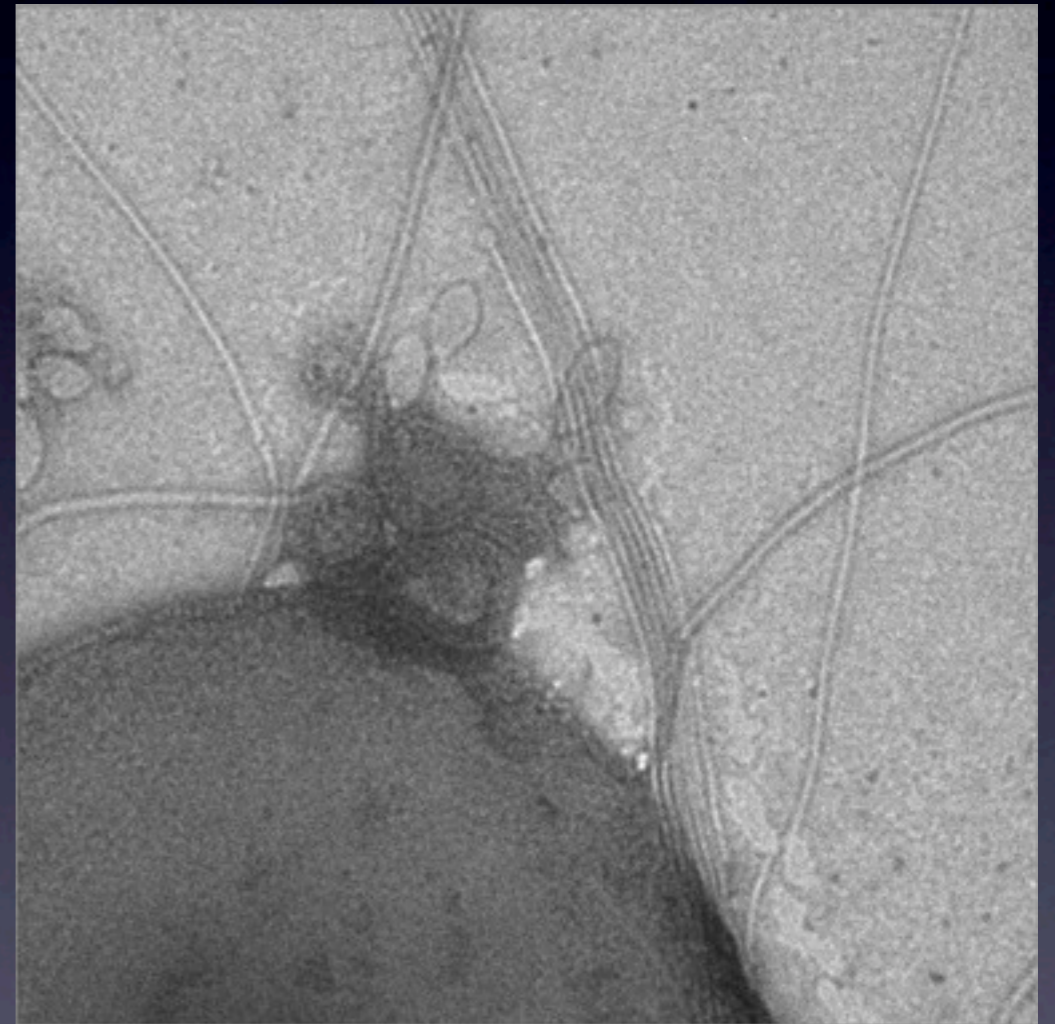


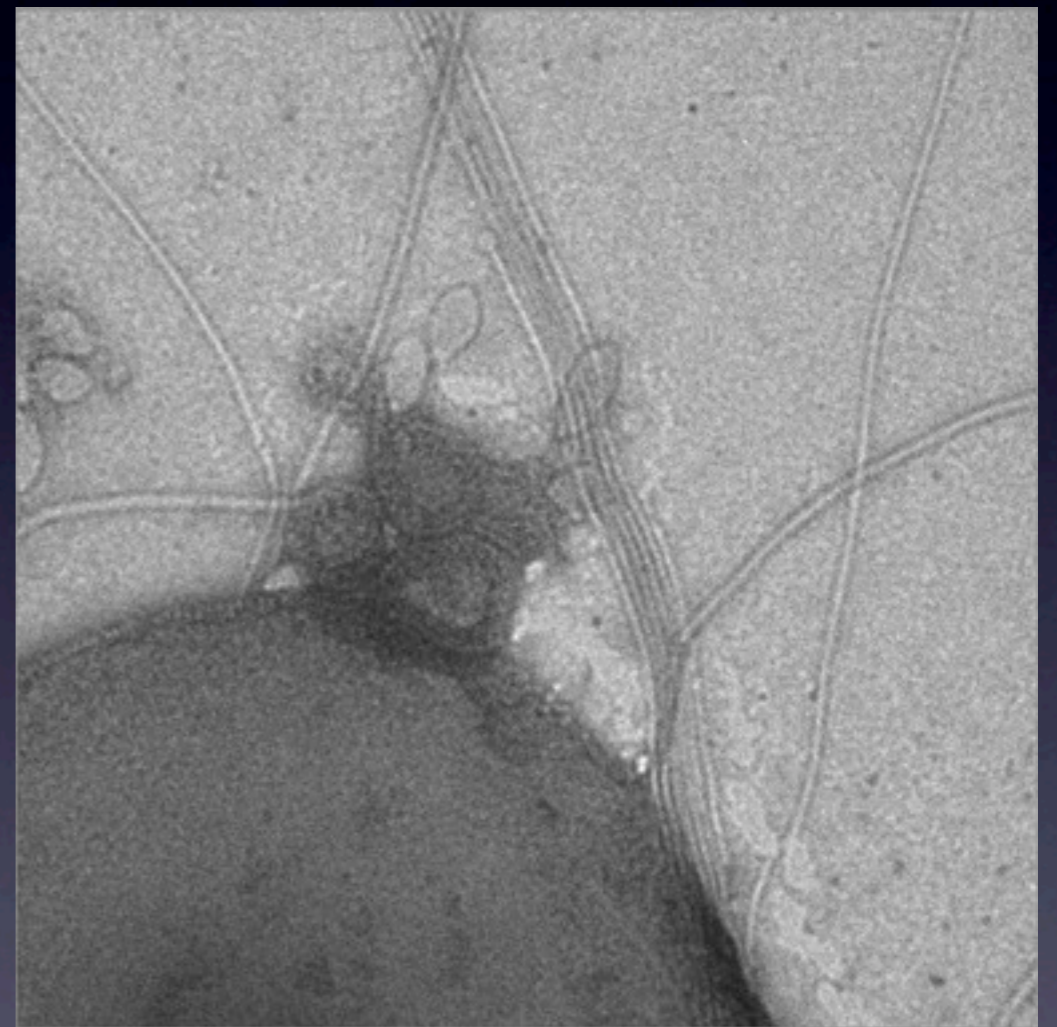
# Evolutionary Dynamics in Wild Microbial Populations



Rachel J. Whitaker  
University of Illinois, Urbana-Champaign



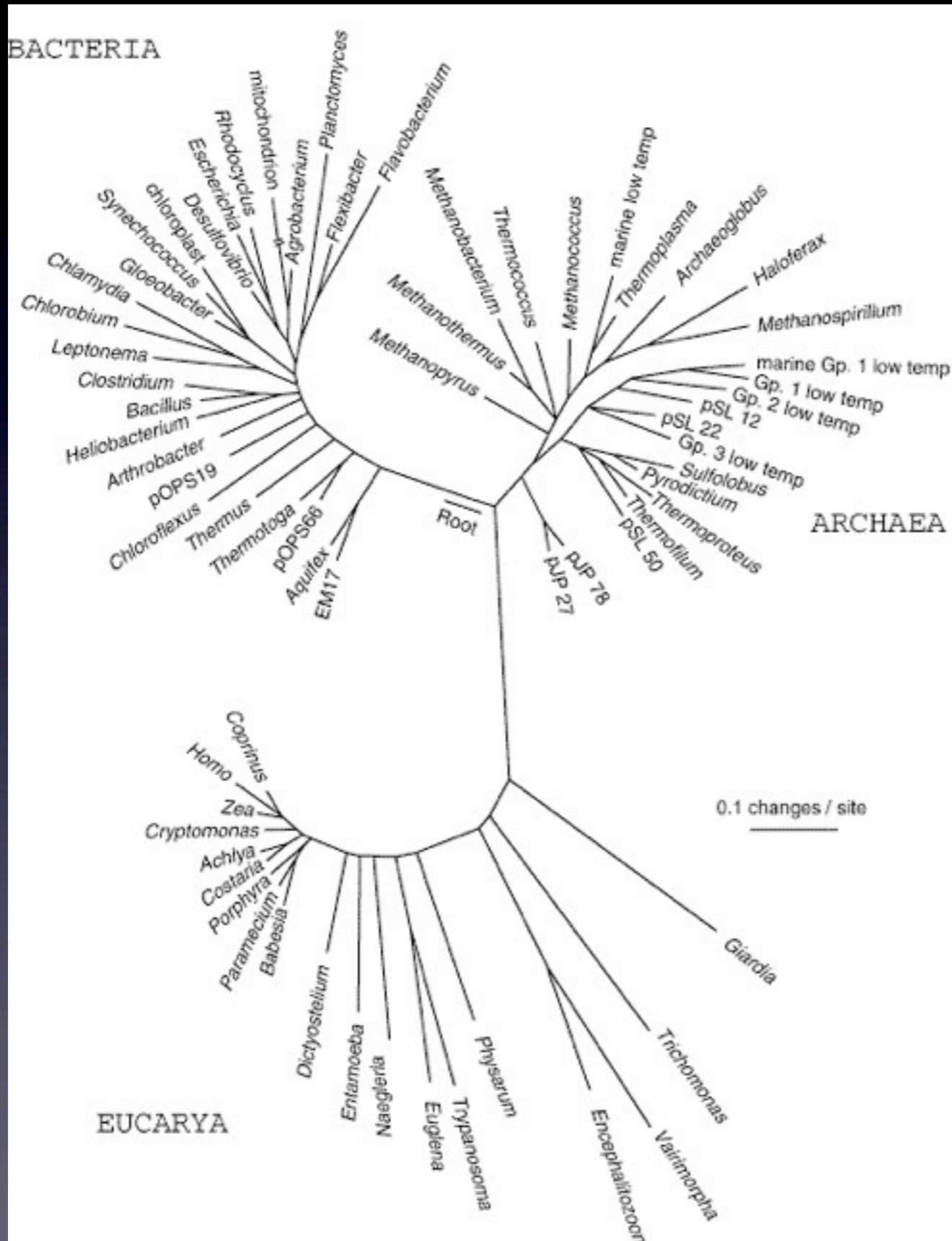
# Evolutionary Dynamics in Wild Microbial Populations



Rachel J. Whitaker  
University of Illinois, Urbana-Champaign

# The "S" Word

Microbiologists believe in diversity but can't define species

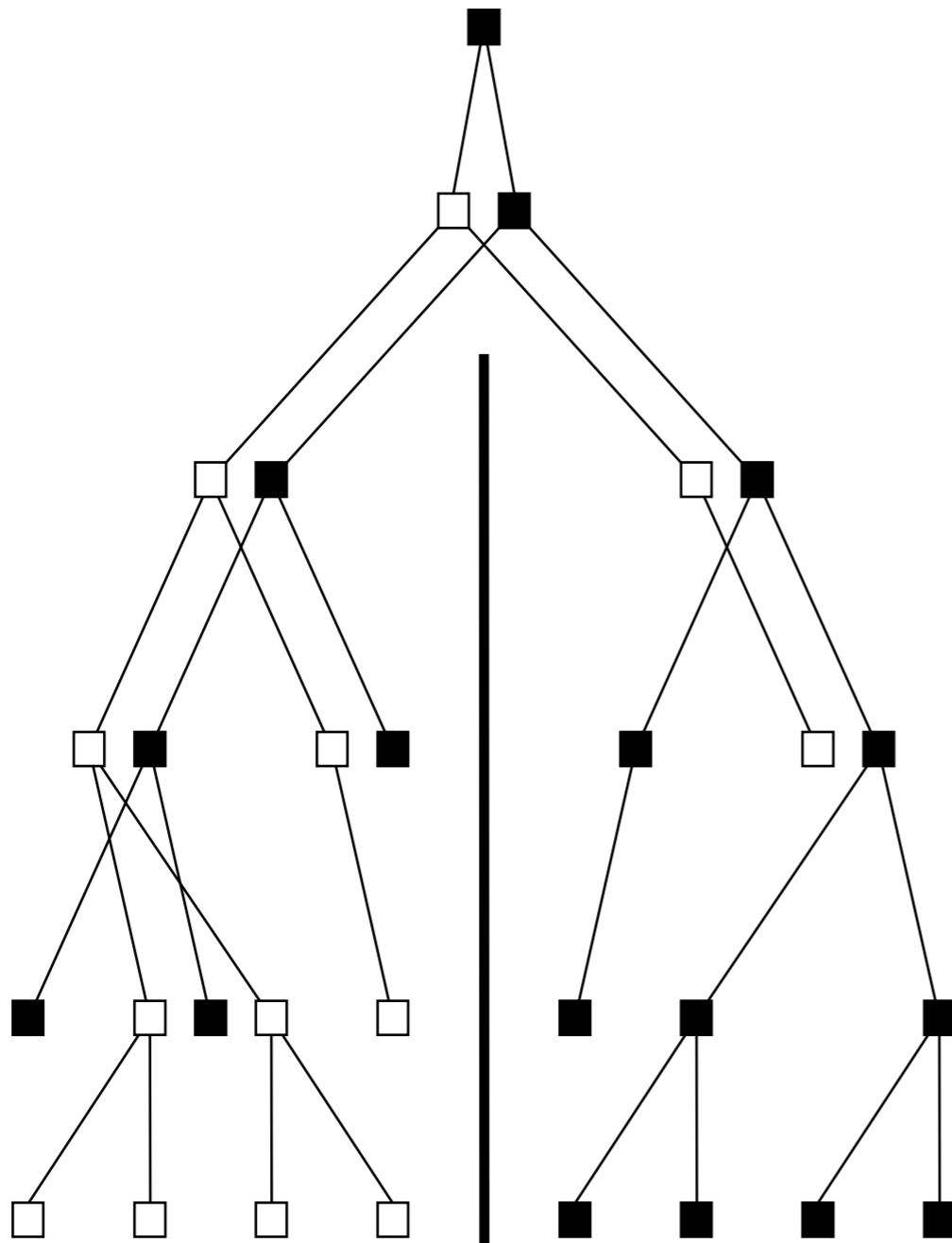


PACE, SCIENCE, 1997



# Isolation mechanisms

Time



geographic  
biological  
ecological

?



# Nature does the experiment

variation  
introduced

*Mutation*



Diversity



variation  
removed

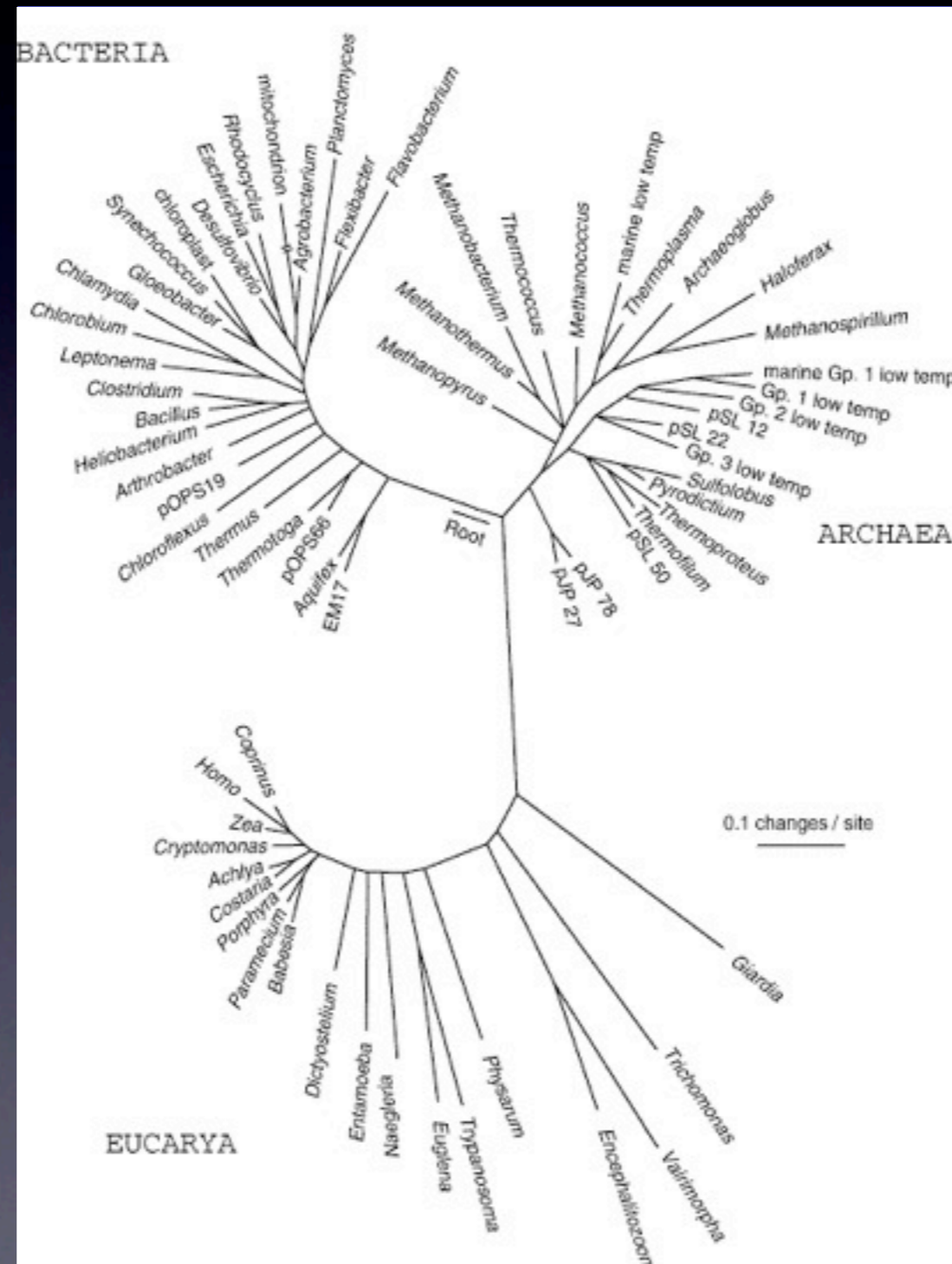
*Selection*  
*Drift*

variation distributed

*Gene flow*



# The beauty of biology -- Diversity



PACE, SCIENCE, 1997



# Model systems: The Importance of Islands

“An island is certainly an intrinsically appealing study subject. It is simpler than a continent or an ocean, a visibly discrete object that can be labeled with a name and its resident populations identified thereby.”

MacArthur and Wilson, *Theory of Island Biogeography*, 1967



Bumpass Hell, Lassen National Park





Islands offer an additional advantage in being more numerous than continents and oceans. By their very multiplicity and variation in shape, size, degree of isolation, and ecology, islands provide the *necessary replications in natural 'experiments' by which evolutionary hypotheses can be tested.*

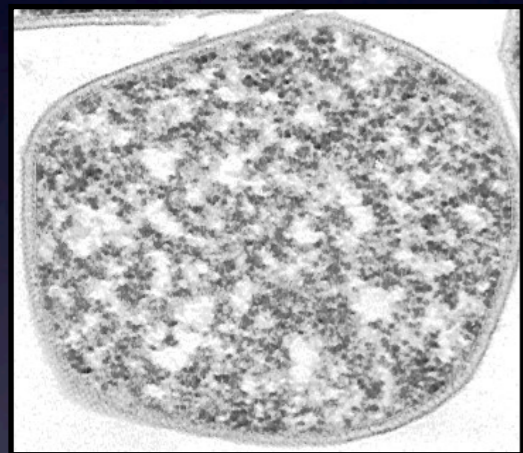
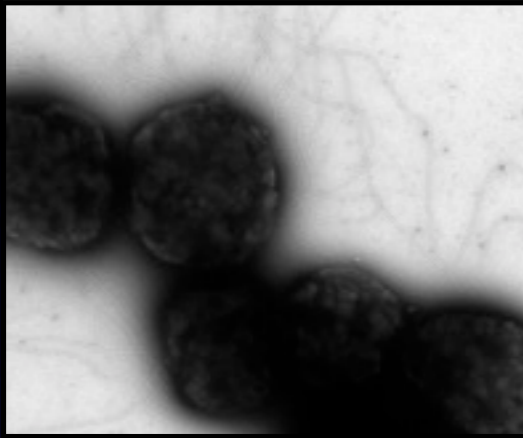
MacArthur and Wilson, *Theory of Island Biogeography*, 1967

Mutnovsky Volcano, Kamchatka Russia



# *Sulfolobus islandicus*

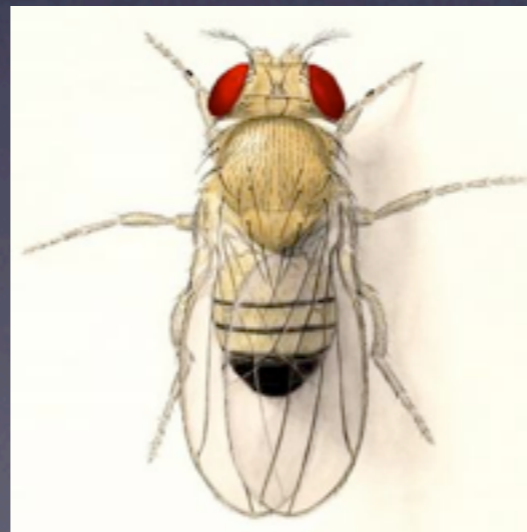
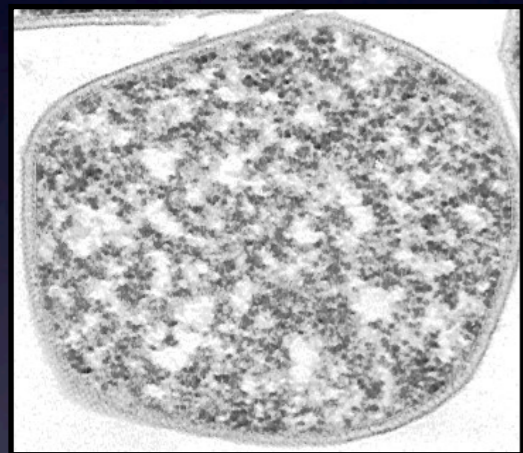
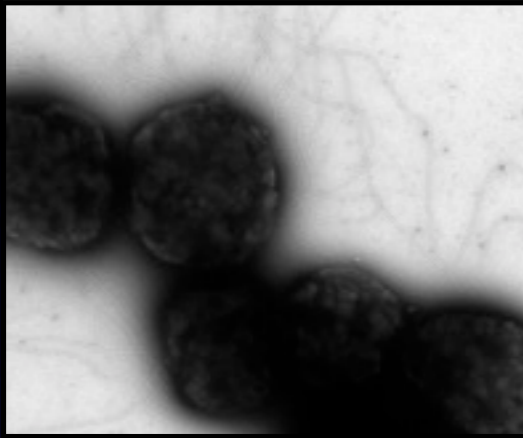
Zillig et al., *Systematic and Applied Microbiology*, 1994





# *Sulfolobus islandicus*

Zillig et al., *Systematic and Applied Microbiology*, 1994





# *Sulfolobus islandicus*



Hyperthermophilic crenarchaeon, lives in geothermal hot springs around pH 3, 80°C.



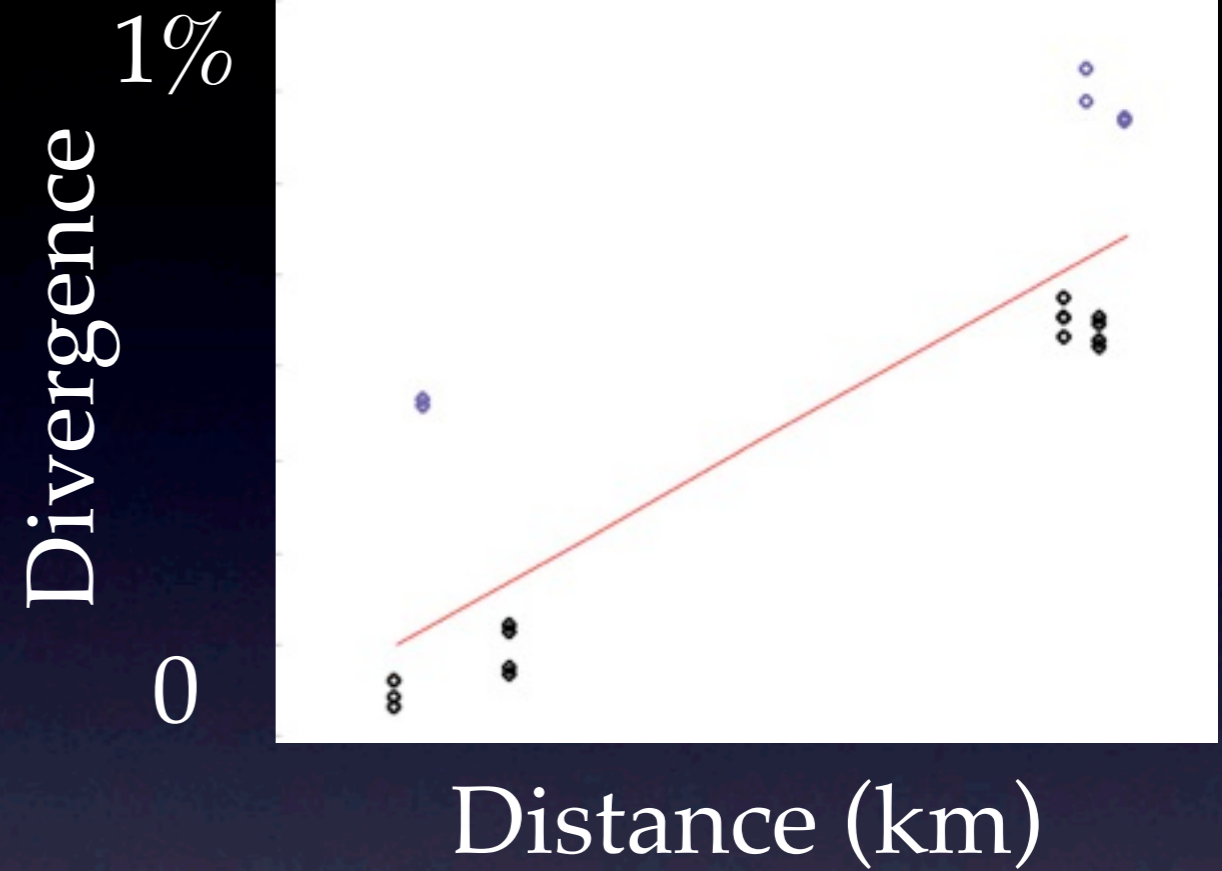
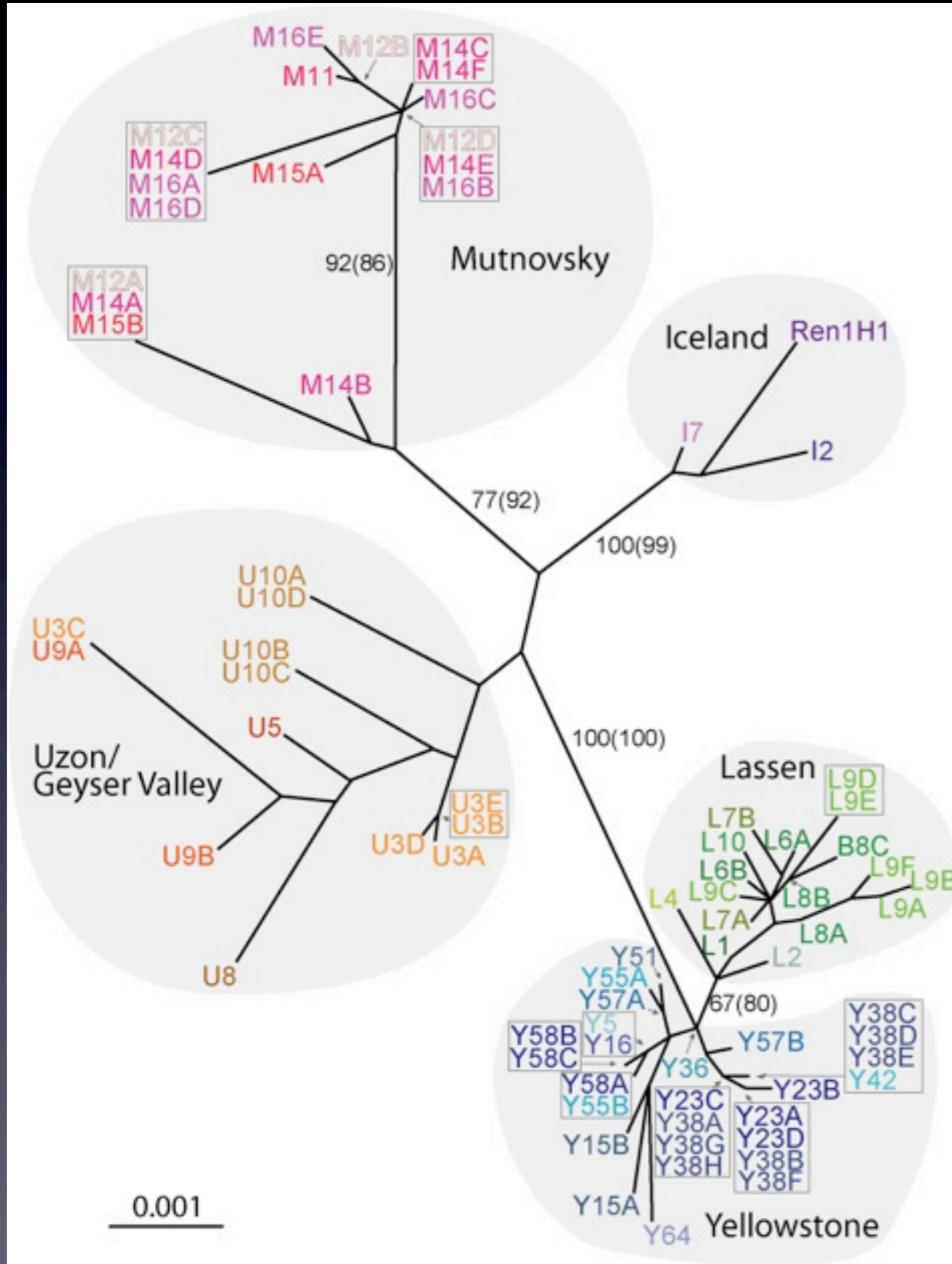
# *Sulfolobus islandicus*



Hyperthermophilic crenarchaeon, lives in geothermal hot springs around pH 3, 80°C.

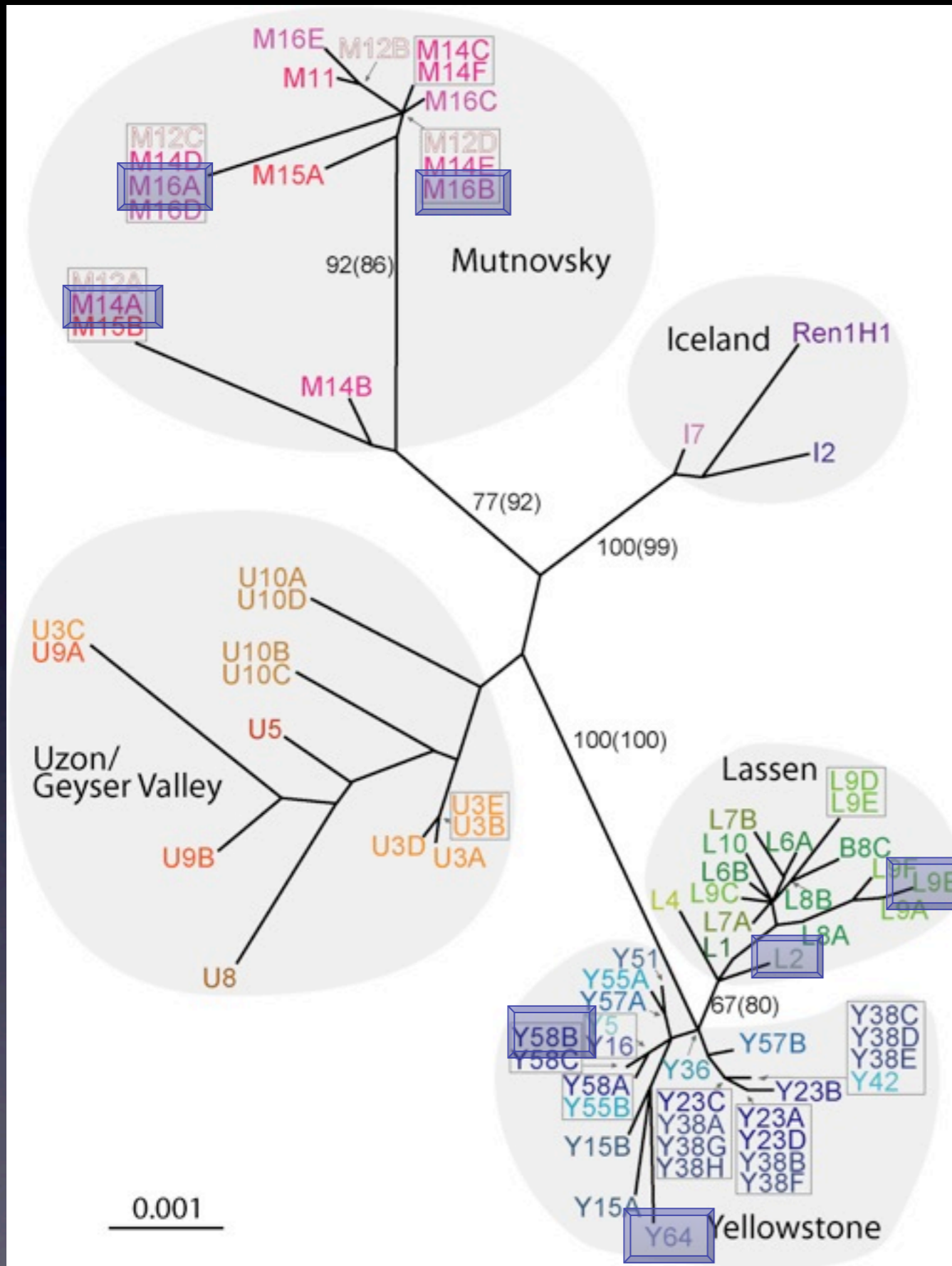


# Isolation by distance



R.J. Whitaker, et al. Science, 2003. 301: p. 976-978.

# Genome sequences of seven strains



Region	Temp °C	pH	Strain name
Yellowstone	59	2.7	Y.N.15.51
Yellowstone	72	3.6	Y.G.57.14
Lassen	78	2.7	L.S.2.15
Lassen	78	2.5	L.D.8.5
Kamchatka	91	3.0	M.14.25
Kamchatka	76	2.0	M.16.27
Kamchatka	76	2.0	M.16.4

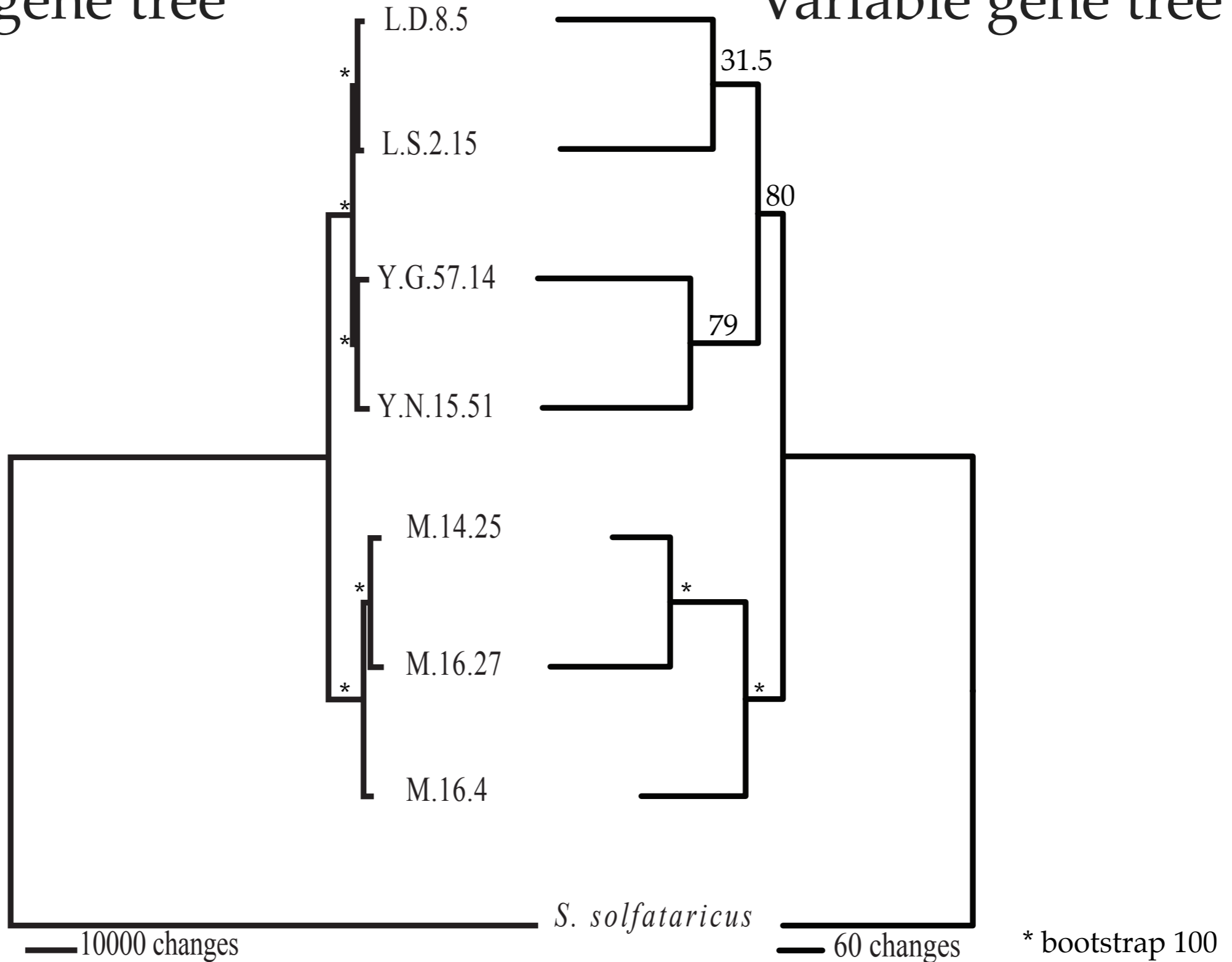
Reno, M.L. *et al.*, PNAS. 2009. 106(21): p. 8605-8610.



# Biogeography of the variable genome

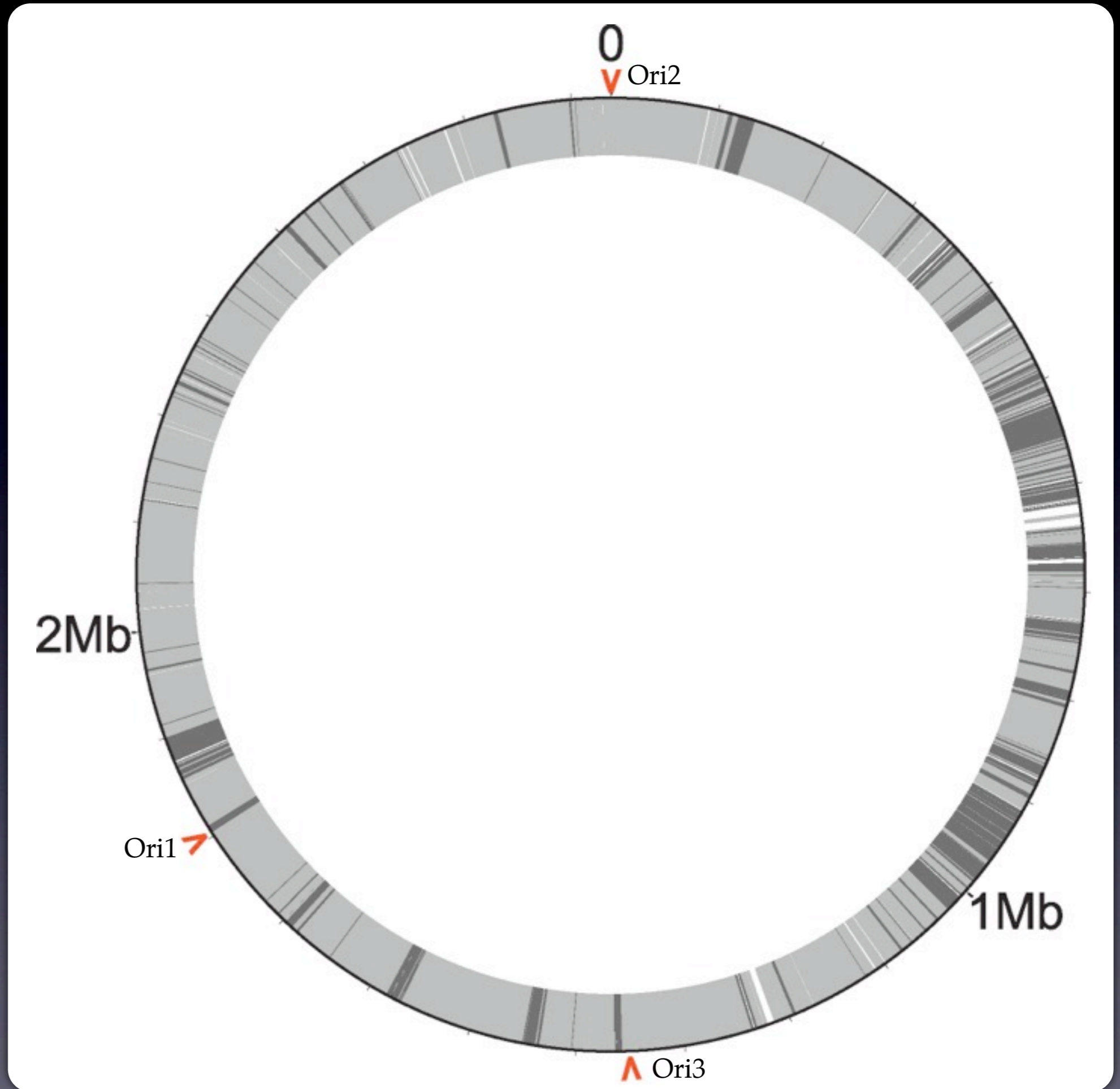
Core gene tree

Variable gene tree



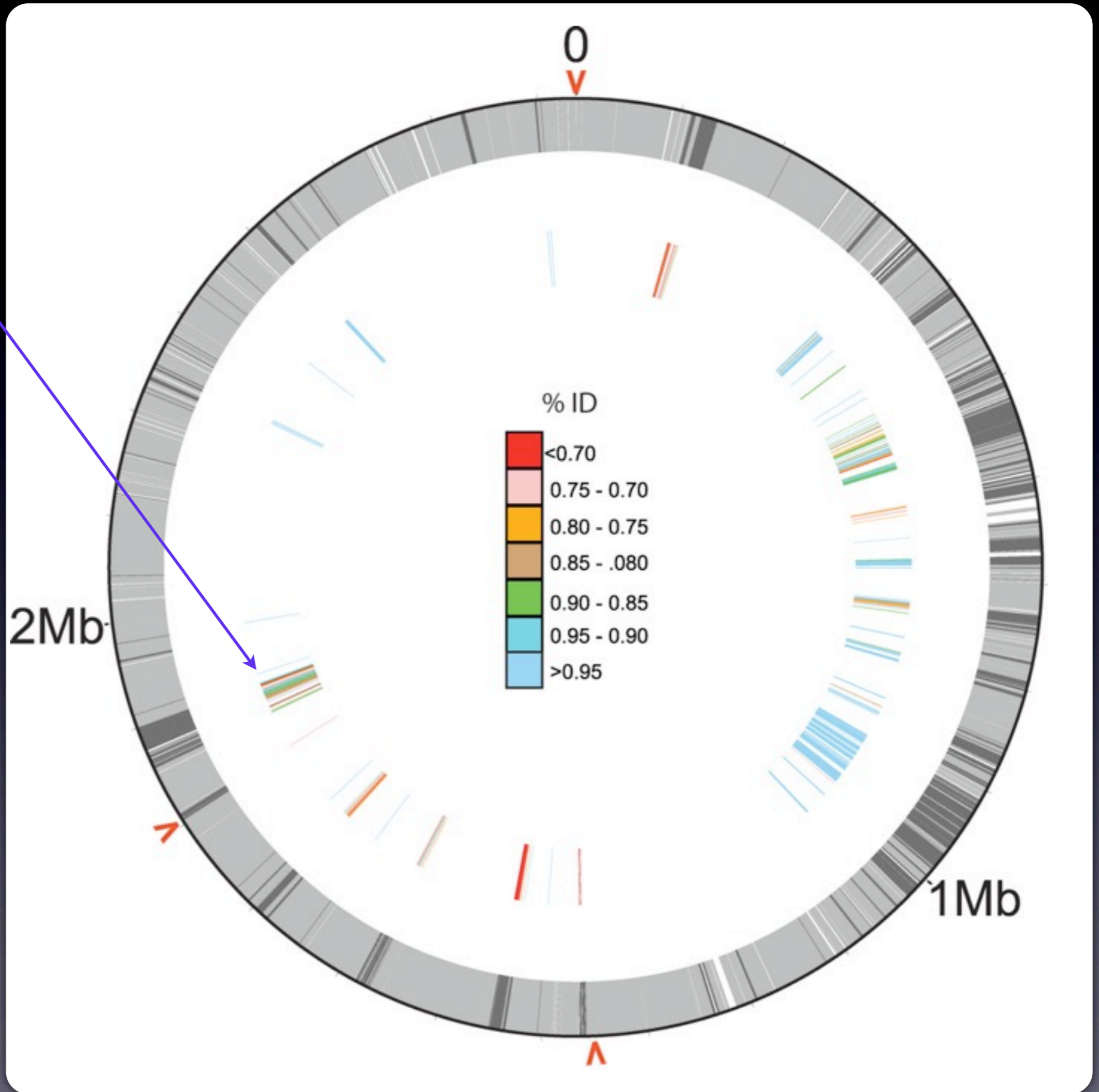
Reno, M.L. *et al.*, PNAS. 2009. 106(21): p. 8605-8610.

- Core
- Variable



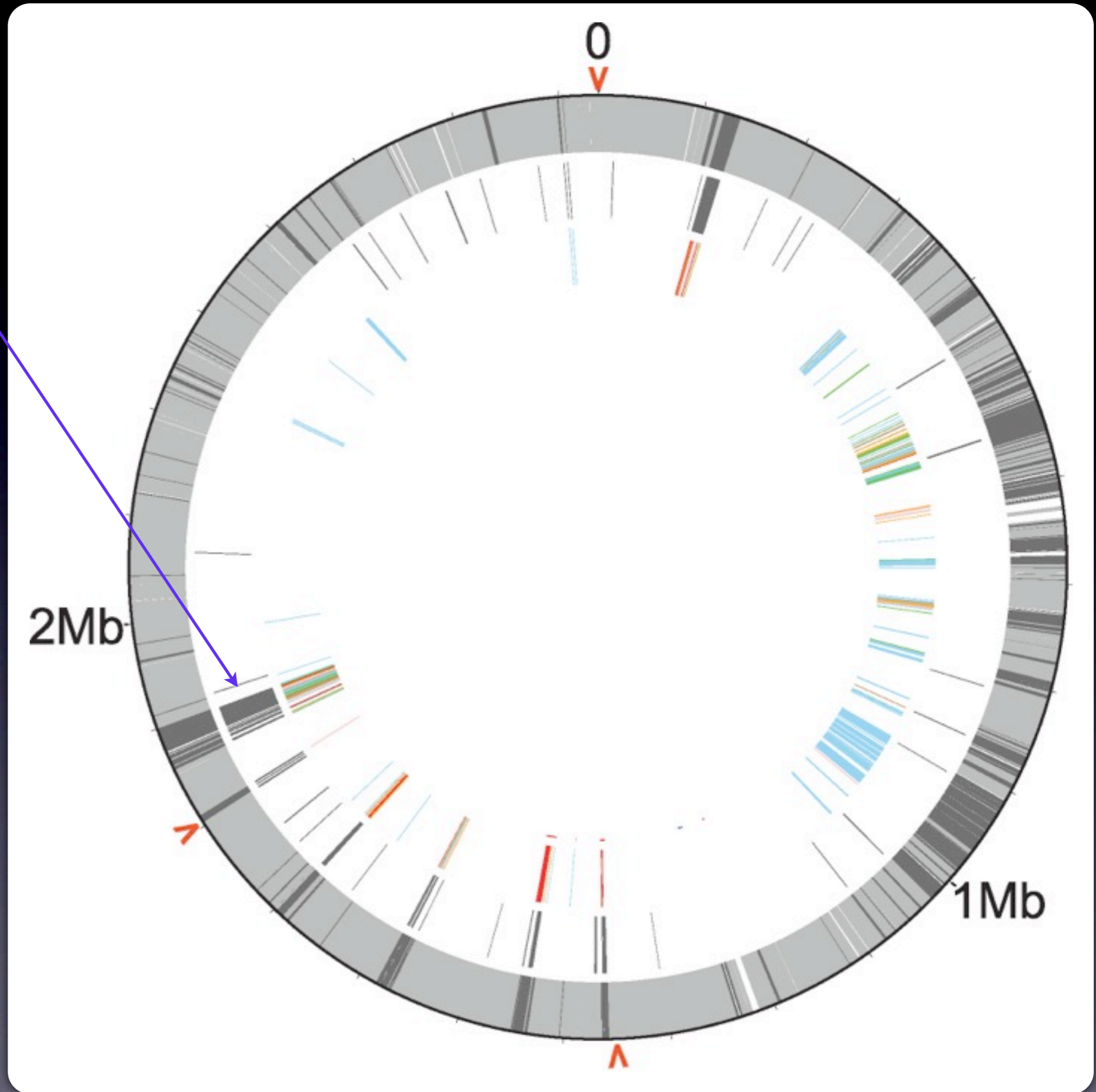


Nucleotide identity of genes shared between populations



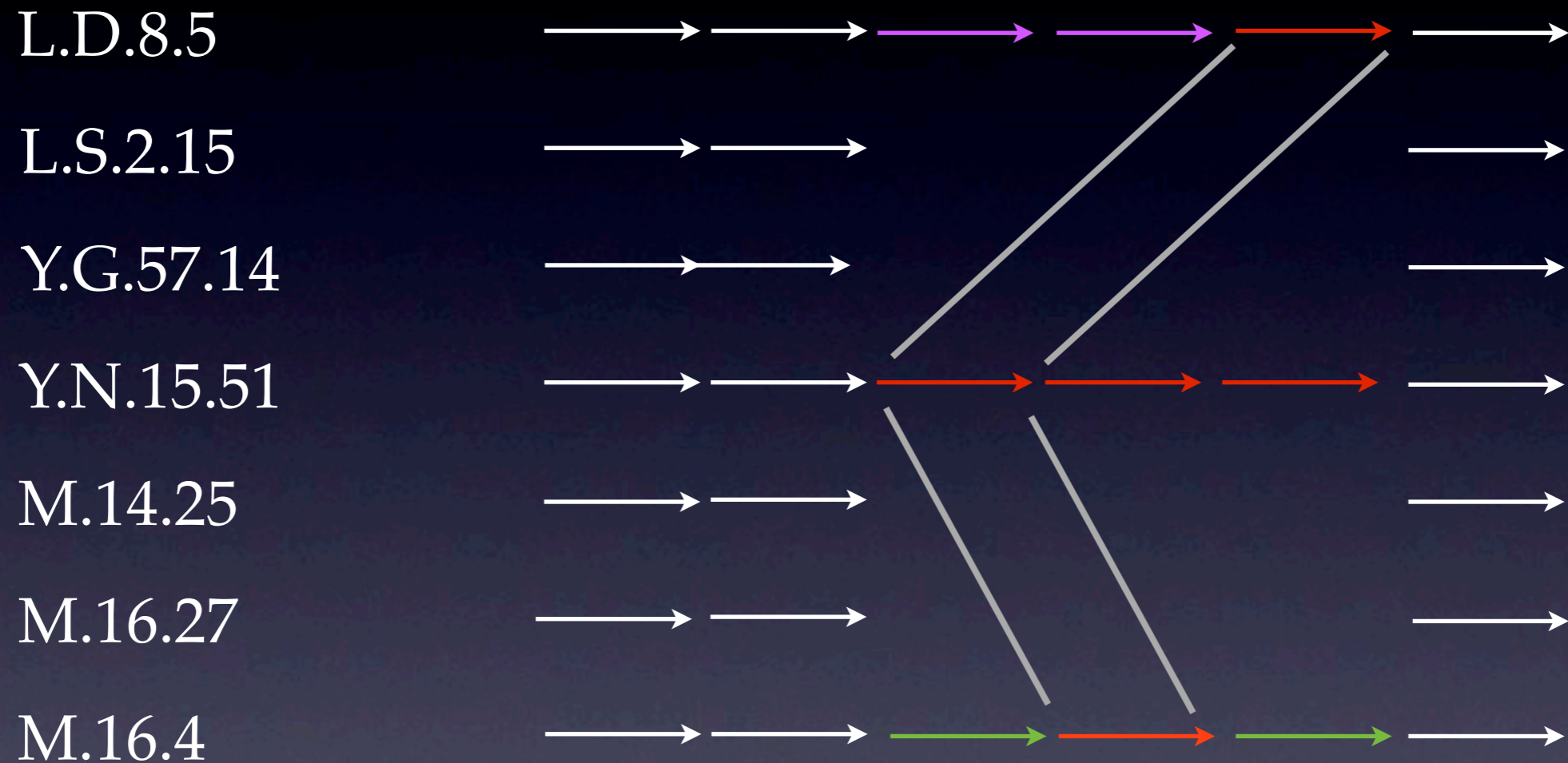


# Viruses and plasmids



Reno, M.L. *et al.*, PNAS. 2009. 106(21): p. 8605-8610.

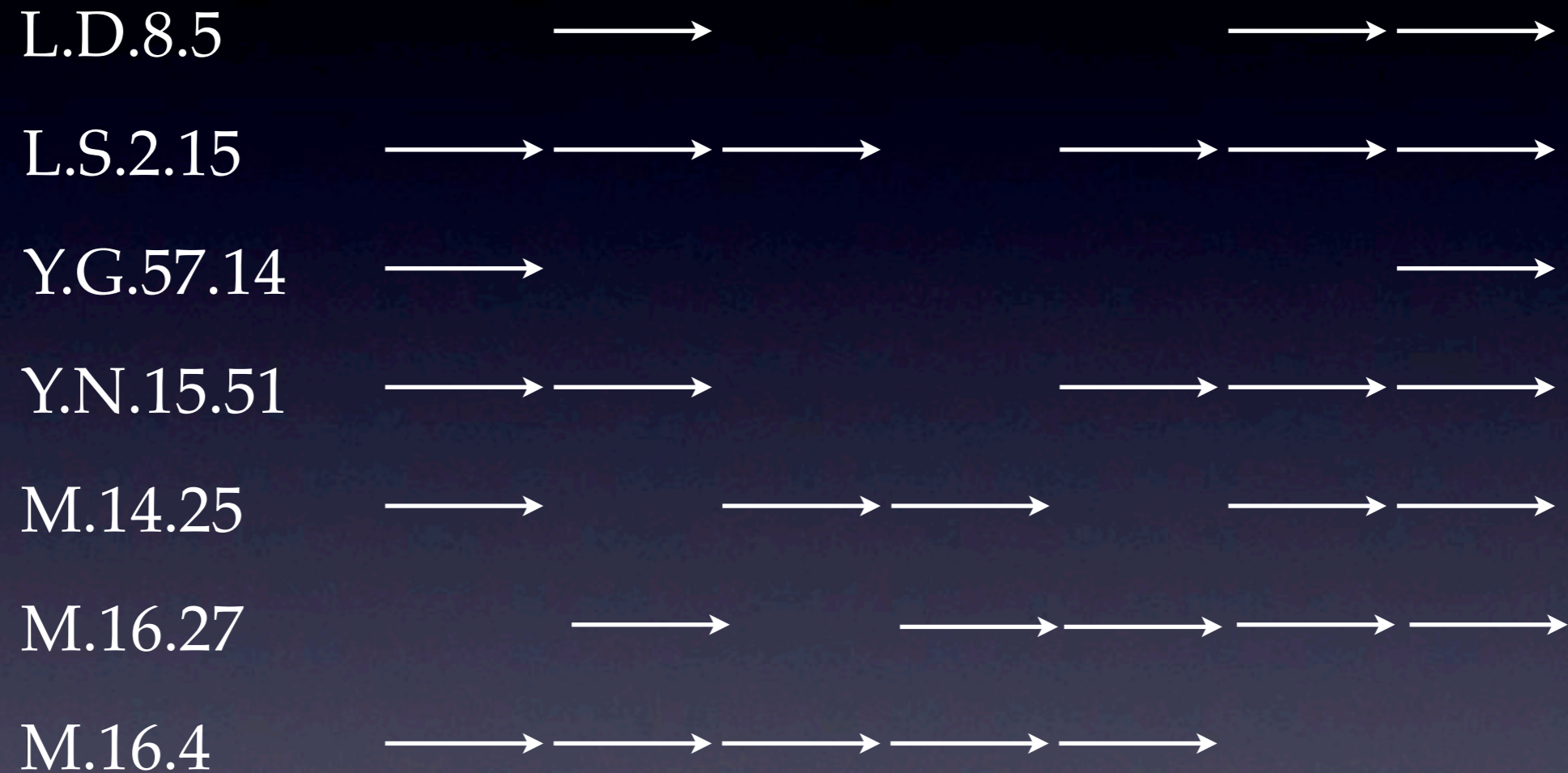
# Genomic signature of gain



< 98.8% nucleotide identity

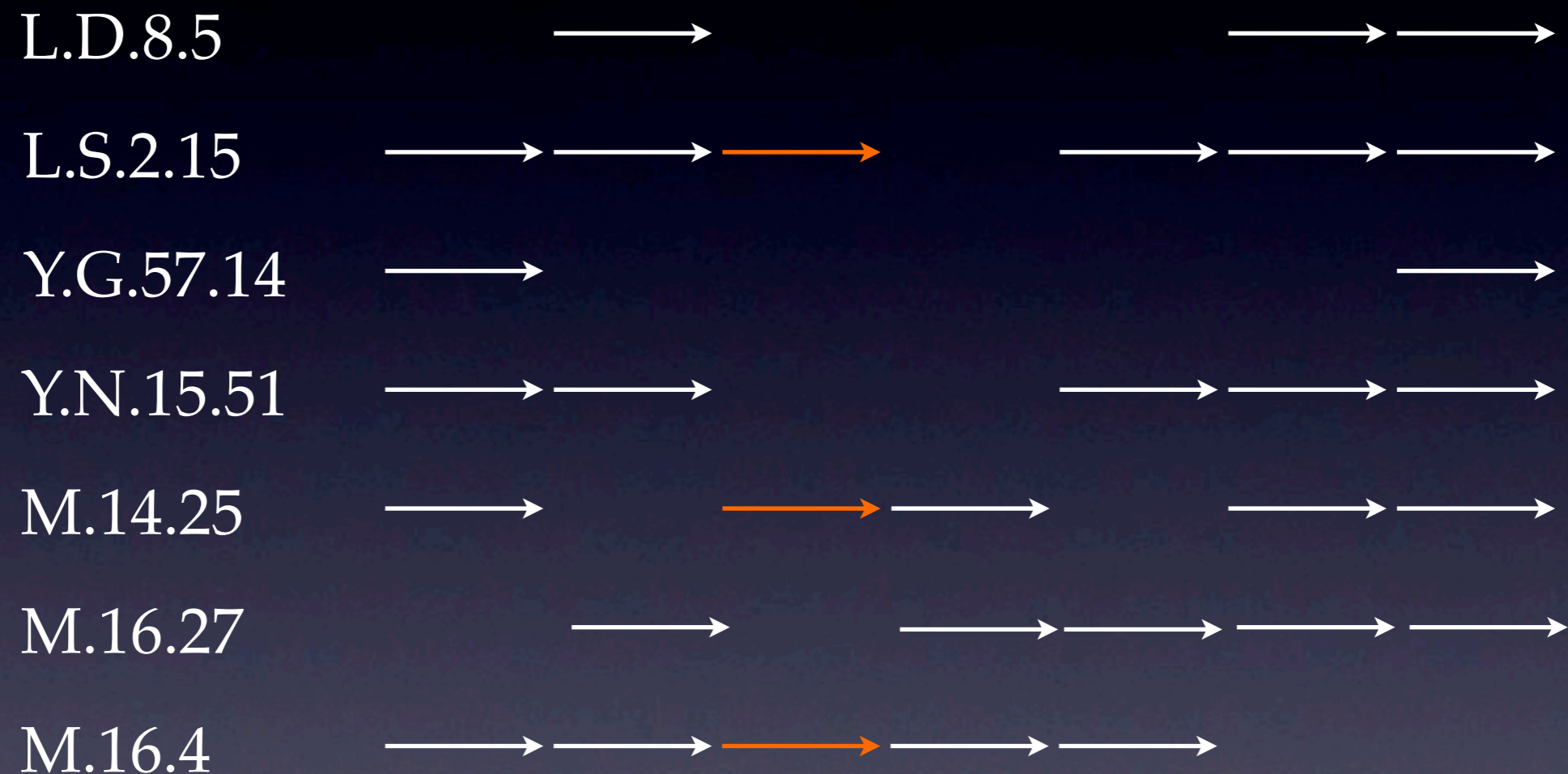


# Genomic signatures of loss



> 98.8% nucleotide identity  
Synteny preserved

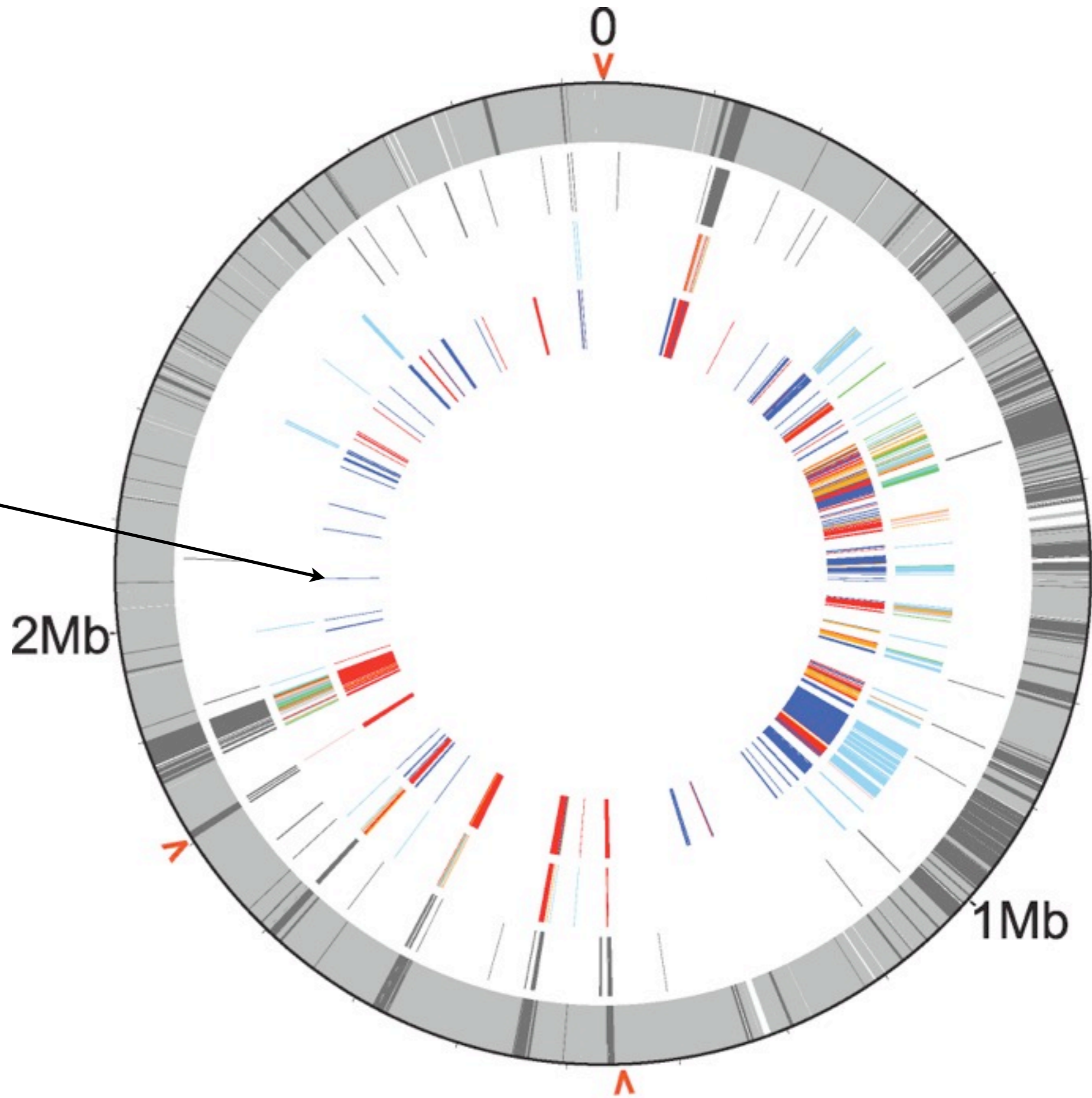
# Genomic signatures of loss



Alternative hypothesis: Subsets of strains from each population *gained same gene in the same place*



- Gain
- Loss
- Multiple



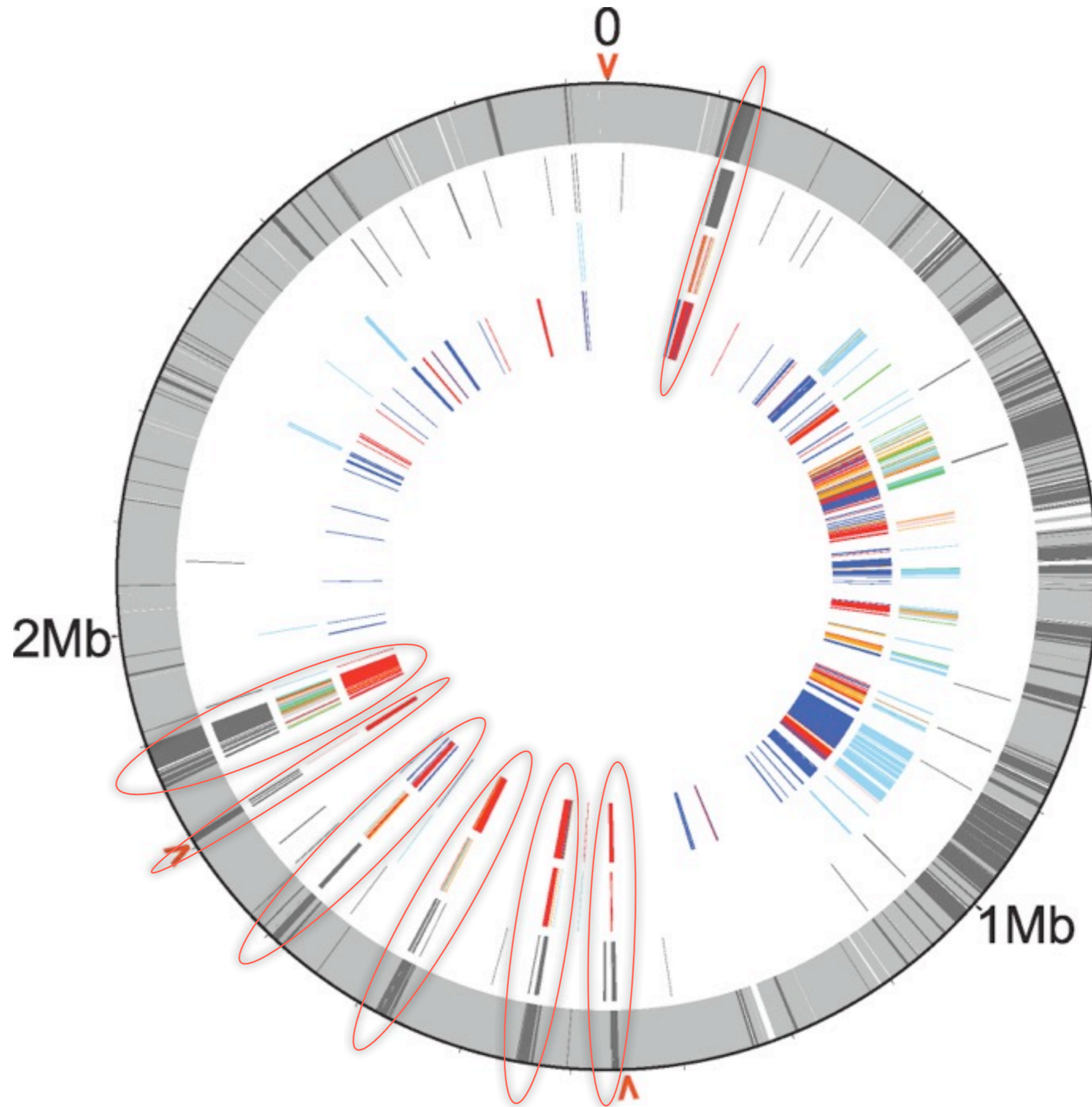
# Sources of gained genes

		Number of genes gained	% of total gains
Sulfolobales	Genomes	438	36%
Sulfolobales	Mobile elements	283	23%
Other		51	4%
No Match *		441	37%

\* by BLAST  $e^{-5}$ ,  $>70\%$  coverage,  $>40\%$  nucleotide identity

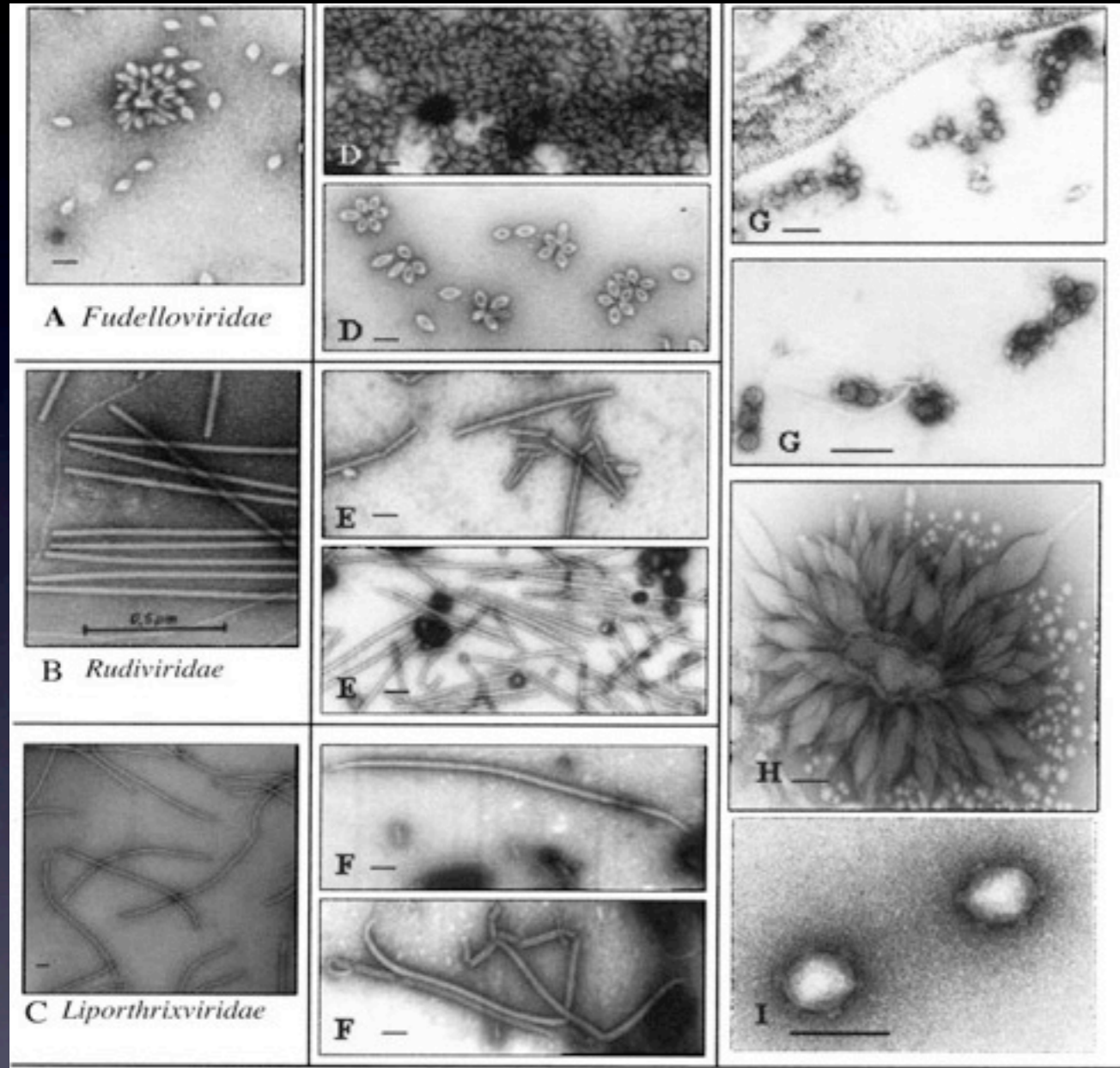


- Gain
- Loss
- Multiple



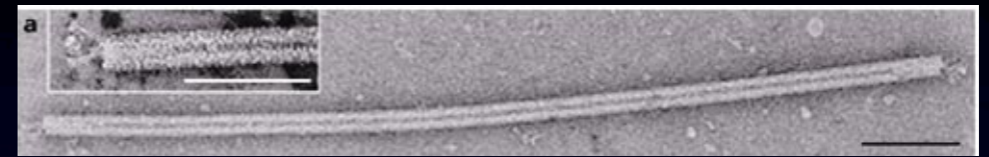


# Sulfolobus viruses



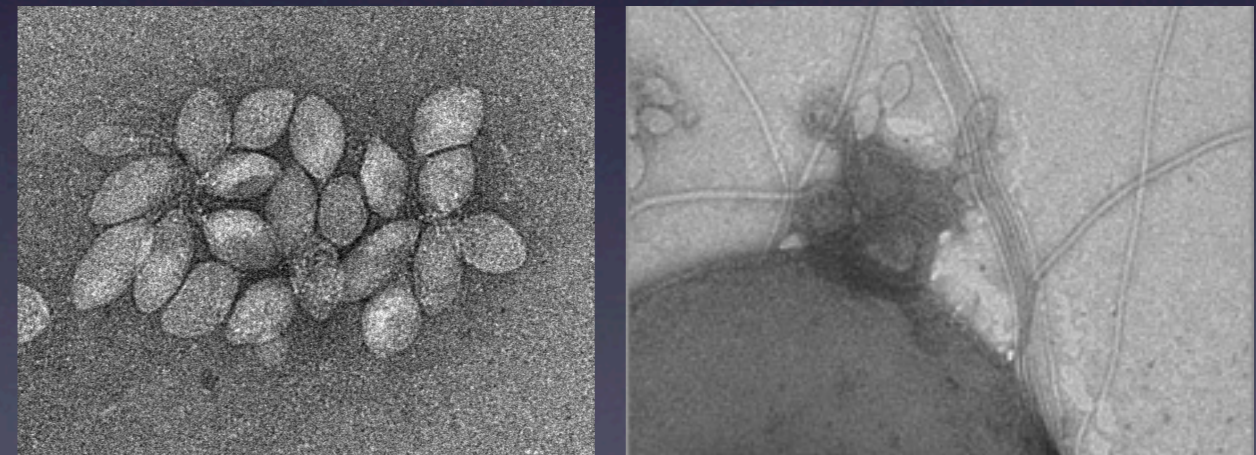
Rice, *et al.* PNAS 2001

## Lytic virus -- SIRV



Prangishvili *et al.* Nature Review  
Microbiology. 4, 837-848, 2006.

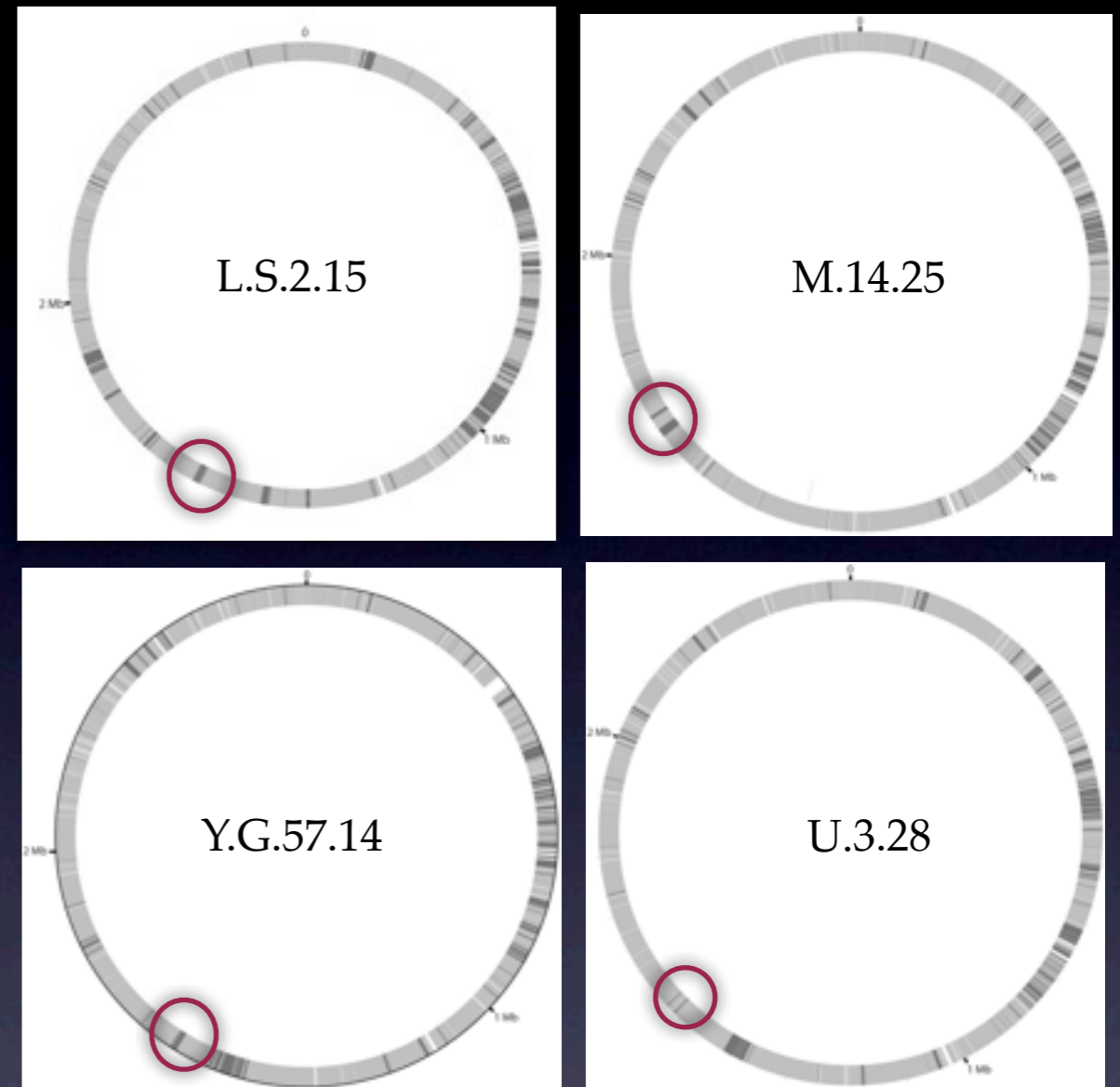
## Chronic virus -- SSV





# Sulfolobus spindle-shaped virus (SSV)

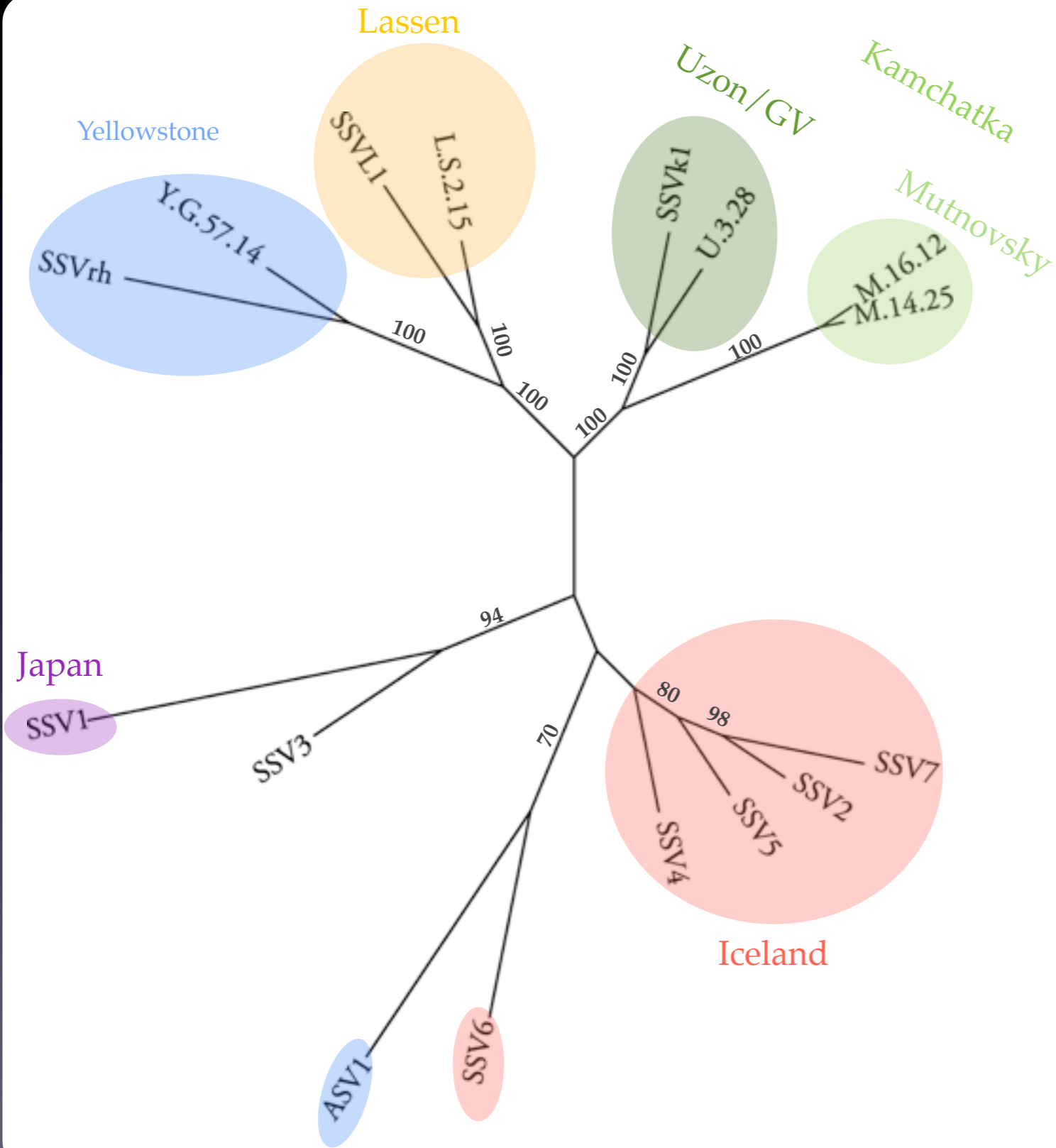
- Integrative, nonlytic, double stranded DNA virus
- 10 fully sequenced SSV nonintegrated virus particles from around the world
  - Japan: SSV1
  - Iceland: SSV2, SSV4, SSV5, SSV6, SSV7
  - Yellowstone: SSVrh, ASV1
  - Kamchatka: SSVk1
  - Lassen: SSVL1 #



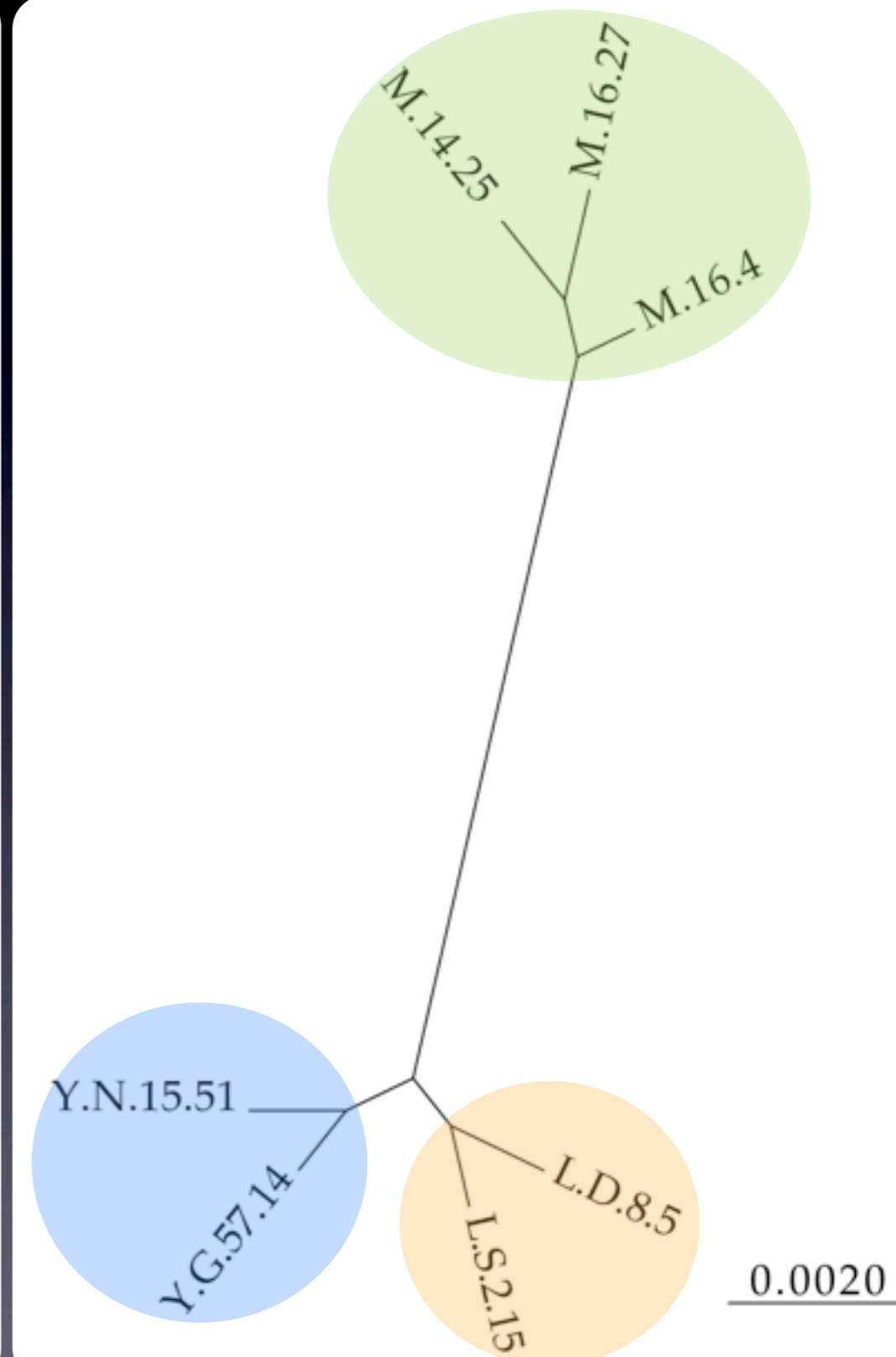
+4 of 8 *S. islandicus* genomes have integrated SSVs

Palm, P., et al., J. Virology, 1991. 185(1): p. 242-250. Wiedenheft, B., et al., J Virol, 2004. 78(4): p. 1954-61.  
Redder, P., X. Peng, et al. (2009). Environmental Microbiology 11(11): 2849-2862. # Kenneth Stedman

# Virus

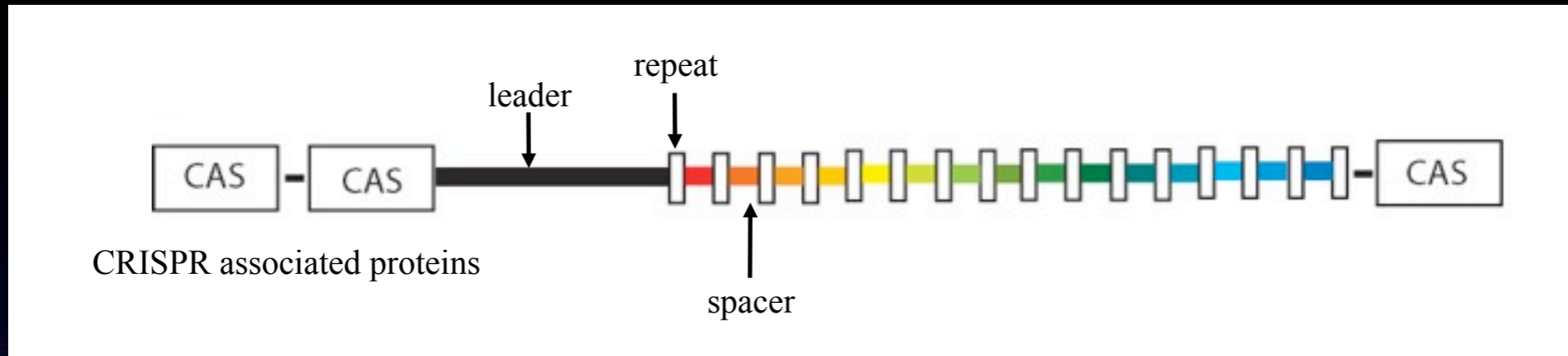


# Host

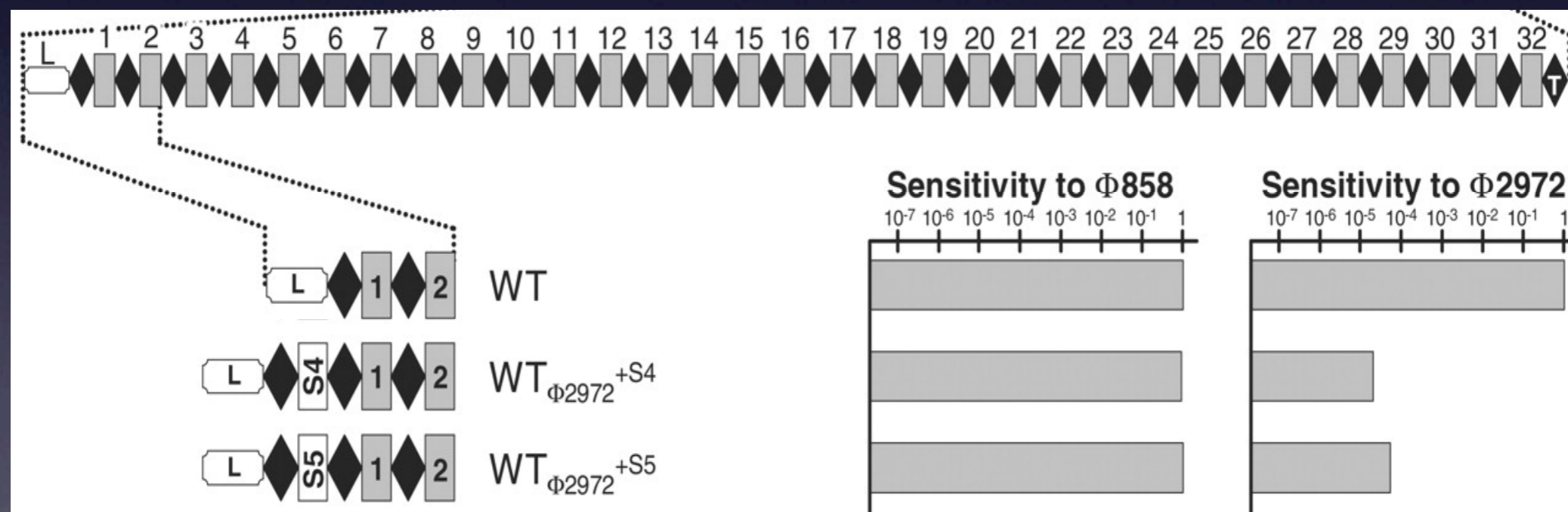
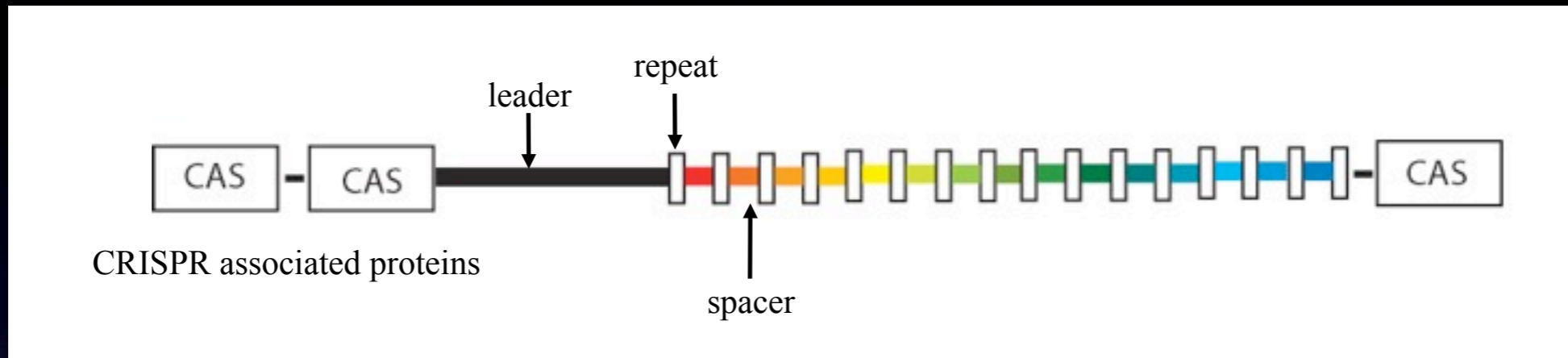




# CRISPR elements - Clustered Regularly Interspaced Short Palindromic Repeats



# CRISPR elements - Clustered Regularly Interspaced Short Palindromic Repeats

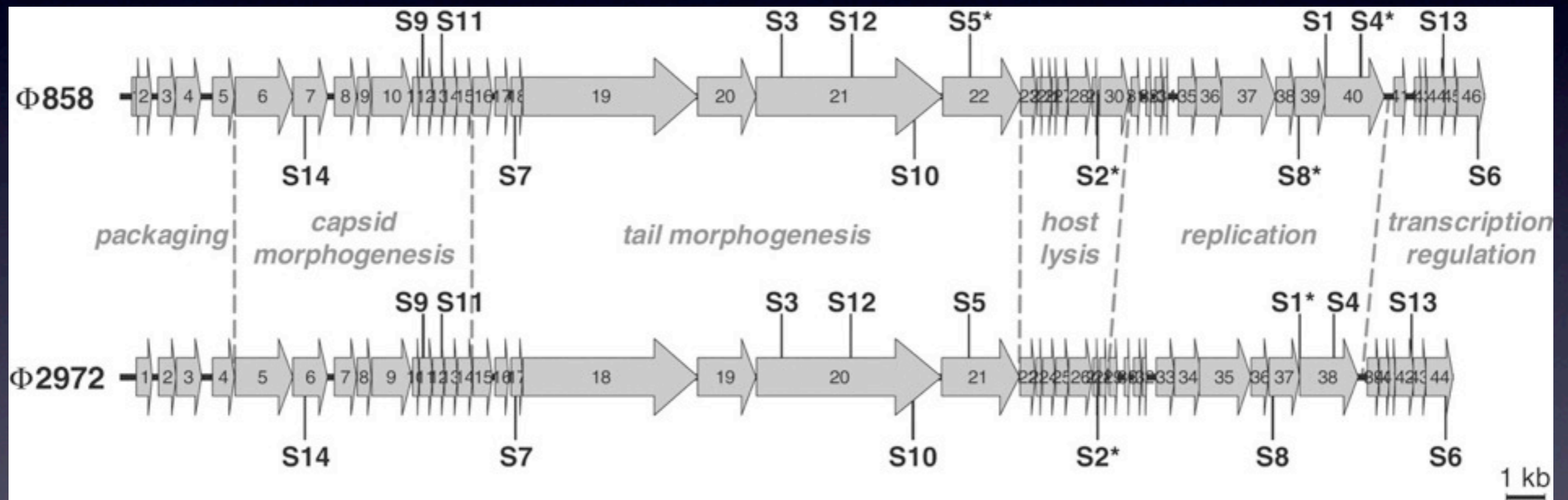


New spacers added to the leader end provide immunity to lytic viruses if they match sequence 100%

Barrangou et al, 2007 Science 315, 1709-1712

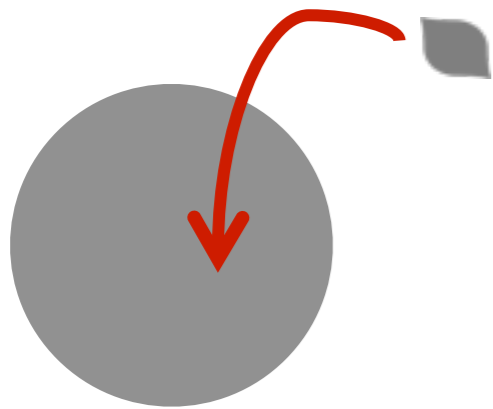


# Different strains acquire different spacers from the same virus

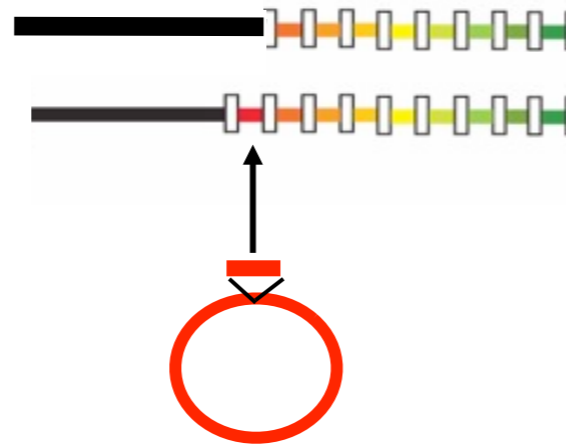


# CRISPR immunity model

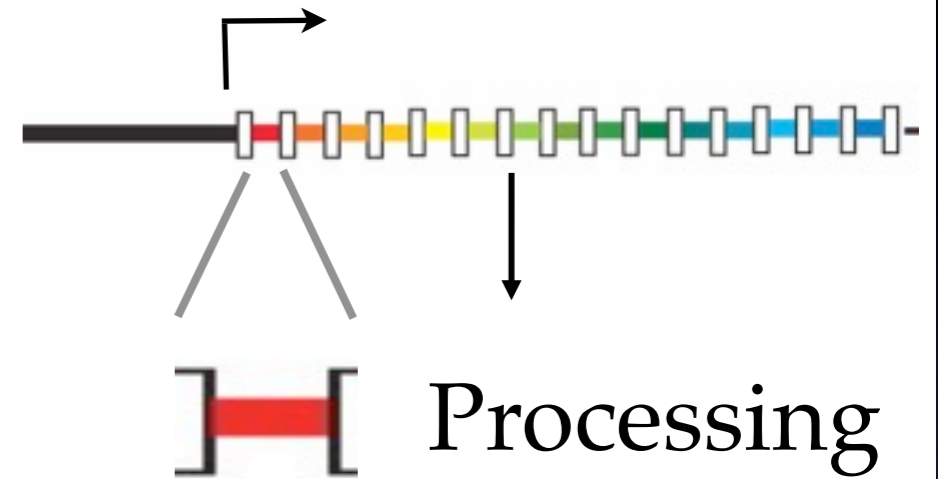
Infection



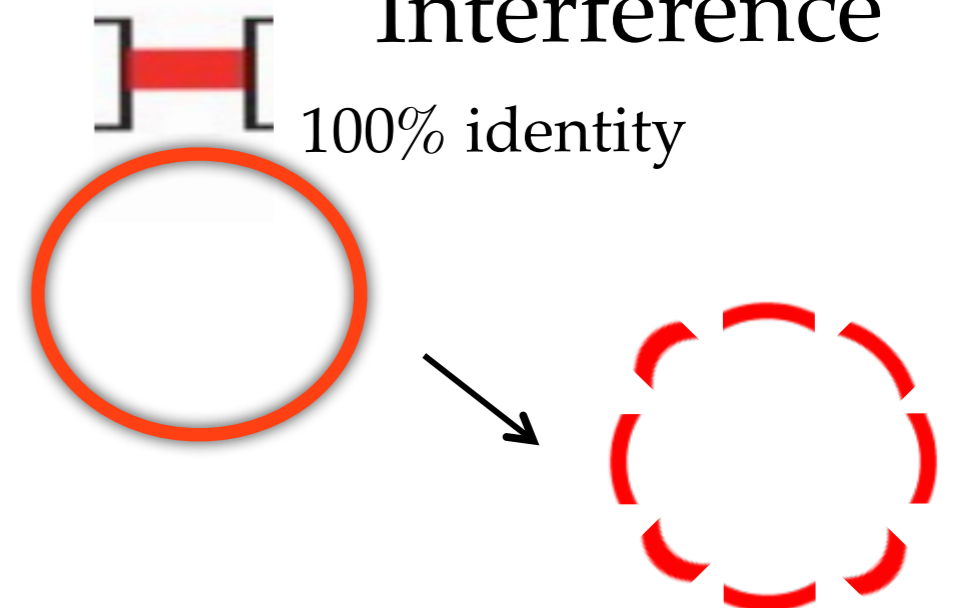
Spacer  
Integration



Expression

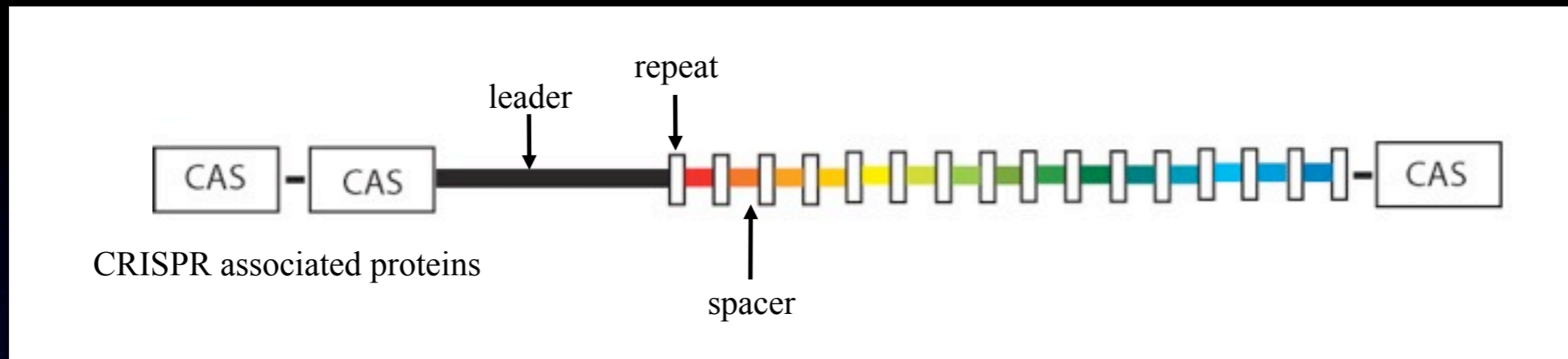


Interference

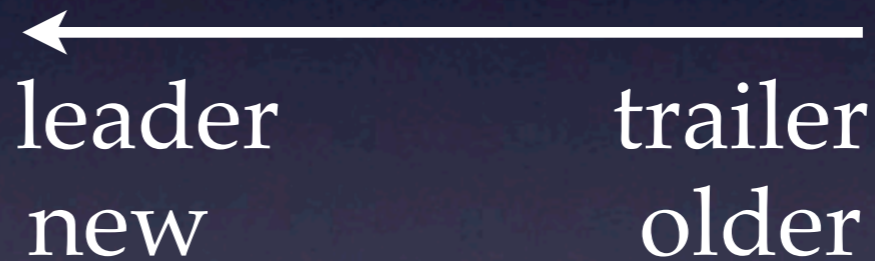




# CRISPR elements - Clustered Regularly Interspaced Short Palindromic Repeats



## History of interactions



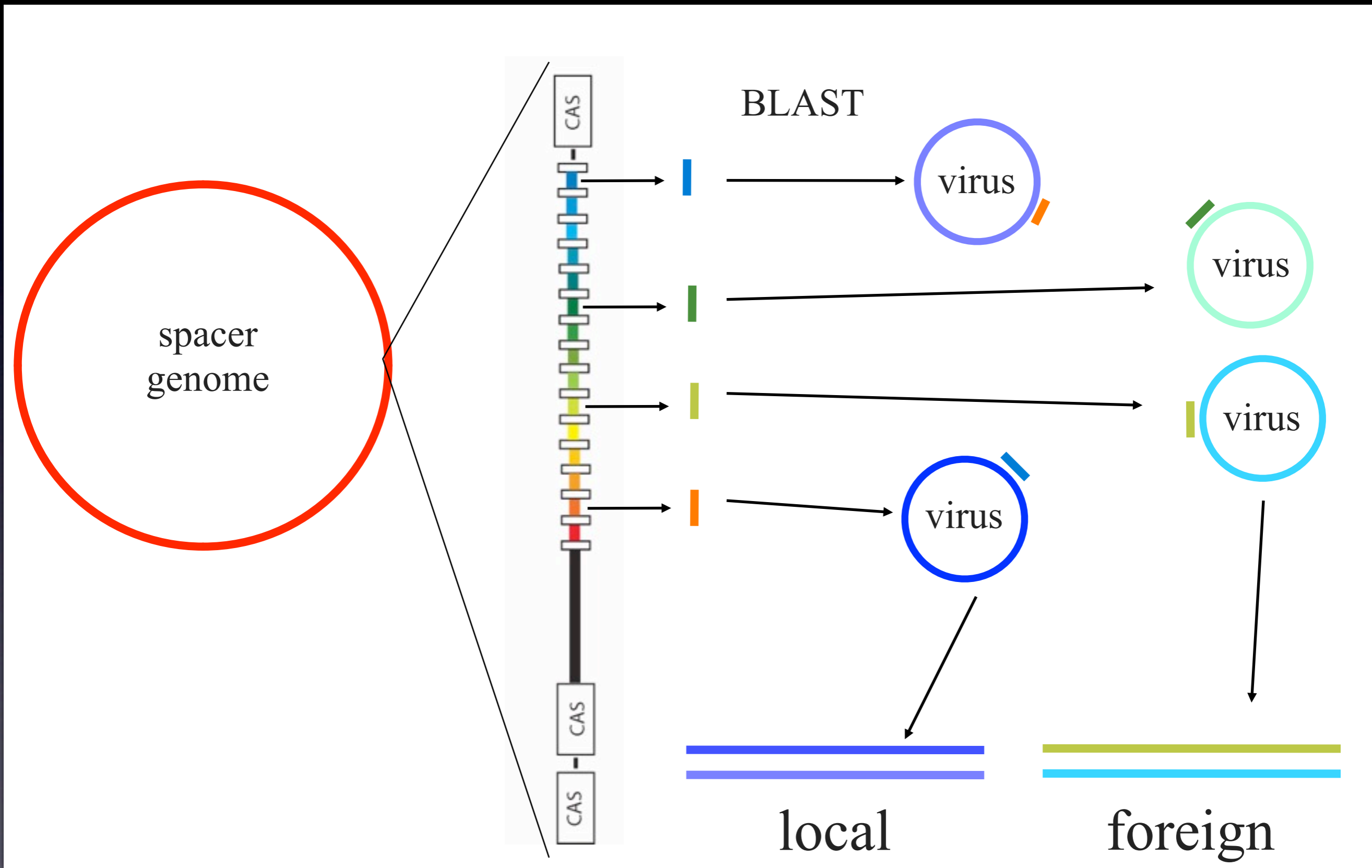
7 *S. islandicus* genomes

20 different CRISPR loci

1393 spacers

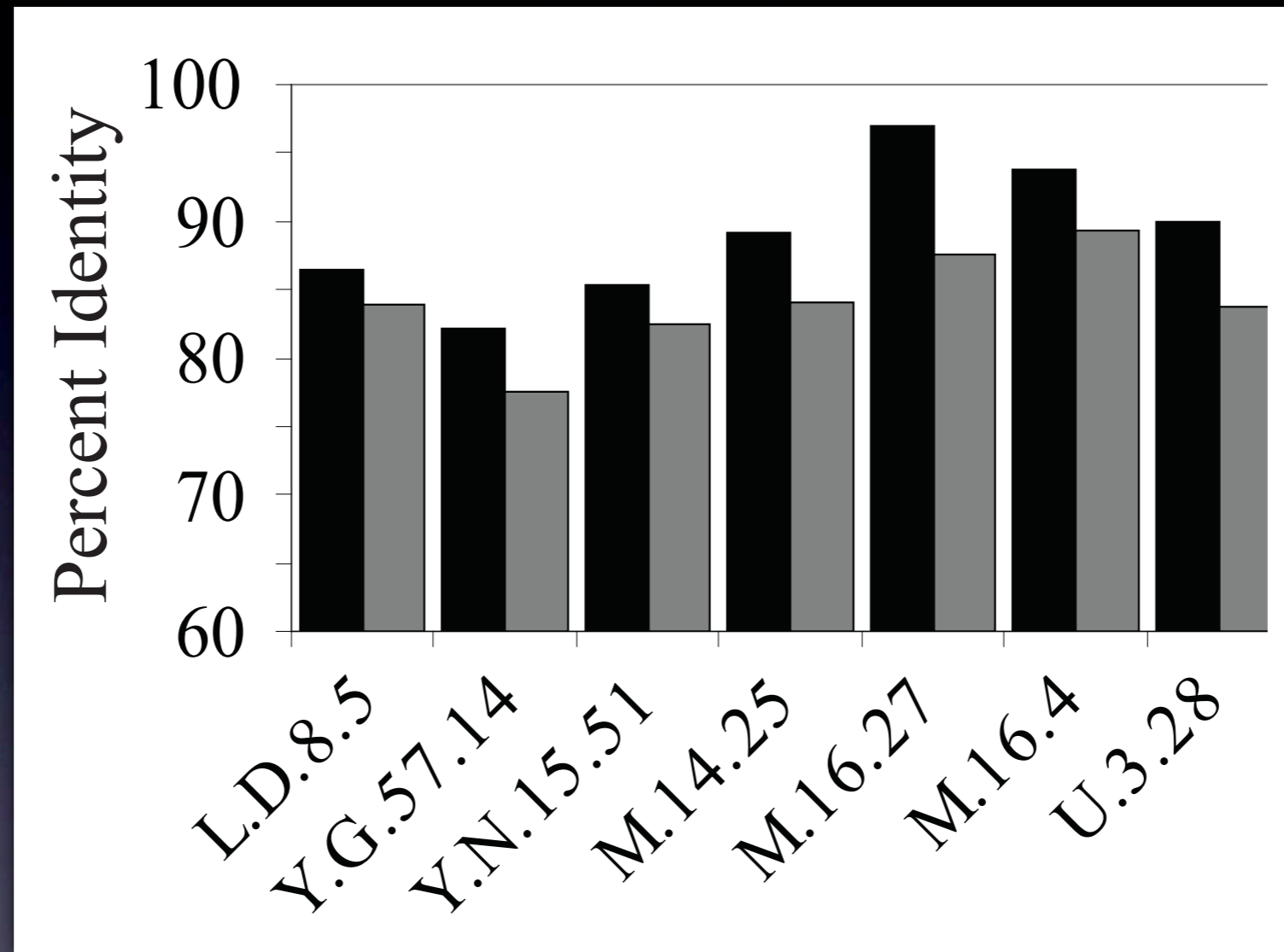
233 matches to genetic elements

# CRISPRs from *Sulfolobus* genomes compared to all known *Sulfolobus* viruses





# Higher matches to local than to foreign viruses



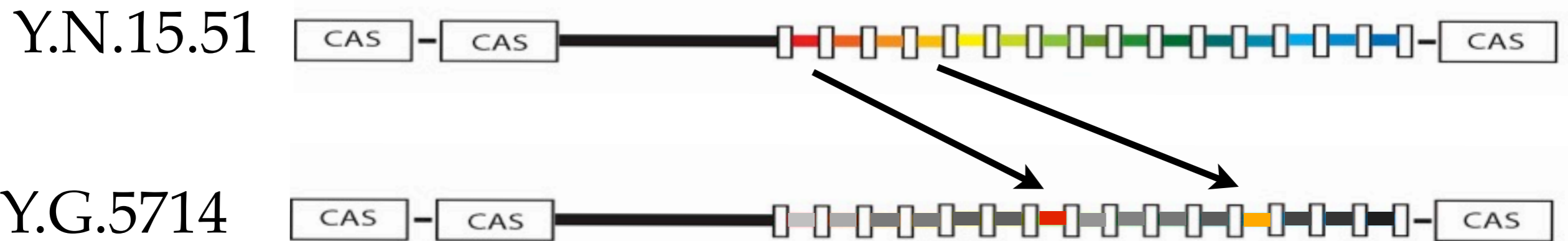
Black: local virus match Grey: foreign virus match

Welch-ANOVA:  $p=0.0113$

$2^{-7}$  probability that local matches are higher than foreign matches in all seven locations

Held, N.L. and R.J. Whitaker, *Environmental Microbiology*, 2009. 11(2): p. 457-466.

# *S. islandicus* strains are sampling the same viral populations

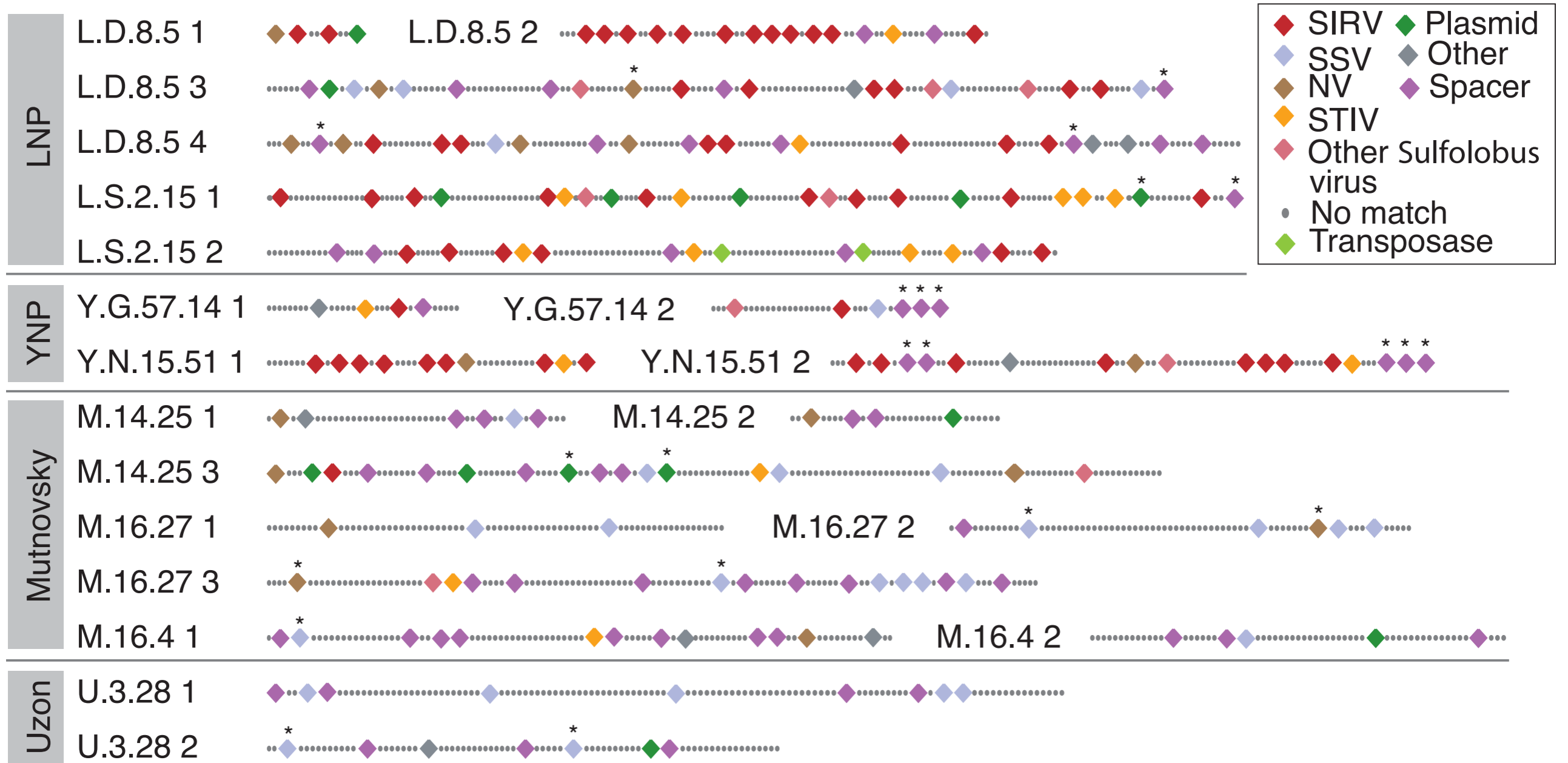


25 of 31 matches between genomes  
from the same region



# Differences in the number of CRISPR spacer matches to the same types of viruses

	SSV	SIRV
Kamchatka	22	4
North America	2	61



Held, N.L. and R.J. Whitaker, Environmental Microbiology, 2009. 11(2): p. 457-466.





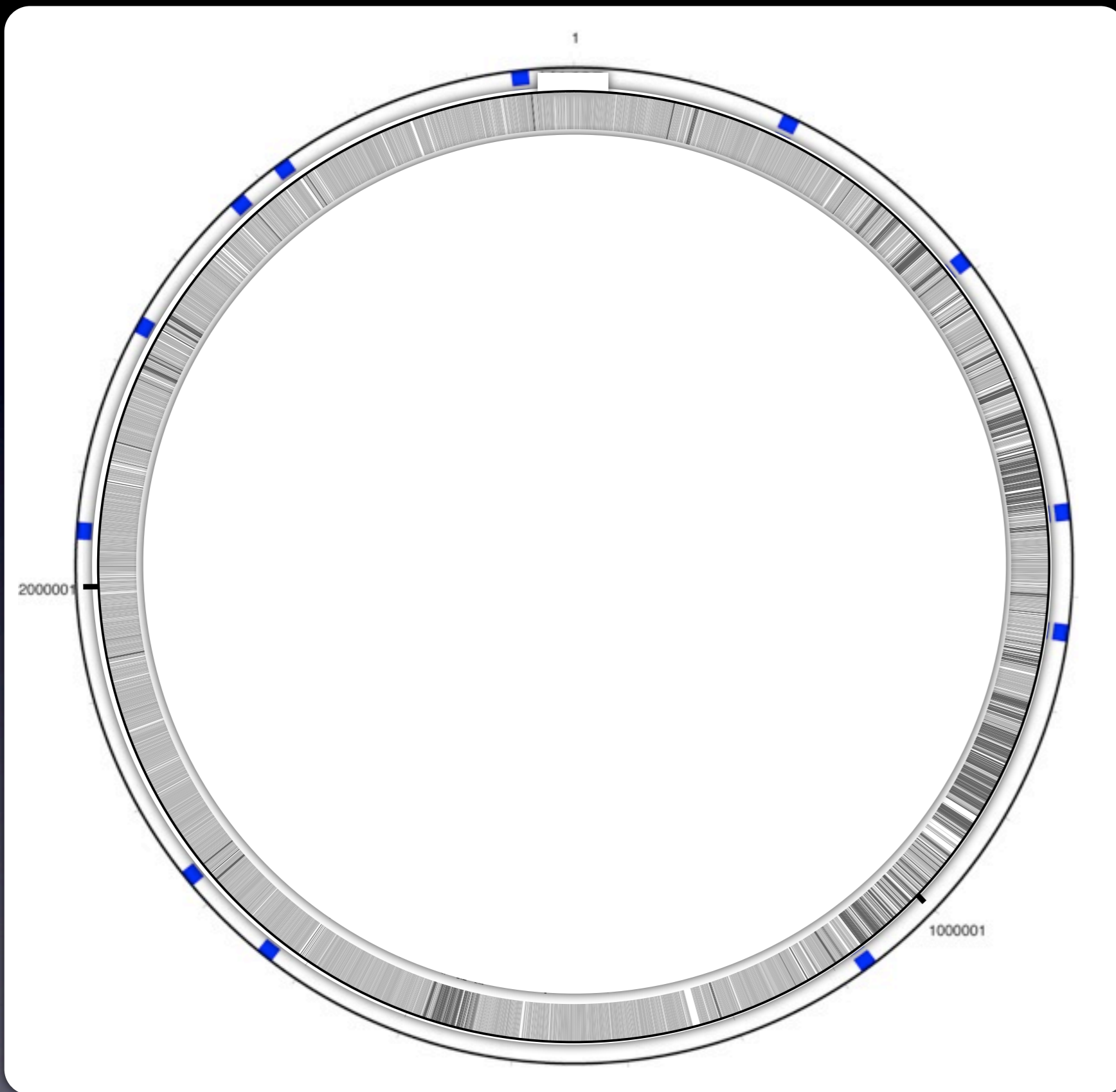
Mutnovsky Volcano  
Kamchatka, Russia



39 strains  
M16 spring



# Multilocus Sequence Typing

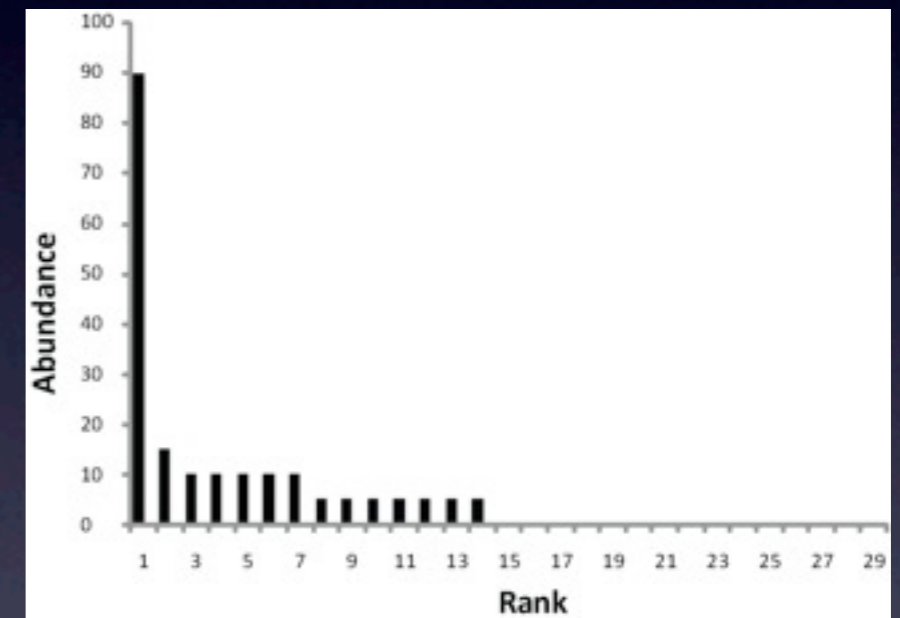
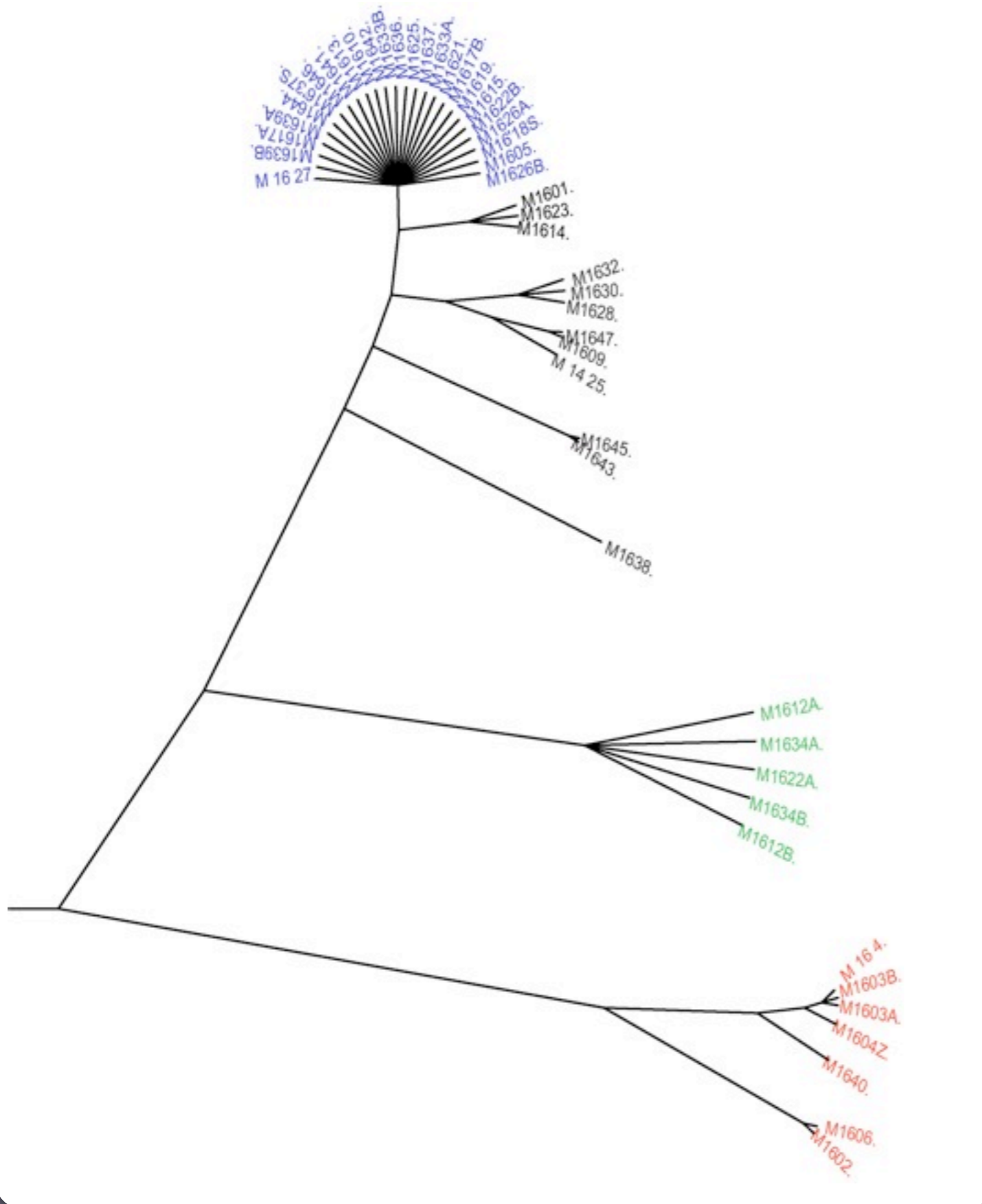


12 loci

39 isolates  
from one  
spring

# Multilocus Sequence Typing (MLST)

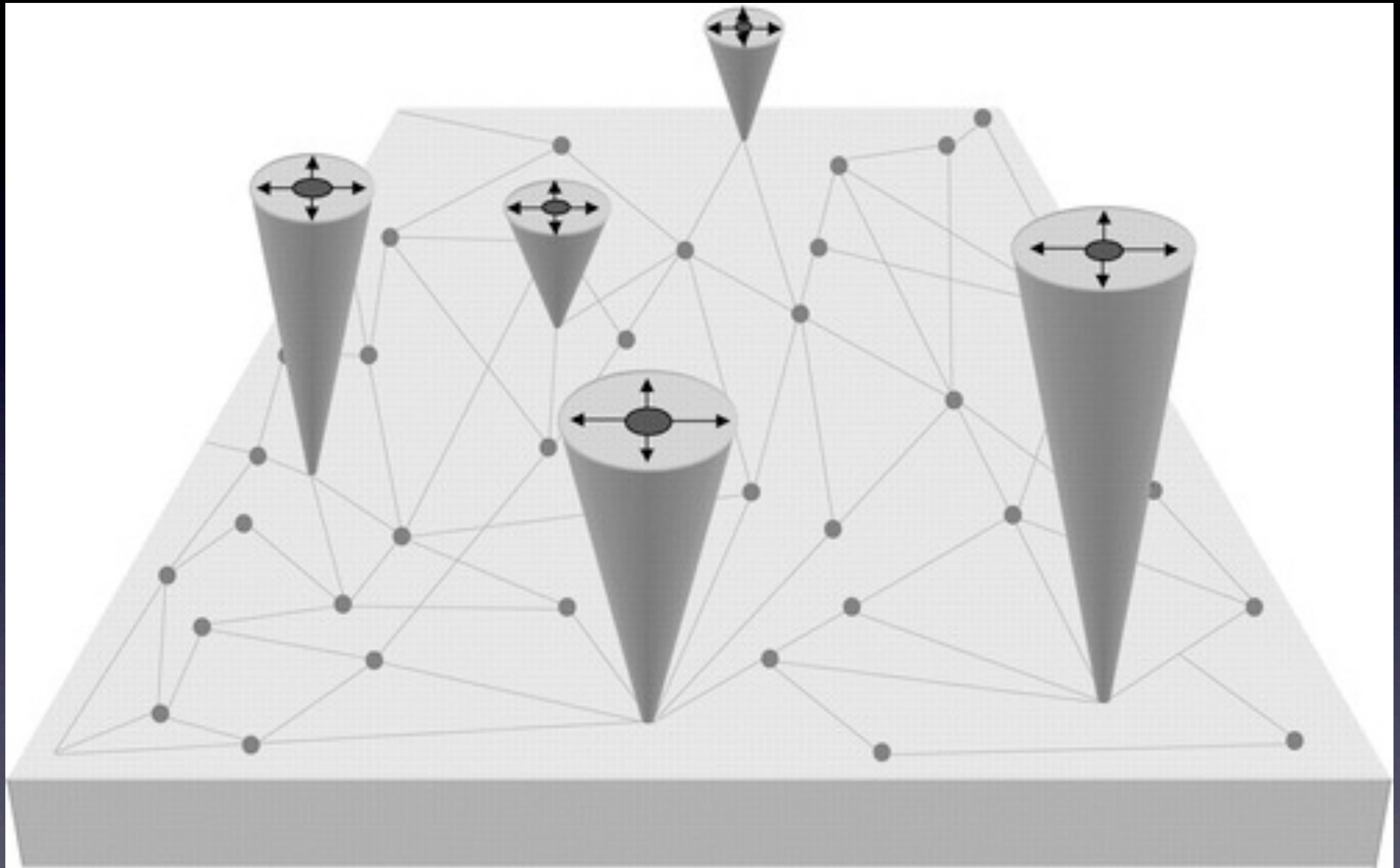
99% nucleotide identity across 12 loci



Clonal expansion

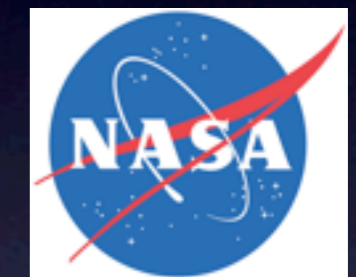


# Epidemic population structure



Maynard Smith *et al.*, *Bioessays*, 2000





Graduate students

Nicole Held  
Michael Reno  
Nicholas Youngblut  
Maria Bautista

Postdocs

Hinsby Cadillo-Quiroz  
Angela Kouris

Undergraduates

Peter Diebold  
Ron Ramirez  
Alfa Herrera  
Jessica Kelliher  
Sara Rienhart  
Brad Dalsing  
Mark Dell'Aringa

Collaborators

Mark Young, Xavier Didelot, Aaron  
Darling