



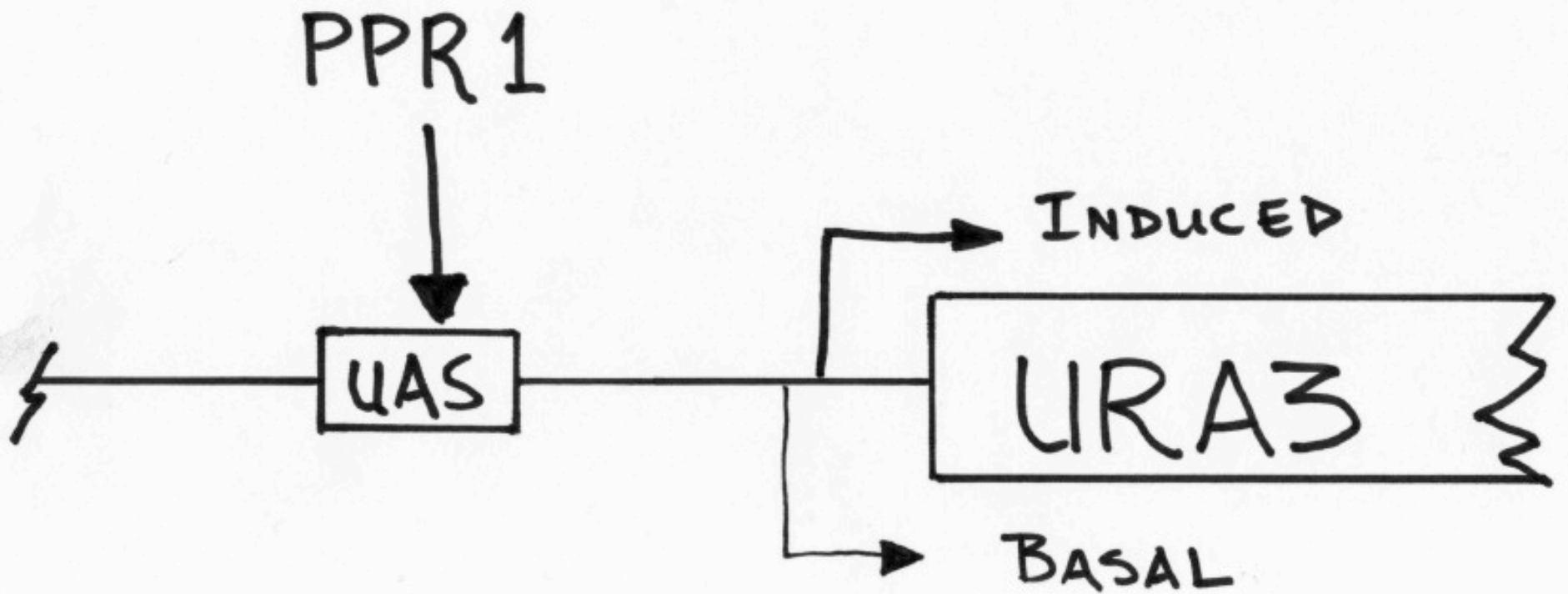


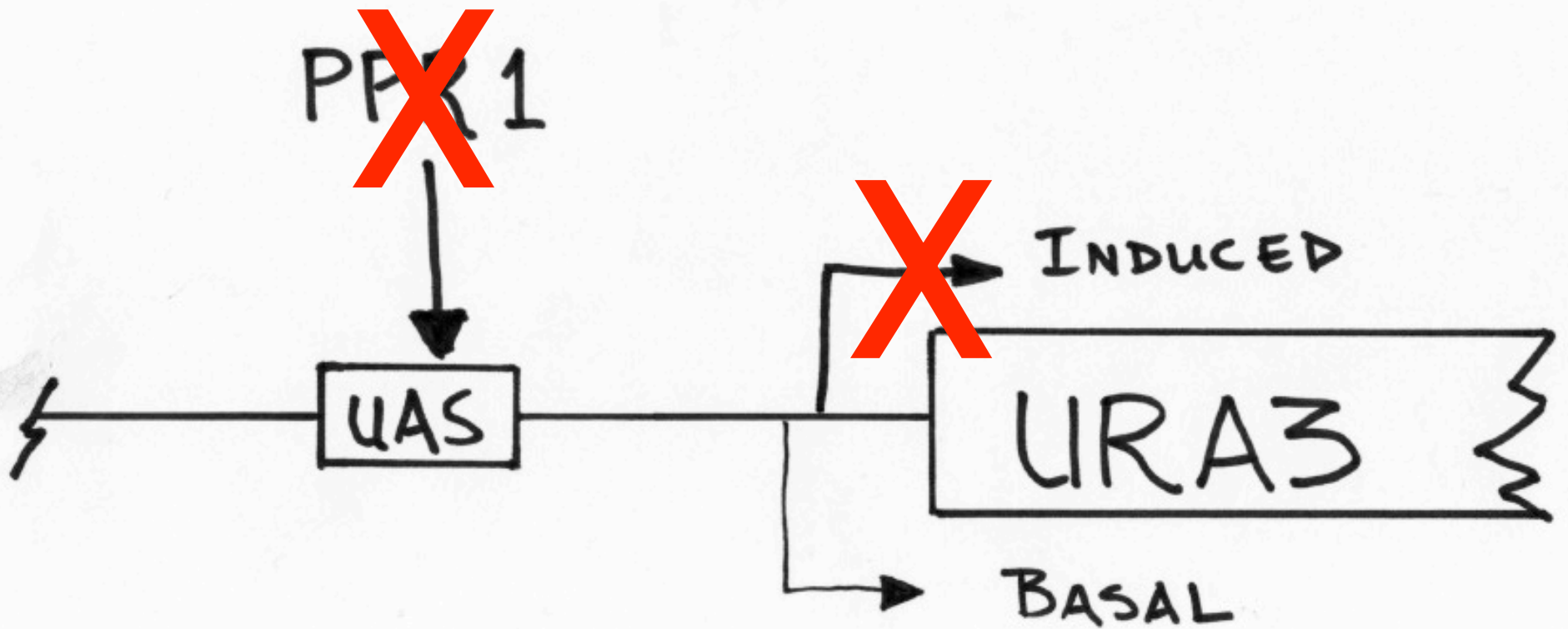
POSITIVE & NEGATIVE SELECTION
FOR URA3.

	<u>-uracil</u>	<u>5-FOA</u>
URA3 ⁺	YES	NO
ura3 ⁻	NO	YES

POSITIVE & NEGATIVE SELECTION
FOR URA3.

	<u>-uracil</u>	<u>5-FOA</u>
URA3 ⁺	YES	NO
ura3 ⁻	NO	YES





POSITIVE & NEGATIVE SELECTION
FOR URA3.

Telomeric - PPR1

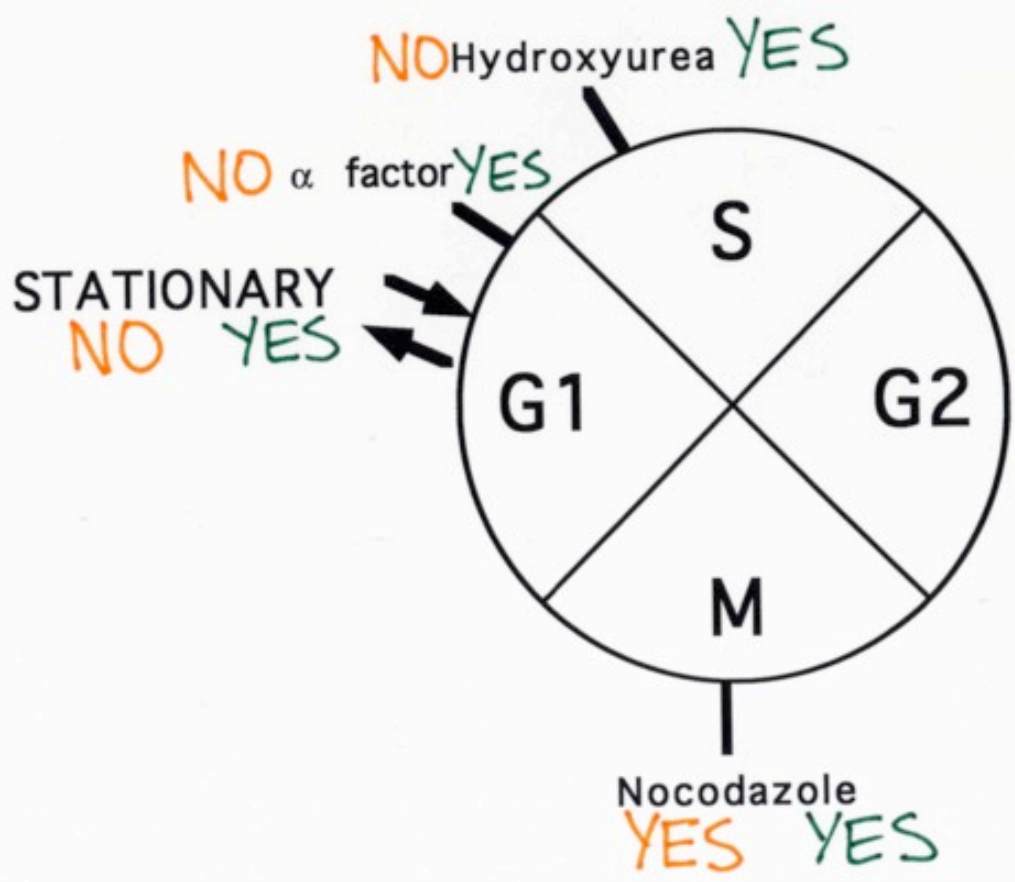
	<u>-uracil</u>	<u>5-FOA</u>
URA3 ⁺	YES	NO
ura3 ⁻	NO	YES

POSITIVE & NEGATIVE SELECTION
FOR URA3.

Telomeric - *ppr1*

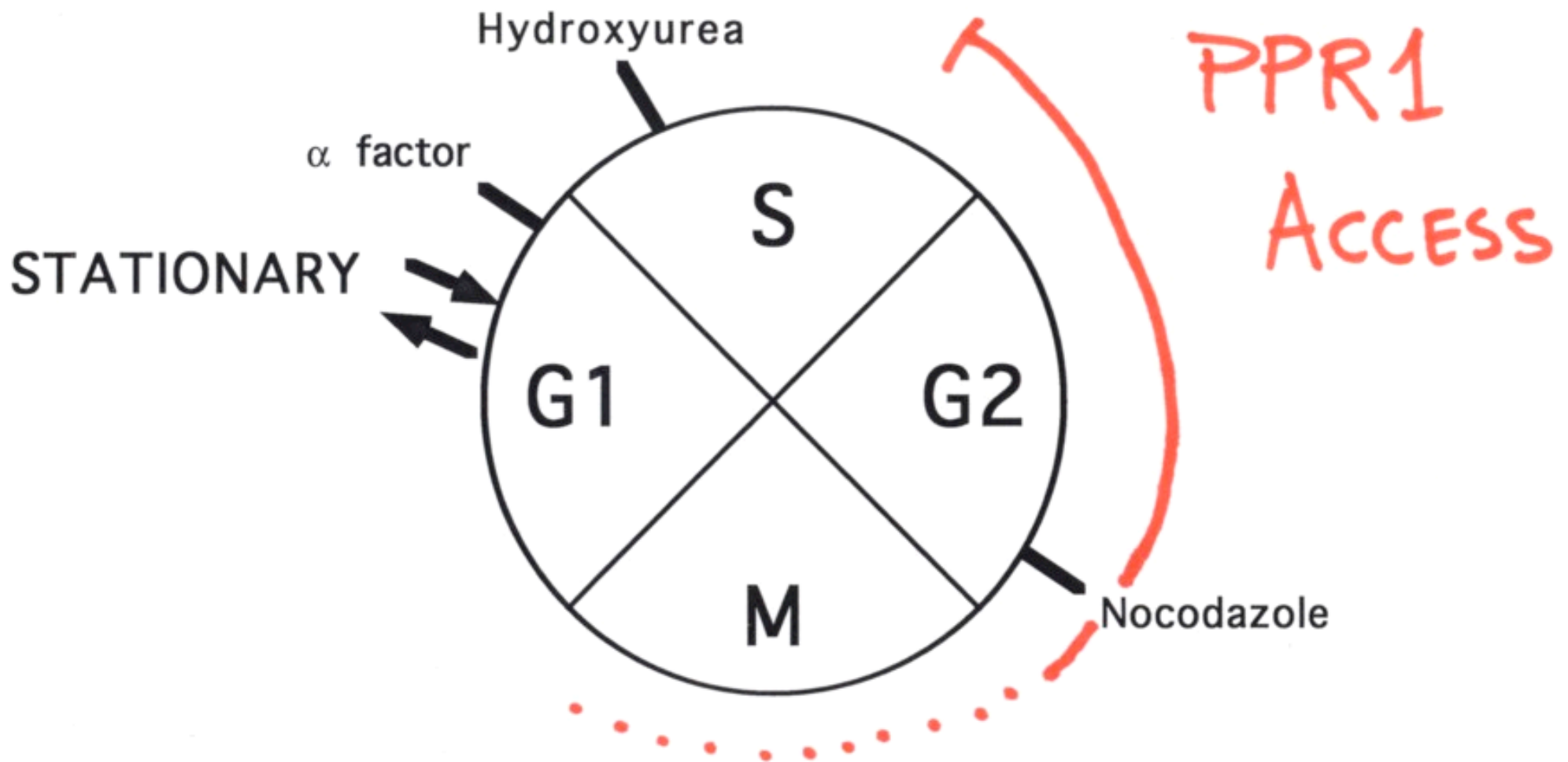
	<u>-uracil</u>	<u>5-FOA</u>
URA3 ⁺	YES	NO
ura3 ⁻	NO	YES

WHEN CAN PPR1 ACTIVATE URA3 EXPRESSION?

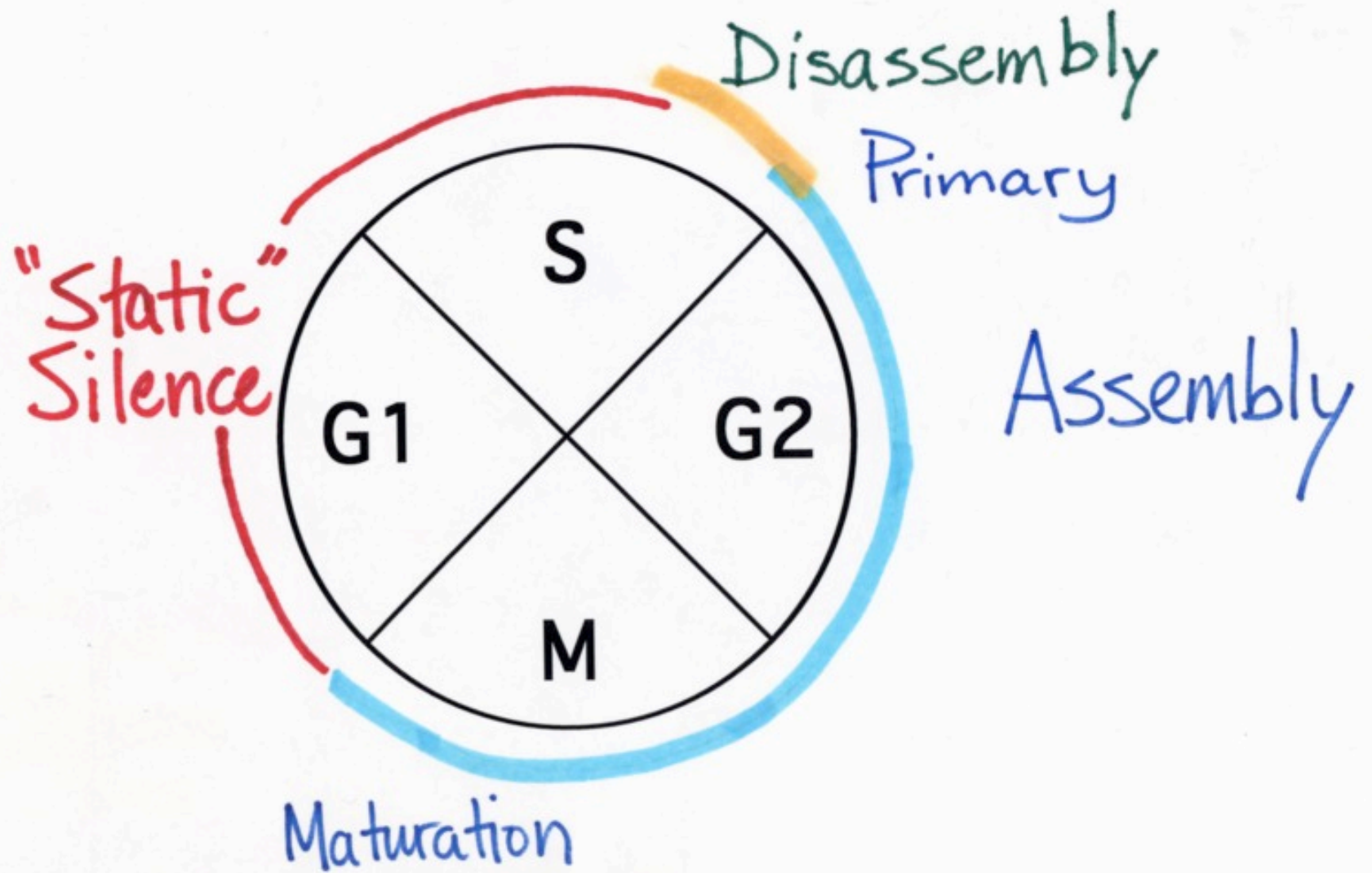


URA3 LOCATION
TELOMERE
INTERNAL

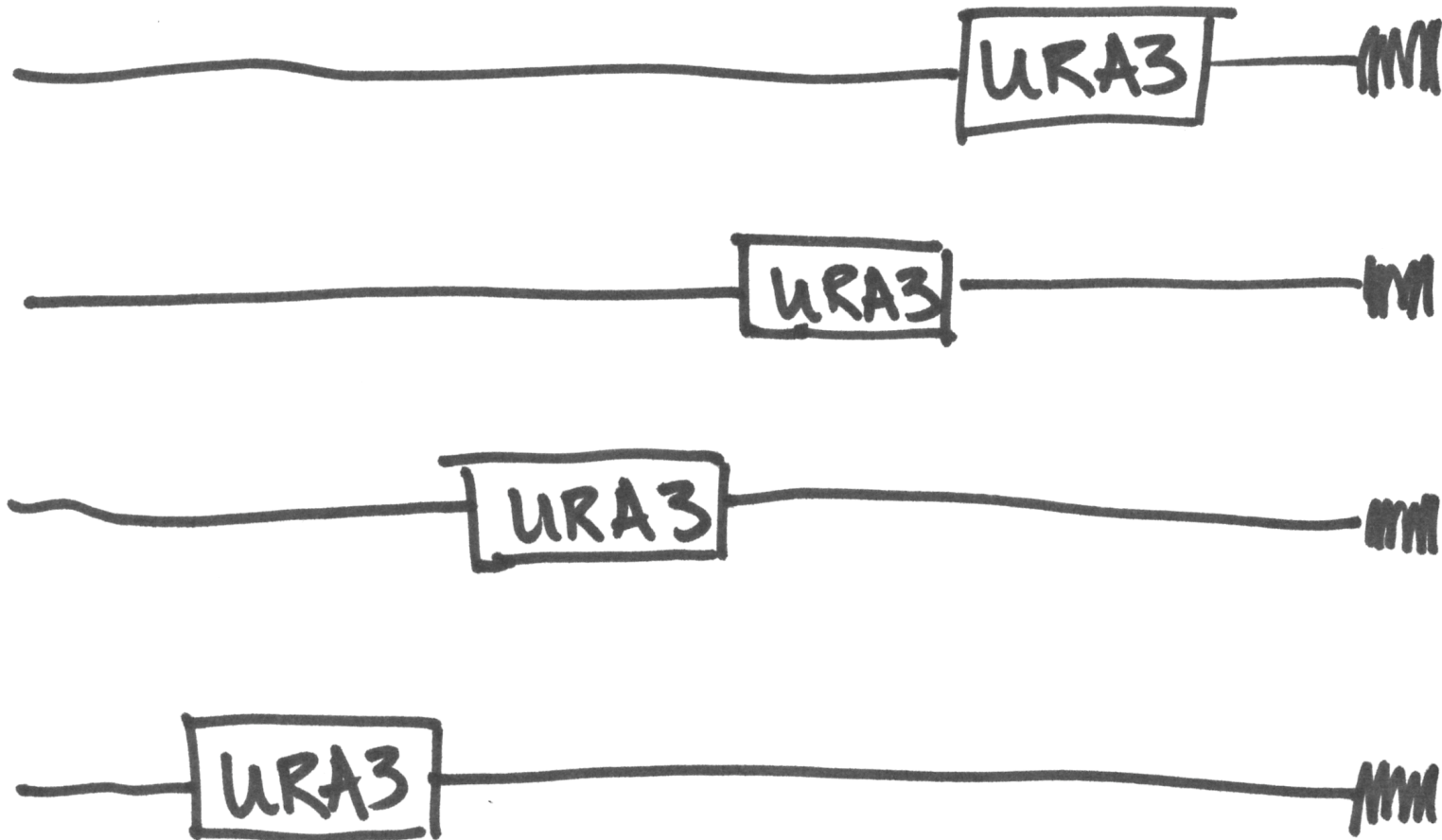
PPR1 has differential access to the telomere during the cell cycle



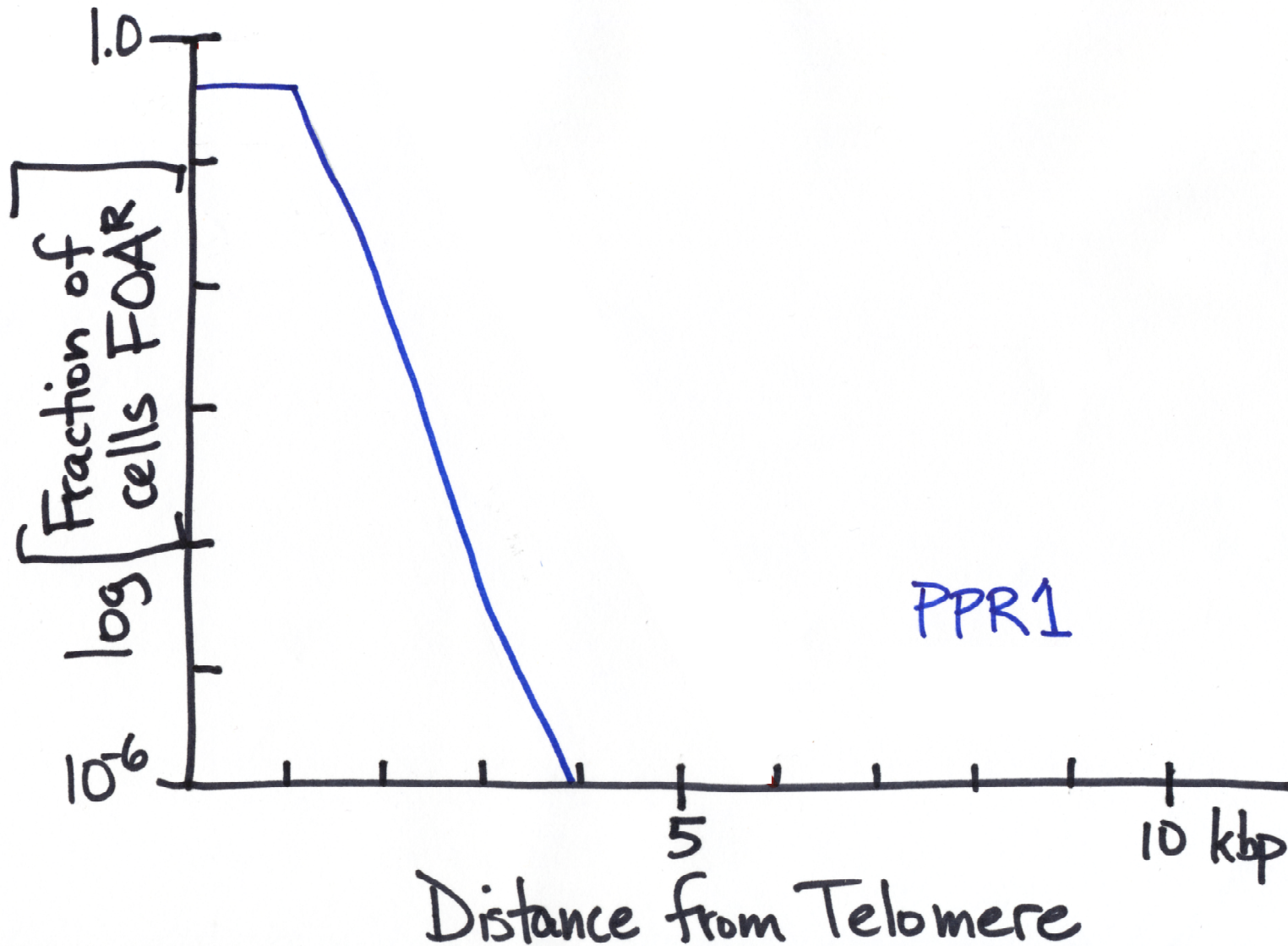
Dynamics of Telomeric Silencing



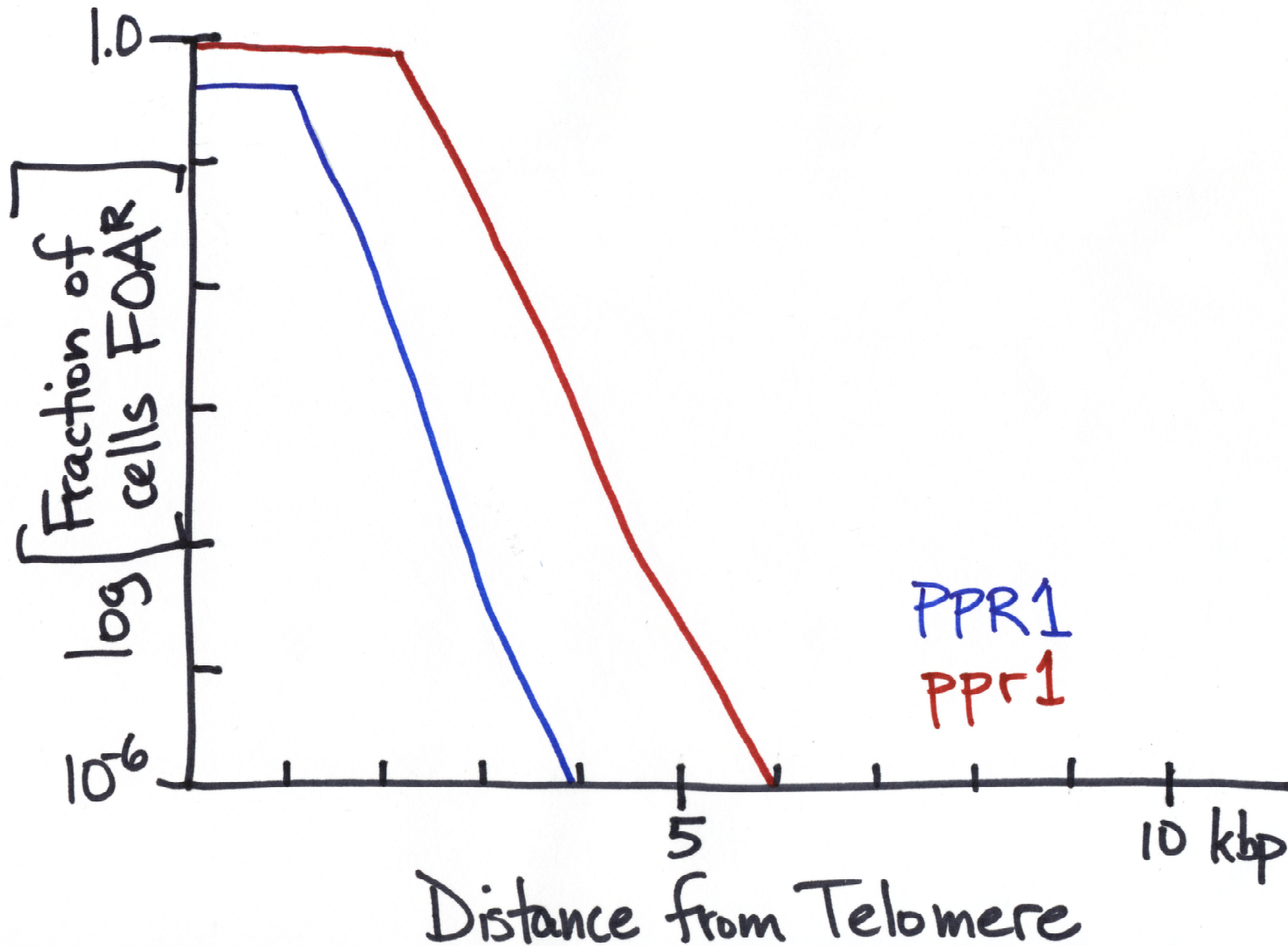
How far from the telomere does silencing occur?



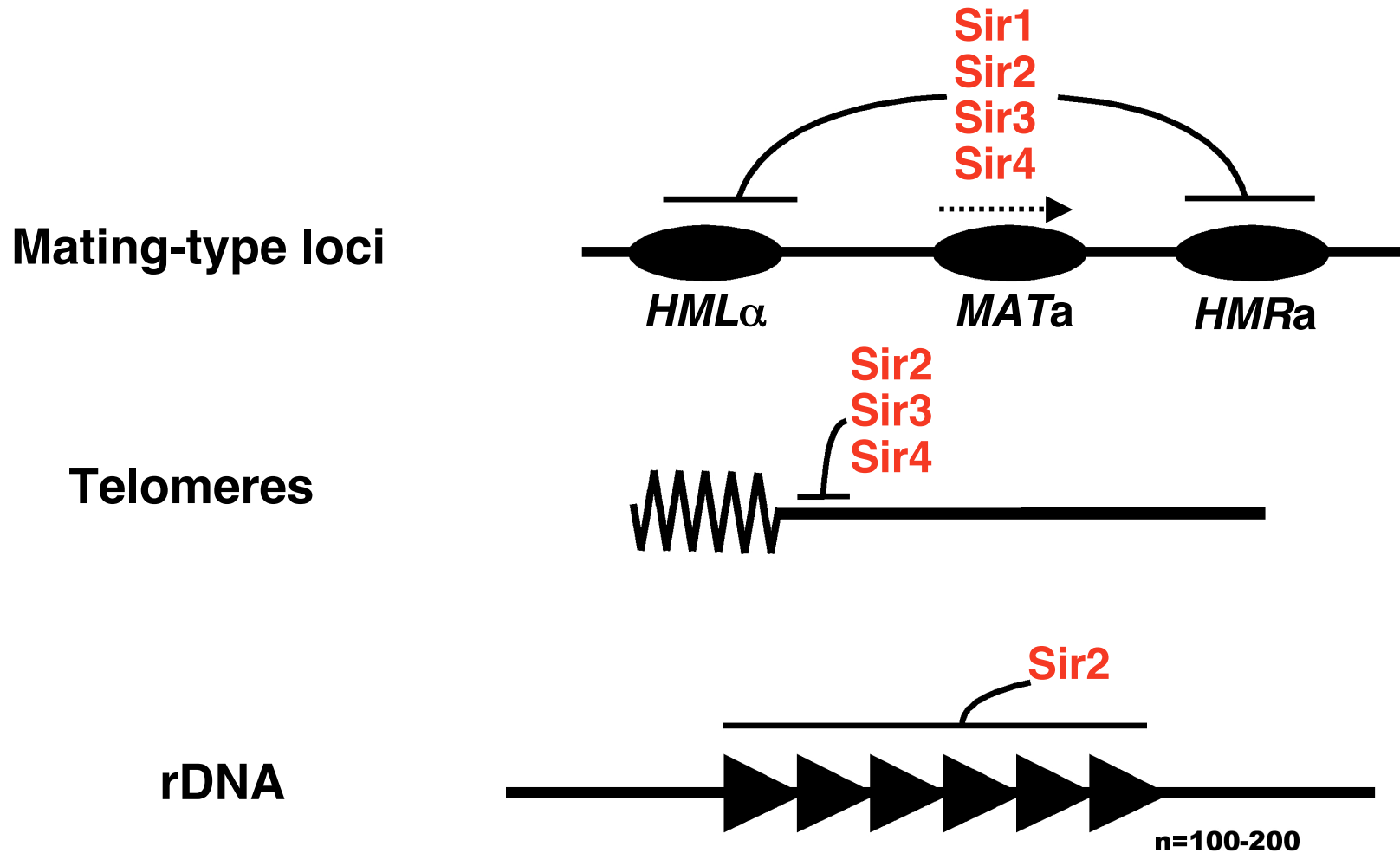
Silencing “spreads” from the telomere



Silencing “spreads” from the telomere

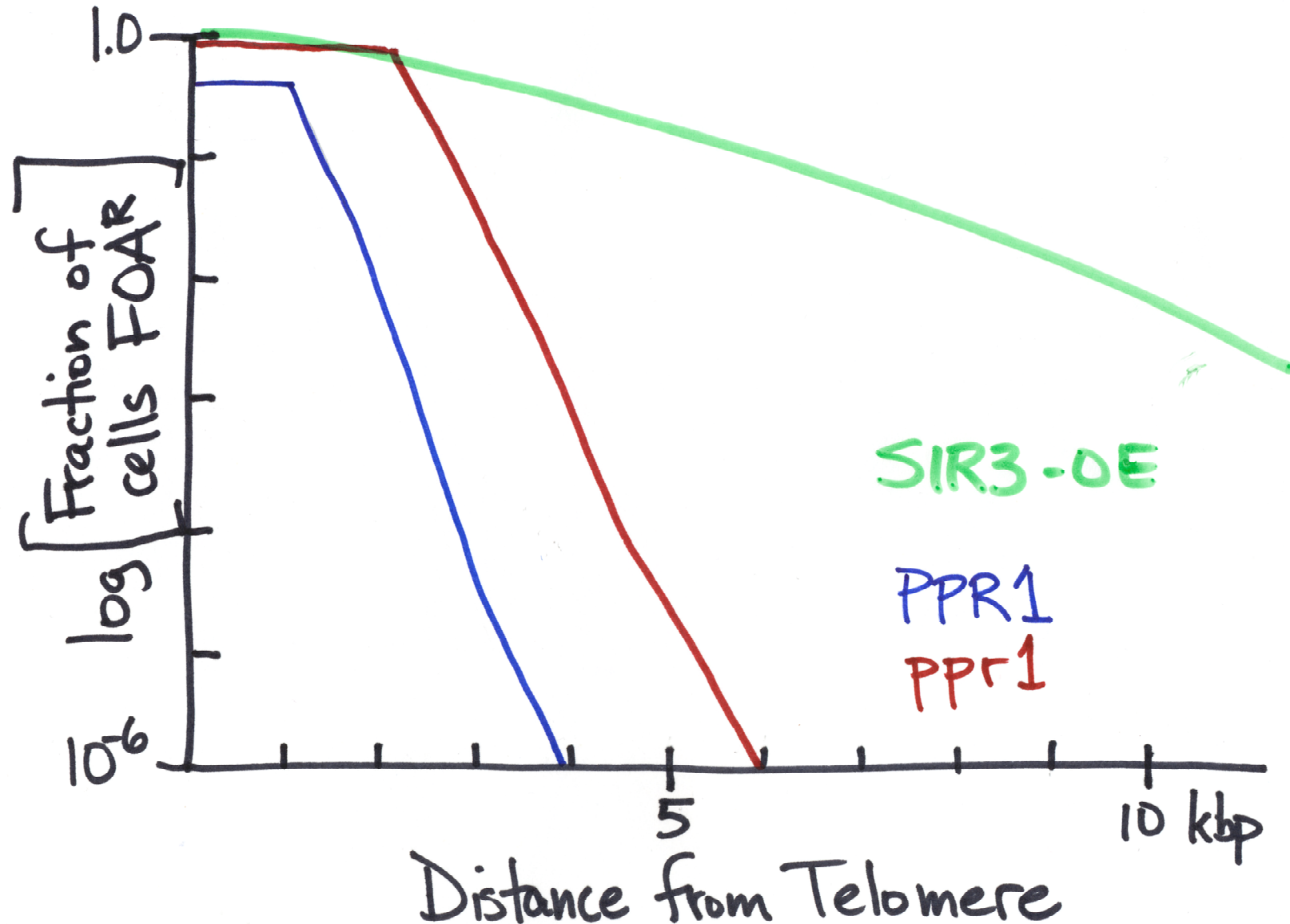


Gene Silencing in *S. cerevisiae*

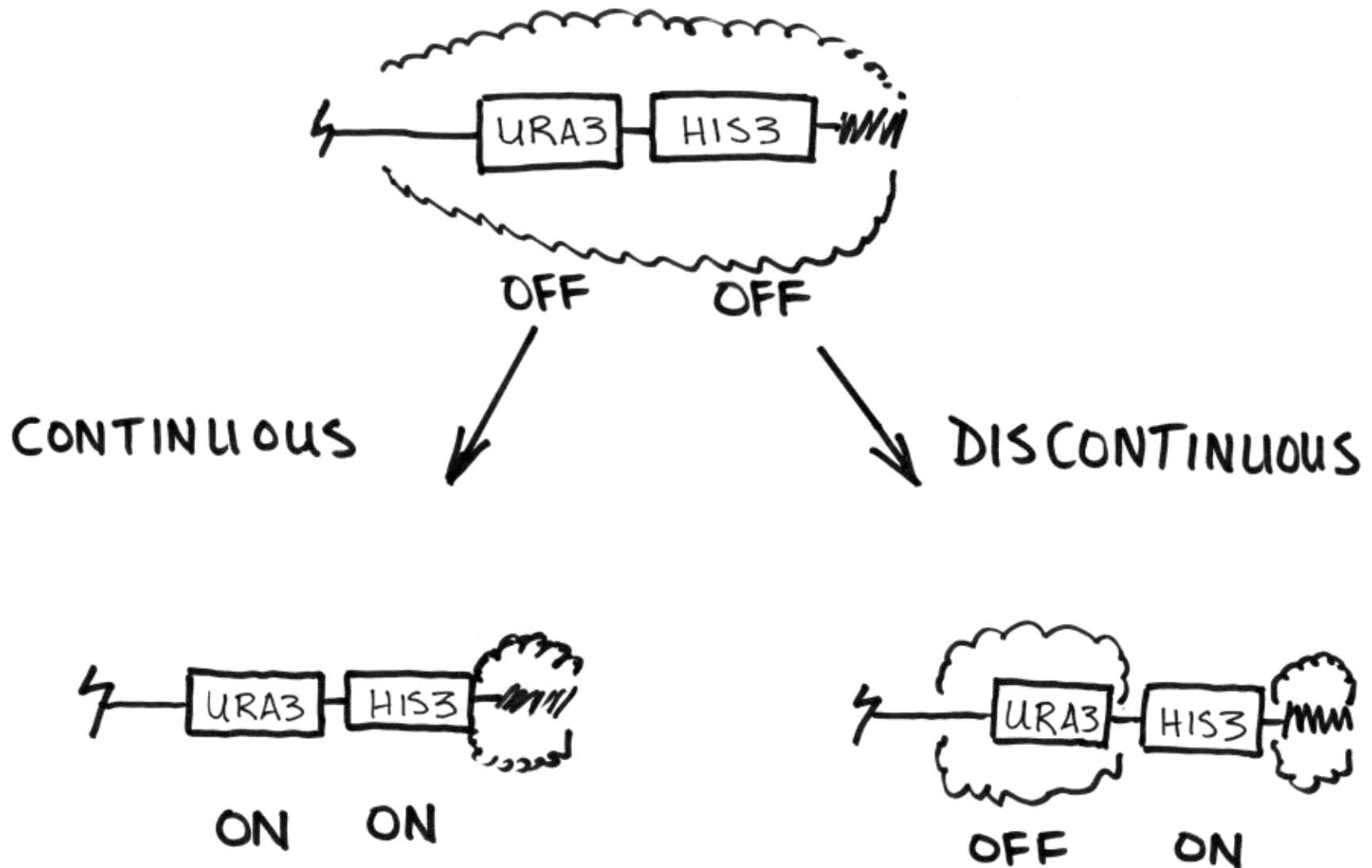


(~10% of the yeast genome is silenced)

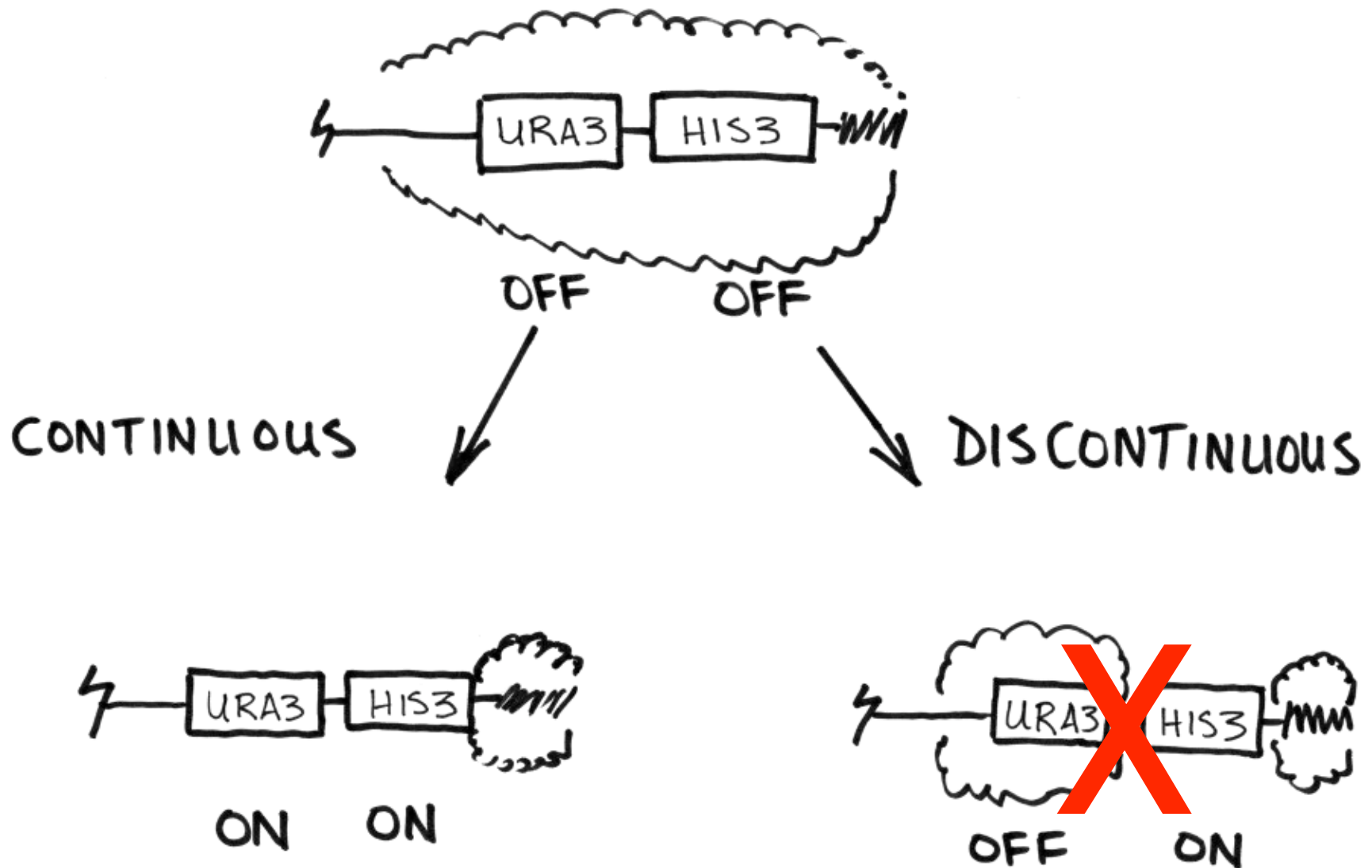
Sir3 is limiting for the spread of telomeric silencing



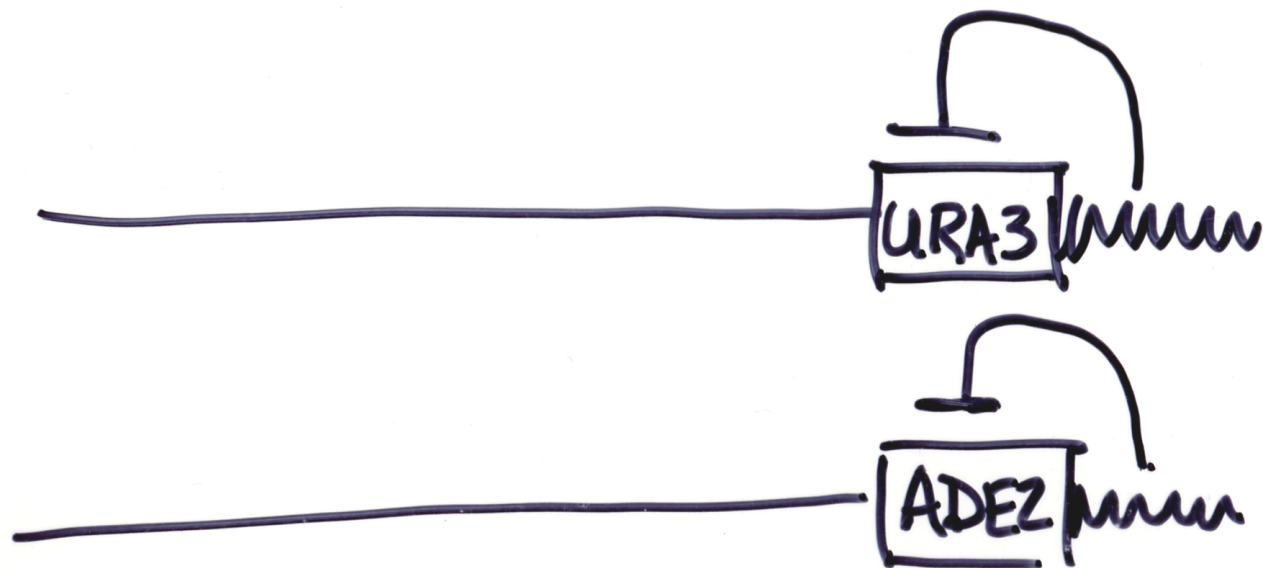
Does telomeric silencing spread continuously?



Does telomeric silencing spread continuously?



Telomeric Silencing



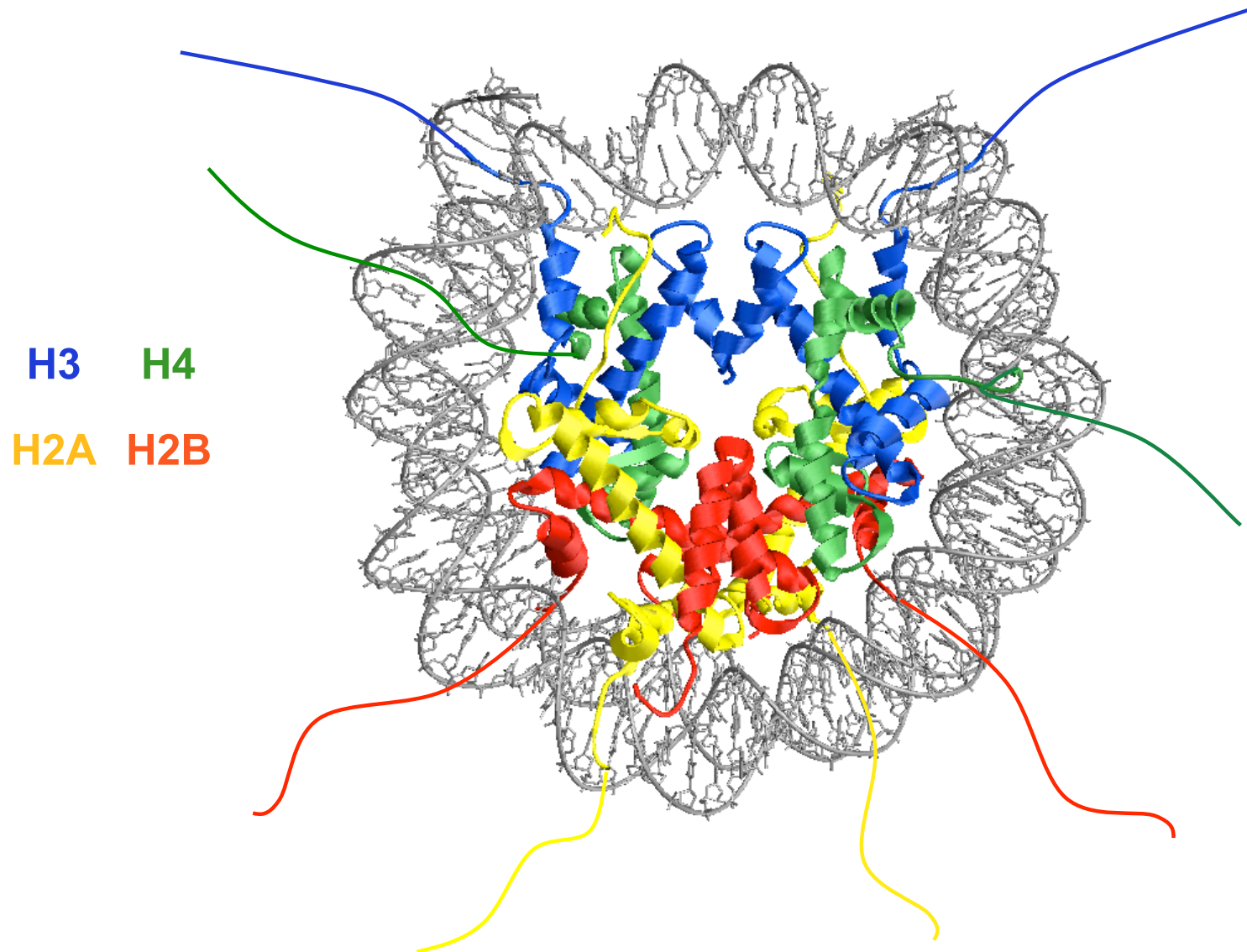
Ura⁻

Red/white
sectorized
colonies

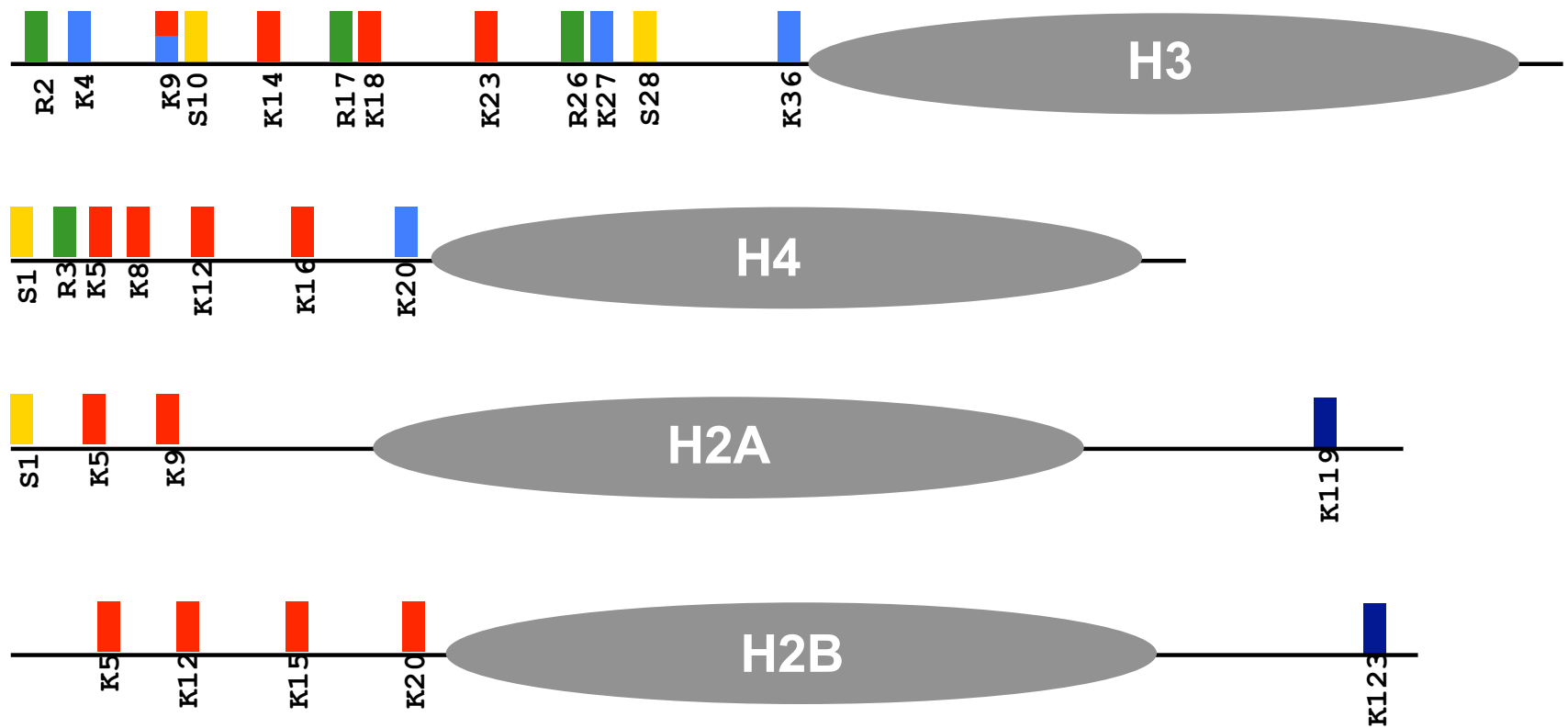
The multi-valent nature of telomeric silencing

- **Rap1** -> telomeric DNA repeats
- **Yku70 & Yku80** -> DNA ends
- **Sir2p** - histone deacetylase
- **Sir3p** -> histones (unmodified)
- **Sir4p** -> Rap1, Ku & histones(?)
- **Nucleosomes - H3 & H4** - via NH₂-tails & core - **H2A & H2B**-?

The Nucleosome: The Building Block of Chromatin

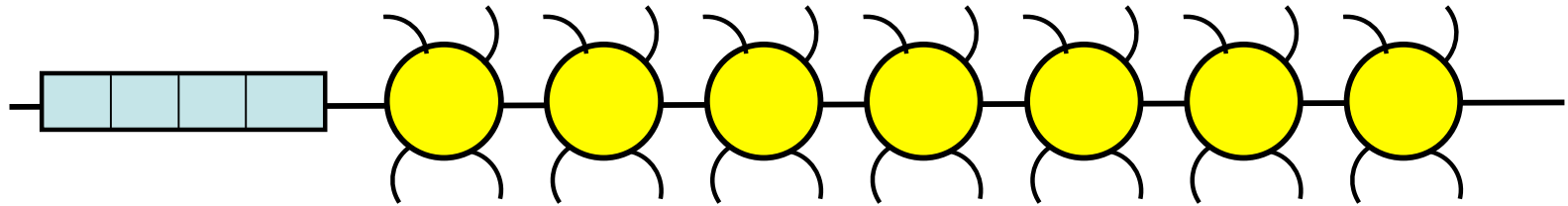


Histone tail modifications



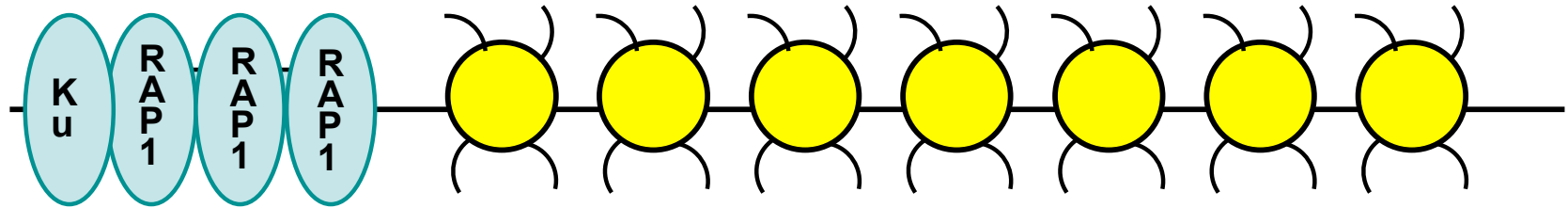
■ R methylation ■ K methylation ■ acetylation ■ phosphorylation ■ ubiquitination

Building Silent Chromatin

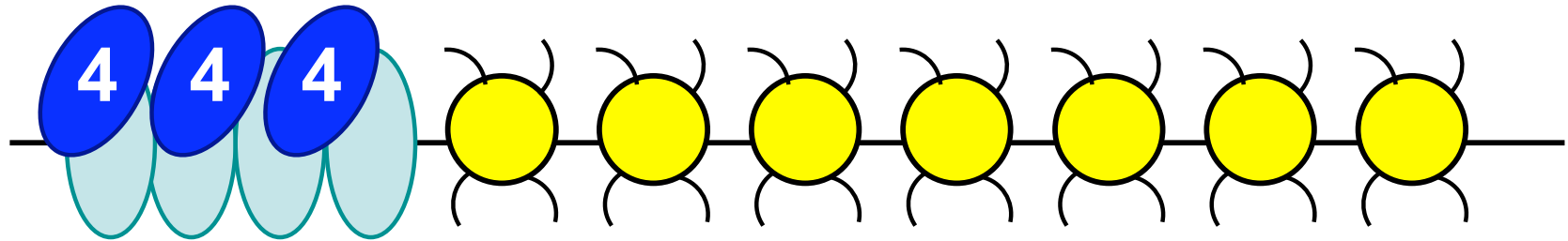


Silencer
(telomeric DNA)

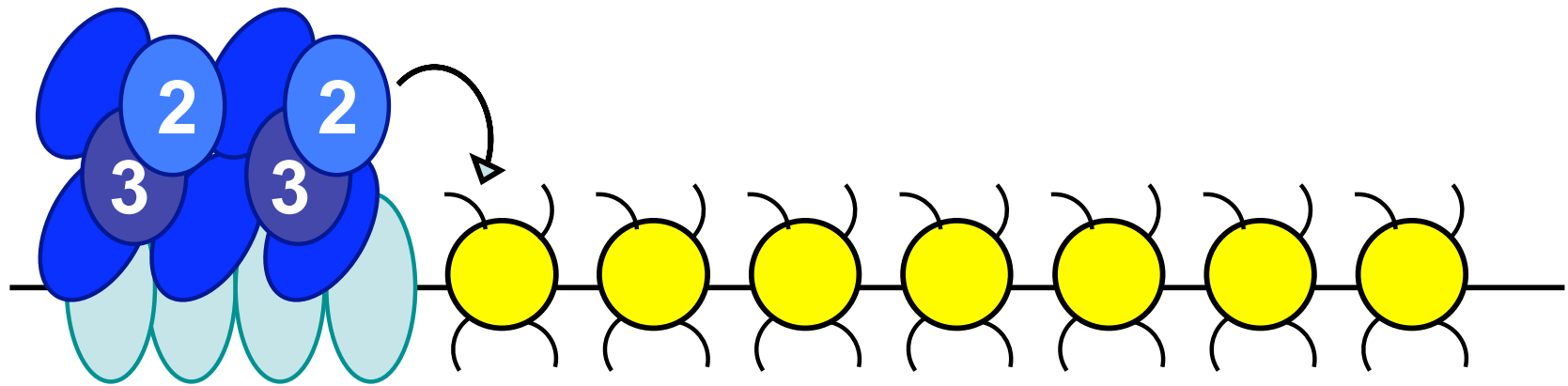
Building Silent Chromatin



Building Silent Chromatin



Building Silent Chromatin

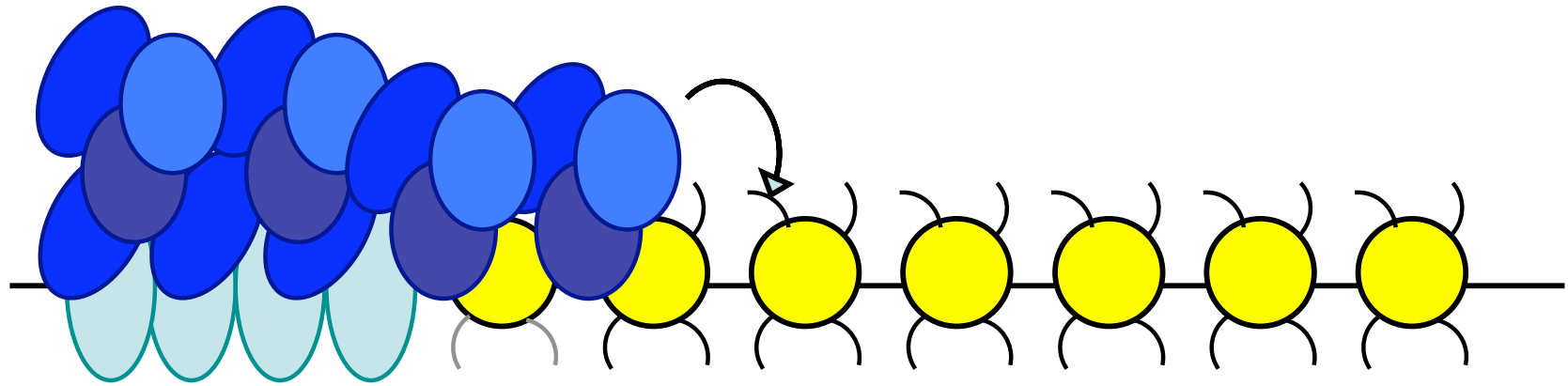


 **SIR complex**

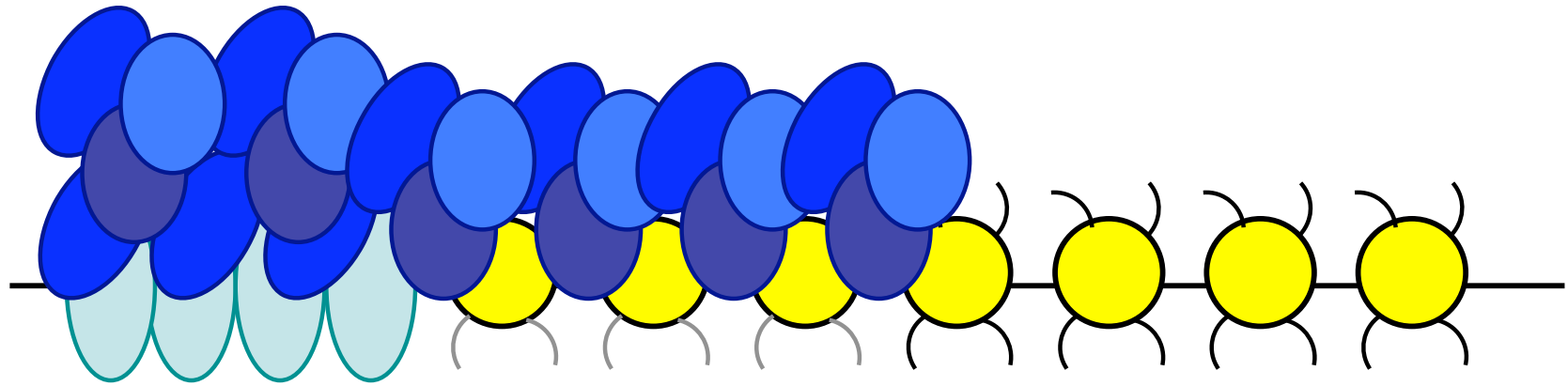
 **NAD⁺-dependent histone deacetylase**

 **bind to nucleosome (unacetylated histone tails)**

Building Silent Chromatin

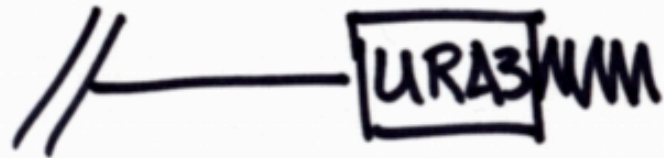


Building Silent Chromatin



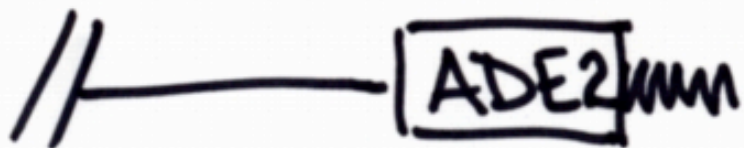


Screen for Disruptors of Telomeric Silencing



WT
ura⁻

DOT (OE)
Ura⁺



red/white
sectorized
colonies

White

The DOT genes

- *SIR4* Silencing protein
- *DOT1* Histone H3 methylase
- *TLC1* Telomerase RNA
- *ASF1* Chromatin assembly protein
- *DNA2* DNA replication protein
- *DOT4* Ubiquitin Hydrolase
- *DOT5* Nuclear thiol peroxidase(?)
- *DOT6* putative Myb-DNA binding domain
- *IFH1* ribosomal RNA expression(?)
- *RPL32* ribosomal protein

Fred

van Leeuwen

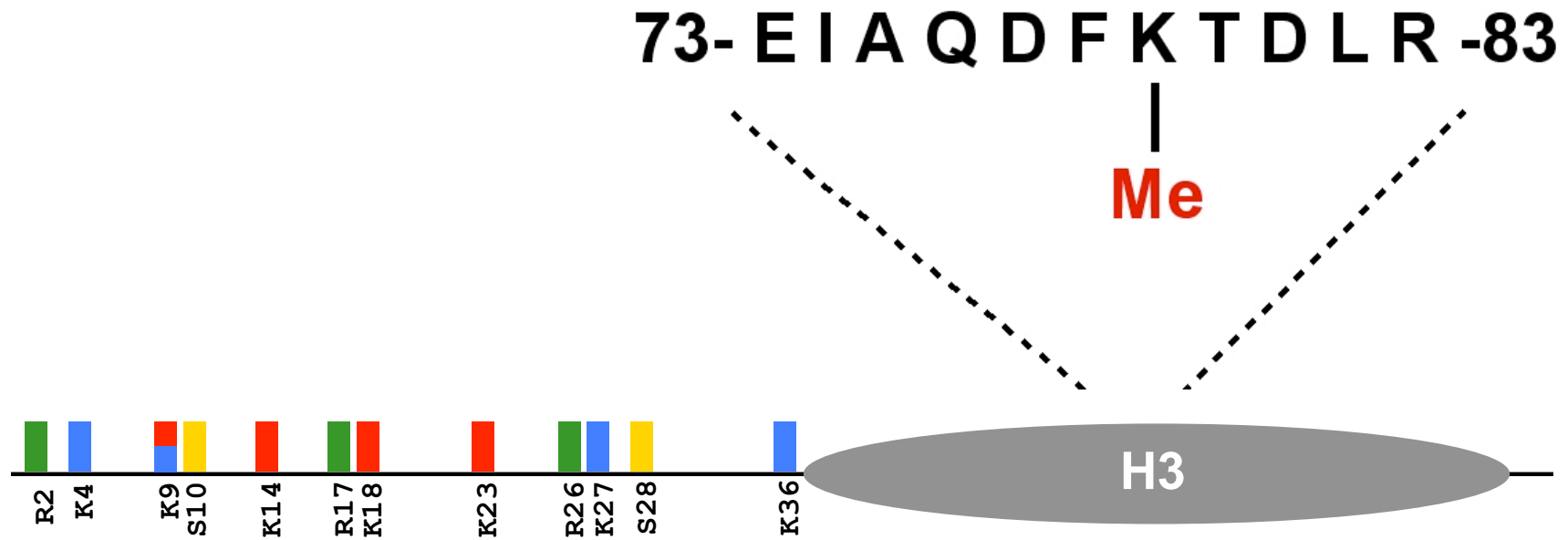
The DOT genes

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DOT1 phenotypes

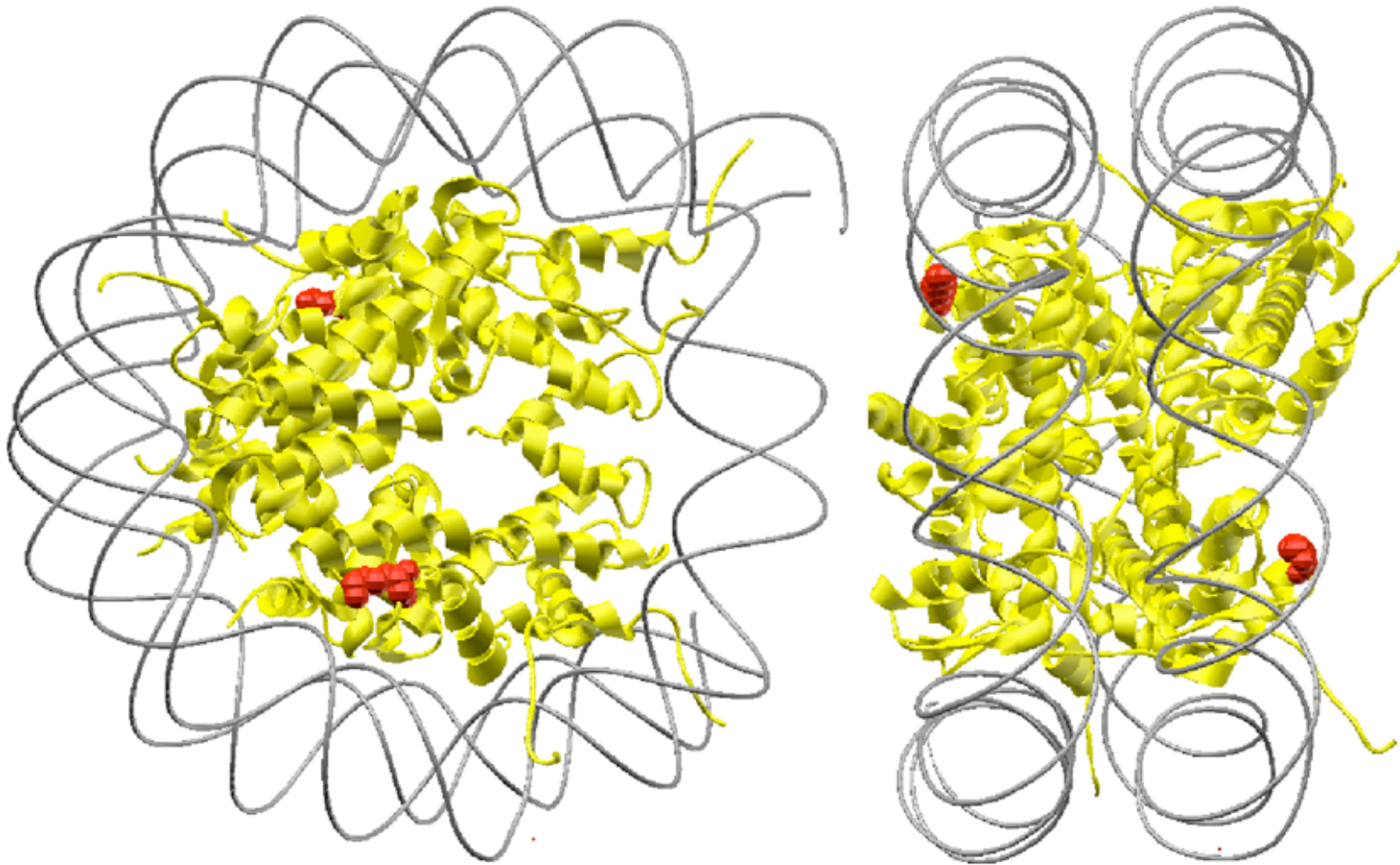
- **Overexpression**
 - Loss of silencing at telomeres & *HM*
 - Modest decrease of silencing at rDNA
- *dot1* Δ
 - Decreased silencing at telomeres & *HM* loci
 - Little or no effect at rDNA
 - Reduced levels of Y' RNA [Hughes et al. (2000)]
 - Diffuse staining of Sir3 along mitotic chromosomes [San-Segundo & Roeder (2000)]

Dot1 methylates histone H3 on Lys79



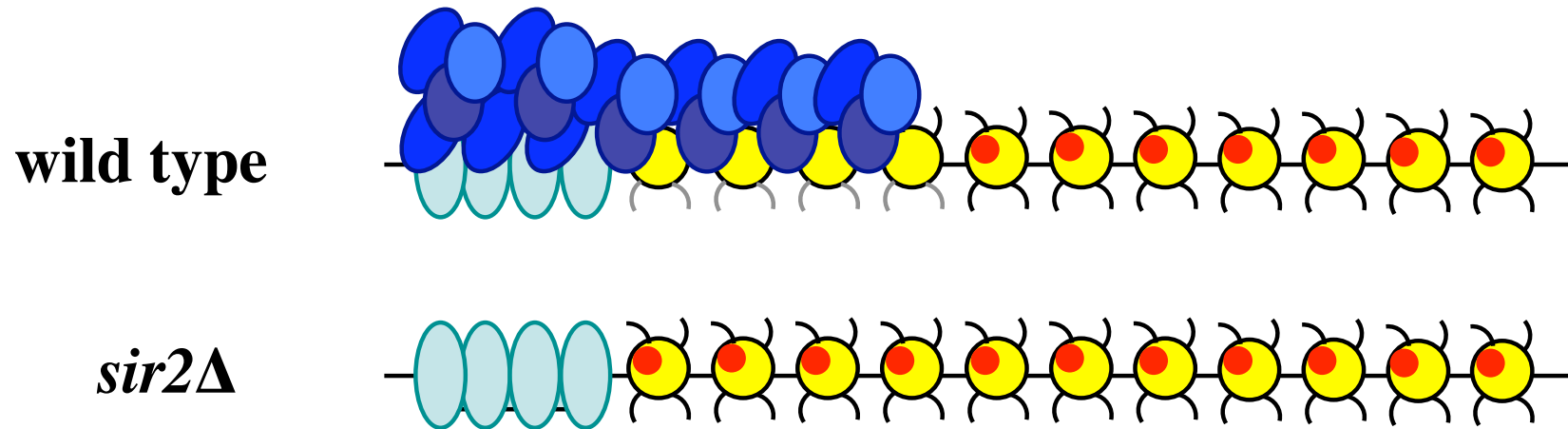
Dot1 methylates histone H3 only in chromatin

Histone H3-Lys79 is located on the top and bottom of the nucleosome core



K. Luger EMBO 20:5207 (2001)

Methylated histone H3-K79 is a mark of euchromatin



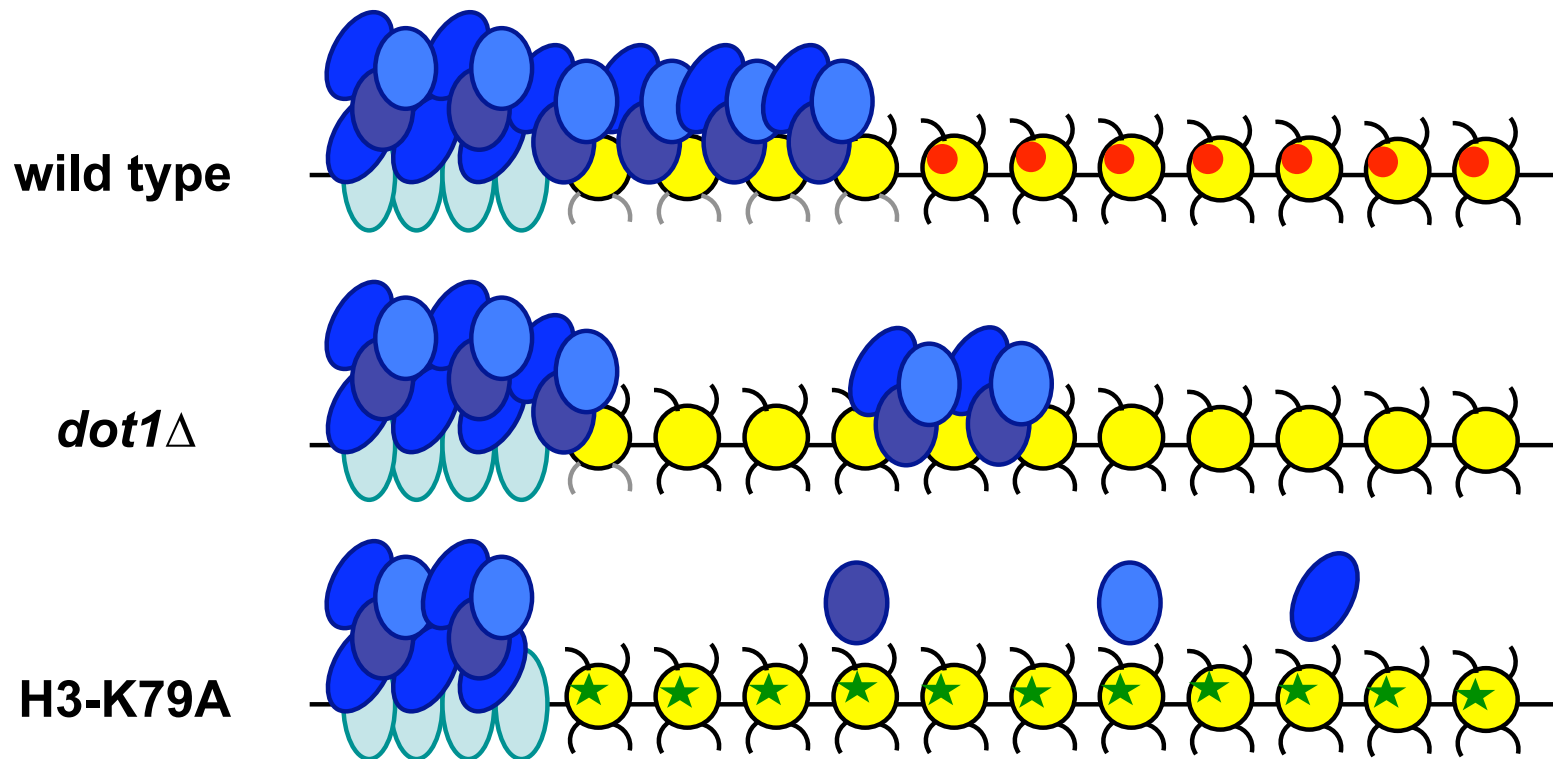
♣ 90% of total chromatin is methylated

♣ Silent loci are hypomethylated at histone H3-K79

♣ Silent chromatin prevents methylation of H3-K79 by

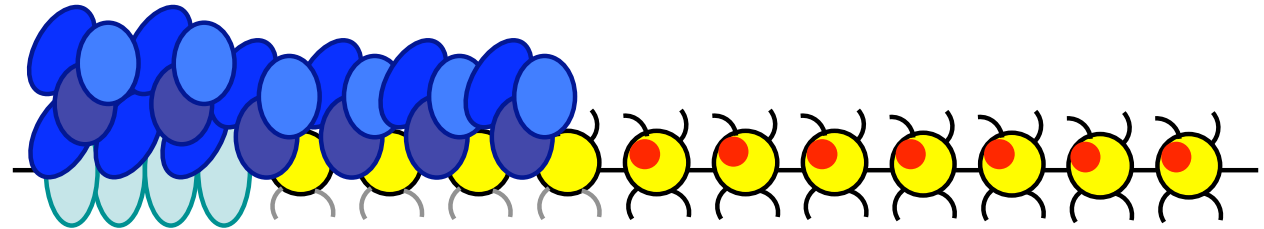
Dot1

Loss of H3-K79 methylation results in redistribution of Sir proteins

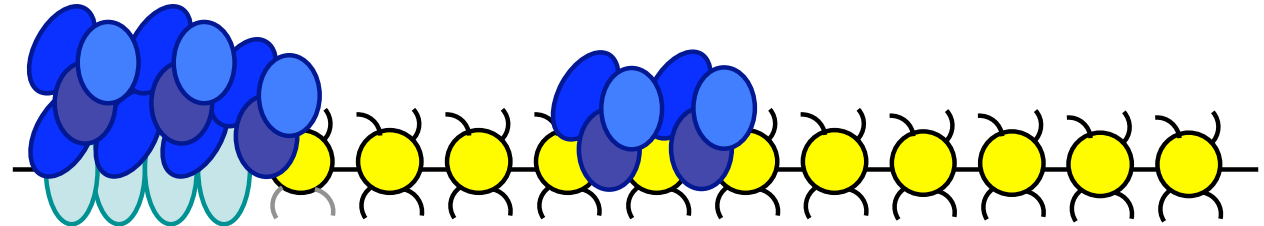


Dot1 reduces promiscuous binding of silencing proteins in euchromatin

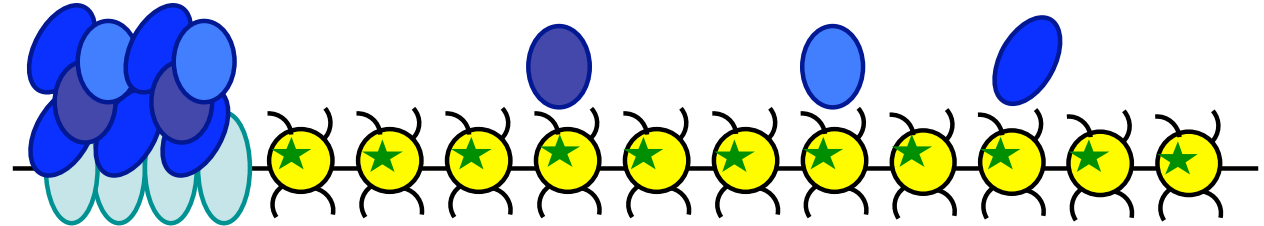
wild type



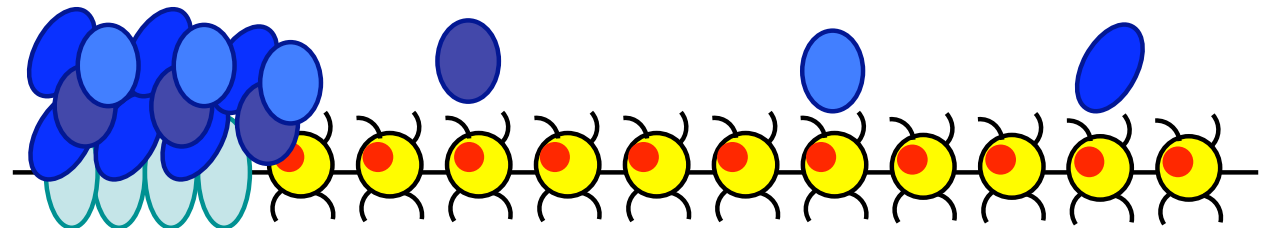
dot1 Δ



H3-K79A

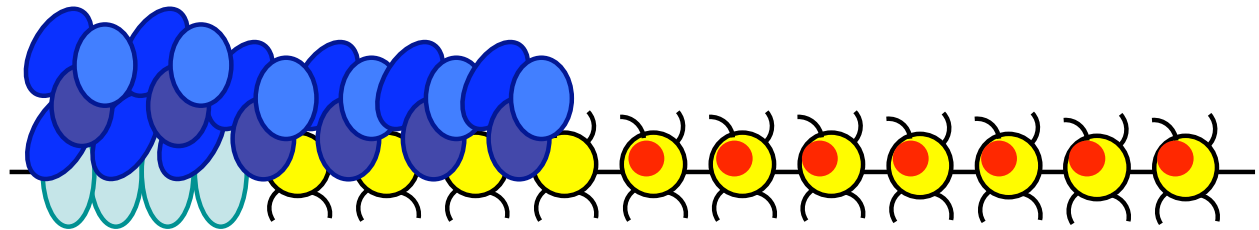


high-copy
DOT1

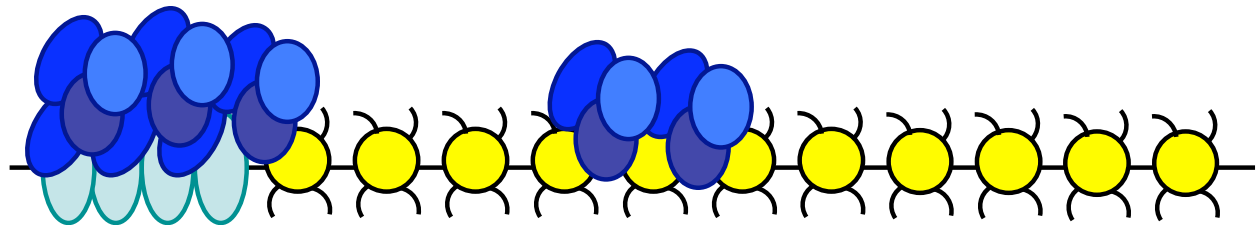


Gaining specificity by preventing promiscuity: A common theme?

wild-type

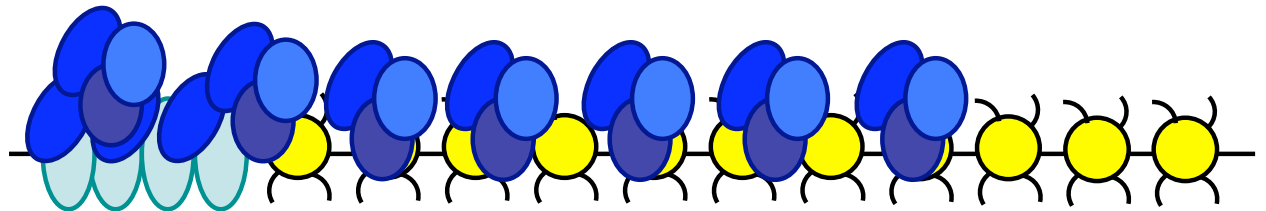


dot1 Δ
(H3-K79 Me)



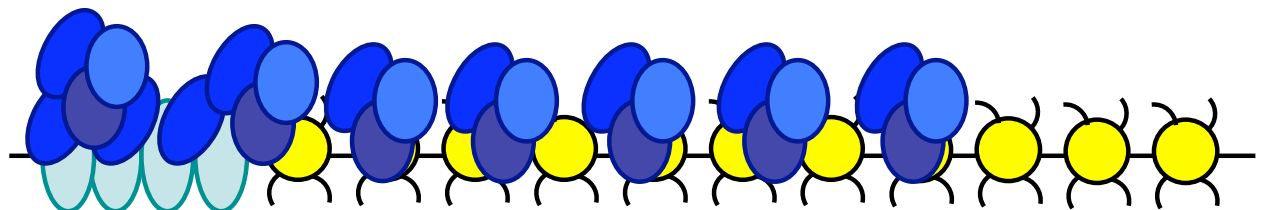
Kimura et al.
&
Suka et al.
(2002)

sas2 Δ
(H4-K16 Ac)



Meneghini et al.
(2003)

htz1 Δ
(H2A.Z)



DOT1 requires RAD6 activity *in vivo*

- **RAD6 mono-ubiquitinates K123 of histone H2B**

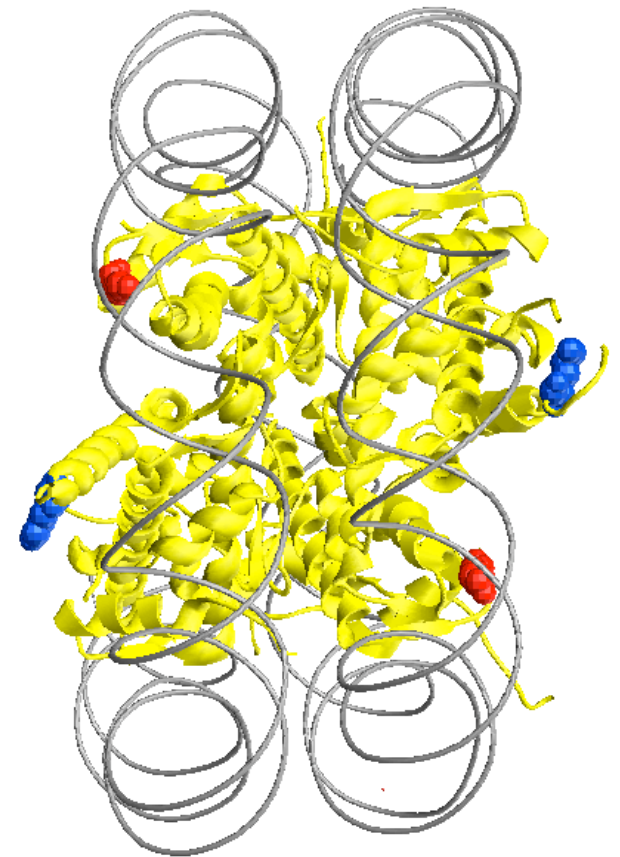
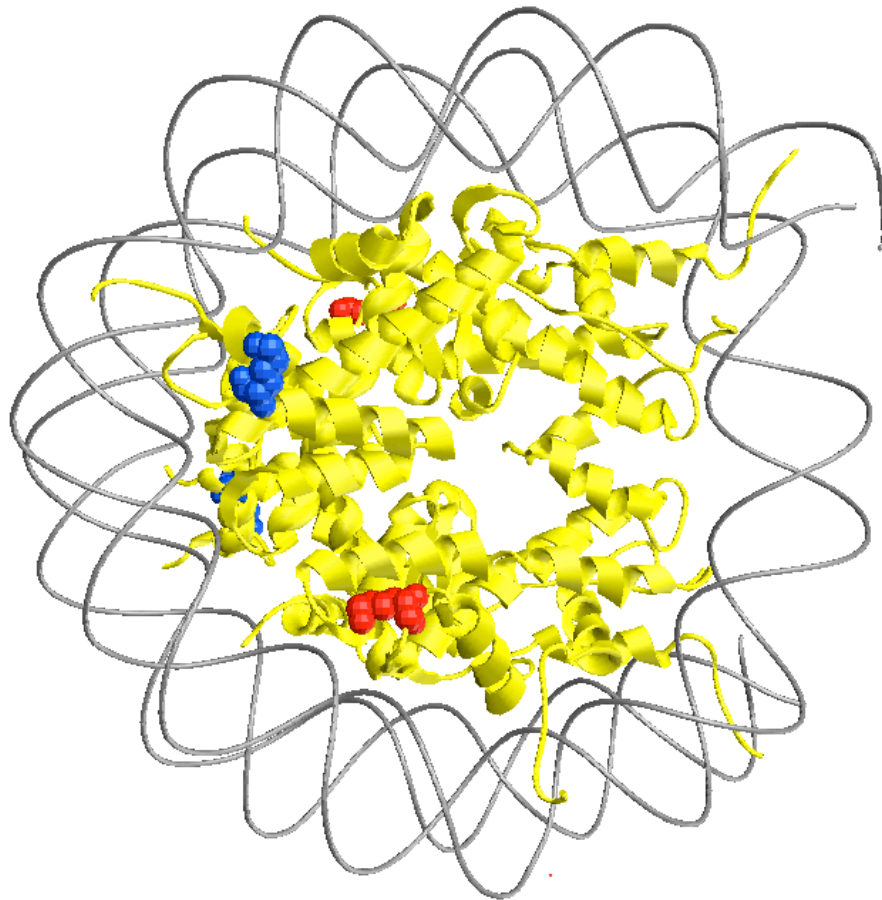
[Robzyk et al. (2000)]

♣ **Required for silencing** [Huang et al. (1997)]

♣ **Required for histone H3 methylation of K79**

[Sun & Allis, Ng et al. & Dover et al. (2002)]

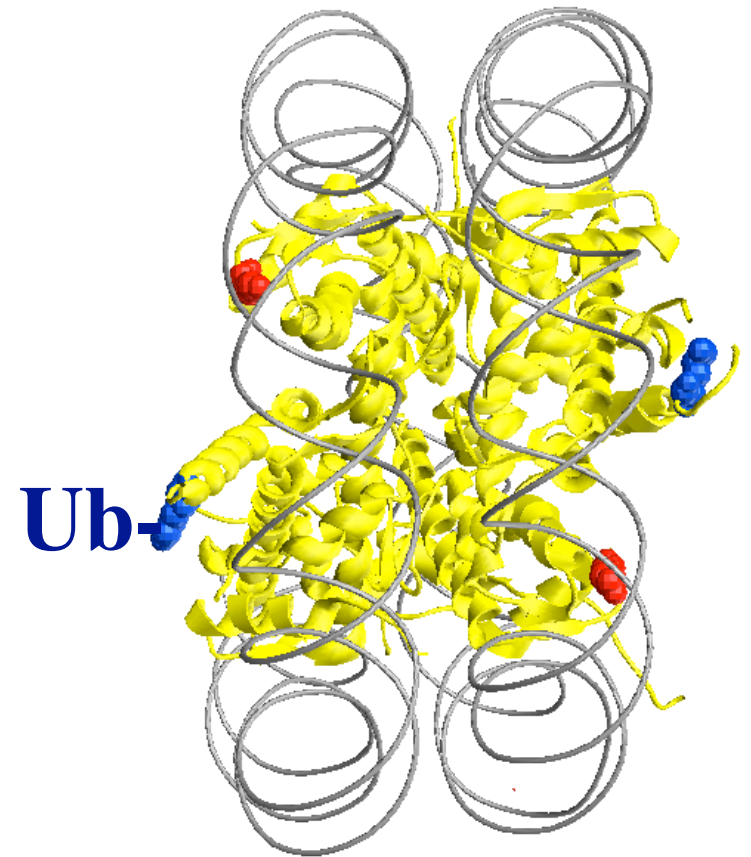
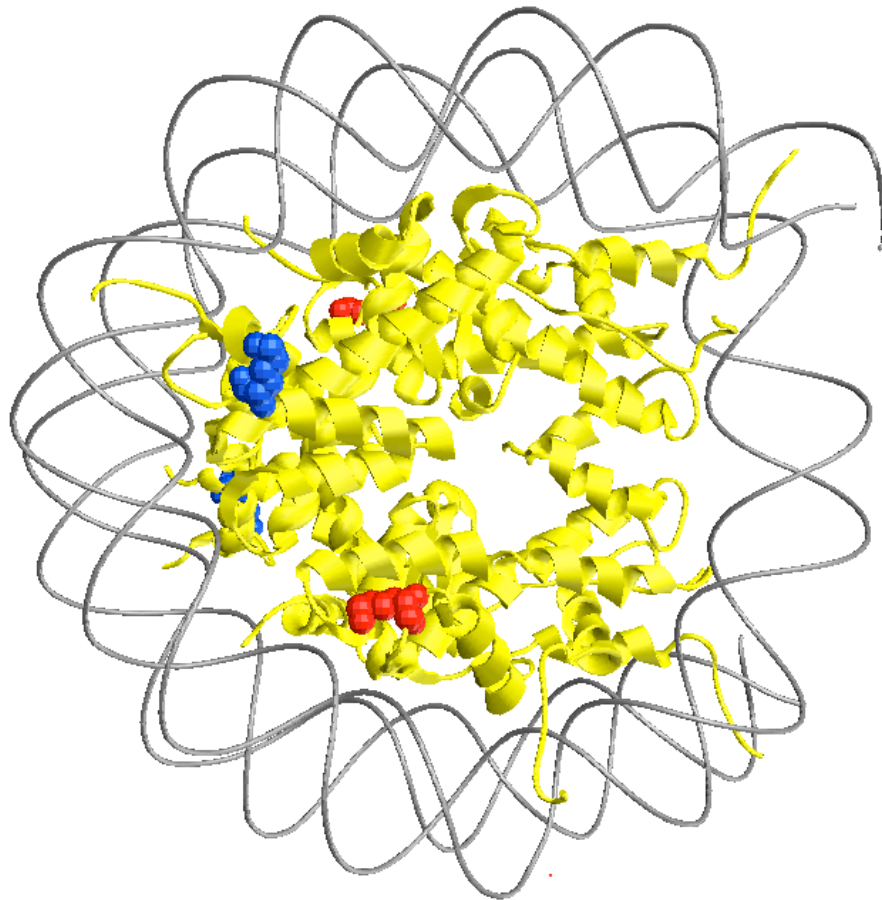
DOT1 needs RAD6 to prevent promiscuous Sir binding



● H3-K79

● H2B-K123

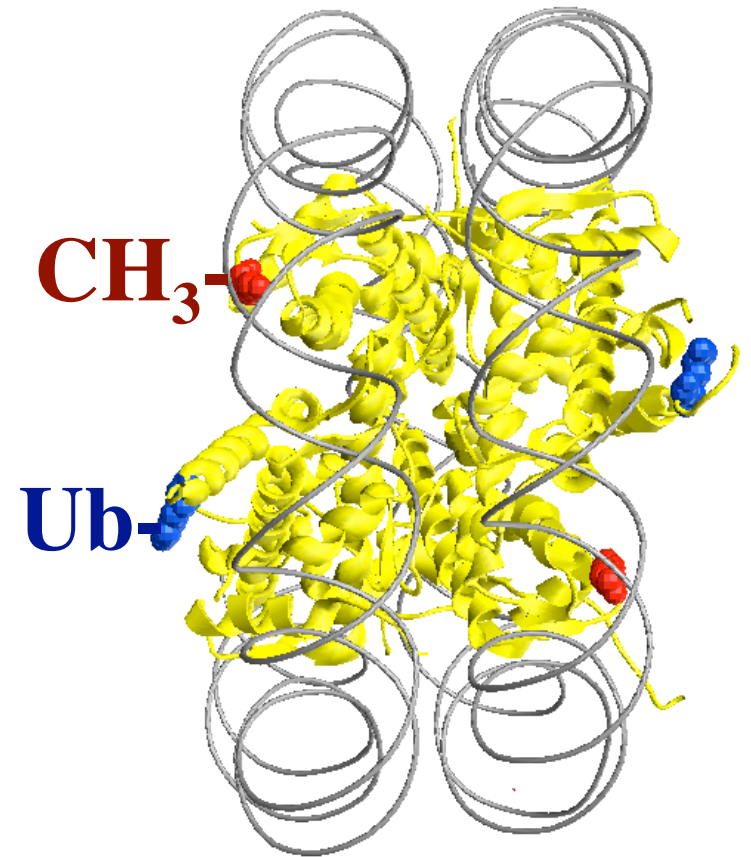
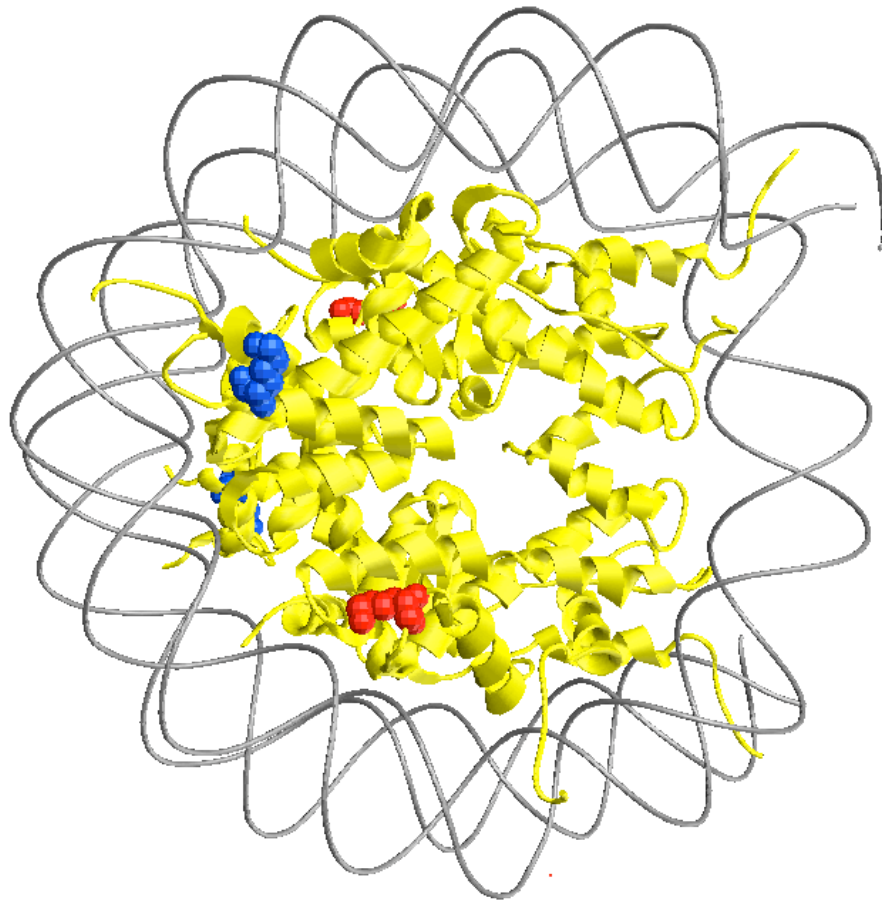
DOT1 needs RAD6 to prevent promiscuous Sir binding



● H3-K79

● H2B-K123

DOT1 needs RAD6 to prevent promiscuous Sir binding



● H3-K79 ● H2B-K123

**A reversible modification can
be converted into a permanent
“memory mark”**

The DOT genes

- *SIR4* Silencing protein
- *DOT1* Histone H3 methylase
- *TLC1* Telomerase RNA
- *ASF1* Chromatin assembly protein
- *DNA2* DNA replication protein
- ***DOT4* Ubiquitin Hydrolase**
- *DOT5* Nuclear thiol peroxidase(?)
- *DOT6* putative Myb-DNA binding domain
- *IFH1* ribosomal RNA expression(?)
- *RPL32* ribosomal protein

DOT4 (UBP10)

[MCB 19:6608 (1999)]

- **Ubiquitin Hydrolase**
- **Binds to Sir4p**

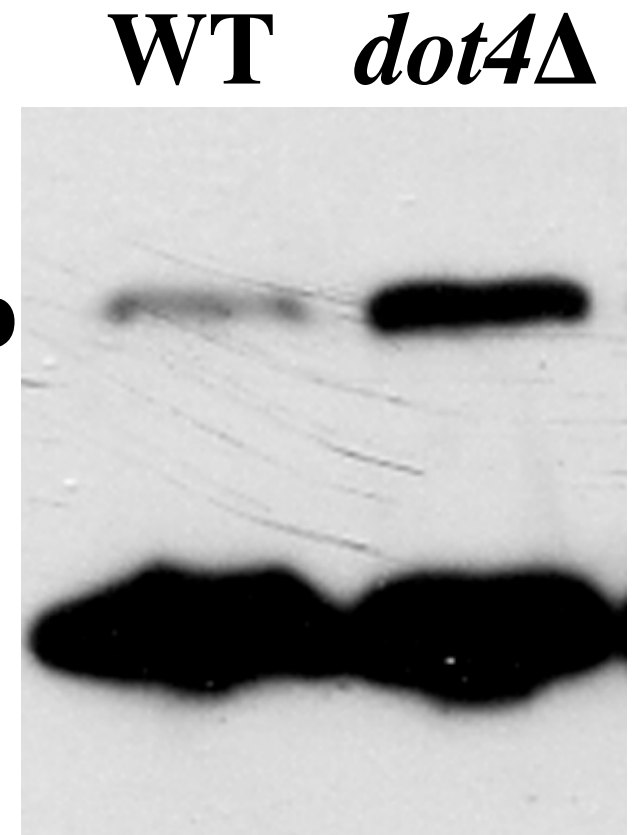
DOT4 keeps nucleosomes from receiving a permanent “active” mark

- Ubiquitin Hydrolase
- Binds to Sir4p
- Antagonizes Rad6p ubiquitination of histone H2B

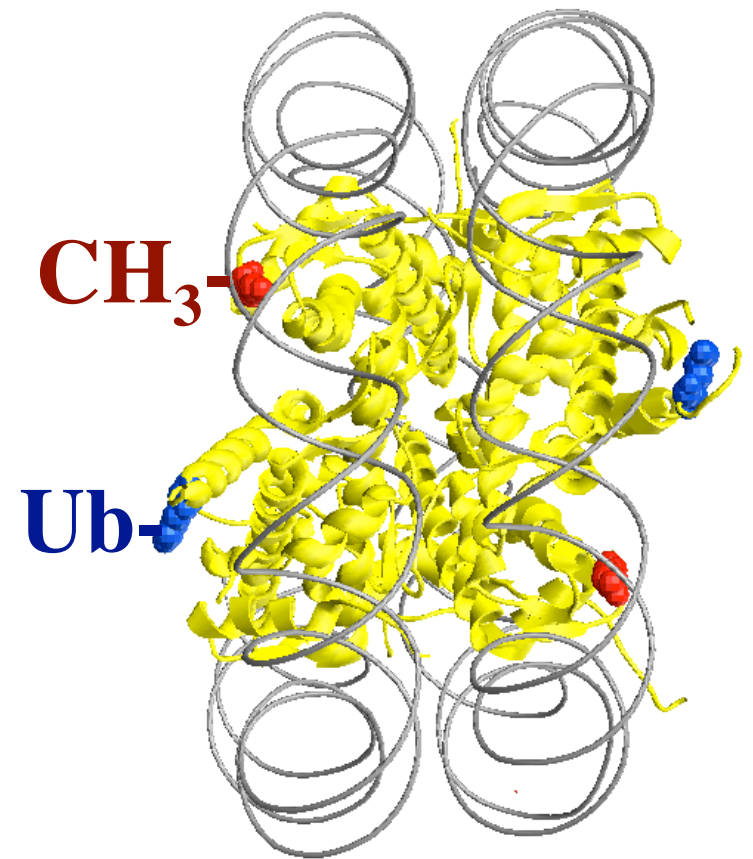
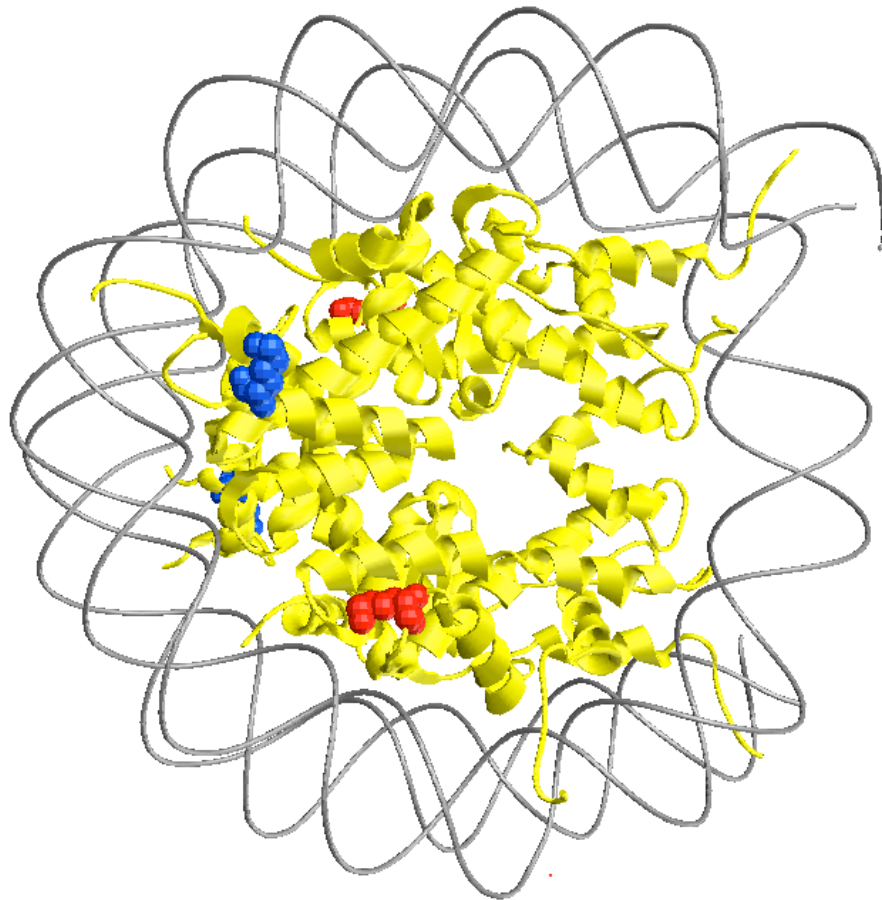
(Rich Gardner)

H2B-Ub

H2B



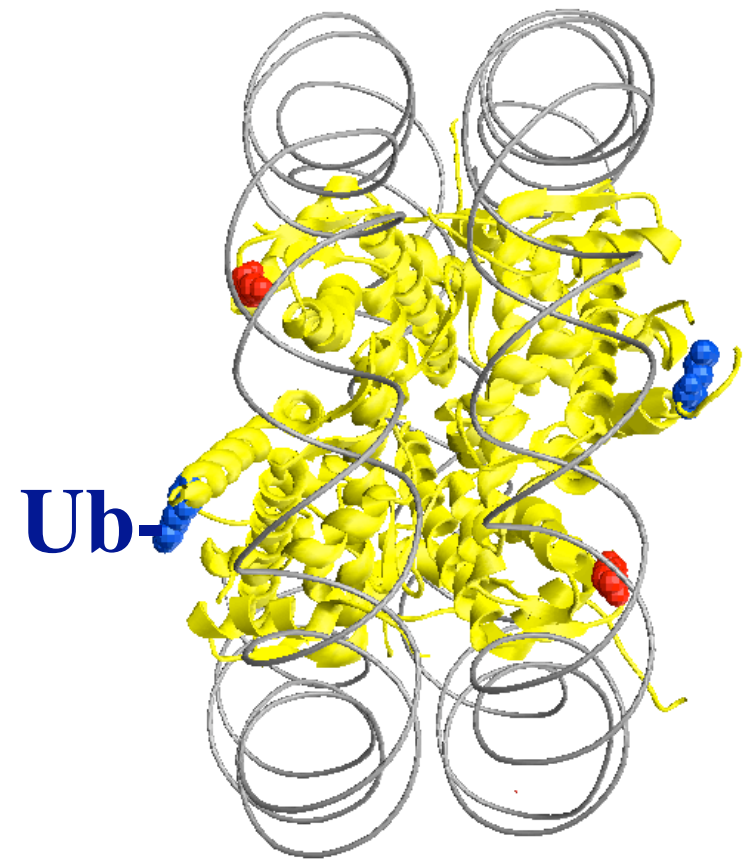
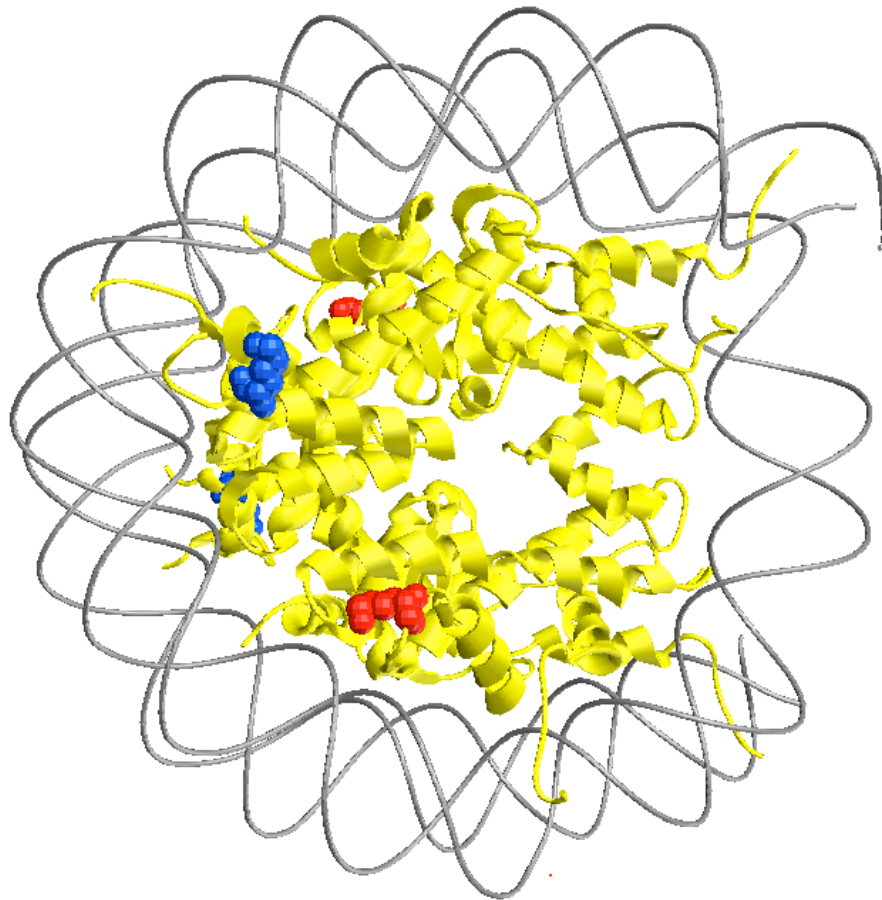
DOT4 keeps nucleosomes from receiving a permanent “active” mark



● H3-K79

● H2B-K123

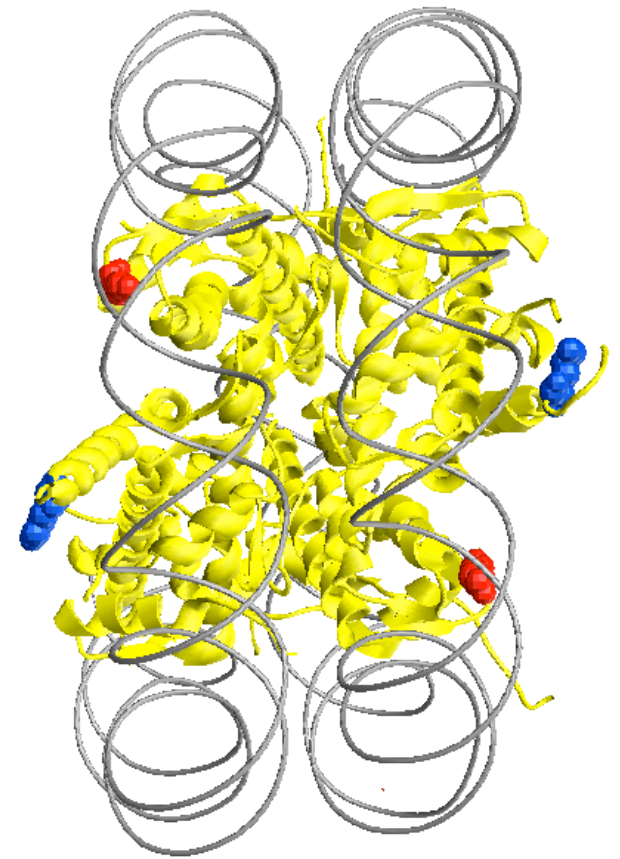
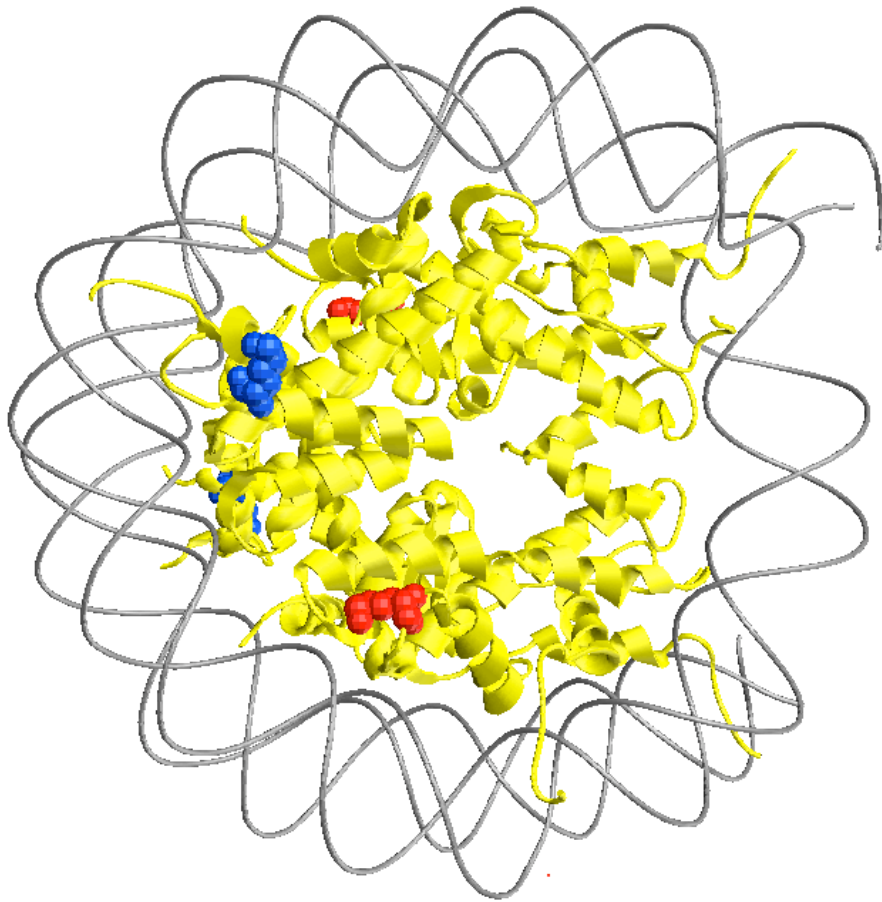
DOT4 keeps nucleosomes from receiving a permanent “active” mark



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DOT4 keeps nucleosomes from receiving a permanent “active” mark

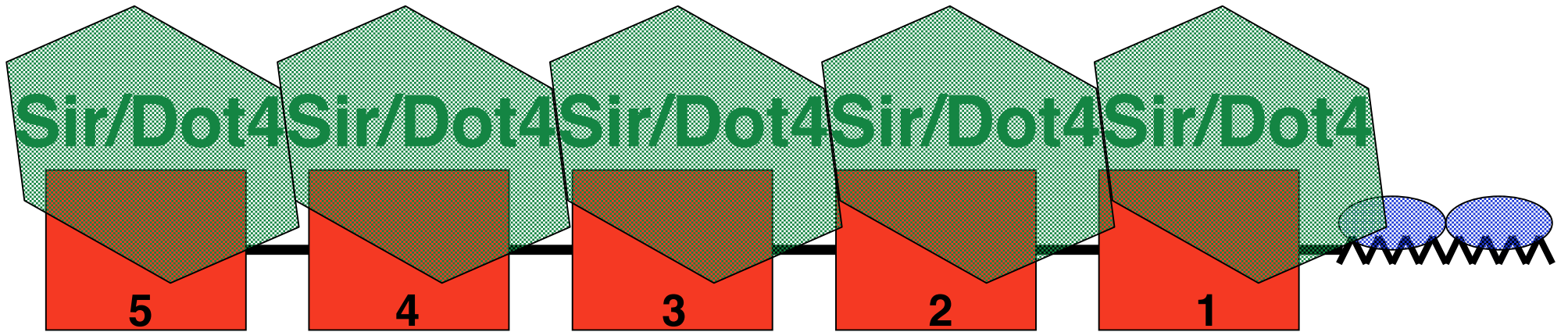


● H3-K79

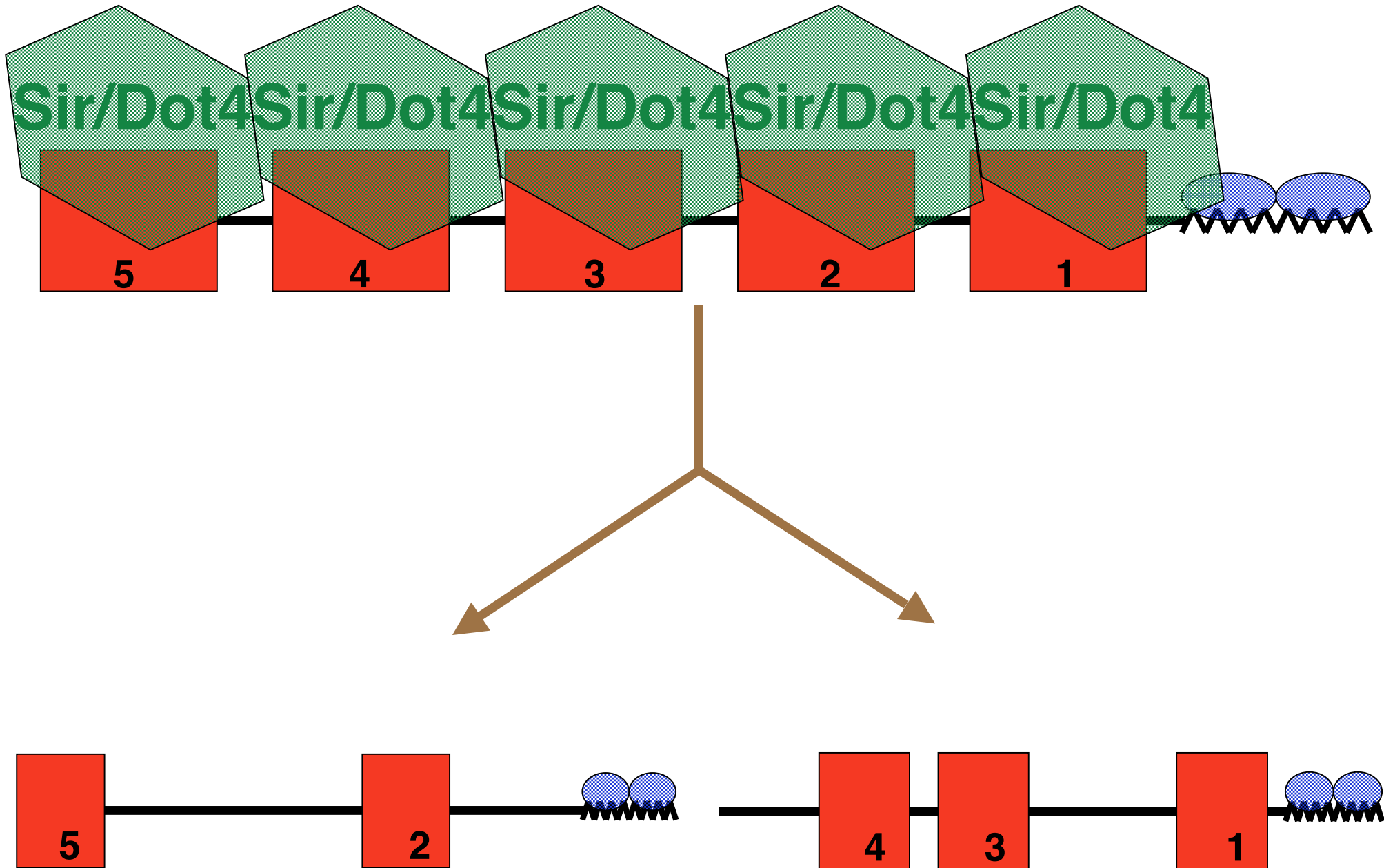
● H2B-K123



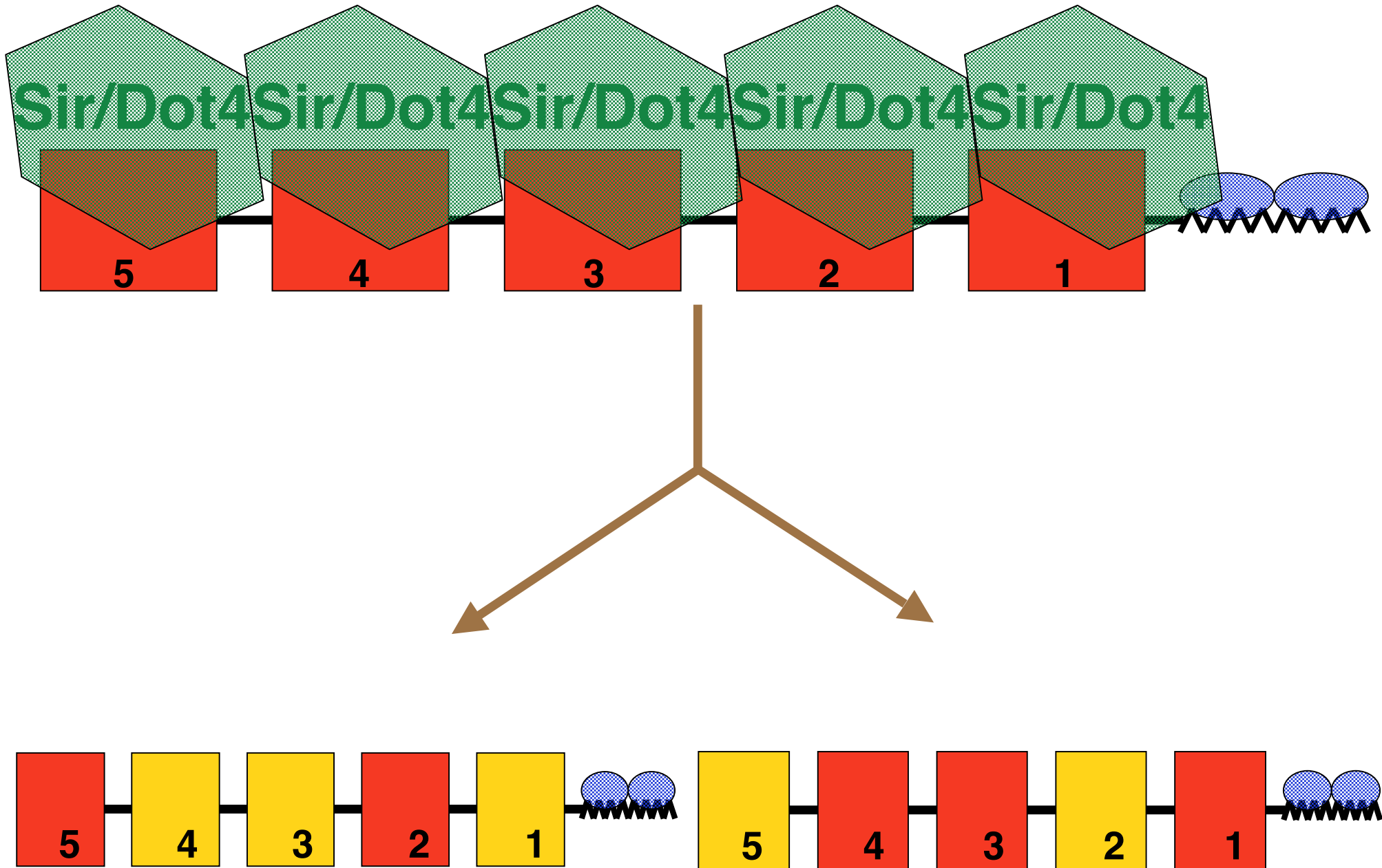
Propagating Silent Chromatin



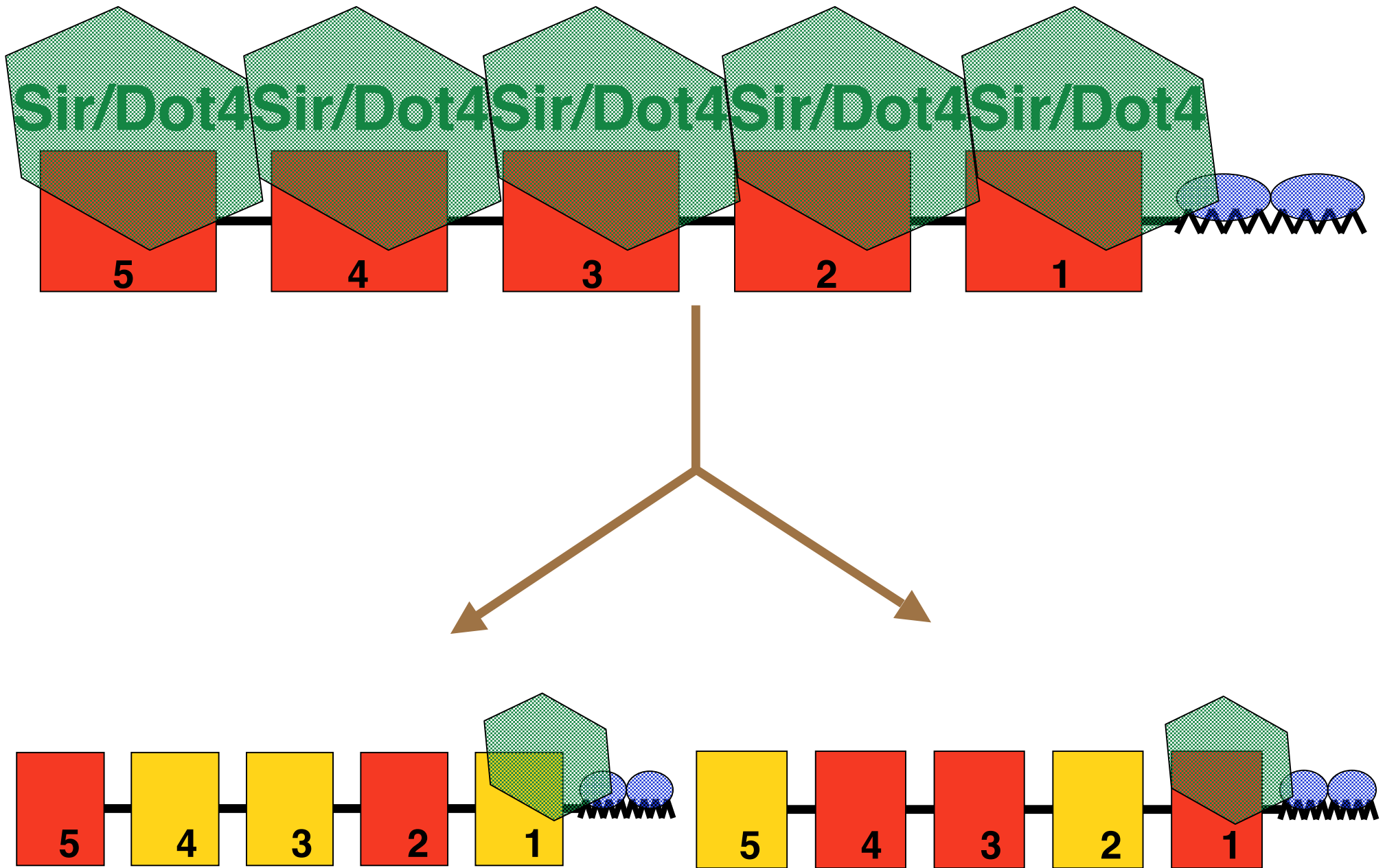
Propagating Silent Chromatin



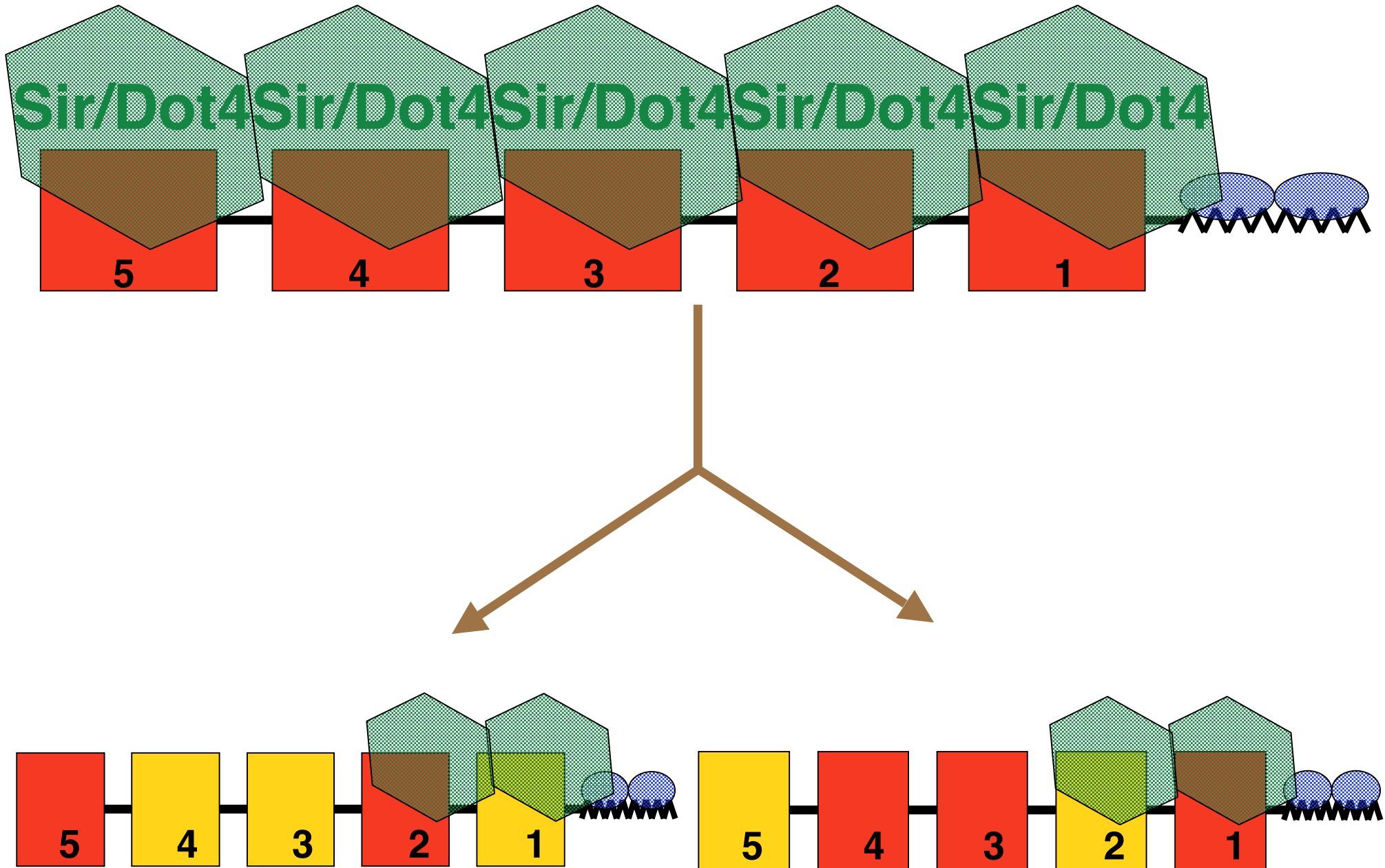
Propagating Silent Chromatin



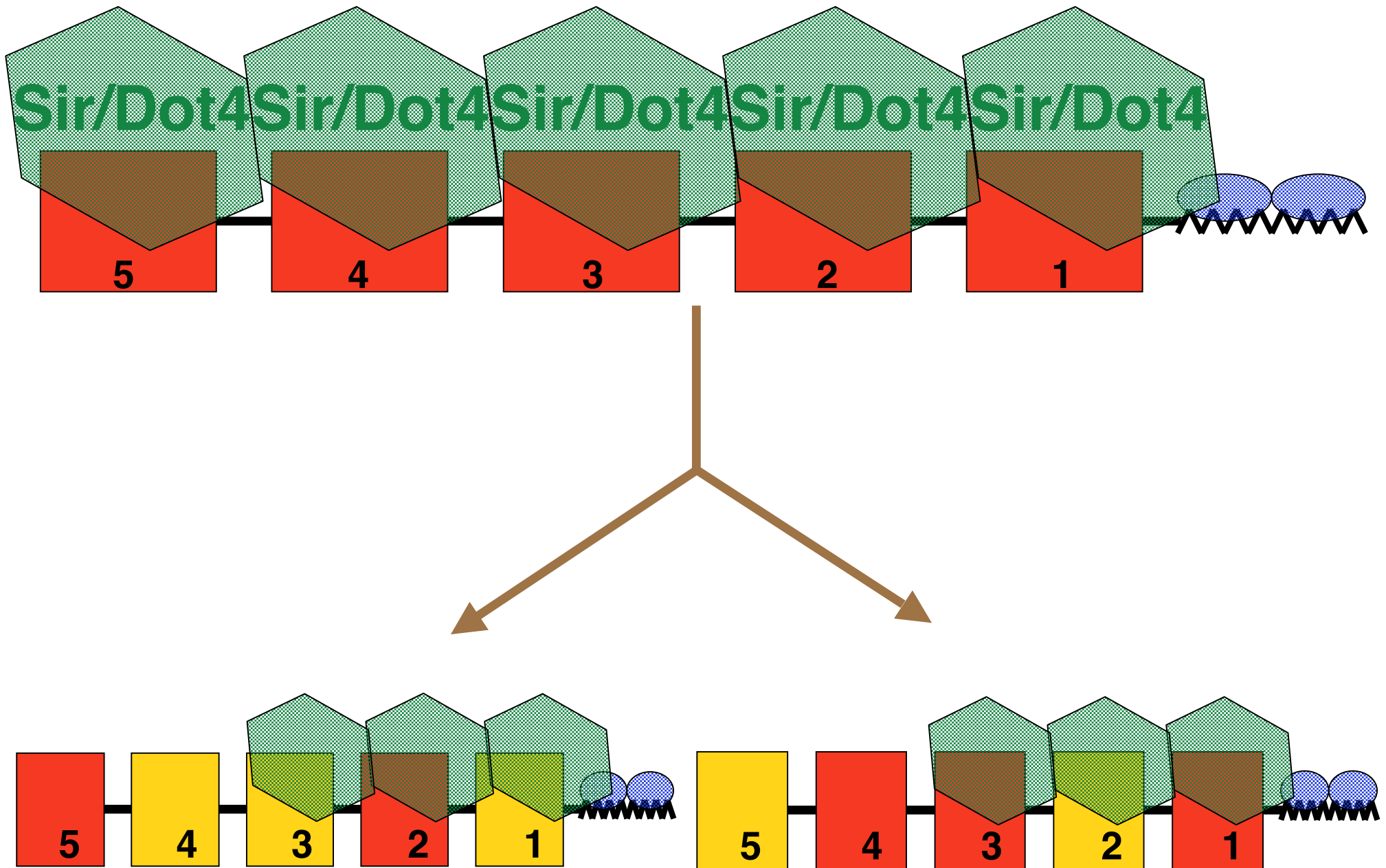
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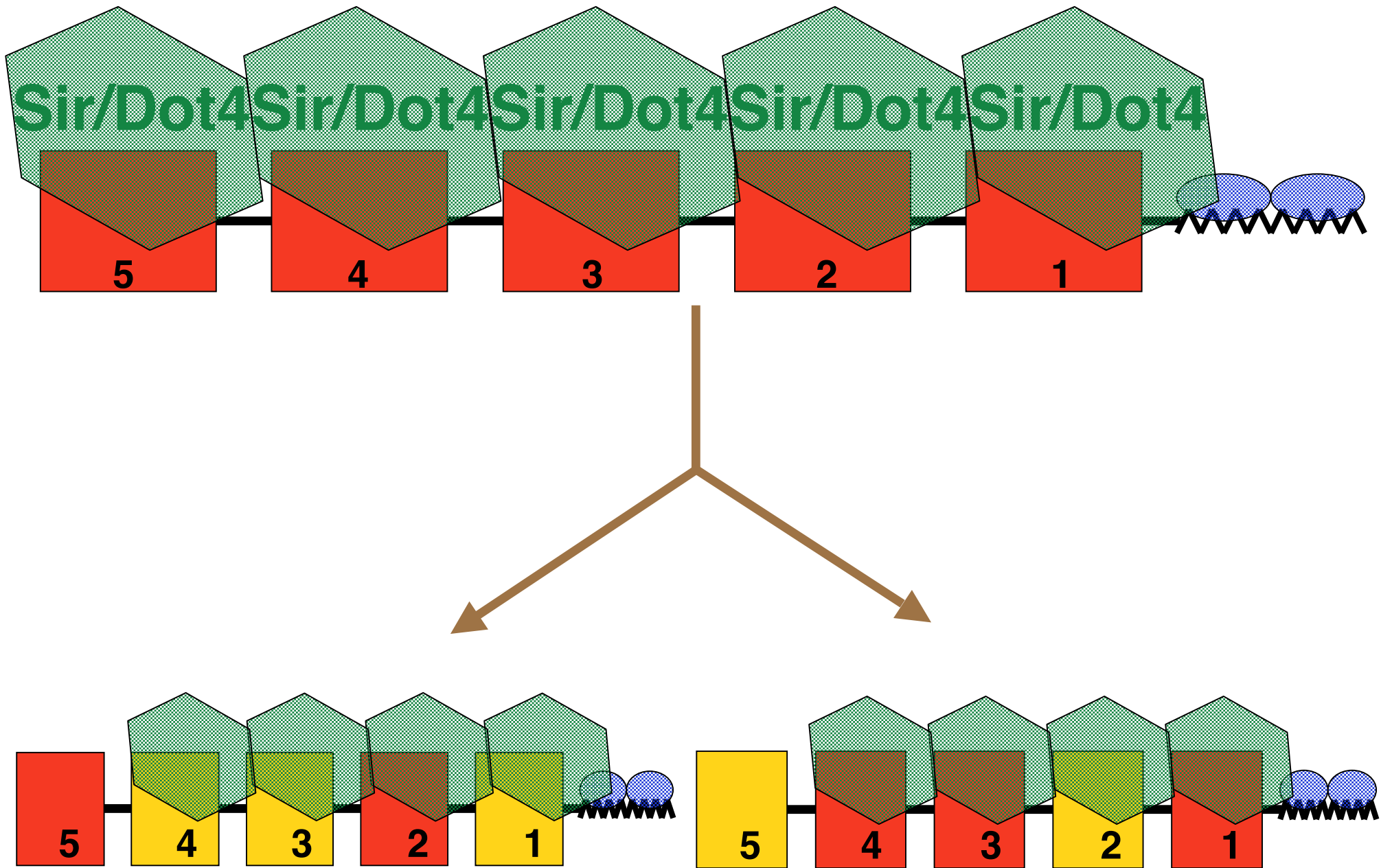
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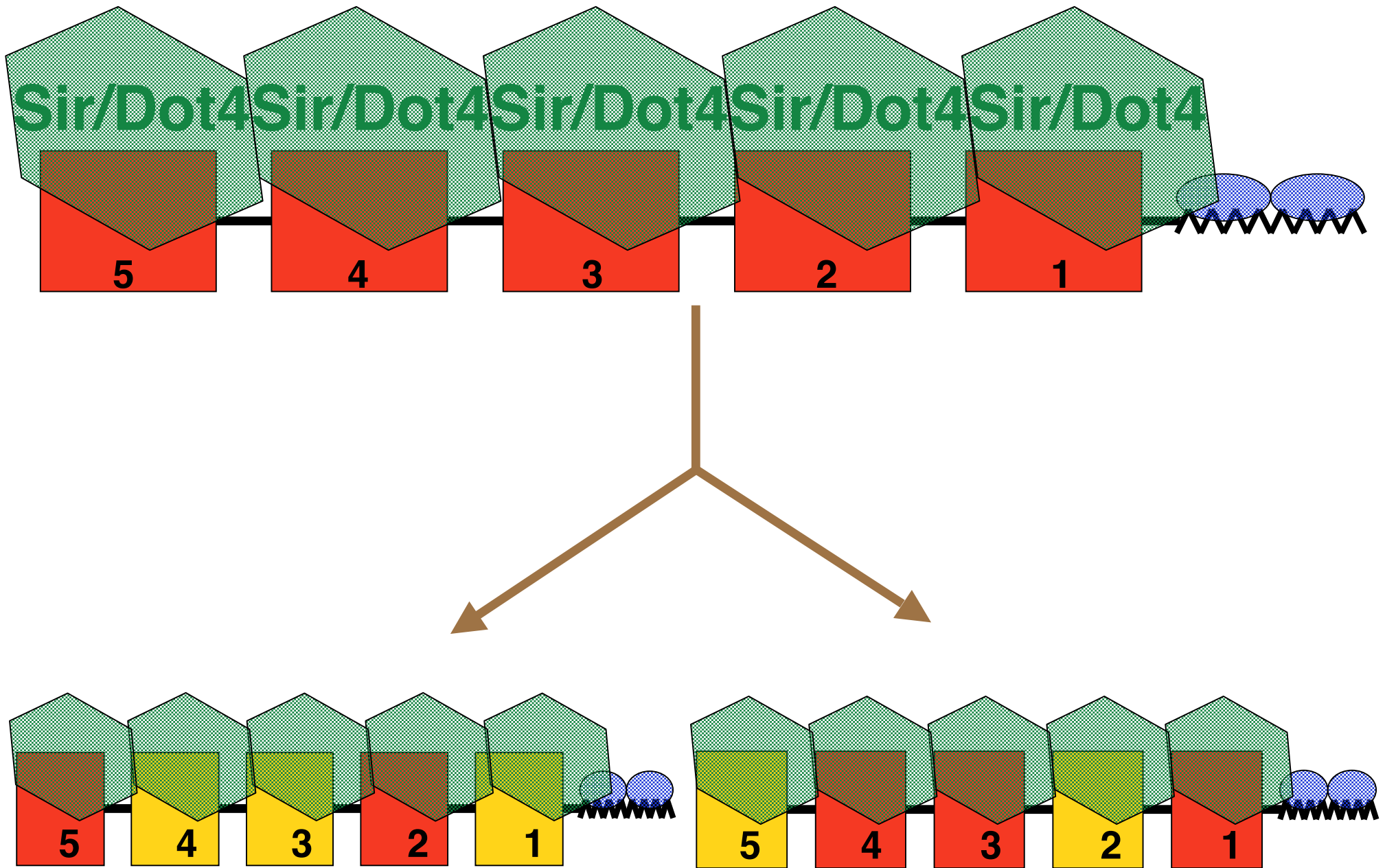
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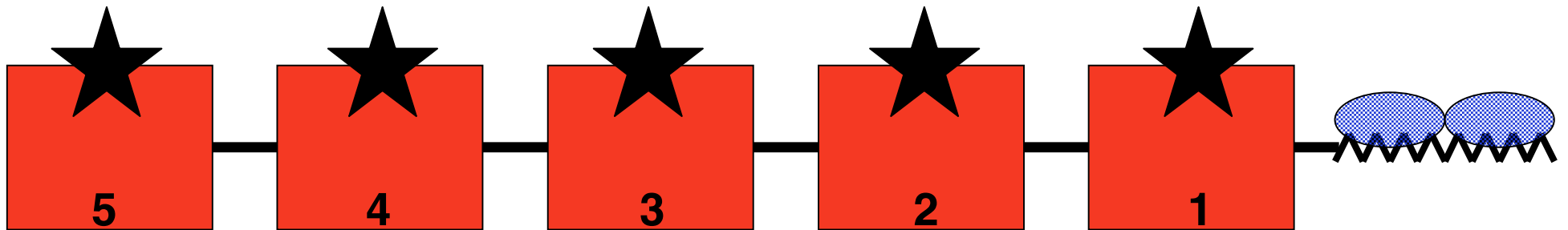
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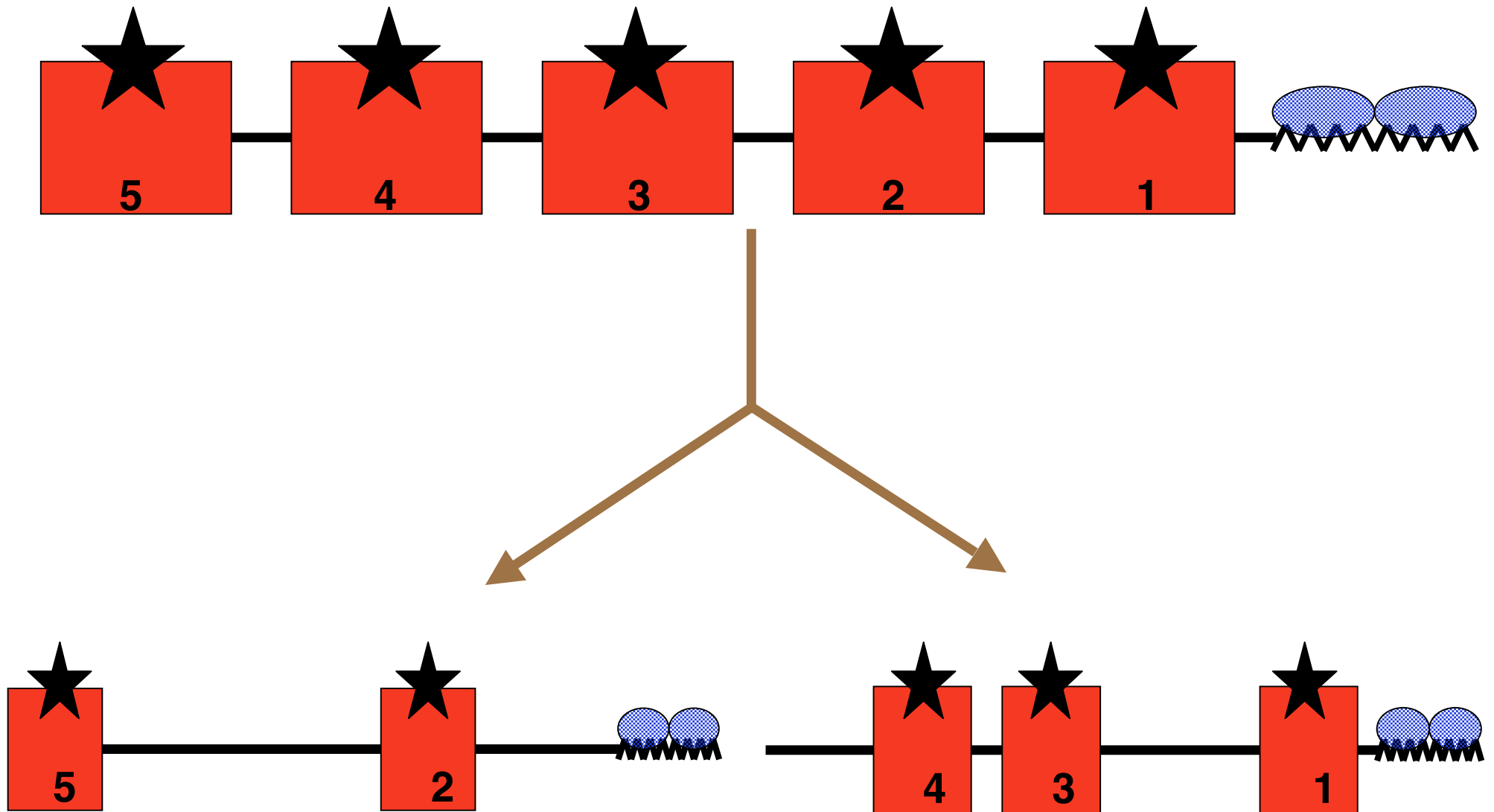
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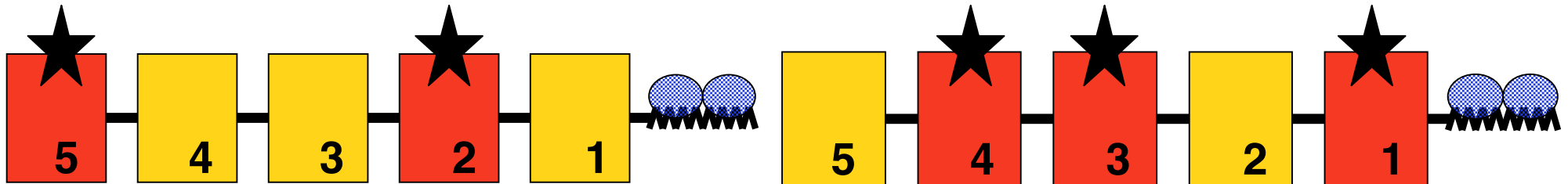
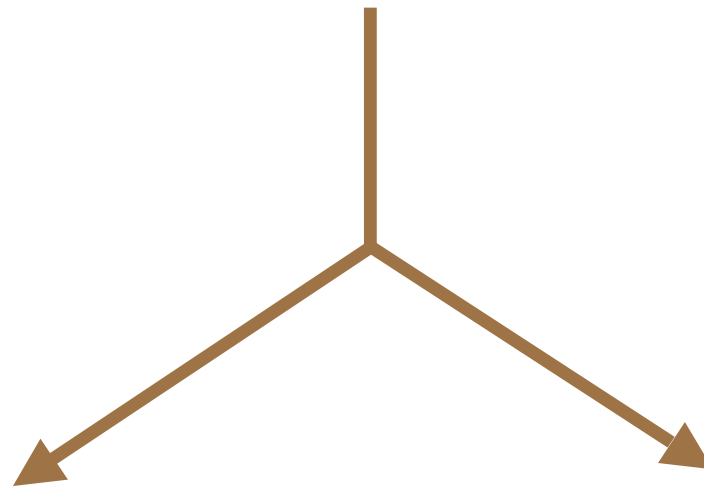
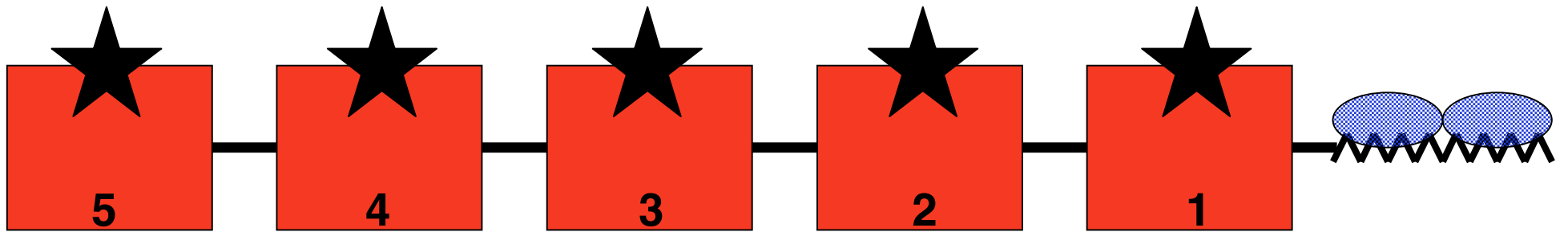
Propagating Active Chromatin



Propagating Active Chromatin



Propagating Active Chromatin



Propagating Active Chromatin

