



Escherichia/Shigella at 1 month impact epithelial cells which expressed higher calprotectin and cathelicidin

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Escherichia/Shigella at 1 month impact epithelial cells which expressed higher calprotectin and cathelicidin

Constance Patin¹, Karine Le Roux¹, Pierre-Yves Ancel^{2,3}, Marie-José Butel^{2,4}, Jean-Christophe Rozé⁵, Patricia Lepage¹

¹ Université Paris-Saclay, INRAE, AgroParisTech, Micalis Institute, Domaine de Vilvert, Jouy-en-Josas, 78350, France ; ² FHU PREMA « Fighting prematurity », 75006, Paris, France ; ³ Université de Paris Cité, Center for Epidemiology and Statistics/CRESS U1153/EPOPé Team, Paris, France & Clinical Investigation Center P1419, Assistance Publique-Hôpitaux de Paris, Paris, France ; ⁴ UMR-S INSERM U1139, 3PHM, Faculté de Pharmacie, Université de Paris Cité, 75006, Paris, France ; ⁵ Neonatal Department, INSERM-CHU Clinical Investigation Center 1413, et UMR-INRA1280, Physiologie des Adaptations Nutritionnelles, Nantes University Hospital, Nantes, France

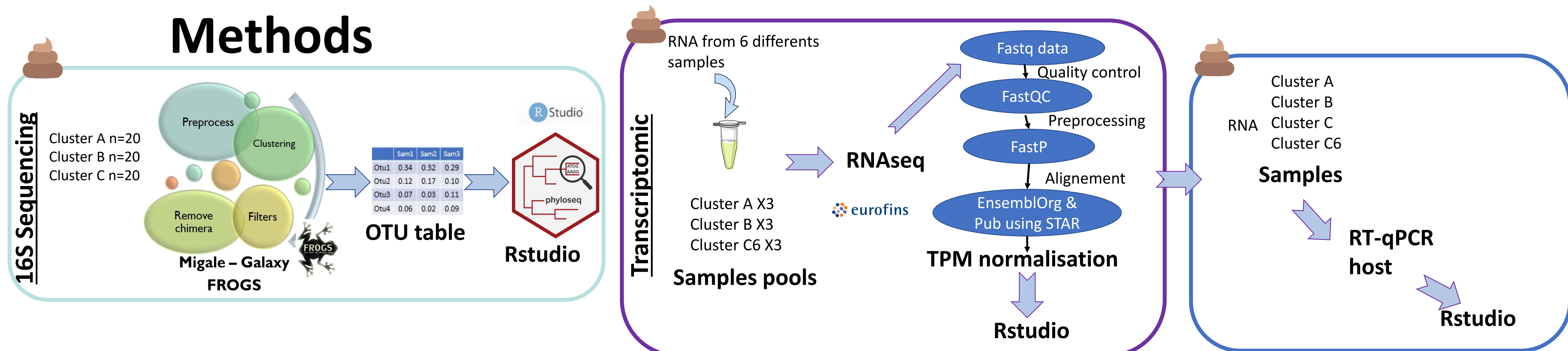
Background

- Preterm birth are 1st cause of death in children under 5 years of age in the world
- Serious psychological and physiological consequences in the short and long term [1]
- High level of fecal calprotectin in healthy infants. Calprotectin is involved in inflammation and is a marker of leucocytes which produces antimicrobial peptides (alpha-defensins and cathelicidin) [2-3]
- Need to develop analyses on non invasive approach

Objective

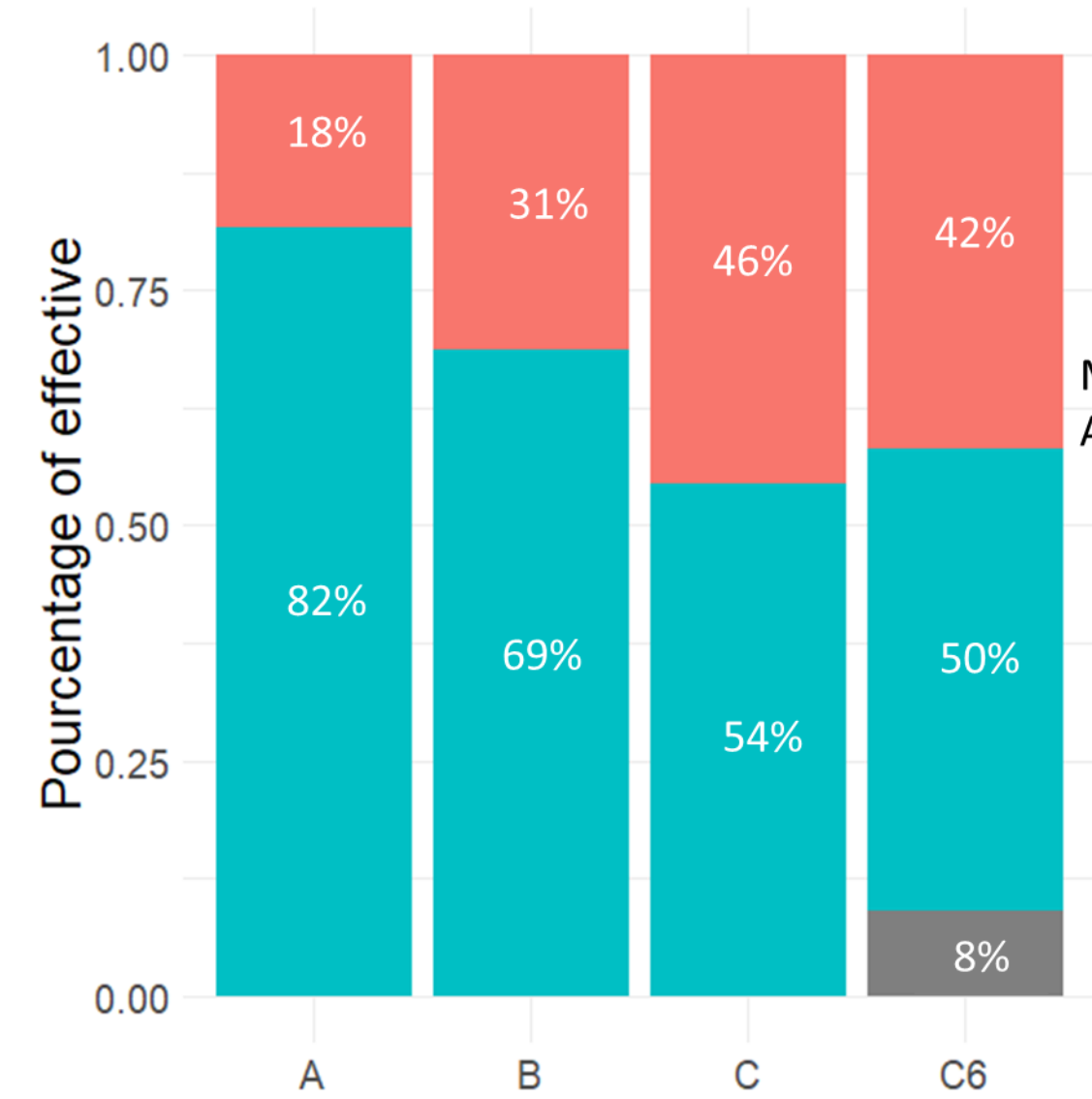
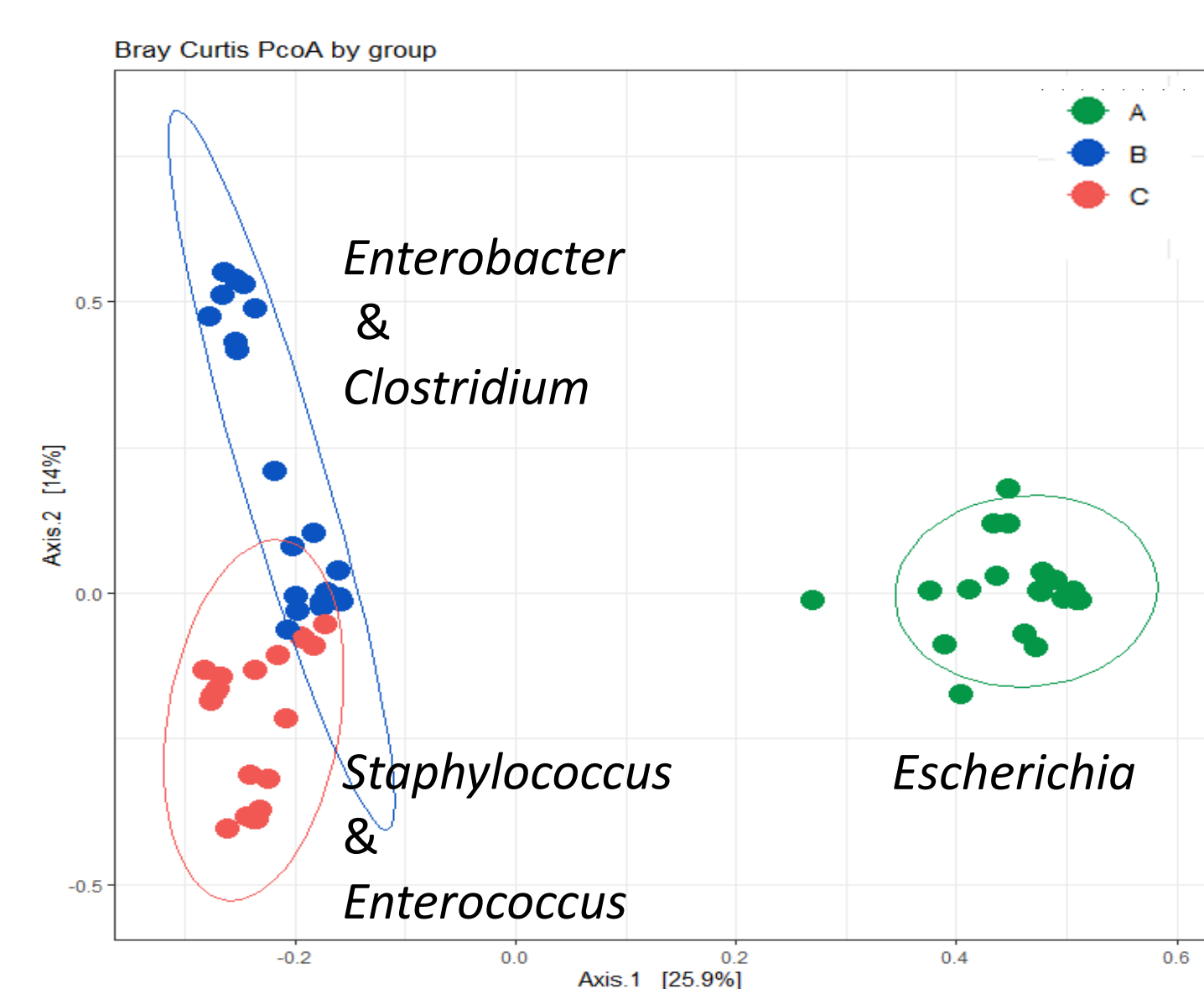
Evaluate impact of gut microbiome colonization at 1 month on calprotectin-mediated physiological inflammation

Methods

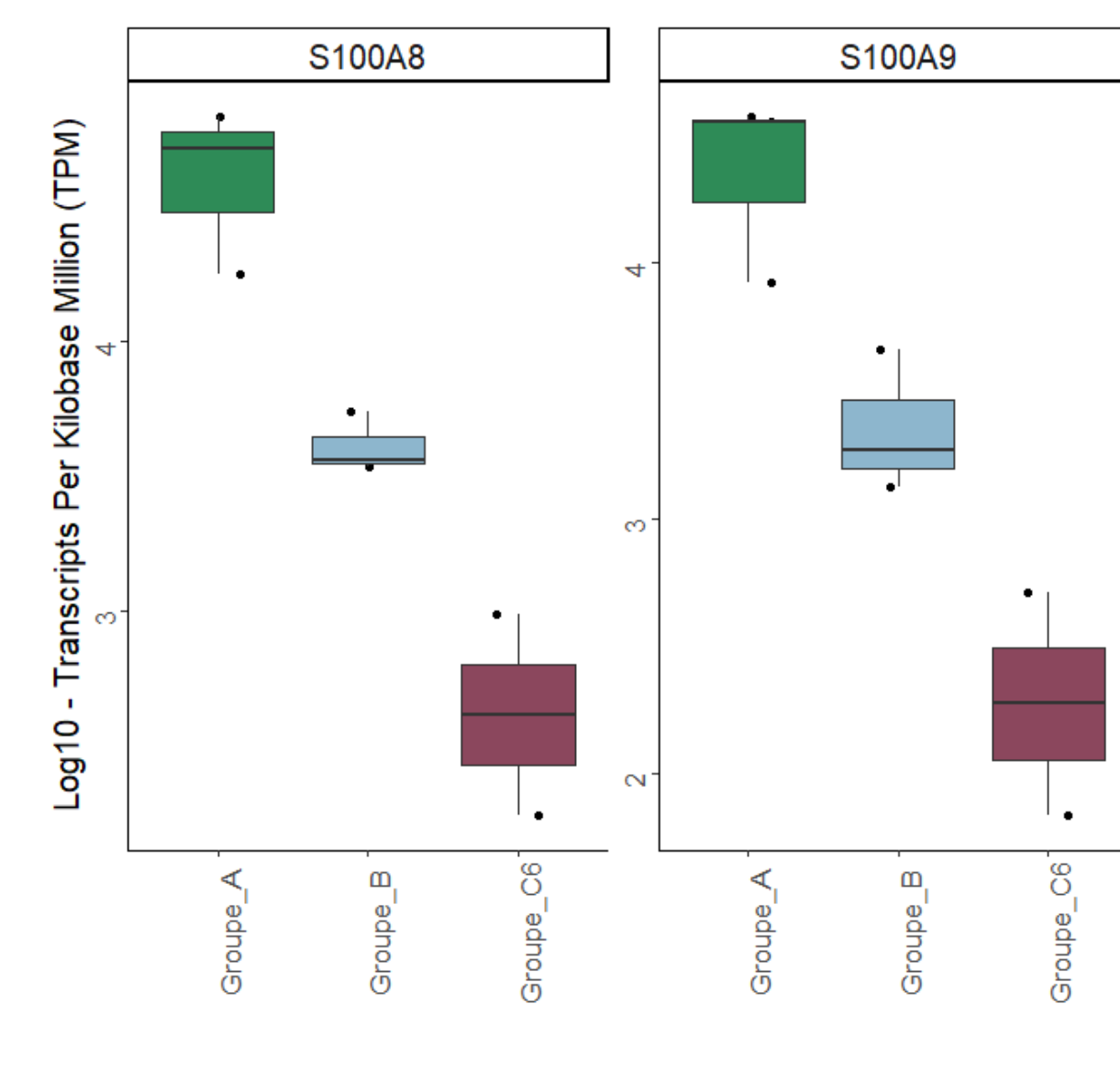
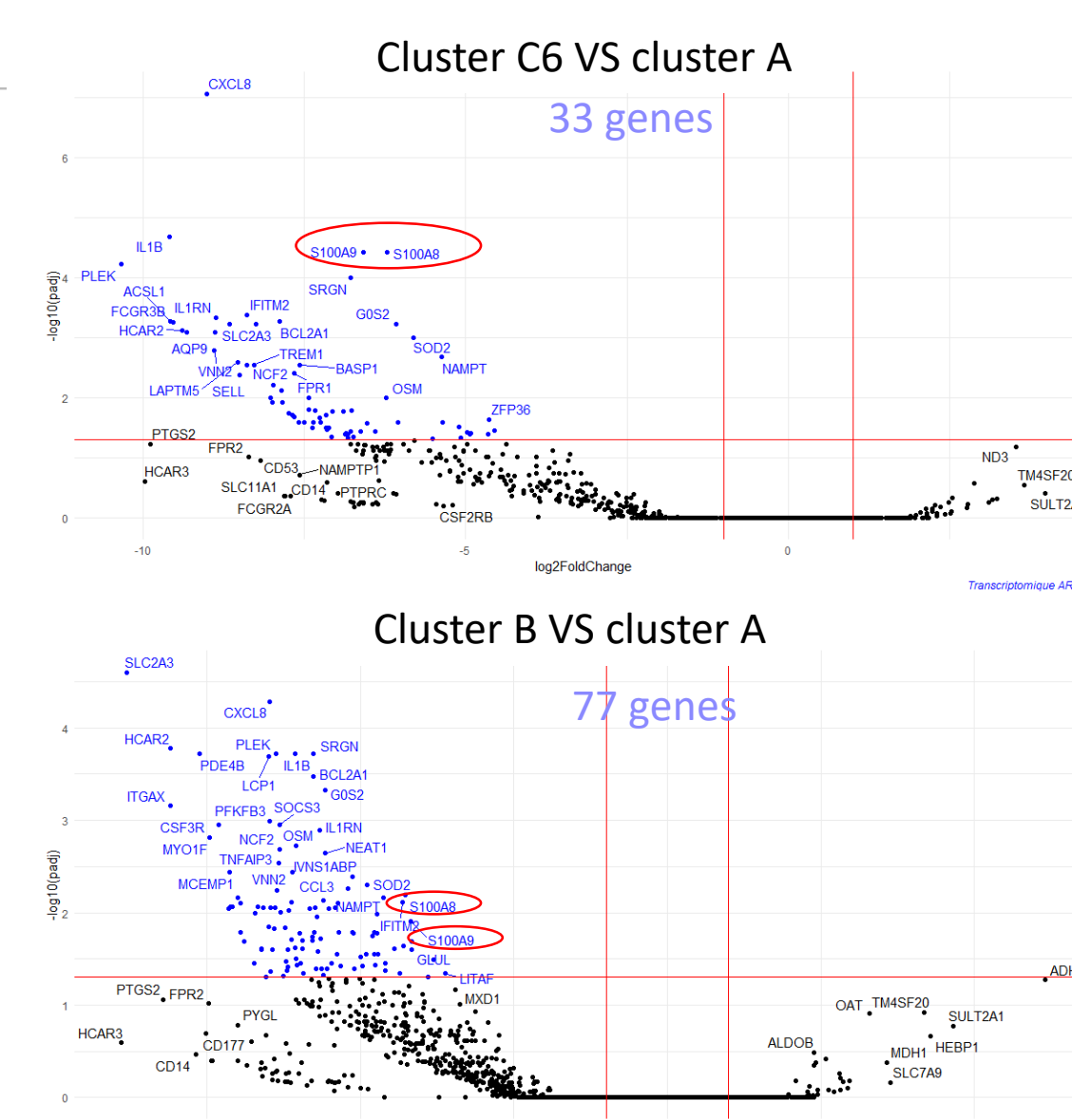
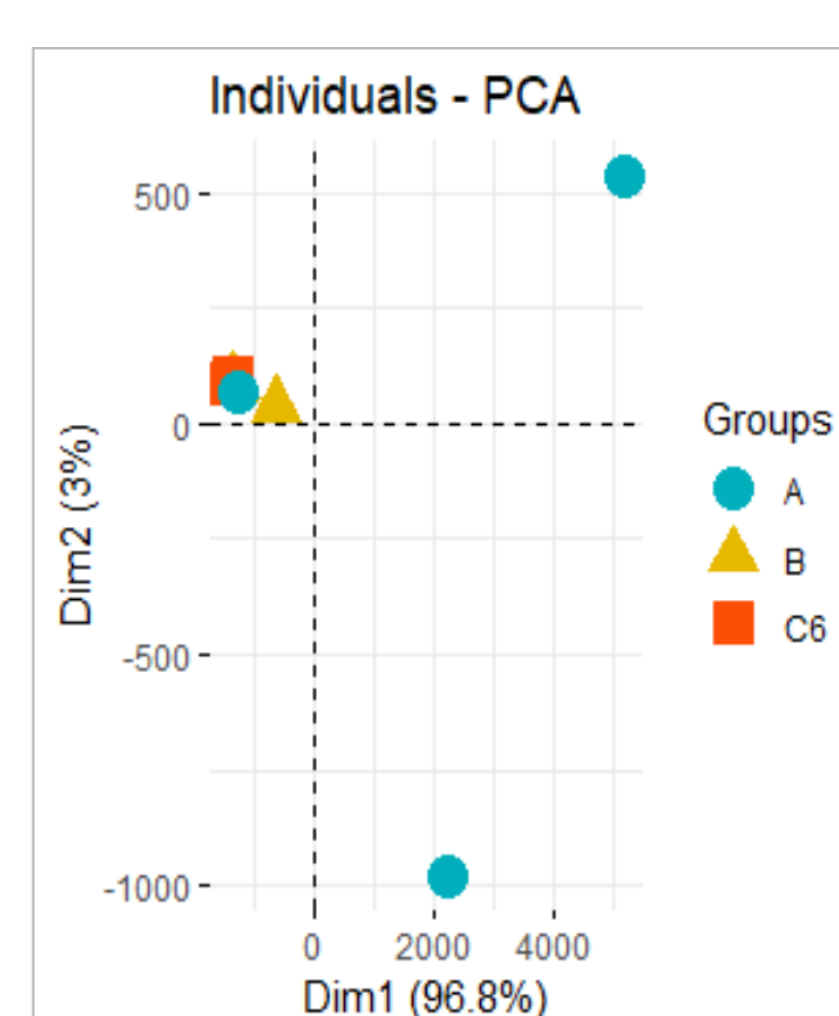


Results

Microbiome of very preterm infants can be stratified in 4 clusters with different outcome



Cluster A genes library have a different gene expression pattern than the other tow groups

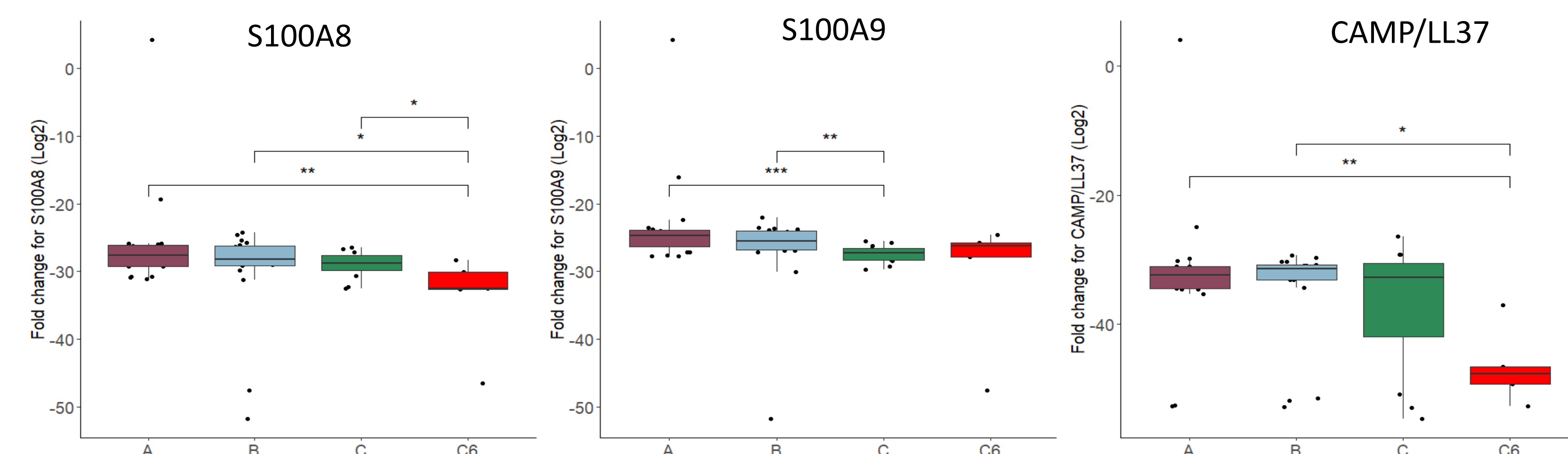


- Clusters are driven by 3 groups of dominant genus
- Cluster C6 has a lower abundance of bacteria to be detected
- Cluster A and B at 1 month have better pronostic at 2 years

- Up-regulation of many genes for the cluster A against B and C6
- Calprotectin subunits (S100A8 and S100A9) are up regulated in cluster A.

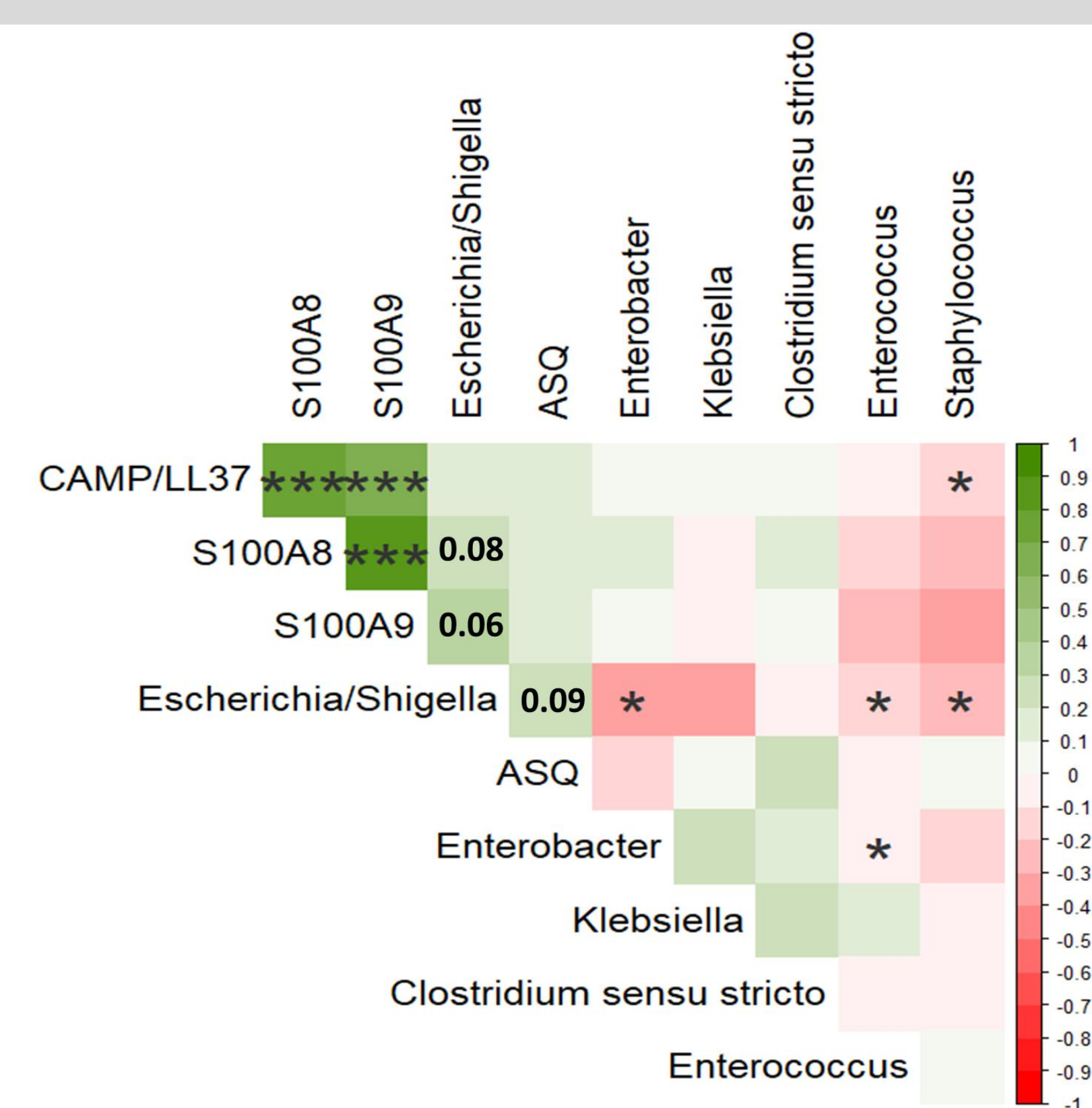
- An increasing trend is observed for expression of calprotectin in group A.

Expression of calprotectin and cathelicidin globally less expressed in children from cluster C and C6



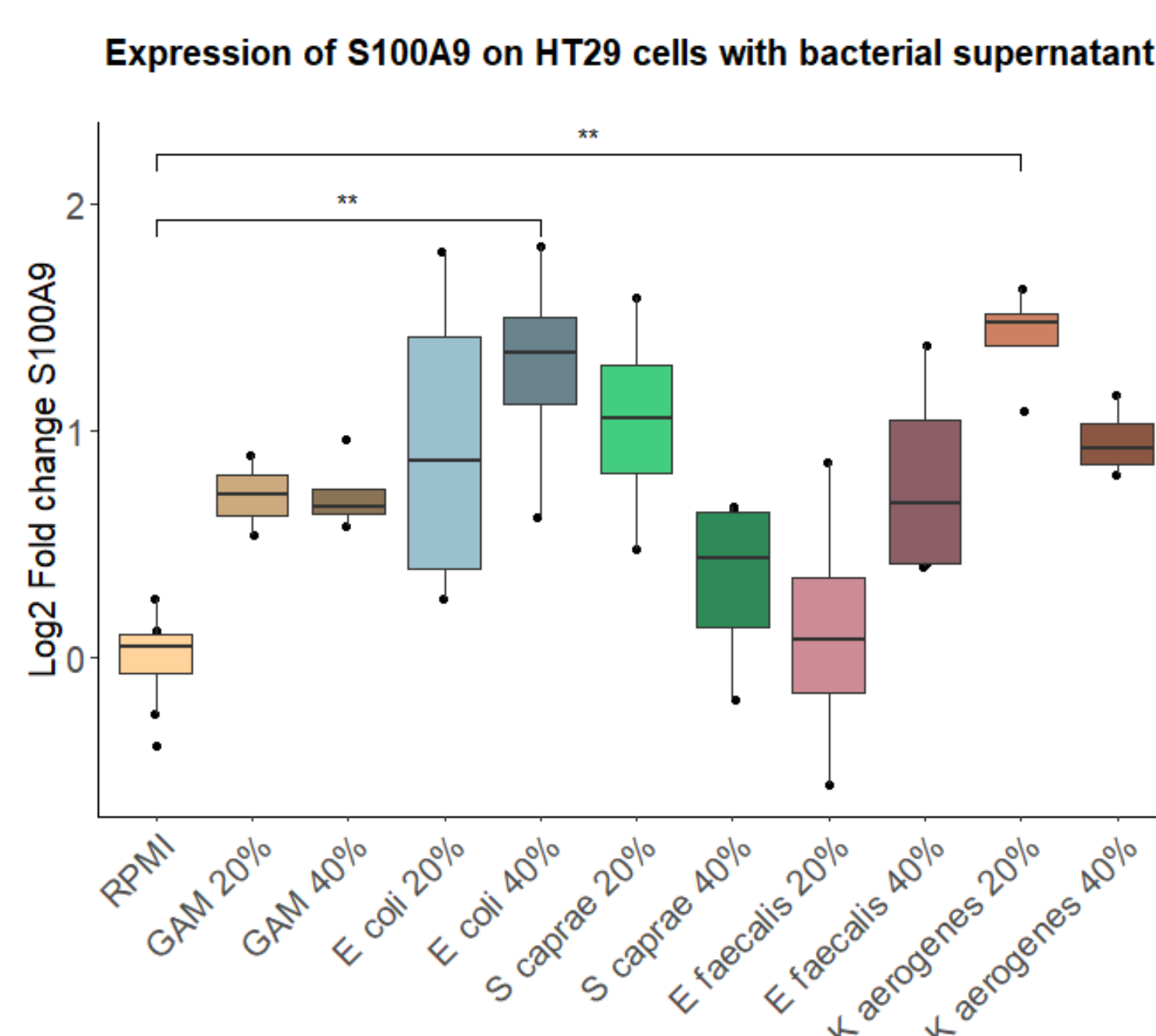
- Globally, cluster A and B have a higher expression of calprotectin and cathelicidin.
- Cluster C6, with non detectable bacteria, has the lowest expression for calprotectin and cathelicidin.

Calprotectin and cathelicidin correlated with gut microbiome



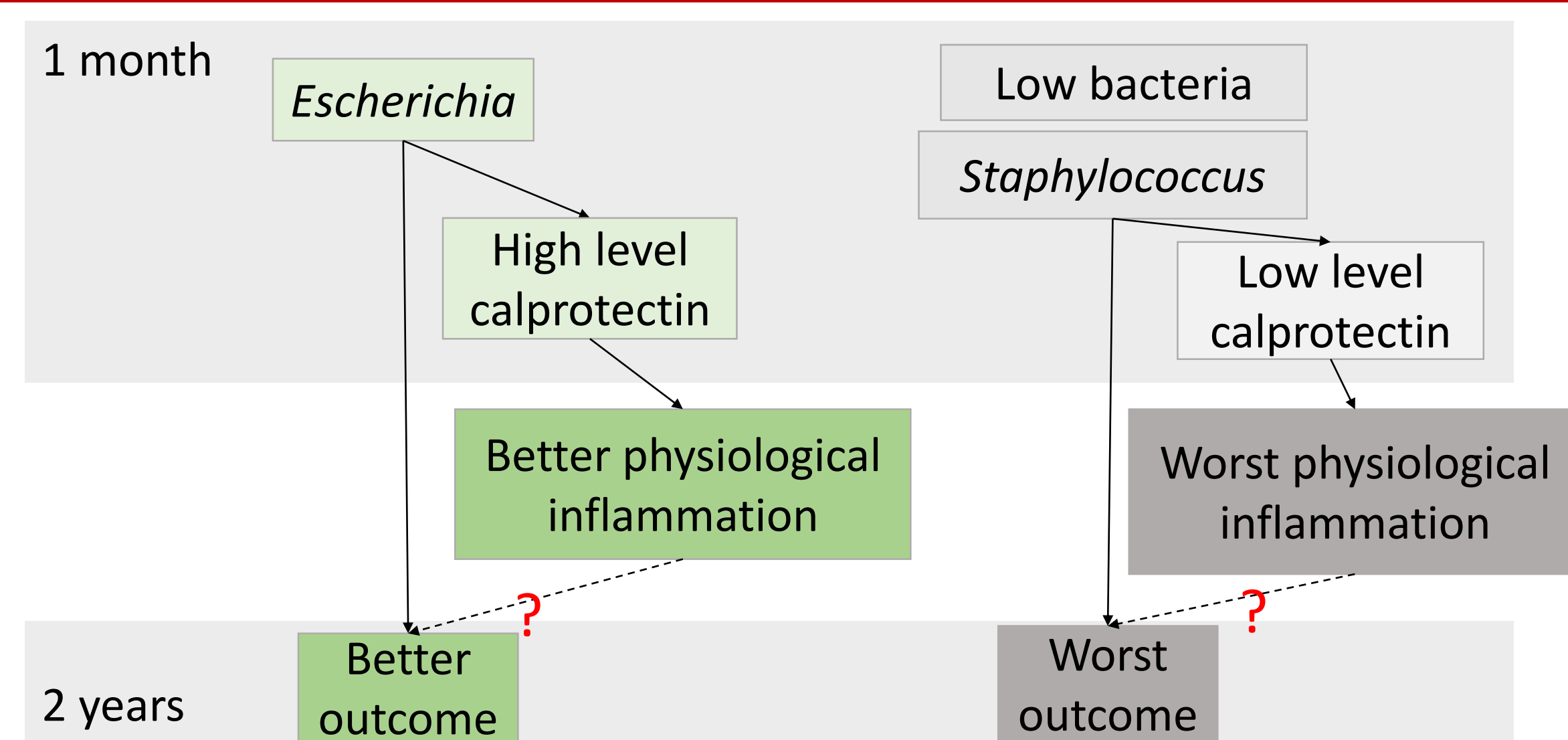
- Calprotectin and cathelicidin were positively correlated together
- Cathelicidin is negatively correlated with *Staphylococcus* (Driver of Cluster C)
- Escherichia/Shigella* and calprotectin were positively correlated (NS)
- ASQ at 2 years and *Escherichia/Shigella* were positively correlated (NS)

No real impact of supernatant of bacteria on epithelial HT29 cells



- S100A8 was not detected in qPCR
- Escherichia coli* and *Klebsiella aerogenes* increased significantly expression of S100A9

Conclusion



- Gut microbiome at 1 month impact calprotectin and cathelicidin expression.
- Having *Escherichia* at 1 month increased the “physiological inflammation” with calprotectin and cathelicidin.
- Meconium ? Cells CCD 841 CoN ? Supernatant of isolates ?