

**Taxonomic  
delimitation of  
*Mammillaria haageana*  
(Cactaceae)**

**Cristian Cervantes**

# Mammillaria



- **Mammillaria** is distributed from the southern United States to Central America.
- Mexico is the center of diversity for the genus
- The number of recognized species varies on the author:  
**Reppenhagen (1992)** considered 320 spp;  
**Pilbeam (1999)** 181 spp and  
**Hunt (2006)** 163 spp.

(Hernández & Gómez-Hinostrosa, 2015)



*Mammillaria zephyranthoides*

*Its name derived from Latin *mammilla*, "nipple", referring to tubercles.*

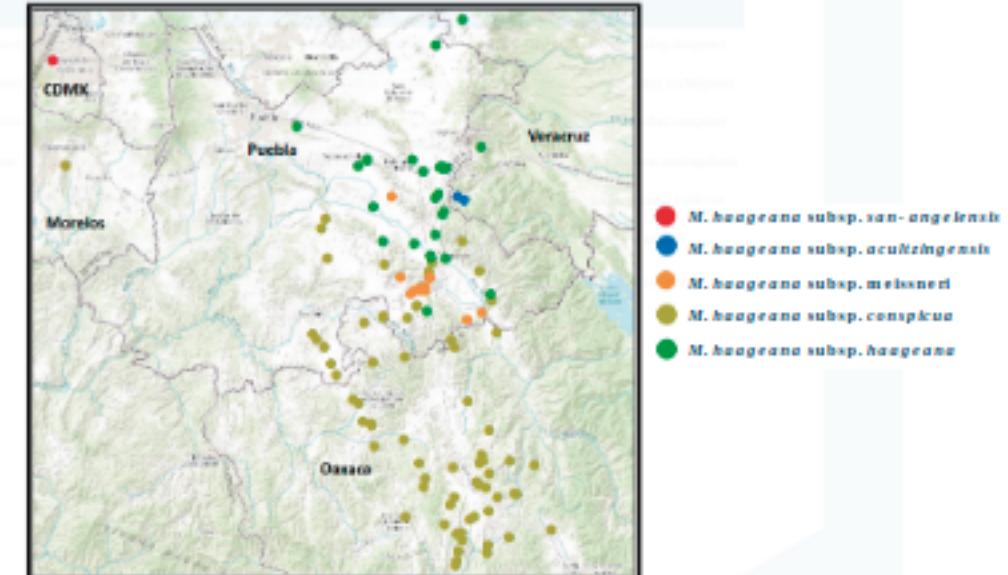
# M. haageana

03

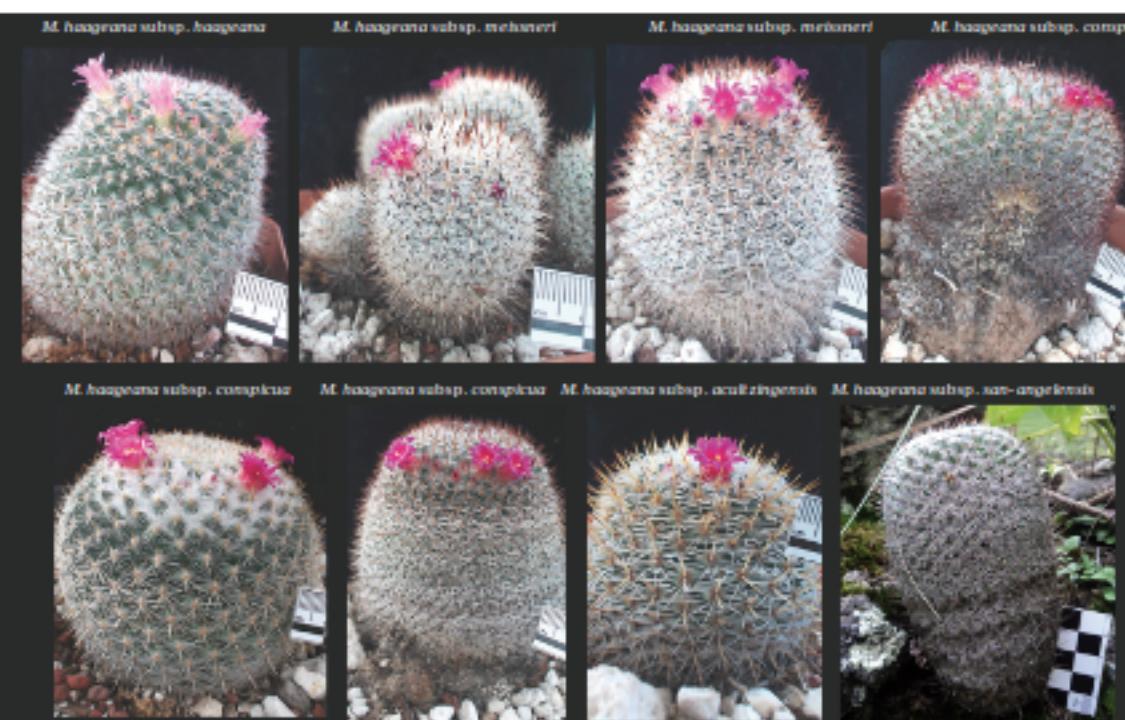
Changes circumscription of *M. haageana* according to some taxonomic proposals.

Bravo-Hollis and Sánchez-Mejorada (1991)	Pilbeam (1999)	Reppenhagen (1992)	Guzmán (2003)	Hunt (2006)
<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>
<i>M. vaupelii</i>	ssp. <i>haageana</i>	<i>M. meissneri</i>	ssp. <i>haageana</i>	
<i>M. collina</i>	ssp. <i>conspicua</i>	<i>M. donati</i>	ssp. <i>acultzingensis</i>	
<i>M. donati</i>	ssp. <i>elegans</i>	<i>M. conspicua</i>	ssp. <i>conspicua</i>	
<i>M. san-angelensis</i>	ssp. <i>san-angelensis</i>	var. <i>vaupelii</i>	ssp. <i>elegans</i>	
<i>M. conspicua</i>	ssp. <i>schmollii</i>	<i>M. albida</i>	ssp. <i>meissneri</i>	
	ssp. <i>acultzingensis</i>	<i>M. elegans</i>	ssp. <i>san-angelensis</i>	
		var. <i>lupina</i>	ssp. <i>vaupelii</i>	
		var. <i>longicaudata</i>		
		var. <i>teyuca</i>		

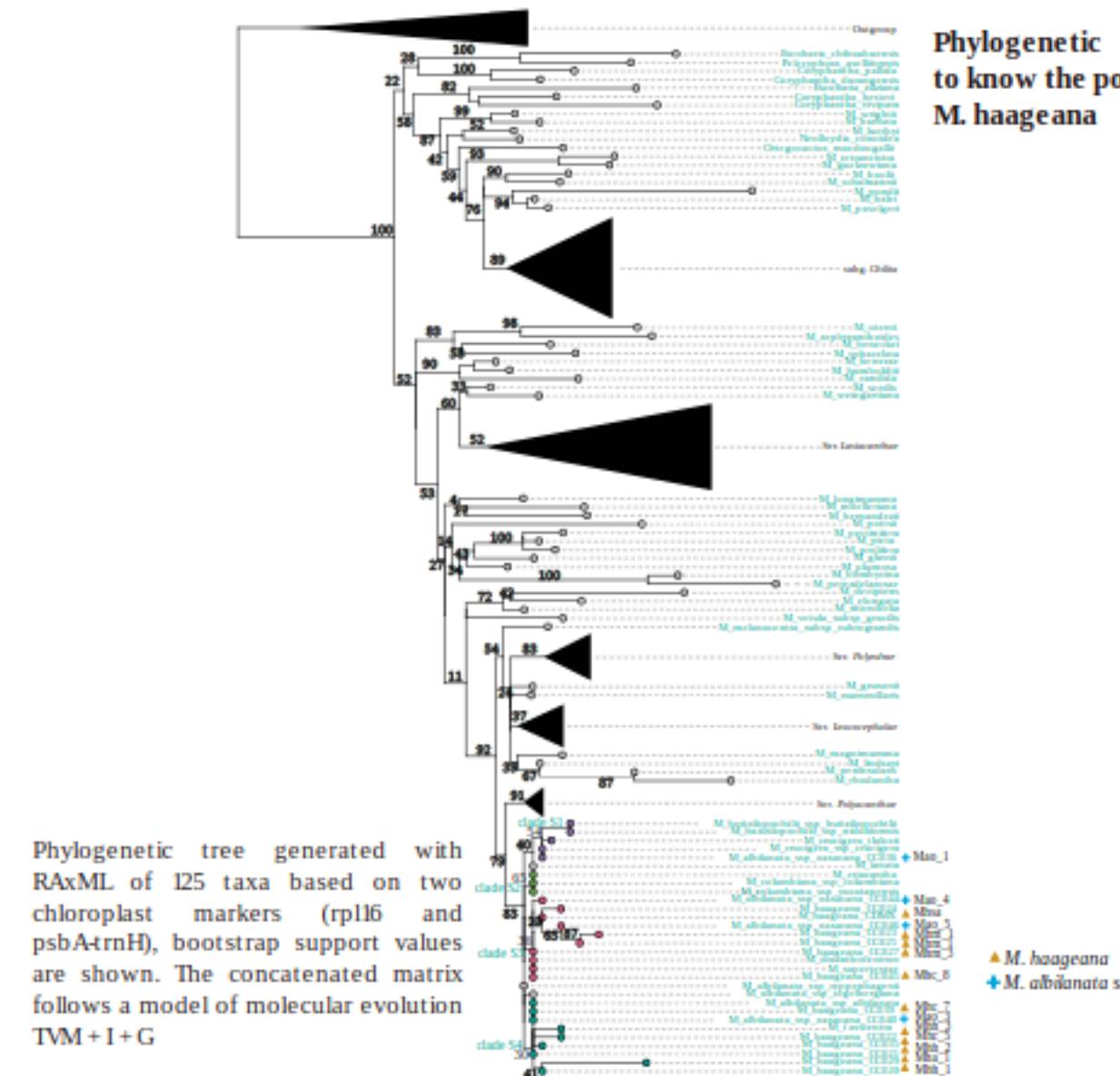
Distribution of *M. haageana*



Morphological variation in *M. haageana*



Phylogenetic analysis to know the position of *M. haageana*



Phylogenetic tree generated with RAxML of 125 taxa based on two chloroplast markers (rpl16 and psbA-trnH), bootstrap support values are shown. The concatenated matrix follows a model of molecular evolution TVM + I + G

## **Changes circumscription of *M. haageana* according to some taxonomic proposals.**

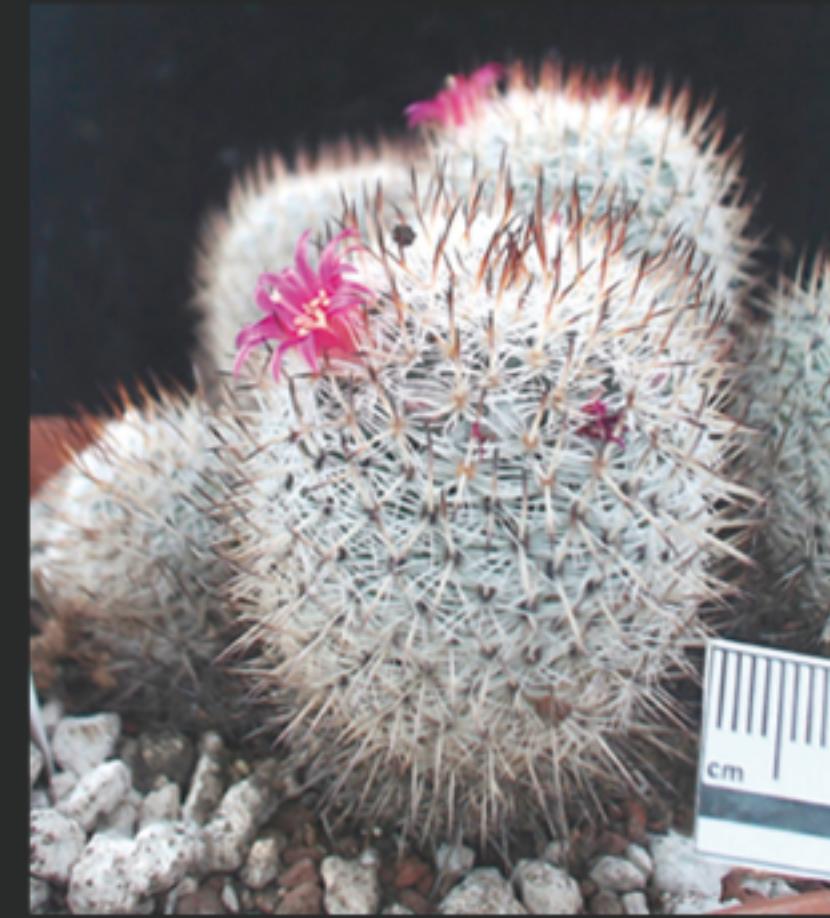
<b>Bravo-Hollis and Sánchez-Mejorada (1991)</b>	<b>Pilbeam (1999)</b>	<b>Reppenhagen (1992)</b>	<b>Guzmán (2003)</b>	<b>Hunt (2006)</b>
<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>	<i>M. haageana</i>
<i>M. vaupelii</i>	ssp. <i>haageana</i>	<i>M. meisneri</i>	ssp. <i>haageana</i>	
<i>M. collina</i>	ssp. <i>conspicua</i>	<i>M. donatii</i>	ssp. <i>acultzingensis</i>	
<i>M. donati</i>	ssp. <i>elegans</i>	<i>M. conspicua</i>	ssp. <i>conspicua</i>	
<i>M. san-angelensis</i>	ssp. <i>san-angelensis</i>	var. <i>vaupelii</i>	ssp. <i>elegans</i>	
<i>M. conspicua</i>	ssp. <i>schmollii</i>	<i>M. albidula</i>	ssp. <i>meissneri</i>	
	ssp. <i>acultzingensis</i>	<i>M. elegans</i>	ssp. <i>san-angelensis</i>	
		var. <i>lupina</i>	ssp. <i>vaupelii</i>	
		var. <i>longicaudata</i>		
		var. <i>teyuca</i>		

# Morphological variation in *M. haageana*

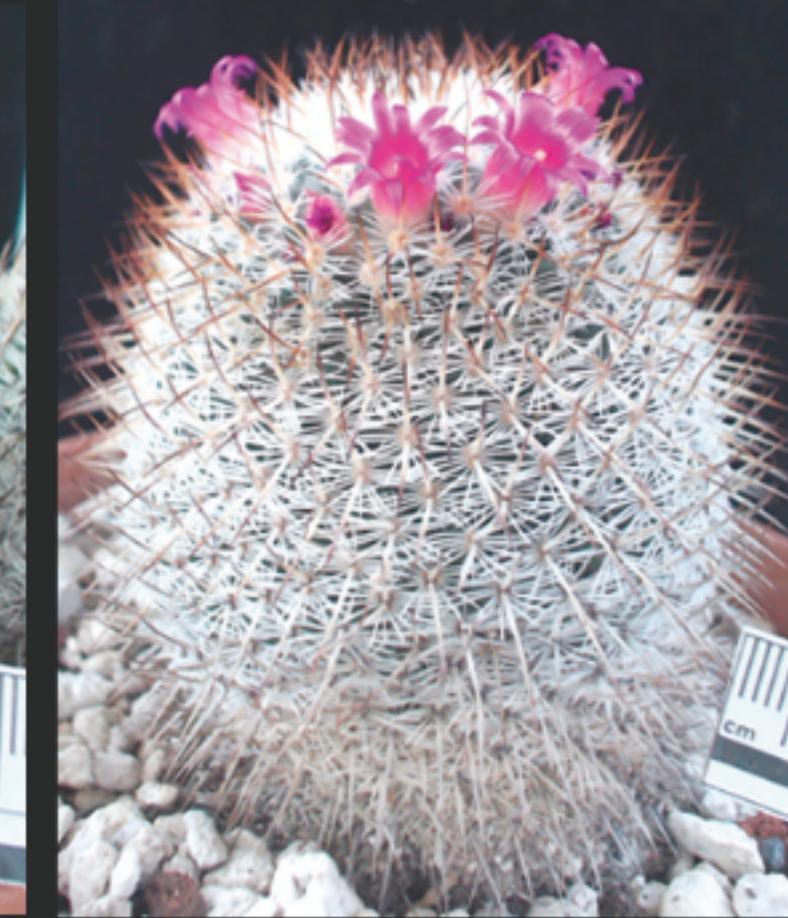
*M. haageana* subsp. *haageana*



*M. haageana* subsp. *meissneri*



*M. haageana* subsp. *meissneri*



*M. haageana* subsp. *conspicua*



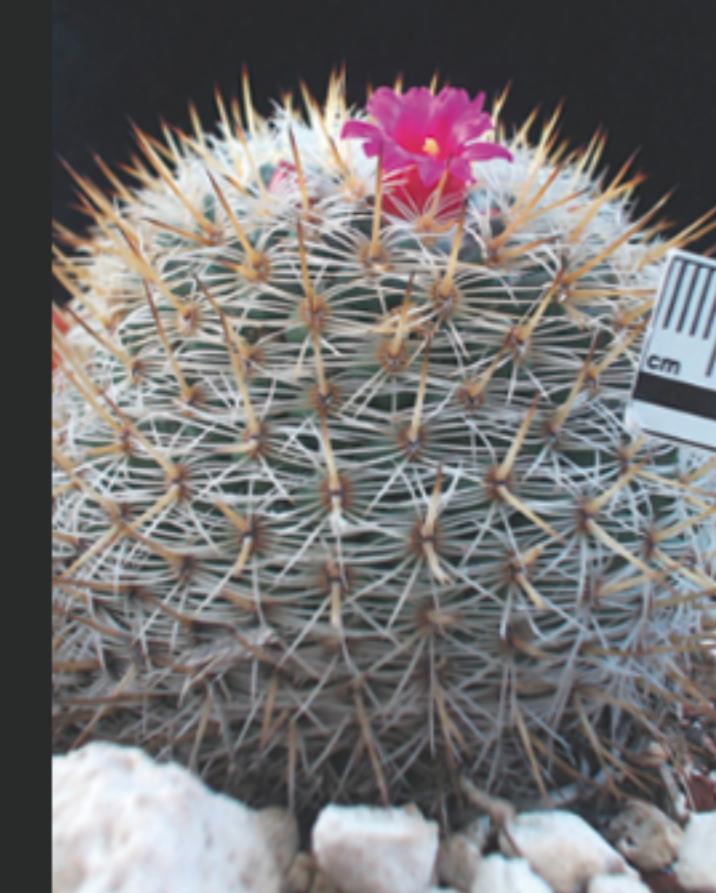
*M. haageana* subsp. *conspicua*



*M. haageana* subsp. *conspicua*



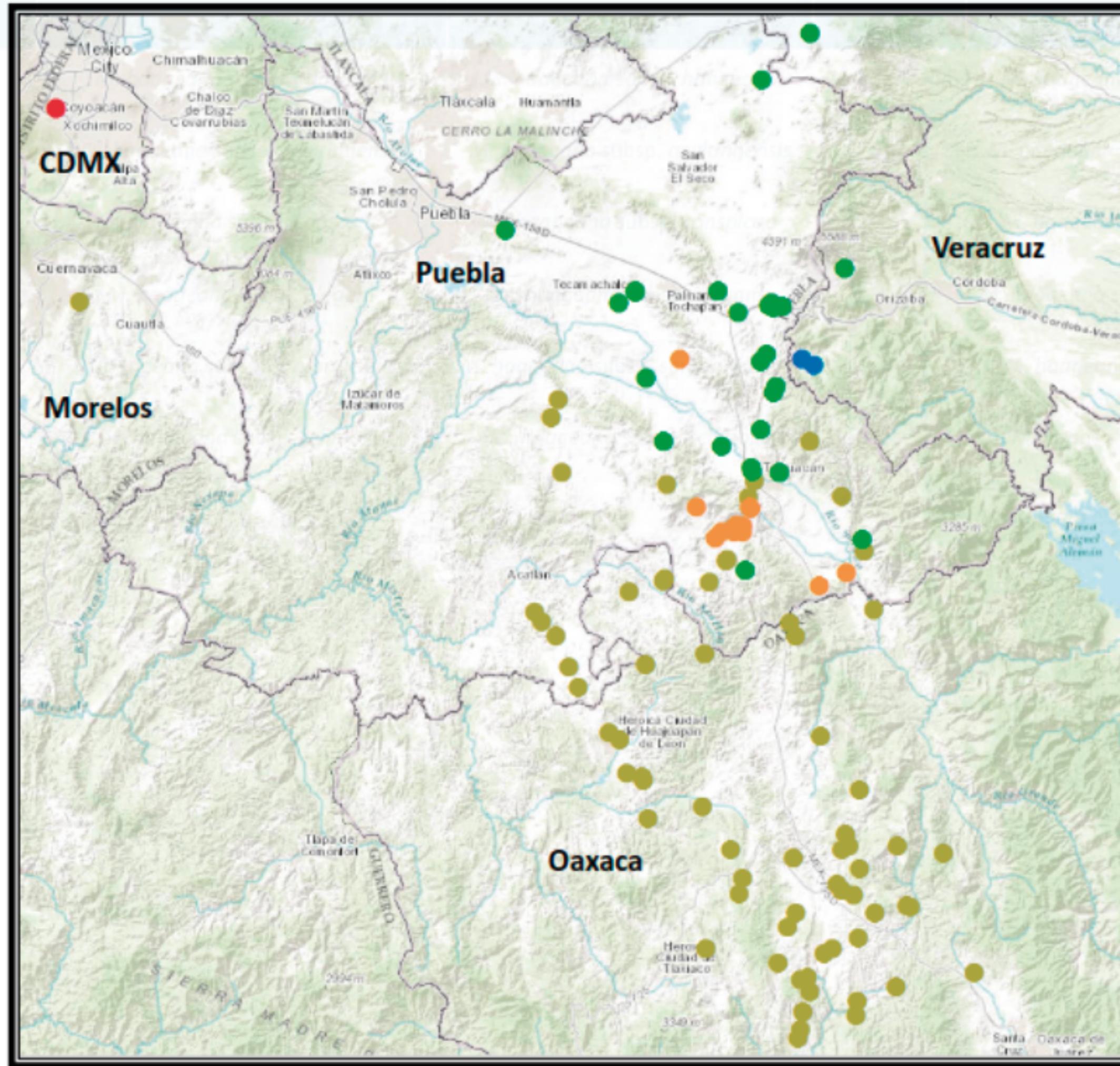
*M. haageana* subsp. *acultzingensis*



*M. haageana* subsp. *san-angelensis*

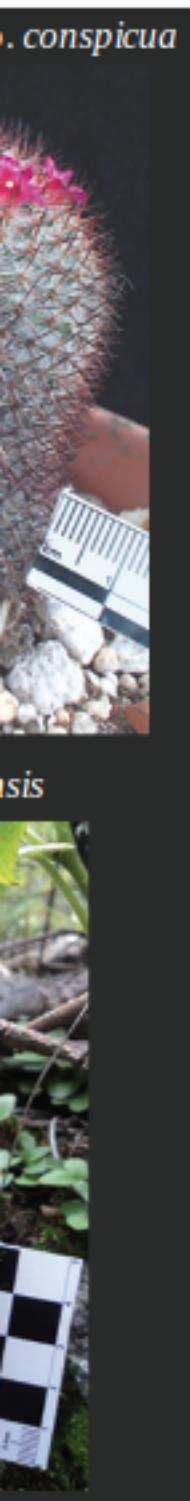
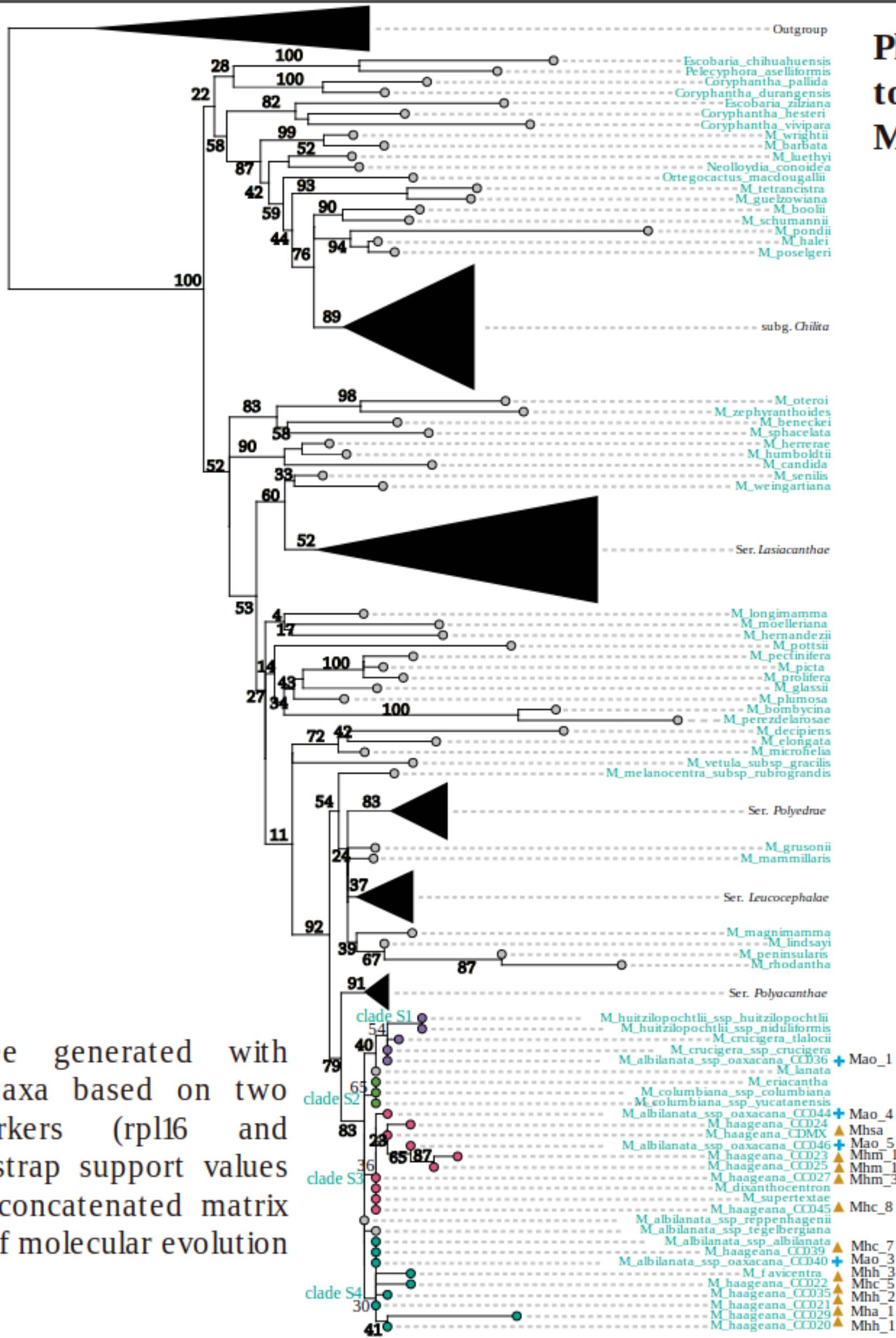


# Distribution of *M. haageana*

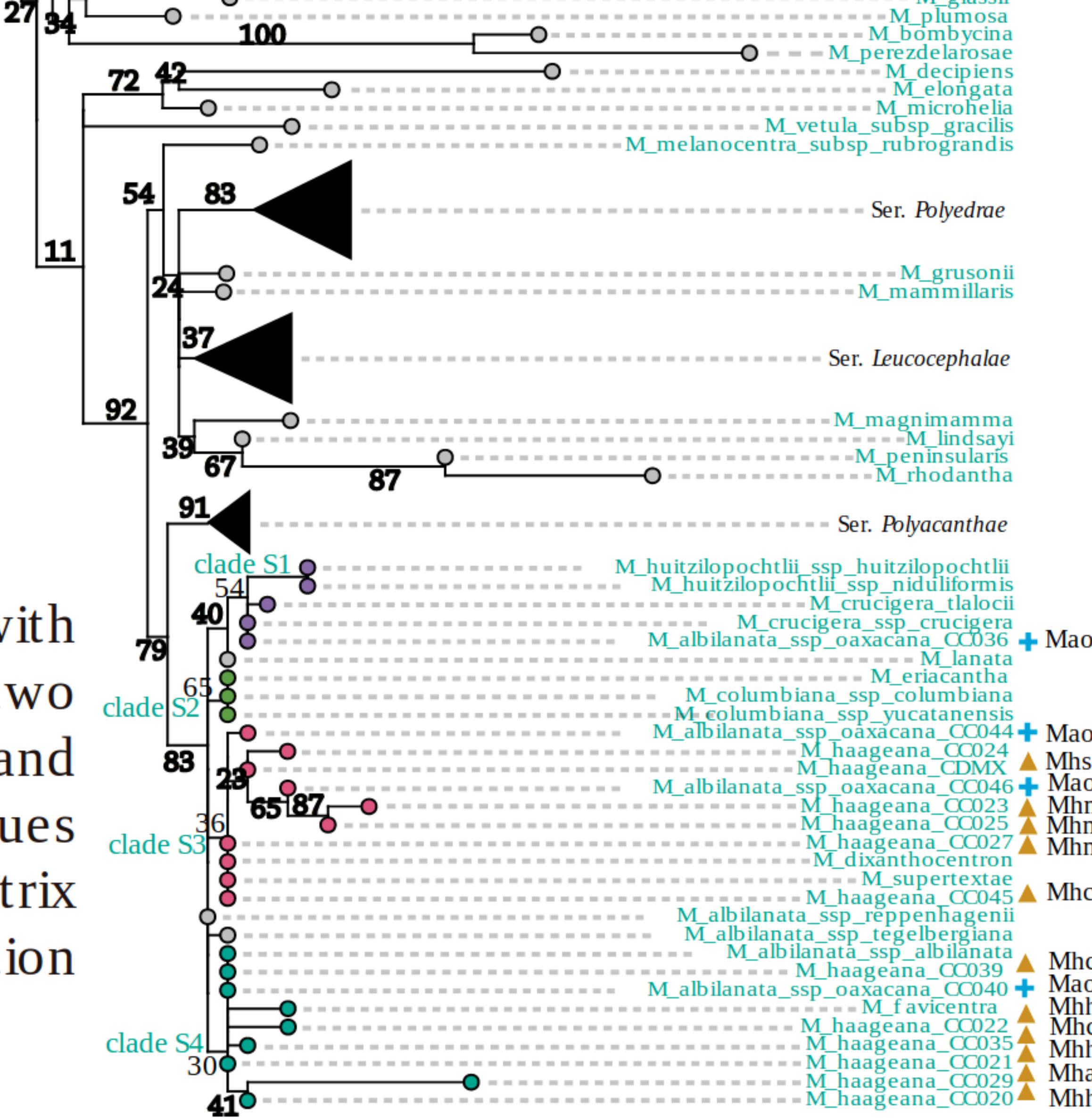


# Phylogenetic analysis to know the position of *M. haageana*

Phylogenetic tree generated with RAxML of 125 taxa based on two chloroplast markers (rpl16 and psbA-trnH), bootstrap support values are shown. The concatenated matrix follows a model of molecular evolution TVM + I + G



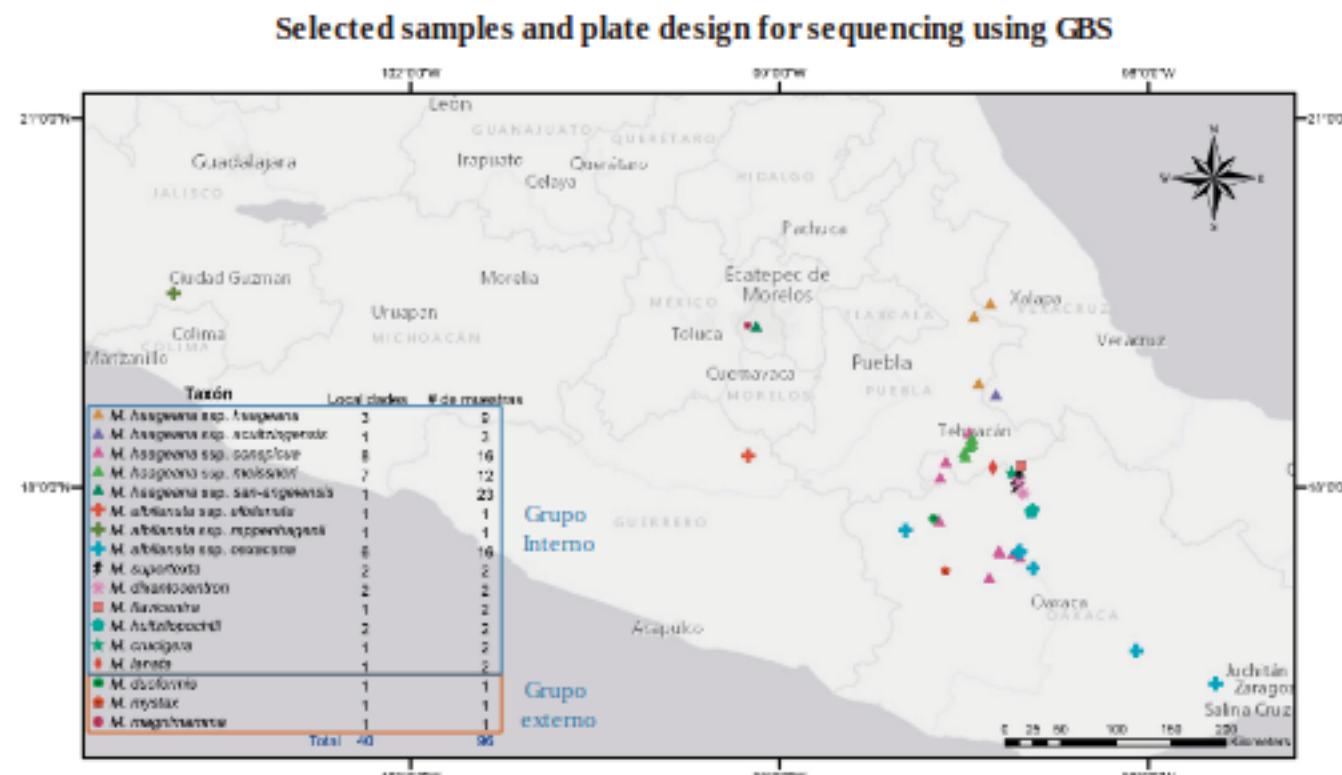
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ed on two  
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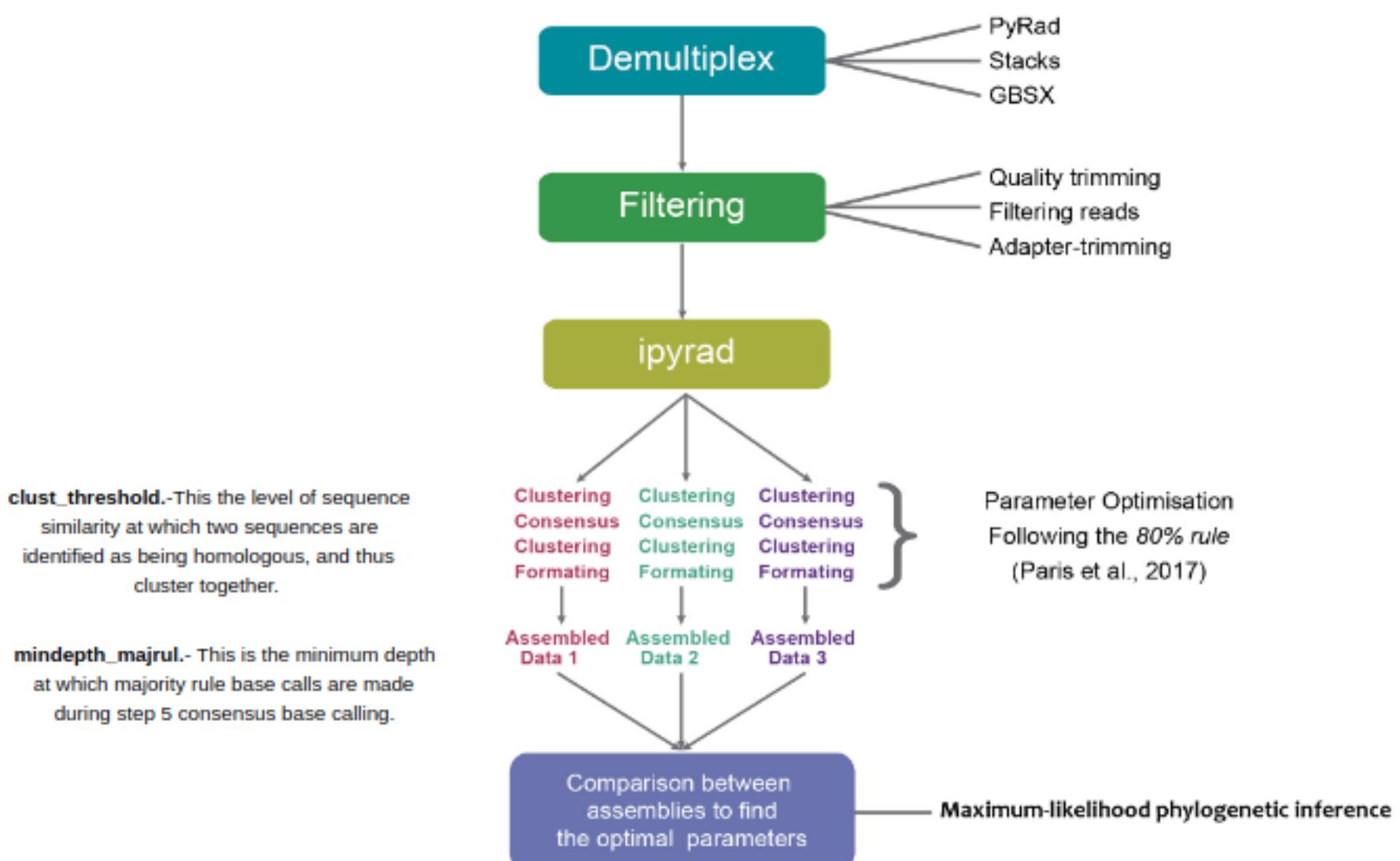
▲ *M. haageana*

+ *M. albilanata* ssp. *oaxacana*

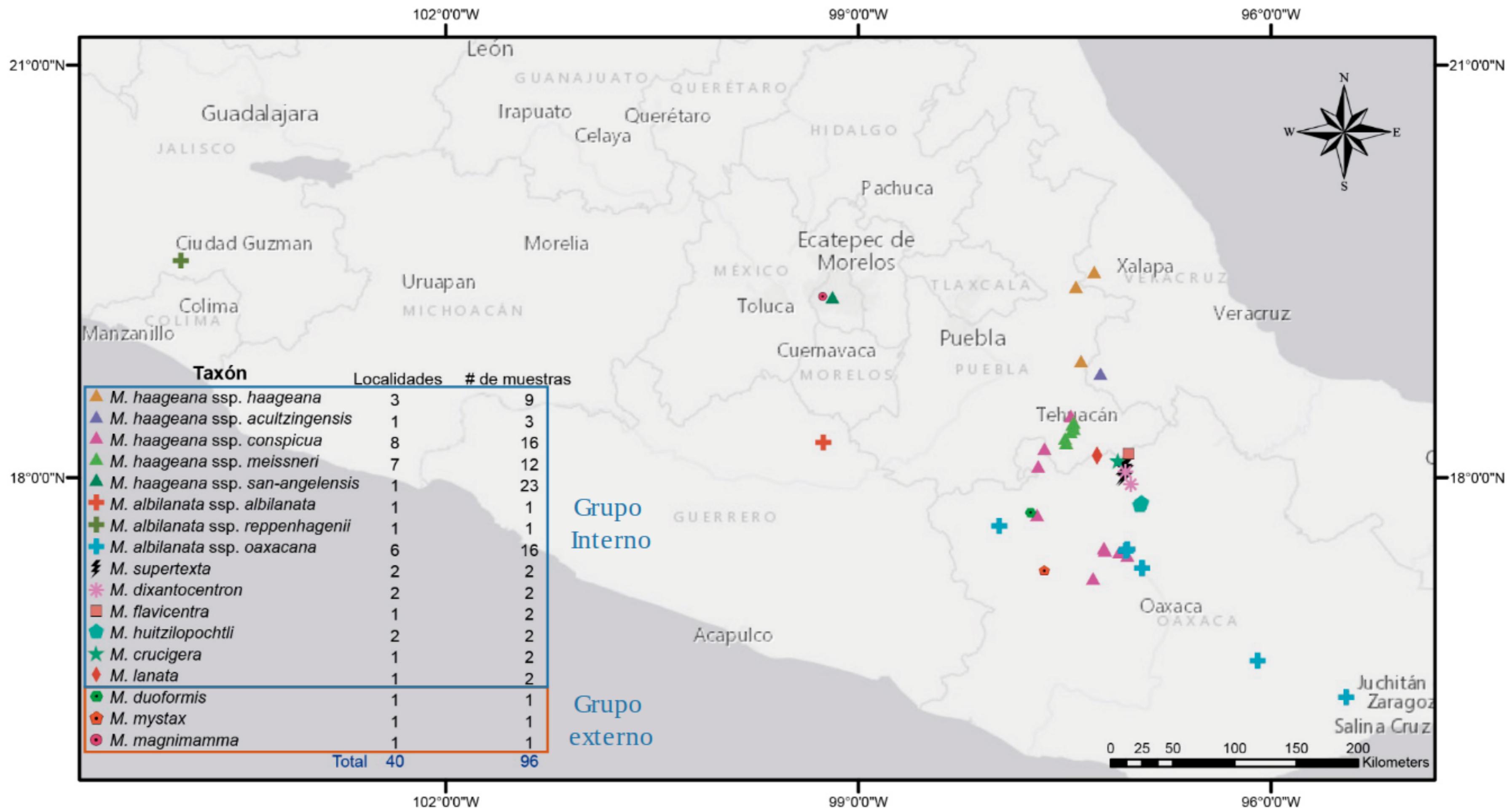
# Material & Methods



## Bioinformatic workflow



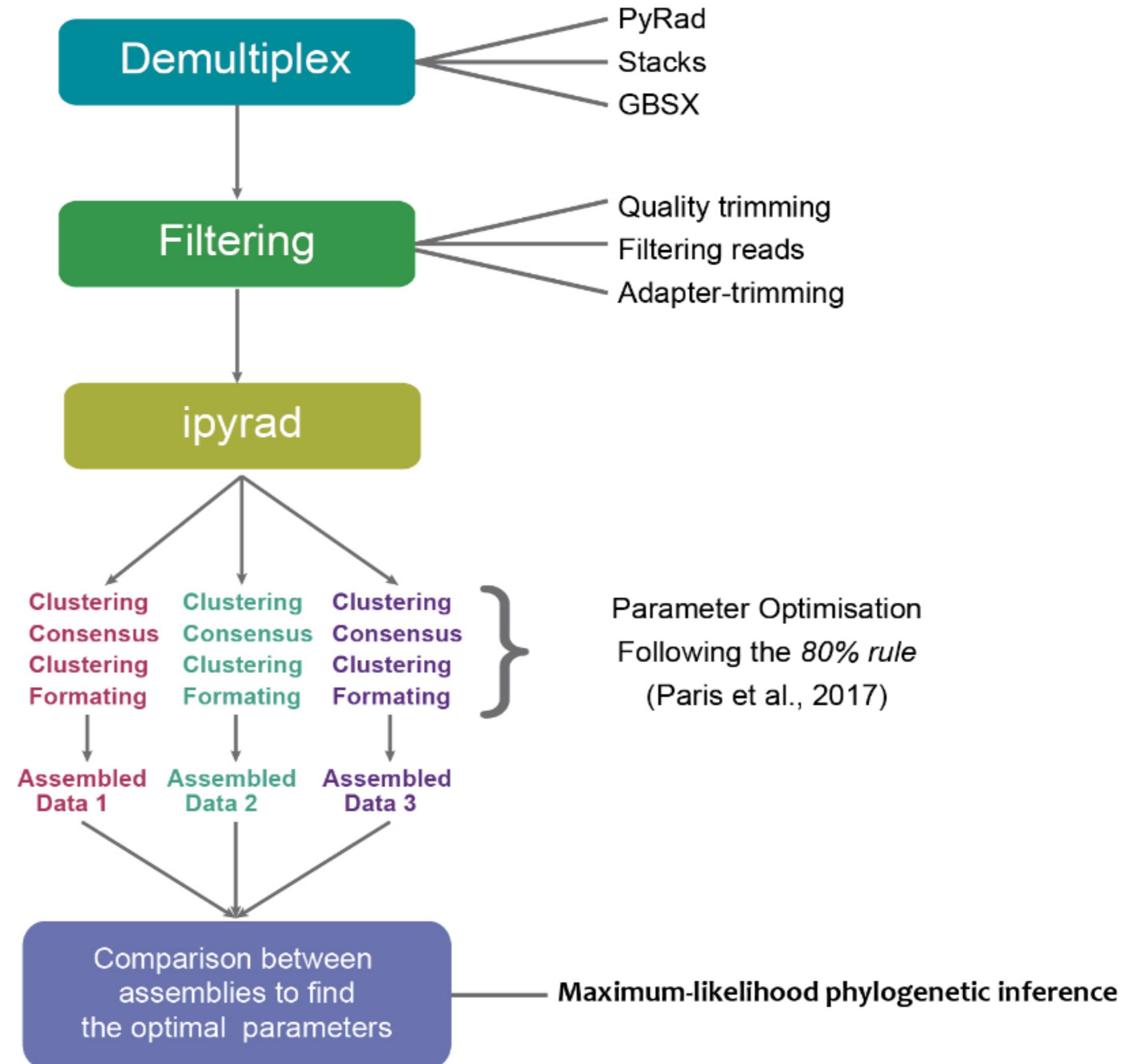
# Selected samples and plate design for sequencing using GBS



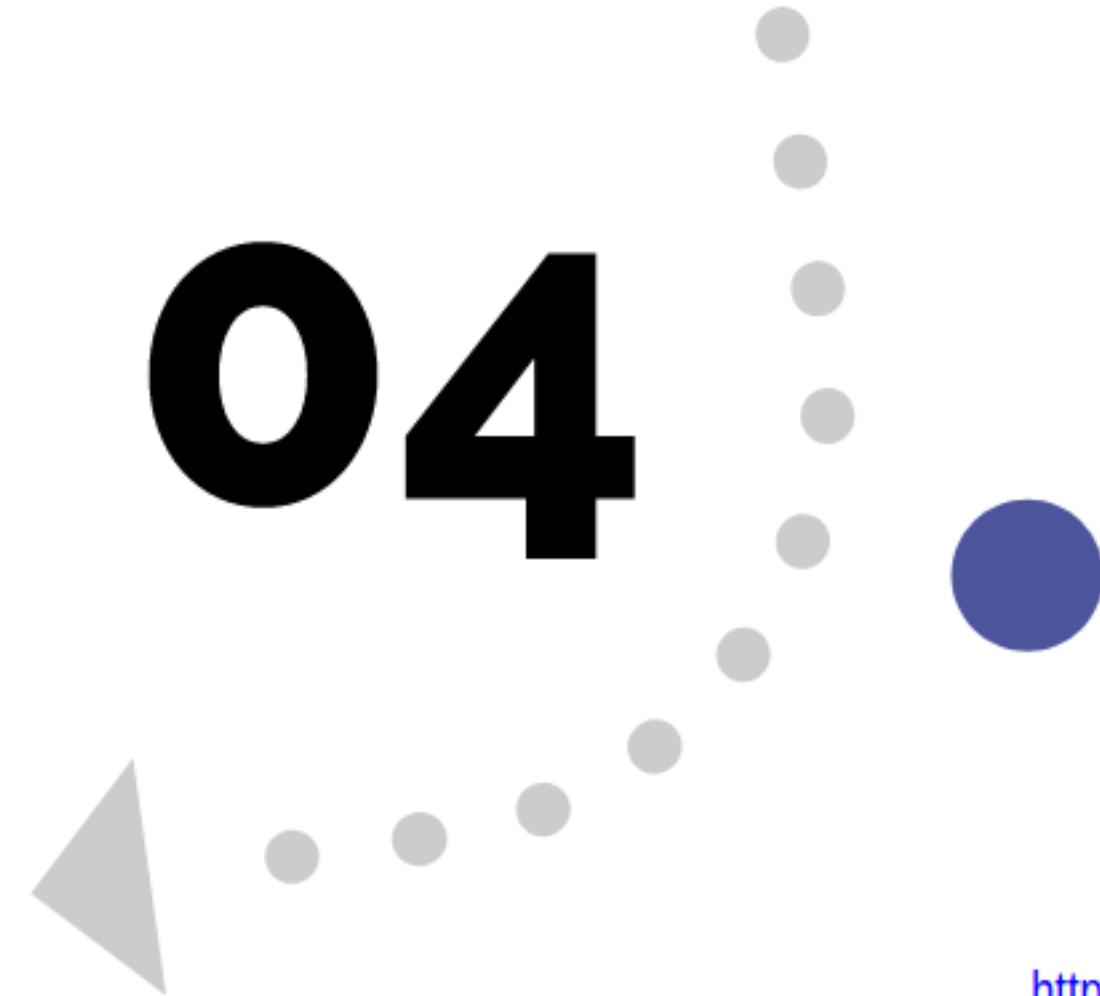
# Bioinformatic workflow

**clust\_threshold.**-This the level of sequence similarity at which two sequences are identified as being homologous, and thus cluster together.

**mindepth\_majrul.**- This is the minimum depth at which majority rule base calls are made during step 5 consensus base calling.

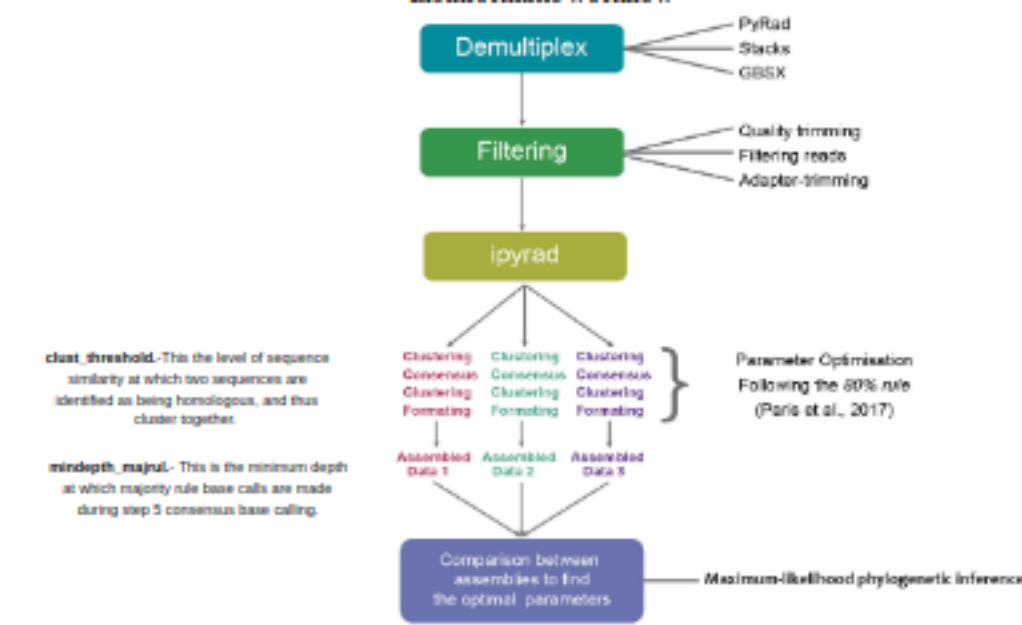


# 04

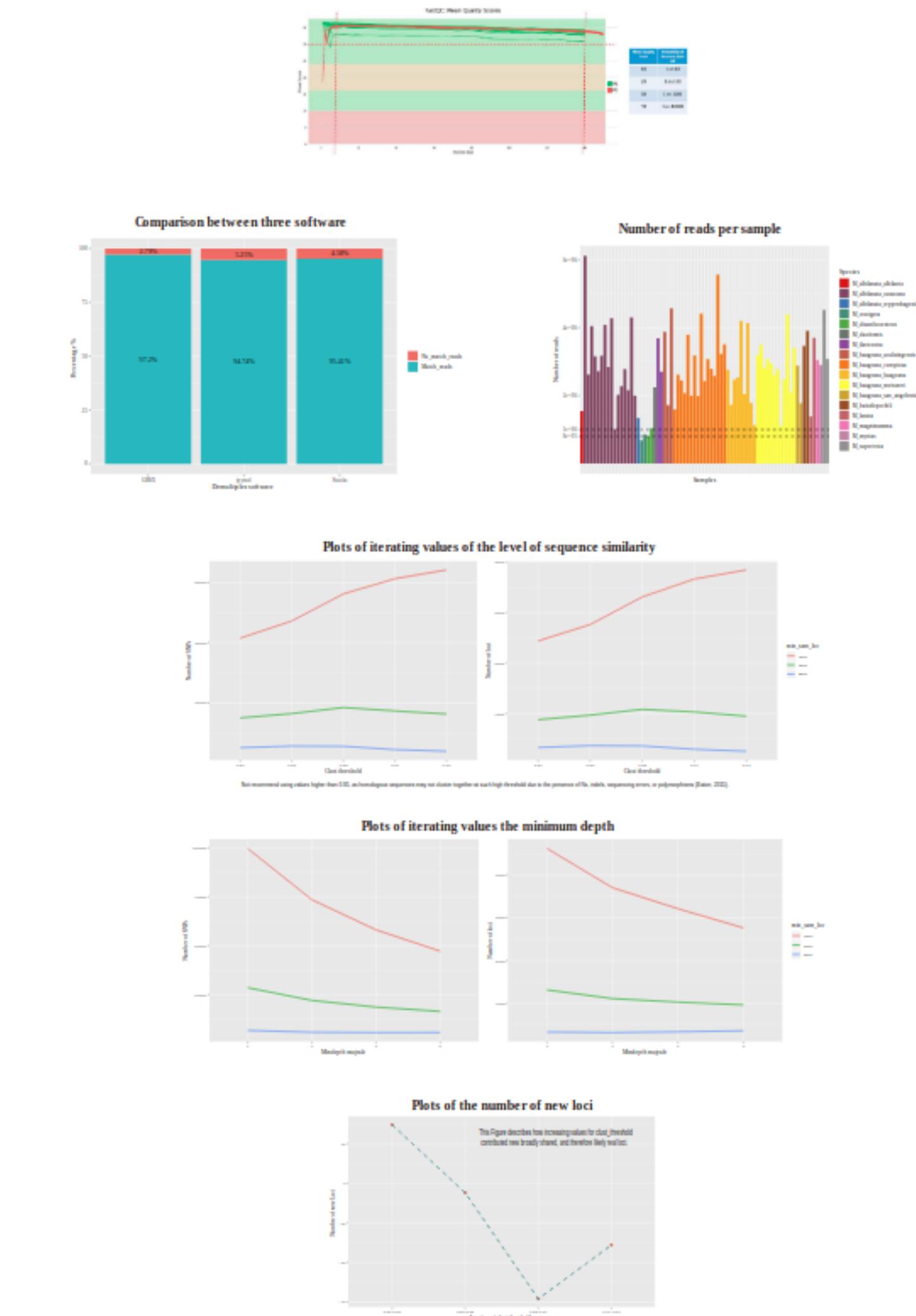


## Bioinformatic process

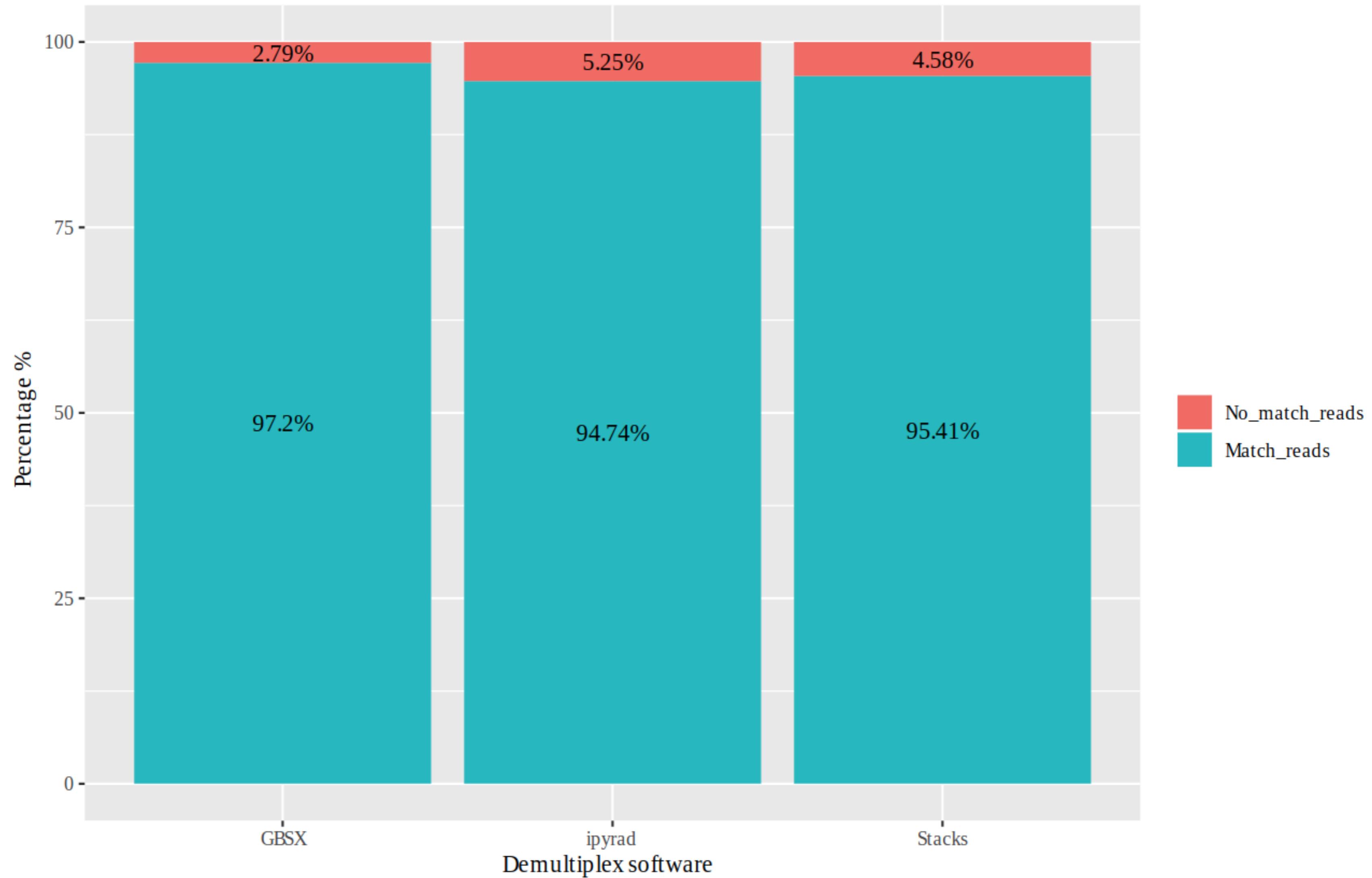
[https://github.com/cristoichkov/GBS\\_Bioinf\\_Process\\_Mamm](https://github.com/cristoichkov/GBS_Bioinf_Process_Mamm)



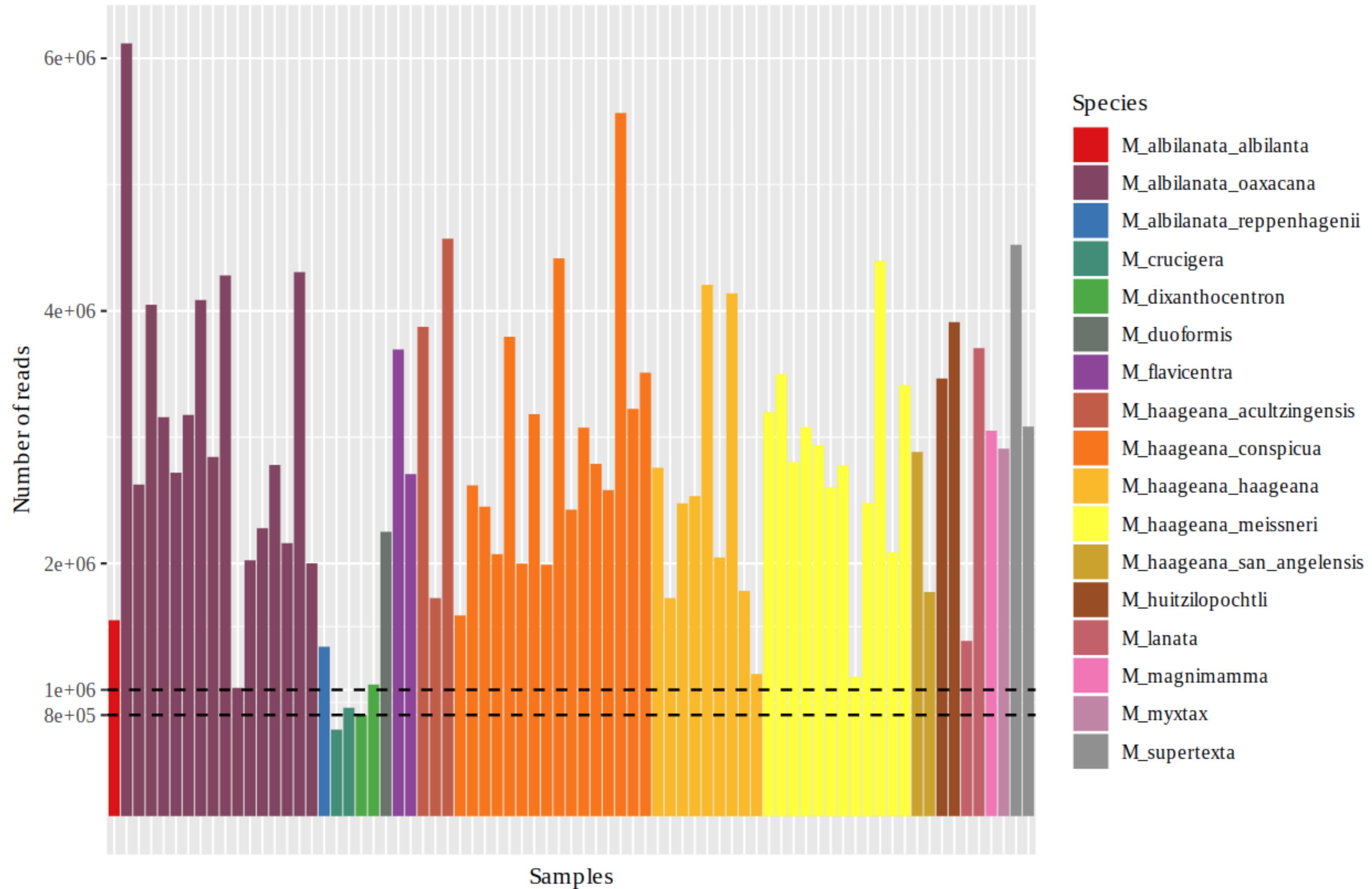
# Results

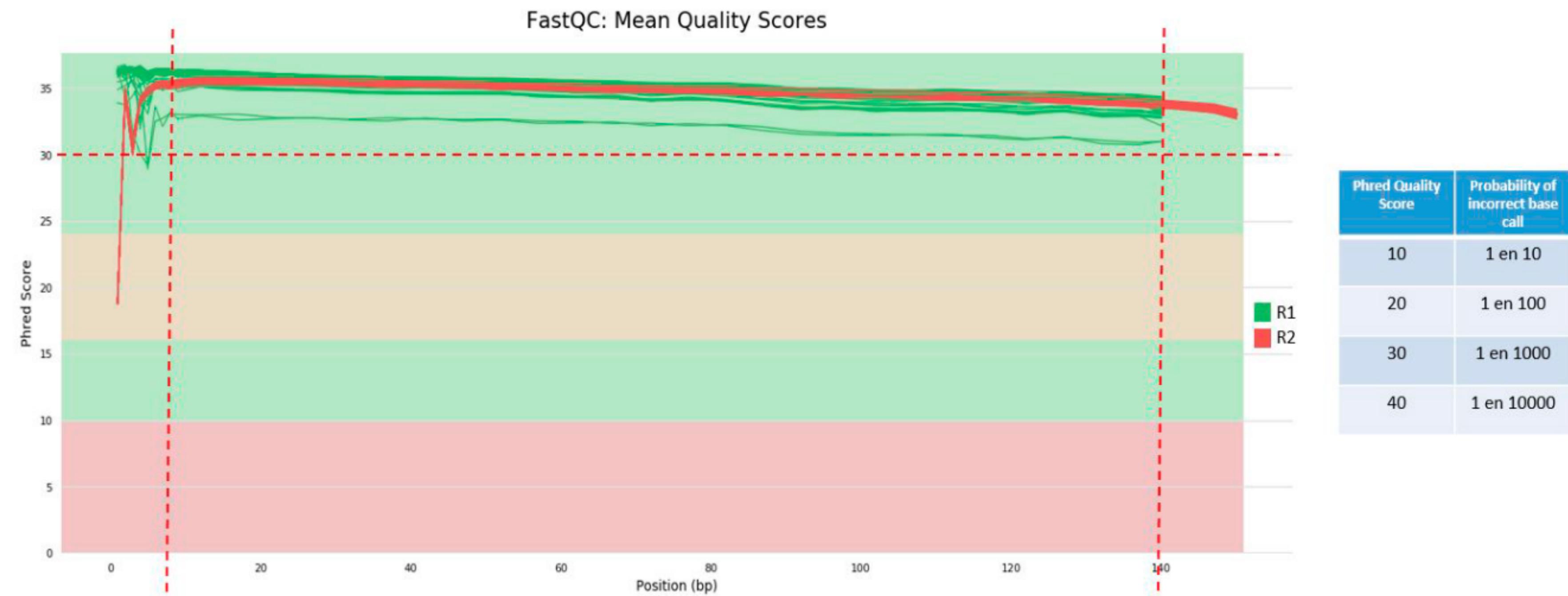


# Comparison between three software



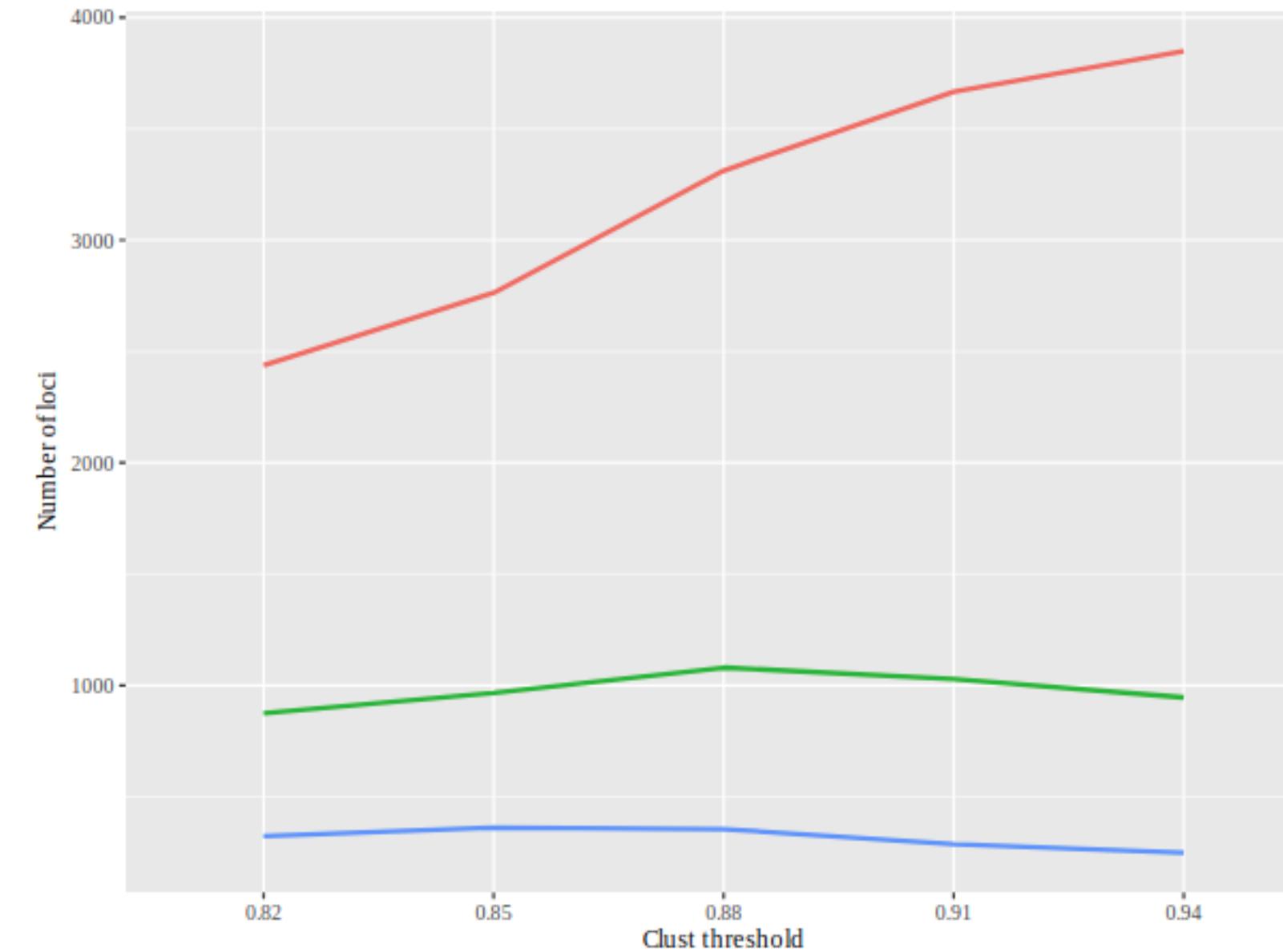
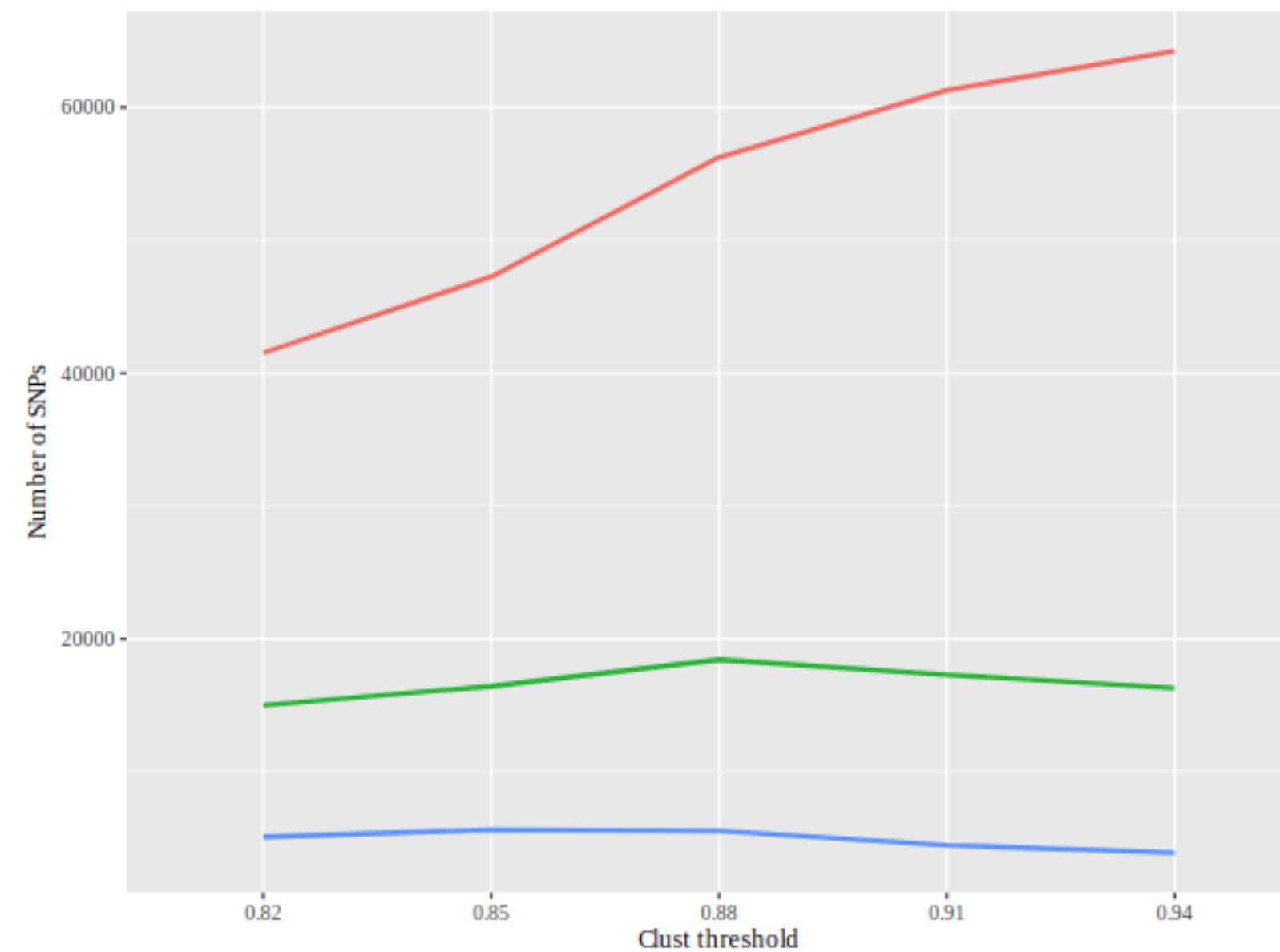
# Number of reads per sample







## Plots of iterating values of the level of sequence similarity

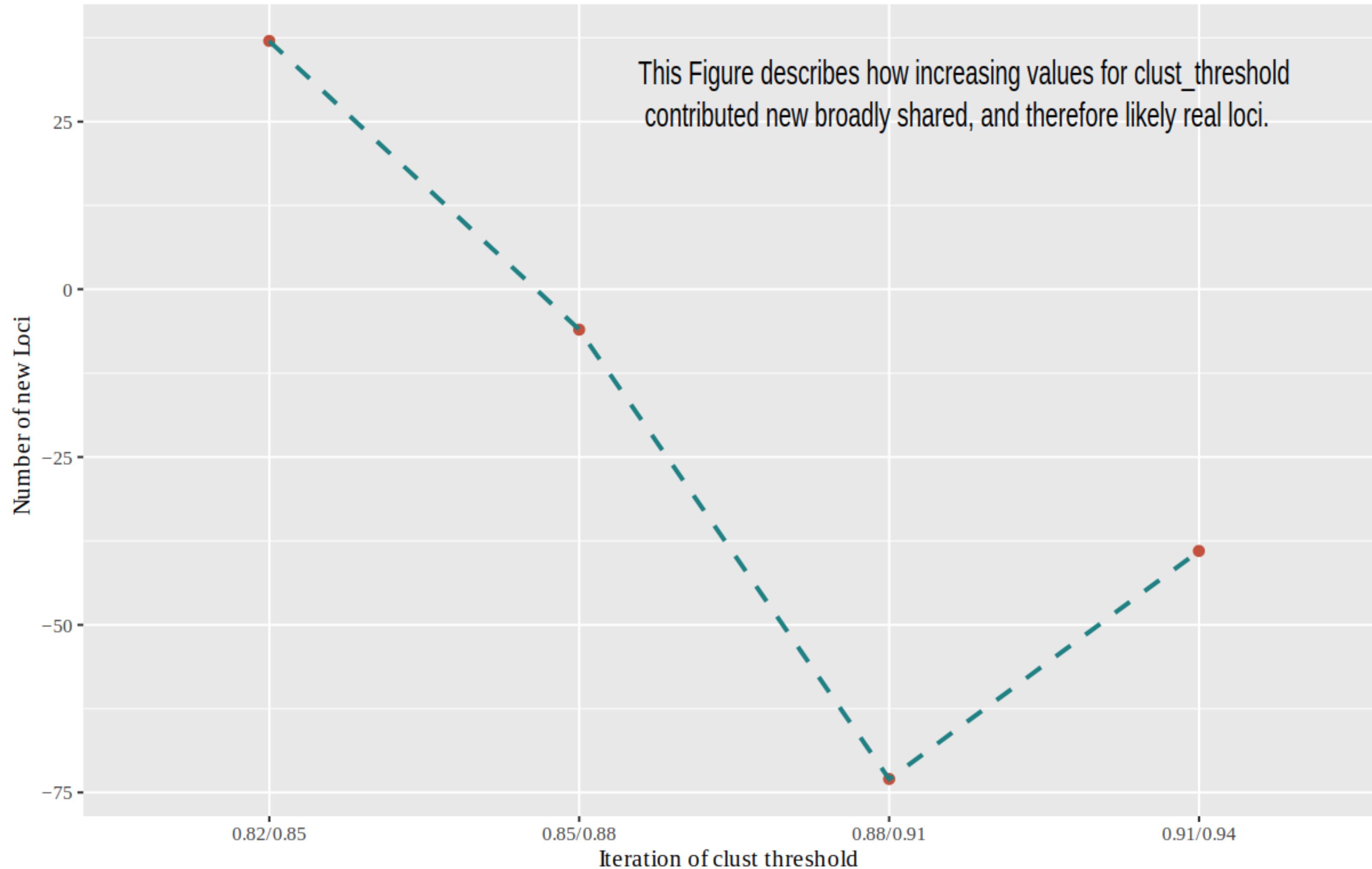


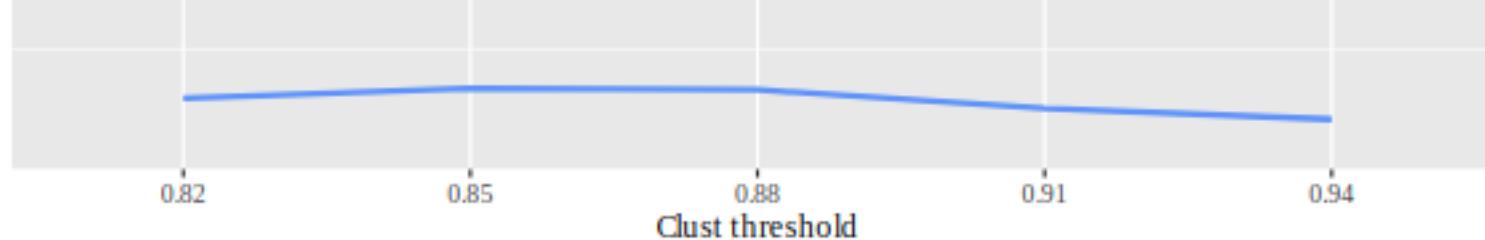
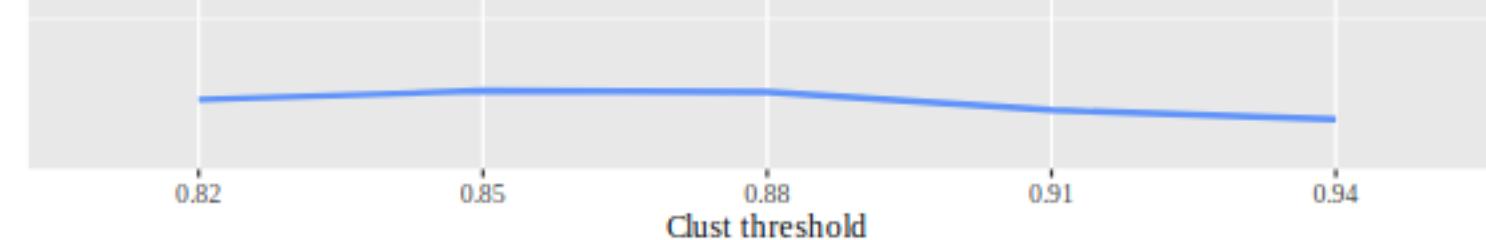
Not recommend using values higher than 0.95, as homologous sequences may not cluster together at such high threshold due to the presence of Ns, indels, sequencing errors, or polymorphisms (Eaton, 2015).

## Plots of iterating values the minimum depth



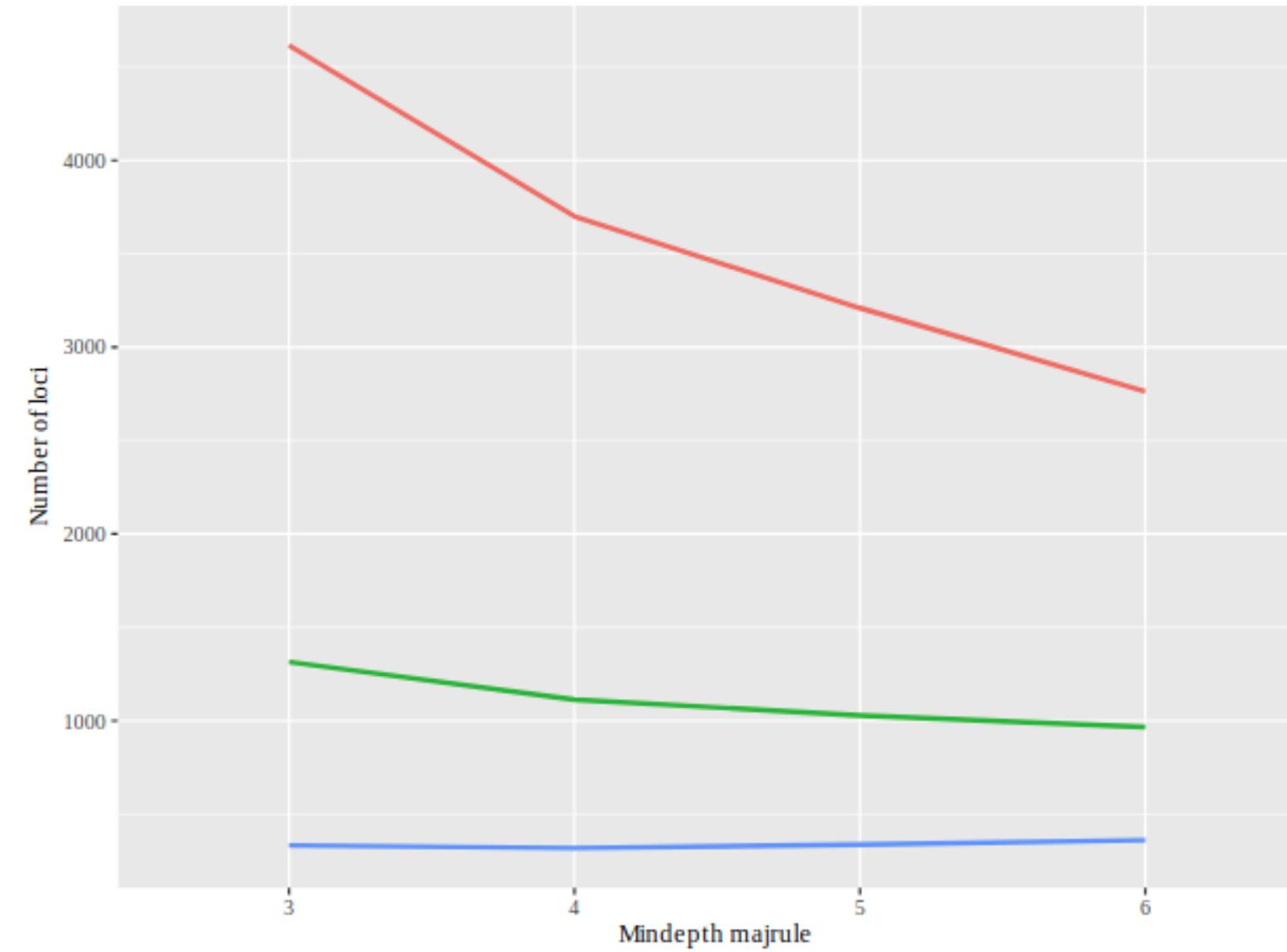
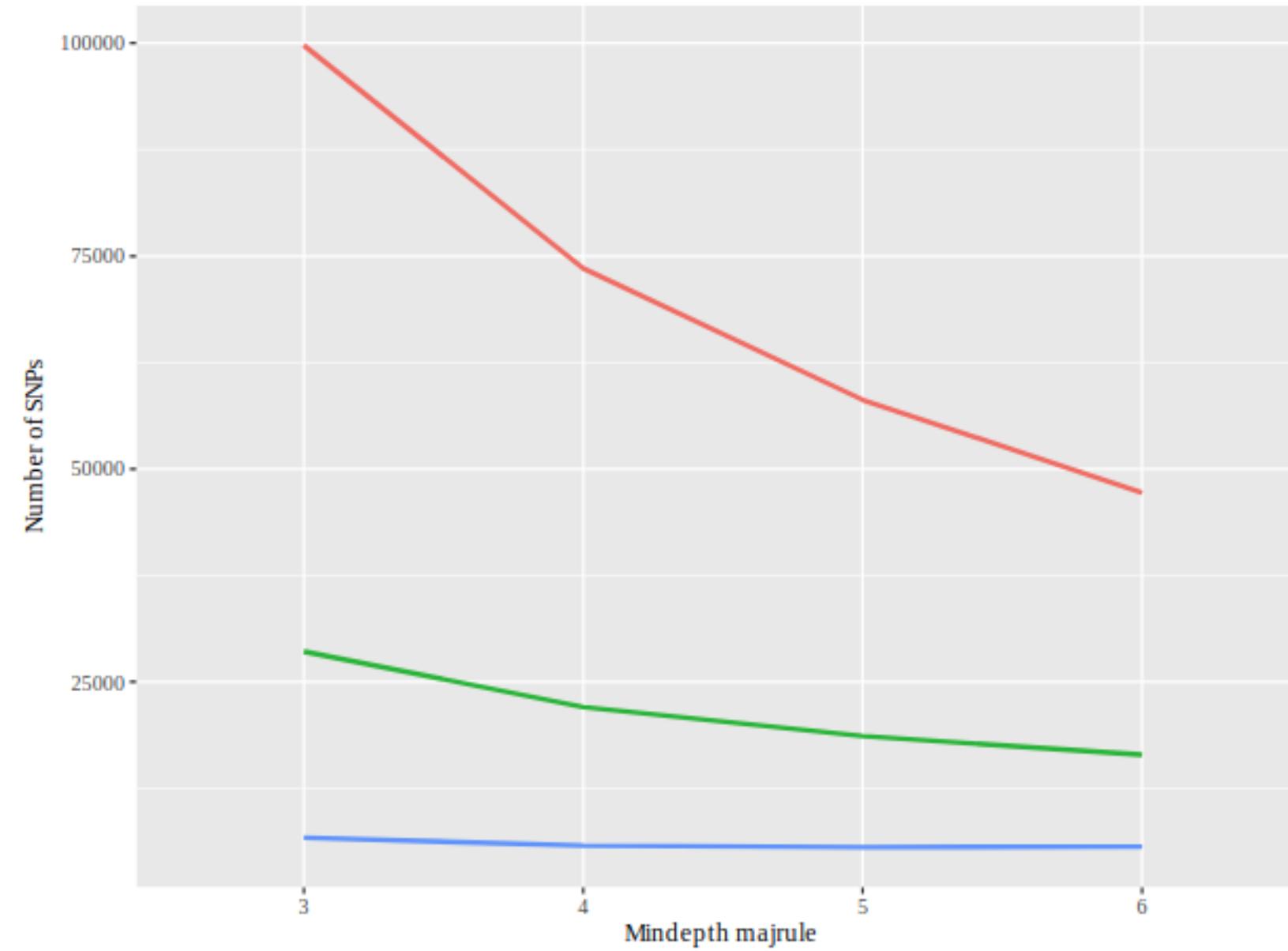
# Plots of the number of new loci





Not recommend using values higher than 0.95, as homologous sequences may not cluster together at such high threshold due to the presence of Ns, indels, sequencing errors, or polymorphisms (Eaton, 2015).

## Plots of iterating values the minimum depth



min\_sam\_loc

- 40%
- 60%
- 80%

## Plots of the number of new loci



This Figure describes how increasing values for `clust_threshold` contributed new broadly shared, and therefore likely real loci.

# Acknowledgment

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U N A M



Reserva Ecológica  
del Pedregal de  
San Ángel UNAM