



# Bacteriophages in human blood metagenome

**Team: “Phage in rage”**

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# Main idea

Genome sequence





# Intrumentary & data


- Sratoolkit
- Trimmomatic
- Bowtie2
- FastQC
- R (data analyze & visualization)
- HIV
- Human virome sequence
- Not human sequence



# Workflow



**HIV**  
sequences




**Human  
virome-HIV**  
sequences



**Human  
virome**  
sequences



# Workflow




Human  
virome-HIV  
sequences



**HIV**  
sequences



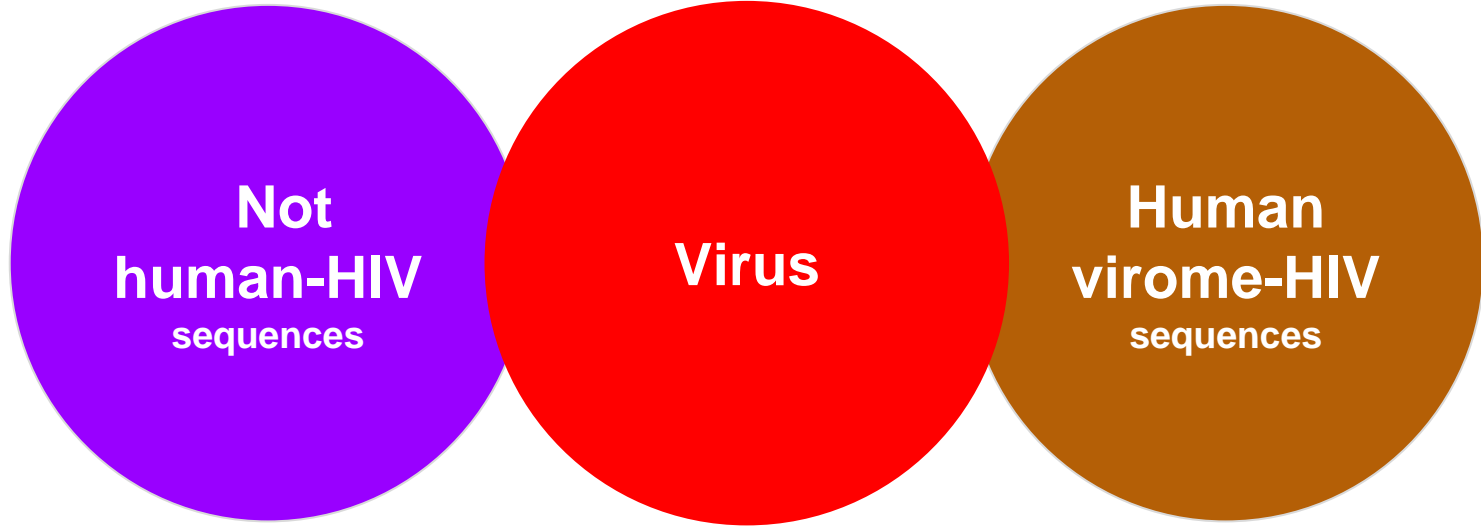
**Not  
human-HIV**  
sequences



**Not  
human**  
sequences




# Workflow



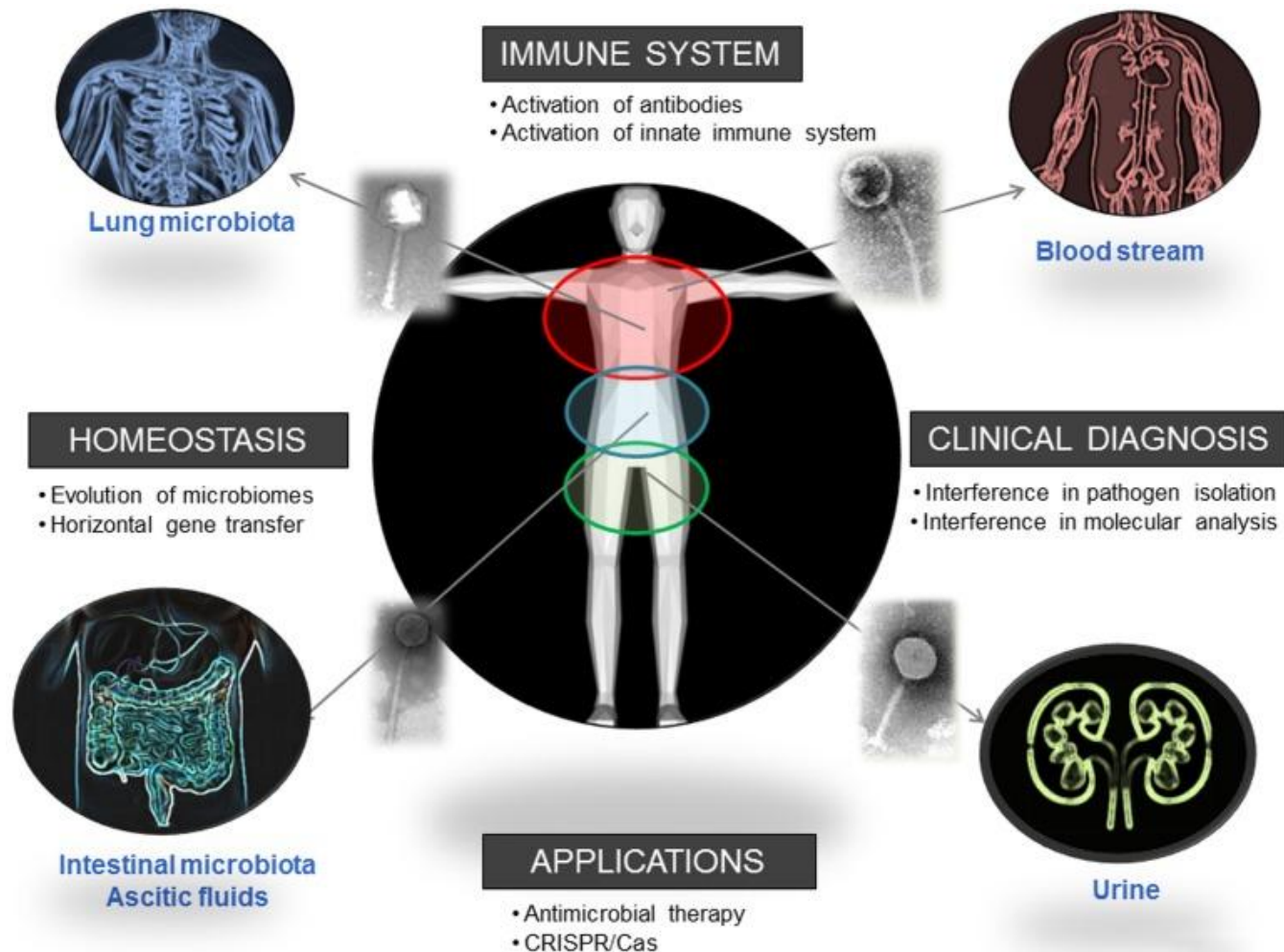
A close-up photograph of a baby with light brown hair and blue eyes, looking directly at the camera with a frustrated or determined expression. The baby is holding a clump of sand in their right hand. They are wearing a white t-shirt with green sleeves. The background is a blurred beach scene with sand and a blue sky. In the top left corner, there is a decorative graphic consisting of two overlapping diagonal lines, one blue and one green.

**TRY HARDER!!**



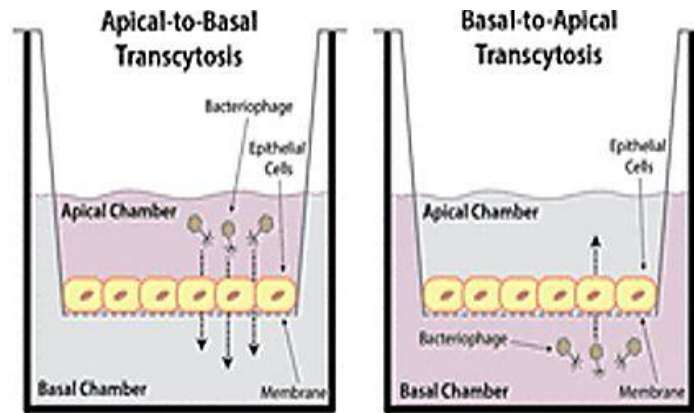
So what about  
phages in human  
body?



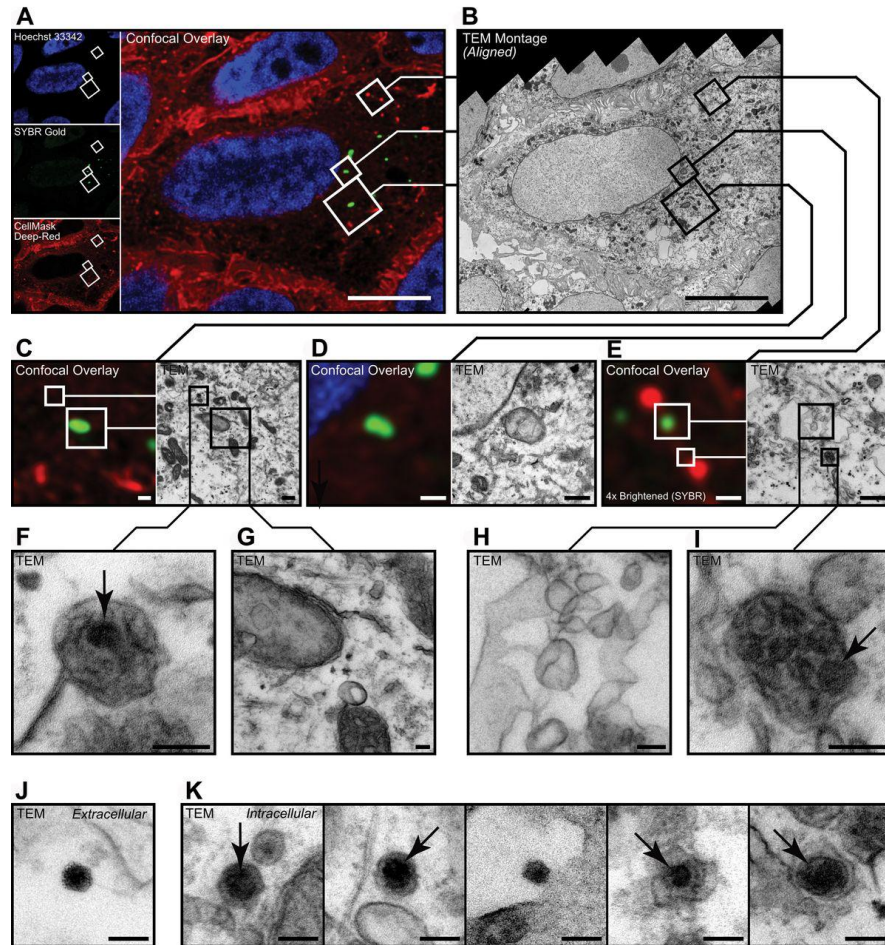


# Idea

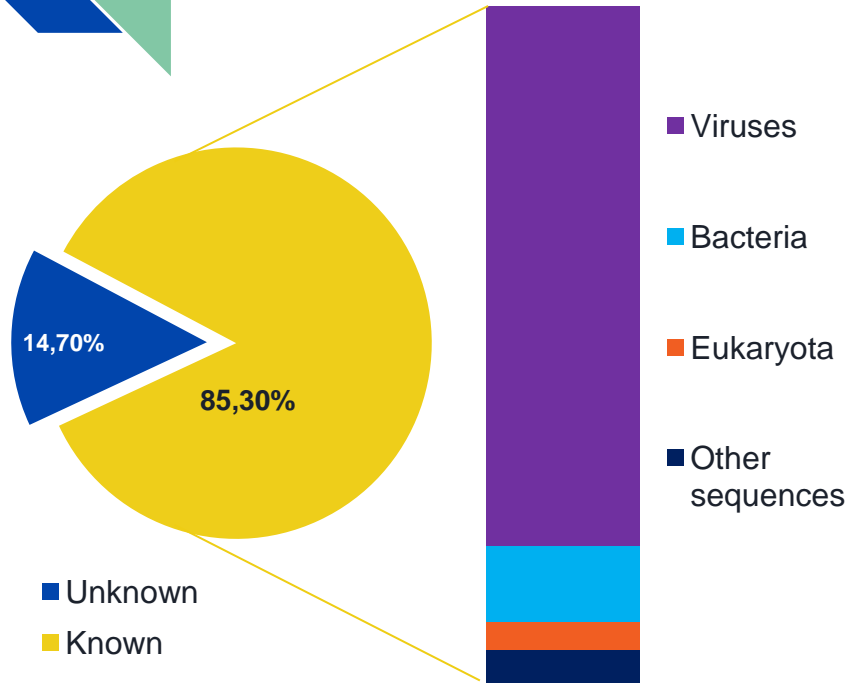
Influence of bacteriophages on physiology and pathology of the human body.



<http://mbio.asm.org/content/8/6/e01874-17.full>



# Data to compare

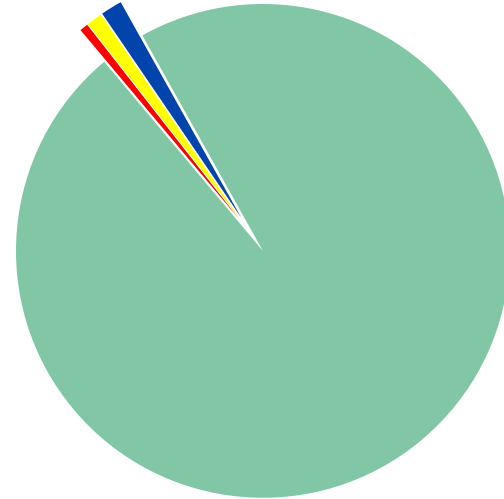
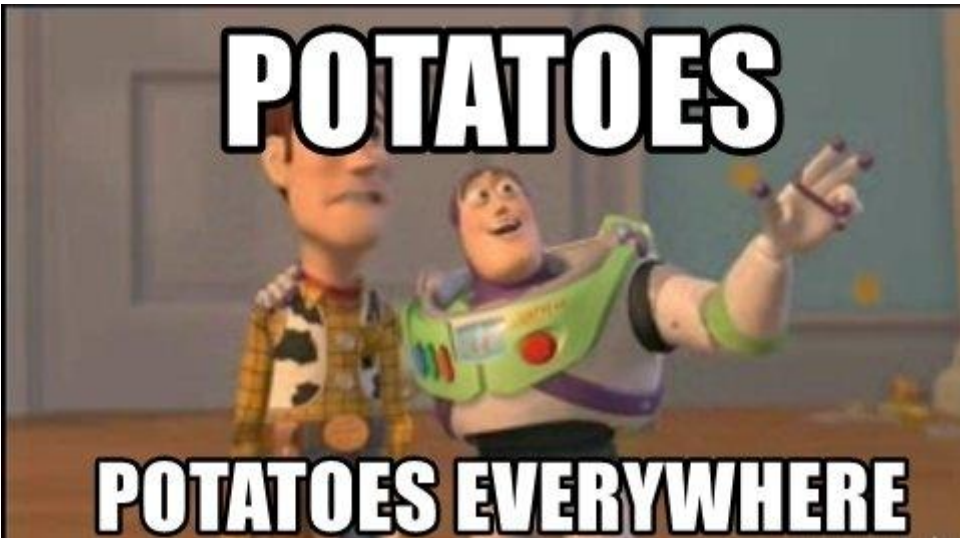


*Marseillevirus-Like Virus Recovered From Blood  
Donated by Asymptomatic Humans  
02 July 2013*

Viral Class, Species	Reads, No. (%)
ssDNA virus	
TTV	11 080 (81.40)
TTV-like virus	1575 (11.57)
SEN virus	576 (4.23)
TTV midi virus	12 (0.09)
TTV-like mini virus	11 (0.08)
RSM1 virus	6 (0.04)
RSM3 virus	11 (0.08)
dsDNA virus	
Marseillevirus	333 (2.45)
Enterobacteria phage	7 (0.05)
λ virus	

# Workflow

Healthy human blood  
metagenome analysis.



- Enterobacteria phage HK629 (NC\_019711.1)
- Enterobacteria phage HK630 (NC\_019723.1)
- Enterobacteria phage lambda (NC\_001416.1)
- Ralstonia phage 1 NP-2014 (NC\_023586.1)

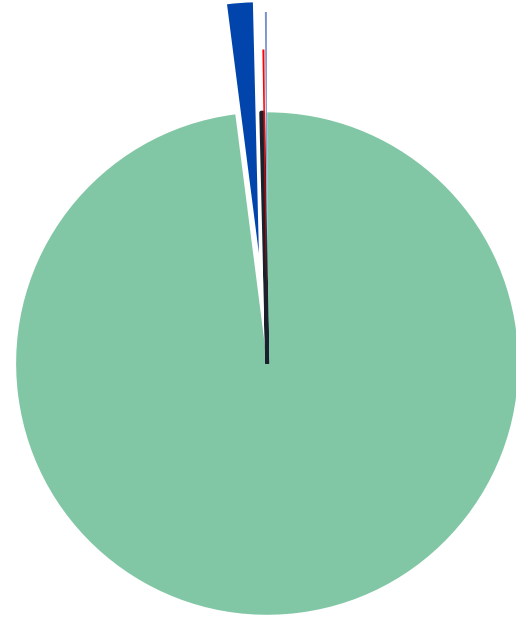
# Workflow

- Mapping phages and bacteria on human blood metagenome



# Workflow

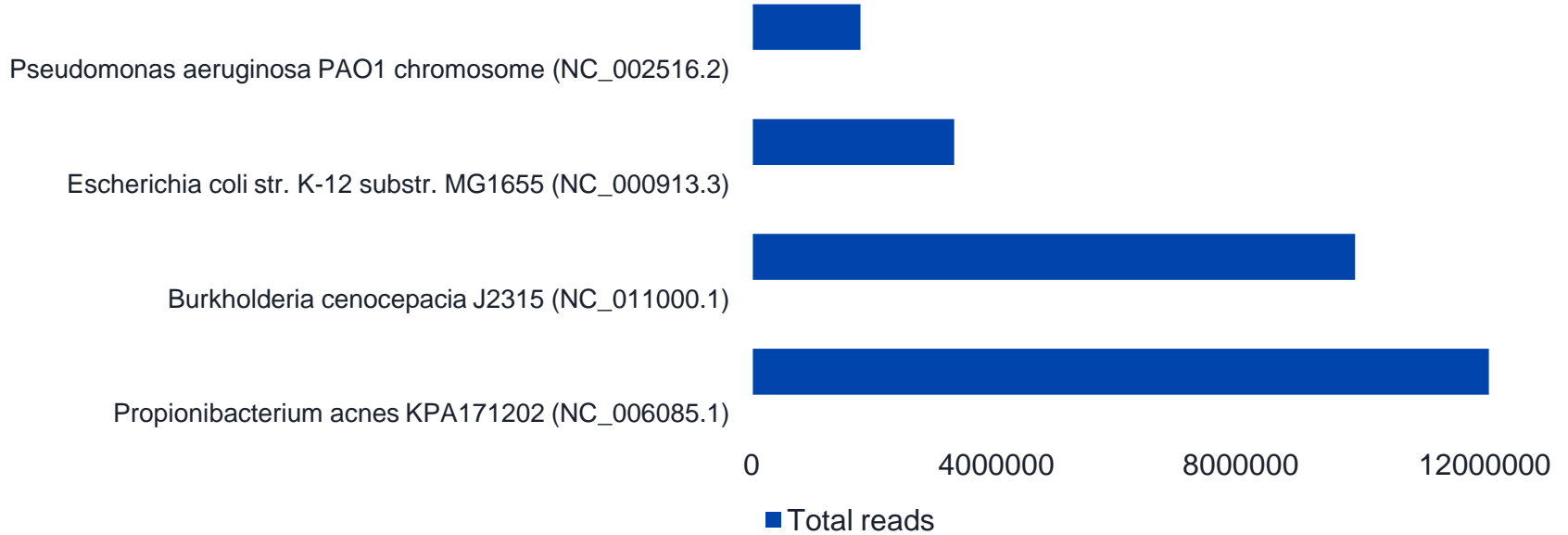
Analyze human blood metagenome infected with HIV analysis



- Bacillus phage Stitch (NC\_031032) - 1548
- Yersinia phage Yepe2 (NC\_011038) - 26
- Enterobacteria phage lambda (NC\_001416) - 2
- Shigella phage SfIV (NC\_022749) - 2
- Enterobacter phage E-2 (NC\_029102) - 2



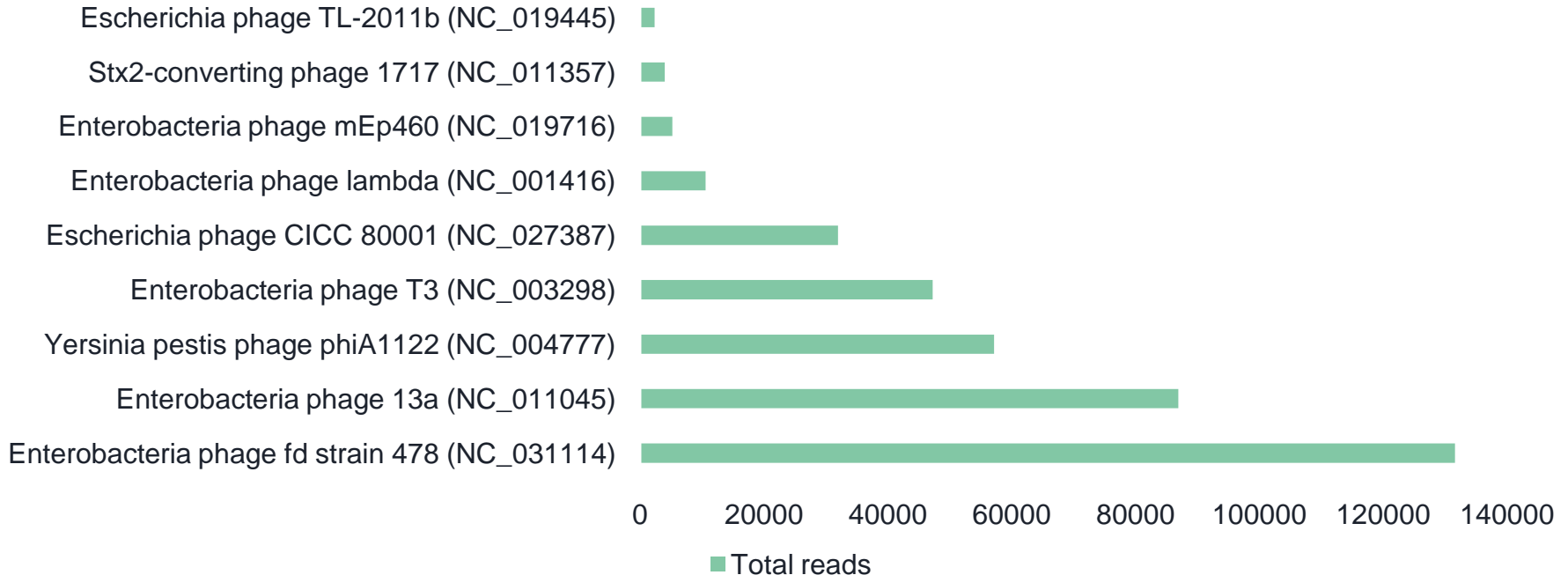
# Workflow (bacteria statistic)





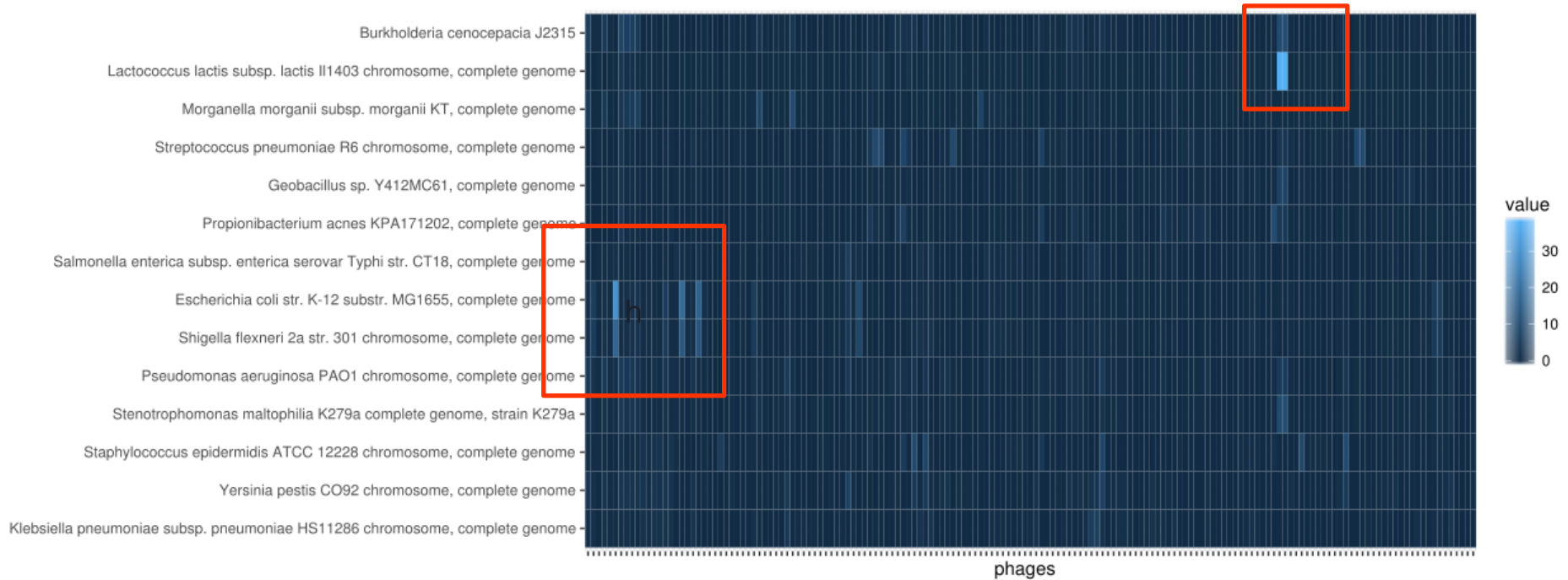
# Workflow (phages statistic)

**The biggest total reads:** Enterobacteria phage fd strain 478 (NC\_025824) – 11 241 609 (reads)



# Correlation results

bacts





# Results

- Было перепроверено старое исследование вирома крови человека с новыми базами данных. Подтверждено наличие фагов в крови, причем в относительно большом количестве.
- Впервые на масштабных данных  $n > 1$  метагенома крови был проанализирован фаговый состав.
- Представленность литических фагов в крови не соотносится с представленностью их хозяев.
- В метагеноме крови проанализированных пациентов лидируют кишечные фаги. При этом по представленности бактерий преобладают пропионобактерии.



Thank you!



# References

- <https://academic.oup.com/jid/article/208/7/1042/2192685>
- <http://onlinelibrary.wiley.com/doi/10.1111/j.1574-695X.2006.00044.x/full>
- <http://mbio.asm.org/content/8/6/e01874-17.full>
- <https://www.frontiersin.org/articles/10.3389/fmicb.2017.00566/full>