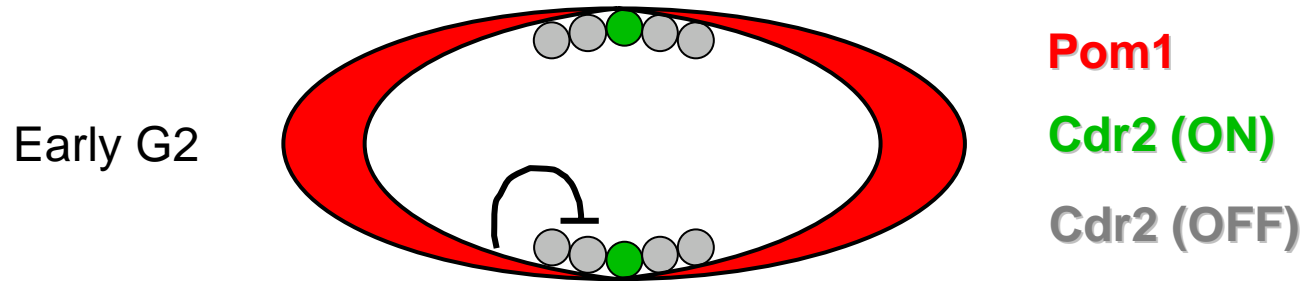


Pom1-GFP



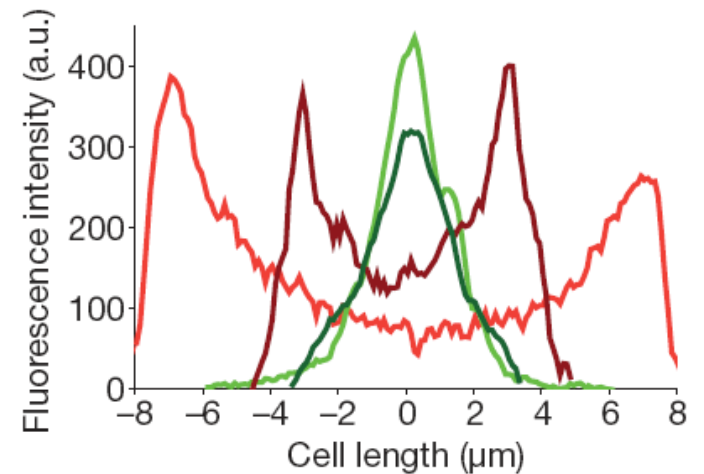
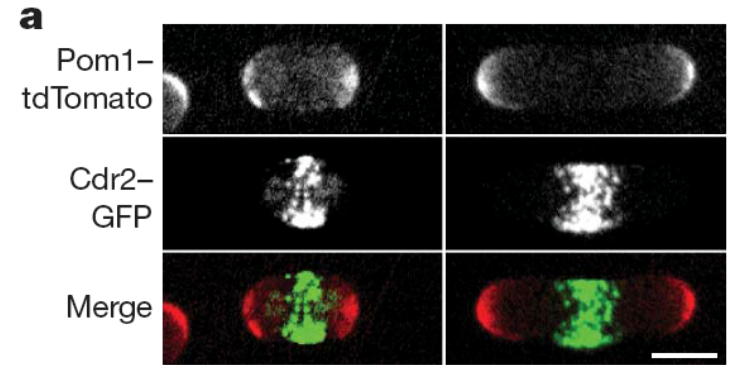
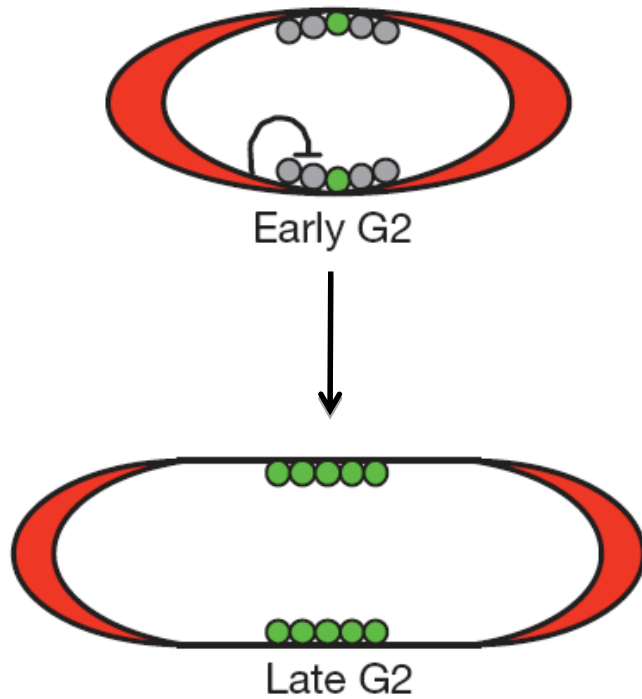
Strain	Length at division (μm)
WT	14.3 ± 0.9
chimera	19.7 ± 1.9
<i>cdr2\Delta</i>	19.9 ± 1.8
<i>cdr2\Delta</i> + chimera	19.1 ± 1.9
<i>cdc25-22</i>	23.8 ± 2.6
<i>cdc25-22</i> + chimera	39.3 ± 7.9

Model for coordinating polarized growth with mitosis



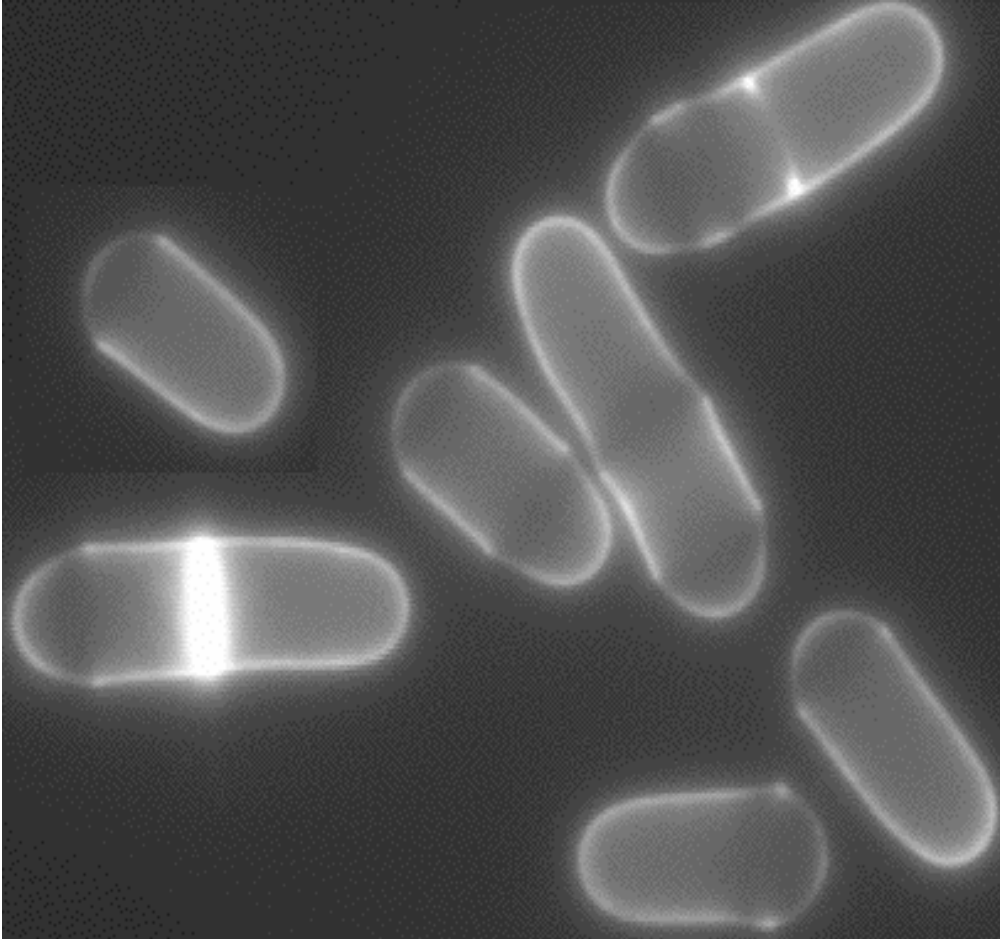
	Cdr2	Wee1	CDK
Early G2	OFF	ON	Low
Late G2	ON	OFF	High

Combined picture of pathway linking cell size and mitotic entry



Pom1 (small cell) Cdr2 (small cell)
Pom1 (large cell) Cdr2 (large cell)

Schizosaccharomyces pombe cells



- Genome 12.4 Mb (exc rDNA)
- 3 chromosomes
- 4914 protein coding genes
- 46% have introns



Jacky Hayles

The background of the slide is a fluorescence microscopy image of yeast cells. The cells are primarily green, with some showing blue fluorescence, likely indicating specific genetic markers or protein localization. The text is overlaid on this image.

Fission Yeast Genome Wide Deletions

KRIBB

Bioneer

Sanger

CRUK

Kwang-Lae Hoe, Dong-Uk Kim

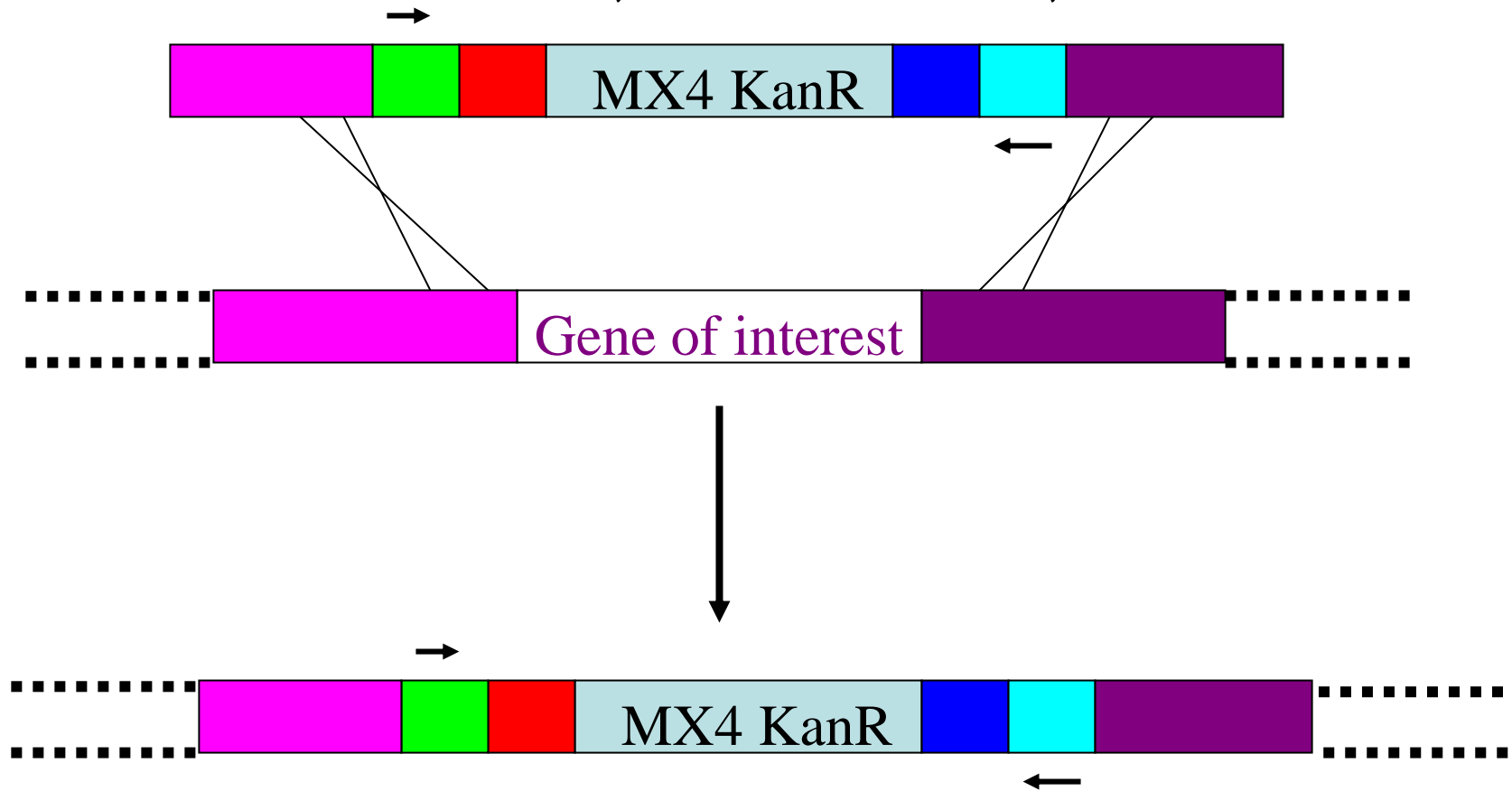
Han-Oh Park





Valerie Wood

Jacky Hayles

Genome wide systematic deletions

Constructed in the diploid h^+/h^+
 $ade6\text{-M210}/ade6\text{-M216}$, $leu1\text{-32}/leu1\text{-32}$, $ura4\text{-D18}/ura4\text{-D18}$



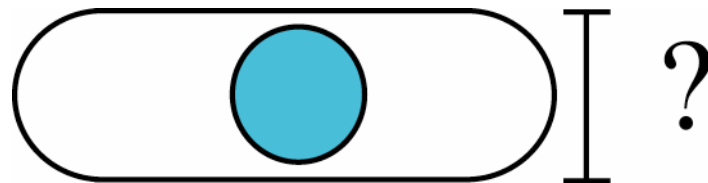
-   Universal priming sequences
-   Unique up & down tags

Progress to date

- **Total data-set of genes:** **4914 (100%)**
- **Deletions constructed to date:** **4836 (98.5%)**
- **Essential genes:** **1260 (26%)**

Encoding a Cellular Ruler

Felice Kelly

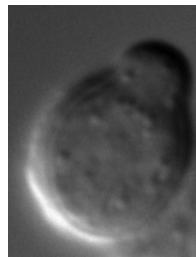
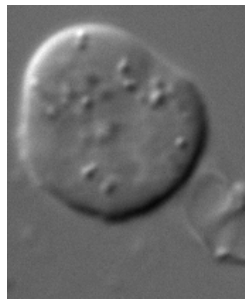
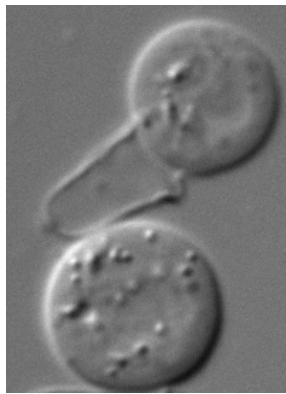
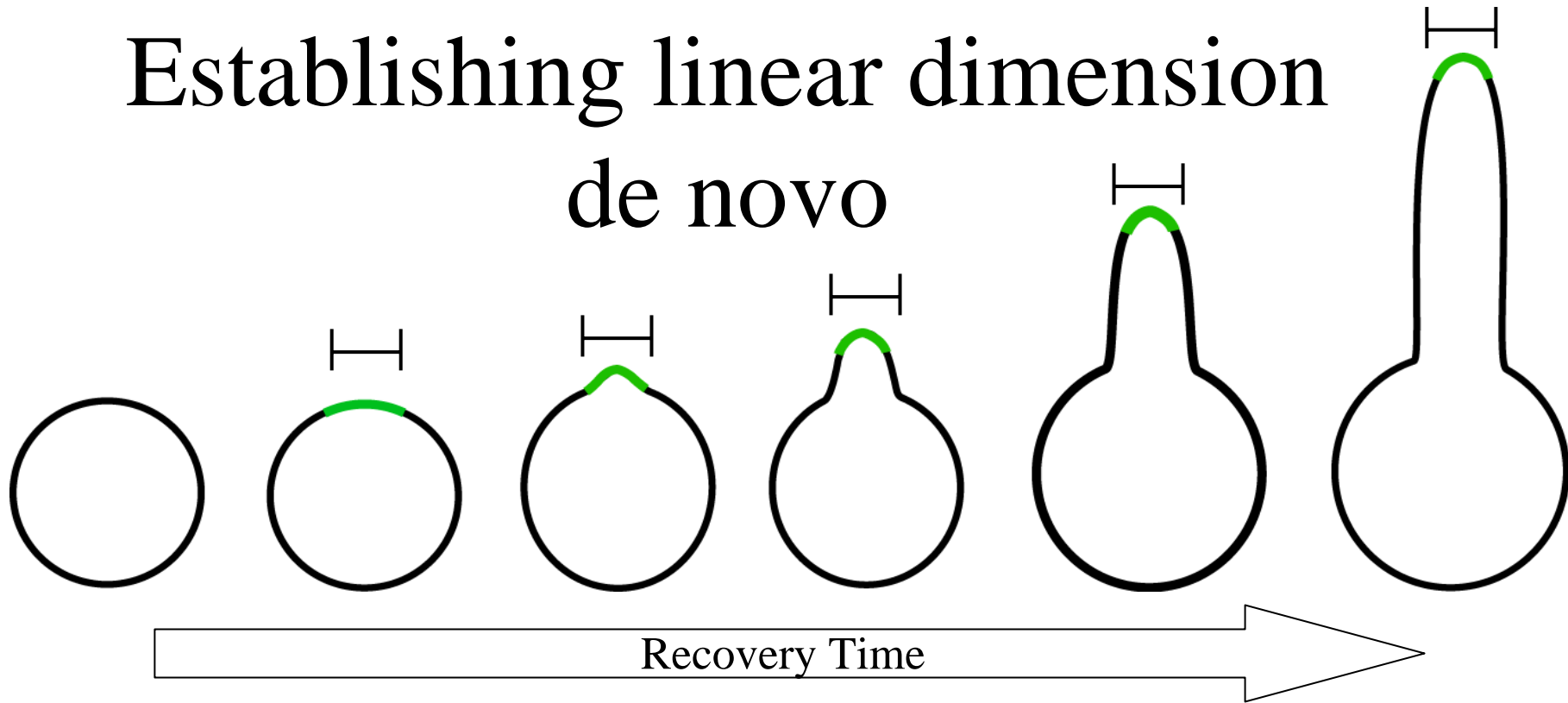


Fission Yeast grow with a constant width



Frank Neumann

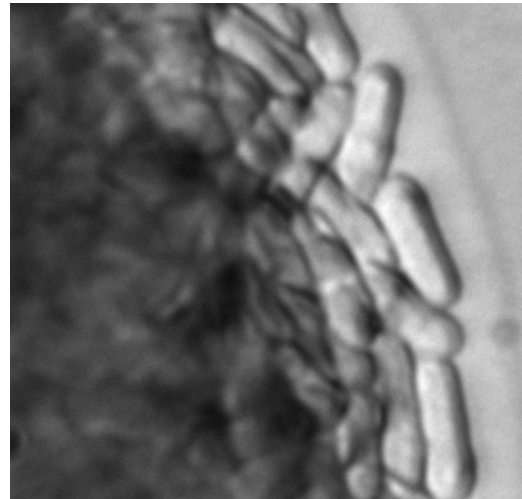
Establishing linear dimension de novo



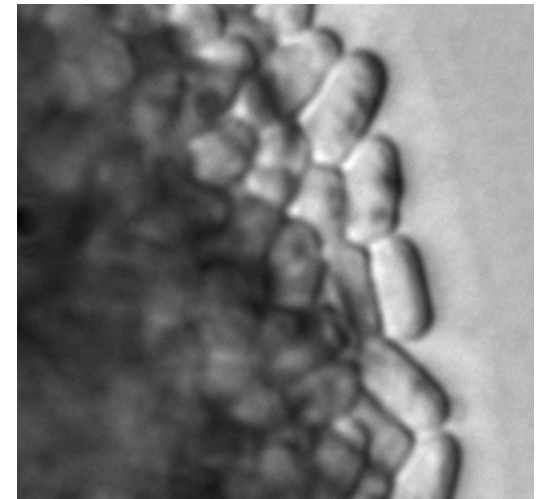
Screening for a subtle phenotype

Initial Categorization
by Jacky Hayles

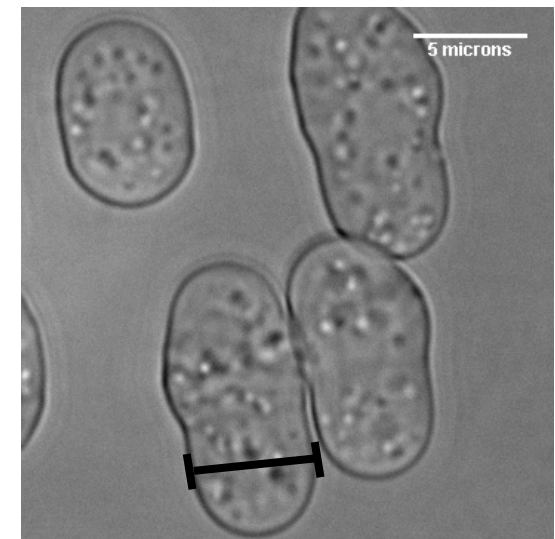
Wild-type cells



Wide mutant cells



Directed Screen
of Exponentially
Growing Cells



Genomic screen for width mutants

3488 viable
deletions



142 putative
width mutants

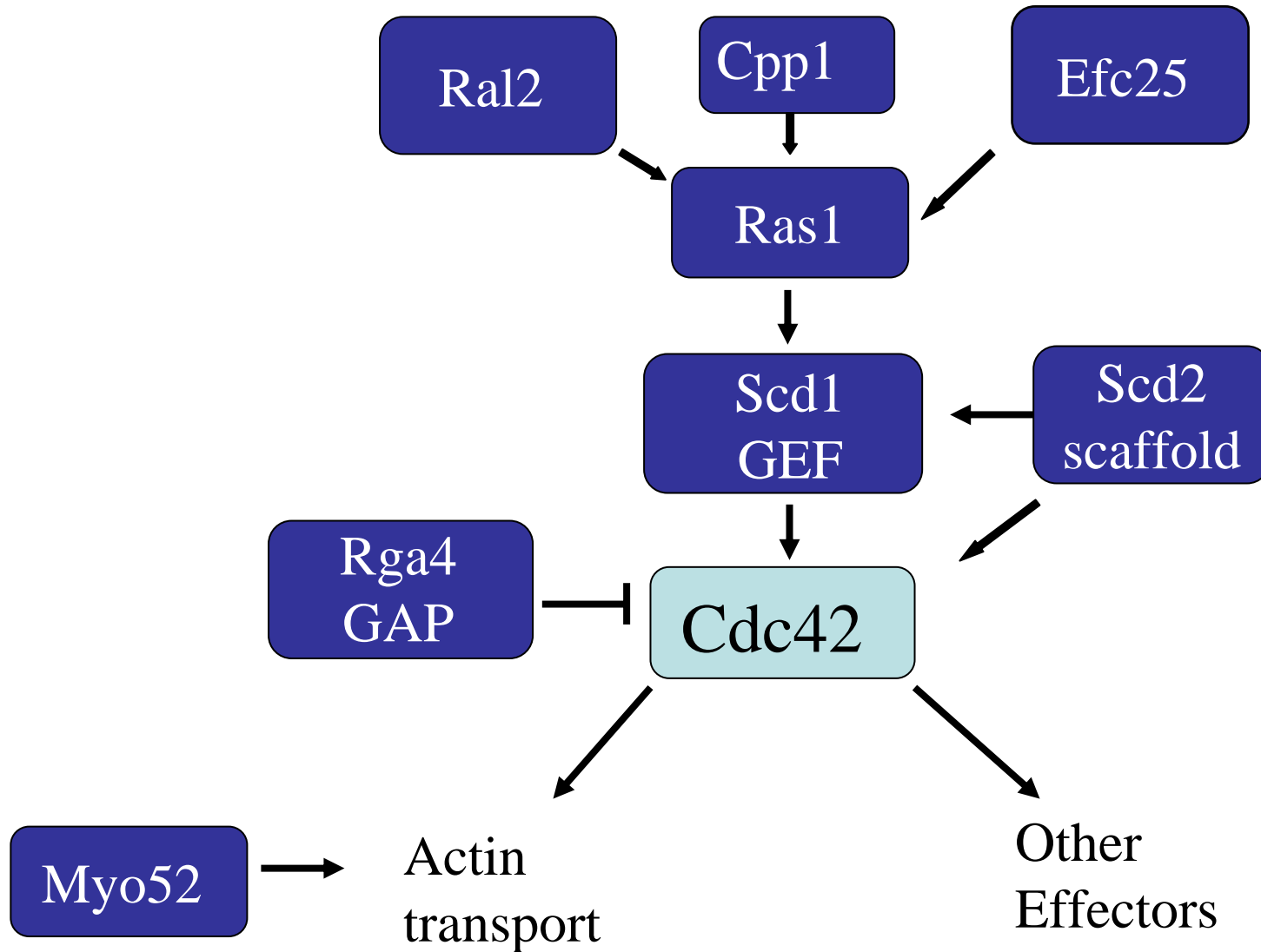


12 confirmed
width mutants



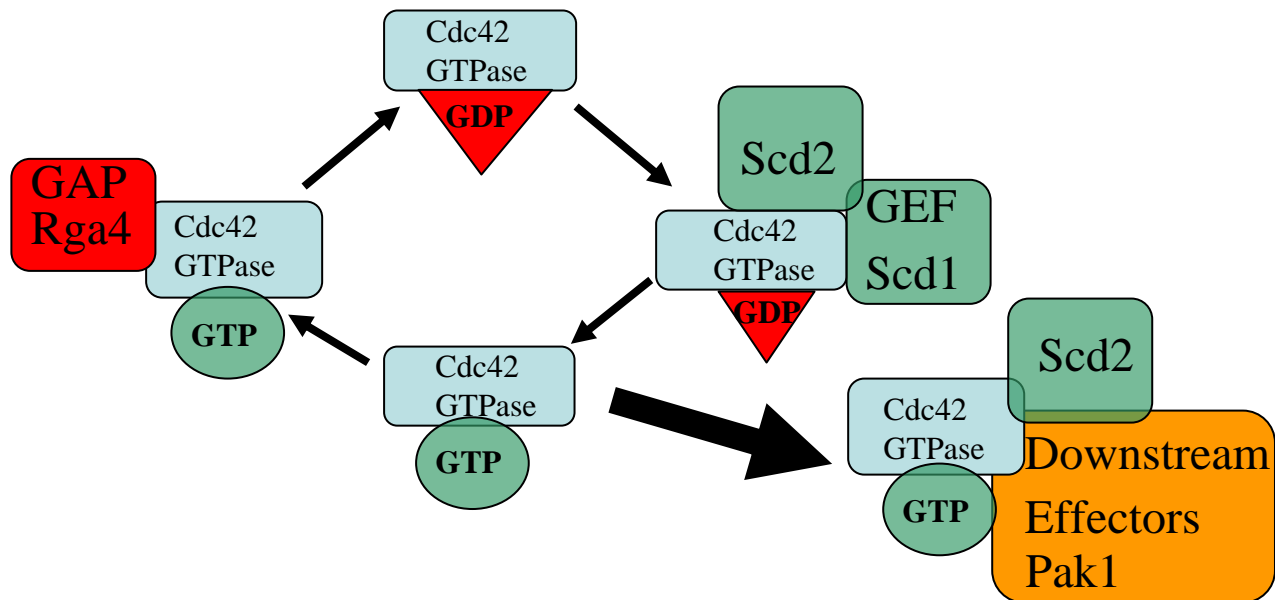
8 genes in a
single pathway

Genomic screen revealed a conserved pathway controlling cell width



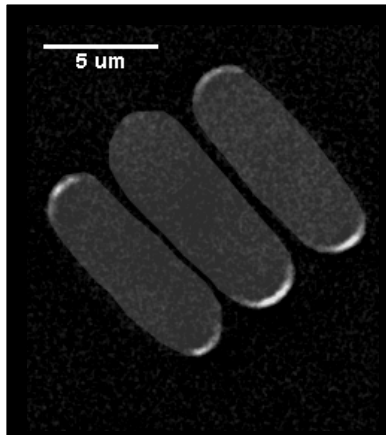
Cdc42 is a conserved polarity regulator in all eukaryotes

- Cdc42 binds GTP (active form) or GDP (inactive form).
- Wide ranging activities include filapodia formation and polarization in mammalian cells.
- Many functions involve actin cytoskeleton polarization.

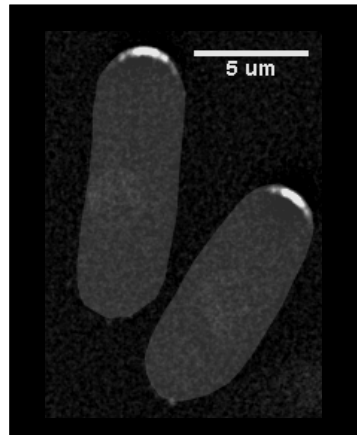


Cdc42 activators localize to the growing cell tip

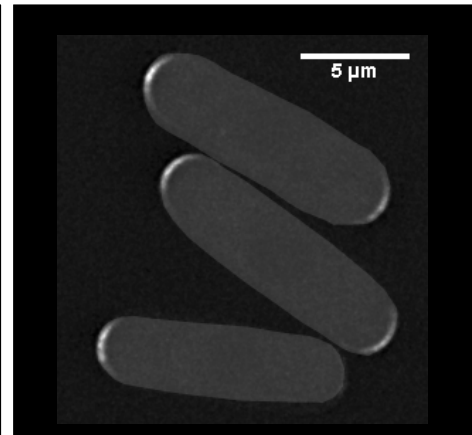
Scd1-GFP
(Cdc42 GEF)



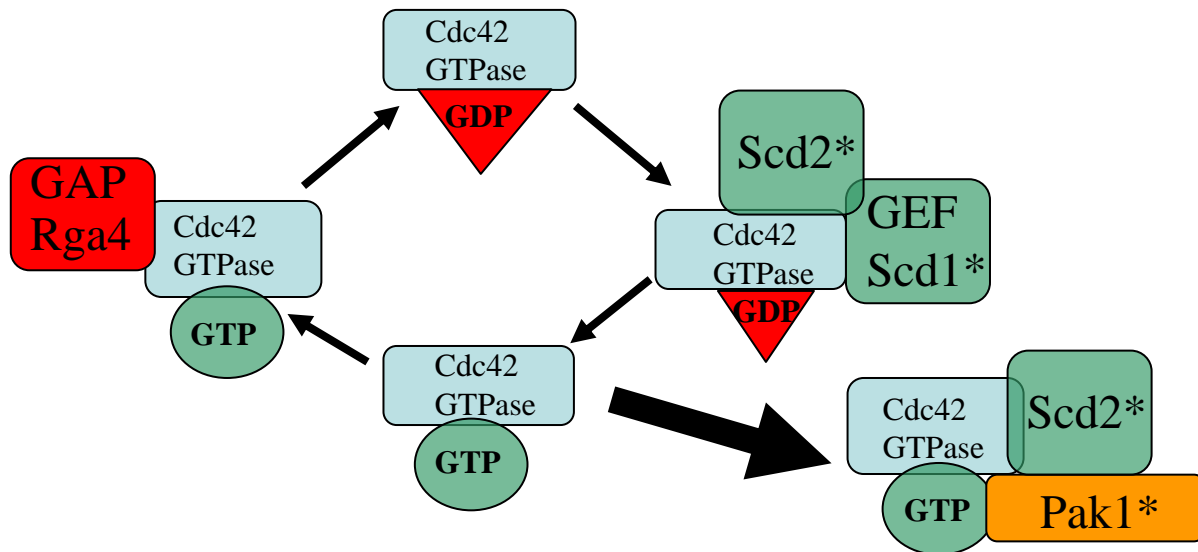
Scd2-GFP
(scaffold)



Pak1-GFP
(effector kinase)

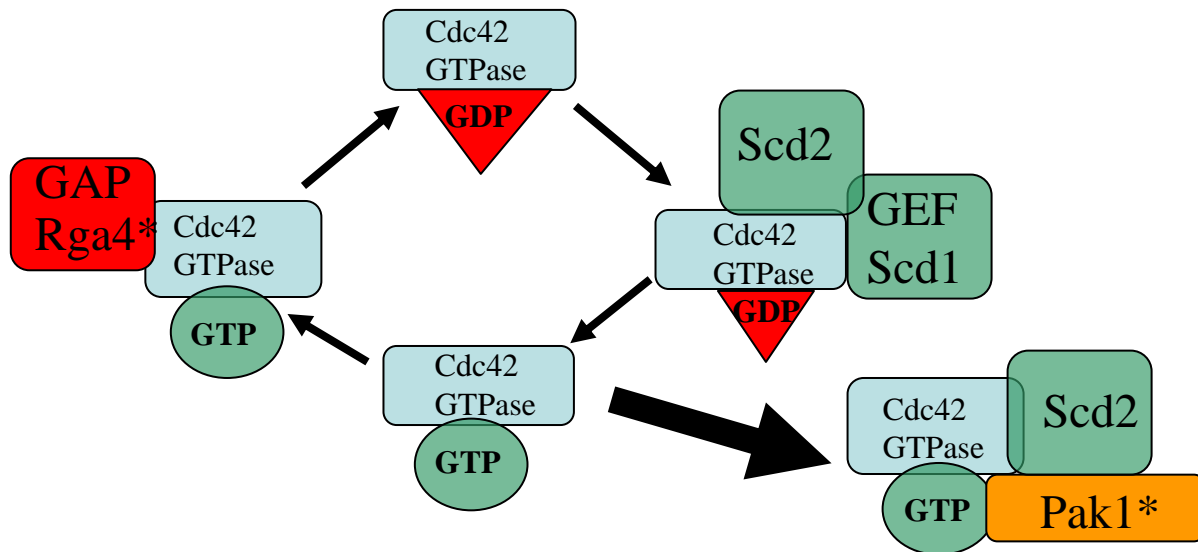
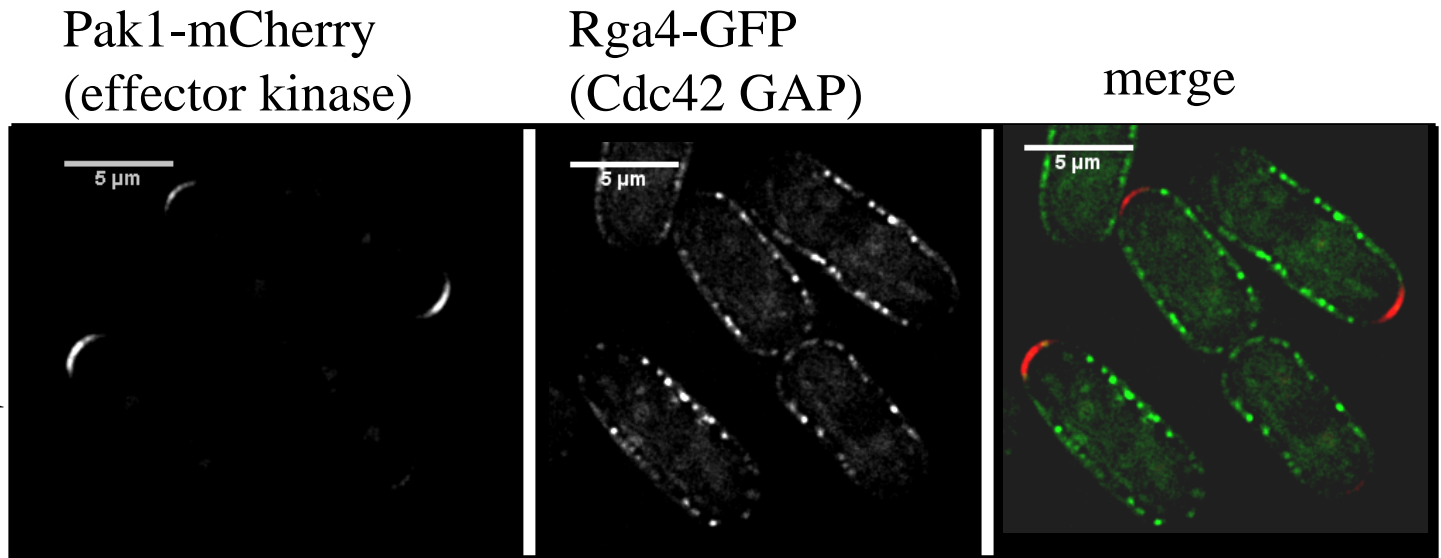


GFP signal
and
cell shape

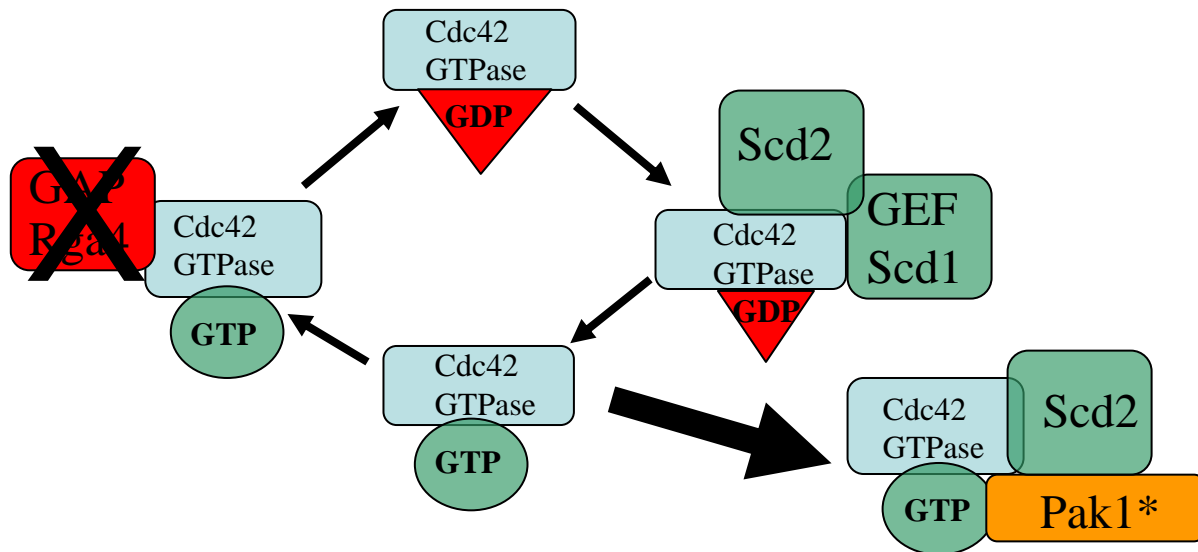
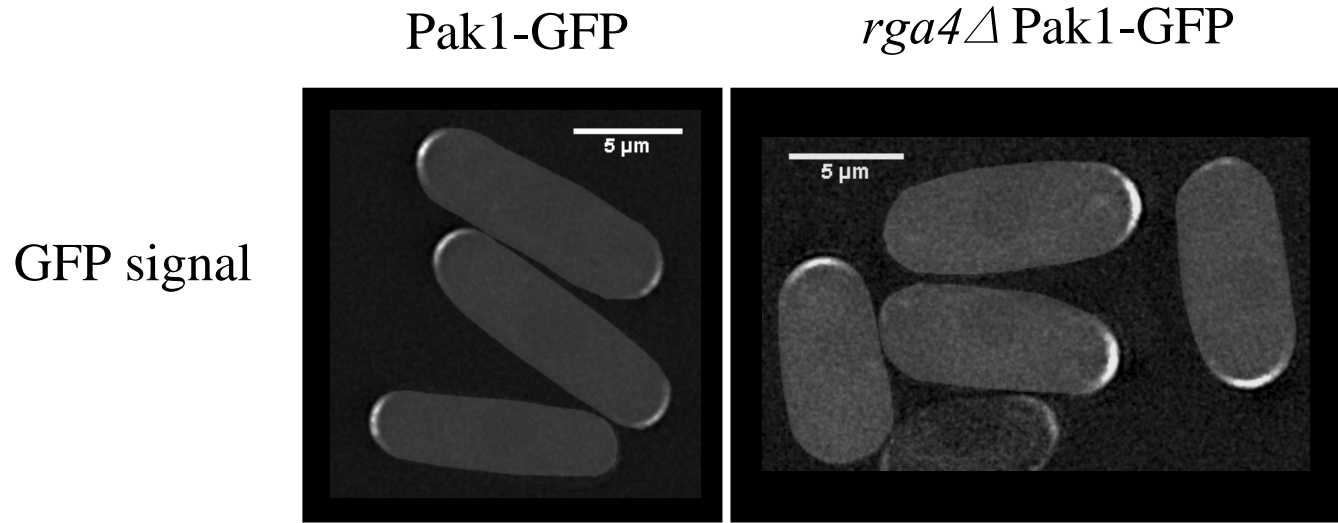


Negative Regulator of Cdc42 is excluded from cell tips

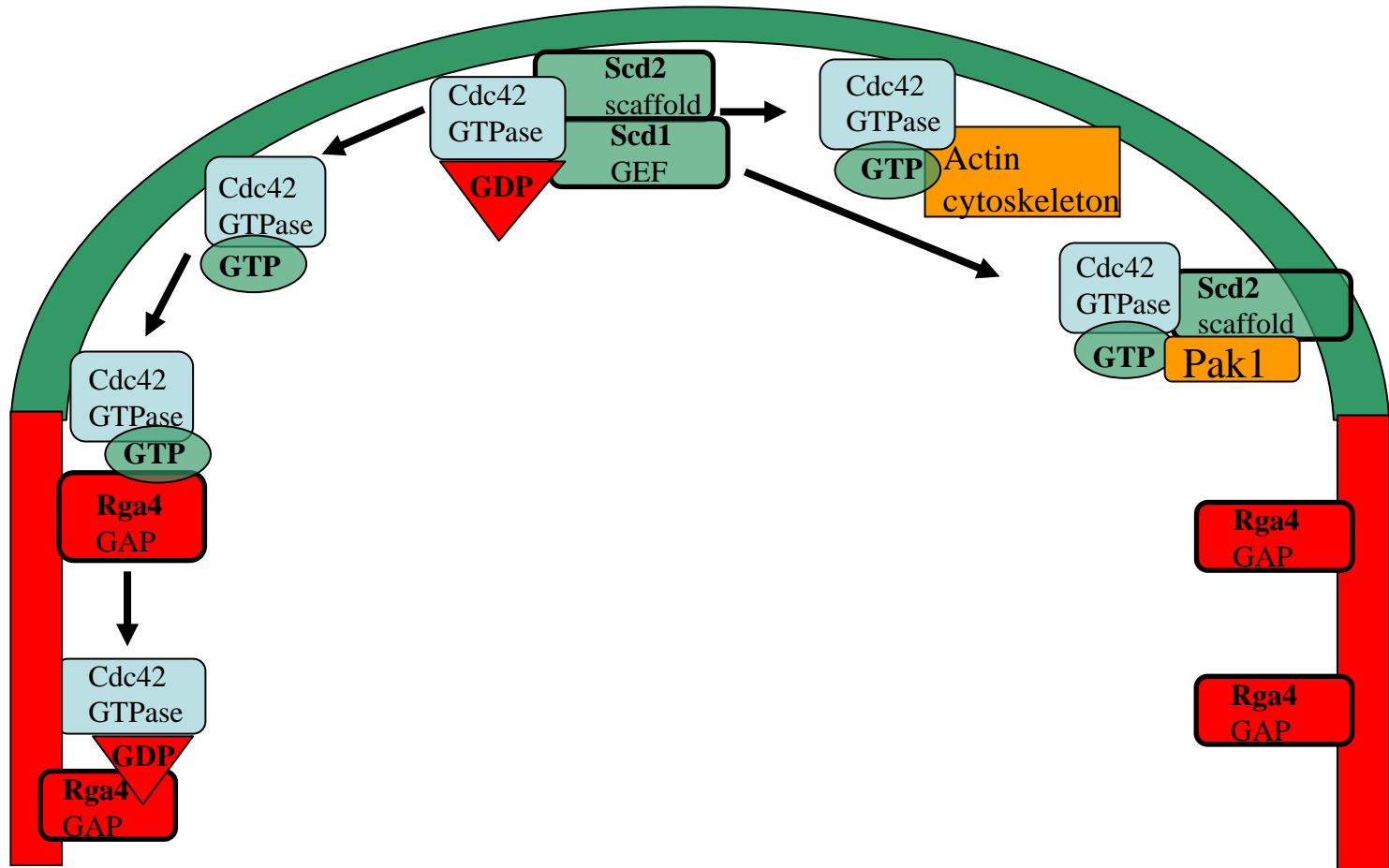
Fluorescent protein signal



Rga4 is required for restriction of Pak1

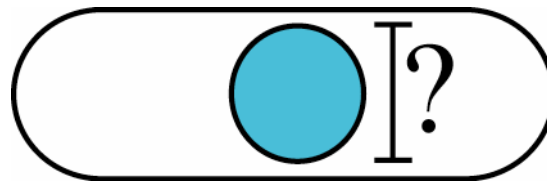


Rga4 forms a negative regulatory zone which limits cell width

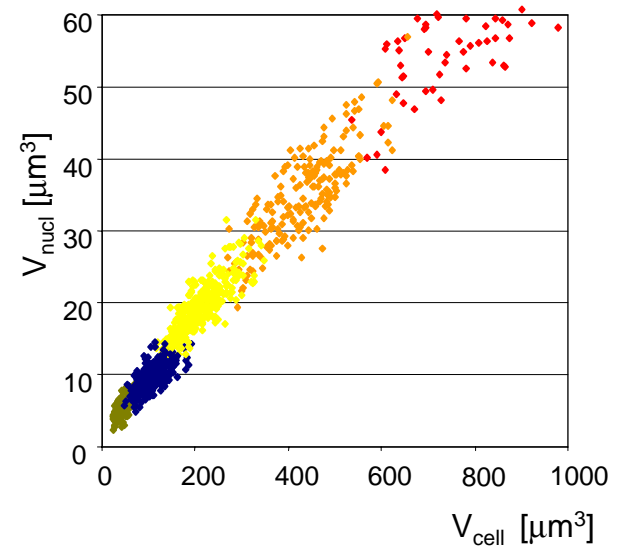
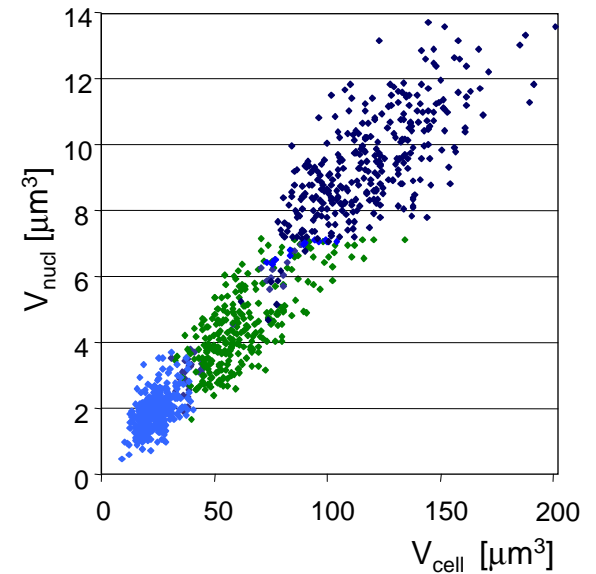
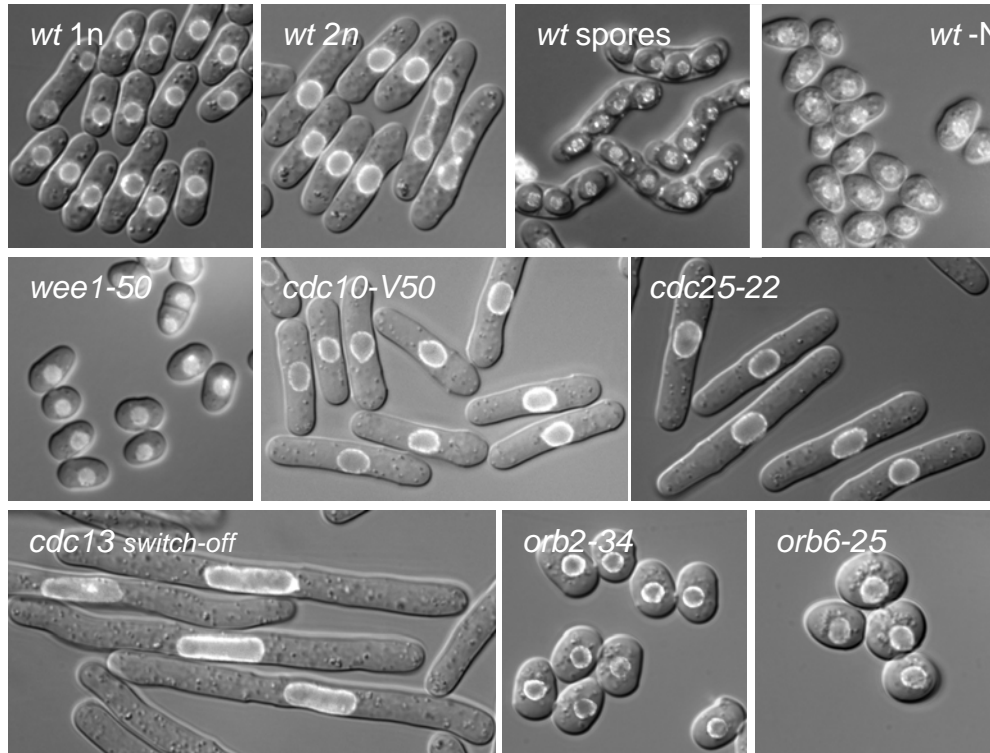


Controlling Nuclear Size

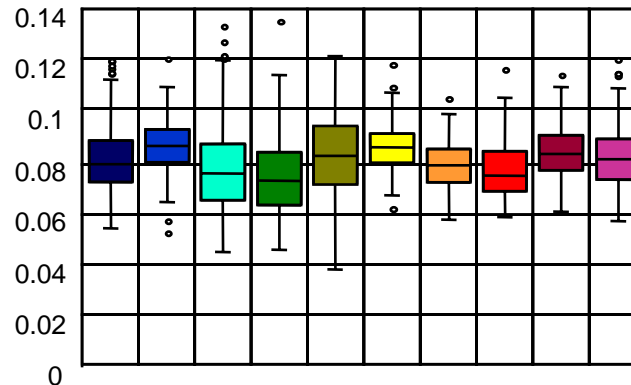
Frank Neumann



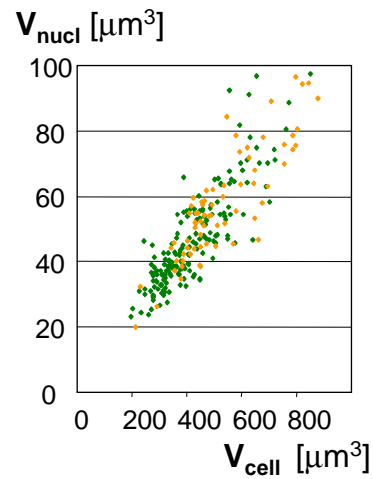
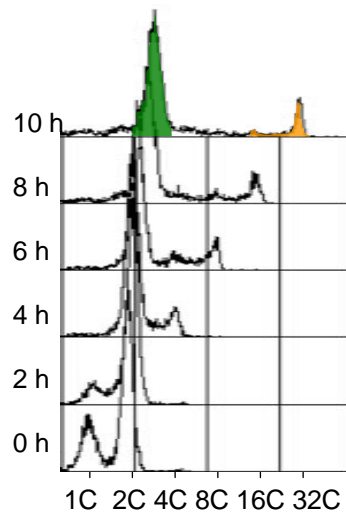
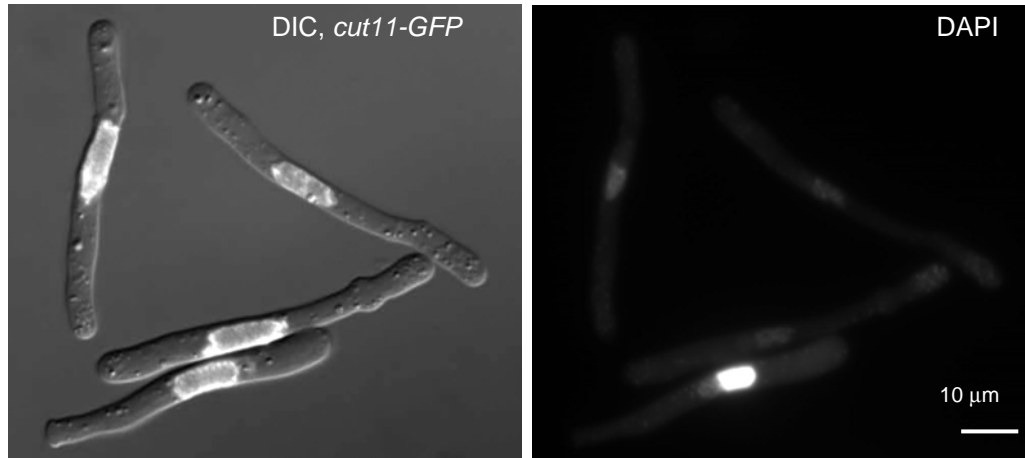
Cell size and shape



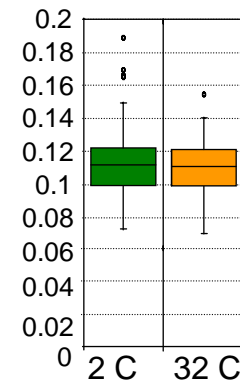
- wt haploid
- wt diploid
- wt spores
- wt -N starvation
- wee1-50 5h 36.5°C
- cdc10-V50 4.5h 36.5°C
- cdc25-22 3h 36.5°C
- cdc13 switch-off 10h
- orb2-34 5h 36.5°C
- orb6-25 5h 36.5°C



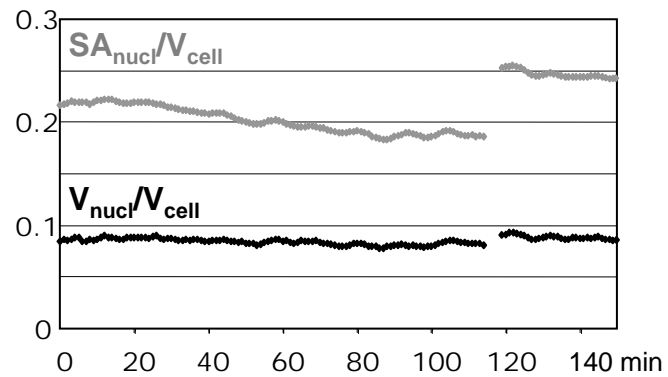
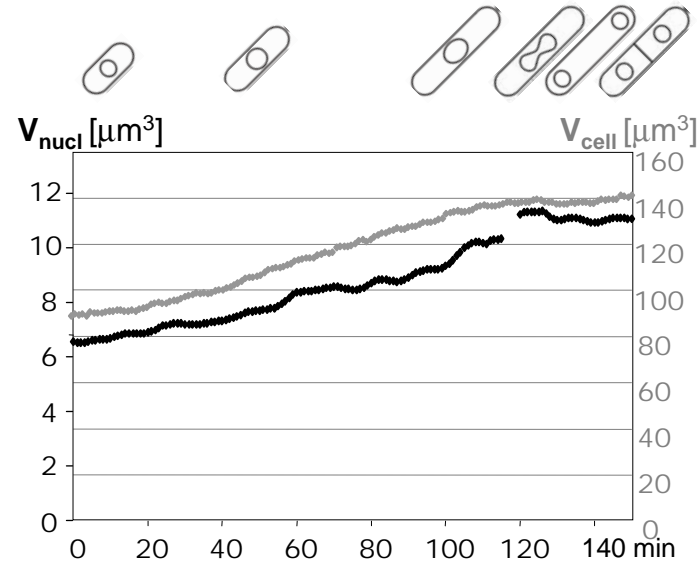
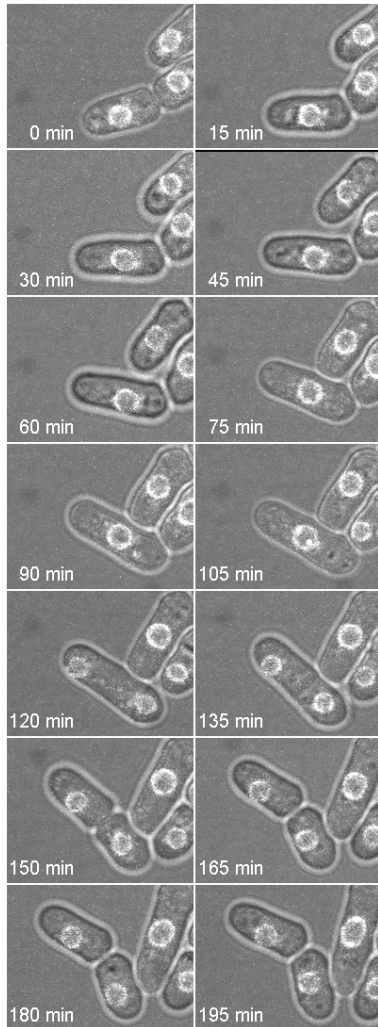
DNA content



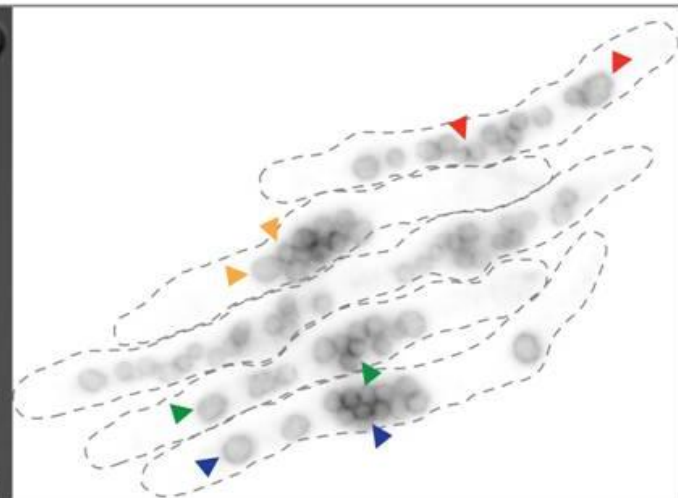
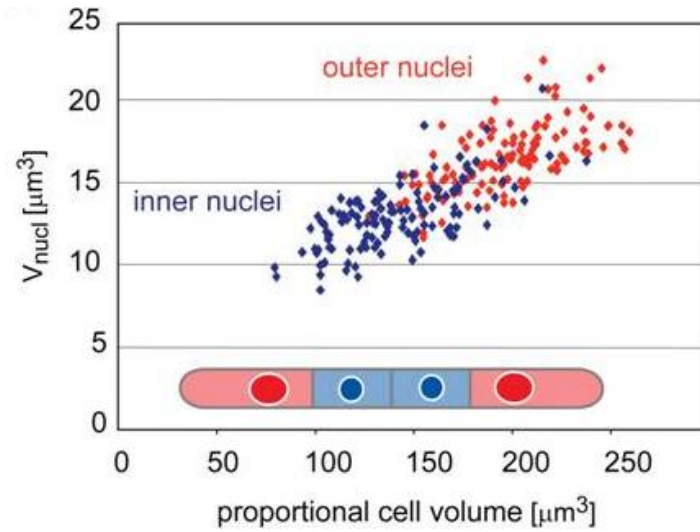
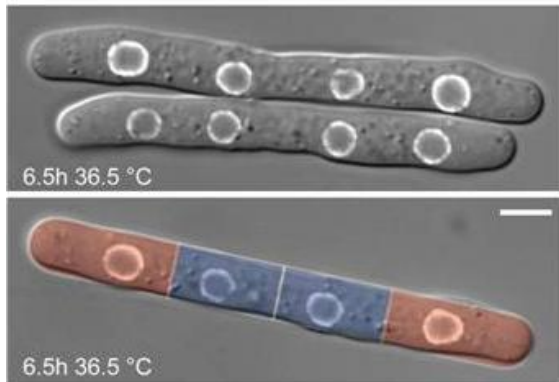
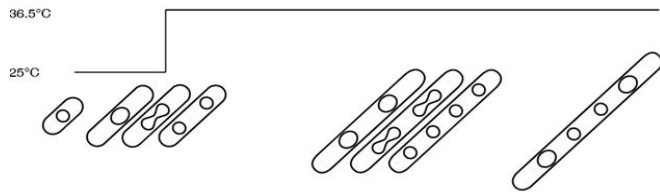
N/C ratio (fixed cells)



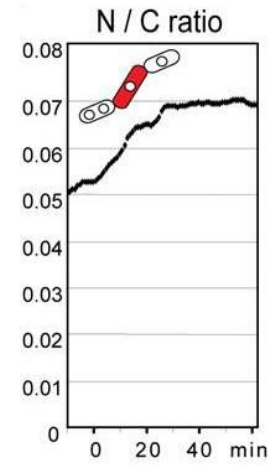
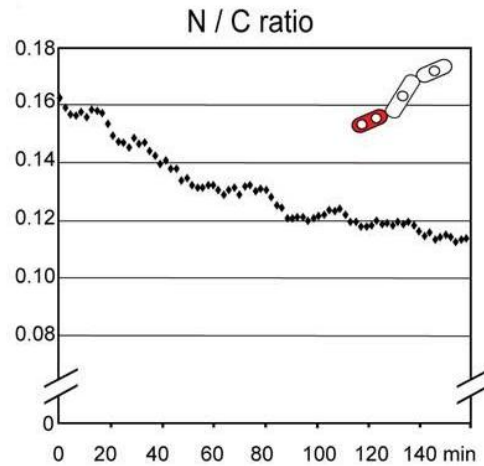
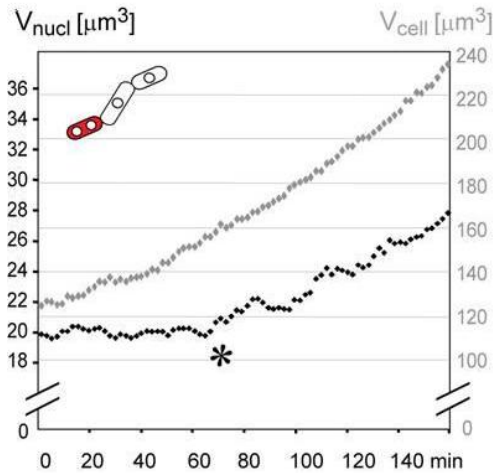
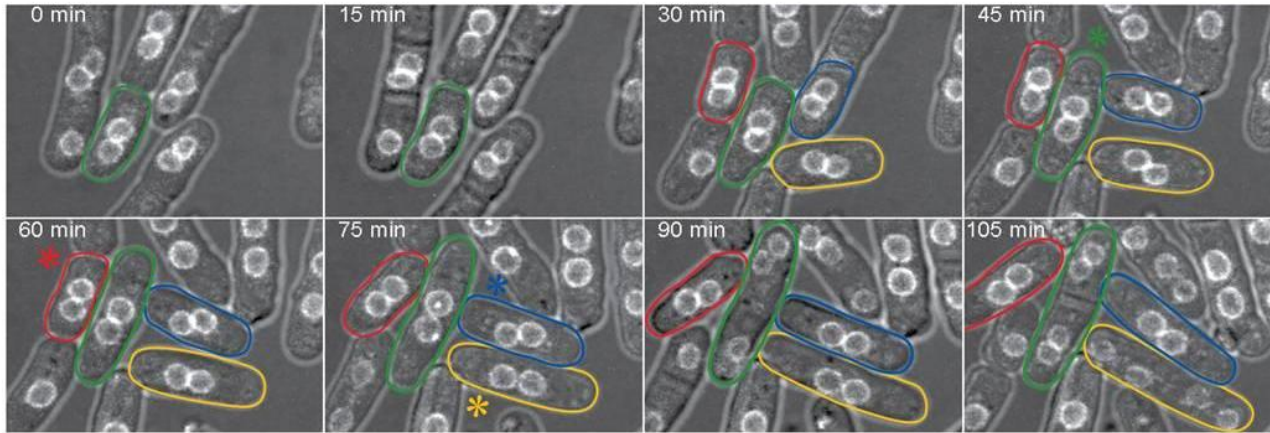
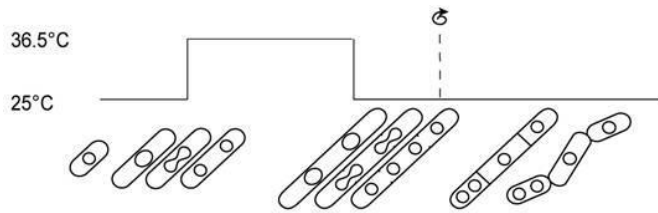
N/C ratio and cell cycle



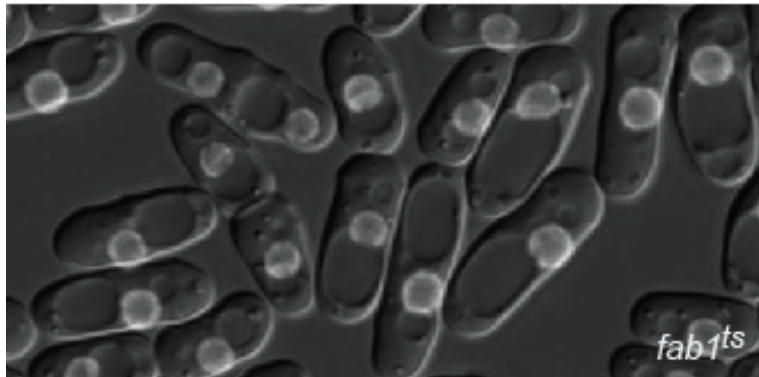
Subcellular environment



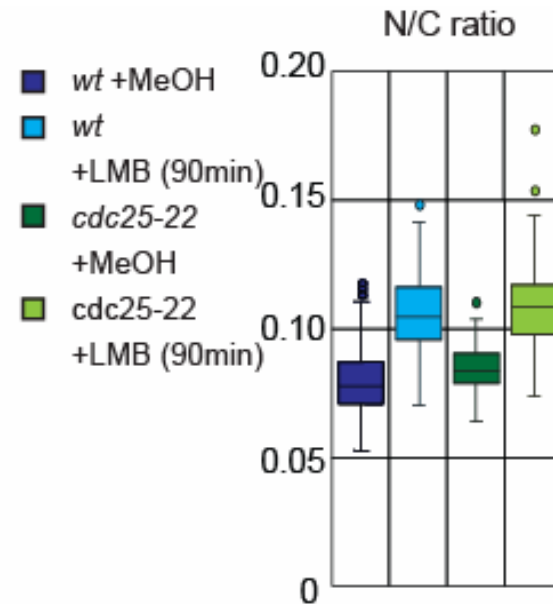
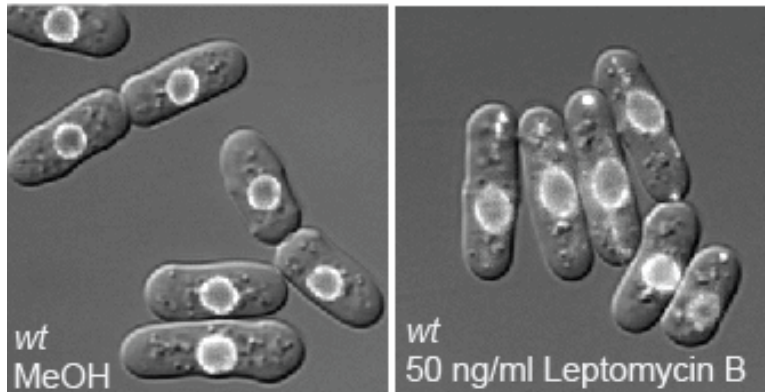
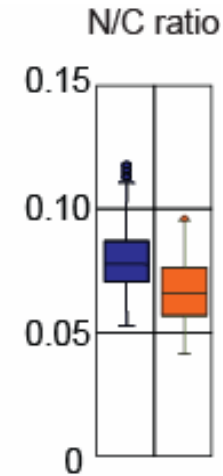
N/C ratio perturbation



Changed N/C ratios



- *wt*
- *fab1ts*

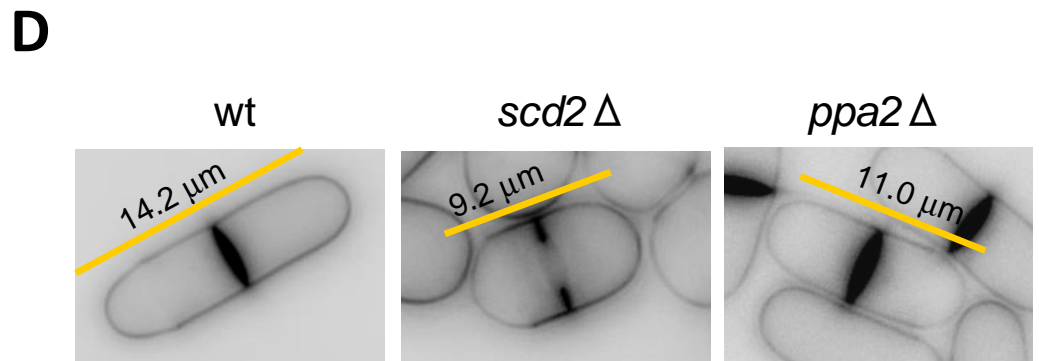
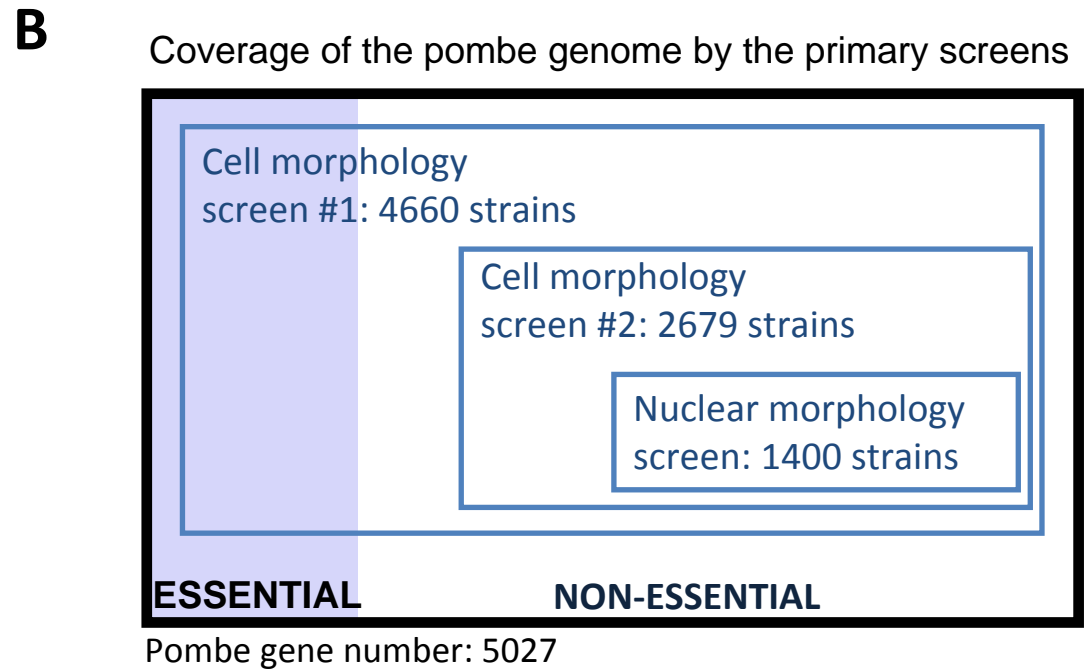
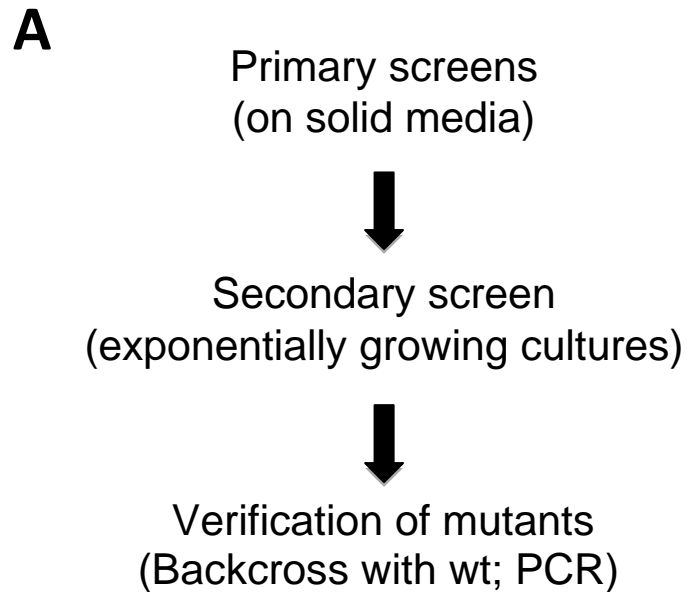


Systems-level study of
cell size control in
fission yeast

Francisco Navarro

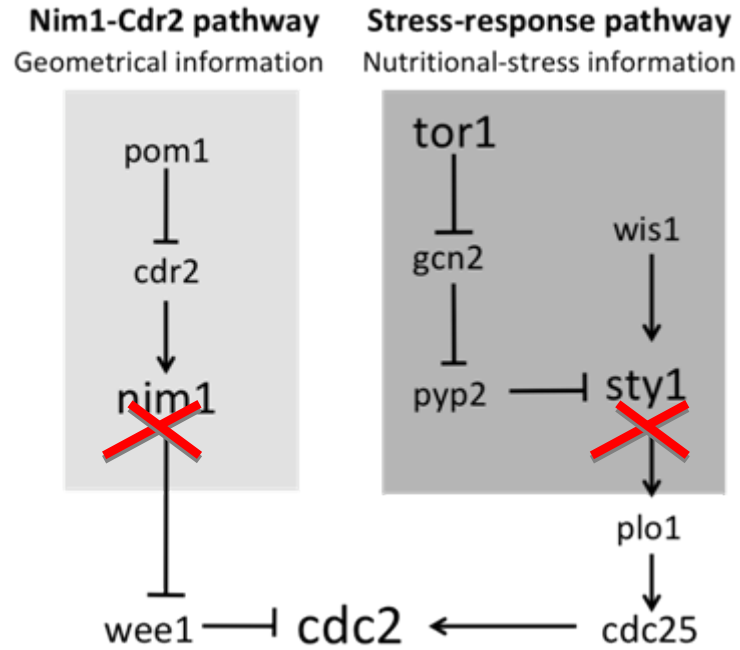


Genome-wide screen of small size mutants

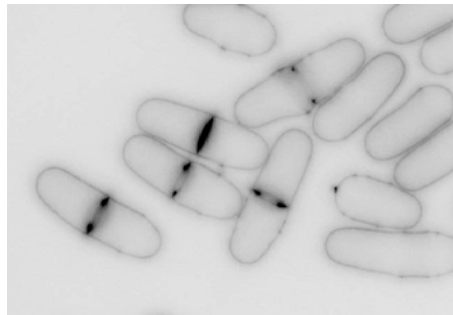


Small size mutants identified in the screen

Sys ID	Cell length (μm)	Doubling time (min)	GO_molecular function	GO_Biological Process
SPCC18B5.03	7.4 \pm 0.7	156	Protein Ser/Thr/Tyr kinase	Regulation of G2/M transition of mitotic cell cycle
SPBC106.10	10.5 \pm 0.7	157	cAMP-dependent protein kinase	cAMP-mediated signaling; negative regulation of transcription by glucose; response to osmotic stress;
SPAC23H3.13c	10.9 \pm 0.9	152	GTPase, α -subunit	
SPCC1753.02c	12.7 \pm 0.8	148	G-protein coupled receptor	
SPBC32H8.07	12.9 \pm 0.9	142	GTPase activity	
SPBC1718.07c	12.3 \pm 0.7	138	Protein binding	
SPAC1782.09c	11.9 \pm 0.9	138	Protein Ser/Thr/Tyr phosphatase	Negative regulation of mitosis; septum formation; mitosis exit; Cytokinesis checkpoint;
SPAC2F7.03c	12.3 \pm 1.6	144	Protein Ser/Thr kinase	Activation of bipolar cell growth; regulation of cytokinesis;
SPBC23G7.04c	12.5 \pm 0.7	126	Protein kinase inhibitor	Negative regulation of mitotic cell cycle
SPAC2F7.08c	12.6 \pm 0.7	137	General RNA polymerase II transcription factor activity	Chromatin remodeling; regulation of transcription from RNA polymerase II promoter
SPBC30B4.04c	12.9 \pm 0.9	131		
SPCC126.04c	12.7 \pm 0.8	163	unknown	Chromatin modification; histone acetylation
SPBC16E9.12c	13.1 \pm 0.8	143	Poly(A) RNA binding	mRNA poly(A) tail shortening
SPCC1919.05	12.4 \pm 0.6	136	Protein binding	mRNA catabolic process; protection against dsRNA virus; 3'-5' directed mRNA degradation.
SPBC19F8.02	12.6 \pm 0.6	149	Protein binding	Cytoplasm organization
SPAC27E2.03	12.3 \pm 0.7	154	GTP binding	unknown
SPBC16H5.07c	11.2 \pm 1.0	136	Phosphoprotein phosphatase activity	Negative regulation of mitotic cell cycle; signal transduction
SPAC26F1.10c	11.3 \pm 0.6	138	Protein tyrosine phosphatase	Negative regulation of stress-activated MAPK cascade
wt	14.1 \pm 0.8	130		

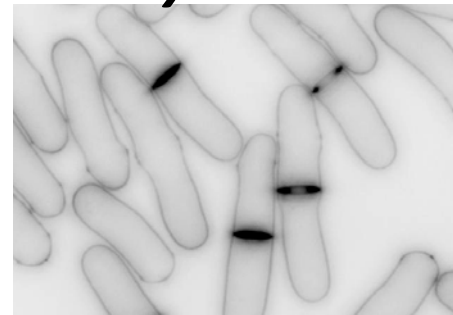


wt



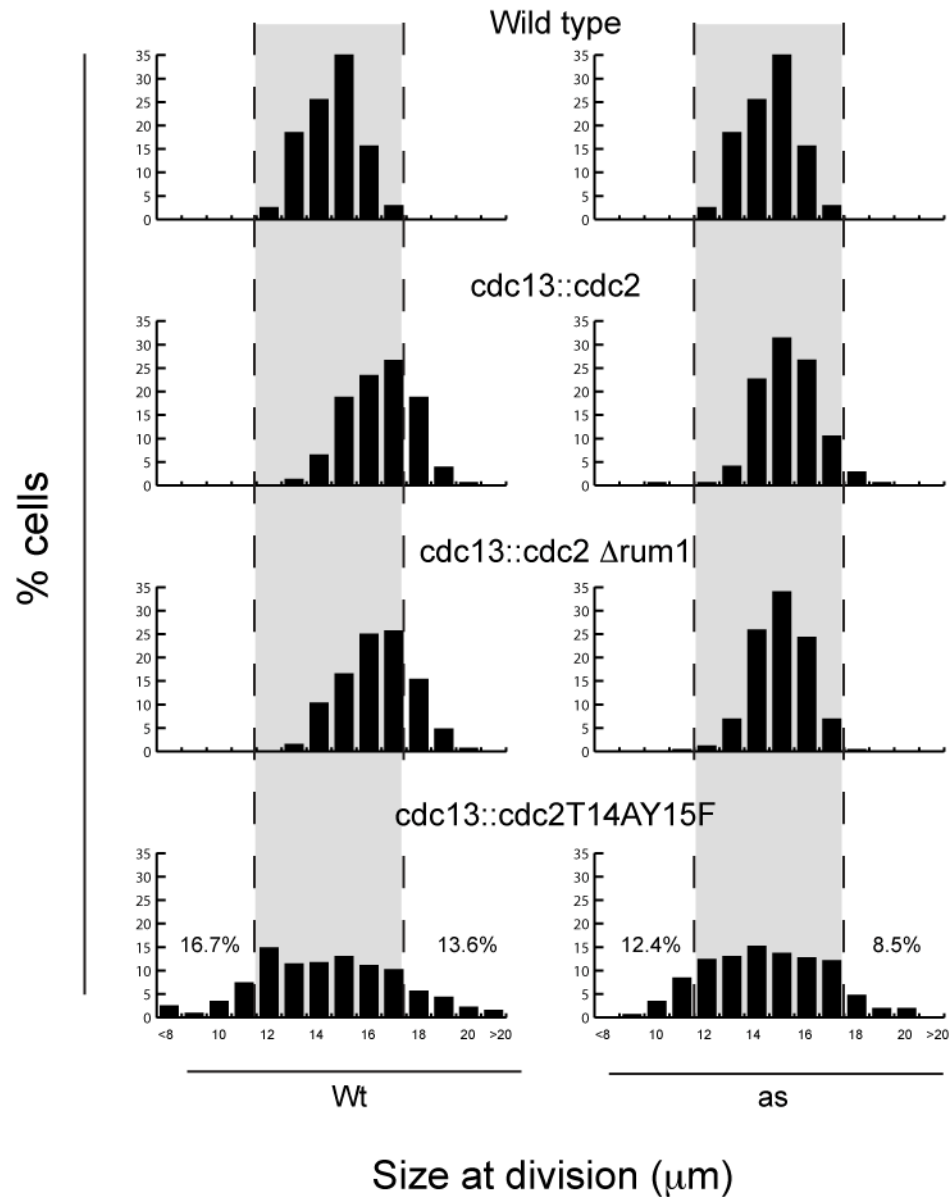
Mean length=14.2m
CV=6.3%

***sty1* Δ *nim1* Δ**

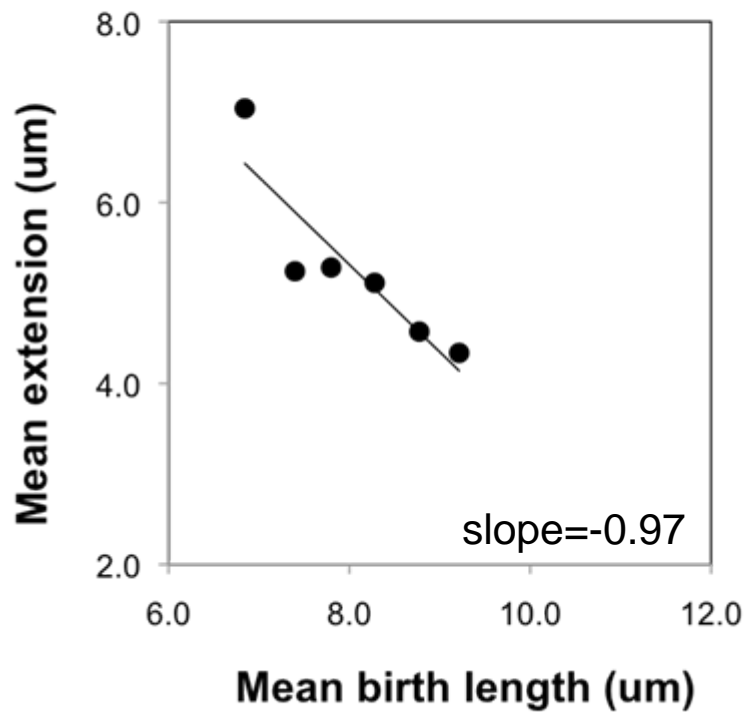


Mean length=22.6 μ m
CV=7.5%

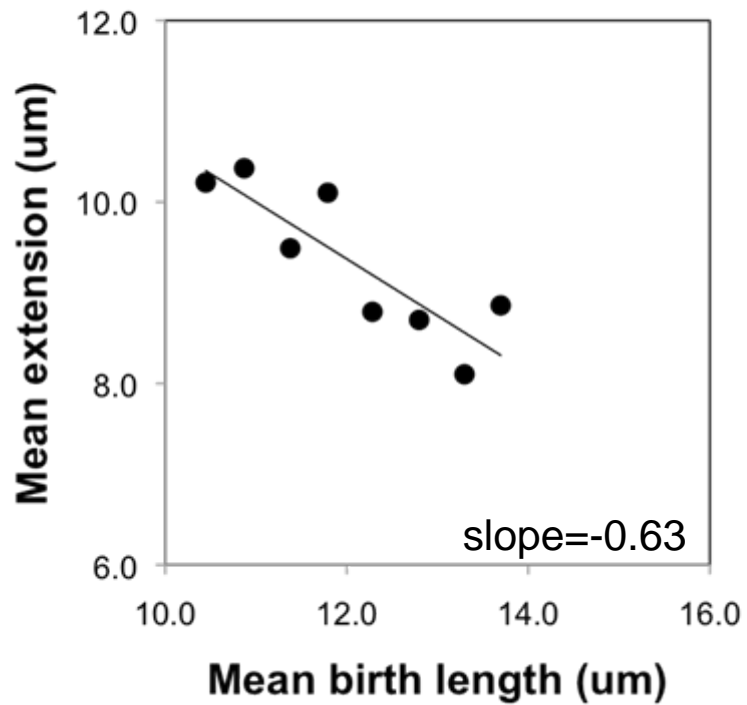
The Wee1/Cdc25 loop is essential for the homogeneity of the population



wt

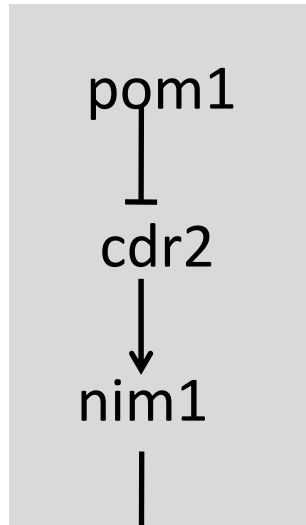


***sty1* Δ *nim1* Δ**



Nim1-Cdr2 pathway

Geometrical information



Stress-response pathway

Nutritional-stress information

