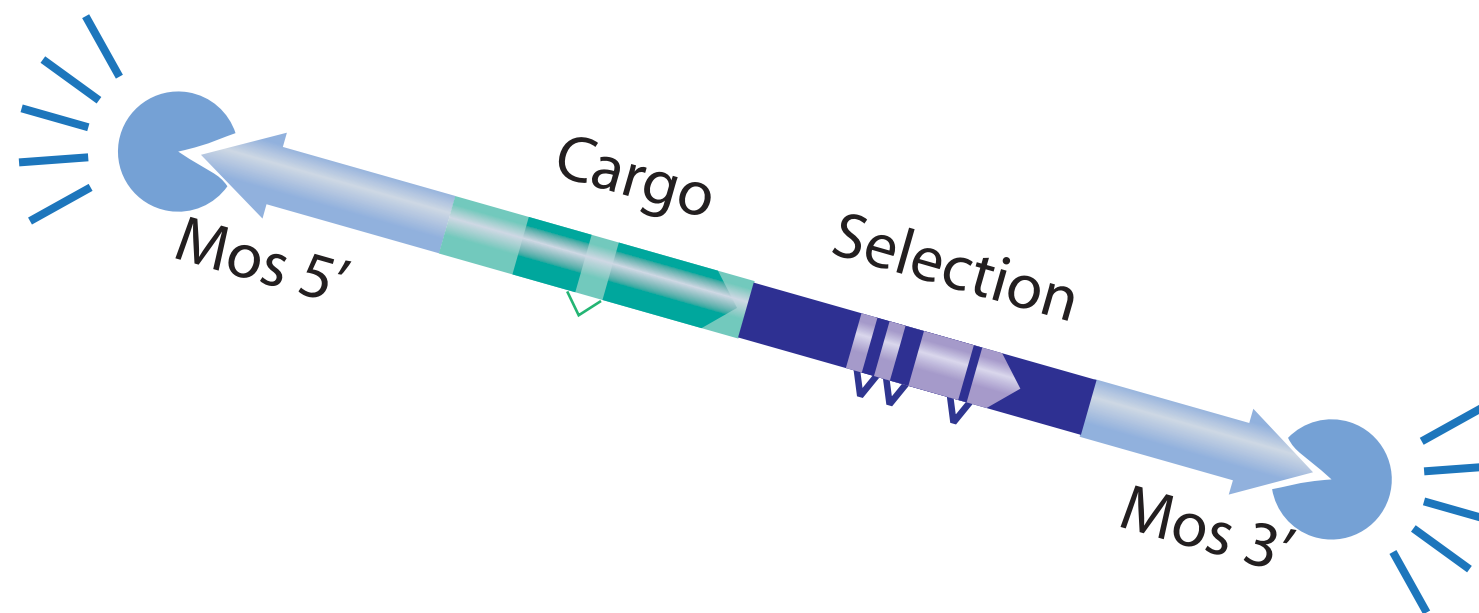
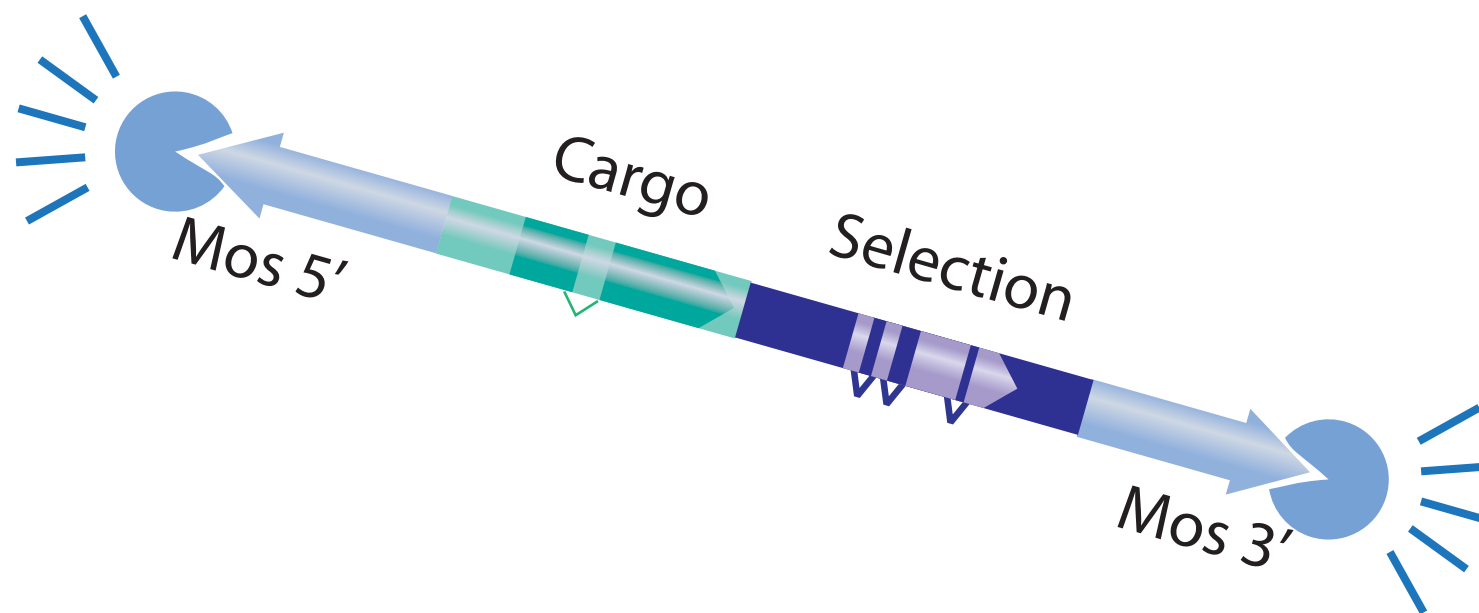


Hopping transgenes and universal MosSCI insertion sites into genomes



Christian Frøkjær-Jensen
Postdoctoral fellow
HHMI, University of Utah

Hopping transgenes and universal MosSCI insertion sites into genomes



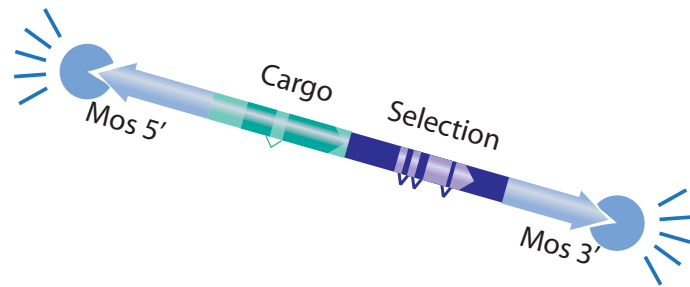
ApE
(A plasmid Editor)

Christian Frøkjær-Jensen
Postdoctoral fellow
HHMI, University of Utah



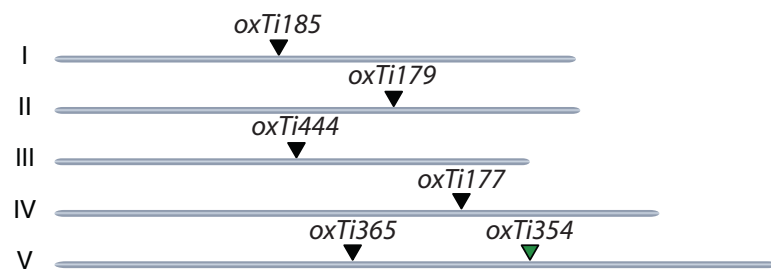
Wayne Davis

Methods to engineer the genome based on Mos I



1. MiniMos transposon

Hopping transgenes into the genome



2. Universal MosSCI sites

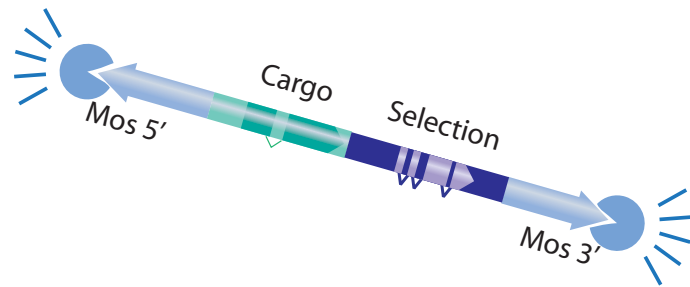
Targeted insertion at different sites across the genome



3. wormbuilder.org

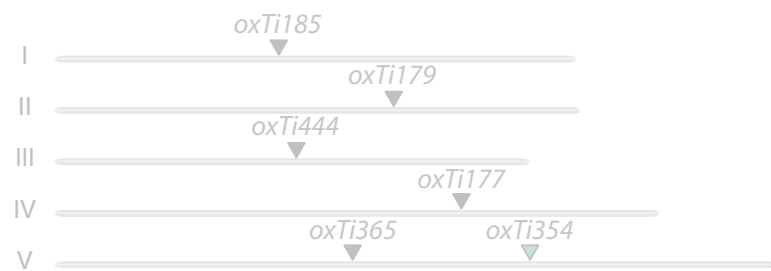
Reagents, strains and troubleshooting advice

Methods to engineer the genome based on Mos I



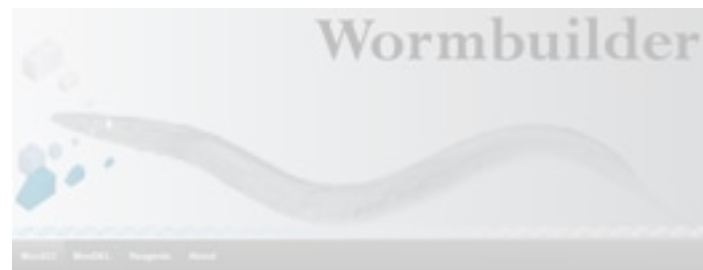
1. MiniMos transposon

Hopping transgenes into the genome



2. Universal MosSCI sites

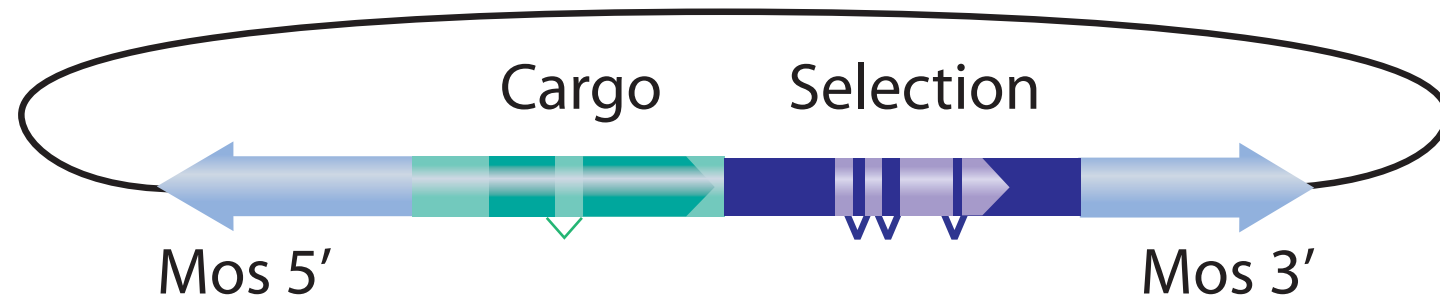
Targeted insertion at different sites across the genome



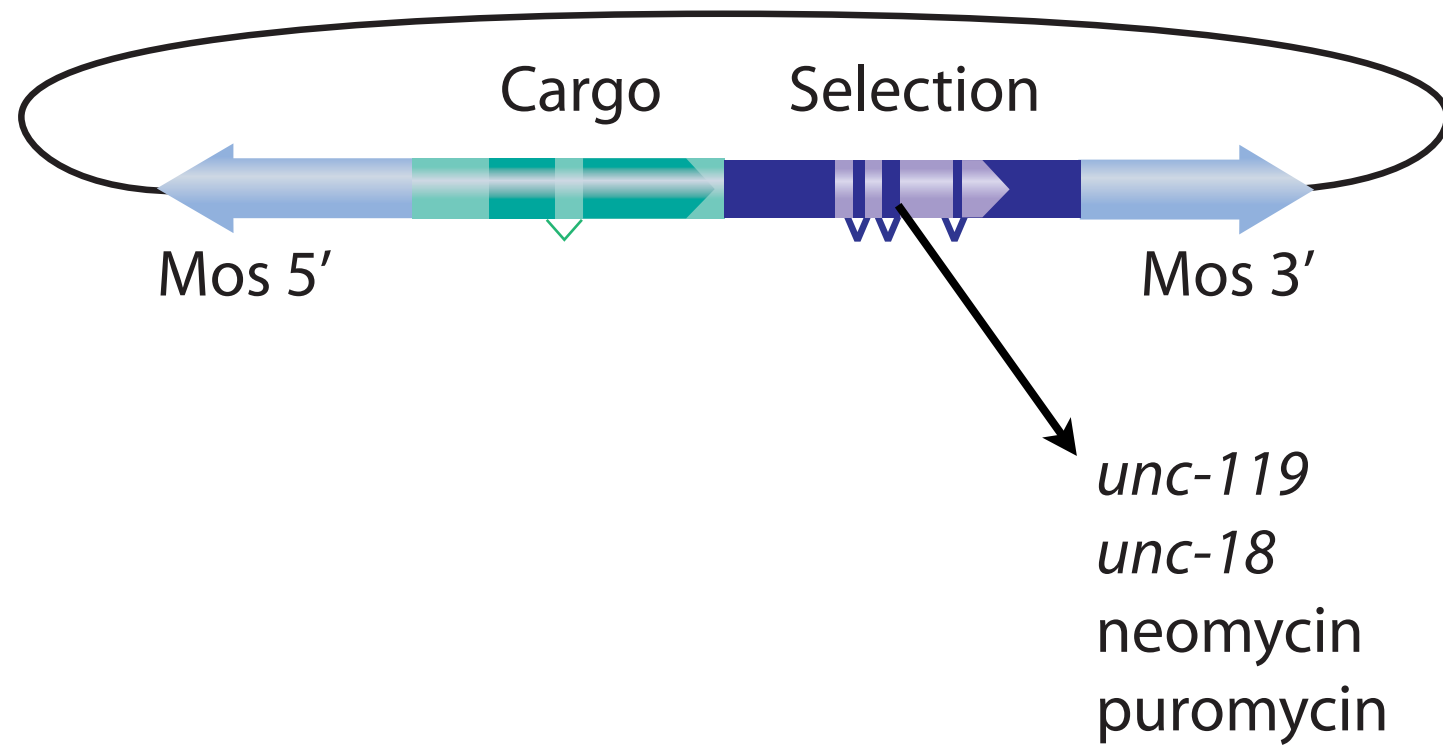
3. www.wormbuilder.org

Reagents, strains and troubleshooting advice

A modified MosI can transpose with cargo in worms

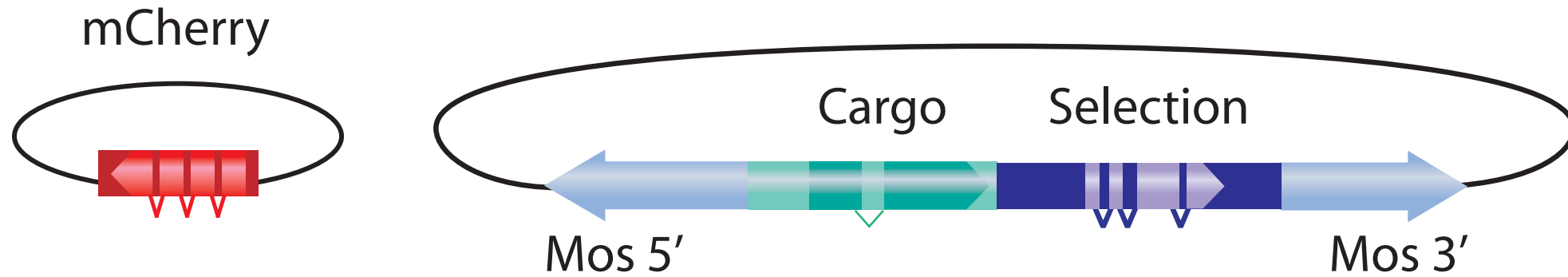


A modified MosI can transpose with cargo in worms



mCherry co-injection plasmid marks array

Injected DNA

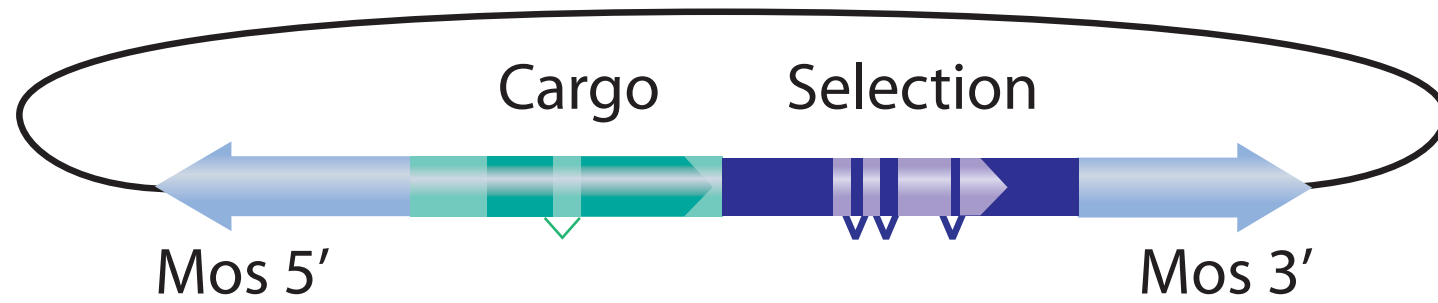
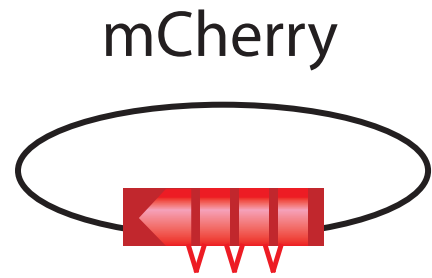


Genomic DNA

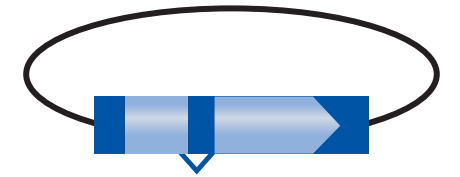


Transposase mobilizes Mos I with cargo

Injected DNA



Mos1 Transposase

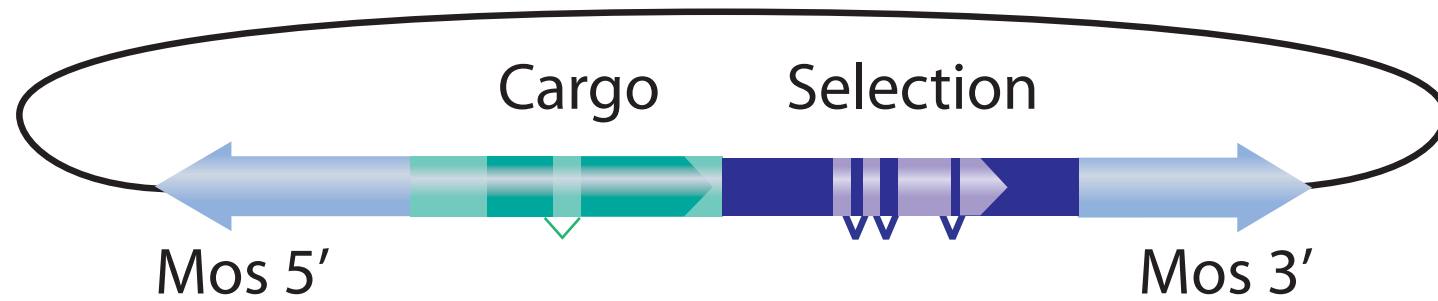
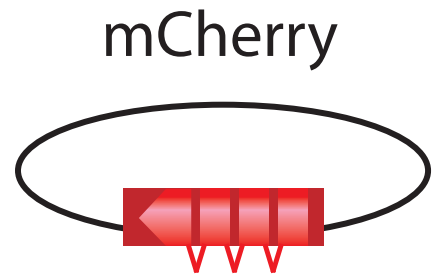


Genomic DNA

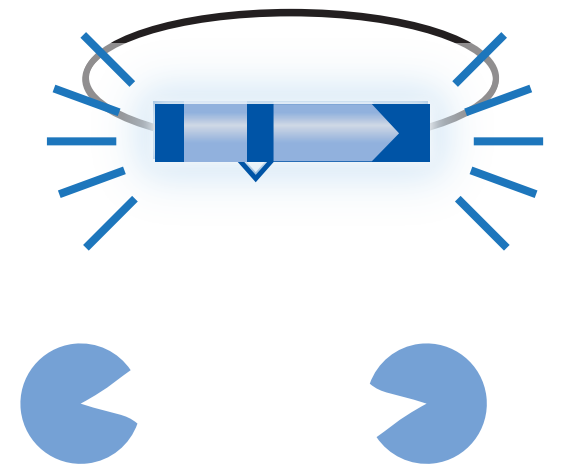


Transposase mobilizes Mos I with cargo

Injected DNA



Mos1 Transposase

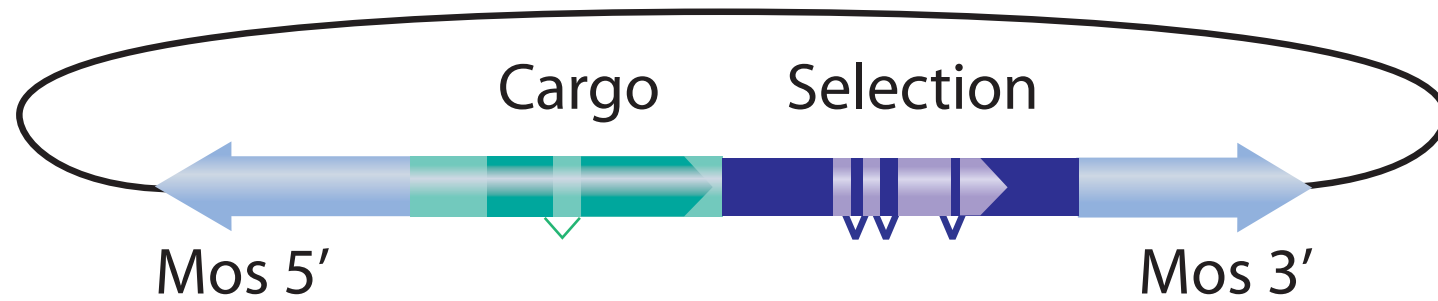
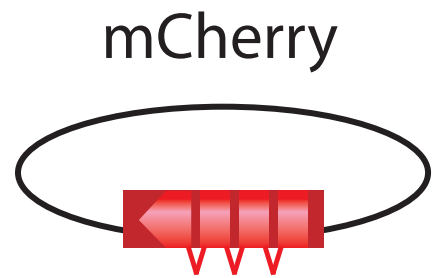


Genomic DNA

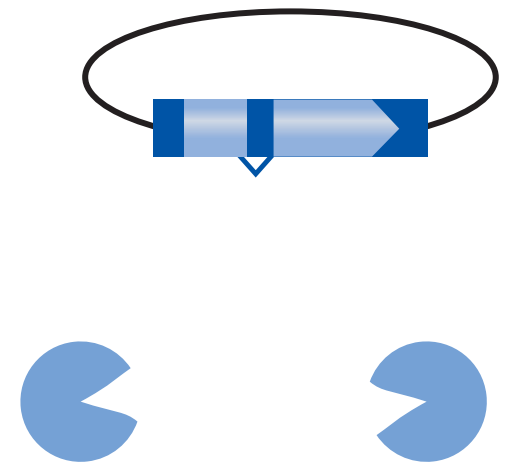


Transposase mobilizes Mos I with cargo

Injected DNA



Mos1 Transposase

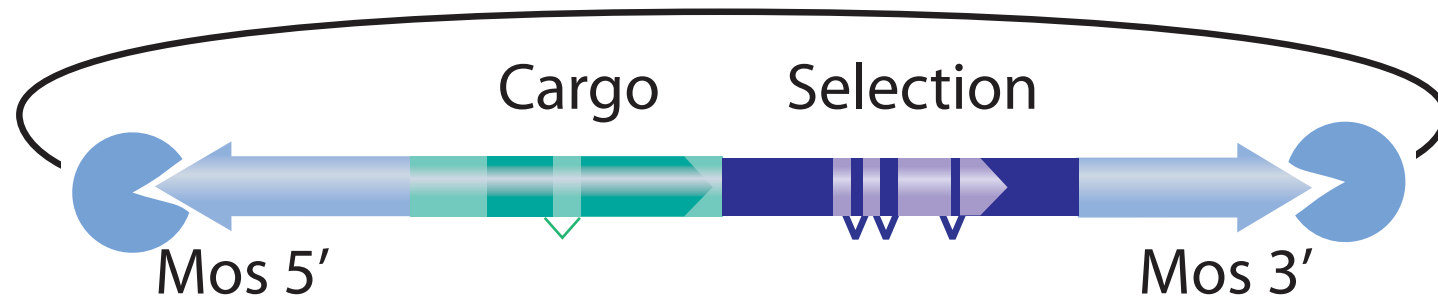
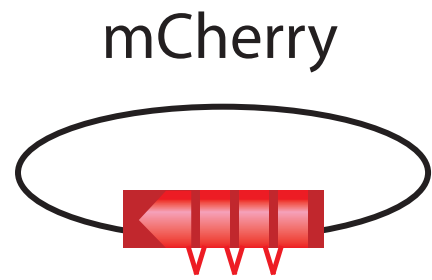


Genomic DNA

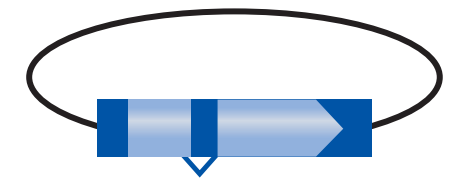


Transposase mobilizes Mos I with cargo

Injected DNA



Mos1 Transposase

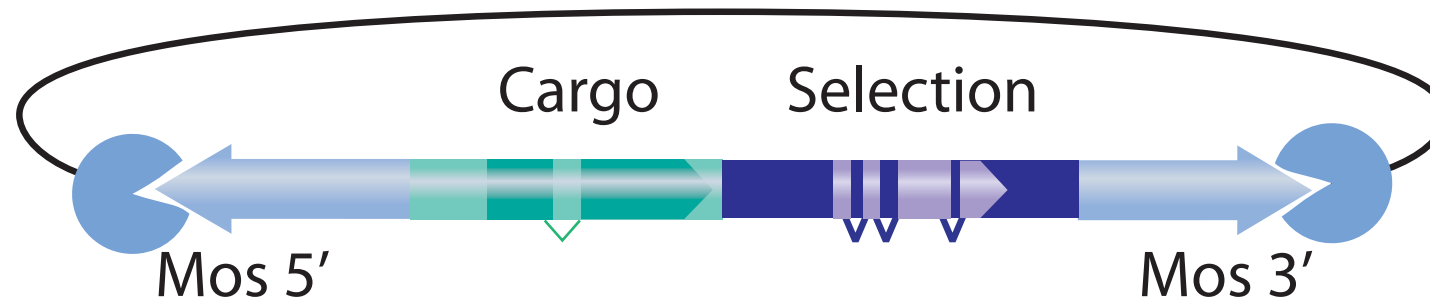
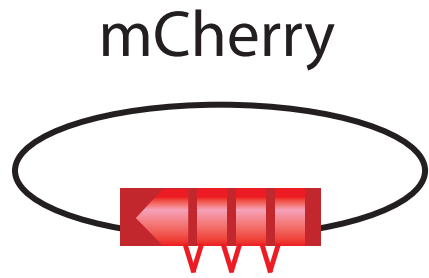


Genomic DNA

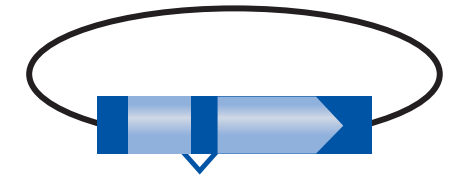


60 % insertion frequency

Injected DNA



Mos1 Transposase



Genomic DNA

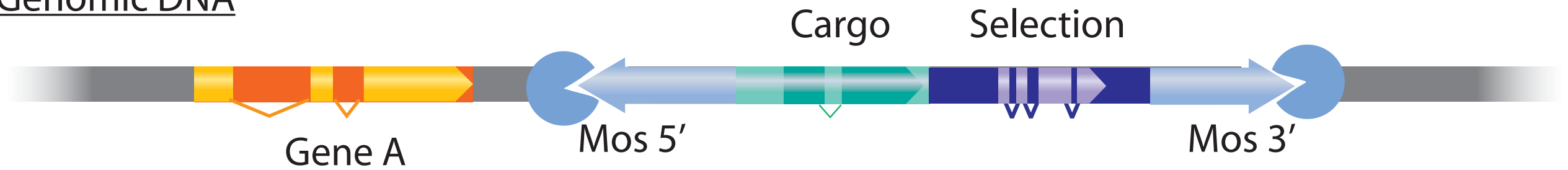


60 % insertion frequency

Injected DNA



Genomic DNA

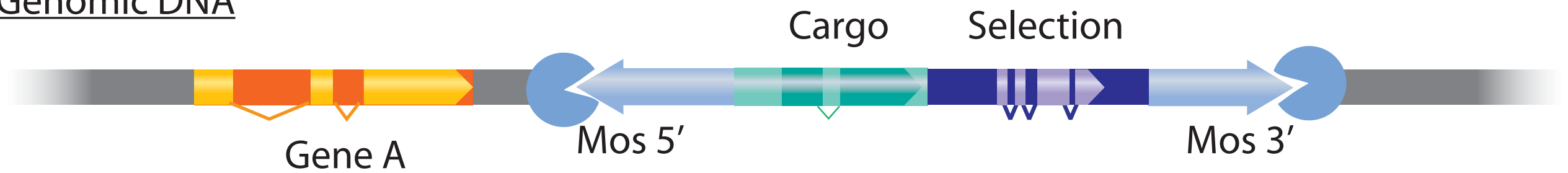


60 % insertion frequency

Injected DNA



Genomic DNA

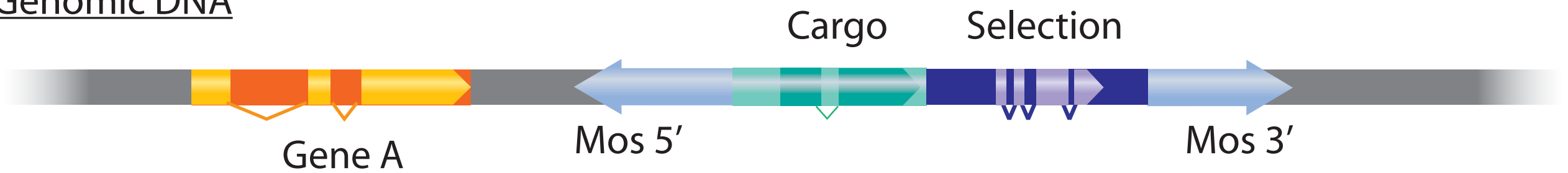


60 % insertion frequency

Injected DNA

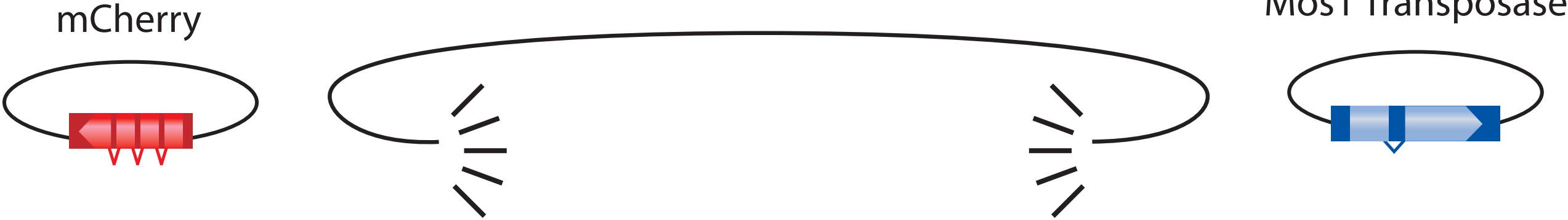


Genomic DNA

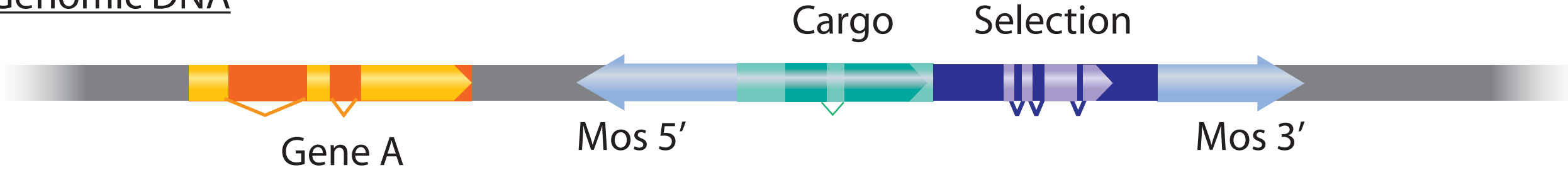


Extrachromosomal array is unstable and lost

Injected DNA

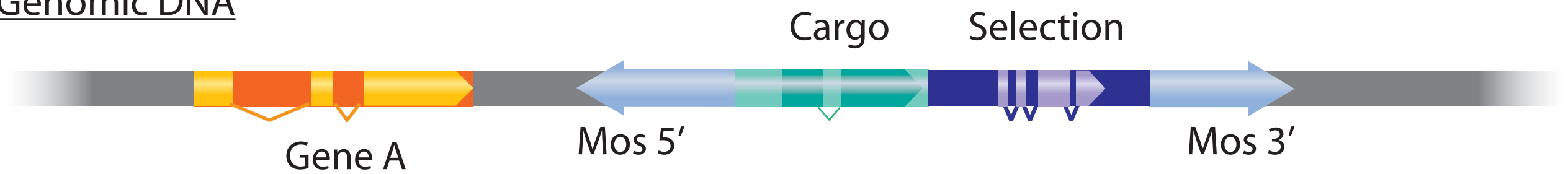


Genomic DNA

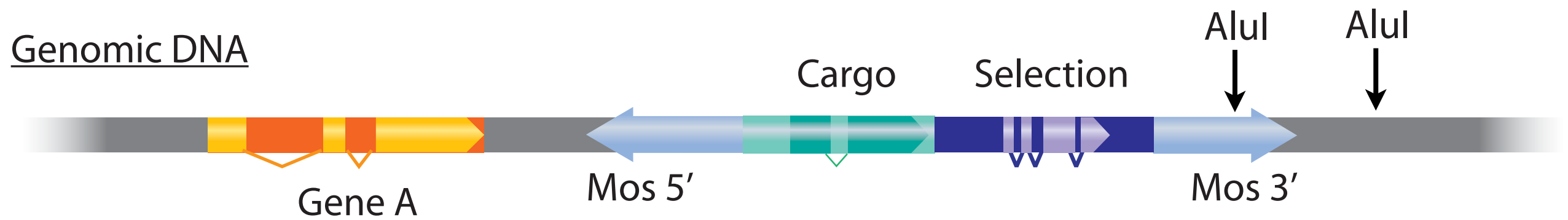


Extrachromosomal array is unstable and lost

Genomic DNA

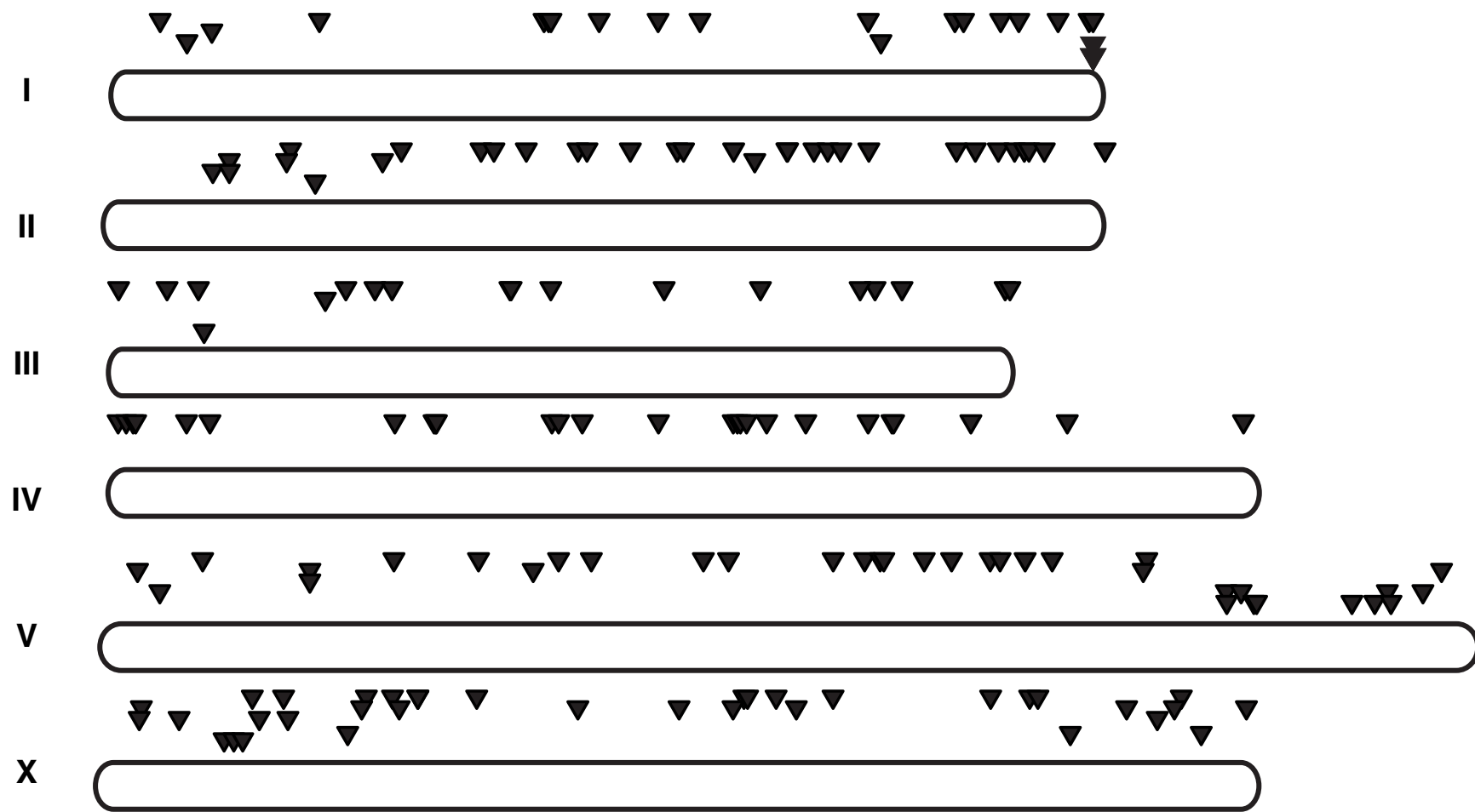


Insertion site can be determined by PCR

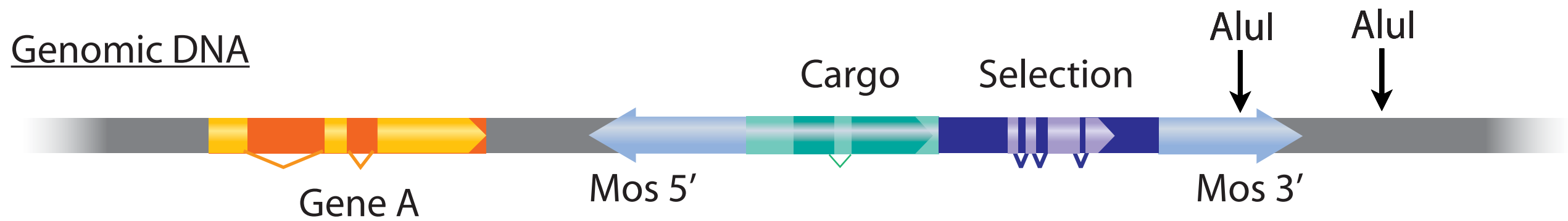


Insertion site can be determined by PCR

Peft-3:tdTomato:H2B insertions

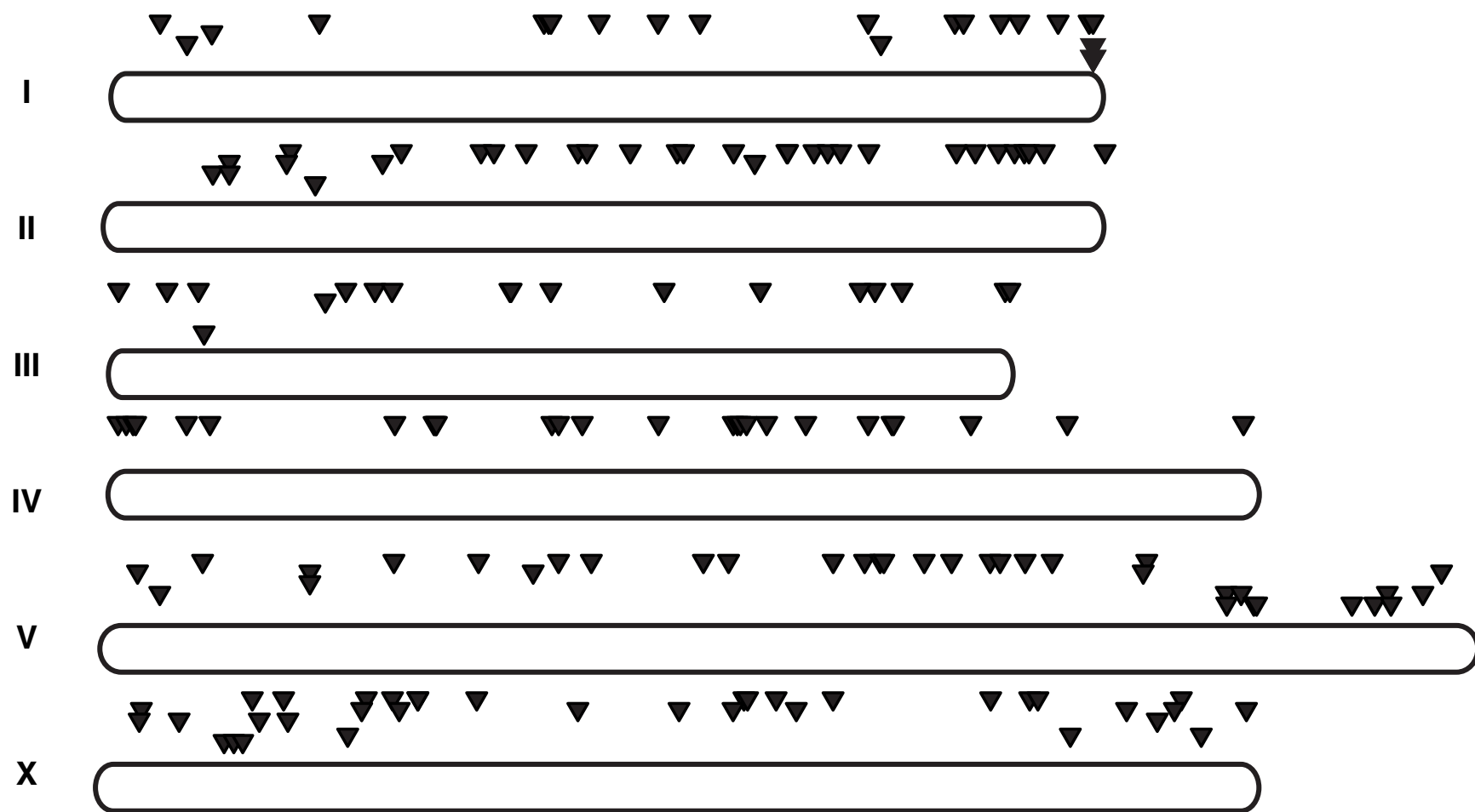


Genomic DNA



Insertion site can be determined by PCR

Peft-3:tdTomato:H2B insertions



These insertions are useful for:

- 1) Moving mutations around (e.g. building doubles and triples)
- 2) Outcrossing mapped mutations
- 3) Mapping new mutations (mapping strains with 3x fluorophores)

Most strains deposited at the CGC

Insertion frequency and fidelity is high

Experiment: Inject a mix of three different miniMos elements
(tdTomato:H2B, mCherry, GFP:H2B)

Injected animal	#1	#2	#3	#4	#5	Total
Singled F1s (rescued)	24	45	40	18	29	156

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Insertions from non-rescued	0	1	0	0	1	2

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Single fluorophore	5	6	1	1	7	20
Multiple fluorophores	0	0	0	0	0	0

Insertion frequency and fidelity is high

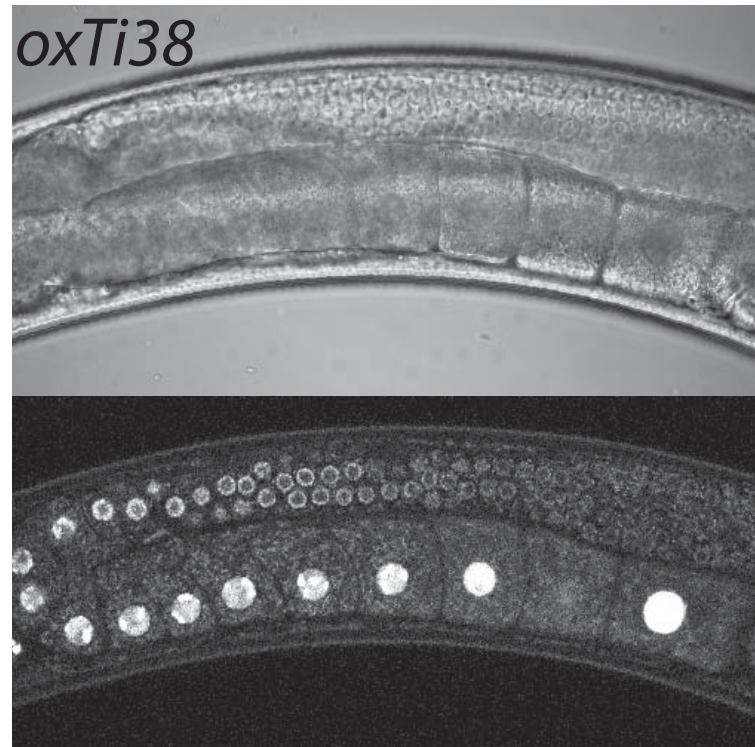
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Single fluorophore	5	6	1	1	7	20
Multiple fluorophores	0	0	0	0	0	0

- 1) Multiple insertions are generated pr. injected worm (1-7 insertions/P0 injected)
- 2) Each strain carries a single transgene insertion
- 3) The fidelity of insertion is high - no non-fluorescent insertions

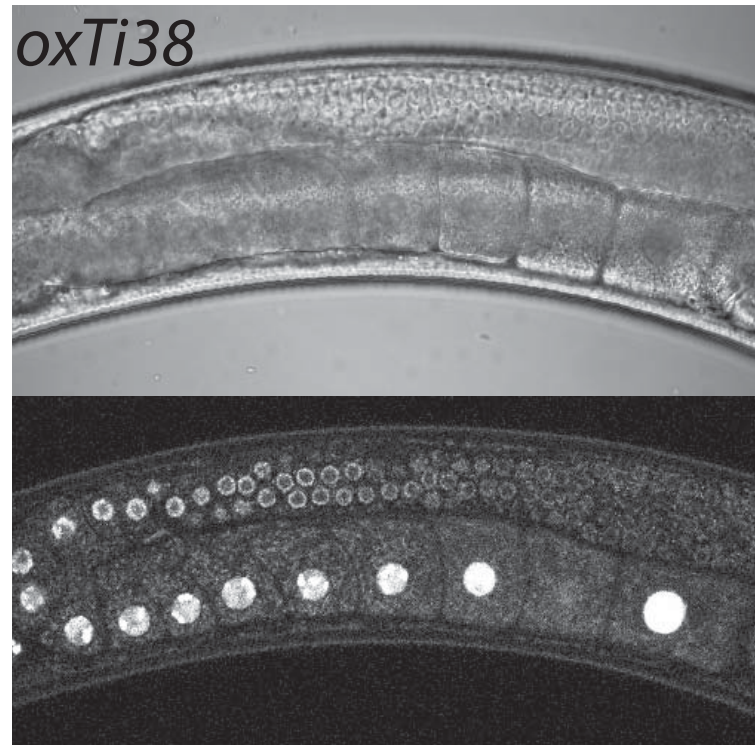
Approx. 50% of insertions are fluorescent in germline

Ppie-1:GFP:H2B

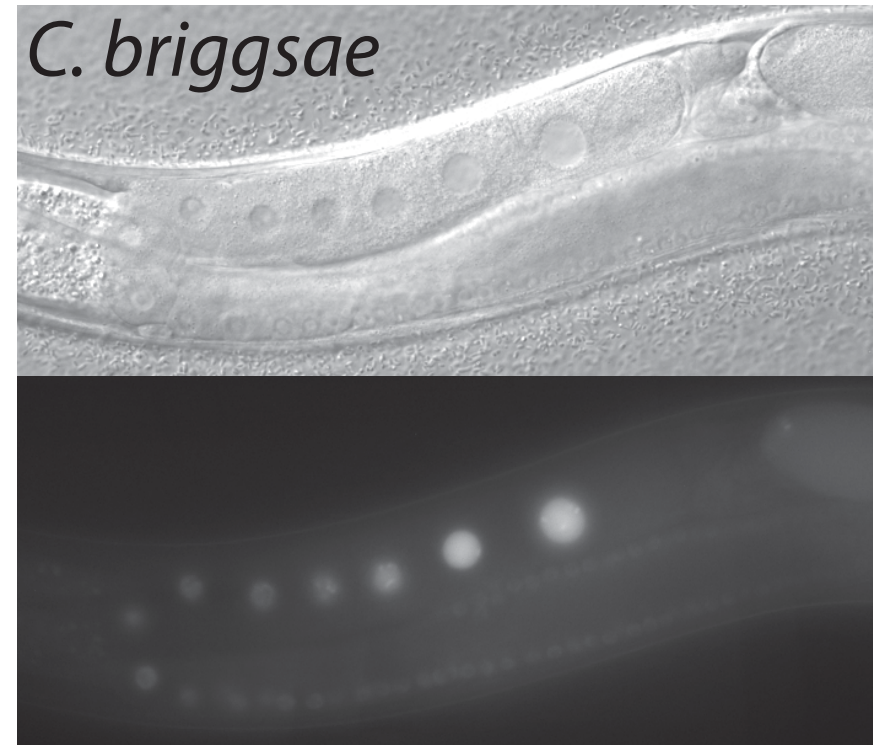


Approx. 50% of insertions are fluorescent in germline

Ppie-1:GFP:H2B



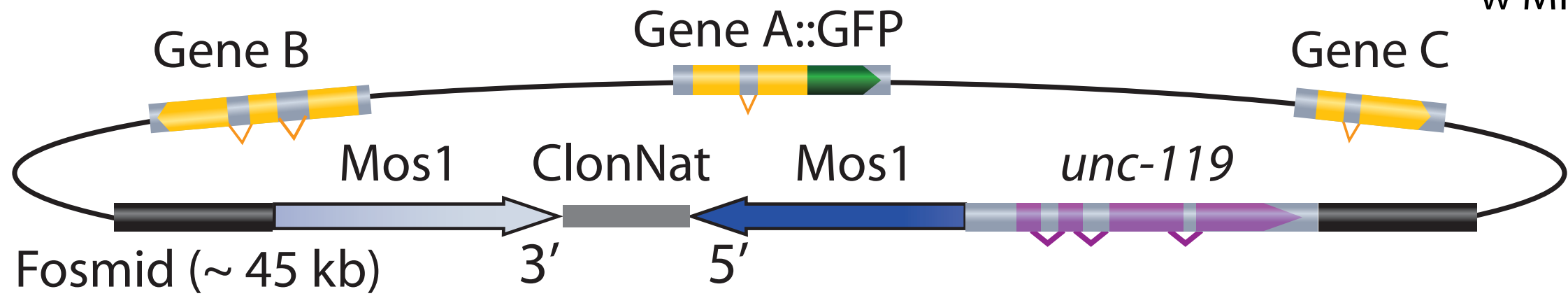
Ppie-1:GFP:H2B



Minimos can carry large transgenes



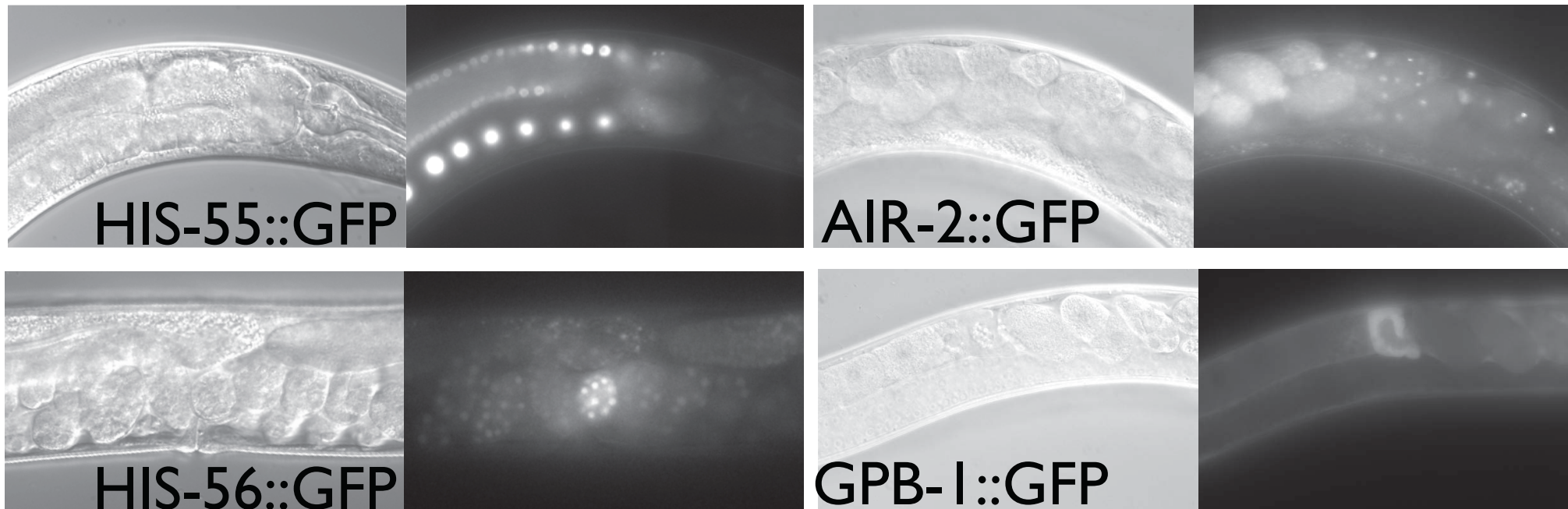
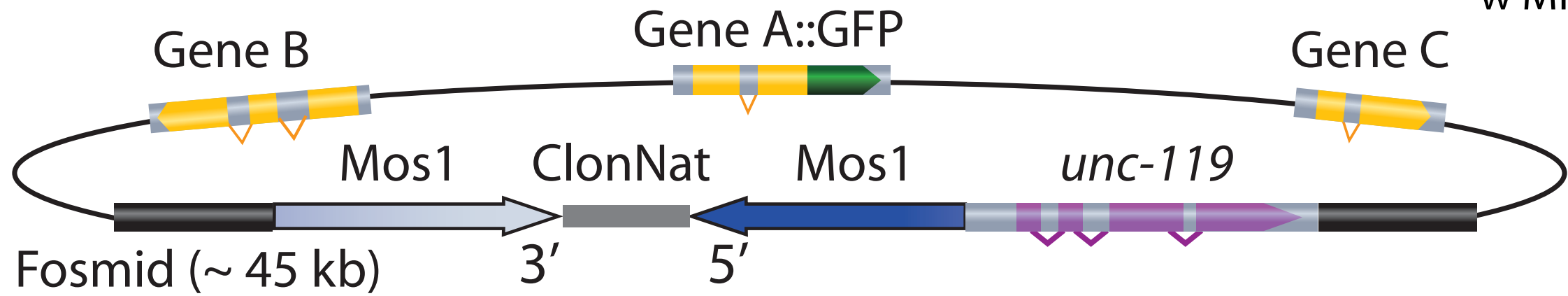
w Mihail Sarov



Minimos can carry large transgenes



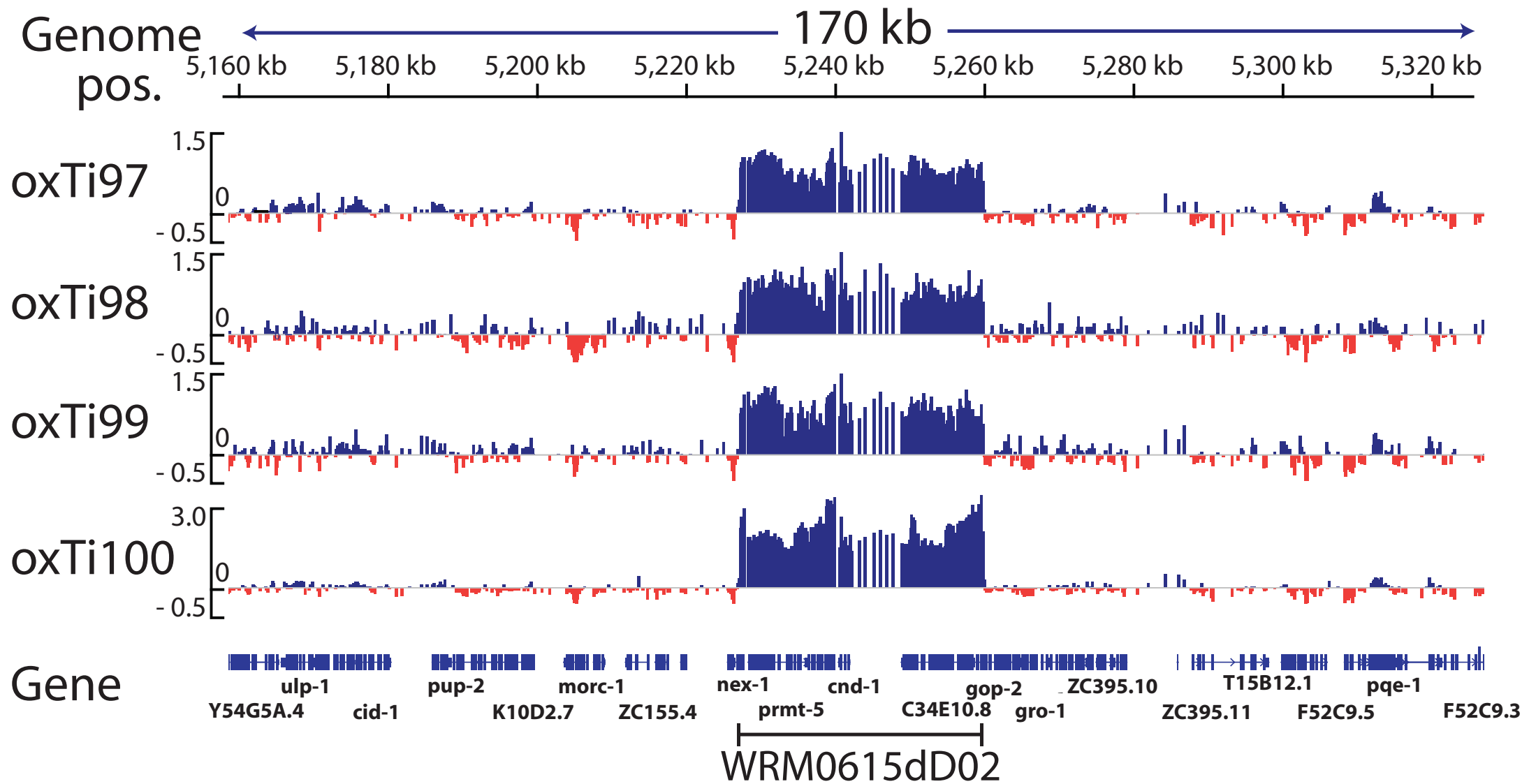
w Mihail Sarov



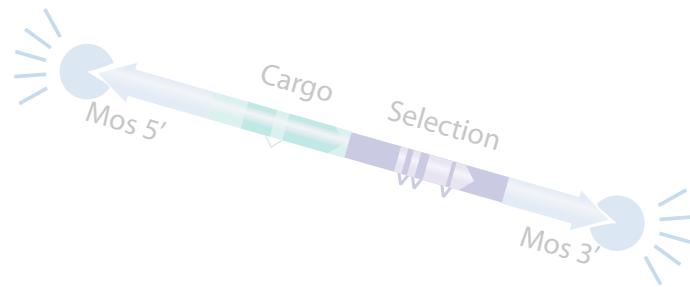
Fully intact fosmids are inserted



w Moerman lab

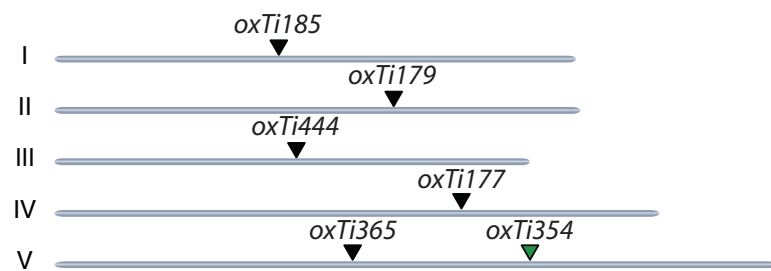


Methods to engineer the genome based on Mos I



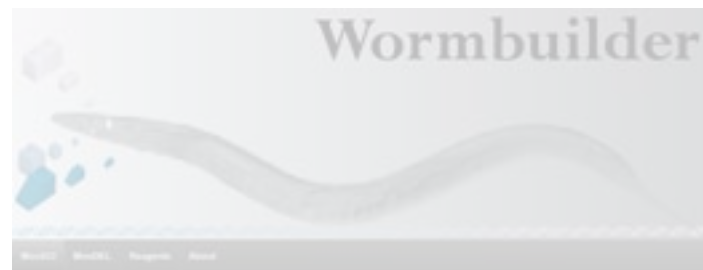
1. MiniMos transposon

Hopping transgenes into the genome



2. Universal MosSCI sites

Targeted insertion at different sites across the genome



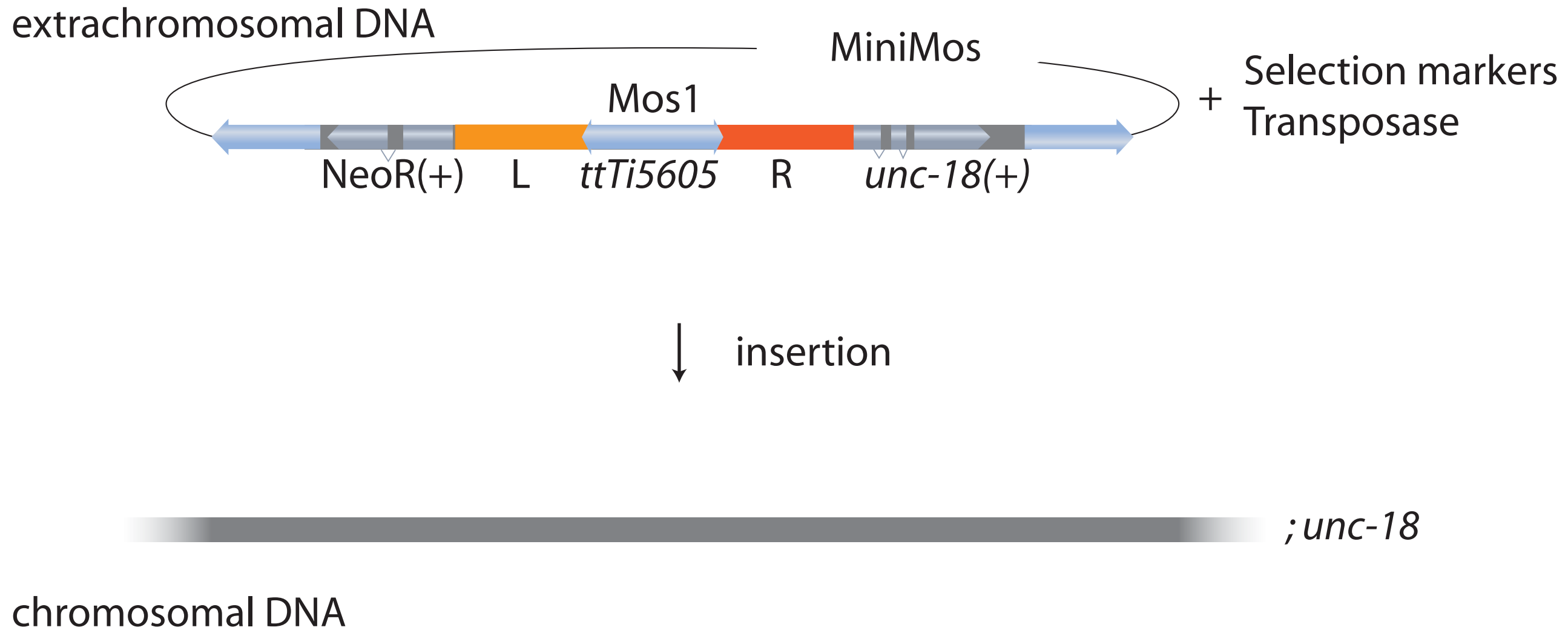
3. www.wormbuilder.org

Reagents, strains and troubleshooting advice

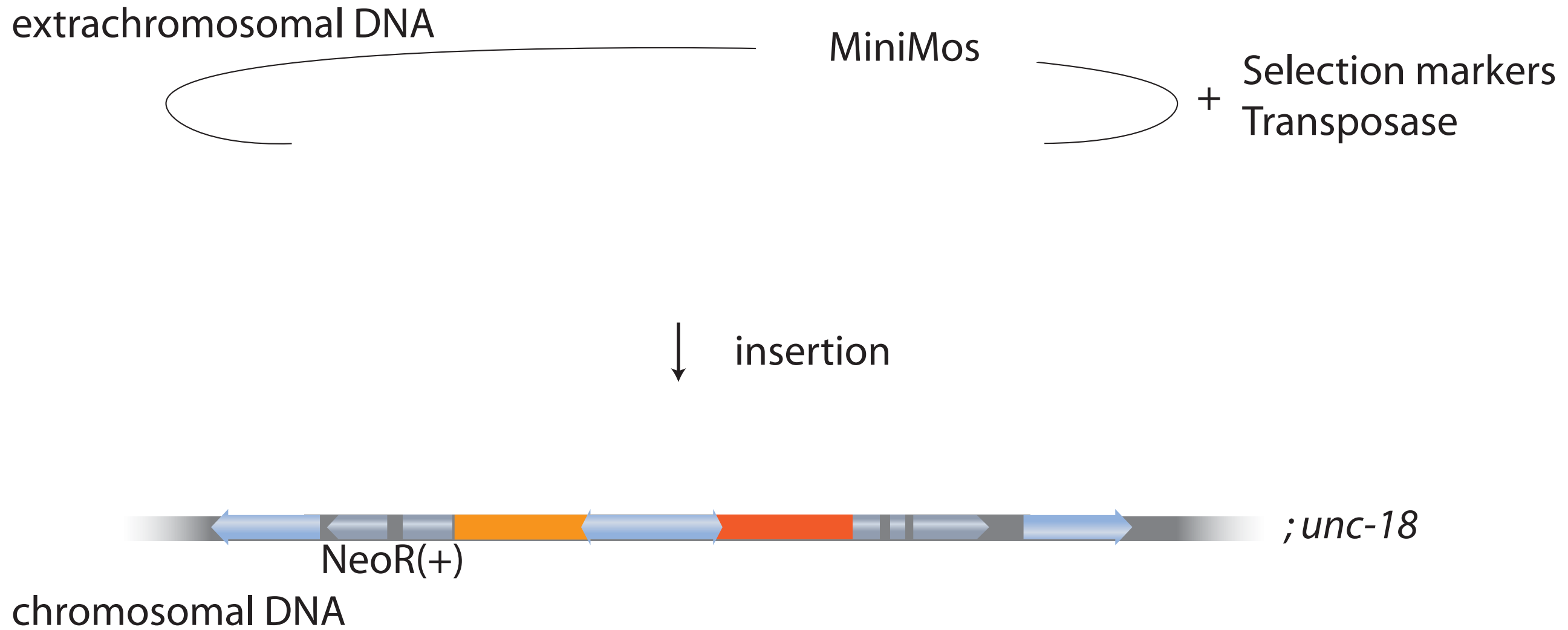
I. Generate universal landing site

chromosomal DNA  ; *unc-18*

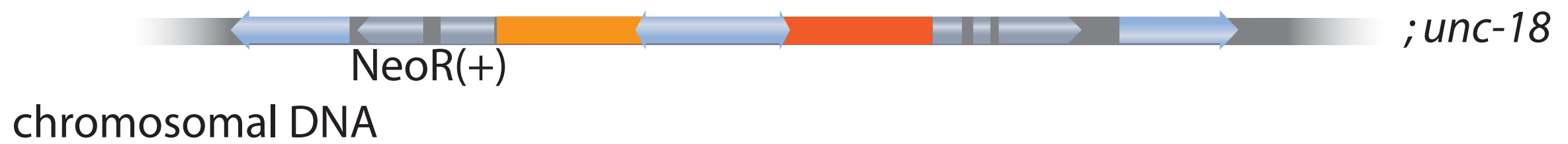
I. Generate universal landing site



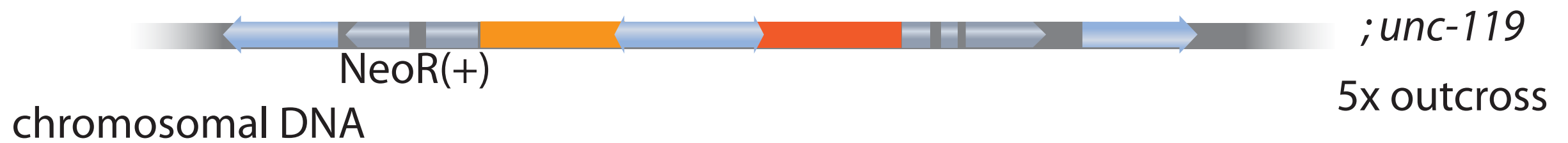
I. Generate universal landing site



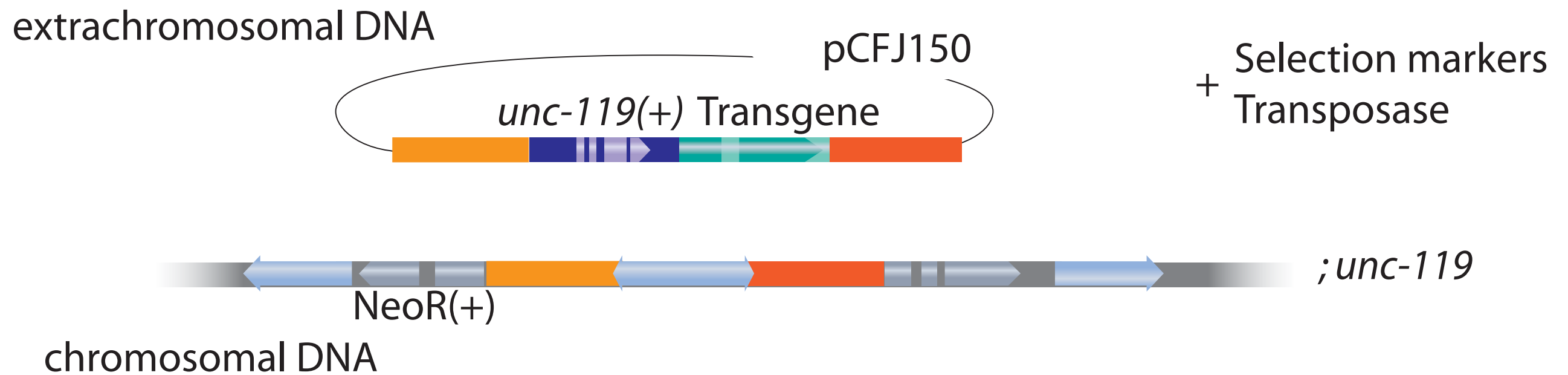
I. Generate universal landing site



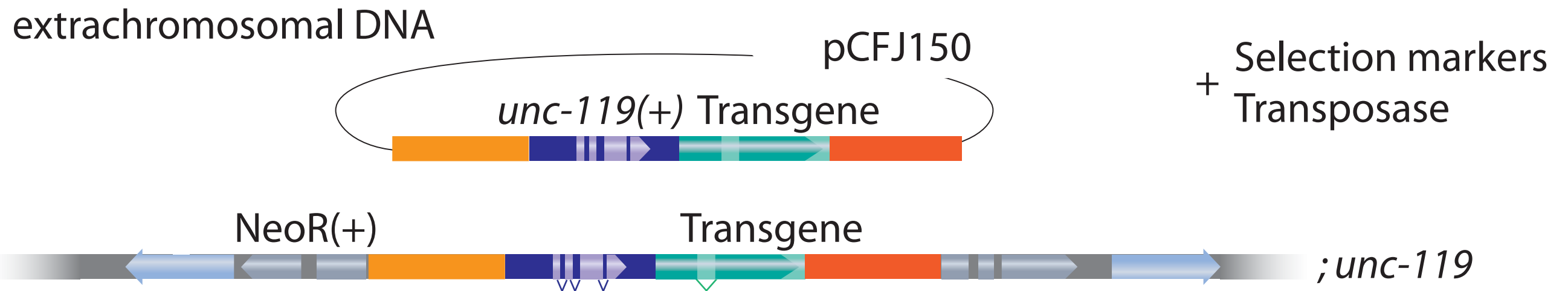
2. Cross into *unc-119* background



3. Inject pCFJ150 based targeting vector



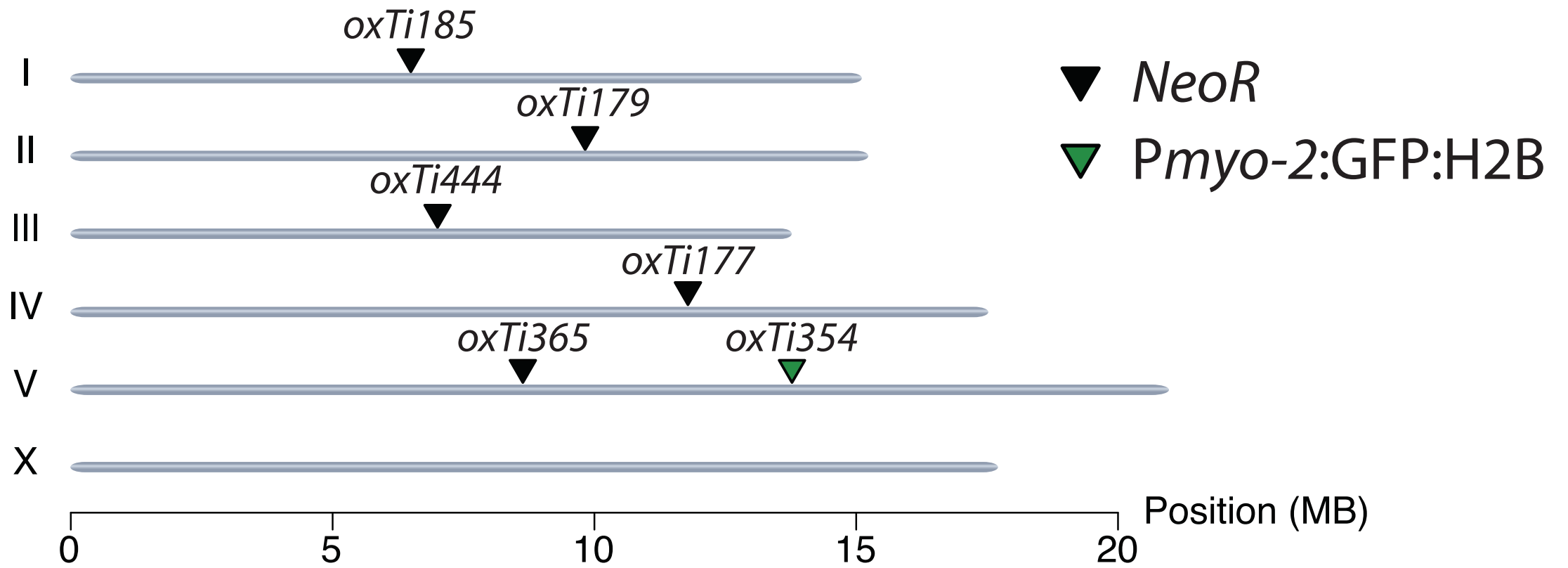
3. Inject pCFJ150 based targeting vector



3. Inject pCFJ150 based targeting vector

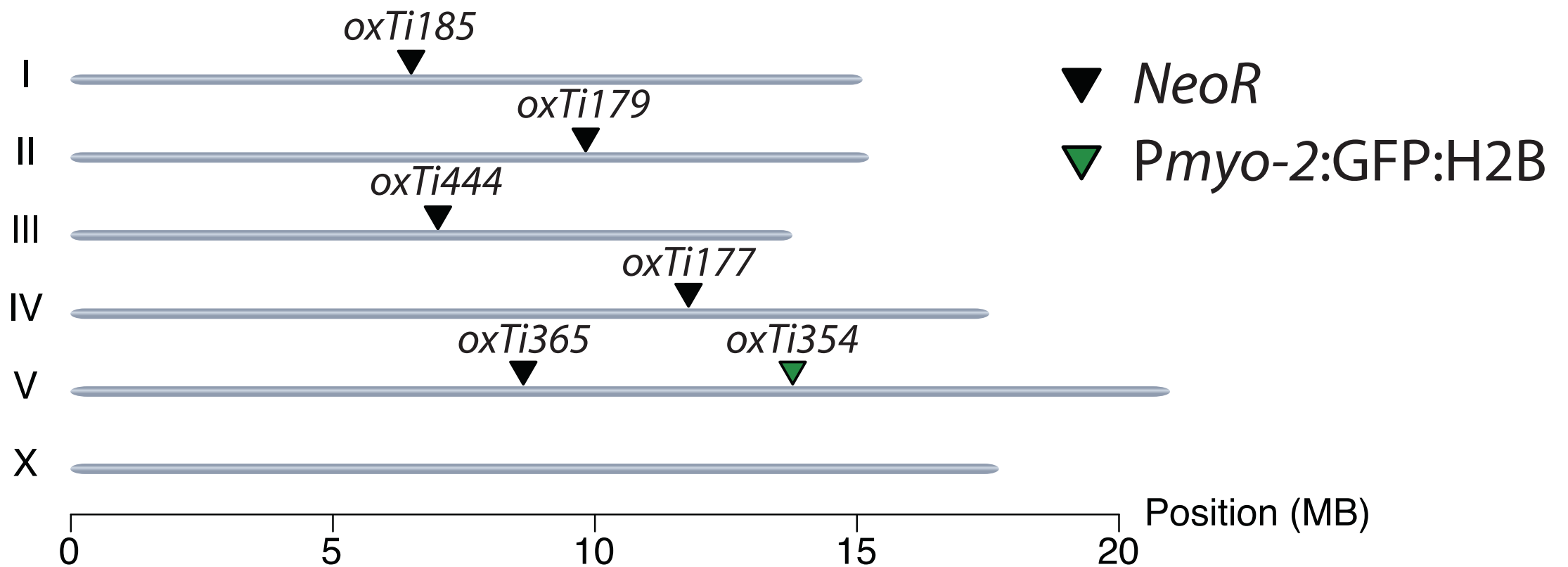


Standard insertion sites



5x outcrossed
Germline fluorescence verified
Available at the CGC

Standard insertion sites

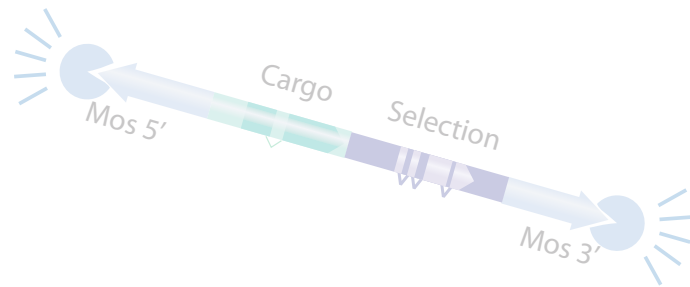


5x outcrossed
Germline fluorescence verified
Available at the CGC

Advantages:

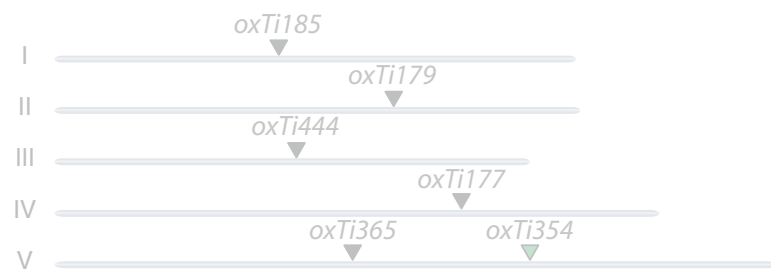
- A single targeting plasmid is compatible with many insertion sites
- Backwards compatible with constructs for Chr. II site (*ttTi5605*)
- MosSCIs can be followed by Neomycin resistance or *Pmyo-2* fluorescence

Methods to engineer the genome based on Mos I



1. MiniMos transposon

Hopping transgenes into the genome



2. Universal MosSCI sites

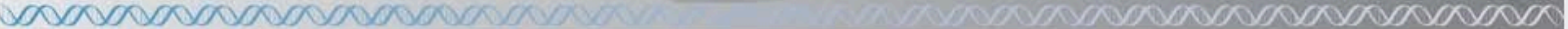
Targeted insertion at different sites across the genome



3. www.wormbuilder.org

Reagents, strains and troubleshooting advice

Wormbuilder



[MosSCI](#) [Universal MosSCI](#) [MosDEL](#) [miniMos](#) [Reagents](#) [Feedback](#) [About](#)

[About MosSCI](#)

[Protocol](#)

[Plasmids](#)

[Insertion strains](#)

[Bright MosSCI inserts](#)

[Comments/FAQ](#)

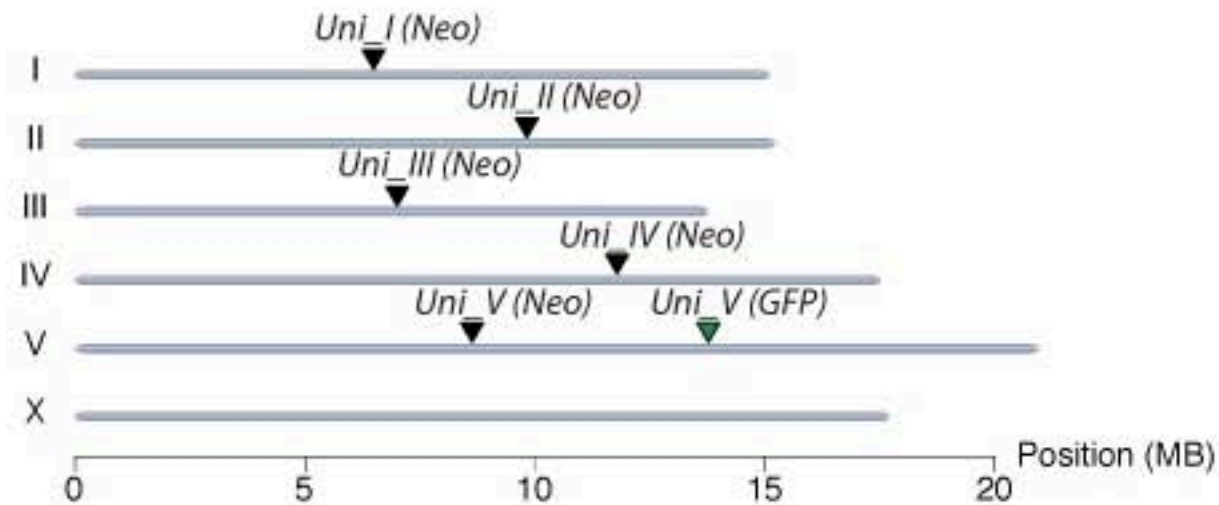
Controlled Single Copy Insertion (mosSCI)

Inserts a single copy of a transgene into a well-defined location in the *C. elegans* genome. The method has the

- Transgenes can be expressed at levels close to endogenous gene expression
- Transgene insertions are stable
- Transgene expression is possible in the germline.

[Home](#) > [Universal MosSCI](#) > Universal MosSCI insertion strains

Universal insertion sites



All universal MosSCI insertion sites are targeted by vectors for the *ttT15605* locus. These vectors include pCFJ150 and pCFJ350.

Insertion site	Locus	Co-insertion marker	Genetic position	Genomic position (WS190)	Genomic environment	Strain	Germline expression
<i>unc-119</i>							
Unil_I (Neo)	<i>oxT1185</i>	NeoR + <i>unc-18(+)</i>	I:1.17	I: 6,503,678	Intergenic	EG8078	Yes
Uni_II (Neo)	<i>oxT1179</i>	NeoR + <i>unc-18(+)</i>	II:1.73	II: 9,833,502	In ZK938.3	EG8079	Yes
Uni_III (Neo)	<i>oxT1444</i>	NeoR + <i>unc-18(+)</i>	III:-0.85	III: 7,014,336	In Igc-38	EG8080	Yes
Unil_V (Neo)	<i>oxT1177</i>	NeoR + <i>unc-18(+)</i>	IV:7.43	IV: 13,048,924	In scl-10	EG8081	Yes

- About reagents
- Fluorescent marker strains
- LacO insertions

[Home](#) › [Reagents](#) › Fluorescent marker strains

Use search box to limit strains to chromosomes (LG1, LG2 etc) or fluorophores (GFP, mCherry, tdTomato).

Please request strains from the [CGC](#).

Strain column has link to the strain info at the CGC.

Show entries

Search:

Chr.	Genetic pos.	Position (WB230)	Promoter	Fluorophore	Allele	Strain	Insertion marker(s)
LG1	l:-18.63	657,302	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi550</i>	EG8004	<i>cb-unc-119(+)</i>
LG1	l:-16.97	1,070,957	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi648</i>	EG7831	<i>cb-unc-119(+)</i>
LG1	l:-14.67	1,455,659	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi638</i>	EG7832	<i>cb-unc-119(+)</i>
LG1	l:-4.48	3,116,556	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi559</i>	EG7833	<i>cb-unc-119(+)</i>
LG1	l:1.23	6,585,618	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi556</i>	EG7835	<i>cb-unc-119(+)</i>
LG1	l:1.28	6,656,763	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi587</i>	EG7836	<i>cb-unc-119(+)</i>
LG1	l:1.29	6,692,324	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi712</i>	EG7837	<i>cb-unc-119(+)</i>
LG1	l:2.07	7,436,394	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi718</i>	EG7838	<i>cb-unc-119(+)</i>
LG1	l:2.75	8,346,811	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi623</i>	EG7839	<i>cb-unc-119(+)</i>
LG1	l:3.35	8,993,439	<i>Peft-3</i>	tdTomato:H2B	<i>oxTi590</i>	EG7840	<i>cb-unc-119(+)</i>

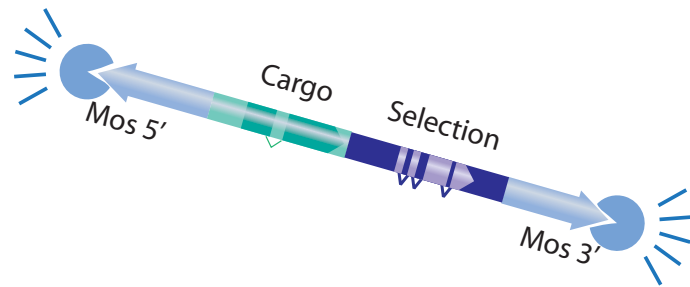


[Edit](#)

Showing 1 to 10 of 158 entries

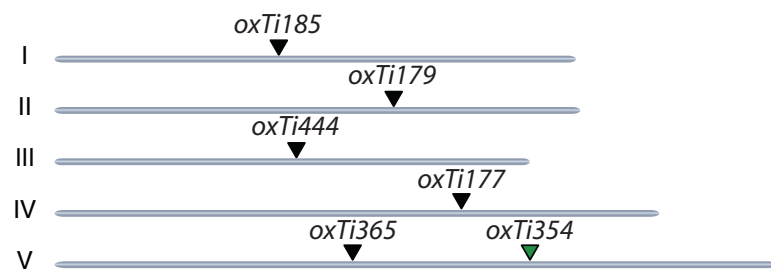
◀ Previous [Next](#) ▶

Methods to engineer the genome based on Mos I



1. MiniMos transposon

- High efficiency
- High fidelity
- Versatile: *C. elegans*, *C. briggsae* and natural isolates
- High frequency of germline expression
- Can carry large transgenes



2. Universal MosSCI sites

- All insertion sites compatible with one targeting vector
- Easier to follow insertion in crosses
- Strains available at CGC



3. www.wormbuilder.org

- Protocols & Reagents
- Search for Universal insertion sites or bright markers
- Troubleshooting advice

Acknowledgements

HHMI, University of Utah

Erik M Jorgensen
M Wayne Davis



Max Planck Institute, Dresden

Mihail Sarov



University of British Columbia, Vancouver

Don Moerman
Stephane Flibotte
Jon Taylor



Postdoctoral funding

LUNDBECKFONDEN



Project funding



Saturday 3:30 - 5:00 pm

Poster 1216C

MiniMos and Universal MosSCI sites

Thanks to Rosina Giordano-Santini & Denis Dupuy for antibiotic reagents.