1 **Interindividual differences in human intestinal microbial conversion**

2 **of (-)-epicatechin to bioactive phenolics**

3 Chen Liu,[*,†] Jacques Vervoort,[‡] Karsten Beekmann,[†,§] Marta Baccaro,[†]

4 Lenny Kamelia,[†] Sebas Wesseling,[†] Ivonne M.C.M. Rietjens[†]

5 [†] Division of Toxicology, Wageningen University and Research, Wageningen, The Netherlands

6 [‡] Laboratory of Biochemistry, Wageningen University and Research, Wageningen, The

7 Netherlands

8 [§] Present address: Wageningen Food Safety Research, PO Box 230, 6700 AE Wageningen, The

9 Netherlands

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Supporting information

Table S1. The limit of detection (LOD) and the limit of quantification (LOQ) of EC and its major colonic metabolites in LC-TQ-MS.

| Compound	EC	3,4-diHPV	3-HPV	3,4-diHPVA	3-HPVA	3,4-diHPPA	3-HPPA	3-HPAA	4-HPAA	Catechol
LOD (nM)	88.05	27.83	50.89	25.07	31.60	443.15	468.66	67.20	25.83	74.56
LOQ (nM)	266.83	84.32	154.20	75.98	95.76	1342.87	1420.18	203.64	78.28	225.93

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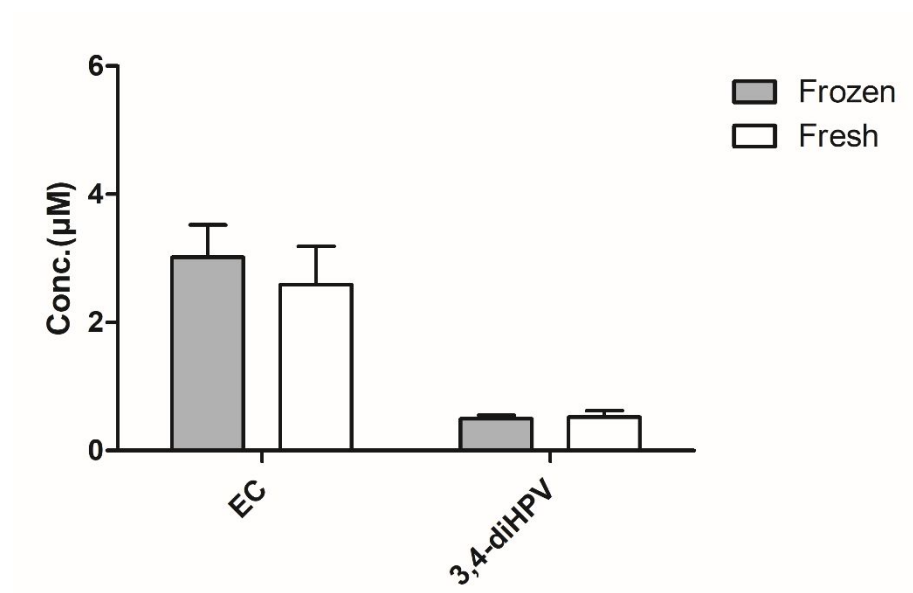
Figure S1. Residual EC and 3,4-diHPV formed in incubations with the fresh faecal

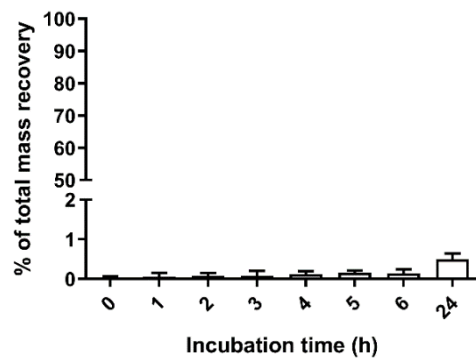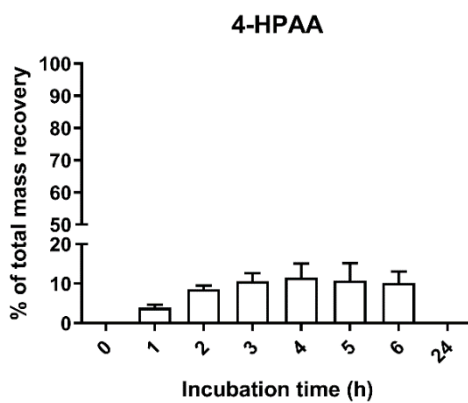slurry and the same faecal slurry but frozen for 1 week prior to incubation.

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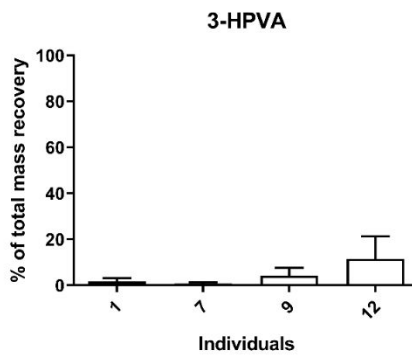
23
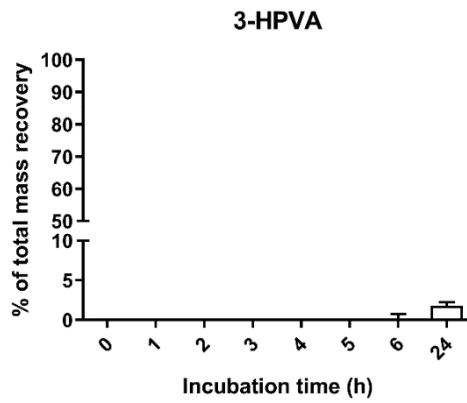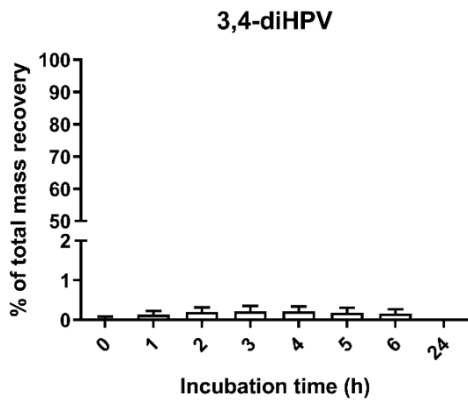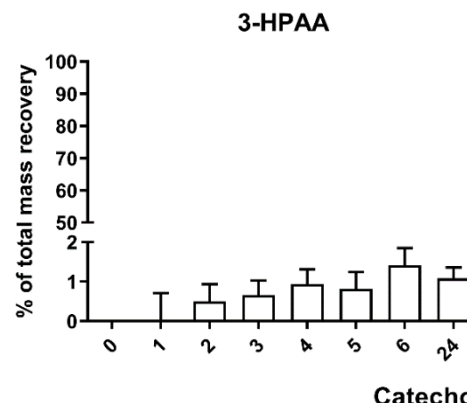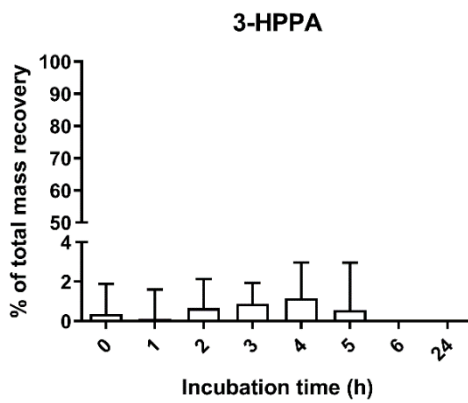
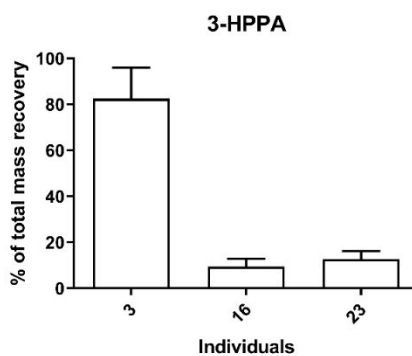**Figure S2.** Phenolic compounds quantified in the negative control samples (without adding EC in pooled faecal incubations) at different incubation timepoints. Results are shown as mean ± SD from 3 independent incubations.

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3,4-diHPV

3-HPVA

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3,4-diHPPA

3-HPPA

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3-HPAA

Gallic acid

30

4-HPAA
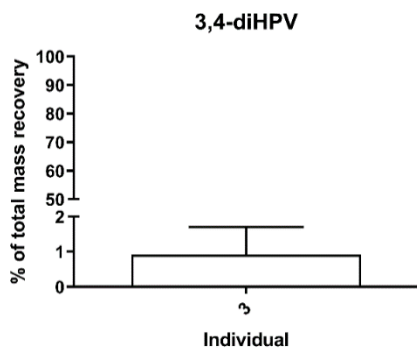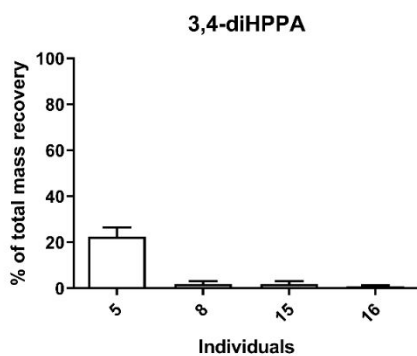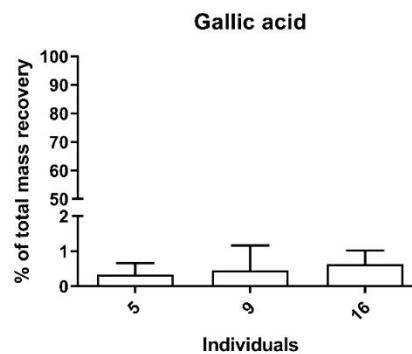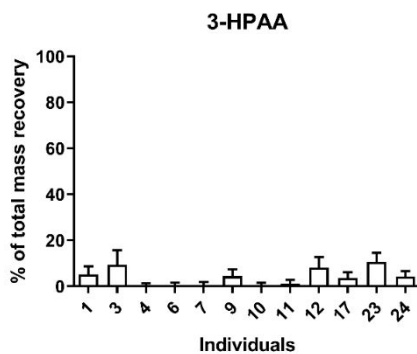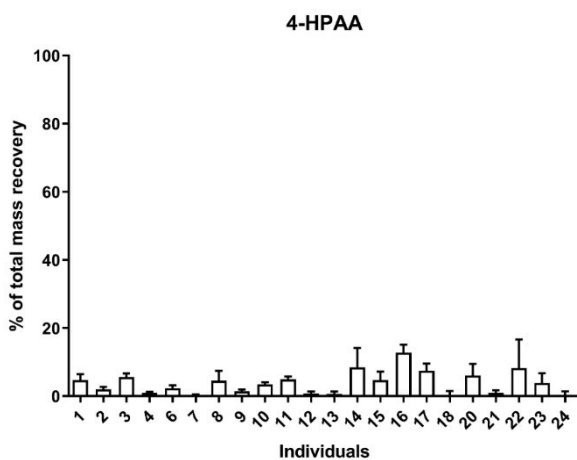
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32   **Figure S3.** Phenolic compounds quantified in different individuals in the negative

33   control (without adding EC in individual faecal incubations) at 2 h of incubations.

34   Results are shown as mean ± SD from 3 independent incubations. Values below the

35   LOD are not presented.

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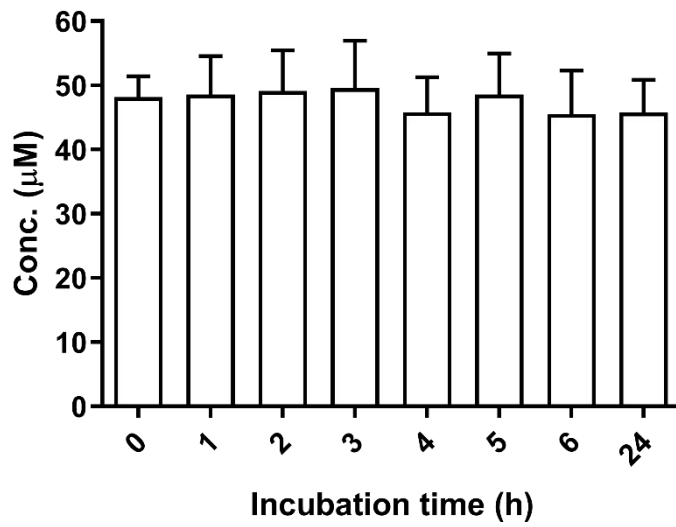
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38 **Figure S4.** EC contents of blank control (incubated without faecal slurry) at different

39 incubation timepoints. Results are shown as mean ± SD from three independent

40 incubations.

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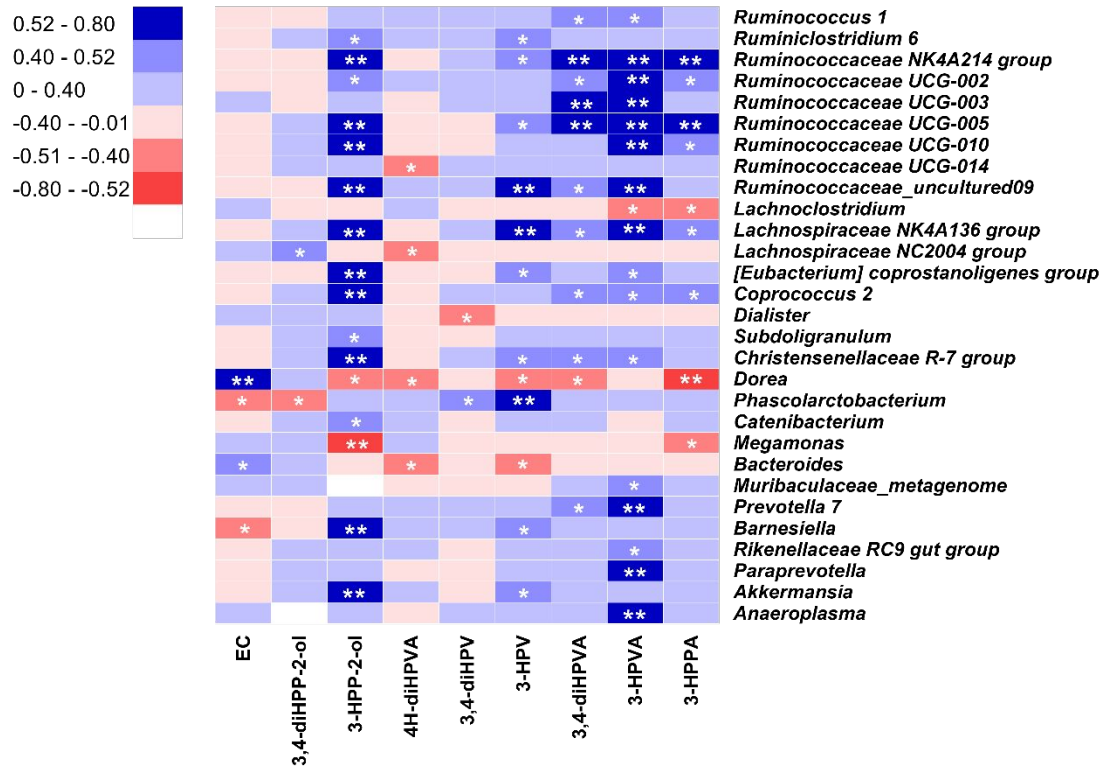**Figure S5.** PCA based on the concentration of residual EC and the 11 EC microbial metabolites present in incubations with faecal slurries from 24 individuals at 2 h.

Legend:

0.52 - 0.80
0.40 - 0.52
0 - 0.40
-0.40 - -0.01
-0.51 - -0.40
-0.80 - -0.52

Row labels (top to bottom):

Ruminococcus 1
Ruminiclostridium 6
Ruminococcaceae NK4A214 group
Ruminococcaceae UCG-002
Ruminococcaceae UCG-003
Ruminococcaceae UCG-005
Ruminococcaceae UCG-010
Ruminococcaceae UCG-014
Ruminococcaceae_uncultured09
Lachnoclostridium
Lachnospiraceae NK4A136 group
Lachnospiraceae NC2004 group
[Eubacterium] coprostanoligenes group
Coprococcus 2
Dialister
Subdoligranulum
Christensenellaceae R-7 group
Dorea
Phascolarctobacterium
Catenibacterium
Megamonas
Bacteroides
Muribaculaceae_metagenome
Prevotella 7
Barnesiella
Rikenellaceae RC9 gut group
Paraprevotella
Akkermansia
Anaeroplasma

Column labels (left to right):

EC
3,4-diHPP-2-ol
3-HPP-2-ol
4H-diHPVA
3,4-diHPV
3-HPV
3,4-diHPVA
3-HPVA
3-HPPA

**Figure S6.** Spearman correlations between the taxon abundances of bacterial genera and the concentration of residual EC and 8 EC microbial metabolites present in incubations with faecal slurries from 24 individuals at 2 h. The sign and strength of the Spearman correlation coefficients are represented as colours (blue: positive; red: negative). The significances of the correlations are indicated by asterisks: *$P < 0.05$, **$P < 0.01$.
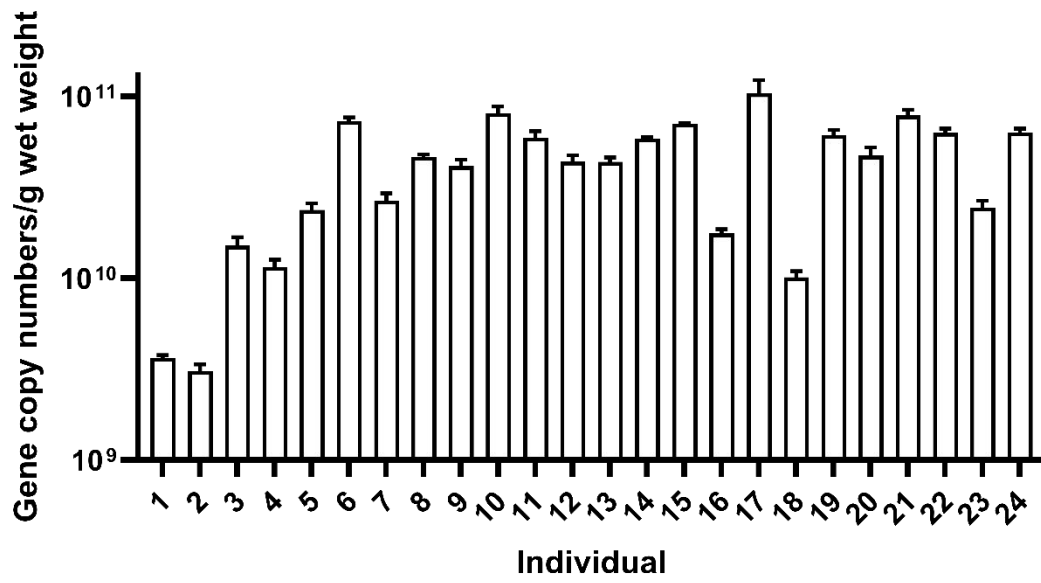
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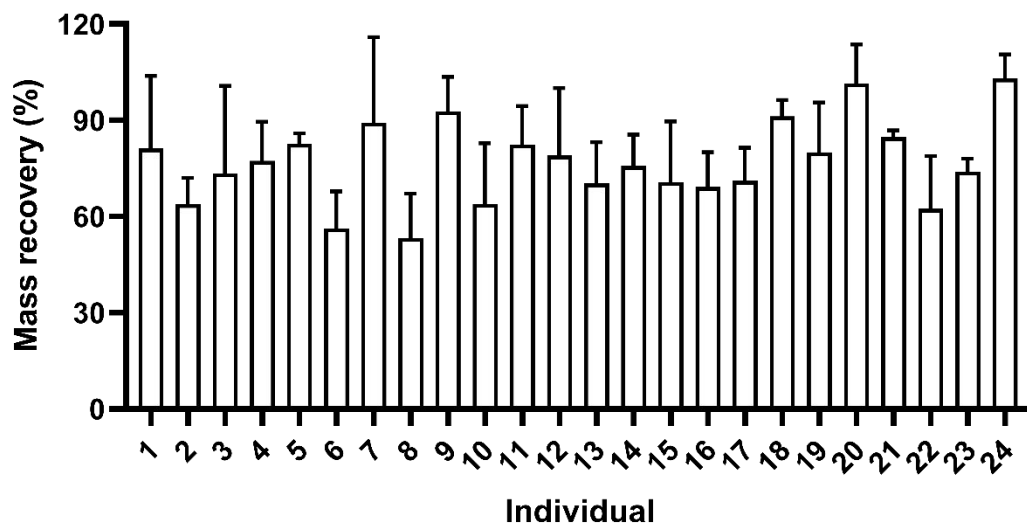
Figure S7. Total mass recoveries of 24 individuals for their EC faecal incubations at t

= 2 h. Results are shown as mean ± SD from three independent incubations.

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Figure S8. Bacterial load of 24 individuals, expressed as gene copy numbers per gram

of wet weight of faecal slurry (mean value $\pm$ SD, n = 3)