butyrate producing genes annotation

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1 butyrate-producing bacterial

Butyrate-producing bacteria have recently gained attention, since they are important for a healthy colon and when altered contribute to emerging disease, such as ulcerative colitis and type II diabetes.

- a butyrate-producing taxonomic core in healthy colons
- two *final* genes in the two primary bacterial butyrate synthesis pathways, butyryl-CoA: acetate Coa-transferase (but) and butyrate kinase (buk).
- butyrate-producing community
- important things let's say it three times:

Eubacterium spp. and Roseburia spp (Clostridum cluster XIVa) and Faealibacterium prausnitzii (Clostridium cluster IV).

1.1 butyrate meta

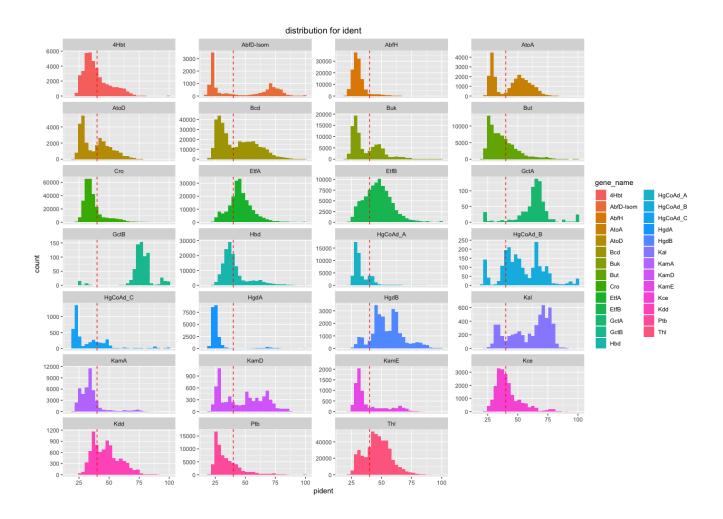
Table 1: butyprate producing genes database first look

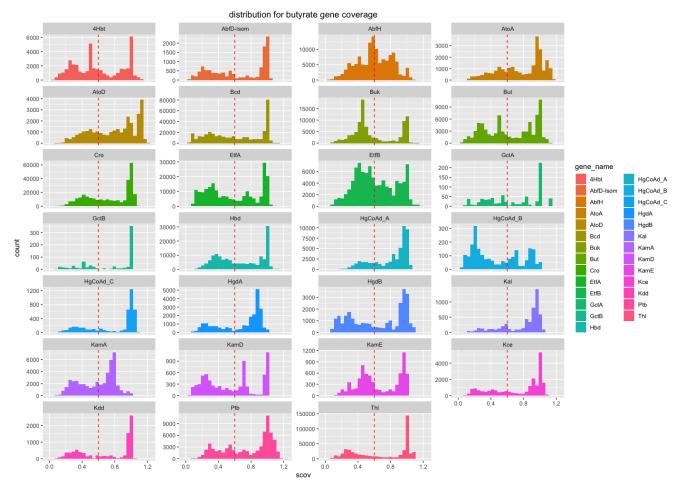
pathway_name	gene_name	n
4aminobutyrate	$4 \mathrm{Hbt}$	68
4aminobutyrate	AbfD-Isom	44
4aminobutyrate	AbfH	38
Glutarate	$\operatorname{Gct} A$	25

pathway_name	${\rm gene_name}$	\mathbf{n}
Glutarate	GctB	27
Glutarate	${\rm HgCoAd}_{\rm A}$	27
Glutarate	${\rm HgCoAd_B}$	27
Glutarate	${\rm HgCoAd_C}$	27
Glutarate	HgdA	27
Glutarate	$_{ m HgdB}$	28
Lysine	AtoA	62
Lysine	AtoD	62
Lysine	Kal	64
Lysine	$\operatorname{Kam} A$	74
Lysine	KamD	66
Lysine	KamE	66
Lysine	Kce	67
Lysine	Kdd	67
Pyruvate	Bcd	475
Pyruvate	Buk	106
Pyruvate	But	79
Pyruvate	Cro	209
Pyruvate	EtfA	254
Pyruvate	EtfB	250
Pyruvate	Hbd	205
Pyruvate	Ptb	92
Pyruvate	Thl	227

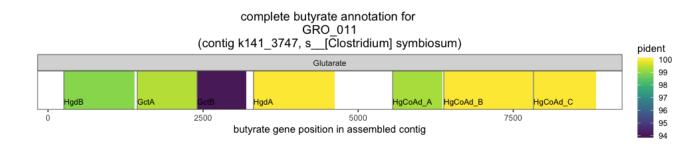
1.2 read in contigs

1.3 pident and scov





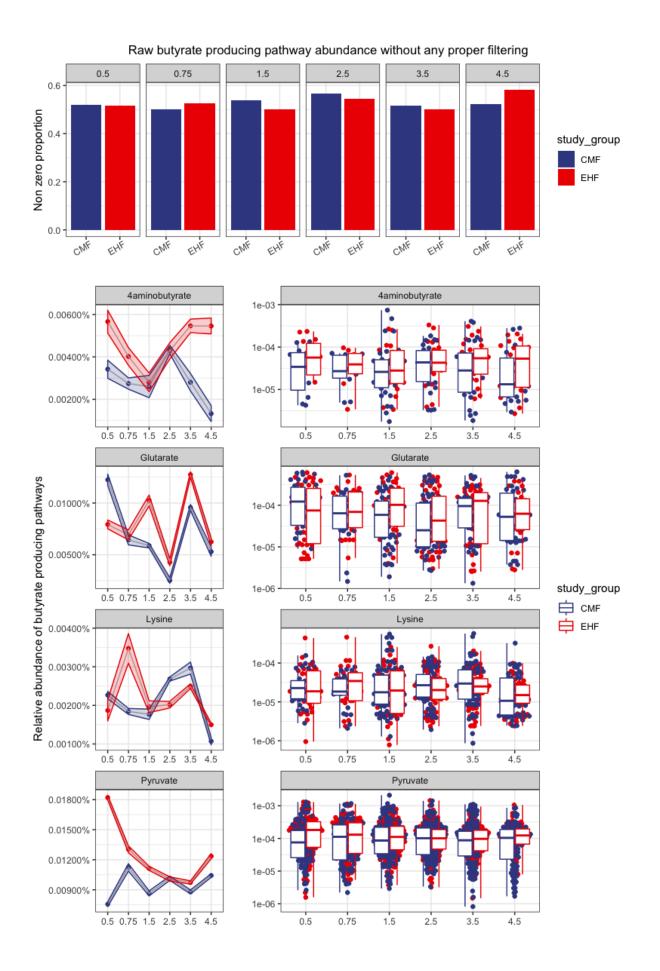
- set pident.cutoff to 40 and scov.cutoff to 0.6 for the downstream analysis.
- 1.4 per base coverage
- 1.5 merga data
- 1.6 a complete butyrate producing pathway



1.7 metadata

2 bysample: total pathway abundance

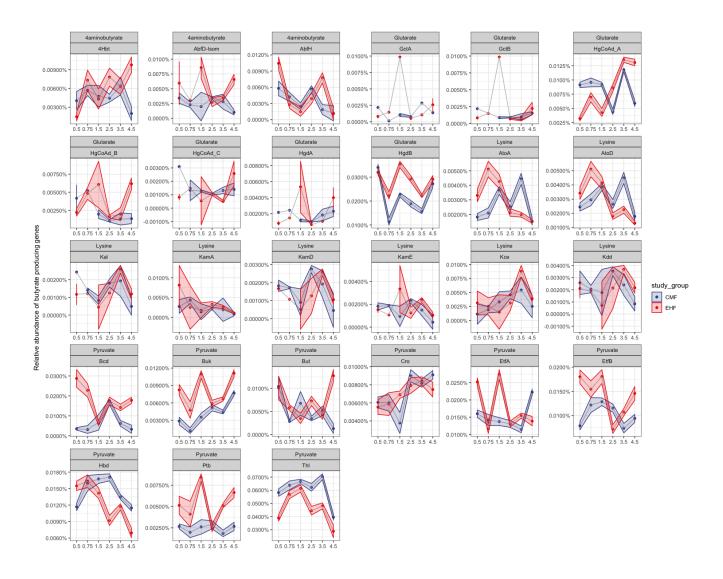
• non zero proportion and non zero regression



2.0.1 gene versus pathway

Table 2: lme result

gene_name	term	Value	Std.Error	DF	t.value	p.value	fdr
Bed	EHF	0.8196	0.2575	28	3.183	0.003558	0.08183
$_{ m HgdB}$	$study_month 0.75$	-0.5106	0.1125	108	-4.537	1.488e-05	0.0003423



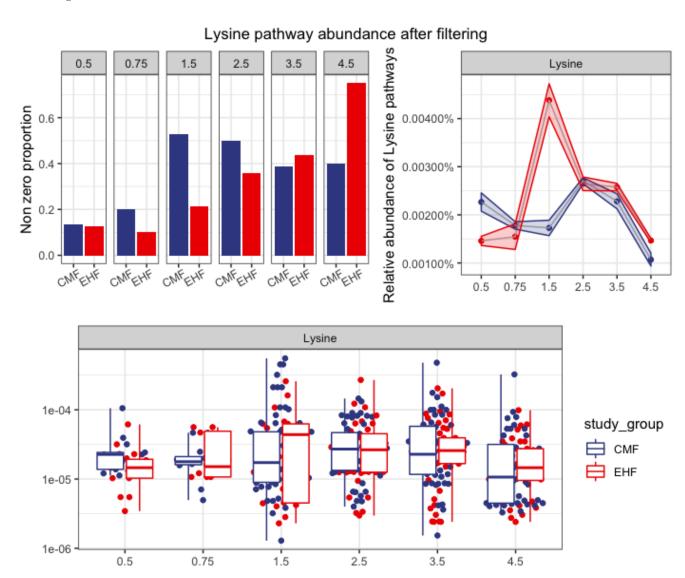
2.0.2 formula effect at 4.5 month

Table 3: lm result

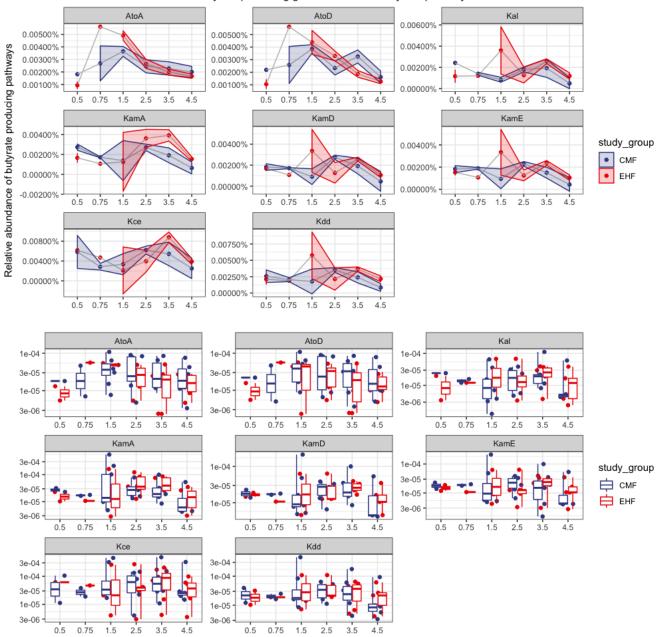
gene_name	term	estimate	std.error	statistic	p.value	fdr
Bcd	CMF-EHF	0.9482	0.4094	2.316	0.03332	0.2999
But	CMF-EHF	0.7213	0.4037	1.787	0.09182	0.3882
KamA	CMF-EHF	0.6796	0.2442	2.783	0.01275	0.2999
KamD	CMF-EHF	0.5419	0.2678	2.023	0.05908	0.3882
Ptb	CMF-EHF	0.7656	0.3145	2.434	0.02623	0.2999

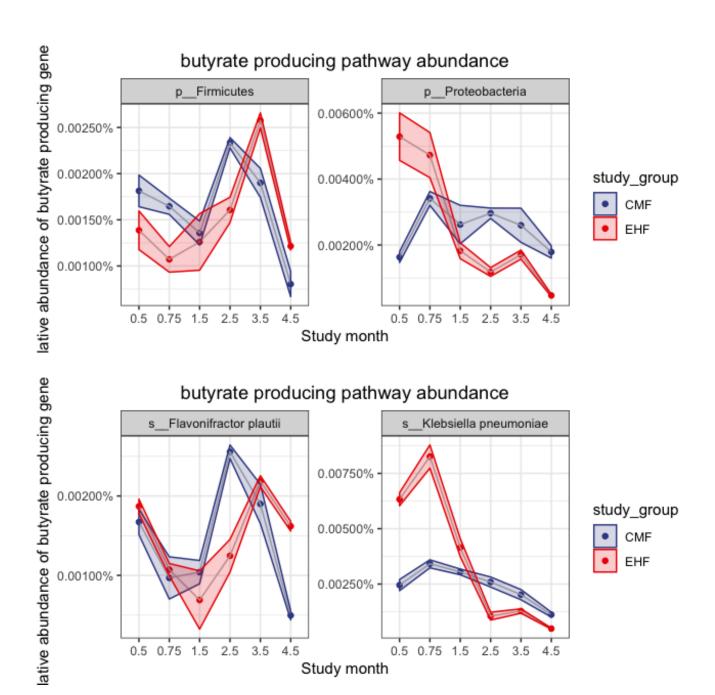
3 lysine pathway

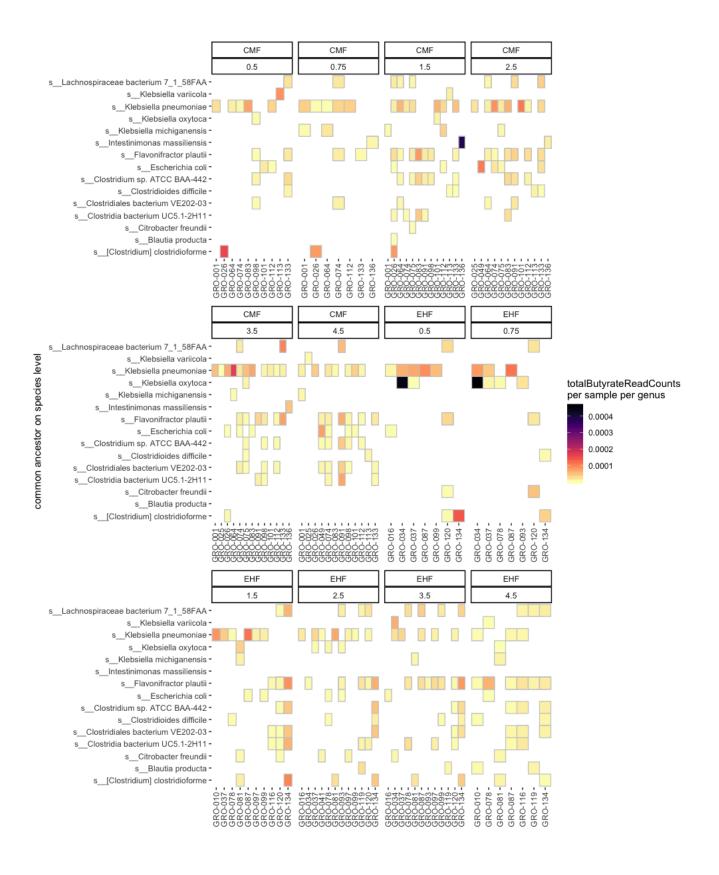
There are eight genes in the lysine pathway and we call present only when at least four genes were detected from the metagenomics data.



butyrate producing gene abundance in Lysine pathway







4 TCA cycle pathway

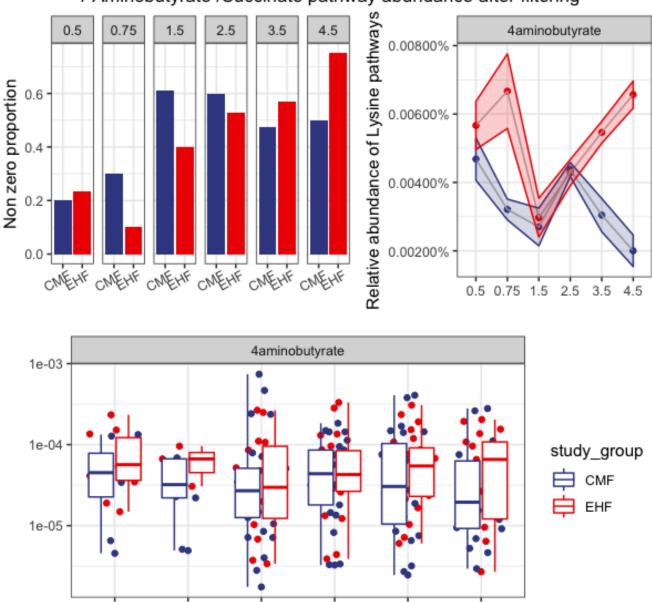
0.5

0.75

1.5

There are three genes in the lysine pathway and we call **present** only when at least **two** genes were detected from the metagenomics data.

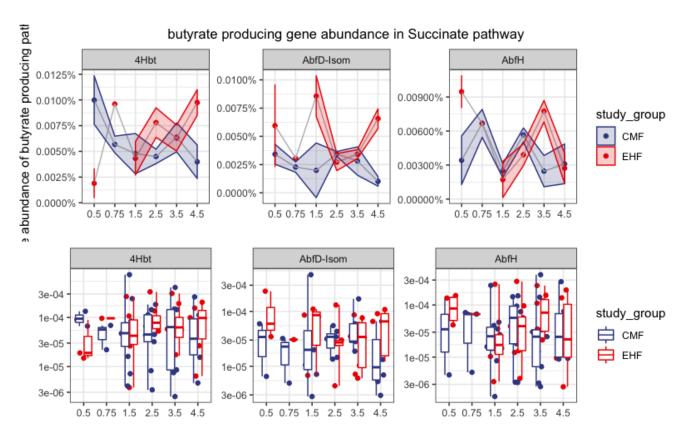
4-Aminobutyrate /Succinate pathway abundance after filtering

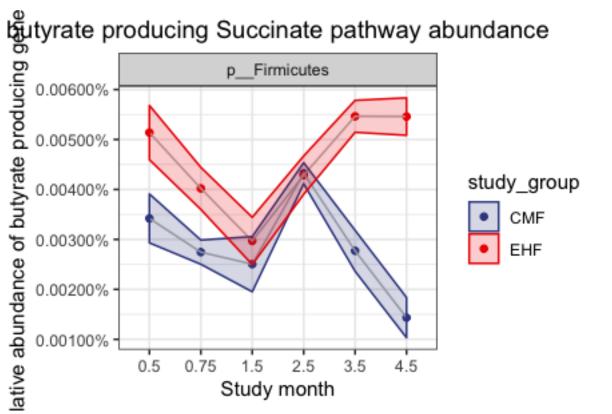


2.5

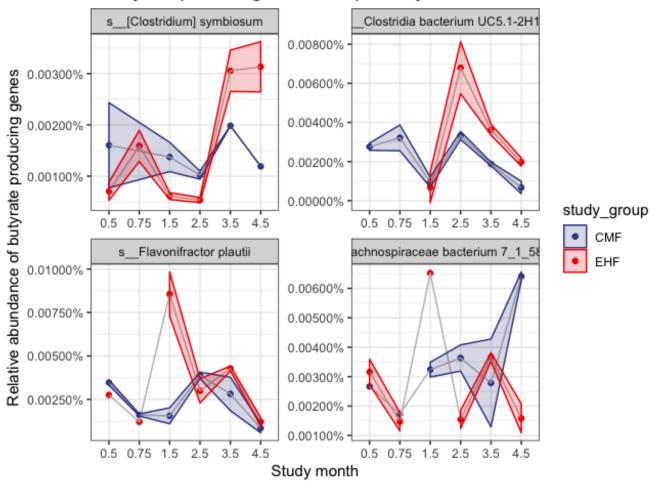
3.5

4.5





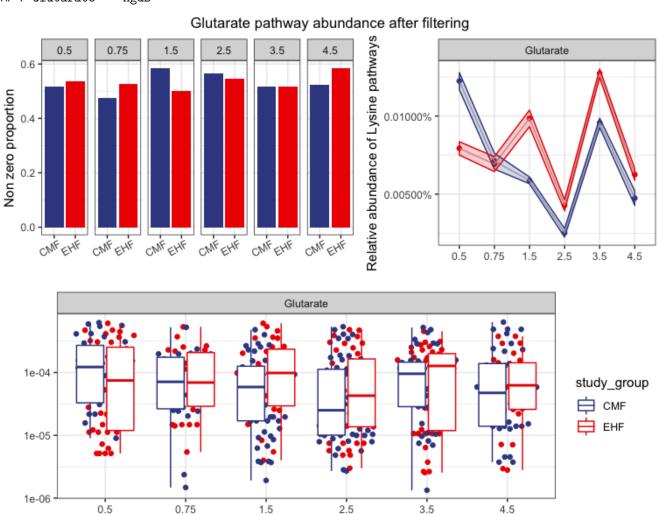
butyrate producing Succinate pathway abundance



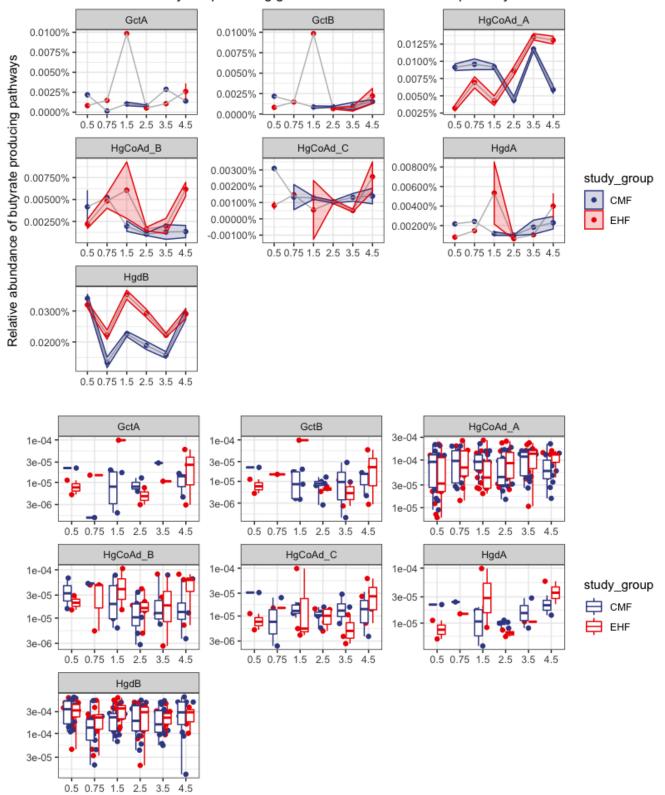
5 Glutarate pathway

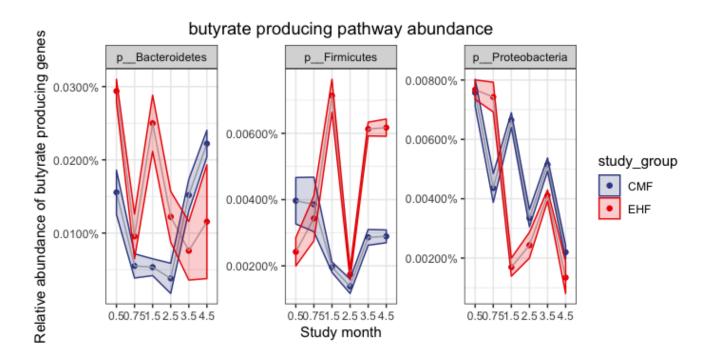
There are eight genes in the lysine pathway and we call **present** only when at least **four** genes were detected from the metagenomics data.

```
## # A tibble: 7 x 2
##
     pathway_name gene_name
##
     <chr>
                   <chr>>
## 1 Glutarate
                   GctA
##
  2 Glutarate
                   GctB
                   HgCoAd_A
##
  3 Glutarate
## 4 Glutarate
                   HgCoAd_B
                   HgCoAd_C
## 5 Glutarate
## 6 Glutarate
                   HgdA
## 7 Glutarate
                   HgdB
```

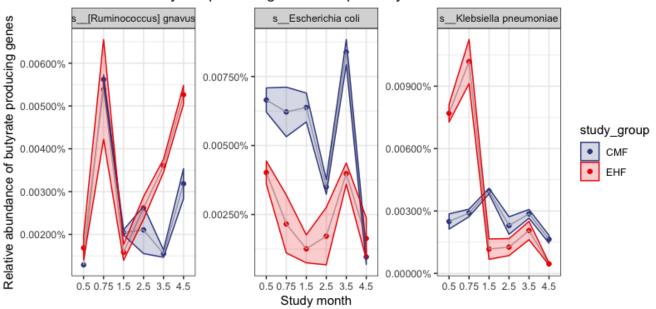


butyrate producing gene abundance in Glutarate pathway





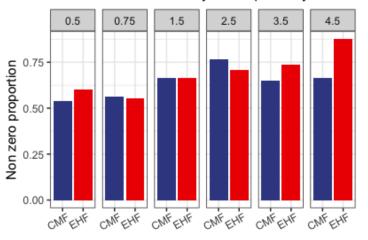


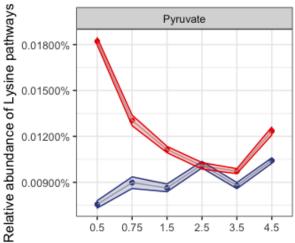


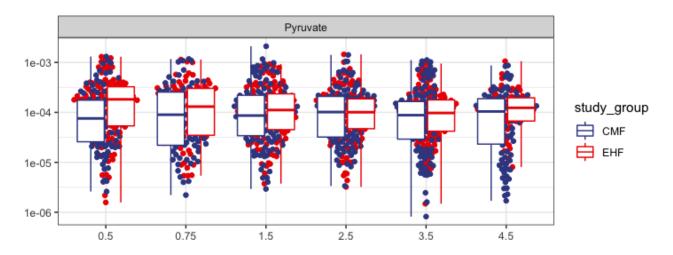
6 Pyruvate

There are night genes in the Acetyl-CoA pathway and we call **present** only when at least **four** genes were deteced from the metagenomics data.

Pyruvate pathway abundance after filtering







butyrate producing gene abundance in Pyruvate pathway

