

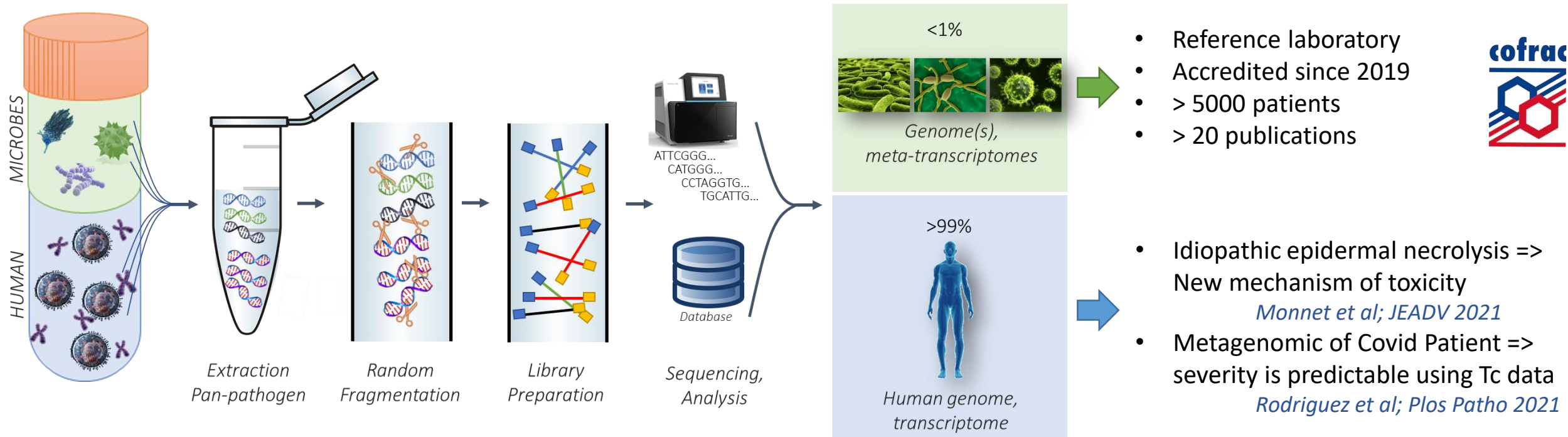
# Diagnosis of meningitis by transcriptomic approach based on metagenomic data

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# Transcriptomic from SMg



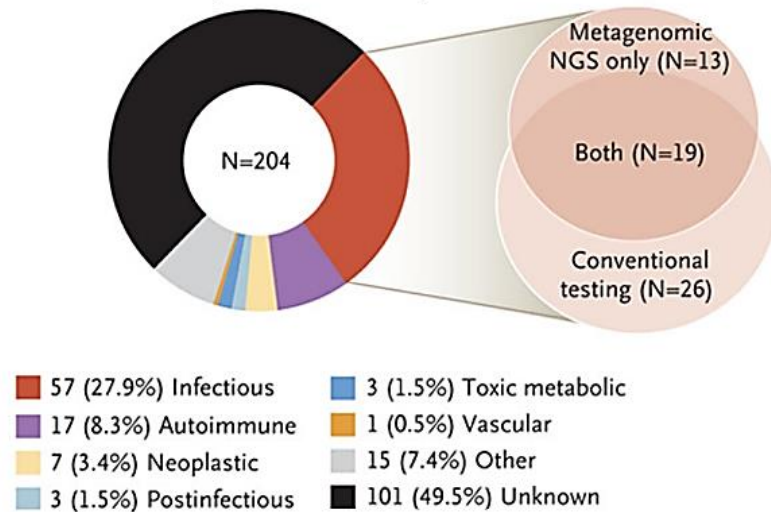
=> Transcriptomic data of Shotgun Metagenomics are usable for clinical questions

# Infection or not infection ?

- Undiagnosed patients in CNS infections ?



A Established Diagnoses in the Study Patients



*Wilson et al, NEJM 2019*



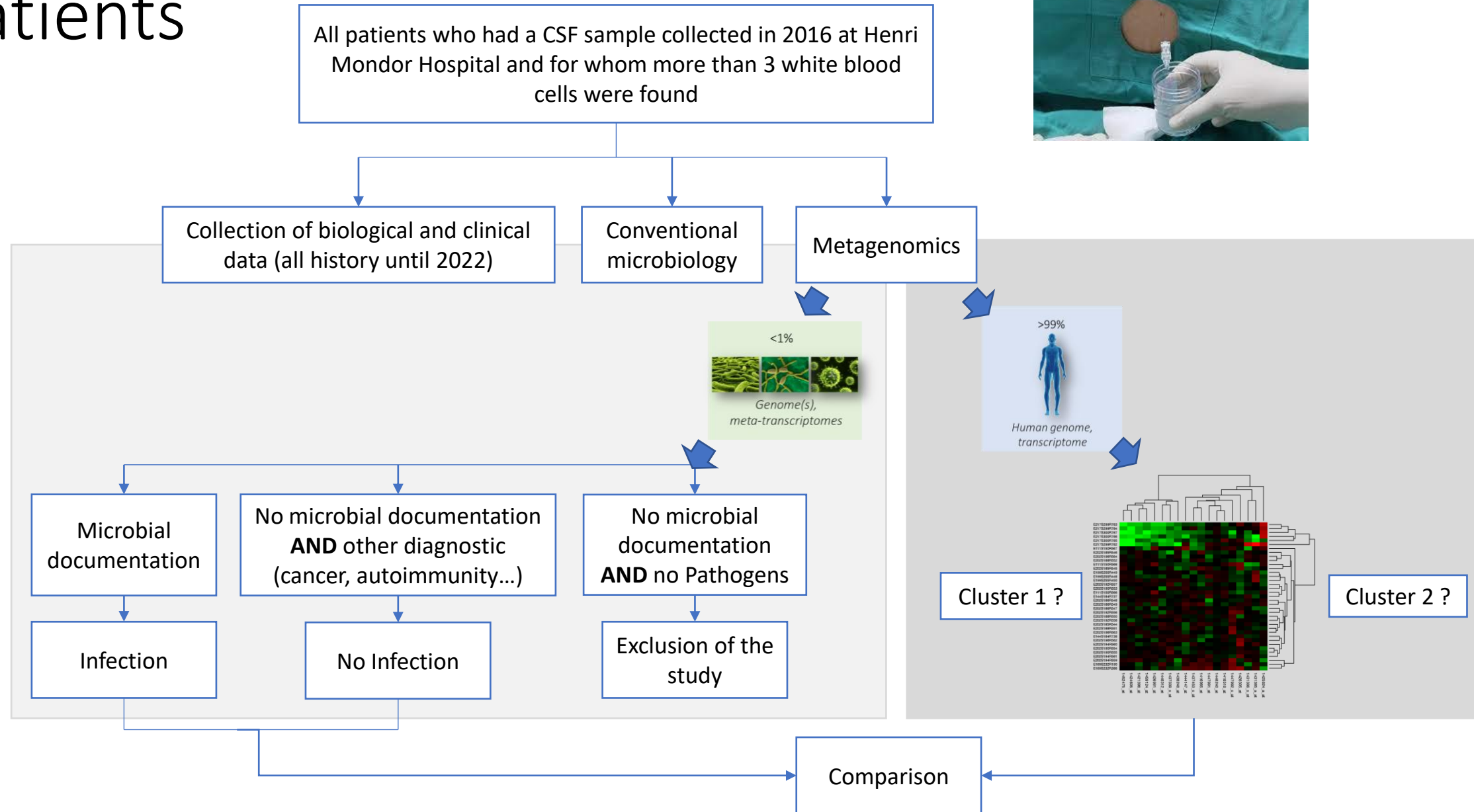
Inability to diagnose infection due to a lack of sensitivity of the techniques, the quality of the sample, the temporality of the disease...



Can the transcriptomic host overcome the inabilities of microbiological diagnostic tools (including Mg) to answer the questions :

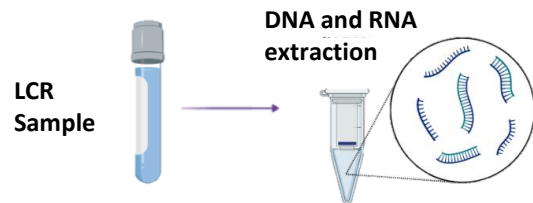
- It is an infection ?
- If yes, it bacterial or viral infection ?

# Patients



# Methods

## Pre-extraction and extraction (triple lysis)



## Library prep

- Nextera XT
- TruSeq Total RNA



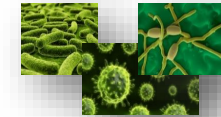
## Sequencing

- NovaSeq 6000

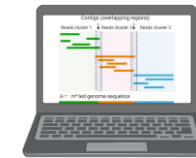


## Bioinformatic analysis

- MetaMIC
- (Microbial documentation)

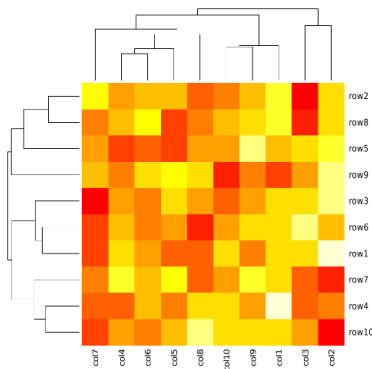


- Transcriptomic pipeline
- Hisat 2, Stringtie, DeSeq2

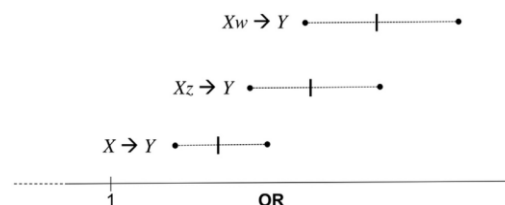


## Heatmap

Cluster ?



## Odd Ratio Risk



## Onological analysis

Pathway enrichment ?  
Gene enrichment ?



# Results Cohort (N=155)

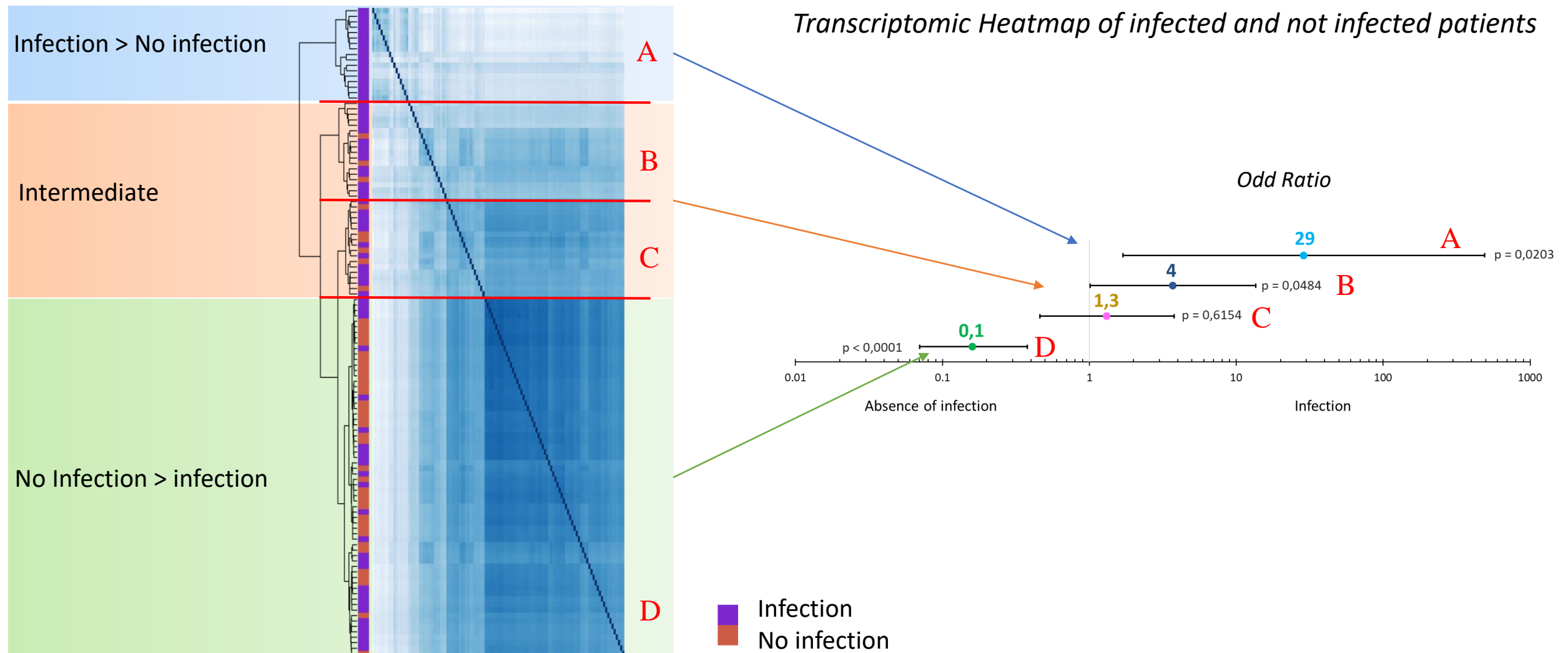
		Infection N=73	No infection N=48	Excluded N=34
Ratio H/F		1.2	0.9	1.6
Age (yo)		54 [31;80]	58 [27;89]	43[14;83]
Unit	Emergency	40%	13%	38%
	Intensive Care	25%	31%	32%
	Various hospital	35%	56%	30%
Infection ratio (bacteria/virus)		18/53	NA	NA



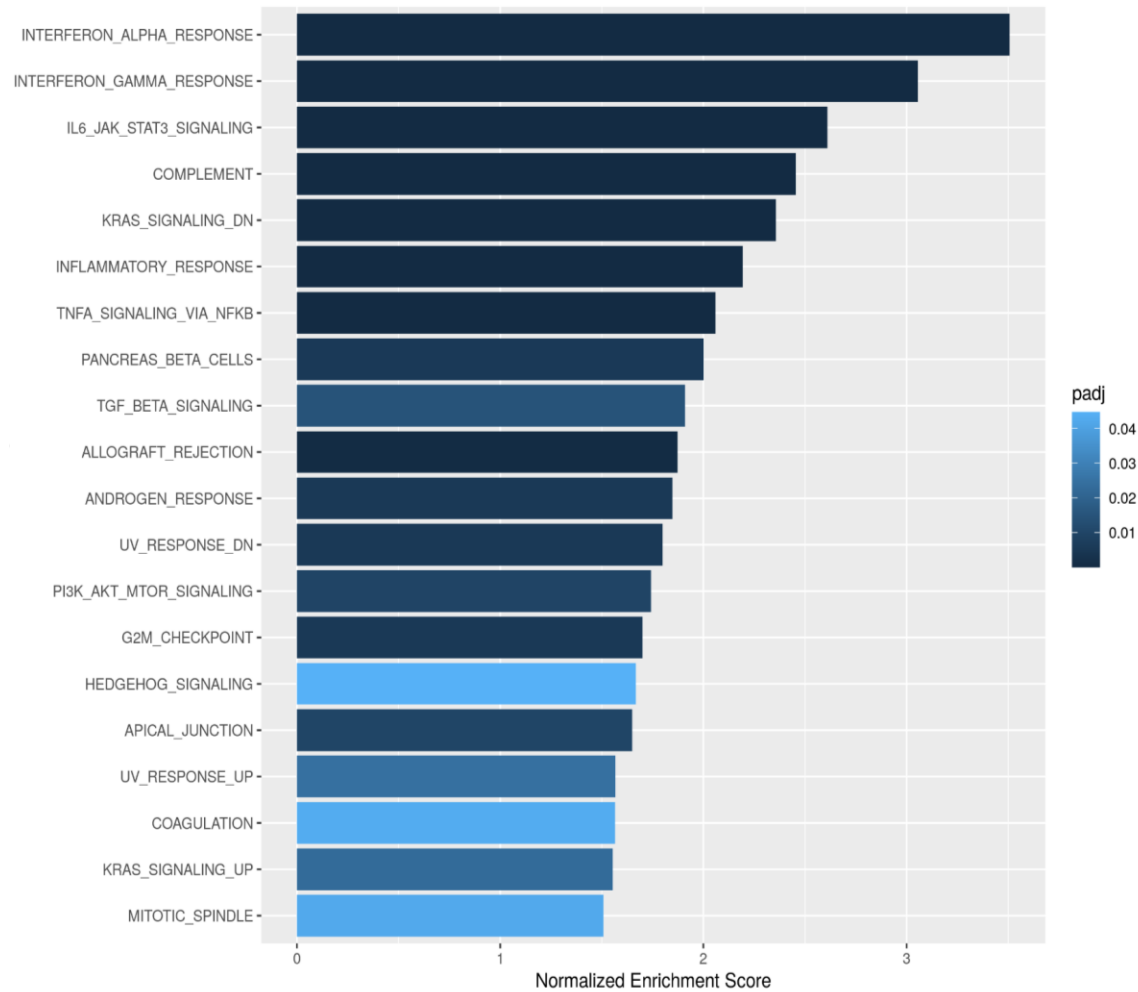
119 Patients



# Infection (N=73) vs no infections (N=48) ?

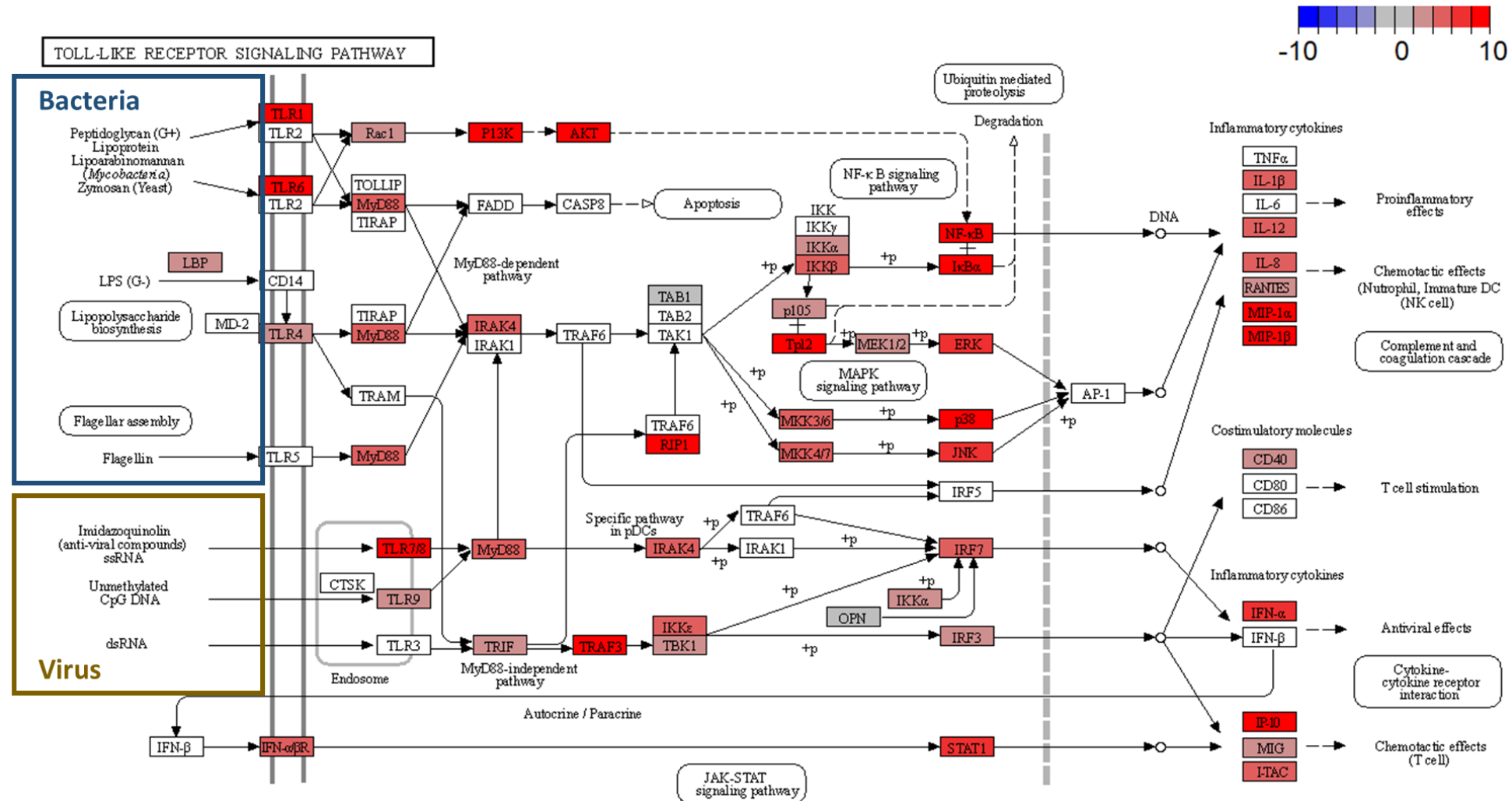


# Results : Infection vs no infections ?

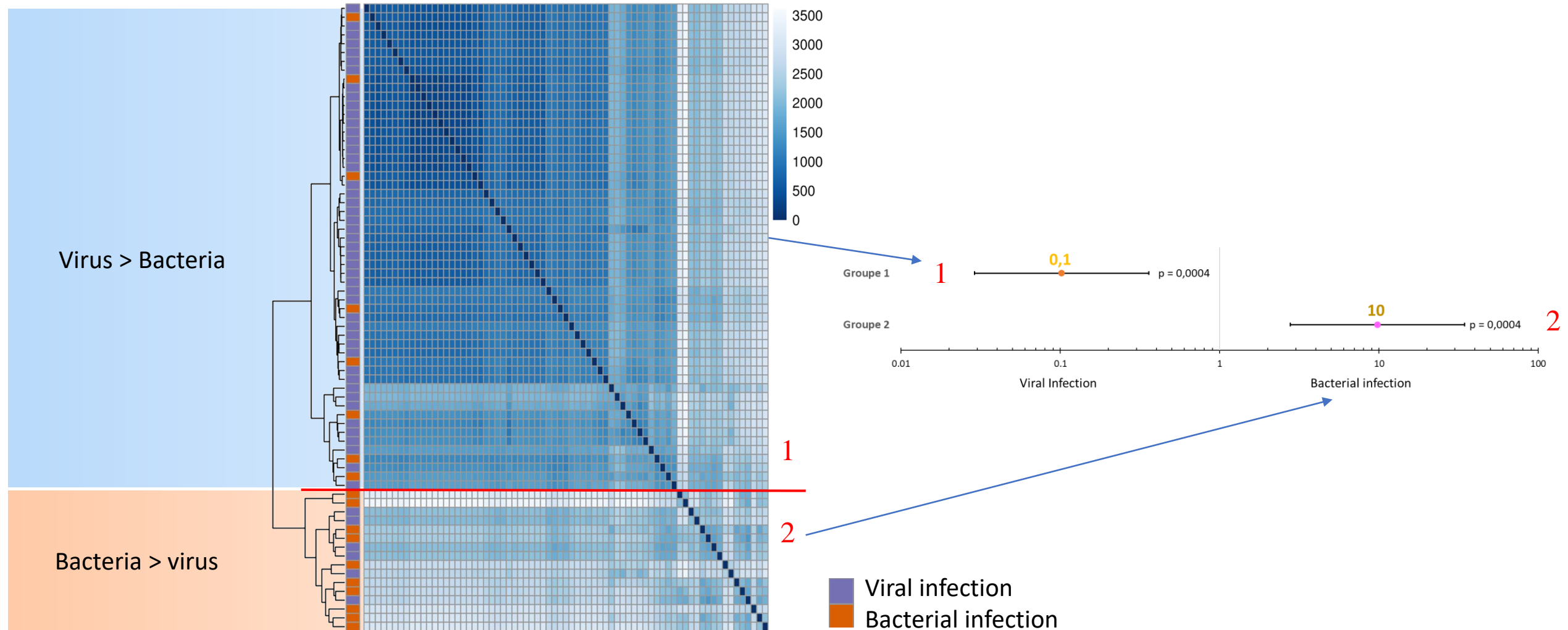




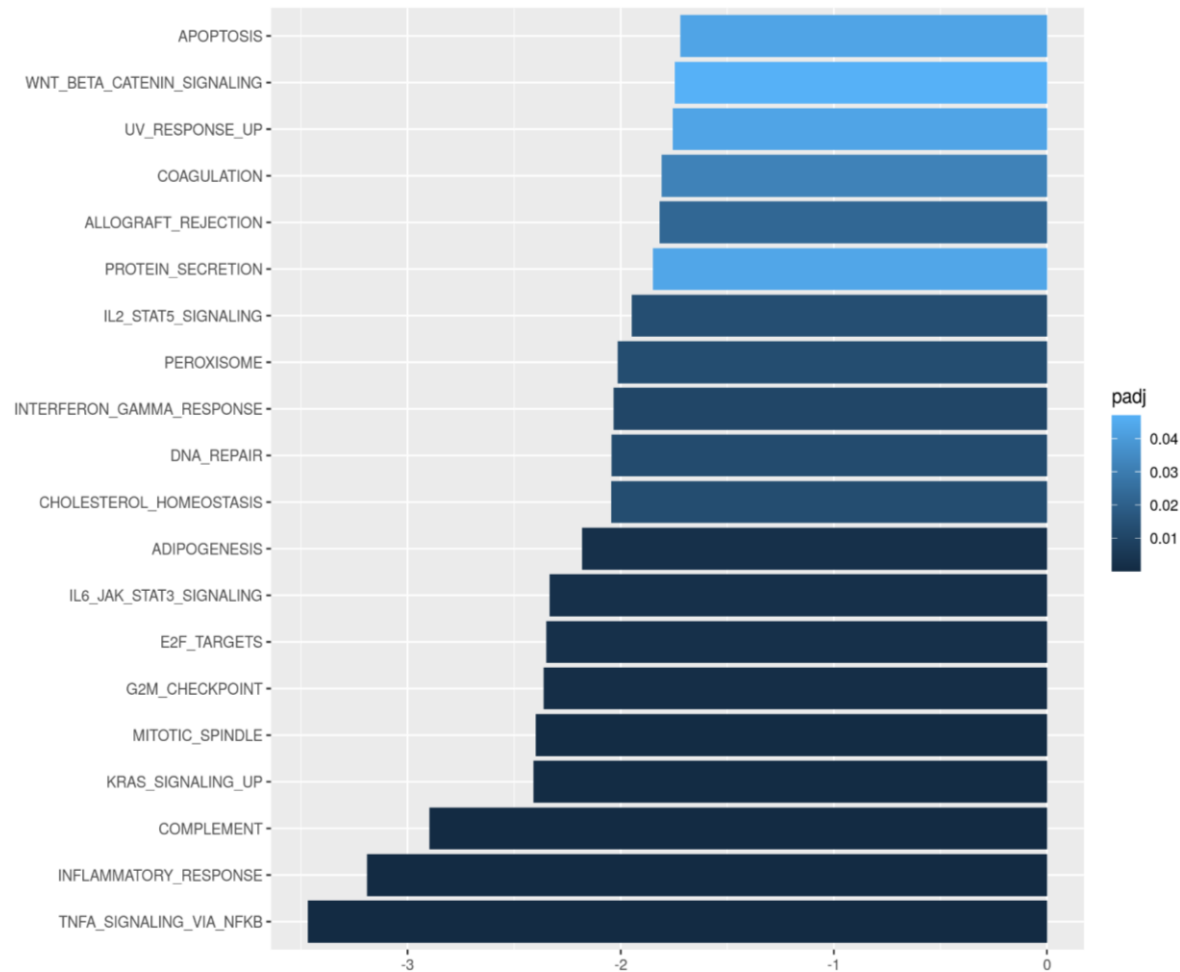
# Results : Infection vs no infections ?



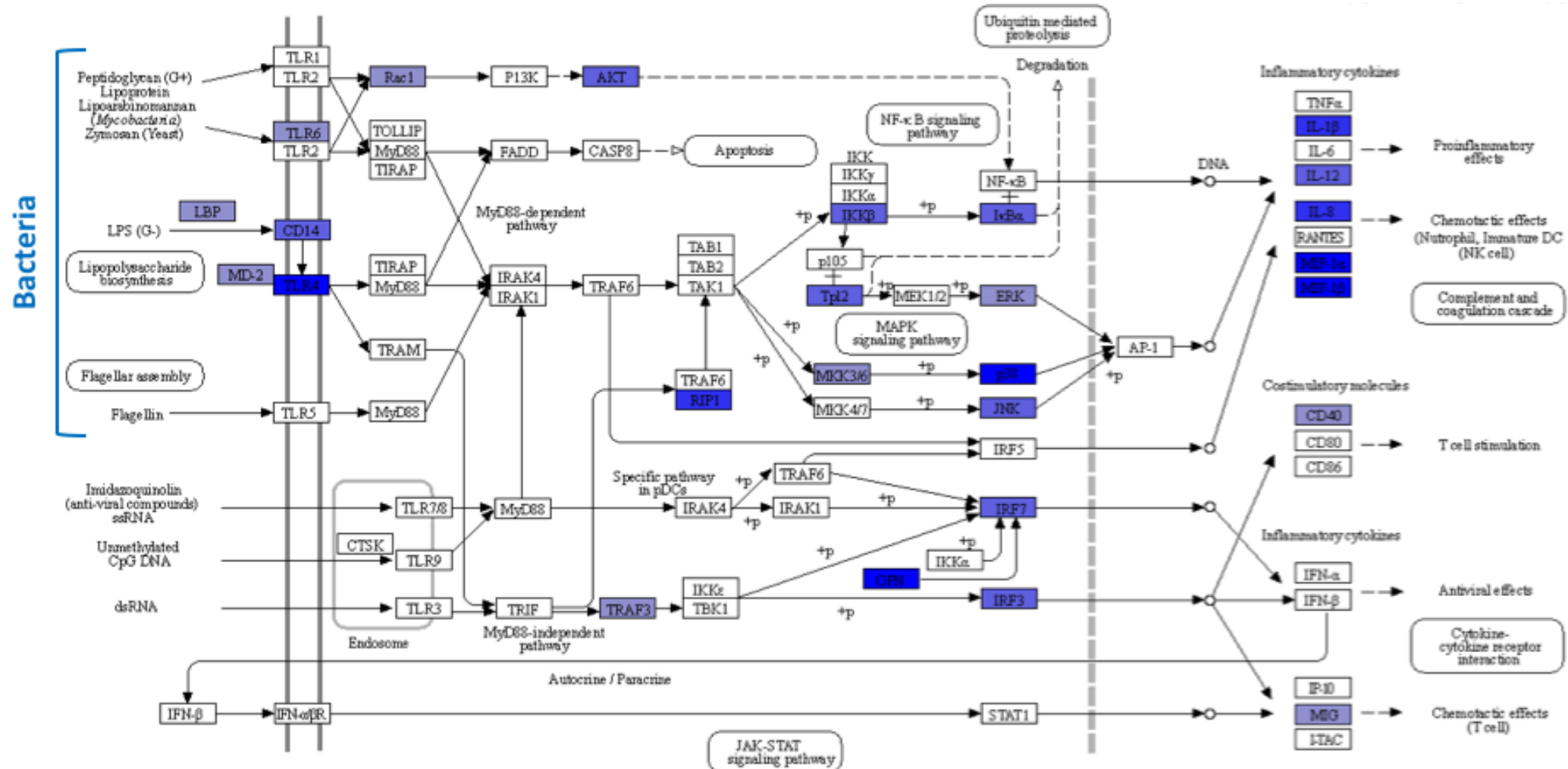
# Viral Infection (N=53) vs bacterial infections (N=18) ?



# Results : Infection vs no infections ?



# Results : Bacteria vs viruses?



# Conclusion/Perspectives

- Human RNA data generated from SMg are usable for transcriptomic profiling
- Transcriptomic profiles are different between infected and not infected patients
- Transcriptomic profiles are different between viral infected and bacterial infected patients
- Enriched pathway are linked with Immunity, TLR pathway is the most impacted
- A cohort of 420 patients is currently tested to confirm the results
- Data mining is pending to identify the better genes in relationship with the different clinical groups

# Thanks to the team !

## NGS METAMIC

### Experimental

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Paul-Louis Woerther (bacterio)  
Cecile Angebault (myco)

### Project Head

Christophe Rodriguez,  
Jean-Michel Pawlotsky



## Clinicians

### Infectious diseases

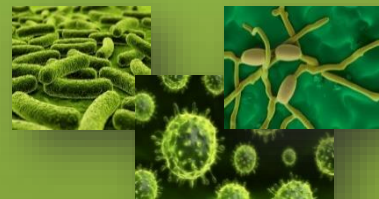
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## Sponsors

