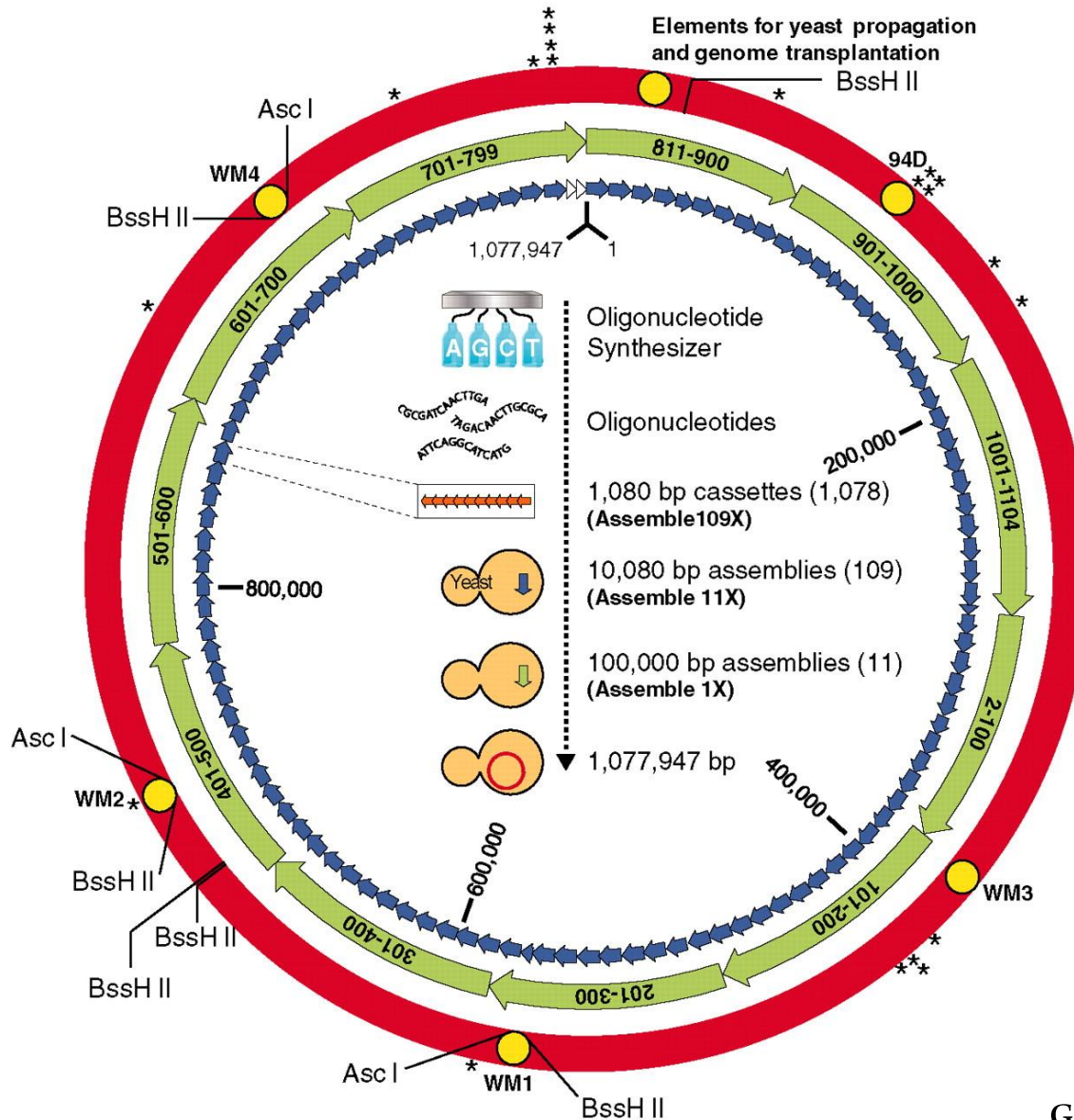
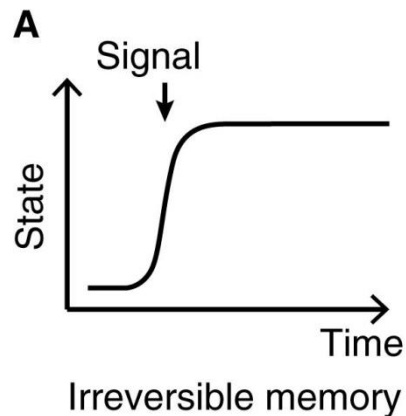


SYNTHETIC BIOLOGY



SYNTHETIC BIOLOGY FOR *DE NOVO* ASSEMBLY OF MEMORY DEVICES – GLOSSARY

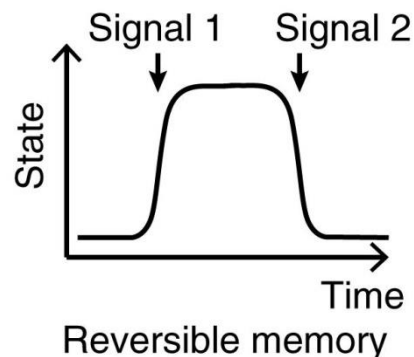
(**Non-**)volatile memory – synthetic memory circuits (**do not**) need active cellular processes to maintain their state



volatile memory > e.g. transcription-based
non-volatile m. > recombination-based

volatile memories are bistable

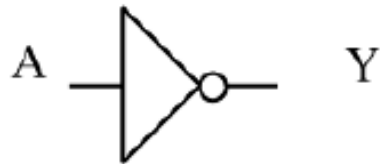
stochastic switching between states should be rare



LOGIC GATES

Basic Logic Gates

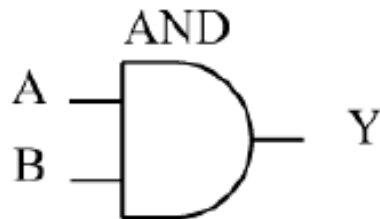
A	Y
0	1
1	0



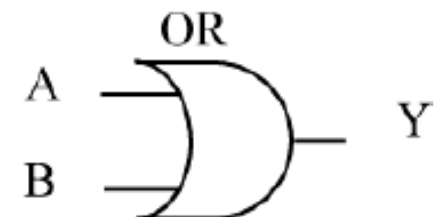
A	B	Y
0	0	0
0	1	1
1	0	1
1	1	0



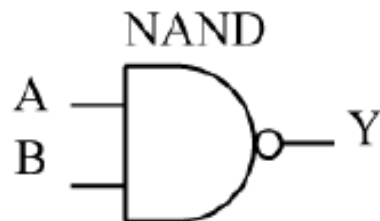
A	B	Y
0	0	0
0	1	0
1	0	0
1	1	1



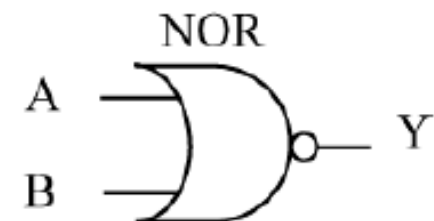
A	B	Y
0	0	0
0	1	1
1	0	1
1	1	1



A	B	Y
0	0	1
0	1	1
1	0	1
1	1	0



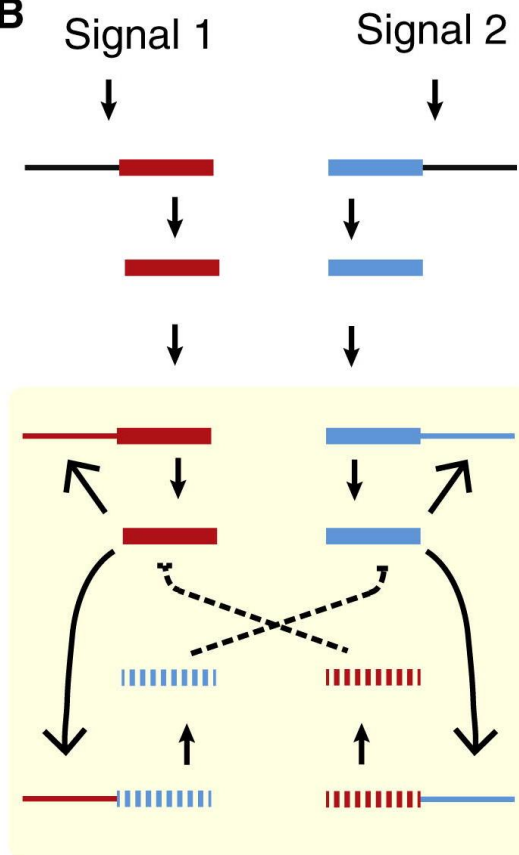
A	B	Y
0	0	1
0	1	0
1	0	0
1	1	0



GENETICALLY ENCODED OPERATORS AND REGULATORS *IN VITRO*

In vitro

B



***In vitro* memory circuits are typically composed of interlocking negative and positive feedback loops that form a bistable core**

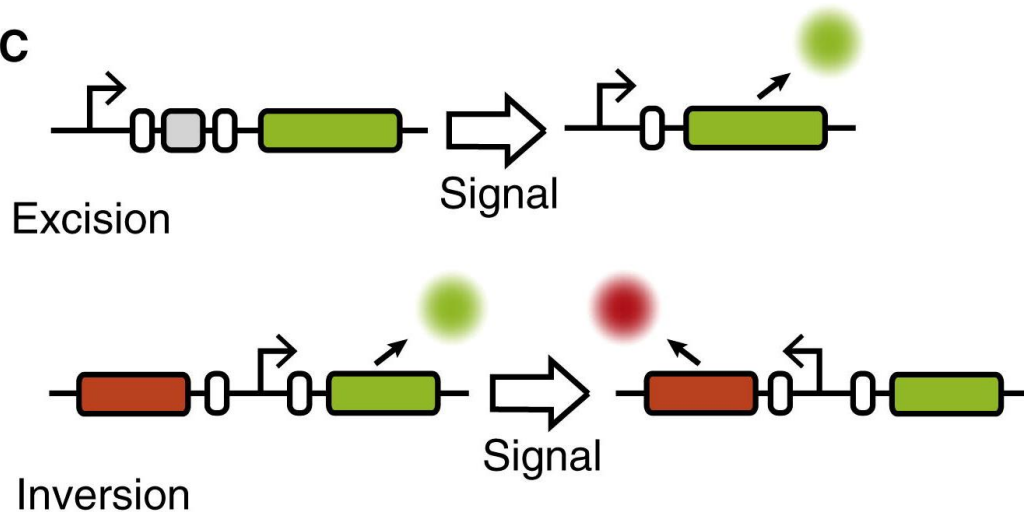
Nucleic acid hybridization

GENETICALLY ENCODED OPERATORS AND REGULATORS *IN VIVO*

In vivo

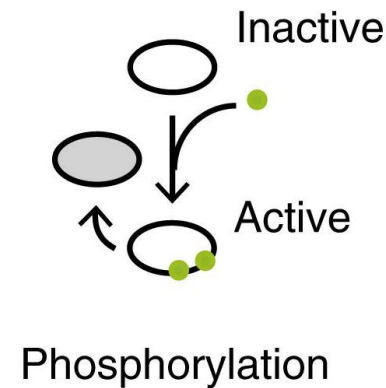
RECOMBINATION-BASED

C



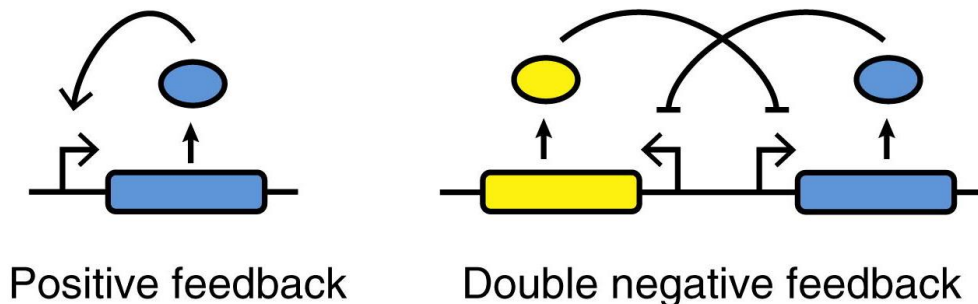
E

PROTEIN PHOSPHORYLATION



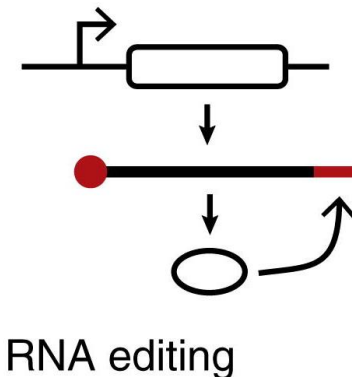
TRANSCRIPTIONAL FEEDBACK LOOPS

D

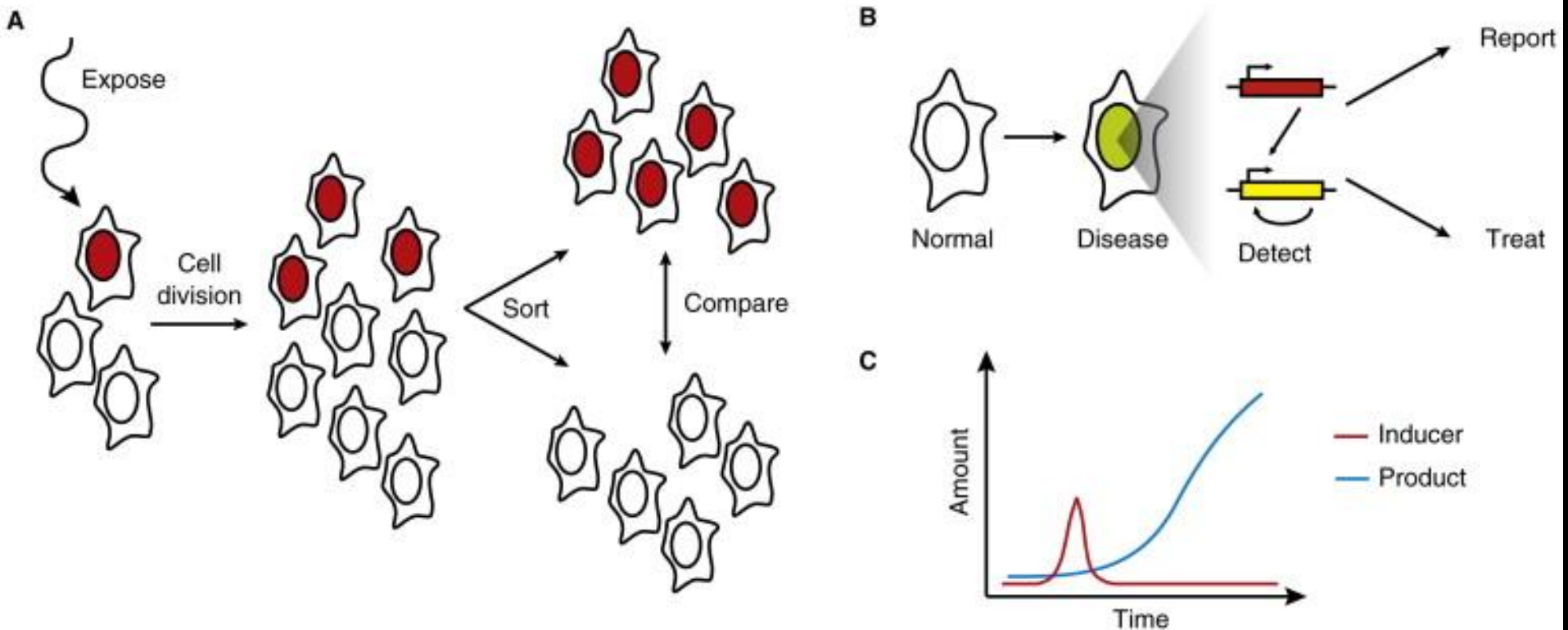


F

RNA EDITING



APPLICATIONS OF SYNTHETIC BIOLOGY

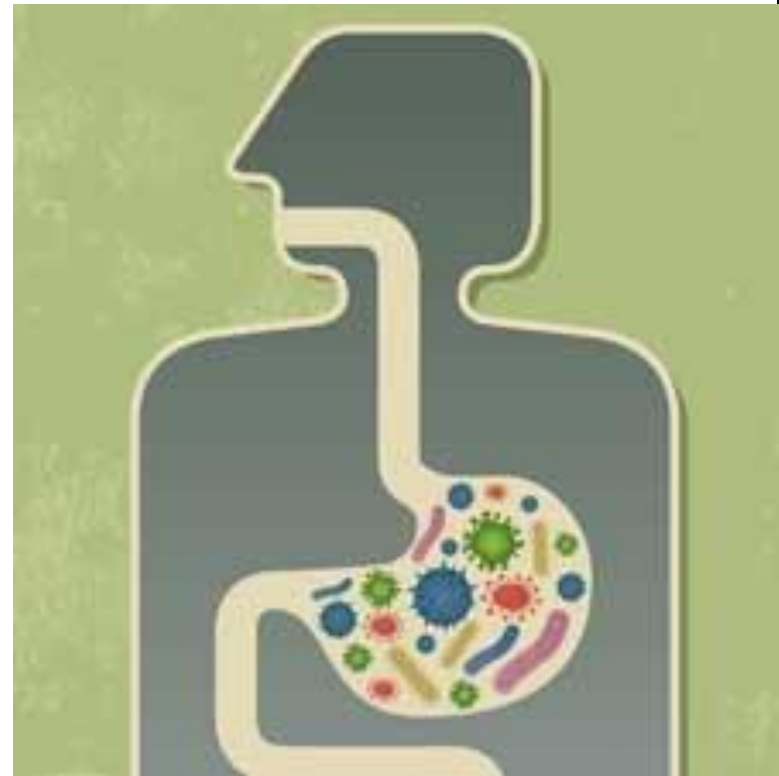


Current Biology

PAPER #1 – KOTULA JW ET AL., PNAS 2014

«PROGRAMMABLE BACTERIA DETECT AND RECORD AN ENVIRONMENTAL SIGNAL IN THE MAMMALIAN GUT»

REPROGRAMMING THE MICROBIOME

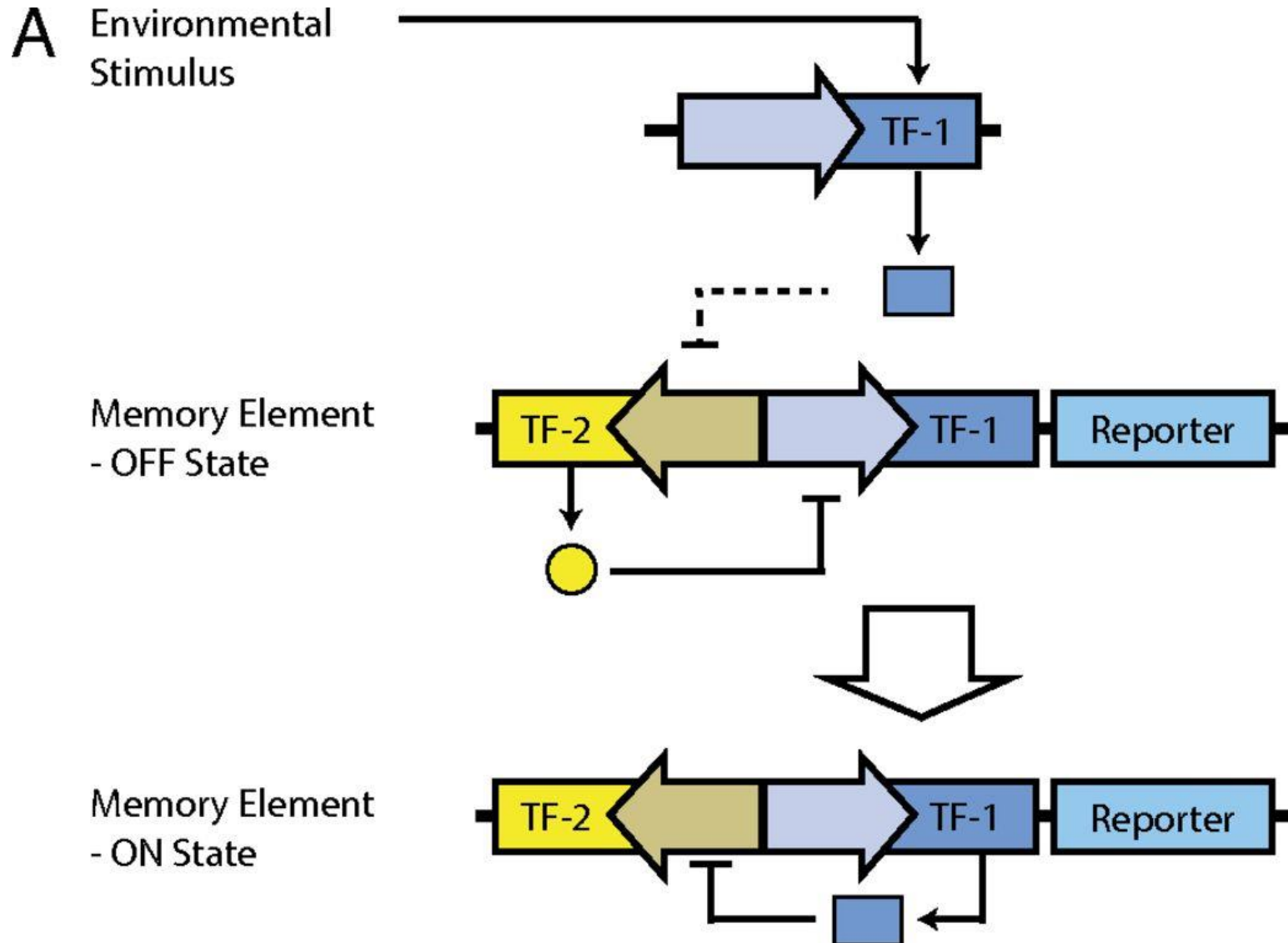


The Scientific American

MEMORY ANALYSIS OF E. COLI

- **Modify E. coli with memory capabilities , transfer into mice, record events during antibiotic exposure**
- **Prerequisites**
 - initial «nonmemory» state should be highly stable, only failing as a result of mutation
 - «memory» state should also be highly stable
 - Chromosomal integration instead of plasmids to minimize loss of genetic information
 - Integrated elements should not impose high fitness burden on the host

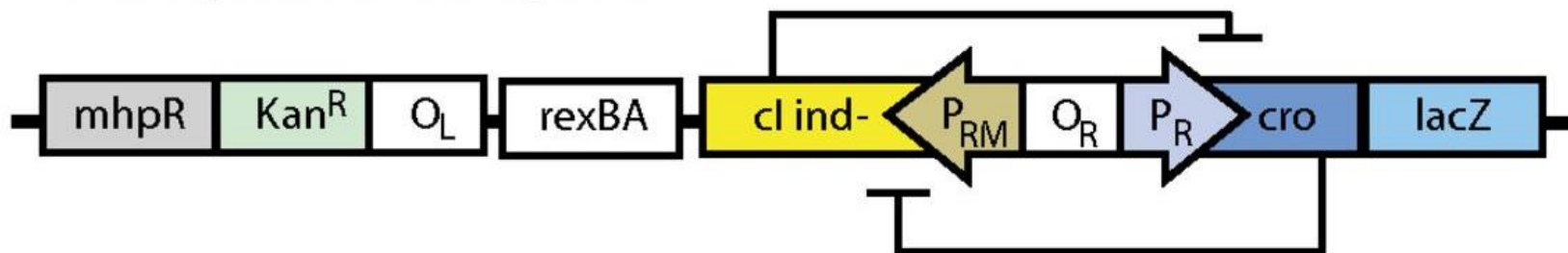
TRIGGER/REPORTER SYSTEM WITH A TOGGLE SWITCH



cl/Cro//tetP-Cro SYSTEM FROM BACTERIOPHAGE LAMBDA

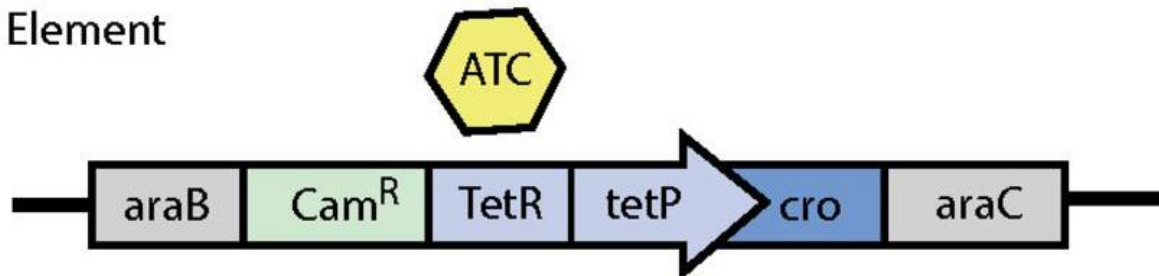
B

Memory Element with Reporter



C

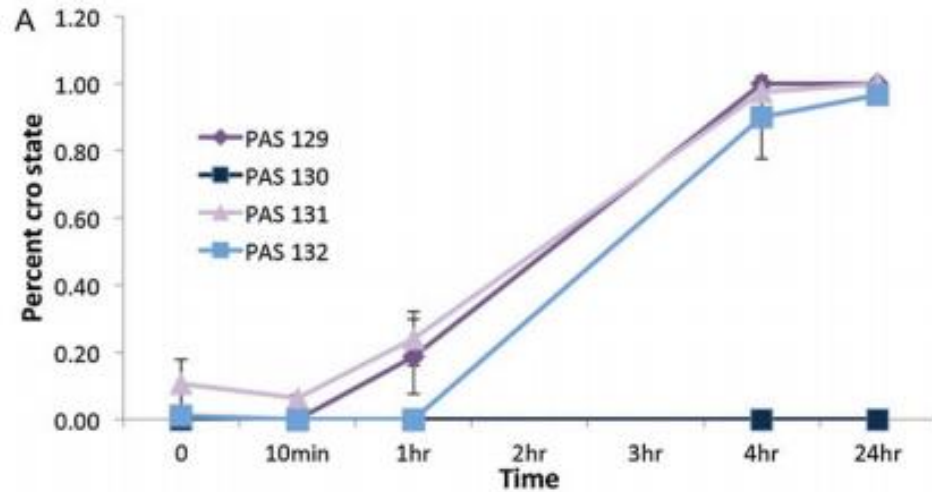
Trigger Element



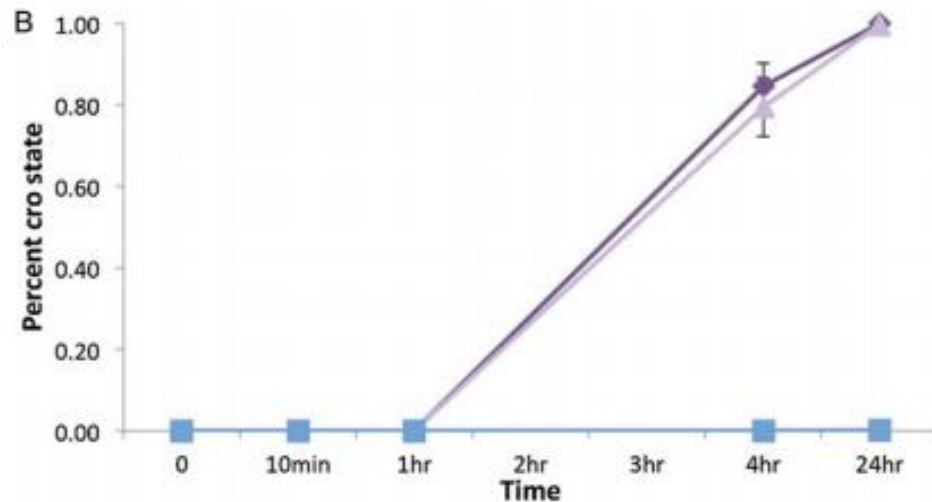
- repressor state of induction-deficient **cl ind-** lysogen only fails due to mutation
- little burden on bacterial host since only 100-200 monomers of **cl ind-** are present per cell, and, if activated < 1000 molecules of **Cro**
- Tn10 tetracycline repressor is particularly sensitive to **anhydrotetracycline (ATC)** >> 100 ng/mL ATC will cause full derepression of the promoter without inhibiting growth of tetracycline-sensitive E.coli

SELECTING THE OPTIMAL MUTANT

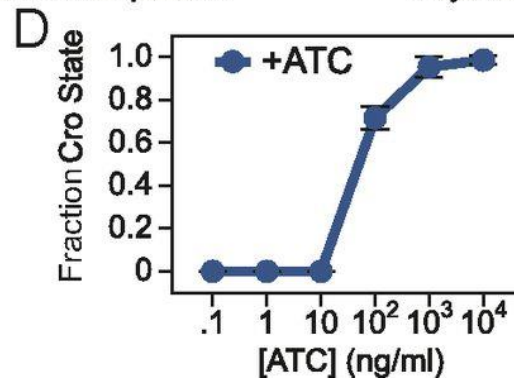
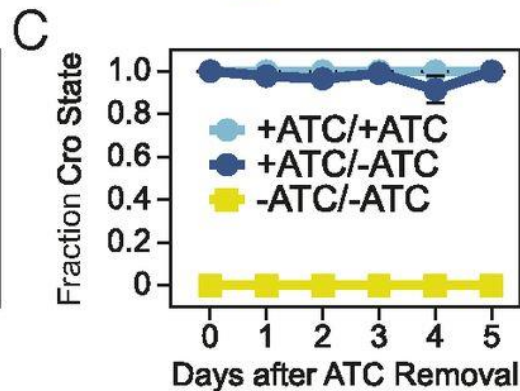
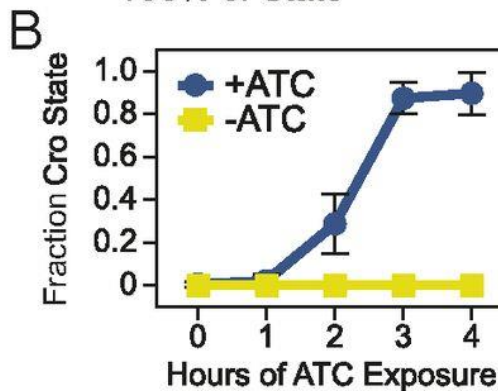
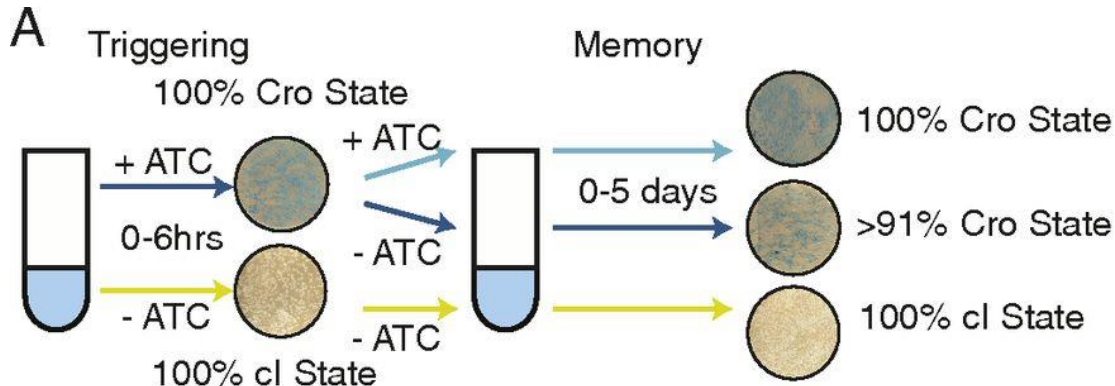
ATC



42°C

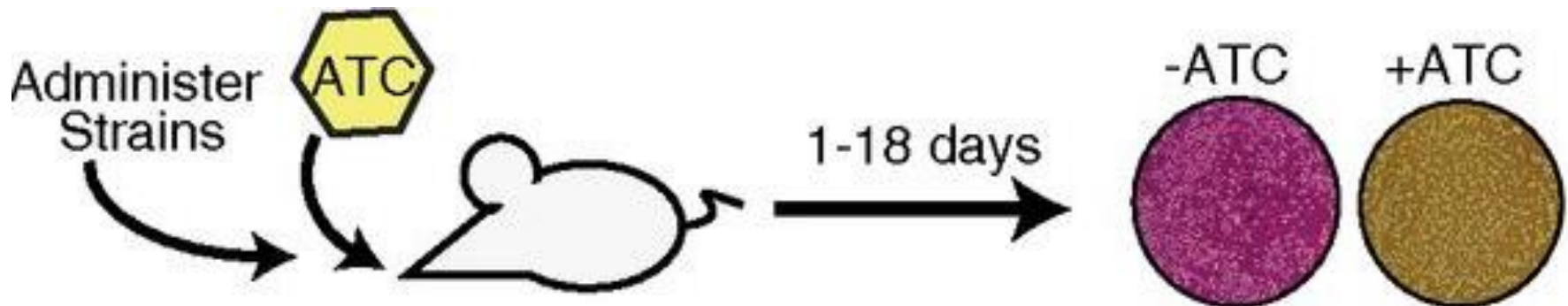


ATC EXPOSURE LEADS TO CI>CRO SWITCH FOR >5D *IN VITRO*

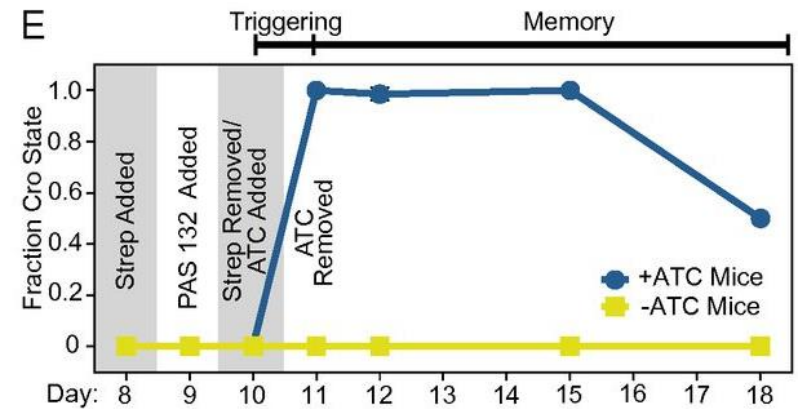
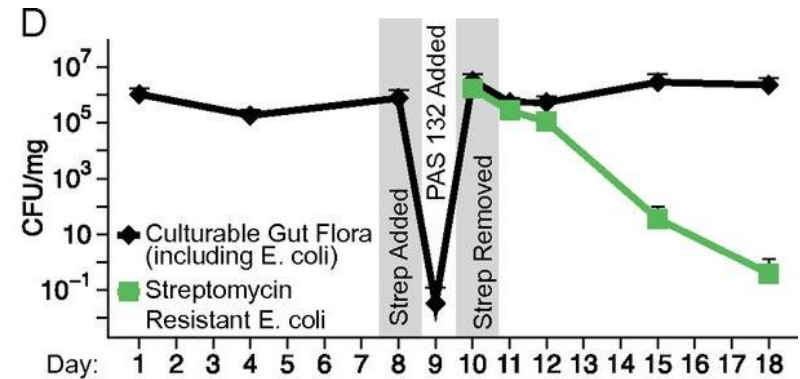
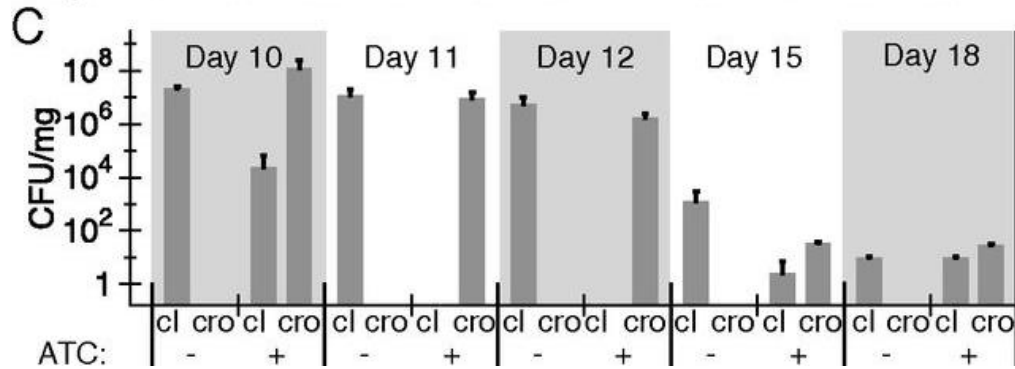
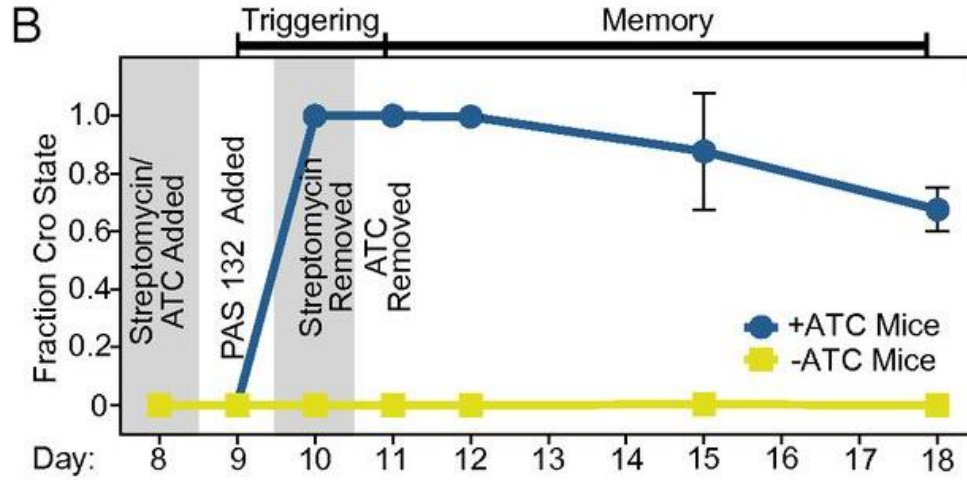


DETECTION OF ATC IN THE MAMMALIAN GUT

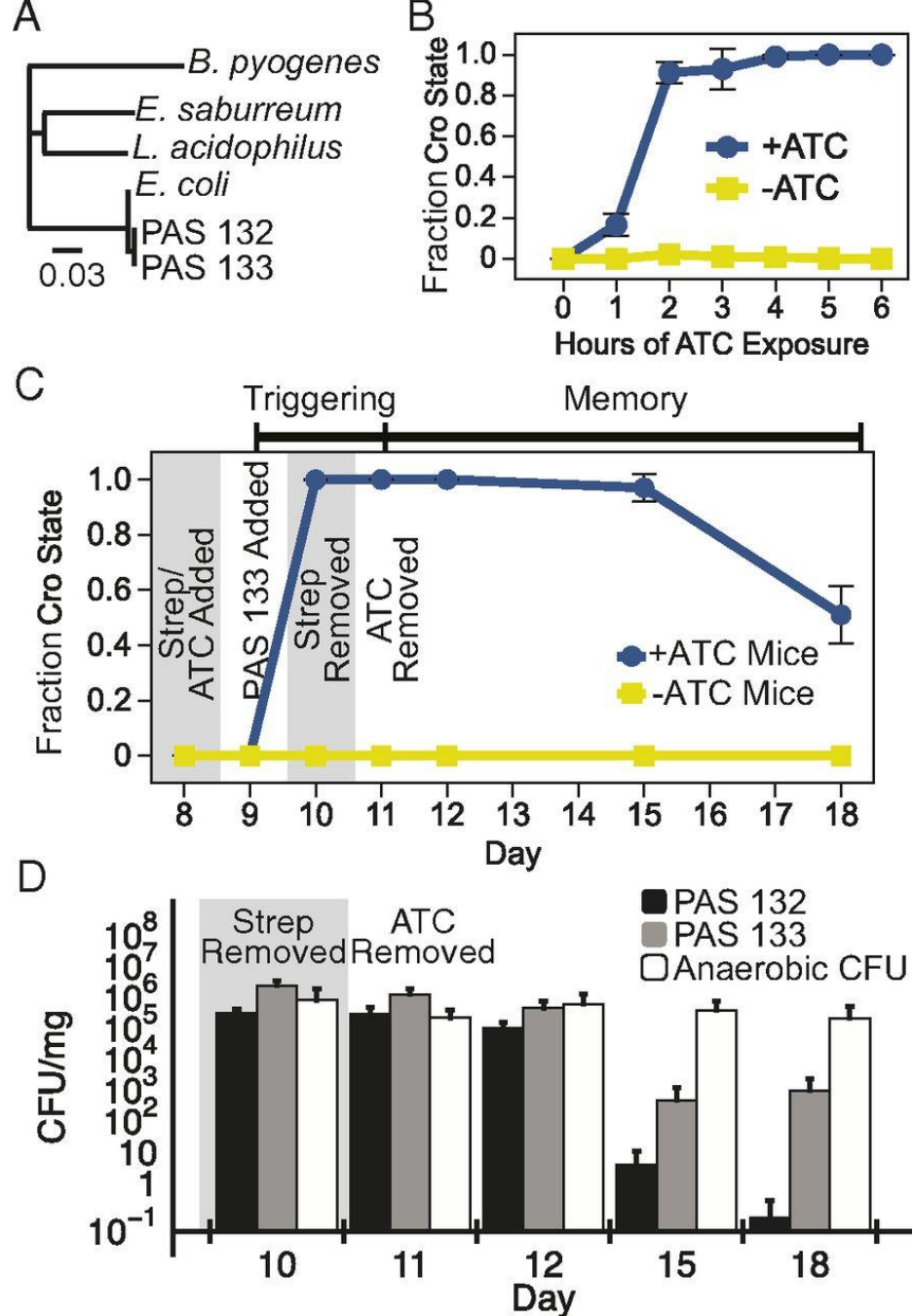
- **PAS132: mutated clone chosen for analysis**
 - Contains a mutation in *rspL*, conferring resistance to Streptomycin
- **Colonization of mice with *E. coli*^{PAS132}**
 - Female Balb/c mice received 10^7 bacteria per animal via oral gavage while receiving streptomycin in the drinking water (+/- ATC)



ATC-INDUCED LASTING CI>CRO SWITCHES *IN VIVO*



ATC-INDUCED LASTING CI>CRO SWITCHES *IN VIVO* IN AN UNCHARACTERIZED (*E. COLI* 16S RIBOSOME CONTAINING) COLIFORM BACTERIUM

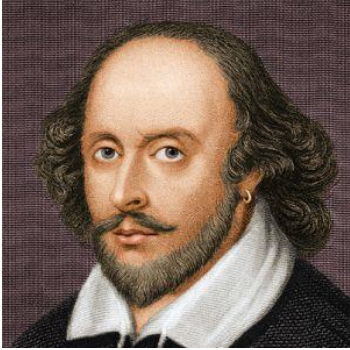


CONCLUSIONS

- **Stable (& bistable) expression system in 2 different E.coli (one as yet uncharacterized) strains to record exposure to antibiotic treatment**
- **Lasting recordings over hours to days (and multiple cell cycles) with no significant fitness burden and no observed «spontaneous», stochastic switching of states**
- **<> FLP based recombination systems are non-volatile and may be leaky due to constitutive low expression of FLP recombinase**
- **Stable cl/Cro system could be completely transformed into E. coli and may further have stabilizing function on the transcripts**
- **May lead to design of efficient, probiotic bacteria for diagnostics or treatment**

PAPER #2 – GOLDMAN N ET AL., NATURE 2014

“TOWARDS PRACTICAL, HIGH-CAPACITY, LOW-MAINTENANCE INFORMATION STORAGE IN SYNTHESIZED DNA”



All 154 of Shakespeare's sonnets
(ASCII «.txt»)

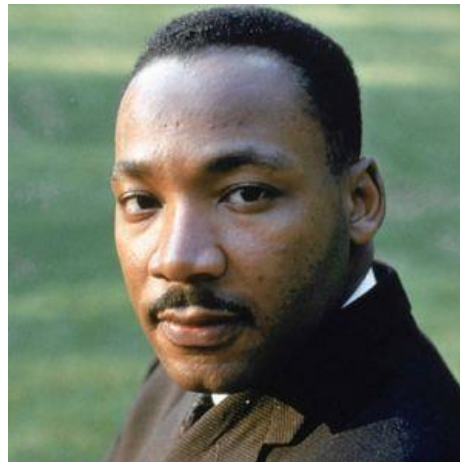


Watson&Crick, Nature 1953
(«watsoncrick.pdf»)

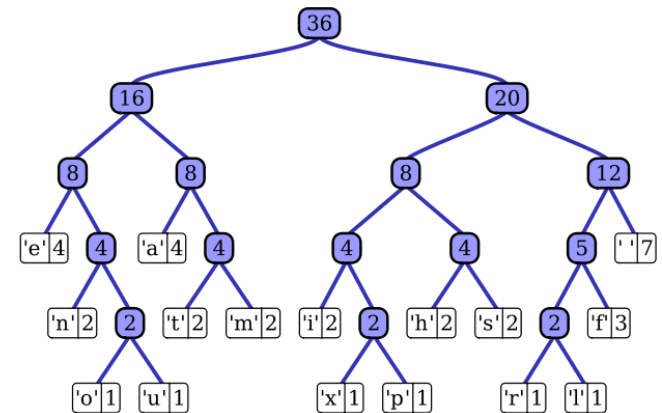
>> 757'051 bytes



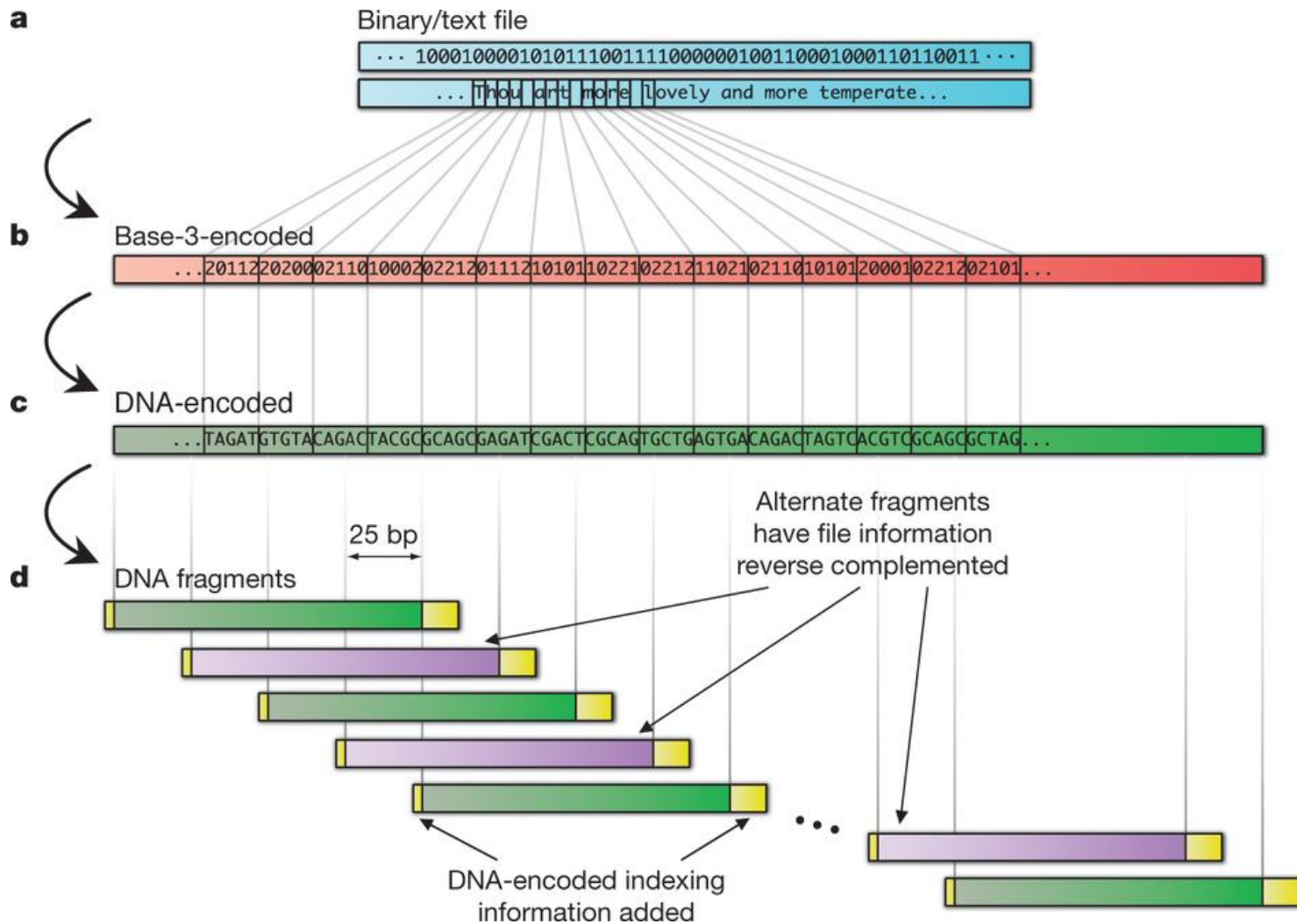
«EMBL-EBI.jpg»



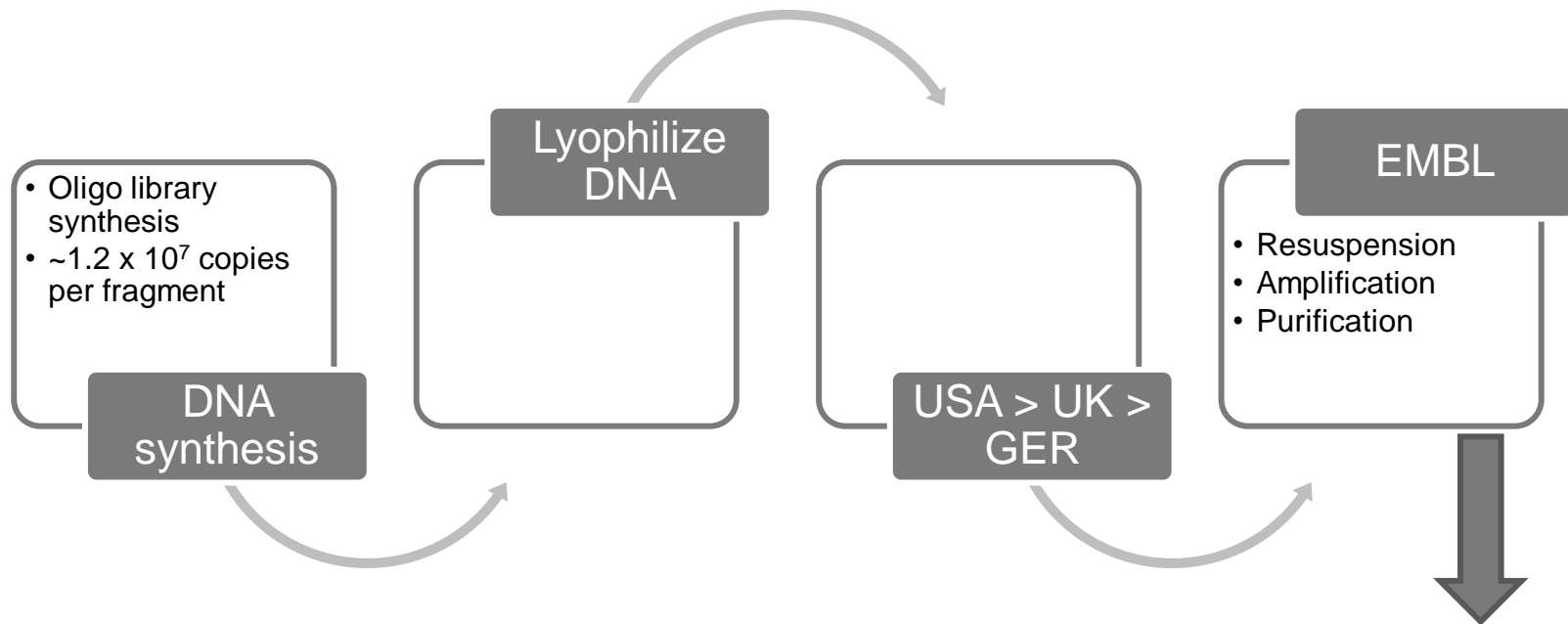
26s, «ihaveadream.mp3»



Huffmann code (ASCII «.txt»)



- 4-fold redundancy per DNA fragment
- Reverse complements of each fragment to minimize data loss
- total of 153,335 strings of DNA, each comprising 117 nt (100 nt data + 17 nt barcoding)
- No homopolymers



Sequencing on
Illumina HighSeq
In «paired-end» mode

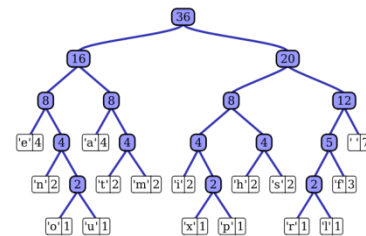
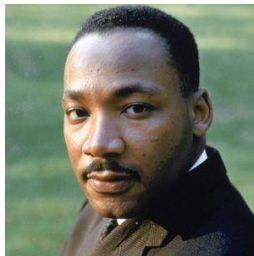
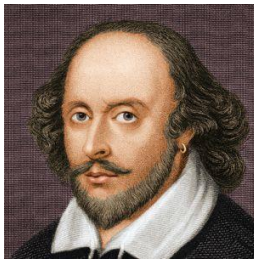




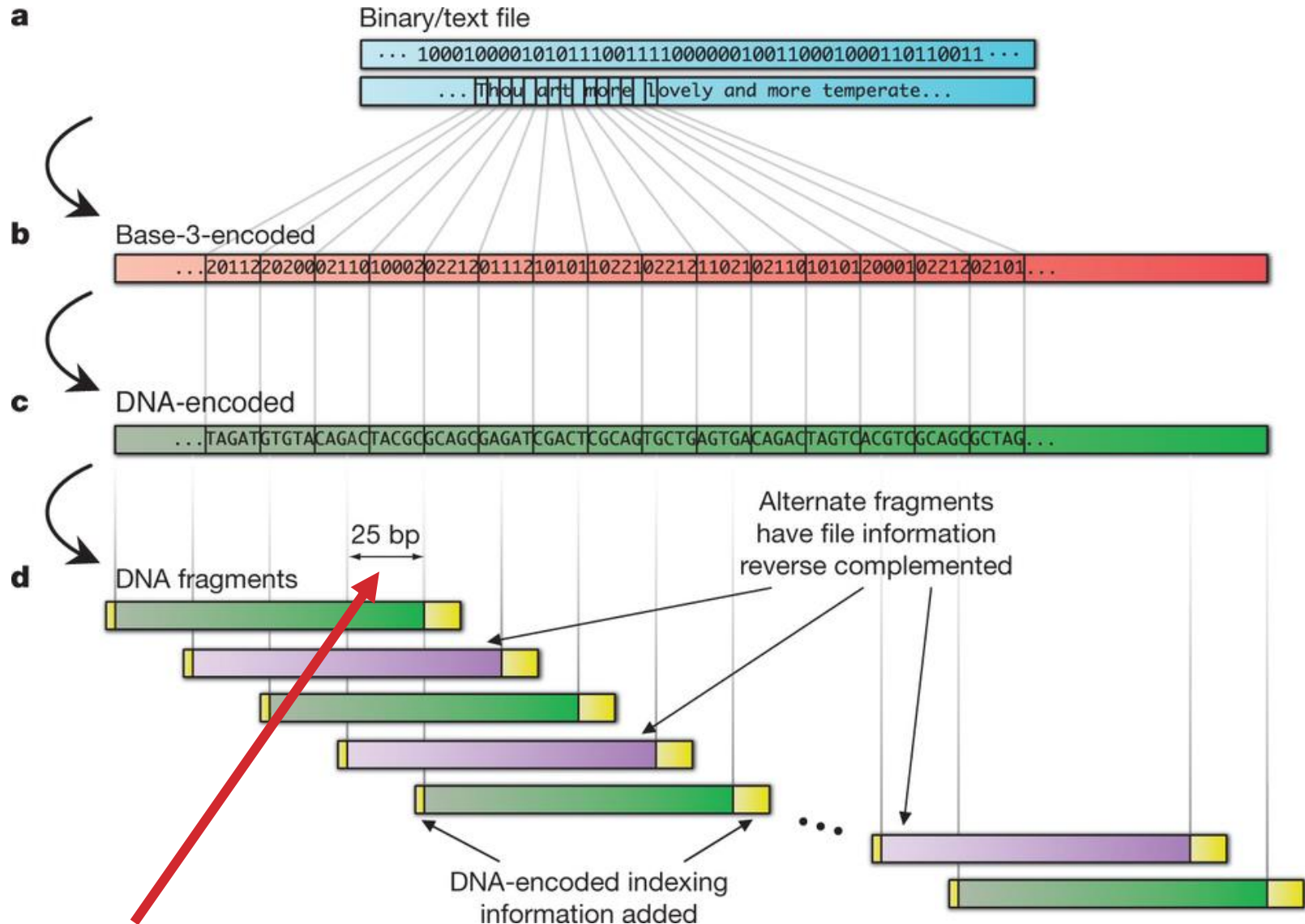
79.6 x 10⁶ read-pairs of 104 bases in length



full-length reconstruction *in silico*

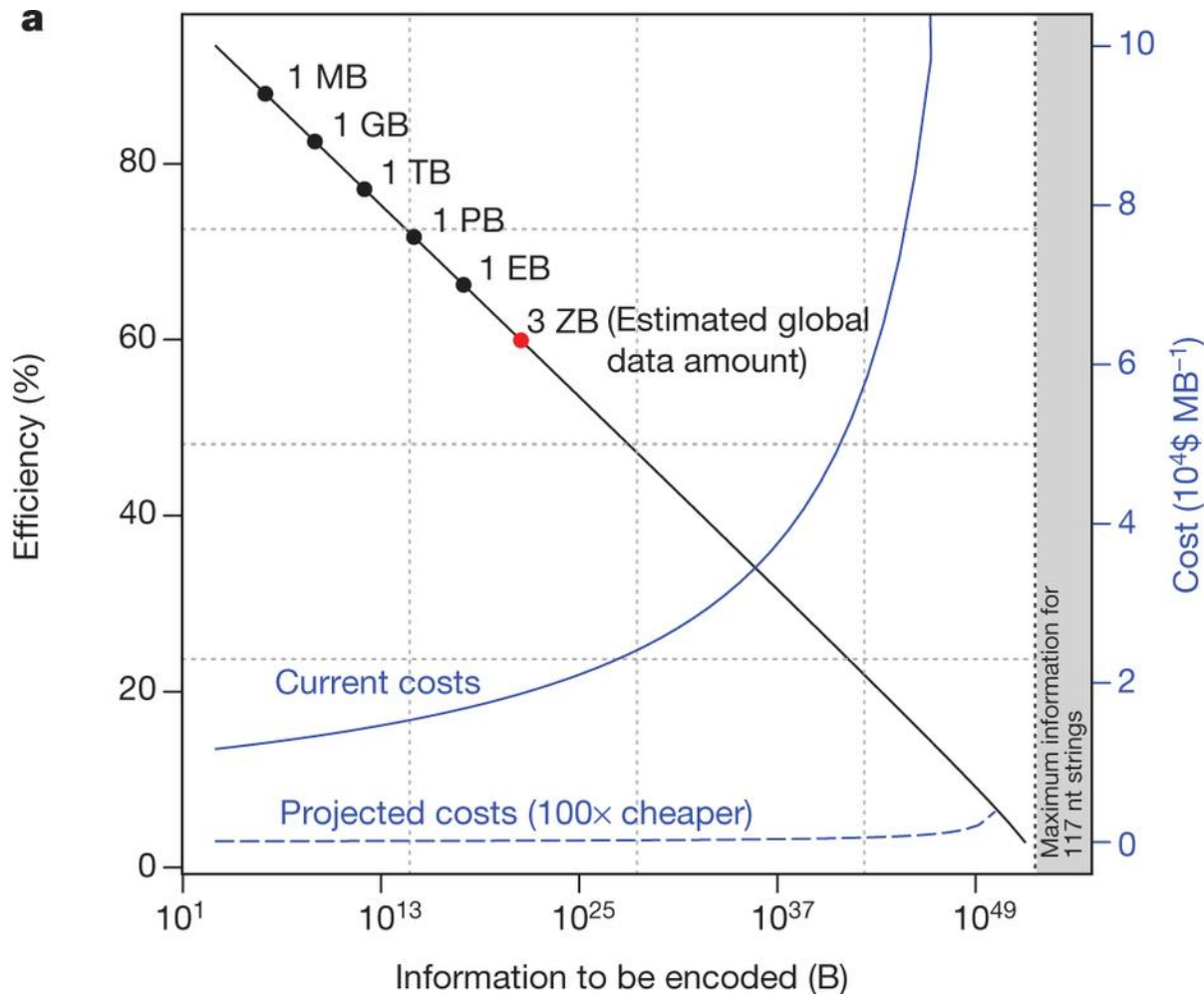


TROUBLESHOOTING



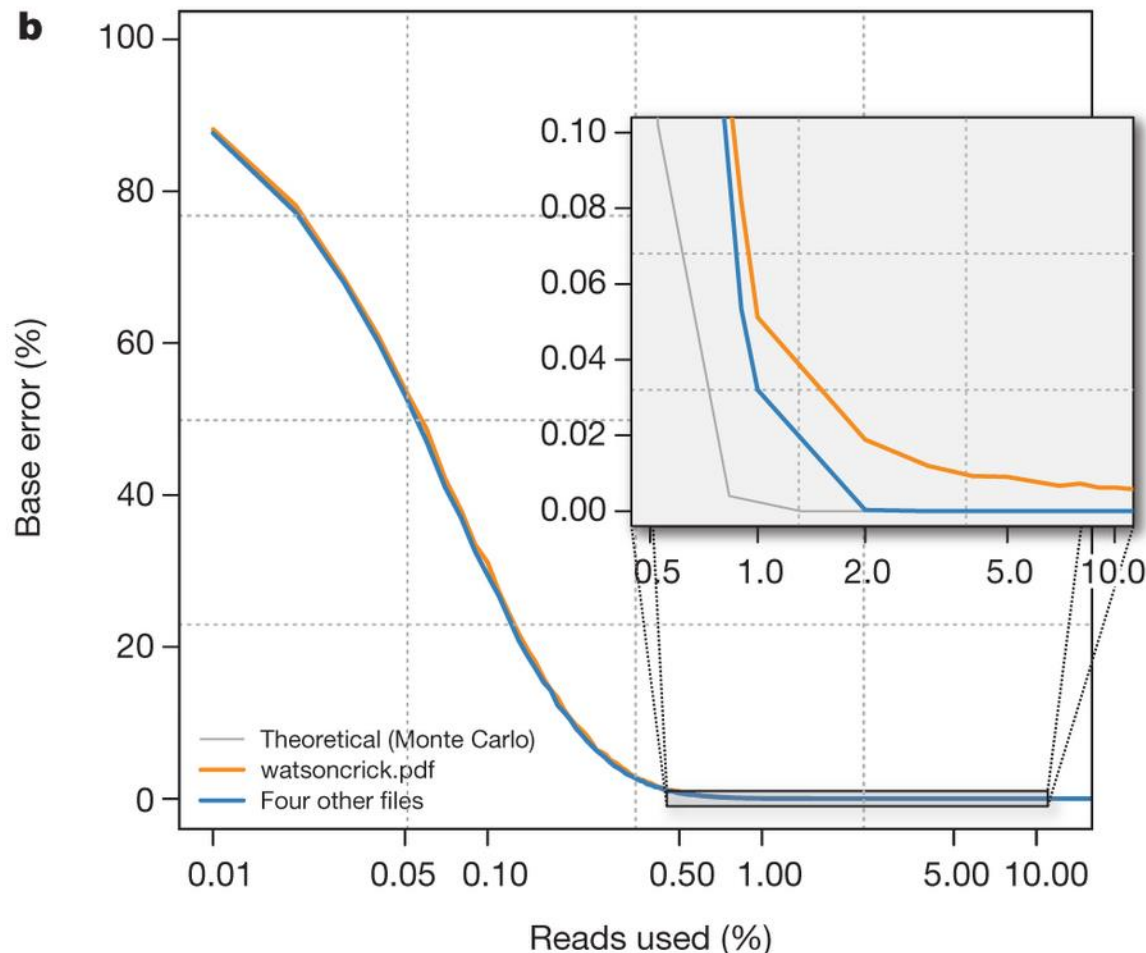
2x25bp could not be assigned > manual filling through neighbor comparison > «100% correctly aligned sequences»

CONCLUSIONS & OUTLOOK – ENCODING LARGER DATA VOLUMES



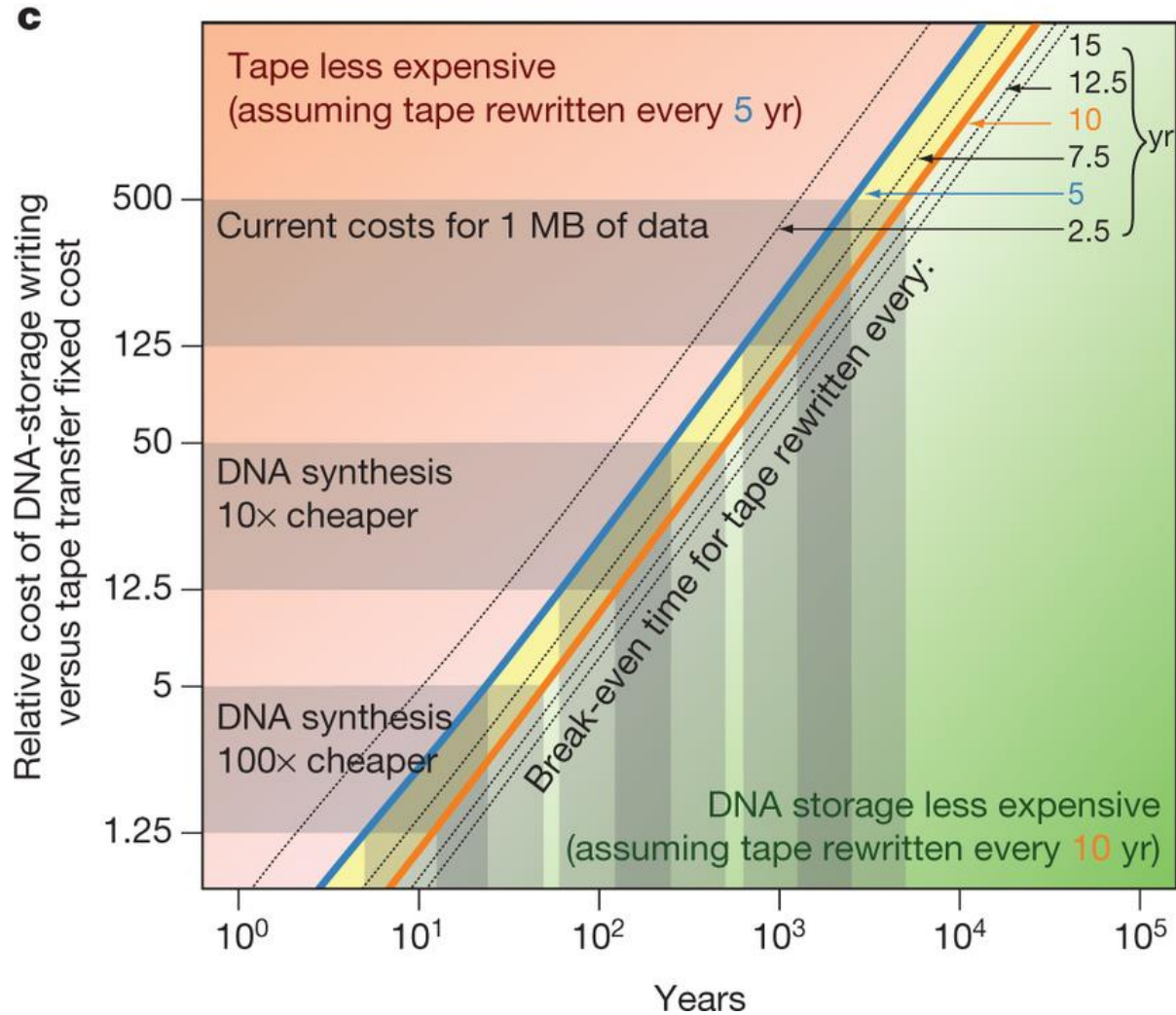
Indexing DNA grows logarithmically to the encodable data, while total amount of synthesized DNA for coding grows sub-linearly

CONCLUSIONS & OUTLOOK – READ ERRORS AS A FUNCTION OF COVERAGE



- Error is zero when $\geq 2\%$ of the reads are used - taken from the originally obtained 79.6×10^6 read-pairs of all but “watsoncrick.pdf”
- Manual correction of «watsoncrick.pdf» leads to a minimal error rate of 0.0036%

CONCLUSIONS & OUTLOOK – COST EFFECTIVENESS



CONCLUSIONS & OUTLOOK – COST EFFECTIVENESS

- Costs can further be decreased by lower sequencing coverage (now mean sequencing coverage $\sim 1'308x$)



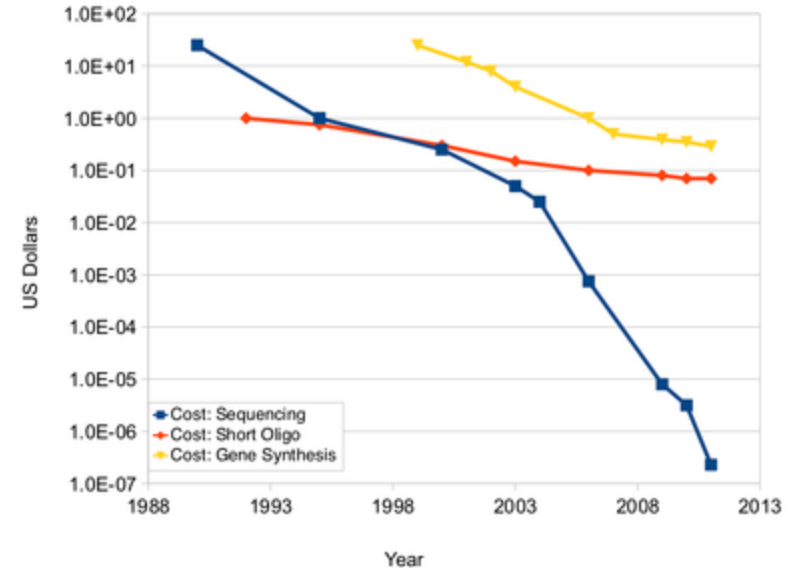
- ~ 80 PB (80x1000 TB) of data as of writing of Paper, growth of ~ 15 PB per year
 - 10% is maintained on disk, CASTOR migrates regularly between tapes
 - Access to old data decreases considerably after 2-3 years after aquisition
 - *Current costs $\sim 12'400\$$ per MB for coding and $\sim 220\$$ per MB for decoding*

CONCLUSIONS & OUTLOOK

- With current synthesis & reading costs as well as current coding scheme, DNA-based storage may be cost-effective for archives of several megabytes within a ~600-5'000 yr period
- If costs decrease by 1 log, ~50-500 yr period
- If costs decrease by 2 logs, < 50 yrs
- ~2.2 PB of information per gram DNA
- long-term storage seems to be evolutionary proven

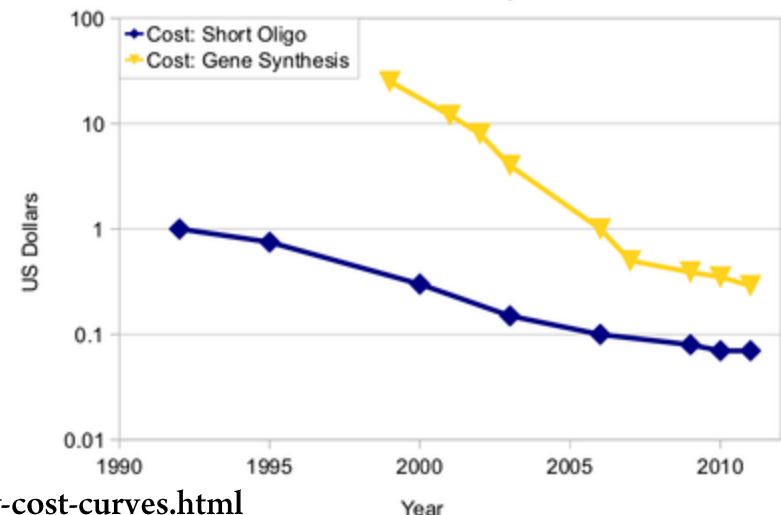
Cost Per Base of DNA Sequencing and Synthesis

Rob Carlson, June 2011, www.synthesis.cc

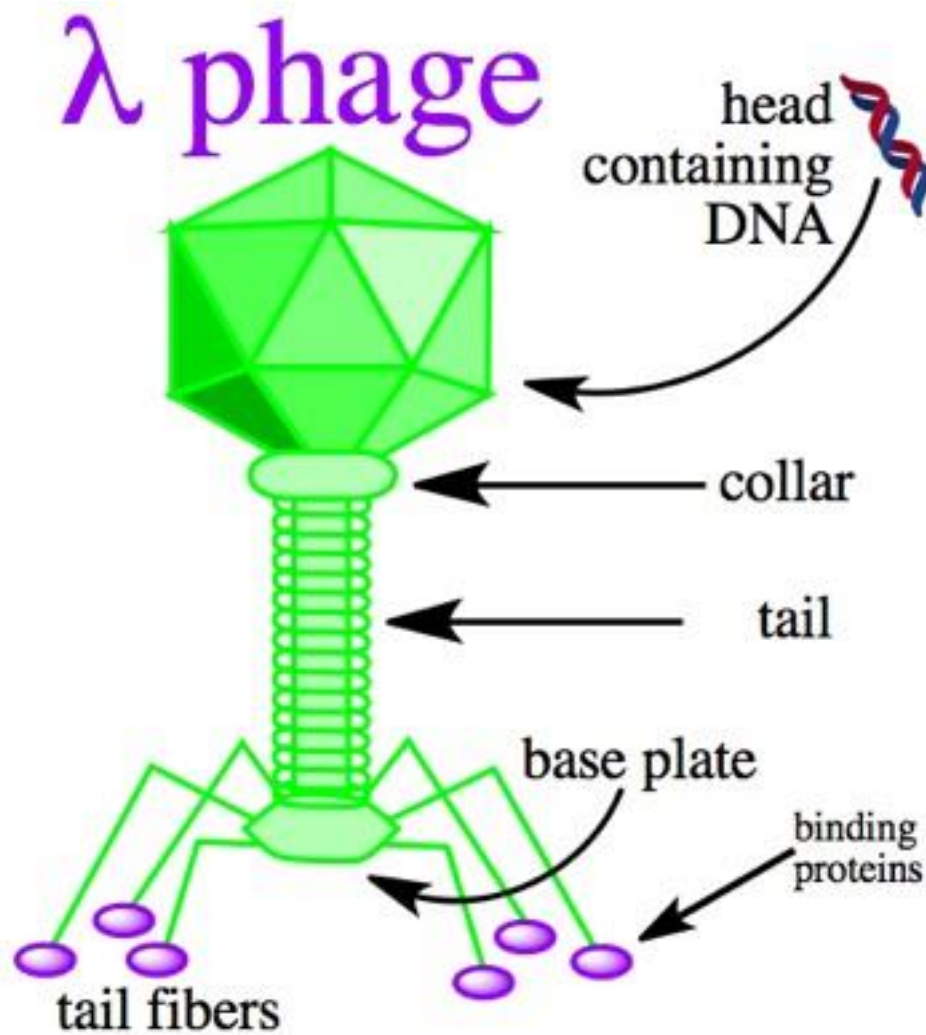


Cost Per Base of Synthetic DNA

Rob Carlson, June 2011, www.synthesis.cc

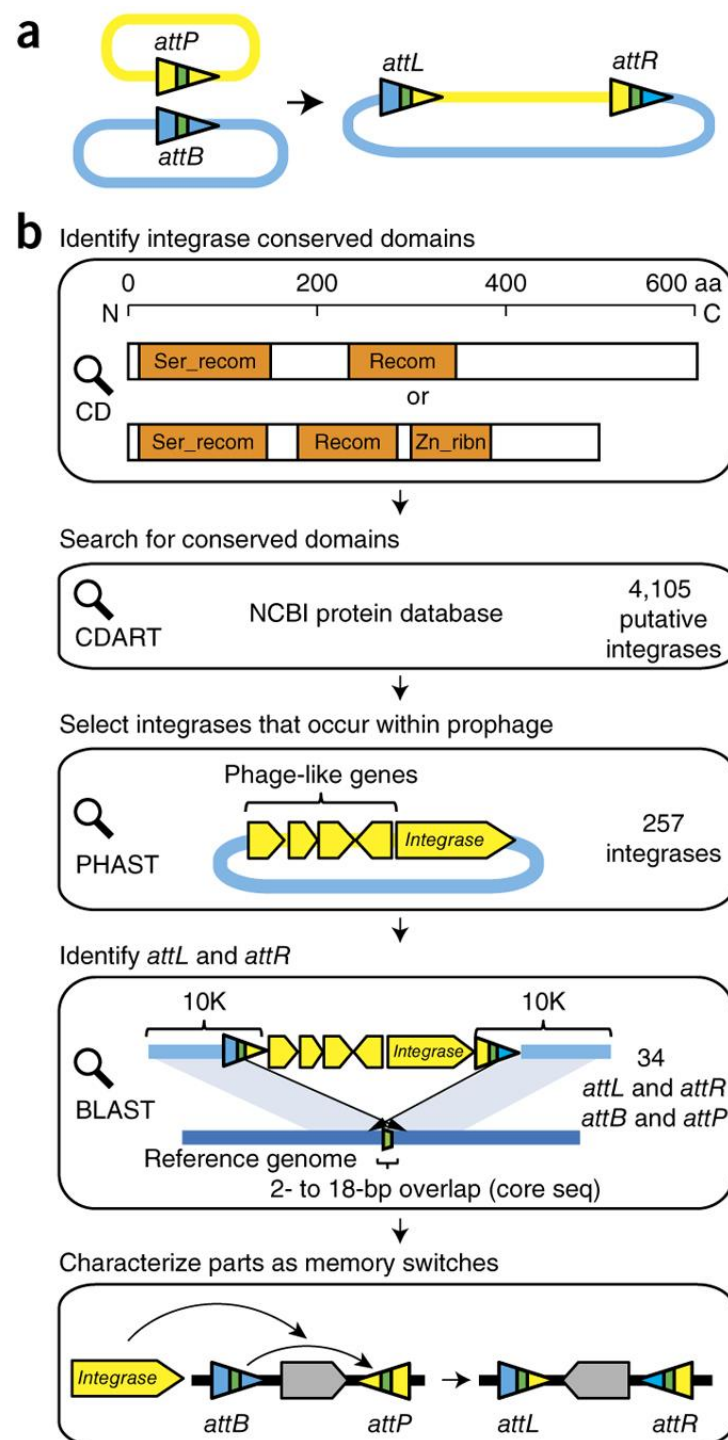


PAPER #3 – YANG ET AL., NATURE METHODS 2014
“PERMANENT GENETIC MEMORY WITH >1-BYTE
CAPACITY”

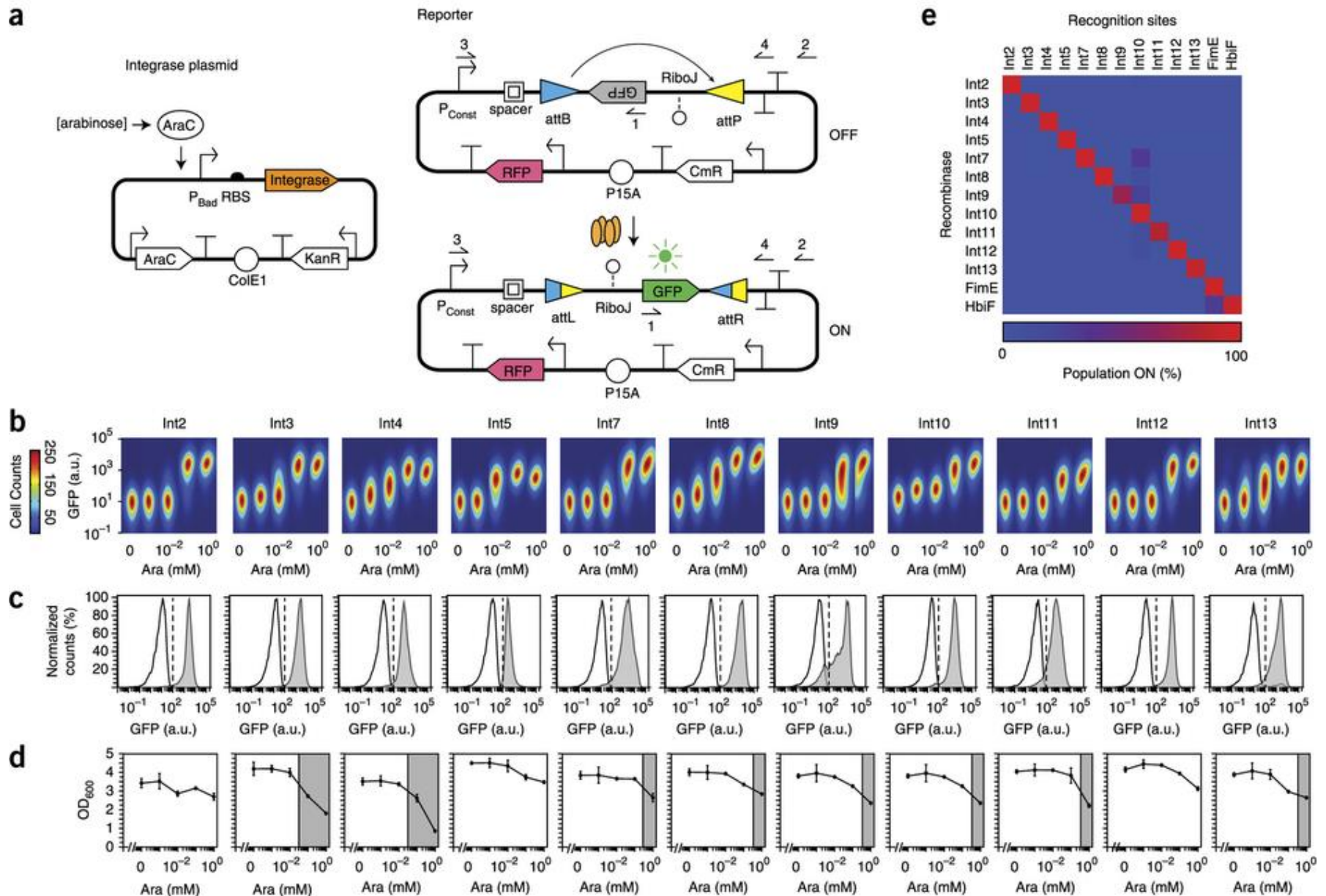


LSTP
«large serine-type phage»
integrates

finding LSTP integrases



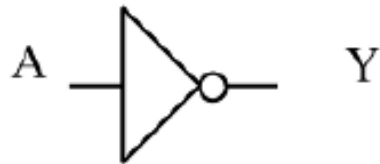
CHARACTERIZATION OF MEMORY SWITCHES AND ORTHOGONALITY



LOGIC GATES

Basic Logic Gates

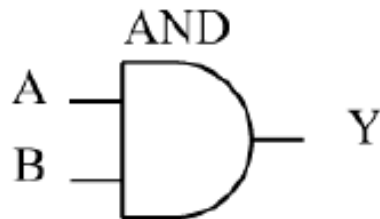
A	Y
0	1
1	0



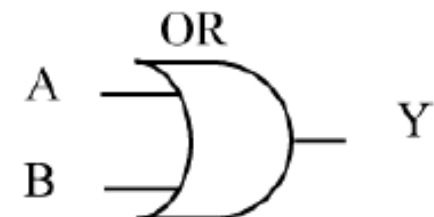
A	B	Y
0	0	0
0	1	1
1	0	1
1	1	0



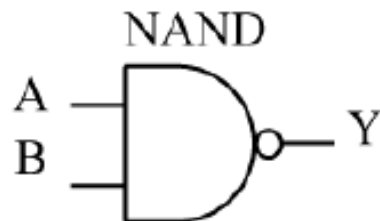
A	B	Y
0	0	0
0	1	0
1	0	0
1	1	1



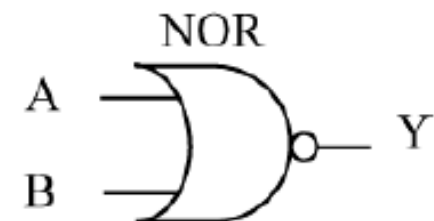
A	B	Y
0	0	0
0	1	1
1	0	1
1	1	1



A	B	Y
0	0	1
0	1	1
1	0	1
1	1	0

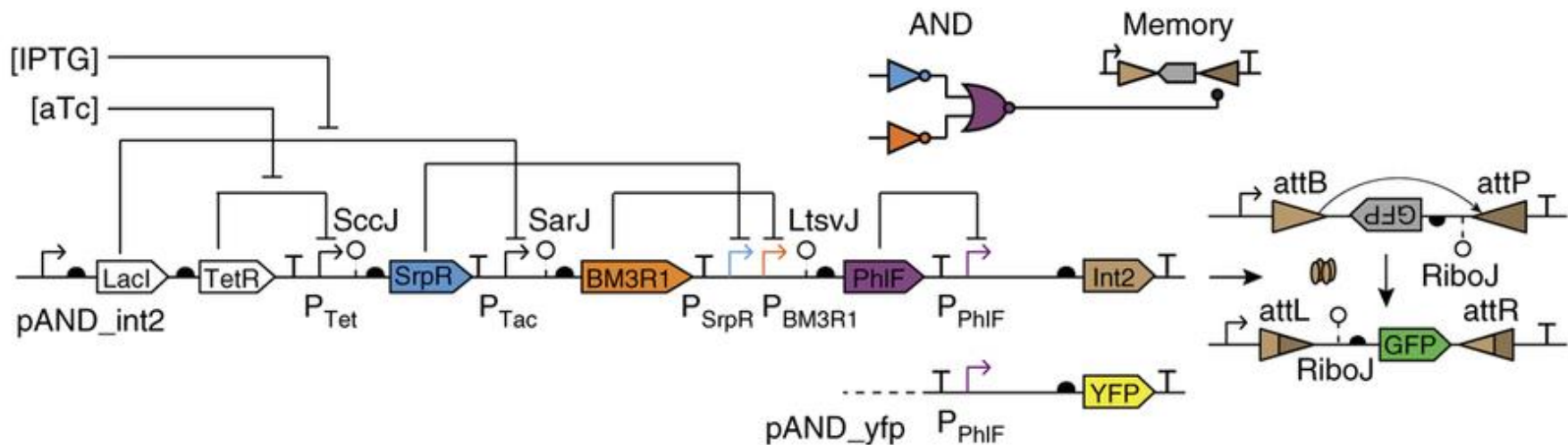


A	B	Y
0	0	1
0	1	0
1	0	0
1	1	0

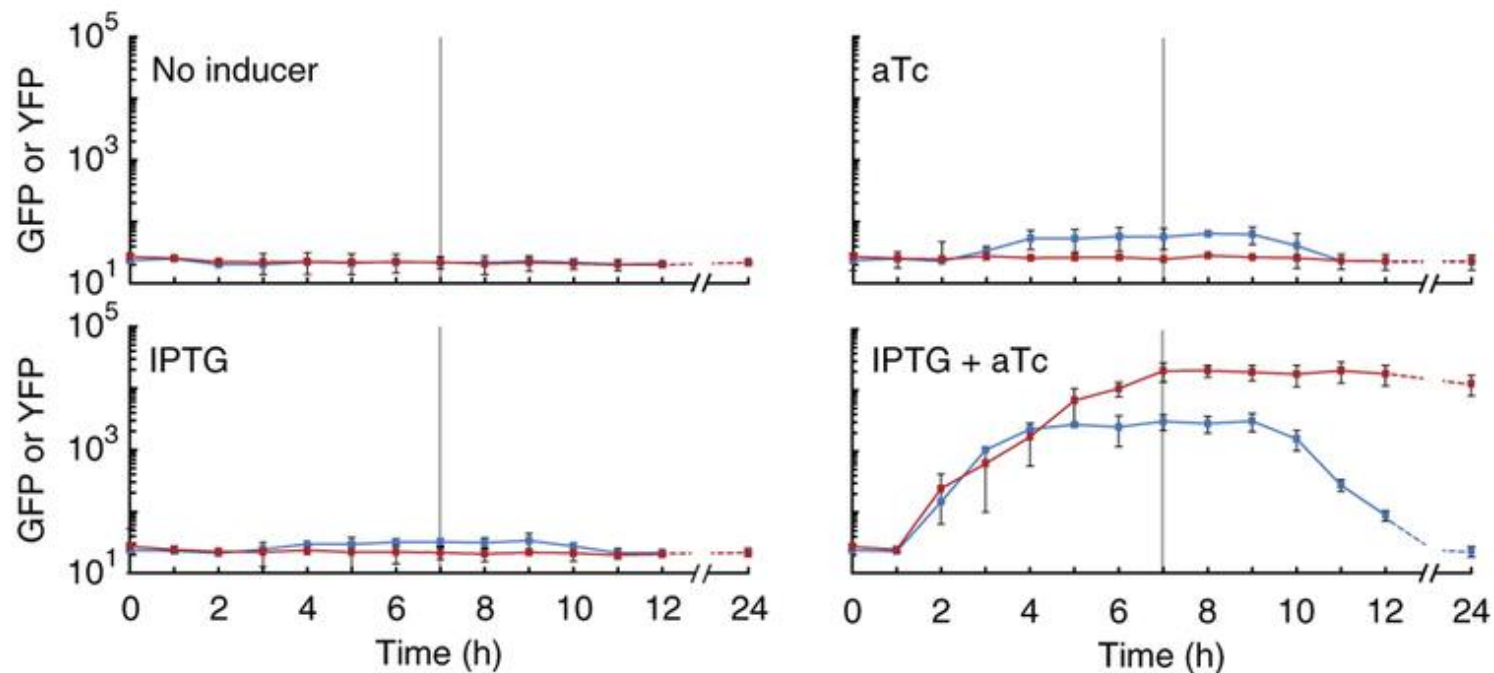


LOGIC AND-GATE

c

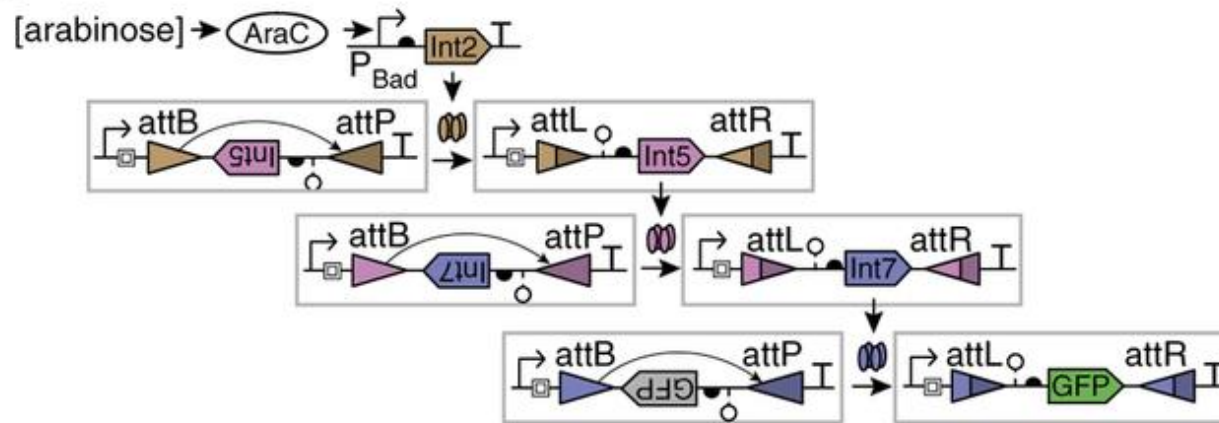


d



CIRCUITS OF MULTIPLE RECOMBINASES

e



f

