

# The Incredible Shrinking Genome

## *Utricularia gibba*

**Enrique Ibarra-Laclette<sup>2</sup>, Eric Lyons<sup>1</sup>**, Gustavo Hernandez<sup>3</sup>, Anahi Perez-Torres<sup>2</sup>, Lorenzo Carretero-Paulet<sup>4</sup>, Tien-Hao Chang<sup>4</sup>, Tianying Lan<sup>4</sup>, Andreanna Welch<sup>4</sup>, Maria Jazmin Abraham Juarez<sup>2</sup>, June Simpson<sup>2</sup>, Araceli Fernandez-Cortez<sup>2</sup>, Mario Arteaga-Vazquez<sup>5</sup>, Elsa Gongora-Castillo<sup>6</sup>, Gustavo Acevedo-Hernandez<sup>7</sup>, Stephan C. Schuster<sup>8</sup>, Heinz Himmelbauer<sup>9</sup>, Andre E. Minoche<sup>9</sup>, Sen Xu<sup>10</sup>, Michael Lynch<sup>10</sup>, Araceli Oropeza-Aburto<sup>2</sup>, Sergio Alan Cervantes-Perez<sup>2</sup>, Maria de Jesus Ortega-Estrada<sup>2</sup>, Jacob Israel Cervantes-Luevano<sup>2</sup>, Todd P. Michael<sup>11</sup>, Todd C. Mockler<sup>12</sup>, Doug Bryant<sup>12</sup>, Alfredo Herrera-Estrella<sup>2</sup>, **Victor A. Albert<sup>4</sup>, Luis Herrera-Estrella<sup>2</sup>**

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2 *CINVESTAV*

3 *Universidad de Guanajuato*

4 *University at Buffalo*

5 *Instituto de Biotecnología y Ecología Aplicada*

6 *Michigan State University*

7 *Centro Universitario de la Ciénega*

8 *Pennsylvania State University*

9 *Center for Genomic Regulation, CRG*

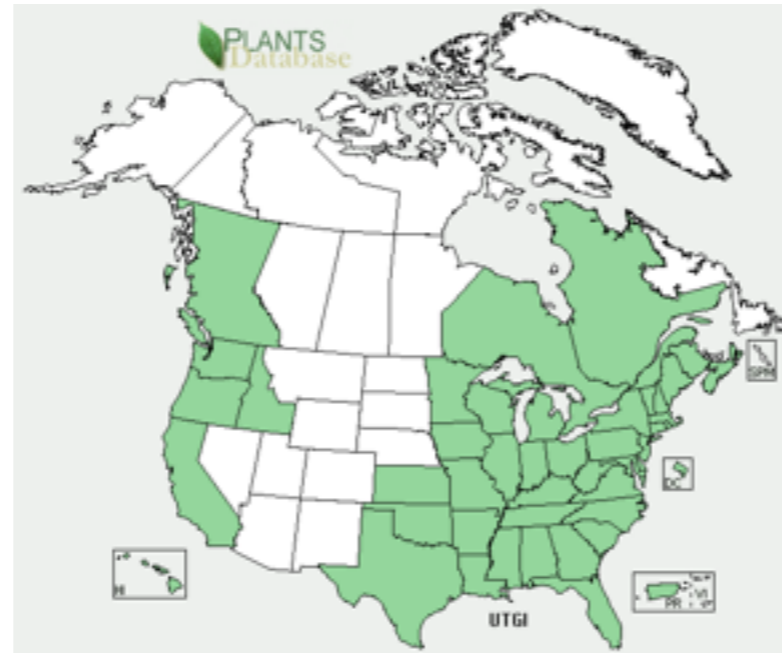
10 *Indiana University*

11 *Rutgers University*

12 *Donald Danforth Plant Science Center*

# Who is *Utricularia gibba*?

The humped bladderwort



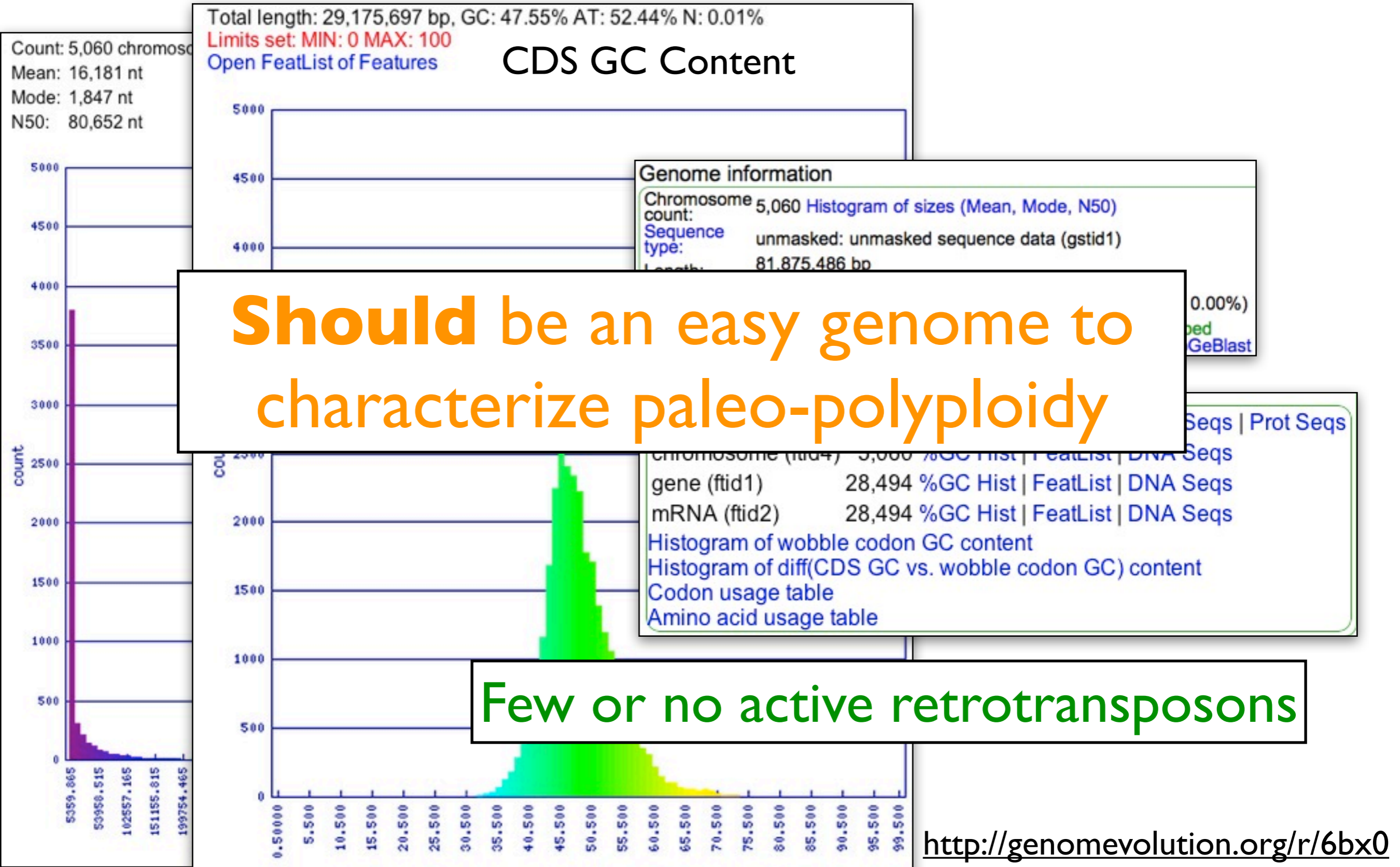
source: USDA



source:  
The Royal  
Society

# U. gibba: genome stats

~82MB genome size



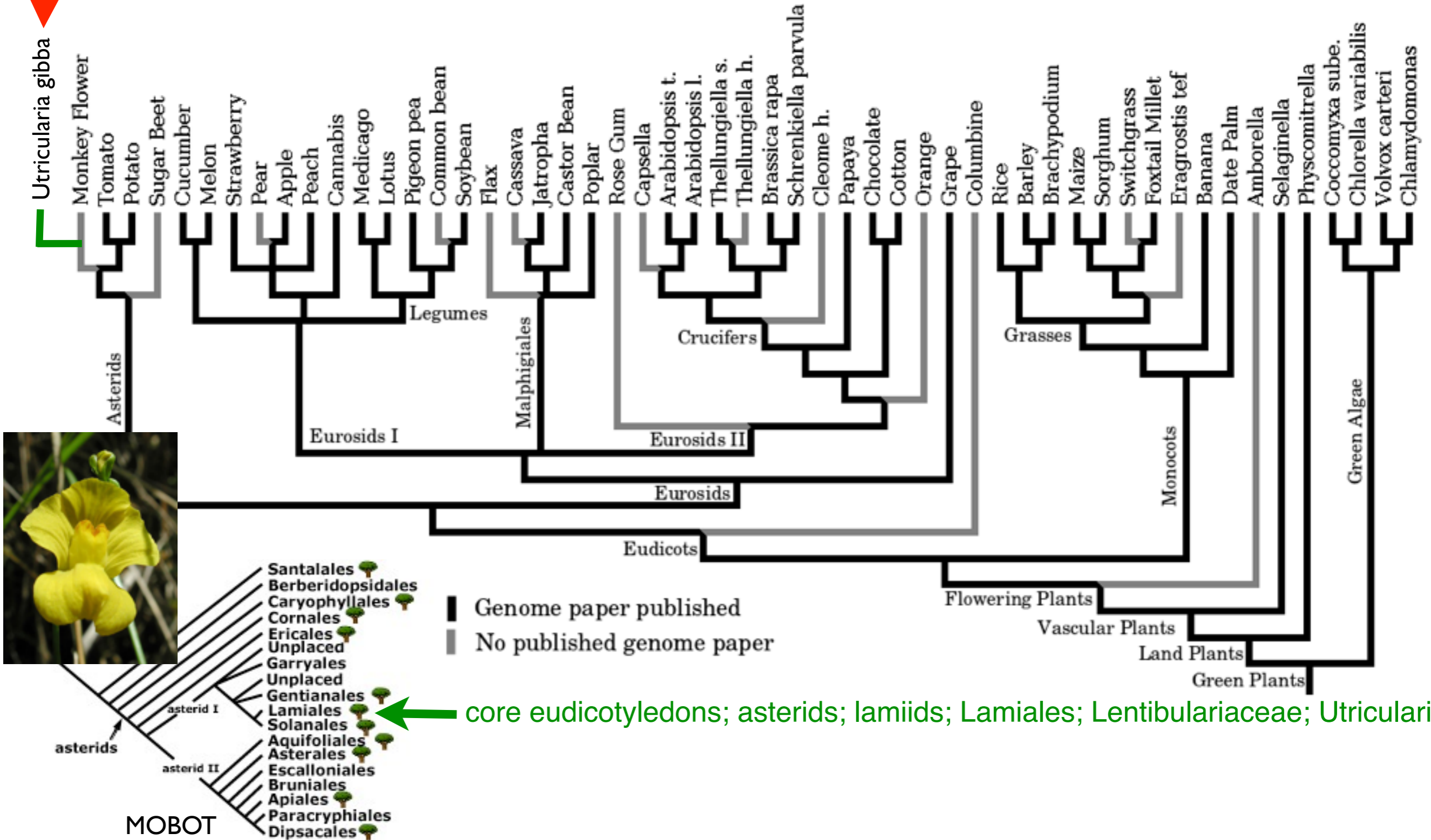
# Sequenced Plant Genomes

<http://genomeevolution.org/r/3118>

Thanks: James Schnable



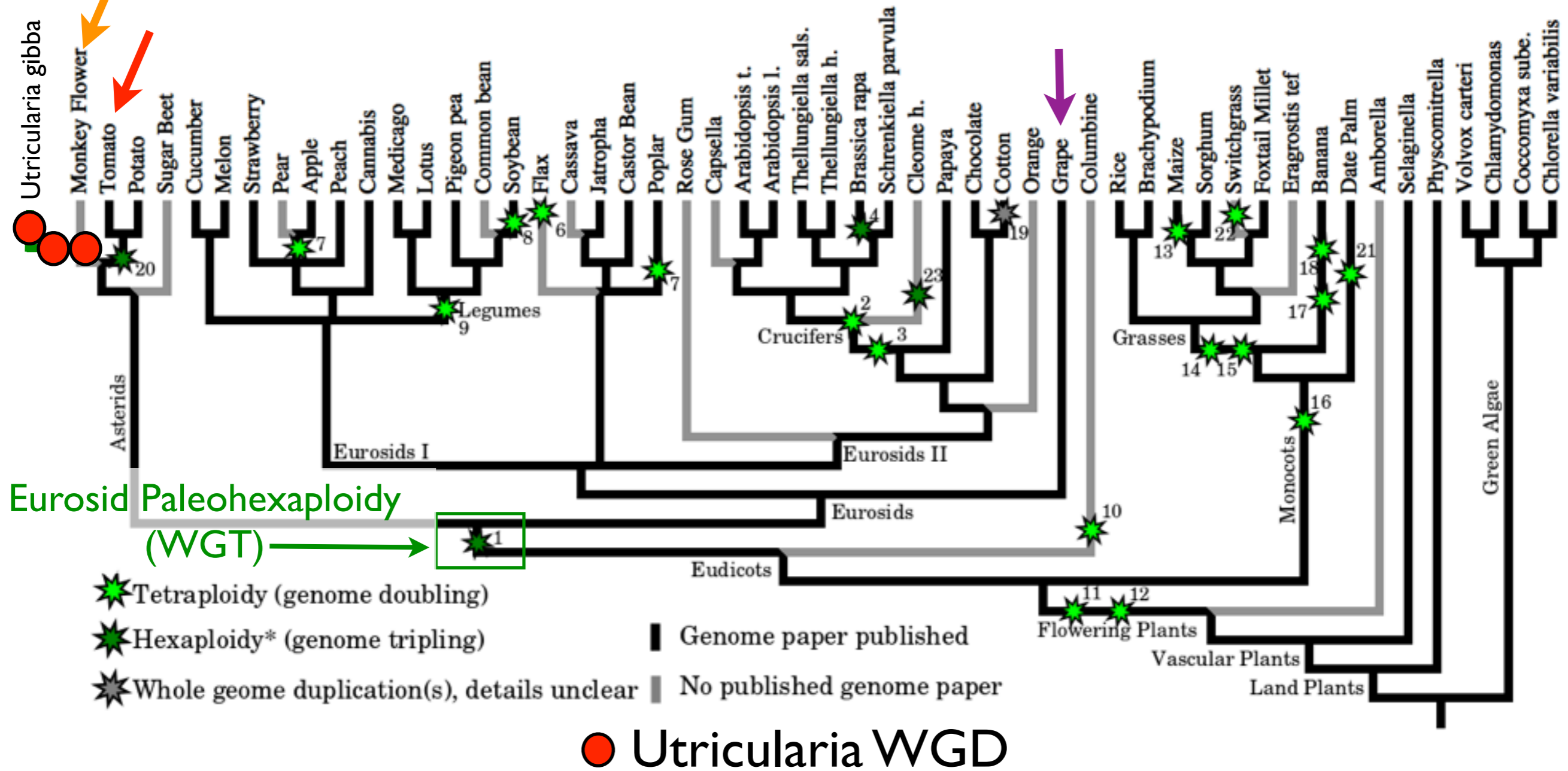
*Utricularia gibba*



MOBOT

# Characterizing paleo-polyploidy

<http://polyploidy.iplantc.org>



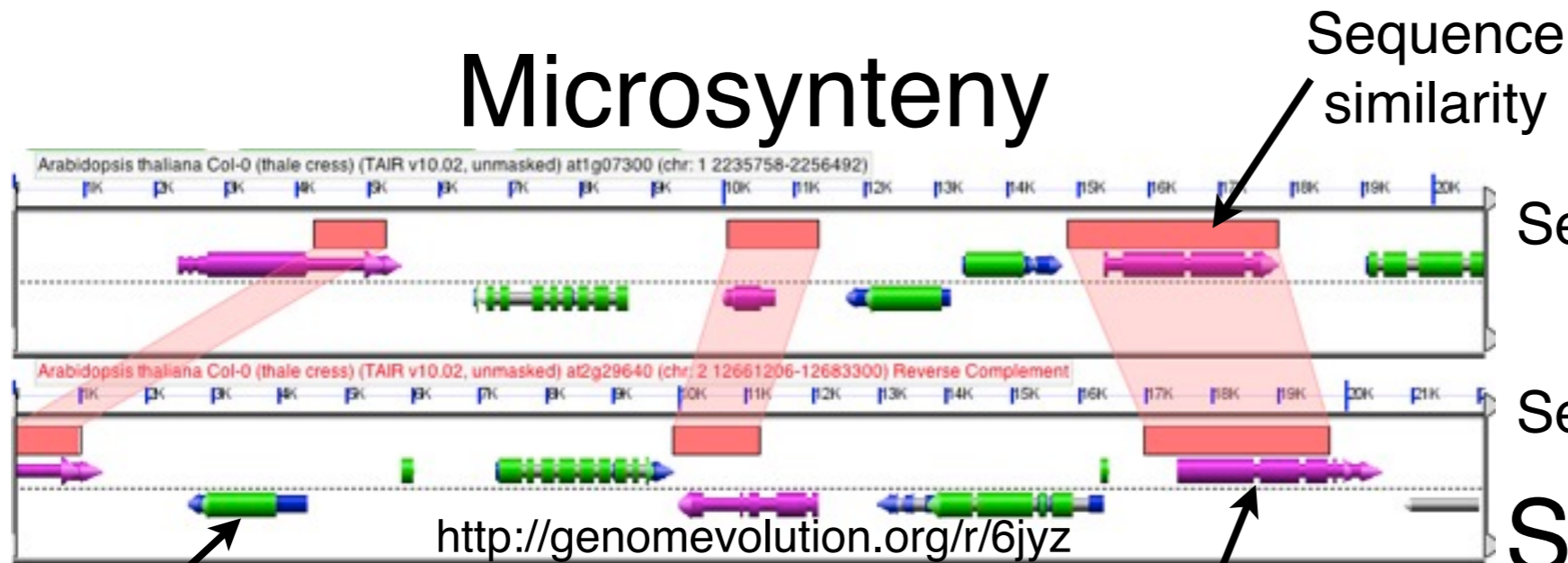
Mimulus is closest, but under-characterized

Tomato is well characterized, but has a WGT

Grape is the de facto eurosid outgroup comparator

# Comparative Genomics

## Microsynteny



Sequence 1

Sequence 2

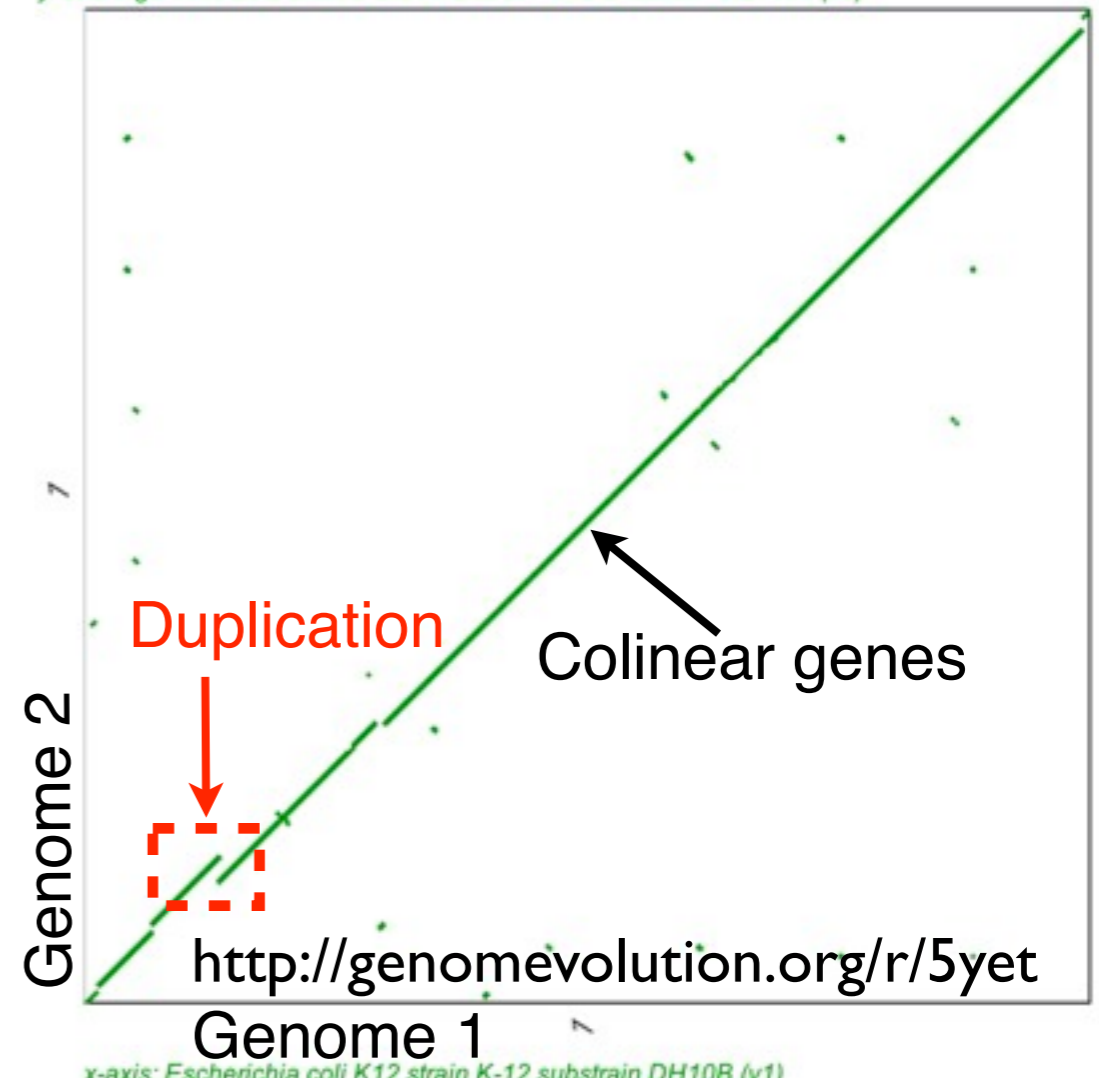
## Syntenic dotplot

Gene model

CoGe link to  
regenerate the analysis

Gene overlapped  
by sequence similarity

y-axis organism: *Escherichia coli* K12 strain K-12 substrain MG1655 (v2)



**Synteny: genomic regions sharing a common ancestry**

**Synteny: inferred by a colinear arrangement of homologous genes**

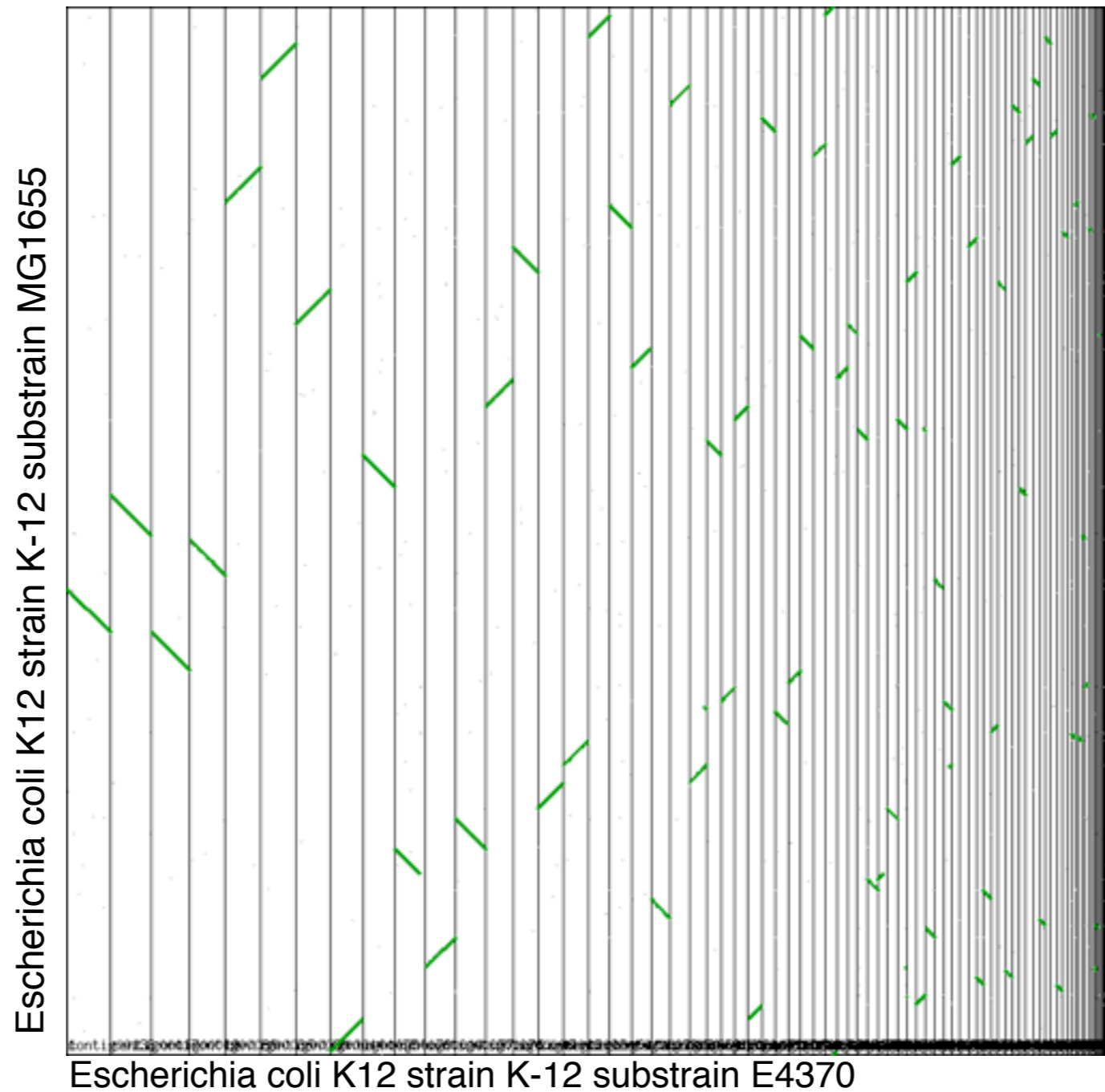
# Syntenic Path Assembly

Making sense of NextGen Genome Assemblies

Utricularia: NextGen Assembly  
with ~5000 contigs

# Syntenic Path Assembly

Making sense of NextGen Genome Assemblies

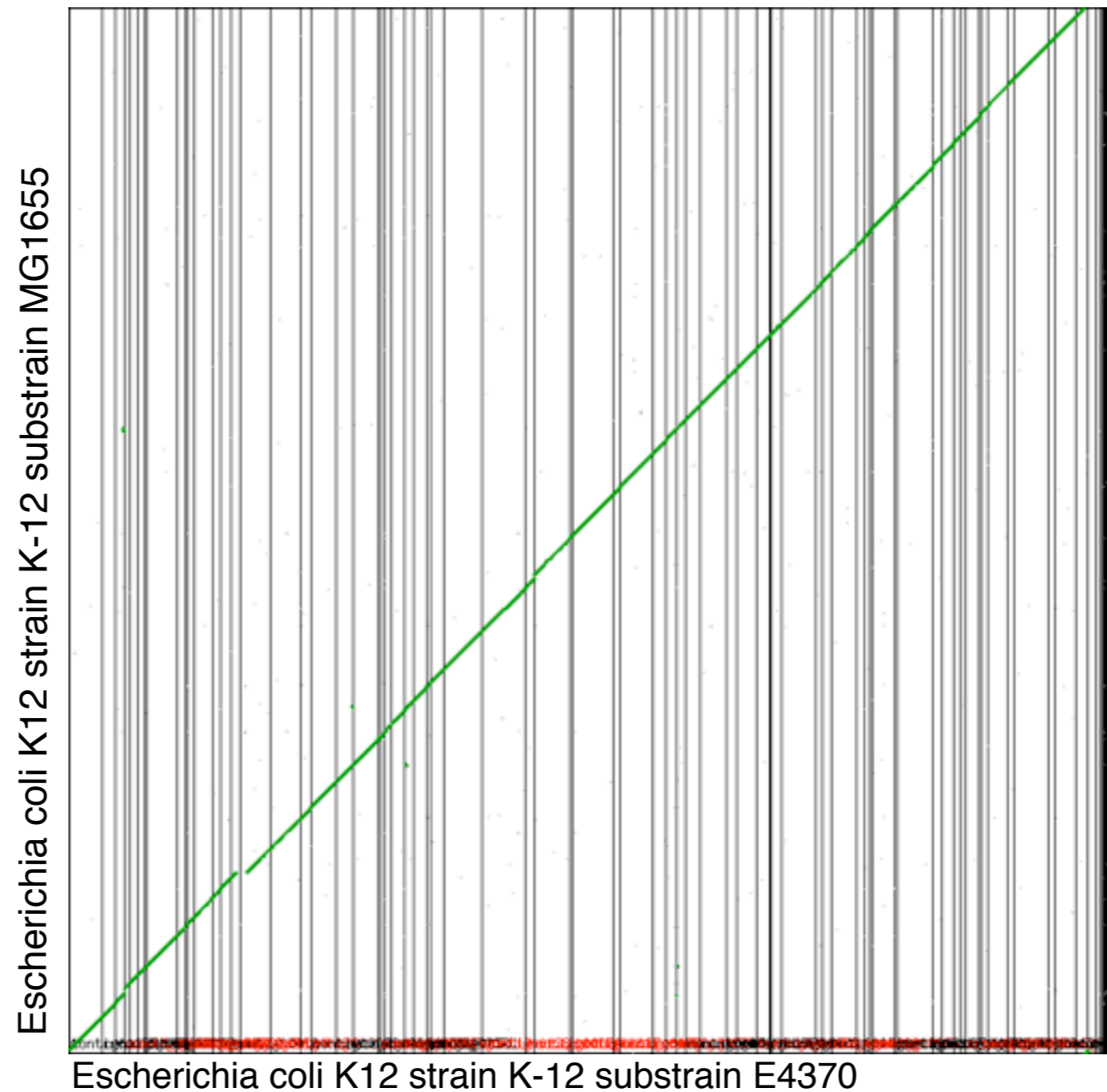




# Syntenic Path Assembly

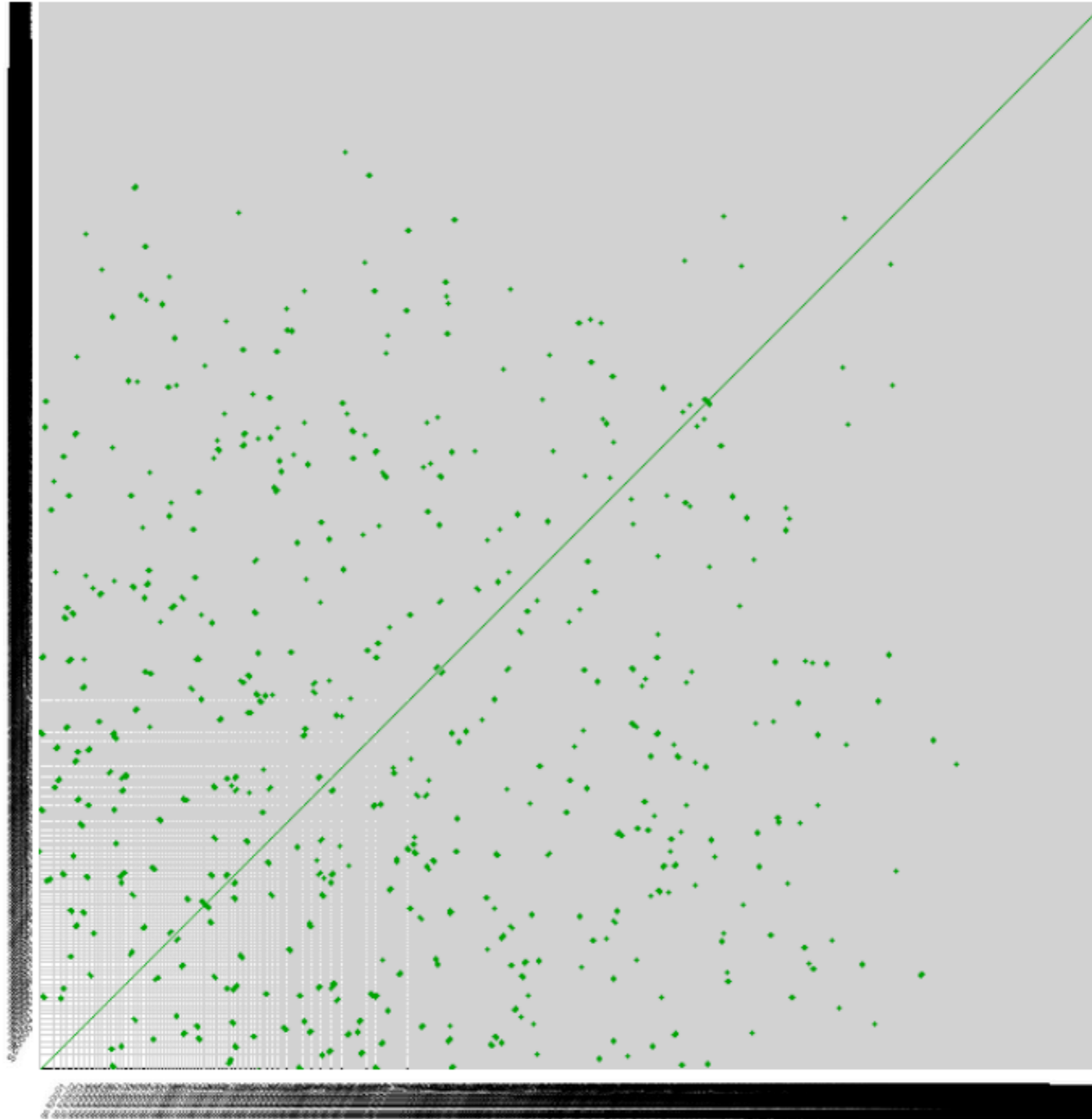
Using synteny to assemble to a reference genome

Assembled by Syntenic Path



# Self-self Utricularia

y-axis organism: *Utricularia gibba* (v4.1)



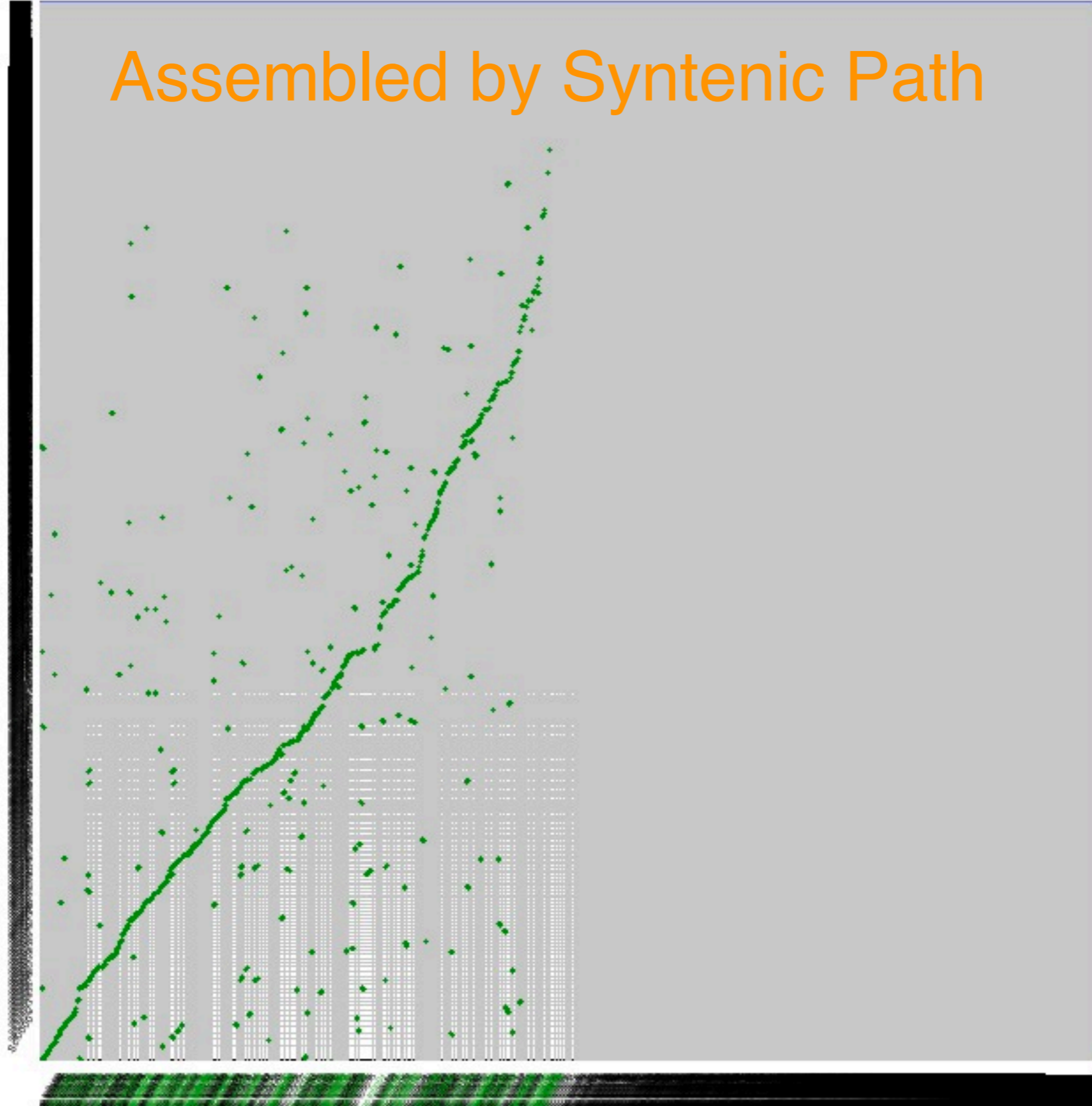
x-axis: *Utricularia gibba* (v4.1)

CoGe SynMap: <http://genomevolution.org/r/6lid>

# Self-self Utricularia

y-axis organism: *Utricularia gibba* (v4.1)

Assembled by Syntenic Path



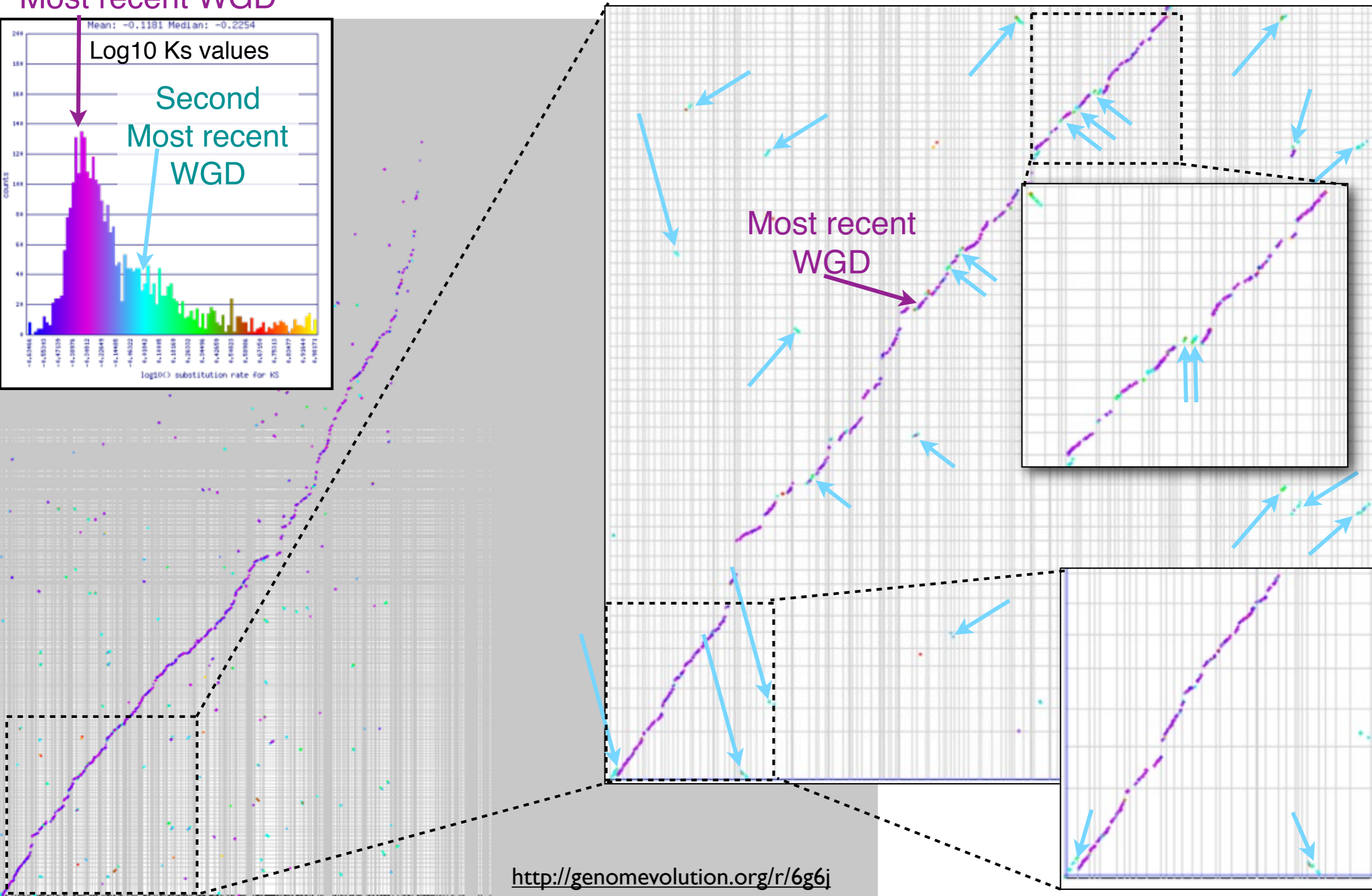
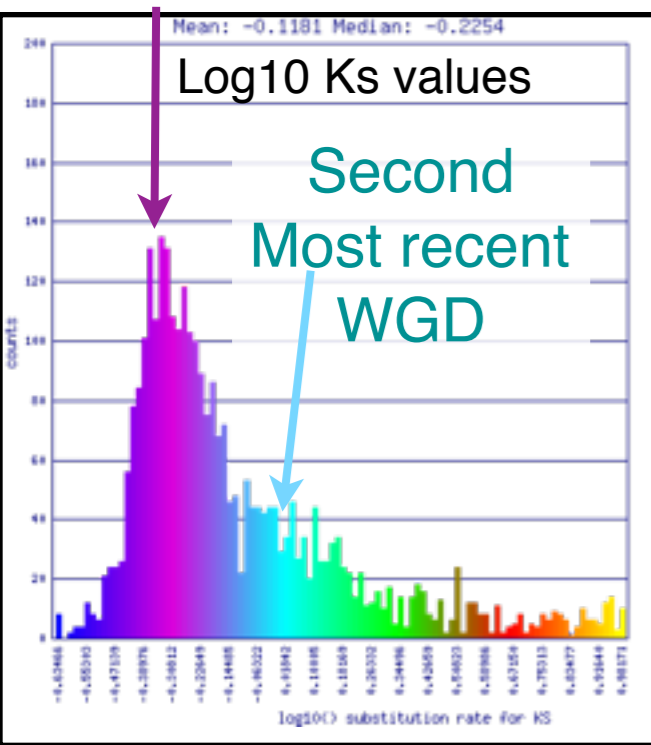
x-axis: *Utricularia gibba* (v4.1)

CoGe SynMap: <http://genomevolution.org/r/6lib>

# Evidence for 2xTetraploidy

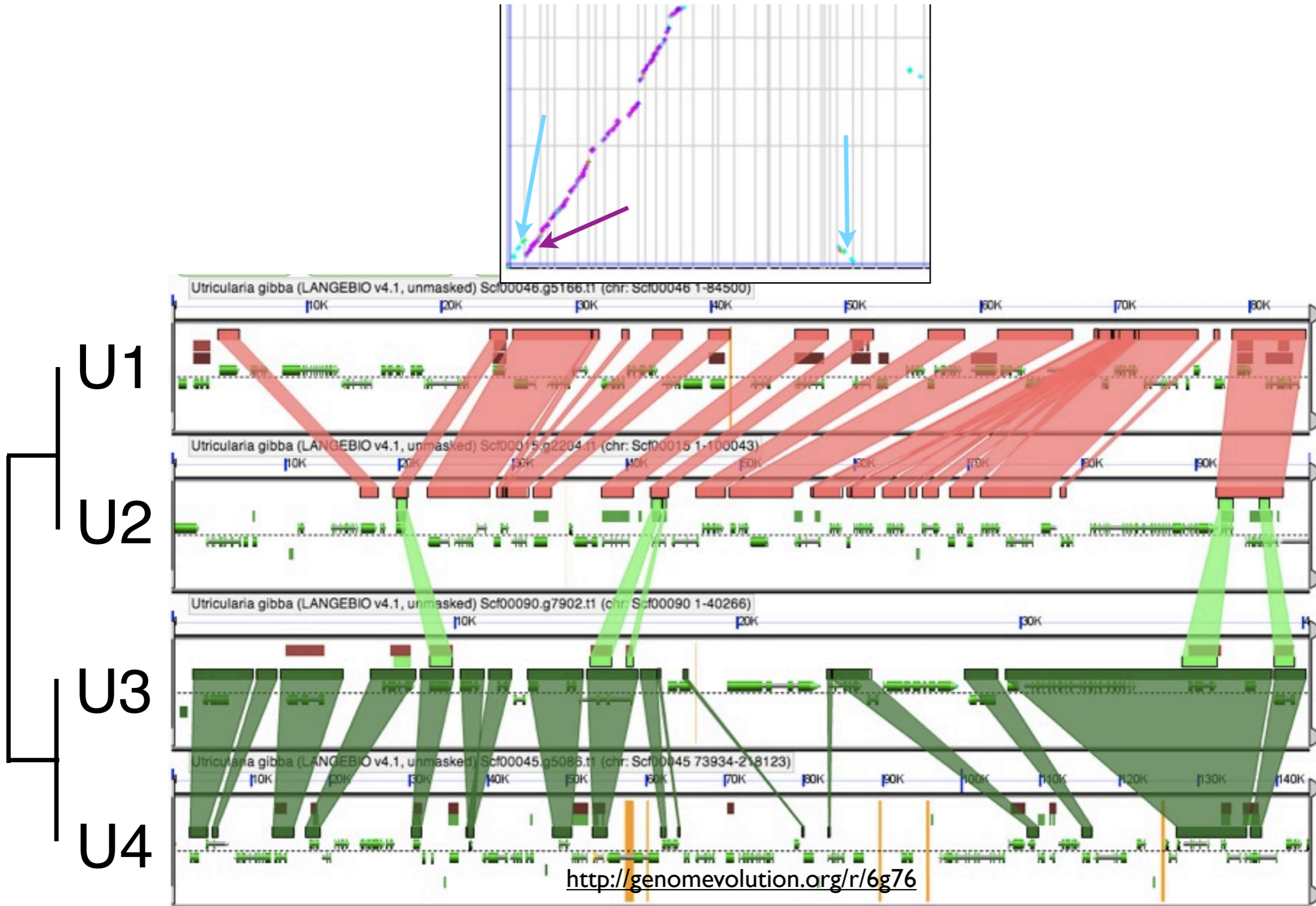
Utricularia Self-Self Sytneic Dotplot: **Synonymous Substitutions (ks)**

Most recent WGD



# Evidence for 2xWDG

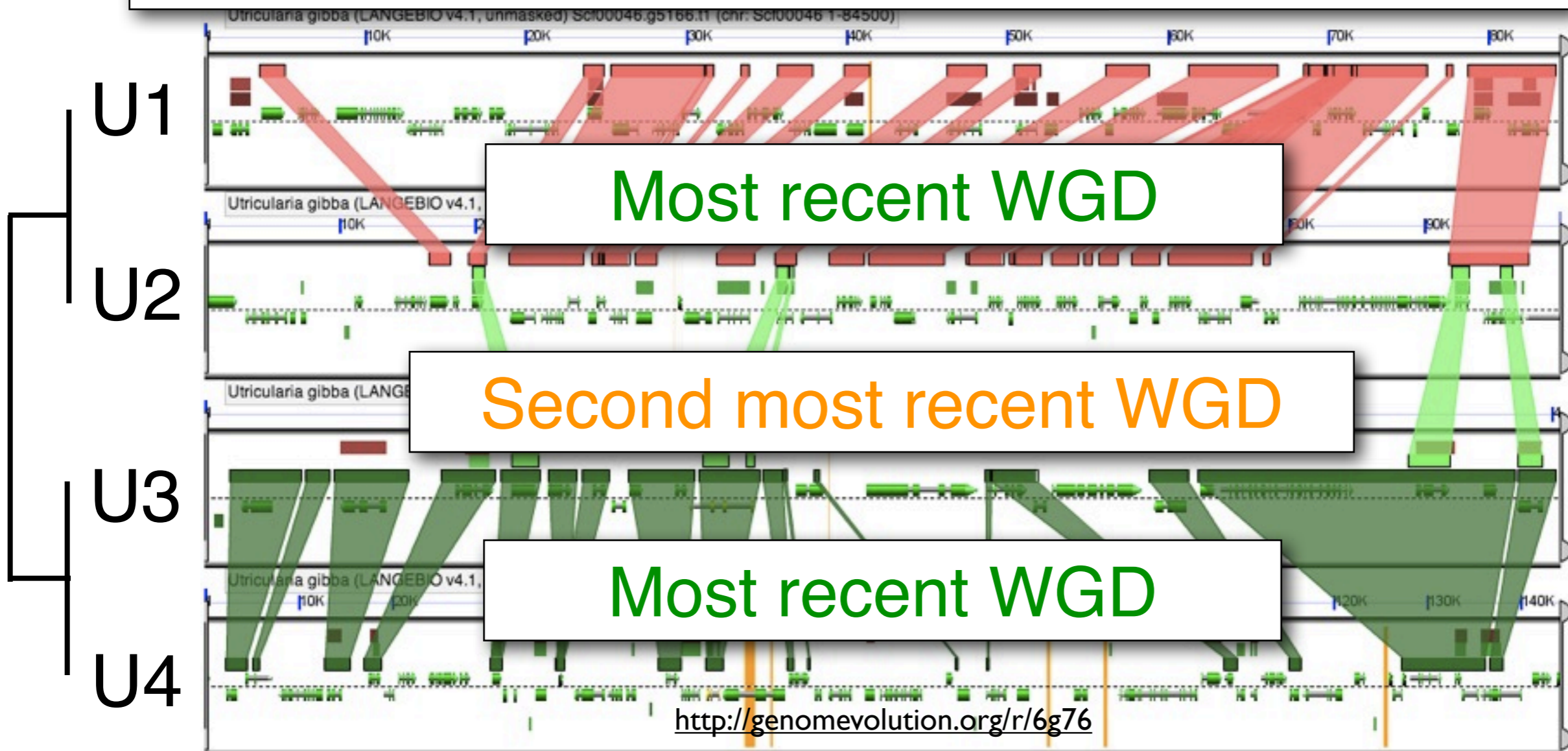
## Utricularia Microsynteny Analysis



# Evidence for 2xWDG

Signal of intragenomic synteny degrades over time through diploidization process: fractionation (deletion of homeologous genes)

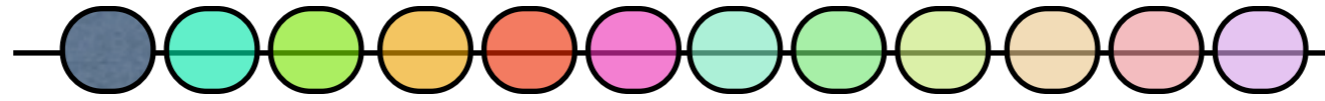
Exacerbated by additional polyploidy events



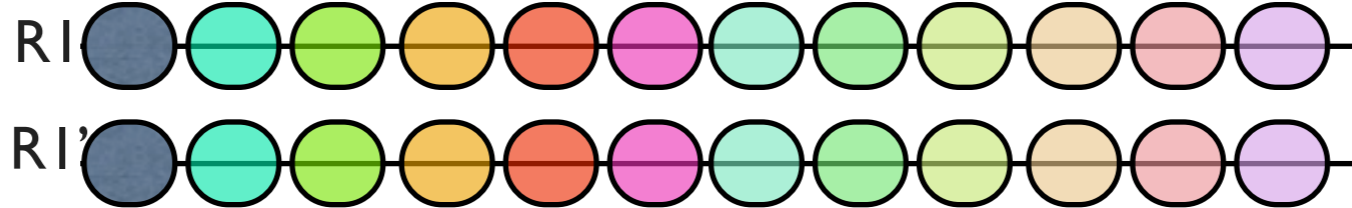
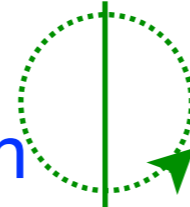
# Fractionation and diploidization:

(Importance of outgroups)

Ancestor



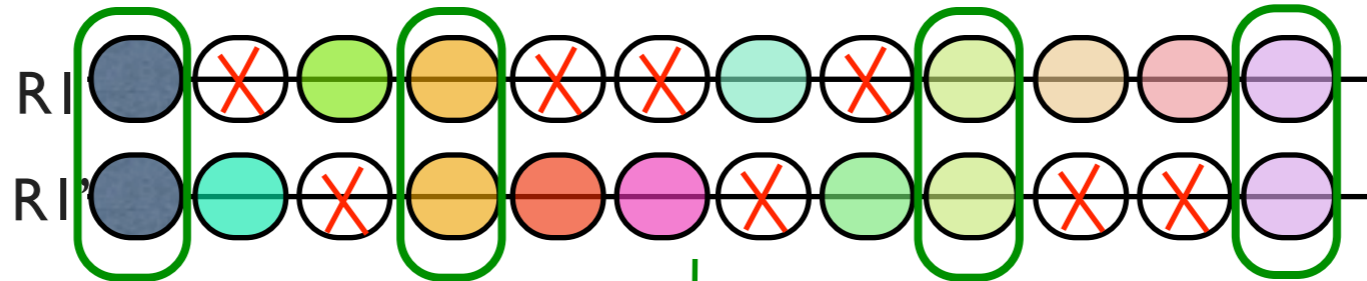
Genome duplication



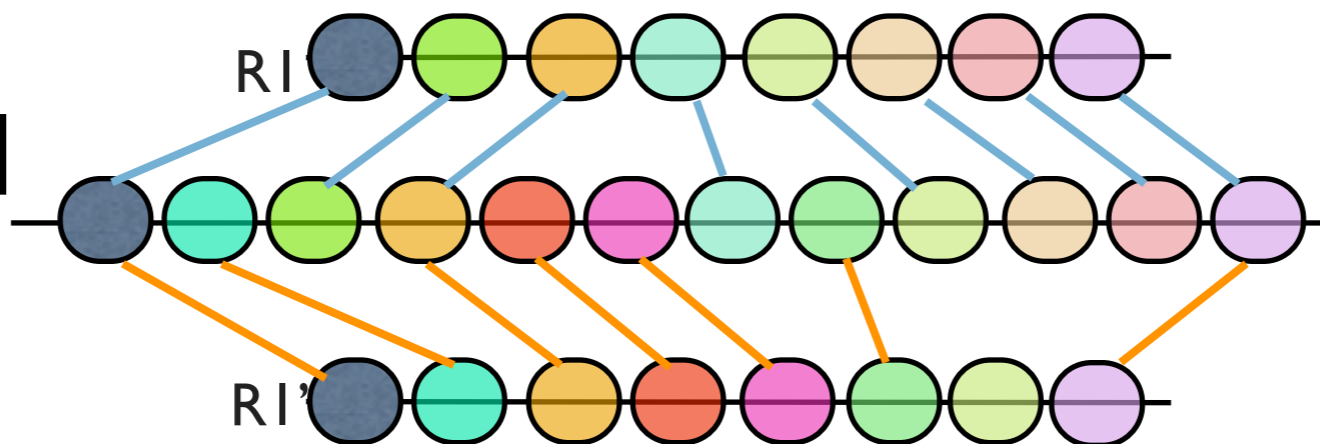
Gene Loss / Fractionation



Syntelogs



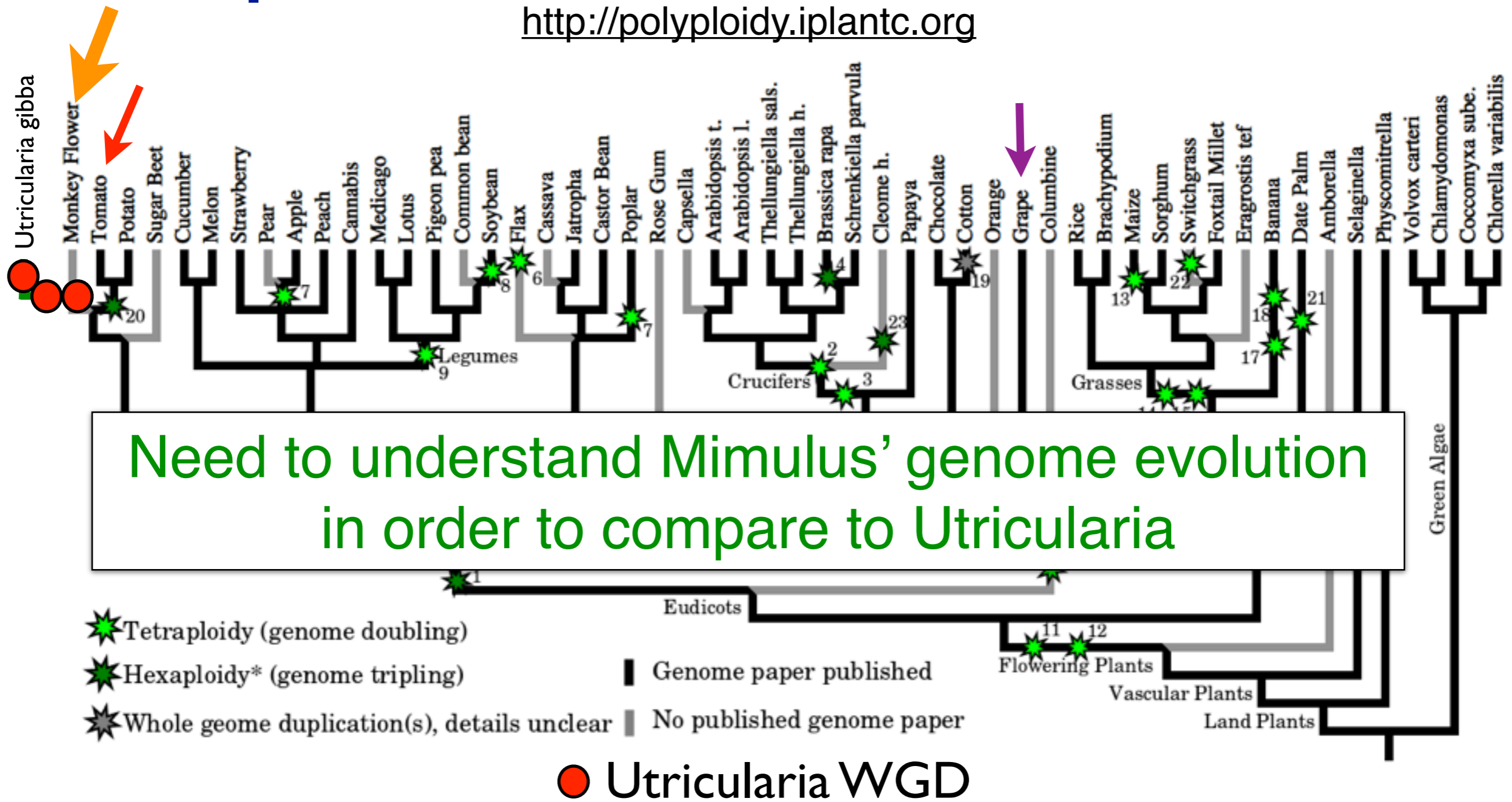
Unduplicated Outgroup



Intercalated Colinear Genes

# Sequenced Plant Genomes

<http://polyploidy.iplantc.org>



**Mimulus is closest, but under-characterized**

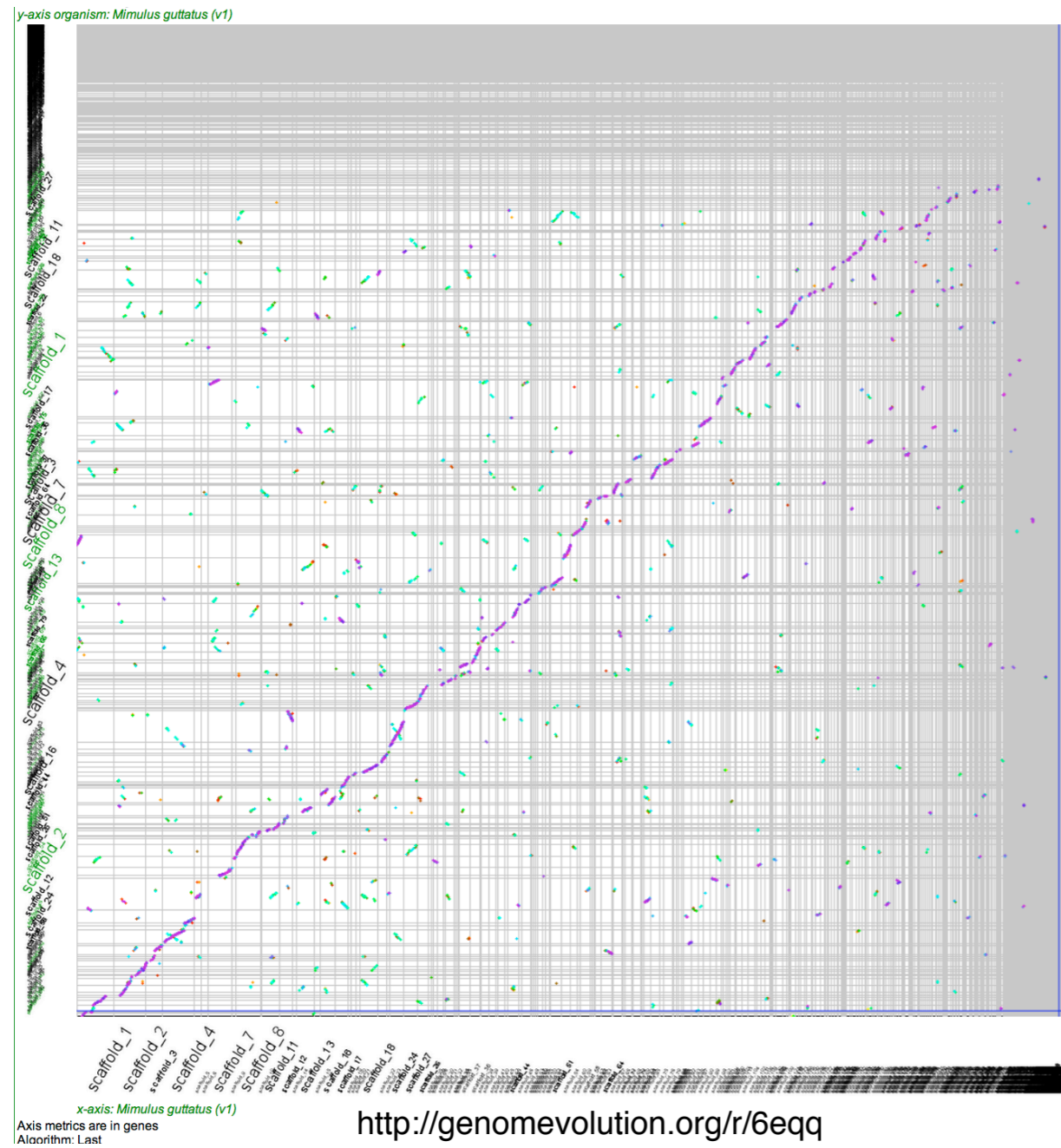
Tomato is well characterized, but has a WGT

Grape is the de facto eurosid outgroup comparator

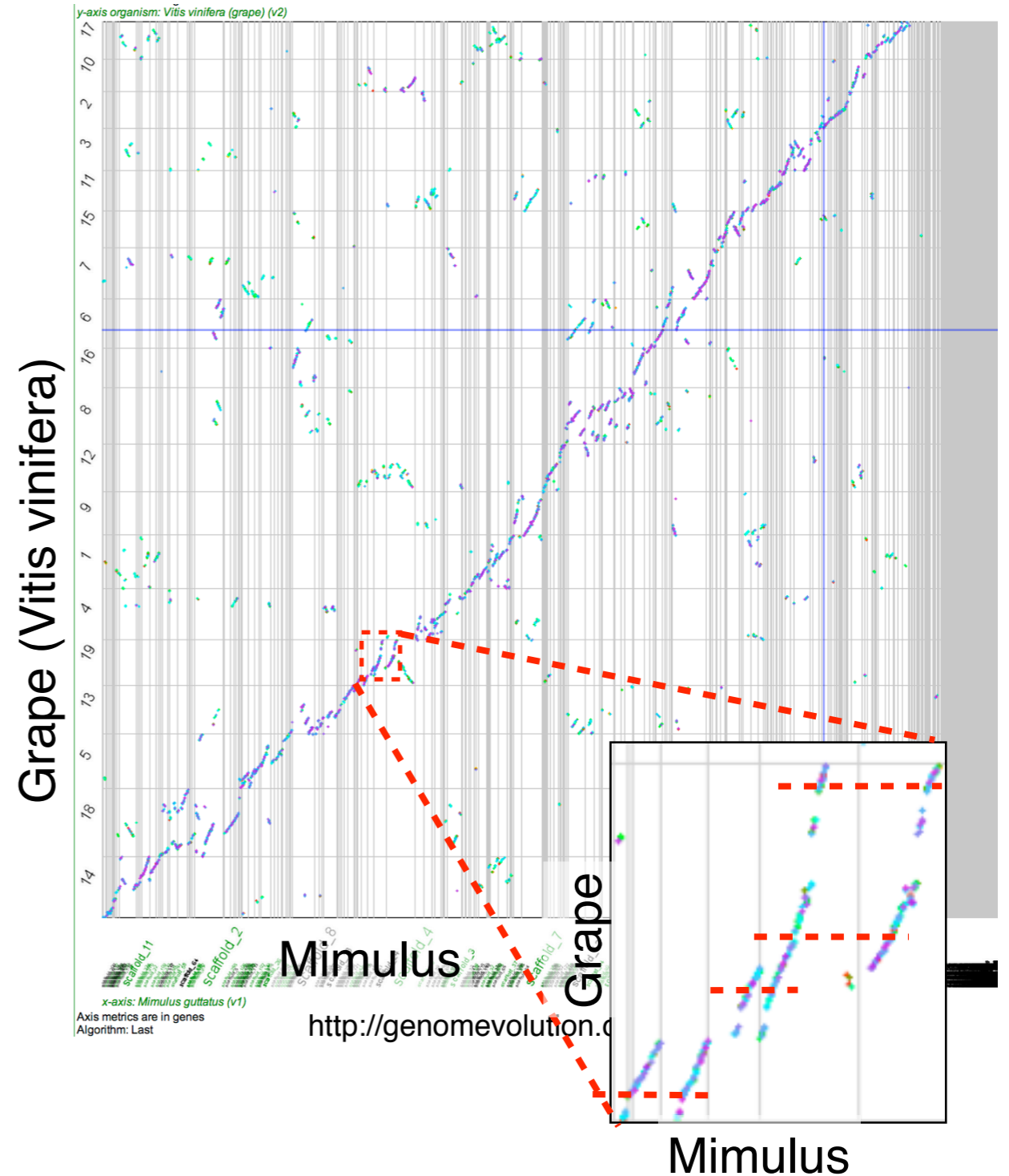


# Mimulus has a WGD

## Self-self Mimulus



## Mimulus v. Grape



# Mimulus has a WGD

## Self-self Mimulus

## Mimulus v. Grape

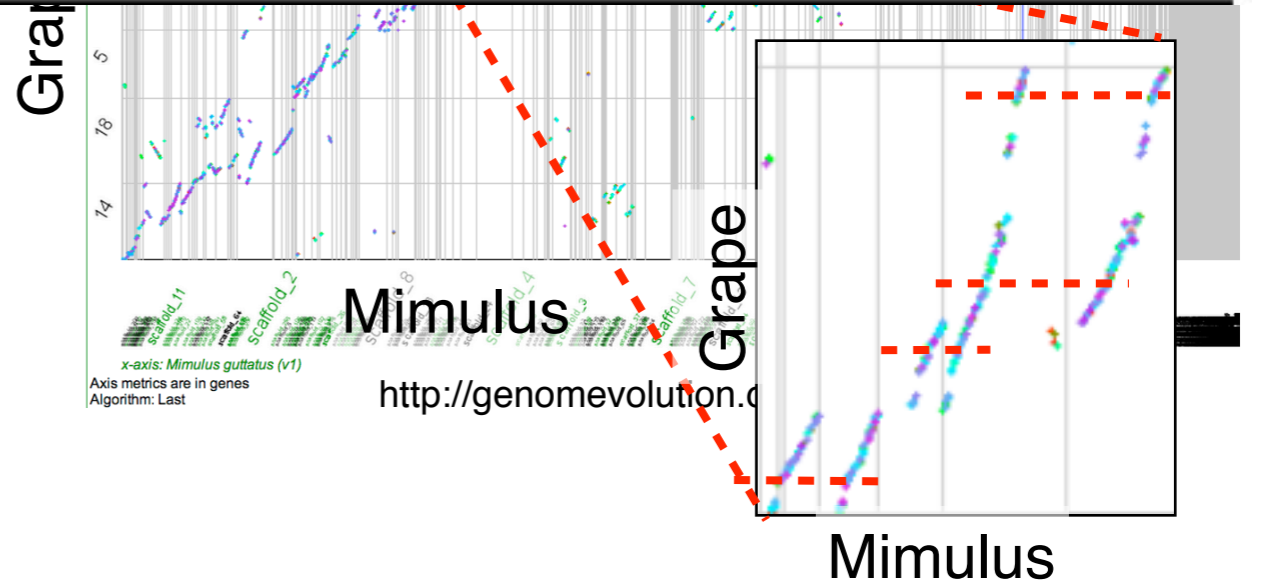
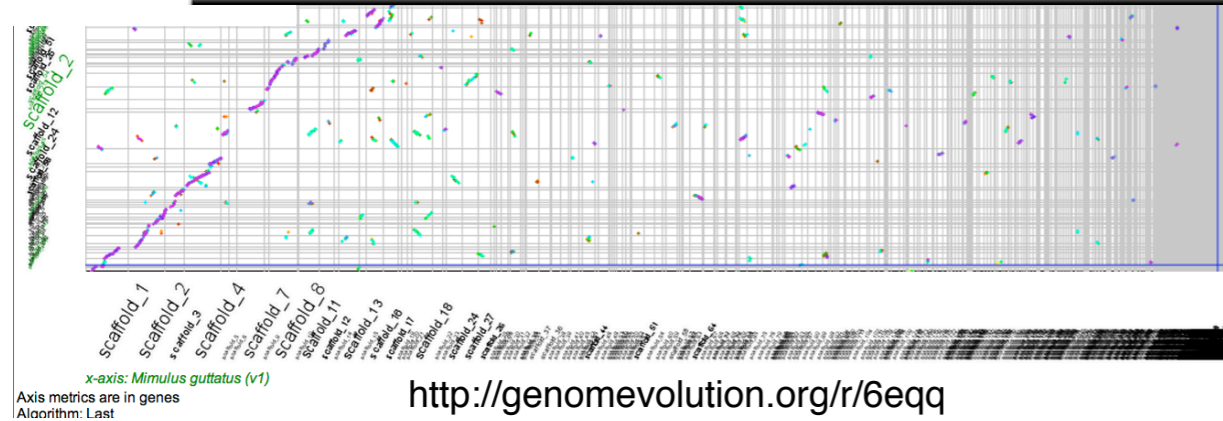
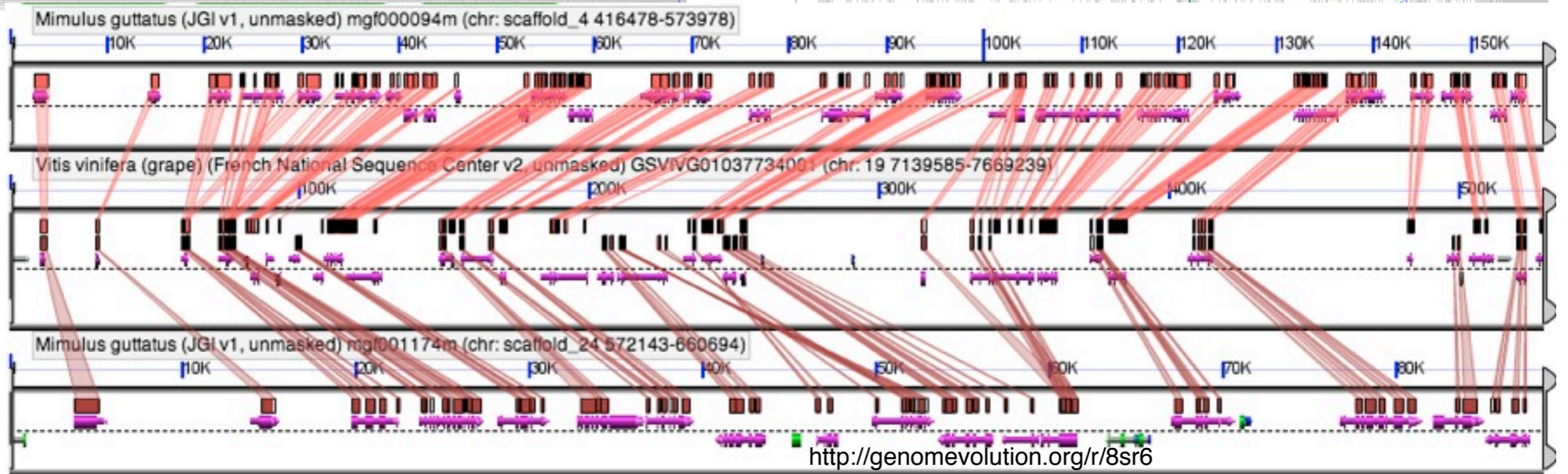
y-axis organism: *Mimulus guttatus* (v1)

y-axis organism: *Vitis vinifera* (grape) (v2)

Mg1

Vv

Mg2



# Mimulus has a WGD

Self-self Mimulus

Mimulus v. Grape

Mimulus had a WGD subsequent to the eurosoid paleohexaploidy

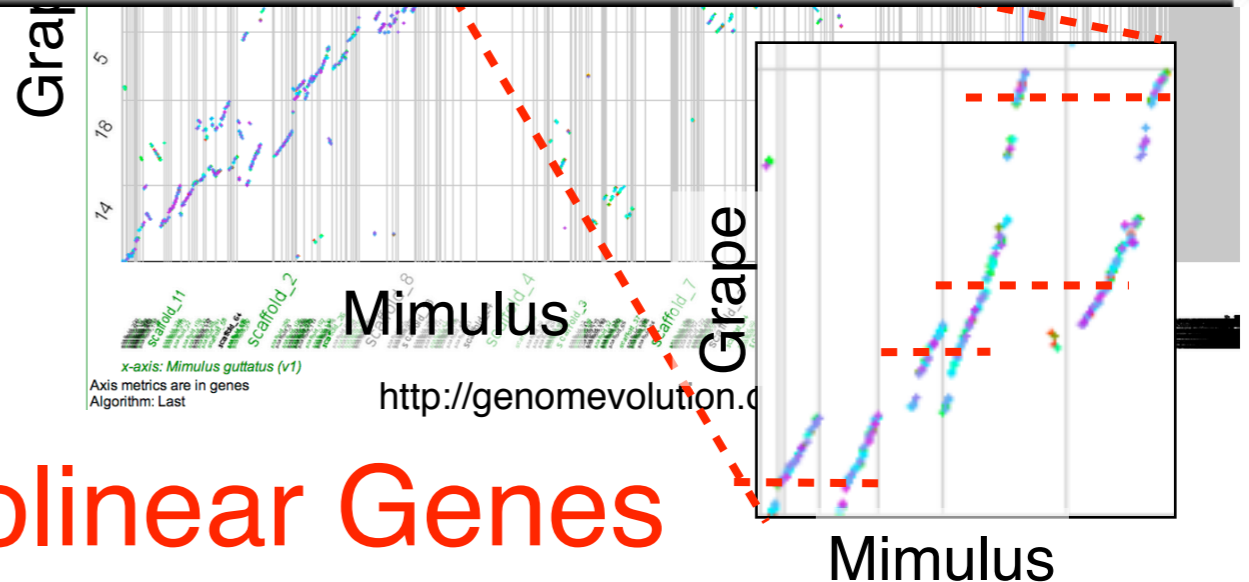
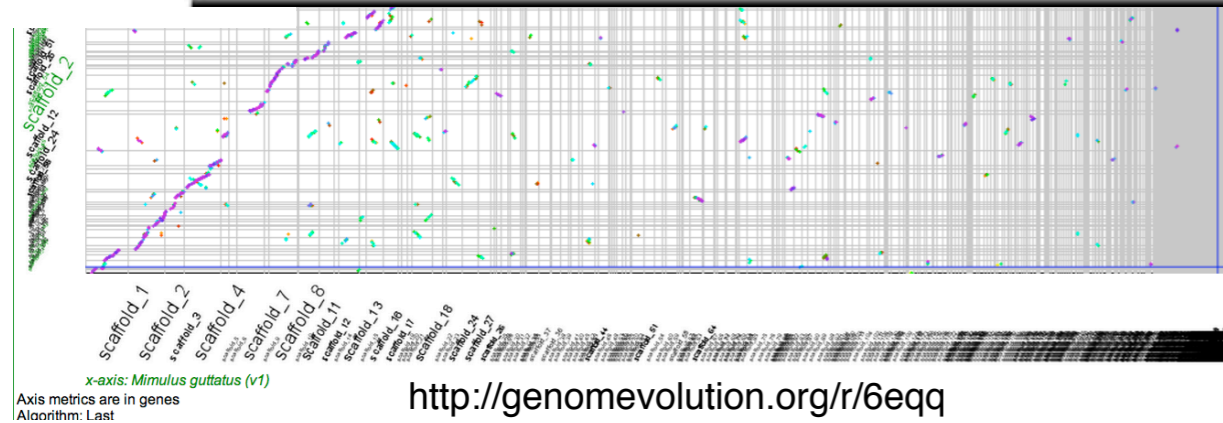
Mg1

Vv

Mg2

2xMg:1xVv

<http://genomeevolution.org/r/8sr6>

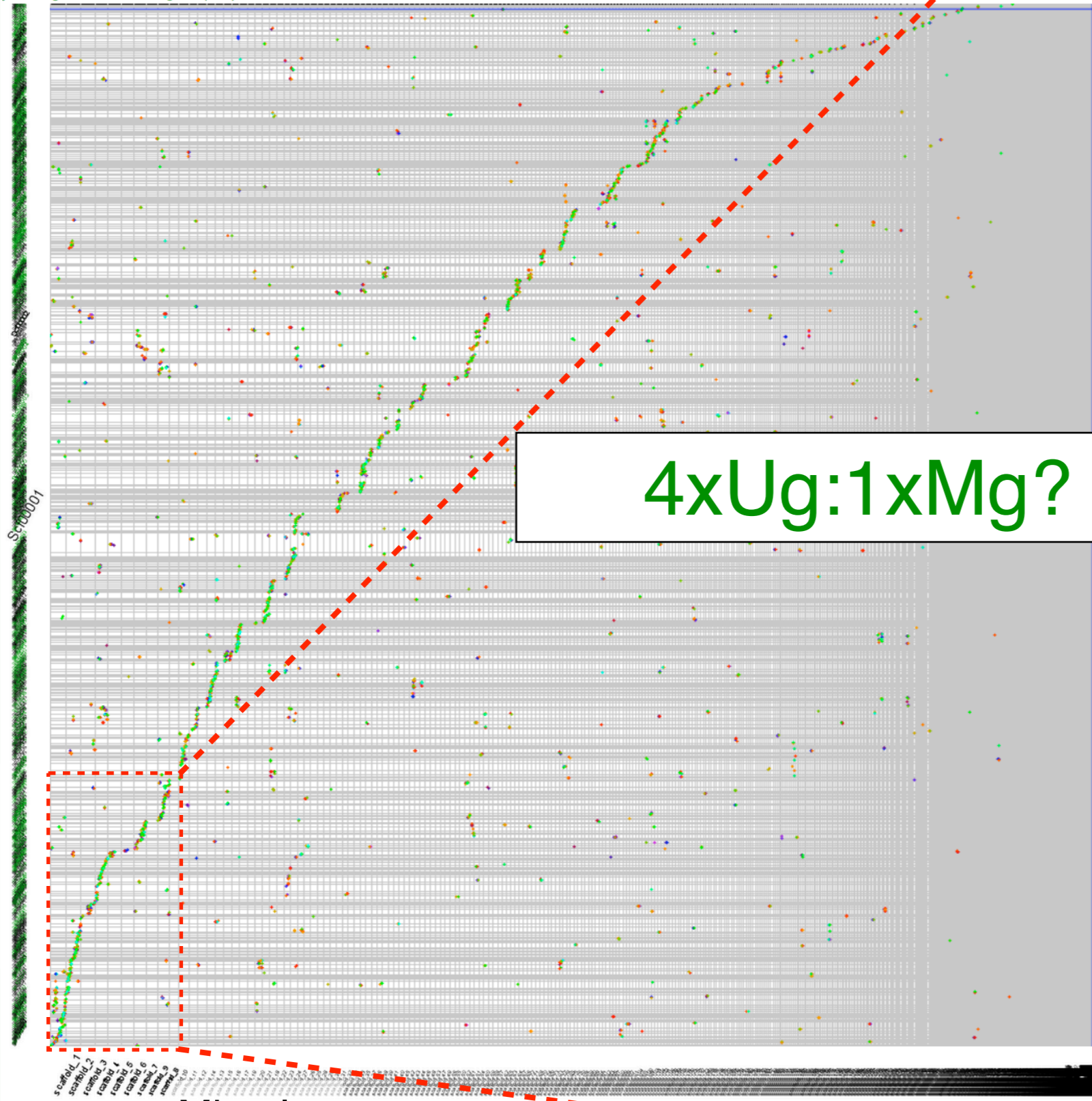


Intercalated Colinear Genes

# Utricularia v. Mimulus

Axis metrics are in nucleotides  
y-axis organism: *Utricularia gibba* (v4.1)

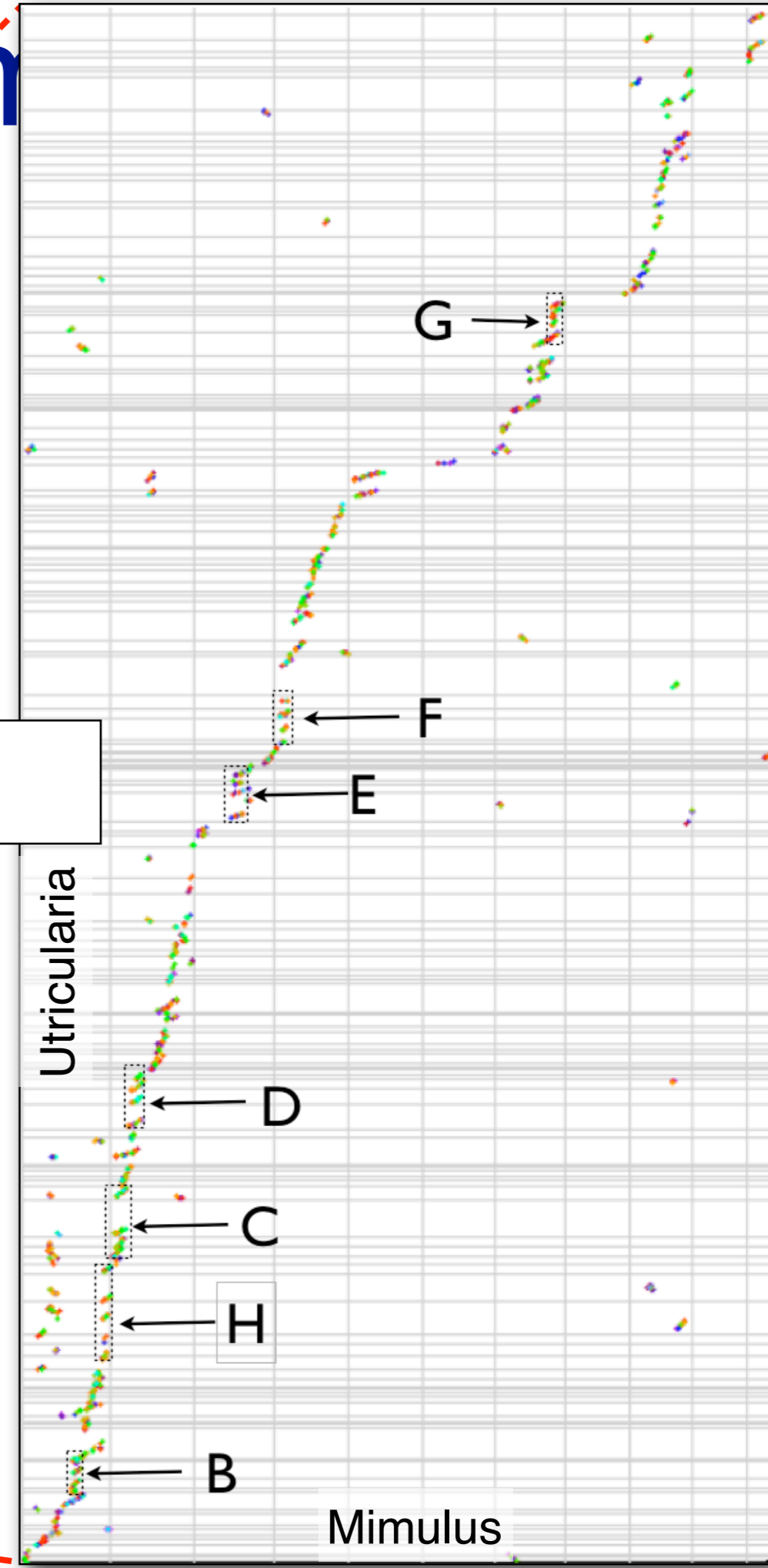
Utricularia



4xUg:1xMg?

x-axis: *Mimulus guttatus*  
Axis metrics are in nucleotides  
Algorithm: Last

<http://genomevolution.org/r/6erk>

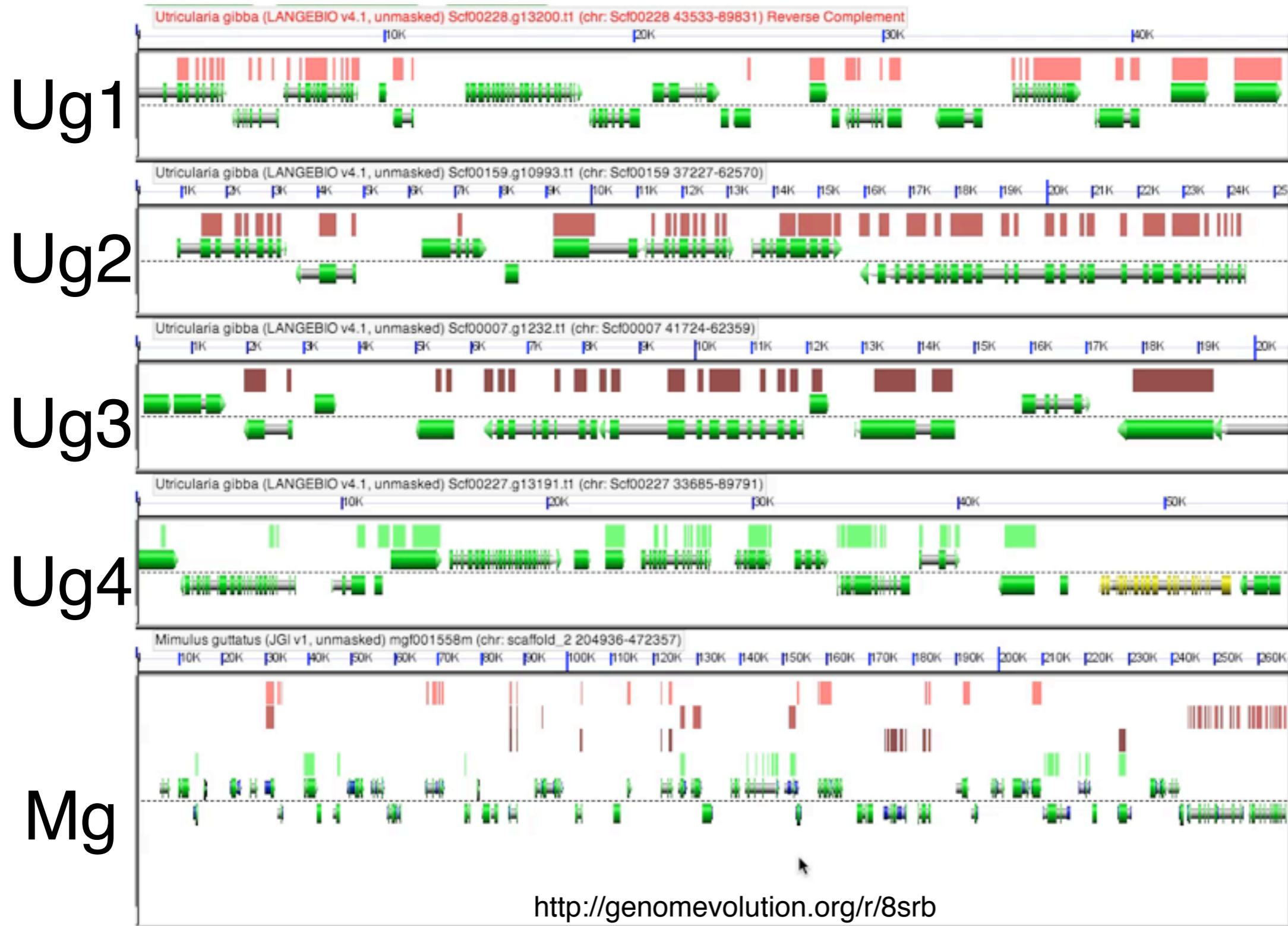


Utricularia

Mimulus

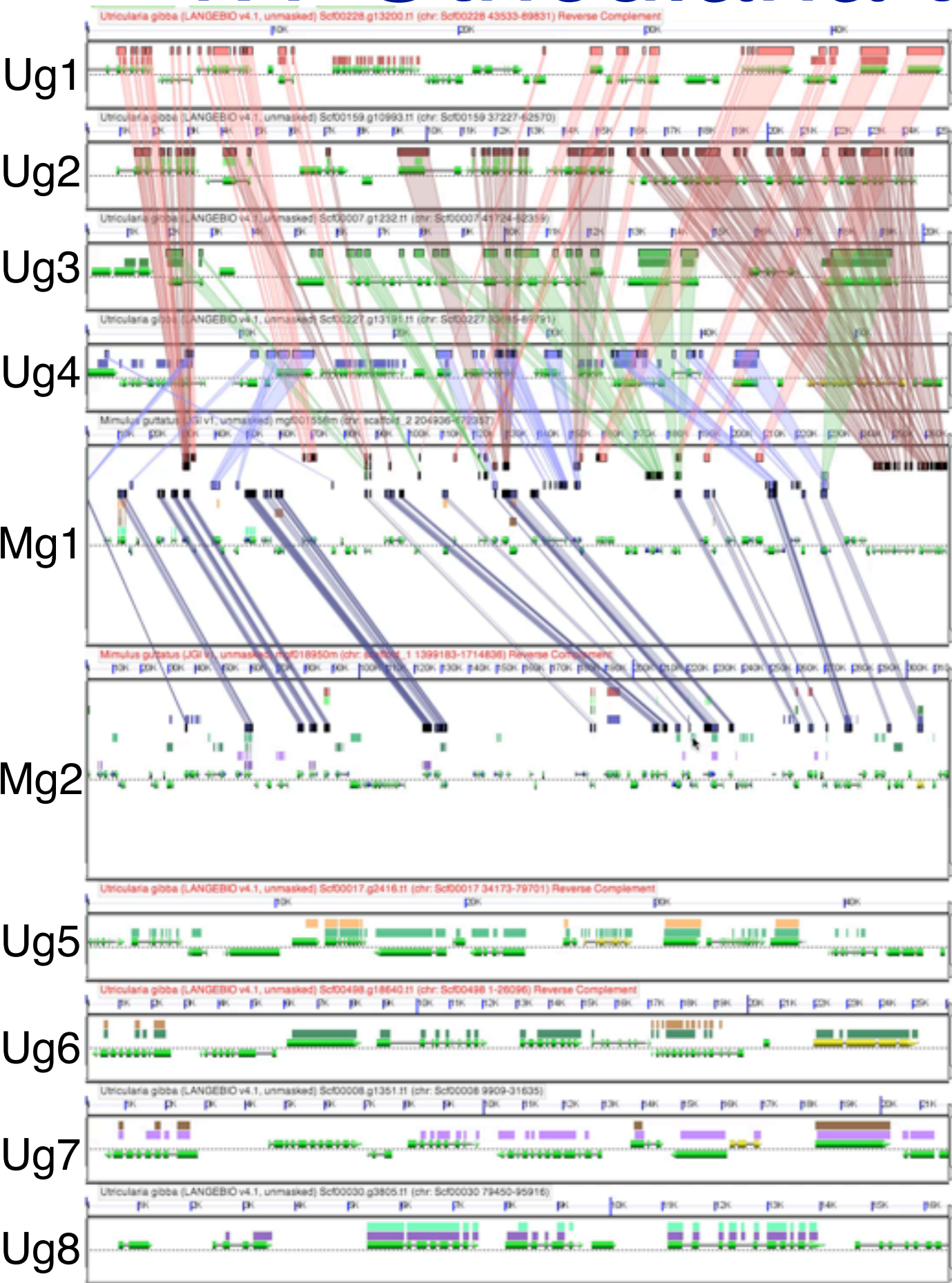
B  
C  
D  
E  
F  
G

# 4:1 Utricularia to Mimulus

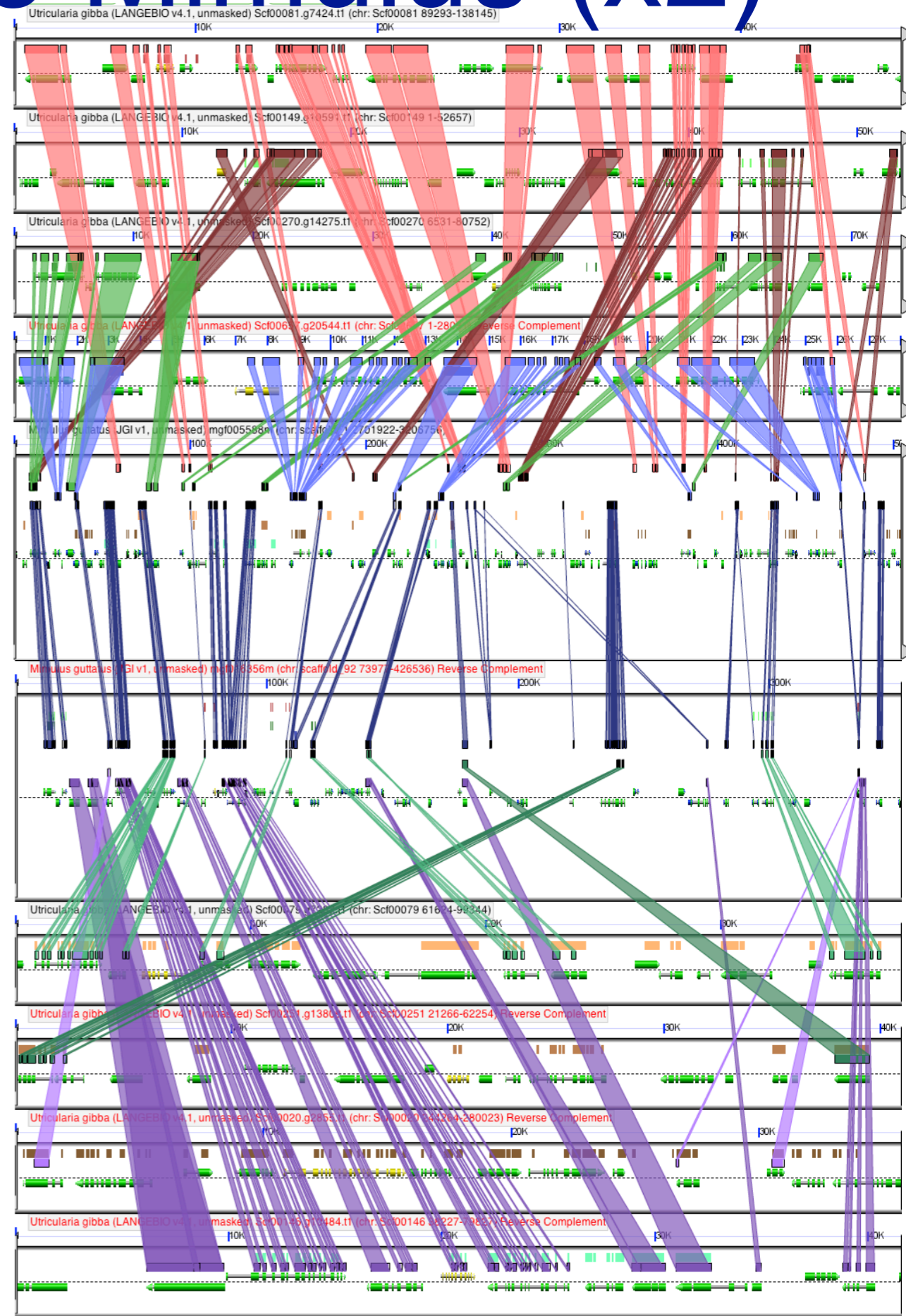


Intercalated Colinear Genes

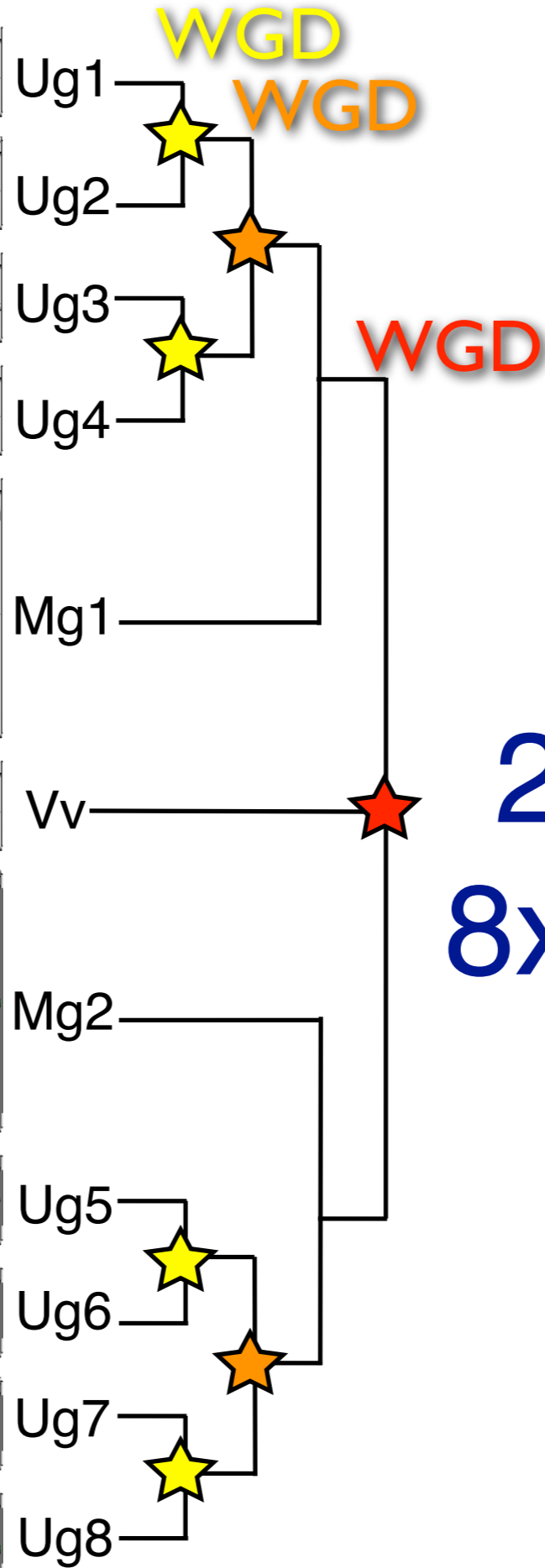
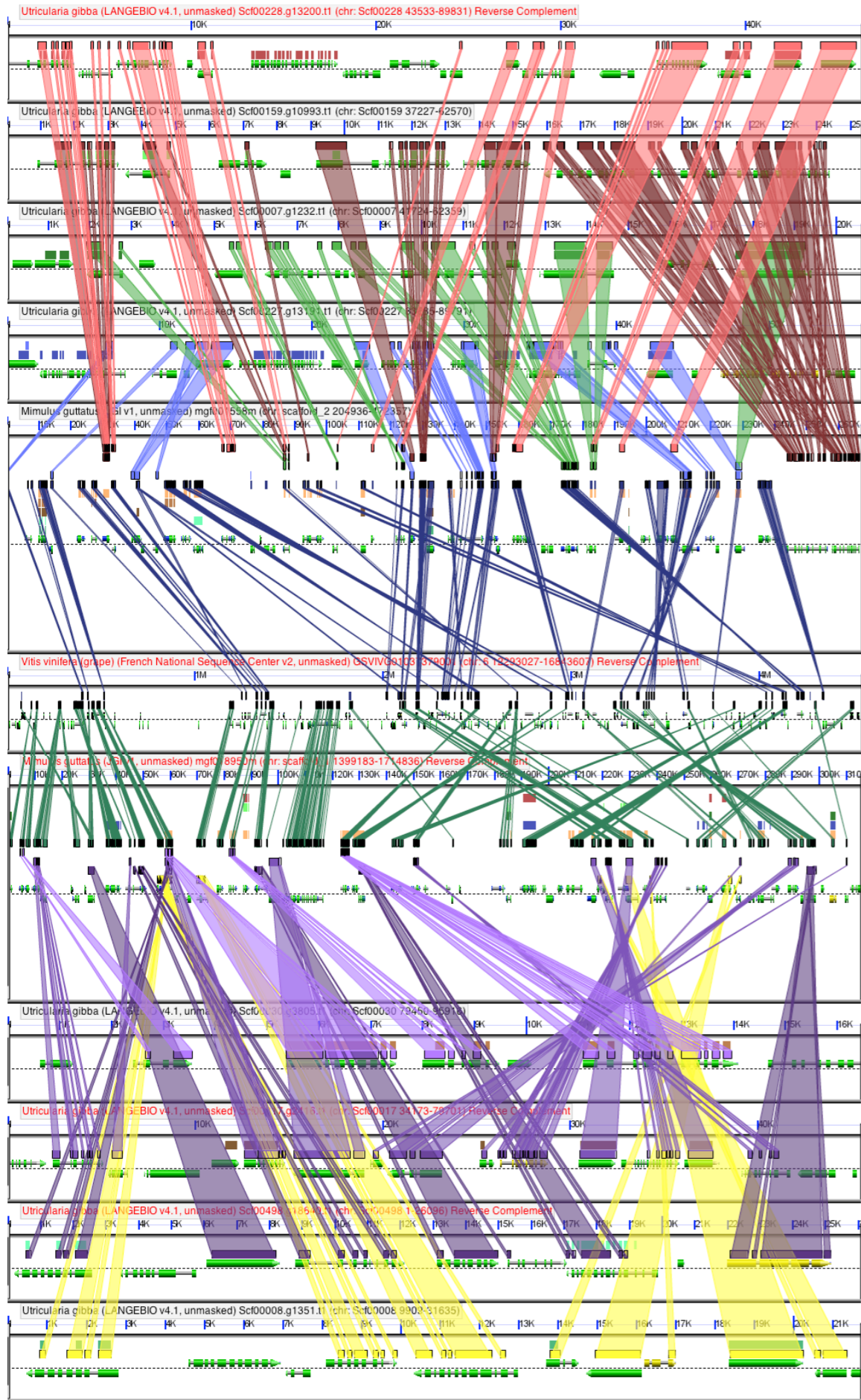
# 4:1 Utricularia to Mimulus (x2)



<http://genomevolution.org/r/6m07>



<http://genomevolution.org/r/6l1r>

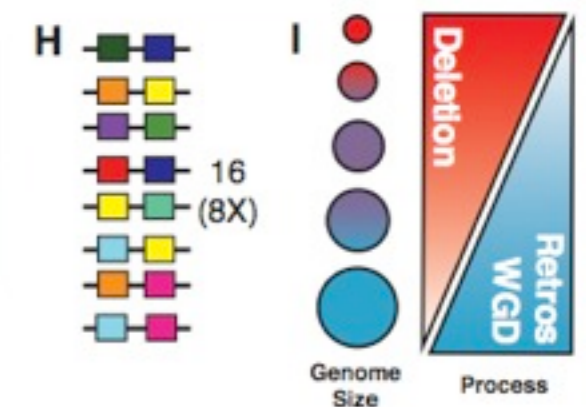
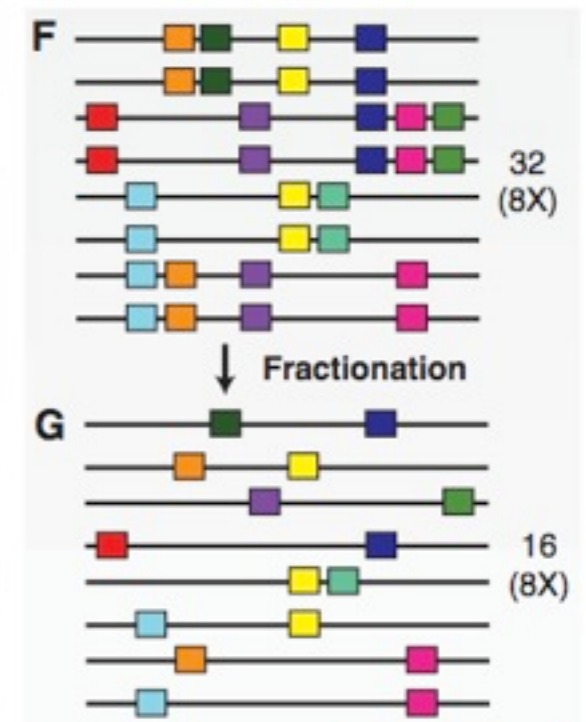
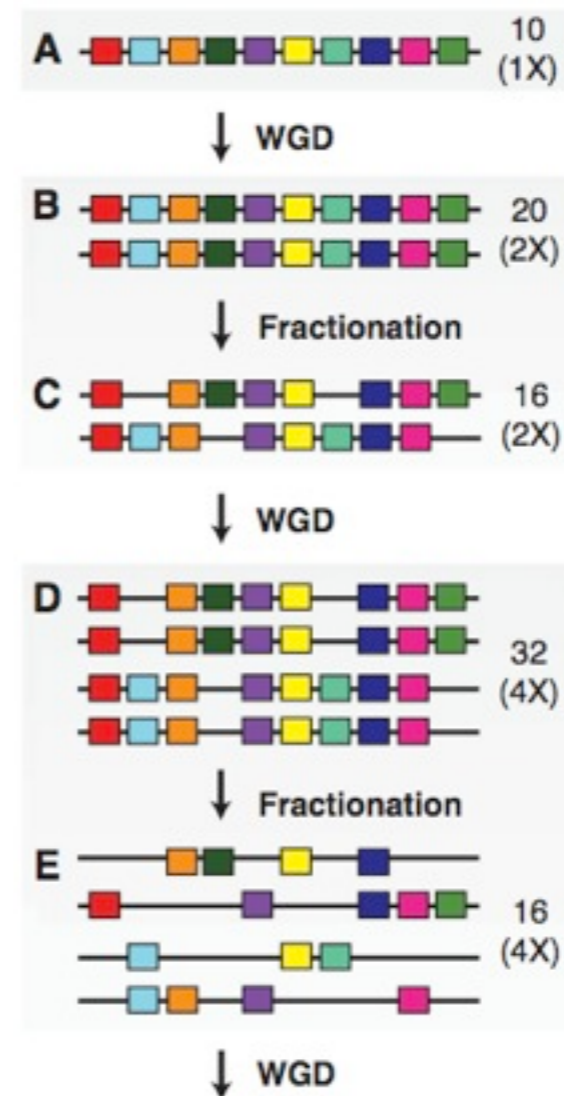
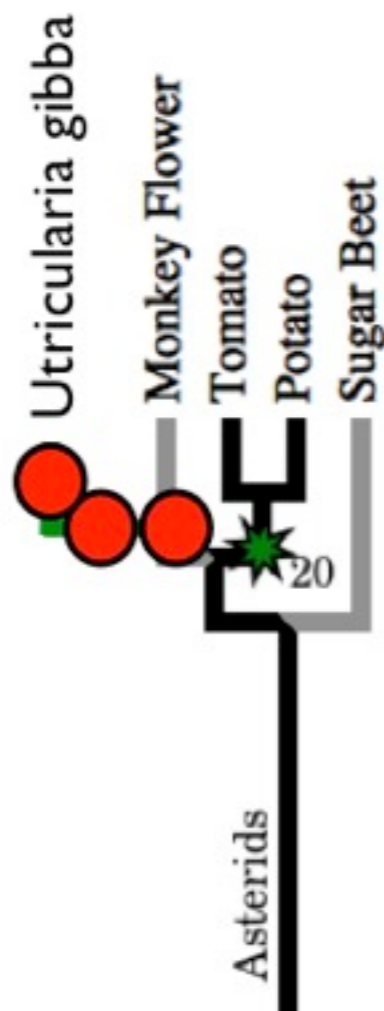


# Conclusions

Utricularia has had three sequential tetraploidy events (8x) subsequent to the Eudicot paleohexaploidy, despite having a **small(est) plant genome**

Utricularia's oldest WGD is **likely** shared with Mimulus; (independent of the Tomato WGT)

Genome Size is a function of genome expansion and contraction mechanisms



Genome Size Process



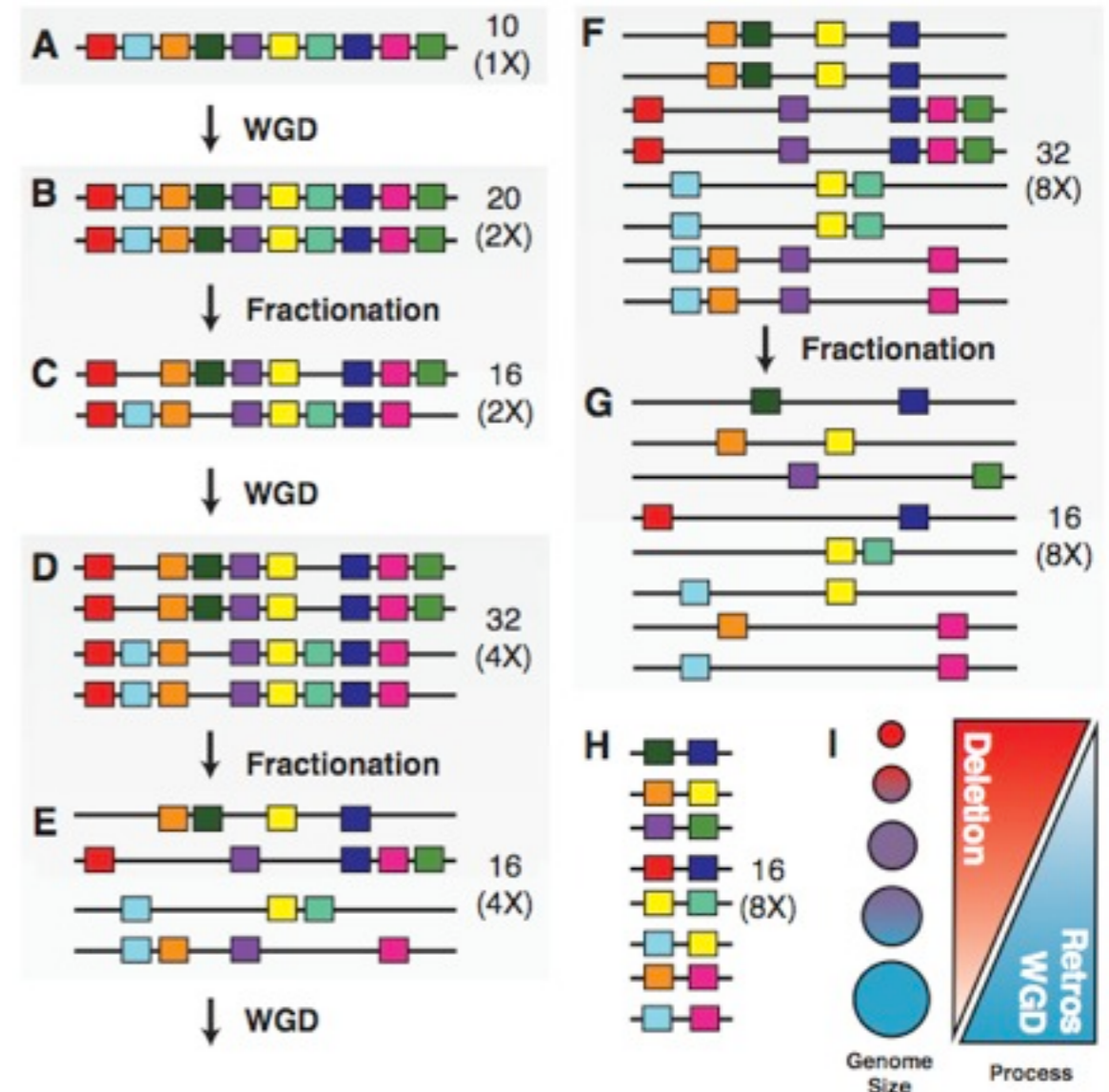
# Conclusions

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Utricularia's oldest WGD is **likely** shared with Mimulus; (independent of the Tomato WGT)

Genome Size is a function of genome expansion and contraction mechanisms

Genus	Species	1C (Mbp)	Original Reference	Paper
Utricularia	gibba	88	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	blanchetii	135	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	parthenopipes	140	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	quelchii	157	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	praelonga	158	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	australis	175	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	microcalyx	214	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	pubescens	216	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	humboldtii	232	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	sandersonii	235	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	subulata	247	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	livida	252	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	reniformis	328	Greilhuber et al., 2006 (Ref. 535)	2011
Utricularia	prehensilis	401	Greilhuber et al., 2006 (Ref. 535)	2011



RBG Kew DNA C-values query results

# Thanks

Download this presentation: <http://genomeevolution.org/r/8t6y>

*Utricularia gibba* sequencing and analysis team:

LETTER

nature

OPEN

doi:10.1038/nature12132

## Architecture and evolution of a minute plant genome

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### CoGe Team:

**Matt Bomhoff, Evan Briones, Haibao Tang**

### Comparative Genomics Collaborators:

**Haibao Tang:** SynMap; SynFind

**James Schnable:** Plant polyploidy



**iPlant Collaborative:**  
Many, many people!

