## **Supporting Information:**

*In silico* prediction and automatic LC-MS<sup>n</sup> annotation of green tea metabolites in urine

Lars Ridder\*<sup>1,2</sup>, Justin J. J. van der Hooft, <sup>1,3,5,†</sup> Stefan Verhoeven, <sup>2</sup> Ric C.H. de Vos, <sup>3,4,5</sup> Jacques

Vervoort, <sup>1,3</sup> Raoul J. Bino<sup>1</sup>

<sup>&</sup>lt;sup>1</sup> Laboratory of Biochemistry, Wageningen University, Dreijenlaan 3, 6703 HA, Wageningen, The Netherlands

<sup>&</sup>lt;sup>2</sup> Netherlands eScience Center, Science Park 140, 1098 XG Amsterdam, The Netherlands

<sup>&</sup>lt;sup>3</sup> Netherlands Metabolomics Centre, Einsteinweg 55, 2333 CC, Leiden, The Netherlands

<sup>&</sup>lt;sup>4</sup> Plant Research International, Wageningen University and Research Centre, P.O. Box 16, 6700 AA, Wageningen

<sup>&</sup>lt;sup>5</sup> Centre for BioSystems and Genomics, P.O. box 98, 6700 AB, Wageningen, The Netherlands.

Table S-1 Reaction rules for intestinal digestion and human phase II biotransformations

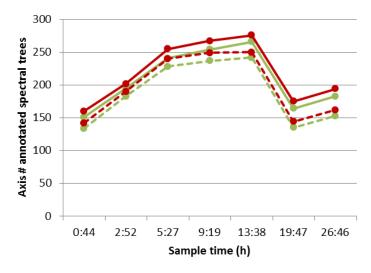
Rule	Smirks			
Conversions in the gut				
glycosidase	[CH1\$(C-&@O):1]-&!@[O:2][#6:3]>>[C:1]O.[O:2][#6:3]			
esterase	[C\$(C=O):1]-&!@[O:2][#6:3]>>[C:1]O.[O:2][#6:3]			
C-ring_fiss_1	[C\$([CH1]c2[cH1]ccc[cH1]2):1]1[CH1]([OH1])[CH2]c3c([OH1])[cH1] c([OH1])[cH1]c301>>[C:1]C(O1)CCC1=0			
lactone_hydrol1	[0:1]=[C:2]1[0:3][CH1\$(C[CH2]c2[cH1]ccc[cH1]2):4][CH2:5][CH2:6] ]1>>[0:1]-[C:2]1=[0:3].[C:4][C:5][C:6]1			
lactone_hydrol2	O=C10[CH1\$(C[CH2]c2[cH1]ccc[cH1]2):4][CH2:5][CH2:6]1>>O=C10.0[ C:4][C:5][C:6]1			
C-ring_fiss_2	[C\$([CH0]c2[cH1]ccc[cH1]2):1]1=C([OH1])C(=0)c3c([OH1])[cH1]c([OH1])[cH			
alpha-ox	[c:1][CH2:2]C(=0)[OH1]>>[c:1][C:2](=0)O			
beta-ox	[CH2:4][CH2]C(=O)[OH1]>>[C:4](=O)O			
reduction	[C;\$(C(=0)[OH1]):1][CH1:2]=[CH1:3][c:4]>>[C:1][C:2]-[C:3][c:4]			
p_dehydrox	[c\$(c1c[cH1]c([CH2]C)[cH1]c1):1][OH1]>>[c:1]			
decarbox	[c\$(c1ccccc1):1]C(=O)[OH1]>>[C:1]			
Phase II conjugations (only rules that applied to the set of tea compounds and their gut metabolites are shown)				
O-gluc_1	[C;!\$(C1CCCC1);!\$(C1CCCCC1);!\$(C(O)=O):1][O:2][H]>>[C:1][O:2] C1OC(C(O)=O)C(O)C(O)C1O			
O-gluc_2	[c:1][0:2][H]>>[c:1][0:2]C10C(C(0)=0)C(0)C(0)C10			
O-gluc_4	[C:1][C;!\$(C(0)(=0)C10CCCC1):2](=[0:3])[0:4][H]>>[C:1][C:2](=[0:3])[0:4]C10C(C(0)=0)C(0)C10			
O-gluc_5	[c:1][C:2](=[0:3])[0:4][H]>>[c:1][C:2](=[0:3])[0:4]C10C(C(0)=0) )C(0)C(0)C10			
O-sulf_1	[c:1][0:2][H]>>[c:1][0:2]S(=0)(=0)0			
O-sulf_2*	[C;!\$(C=0);!\$(CC[OH1]):1][O:2][H]>>[C:1][O:2]S(=0)(=0)O			
O-methyl	[c:1][0:2][H]>>[c:1][0:2]C			
glycination_1	[c:1][C:2](=[0:3])[O][H]>>[c:1][C:2](=[0:3])NCC(=0)O			
glycination_2*	[C!\$(CN):1][C:2](=[0:3])[O][H]>>[C:1][C:2](=[0:3])NCC(=0)O			

<sup>\*</sup> These rules were excluded in the "selected" set described in Table S-2  $\,$ 

**Table S-2** Effects of the number of reaction steps and selecting a subset of most common phase 2 biotransformation rules on the number of generated compounds and computation times.

The selection of most important rules was based on the criterion that more than 5% of the metabolites they predict for a large and diverse set of clinically studied compounds<sup>43</sup> agreed with the clinical observations. The selected rules included glucuronidation of aromatic as well as aliphatic hydroxyl and carboxyl groups, methylation and sulfation of aromatic hydroxyl groups only, and glycination of aromatic carboxyl groups only.

phase II rules	# reaction	# total	computation	#annotations
	steps	compounds	time (min.) *	presented in Fig S-1
selected	2	4905	6	
all	2	6086	7	<del></del>
selected	3	18952	30	
all	3	27245	41	<del></del>



**Figure S-1** The number of automatically annotated parent ions in seven consecutive urine sample data sets, after consumption of tea, using four different virtual metabolite libraries. Legend as indicated in Table S-2.

**Table S-3** Overview of the metabolites identified in urine. Consecutive columns provide details of the main original components in tea, the intermediate species that may be absorbed from the intestinal tract and the metabolites that were assigned to urine components on the basis of our automatic annotation. Compounds newly identified in the present urine samples are underlined. Asterisks indicate structures that were not present in PubChem (on Jan. 28, 2013)

Tea components	Intermediate after hydrolytic and microbiotic	Phase 2 conjugates generated and
	conversion rules	annotated in urine (# positional isomers)
Kaempferol	. OH	O-glucuronide
Kaempferol-3- <i>O</i> -glucoside	HO O.	o gracuromae
Kaempferol-3- <i>O</i> -polyglycoside		
1 1 363	у у у он	
	он о	
	Kaempferol	
(Epi-)afzelechin-3-O-gallate	OH	(Epi-)afzelechin-O-glucuronide
	но	(Epi-)afzelechin-O-sulfate
	ОН	
	ОН	
(Epi-)catechin	ОН	O-sulfate-O-methyl (4*)
(Epi-)catechin-3-O-gallate	но	
	OH	
	(Epi-)catechin	
(Epi-)gallocatechin	ОН	O-sulfate-O-methyl (2*)
(Epi-)gallocatechin-3-O-gallate	ОН	O-glucuronide-O-methyl (2*)
	но	O-sulfate-di-O-methyl (2*)
	ОН	
	ОН	
	(Epi-)gallocatechin	
(Epi-)afzelechin-3-O-gallate	OH OH	O-glucuronide(2*)
(Epi-)catechin	O O O O O O O O O O O O O O O O O O O	O-sulfate*
(Epi-)catechin-3-O-gallate	or 5-(4'-hydroxyphenyl)-γ-valerolactone	
(Epi-)catechin	οH	non-conjugated
(Epi-)catechin-3-O-gallate	OH	O-glucuronide (3*)
		O-sulfate (2*)
	or or	O-sulfate-O-methyl (2*)
	5-(dihydroxyphenyl)-γ-valerolactone	O-glucuronide-O-sulfate (1*)
		O-glucuronide-O-methyl (4*)
(Epi-)gallocatechin	OH ,OH	O-glucuronide (2*)
(Epi-)gallocatechin-3-O-gallate		O-glucuronide-O-methyl (3*) O-glucuronide-di-O-methyl*
	ООООН	O-sulfate (2*)
	5-(3',4',5'-trihydroxyphenyl)-γ-valerolactone	O-sulfate-O-methyl (2*)
		O-sulfate-di-O-methyl*
		O-glucuronide-O-sulfate*
(Epi-)afzelechin-3-O-gallate	он 💮	O-glucuronide*
	но	O-sulfate*
	Ö	
	4-hydroxy-5-phenyl-valeric acid	
(Epi-)catechin	OH OH	O-glucuronide (2*)
(Epi-)catechin-3-O-gallate	HO OH OH OH	O-sulfate (2*) O-glucuronide-O-methyl (4*)
	or o	O-sulfate-O-methyl (2*)

	4-hydroxy-5-dihydroxyphenyl-valeric acid	
(Epi-)gallocatechin (Epi-)gallocatechin-3- <i>O</i> -gallate	ОНОНОН	O-glucuronide-O-methyl (2*)
Chlorogenic acid	4-hydroxy-5-trihydroxyphenyl-valeric acid	Caffeic acid-O-sulfate*
(Epi-)gallocatechin-3- <i>O</i> -caffeate (Epi-)gallocatechin-3- <i>O</i> -ferulate	но	Ferulic acid- <i>O</i> -glucuronide (2) Ferulic acid- <i>O</i> -sulfate (2)
	Caffeic acid	
	но	O-sulfate O-methyl-O-sulfate (dihydroferulic acid-O-sulfate)
	3-(3,4-dihydroxyphenyl)propionic acid	
(Epi-)afzelechin-3- <i>O</i> -gallate (Epi-)catechin (Epi-)catechin-3- <i>O</i> -gallate (Epi)gallocatechin-3- <i>O</i> -ferulate (Epi-)gallocatechin-3- <i>O</i> -p-coumarate	ог	O-methyl-O-glucuronide (2*)
Quercetin, kaempferol	3-(hydroxyphenyl)propionic acid	<i>O</i> -sulfate
Querceini, kaempieroi	но	<u>O-surface</u>
(Epi-)catechin	Hydroxyphenylacetic acid	Non conjugated
(Epi-)catechin (Epi-)catechin-3- <i>O</i> -gallate	но	Non-conjugated Vanillic acid glucuronide (2*) Vanillic acid sulfate
	Protocatechuic acid	
(Epi-)catechin- <i>O</i> -p-benzoate (Epi-)gallocatechin- <i>O</i> -p-benzoate	но—Он	Non-conjugated Hippuric acid 2-hydroxyhippuric acid
	Hydroxybenzoic acid	3-hydroxyhippuric acid 4-hydroxyhippuric acid Methoxyhippuric acid
(Epi-)catechin- <i>O</i> -p-benzoate	HO.	O-glucuronide
(Epi-)gallocatechin- <i>O</i> -p-benzoate	Phenol	O-sulfate
	но	O-glucuronide O-sulfate O-methyl-O-sulfate (2x)
	Benzenediol (e.g. catechol)	
Gallic acid	он	O-glucuronide (1*+1)
Catechin-3- <i>O</i> -gallate Gallocatechin-3- <i>O</i> -gallate	HO	O-sulfate (2*) O-sulfate-O-methyl (5*)
Prodelphinidin- <i>O</i> -gallate (2)	но	O-sulfate-di-O-methyl*
Gallocatechin-catechin-gallate (3)	Benzenetriol (e.g. pyrogallol)	O-glucuronide-O-methyl (3)
Procyanidin-O-gallate (2)		O-glucuronide-di-O-methyl*
Epiafzelechin-3- <i>O</i> -gallate (1) Epicatechin 3,5-di- <i>O</i> -gallate (1)		O-glucuronide-O-sulfate* O-glucuronide-O-sulfate-O-
-rsteeming, and guillet (1)		methyl* di-O-glucuronide*

**Figure S-2.** The *in silico* pathways via which 3-(hydroxyphenyl)propionic acid-*O*-methyl-*O*-glucuronide is generated from (epi)gallocatechin-3-*O*-ferulate, caffeoyl-hexose, caffeoylquinic acids (e.g. chlorogenic acid) as well as (epi-)catechin, corresponding to the highlighted pathways in Figure 5. Green structures represent green tea components and red structures represent metabolites confirmed in the urine LC-MS<sup>n</sup> profile at t=9:19 h.