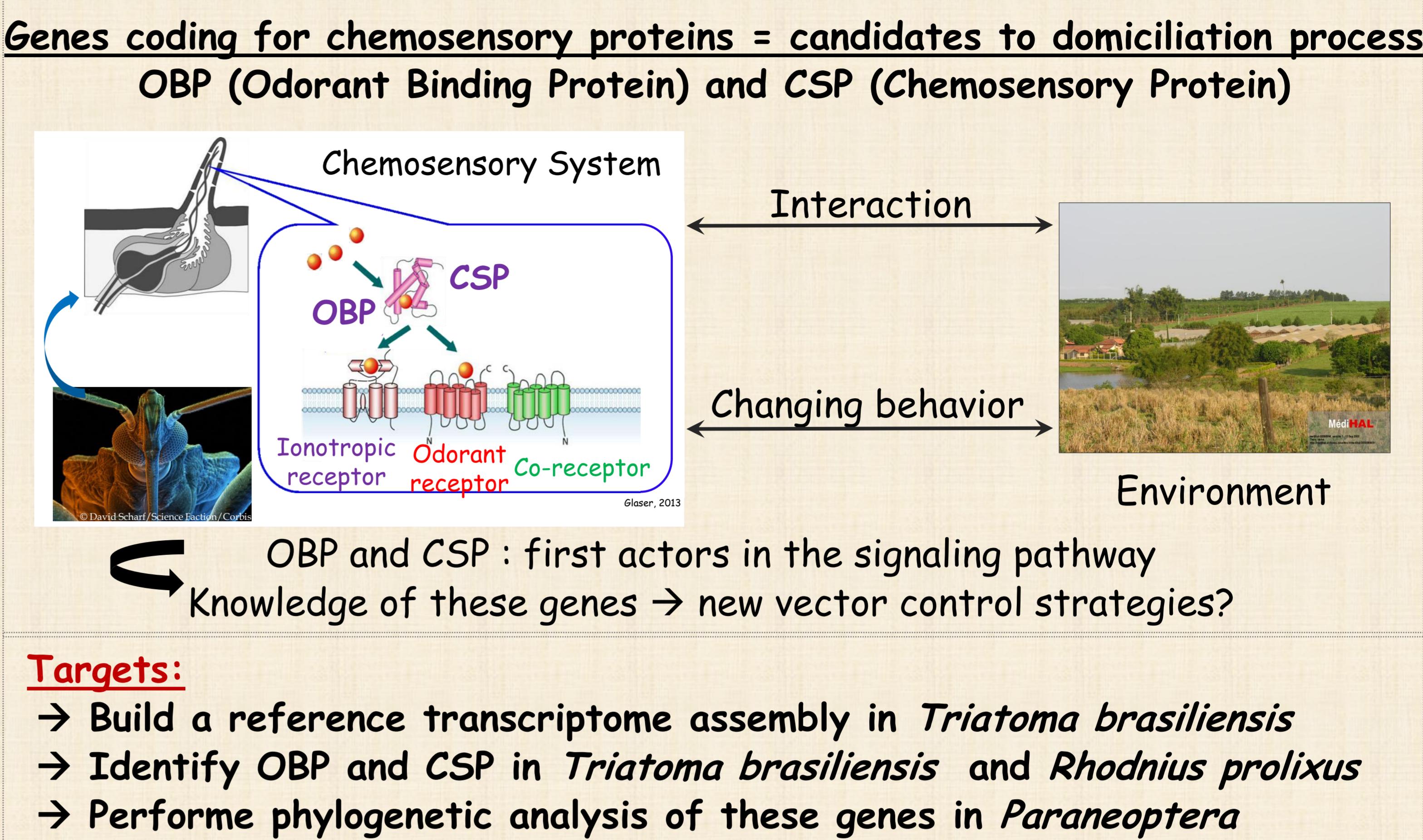
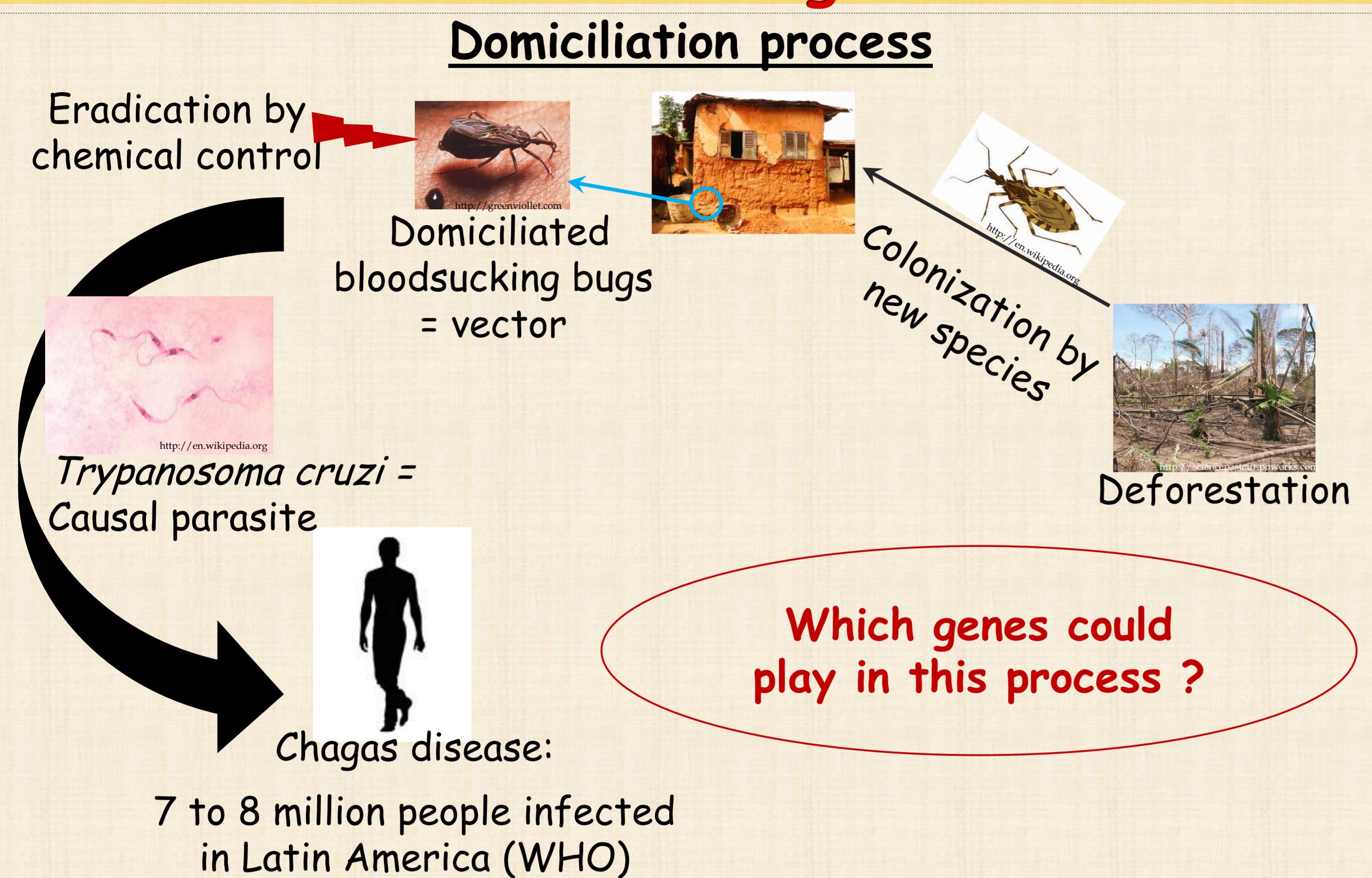




# Exploring the chemosensory system using transcriptome analysis to explain the domiciliation process in Chagas disease vector

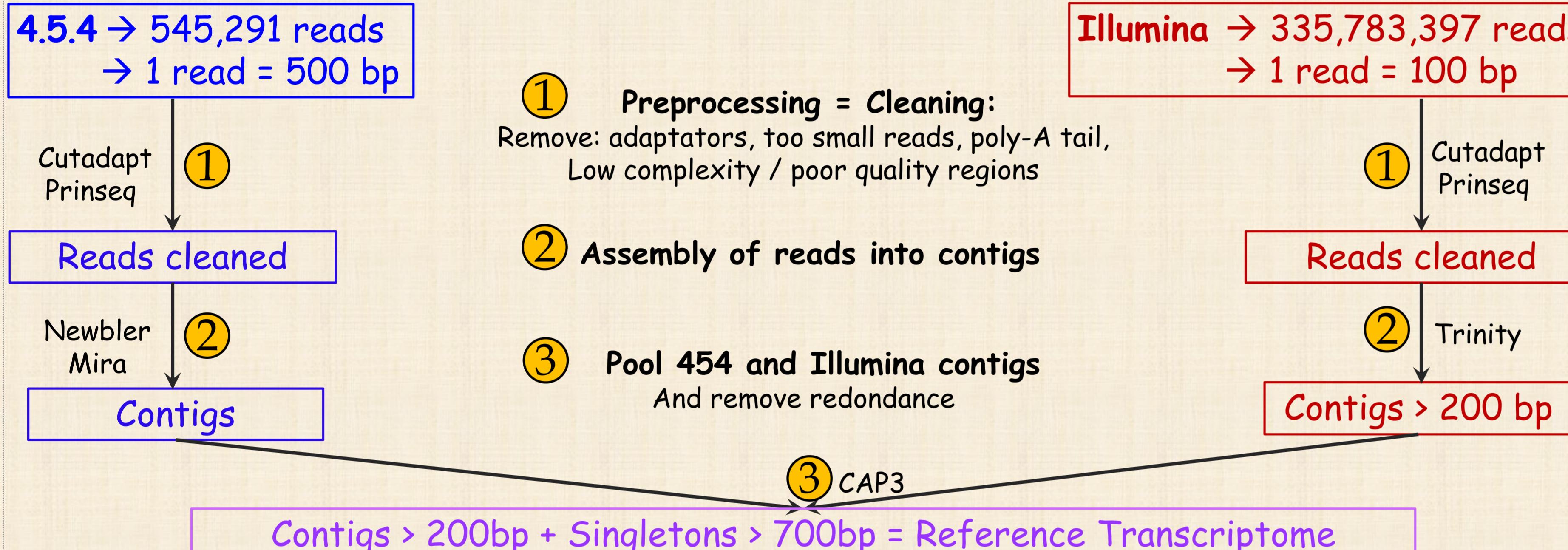
A. Marchant<sup>1, 2</sup>, F. Mougel<sup>2, 3</sup>, E. Jacquin-Joly<sup>4</sup>, M. Harry<sup>2, 3</sup>  
 1 : ED Science Du Végétal - UPSud, Orsay - 2: LEGS - CNRS : UPR9034 - IRD: UR072, Gif sur Yvette - 3: UPSud, Orsay - 4: PISC INRA: UMR1272, Versailles

## Context : Chagas disease vectors and the domiciliation process



## Methods : Analysis of transcriptome

### Transcriptome assembly of *T. brasiliensis*

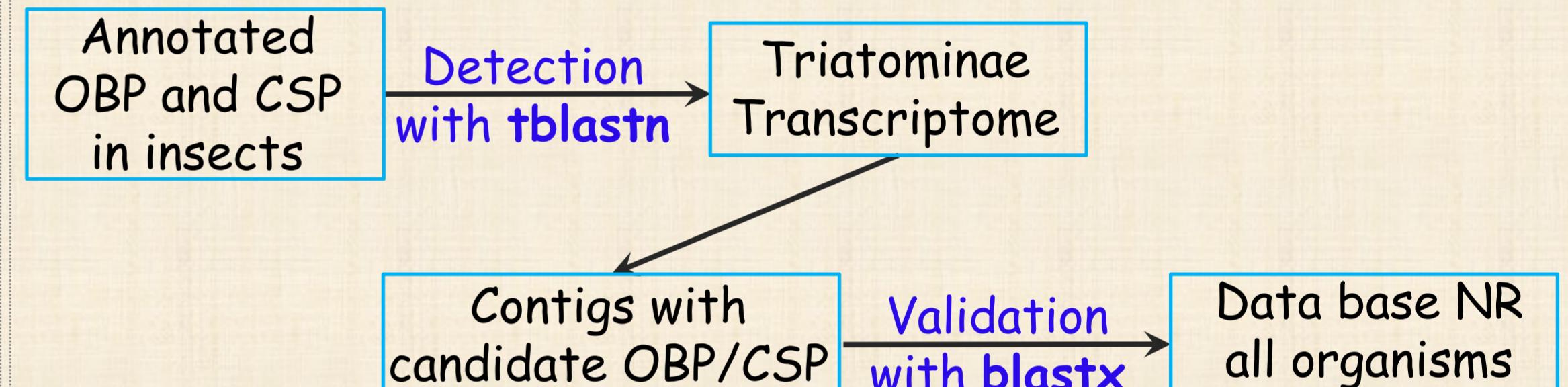


### Data for *R. prolixus*

→ Genome sequence (international consortium)  
OBP and CSP annotated (do Amaral Melo et al, 2013)

→ Transcriptome sequenced using 454 → 500 bp  
Assembled with Newbler (+ Illumina in progress)

### Search for genes of interest



## Results : OBP and CSP variants

### De novo assembly of *T. brasiliensis*

Expected size and number of transcripts	Number of contigs	N50	Size distribution				% CEGMA* complete	% CEGMA* partial
			min	max	median	average		
	25276	1028	201	26222	750	884	61	80

\*: Core Eukaryotic Genes Mapping Approach

Sufficient information

### Trees of chemosensory genes in Paraneoptera

Triatominae

*T. brasiliensis* → 16 CSP / 22 OBP

*R. prolixus* → 19 CSP / 27 OBP

*A. lineolatus* → 3 CSP / 13 OBP

*A. icororum* → 12 CSP / 15 OBP

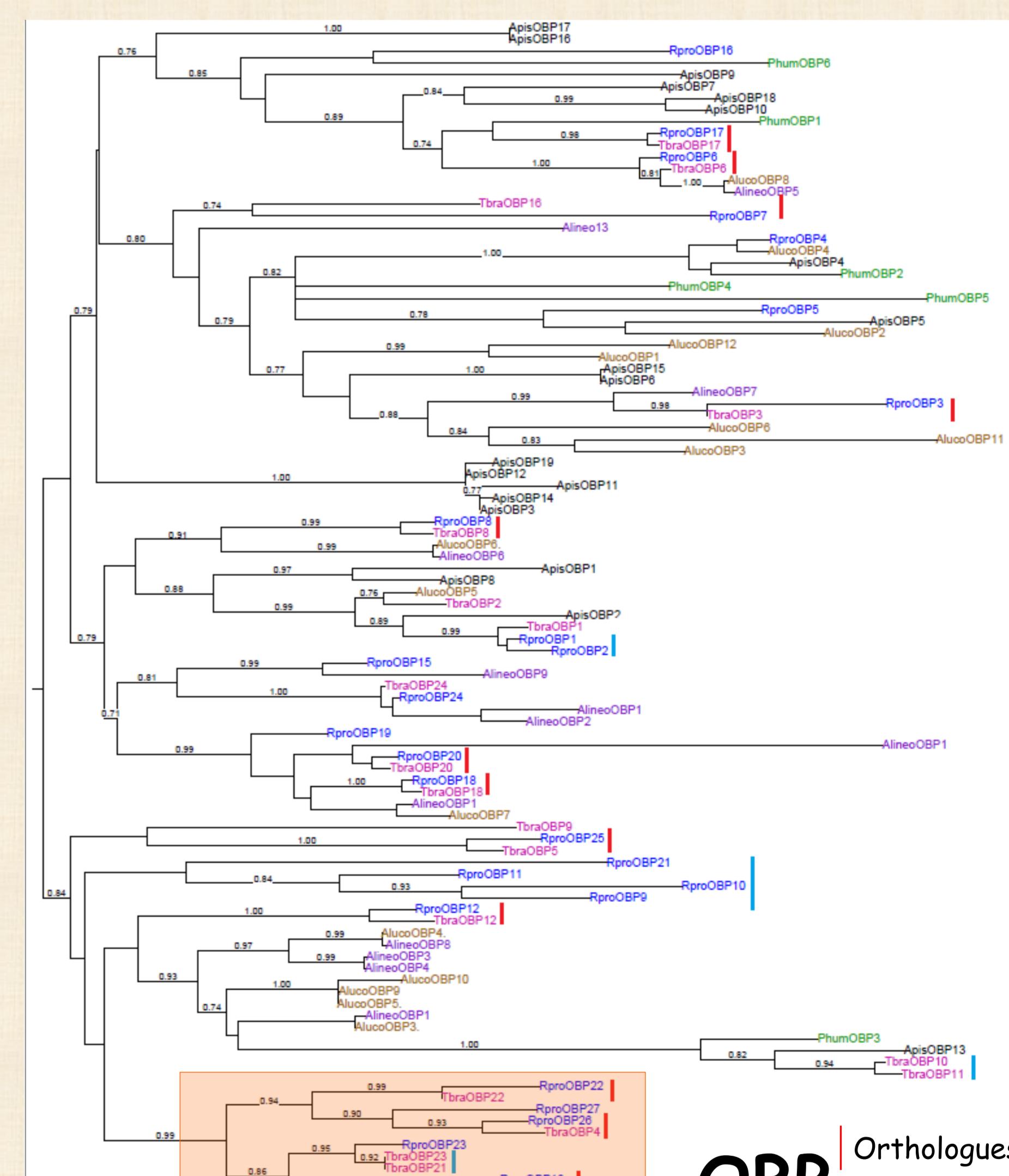
*A. pisum* → 13 CSP / 18 OBP

*P. humanus* → 8 CSP / 6 OBP

Specific clades to *R. prolixus* & *T. brasiliensis*  
Diversity within these clades:  
4-7 CSP per bug  
6-7 OBP per bug

More CSP and OBP variants in Triatominae compared to other Paraneoptera

→ Bloodsucking adaptation?  
→ Adaptation to new and changing environment?



## Perspectives: differential expression analysis

