Additional files

FIG. S1: IolCatGC-positive genomes per species. The dot plot indicates the relative prevalence of *iol* gene-positive genomes belonging to the same species (left). The total number of genomes available for one species is given in a logarithmic scale. For most species, one representative genome sequence only was found in the databases (relative prevalence = 1). The colors indicated the phylum to which a genome sequence set belongs to (right). The plot was generated with the help of R package ggplot2 (3.3.2).

Table S1: Functions encoded by *iol* genes

xlsx-files:

Table S2: Summary table with representative species

Table S3: IolCatGC-positive species

Table S4: Values Sankey diagram

Table S5: Bacterial phyla overview of IolCatGC-positive species

Table S6: IolCatGC-positive species in bacterial genera

Table S7: Pathogenic bacteria harbouring IolCatGC

Table S8: Gut commensals harbouring IolCatGC

Table S9: Archaea with Iol protein homologs

FIG. S1: IolCatGC-positive genomes per species.

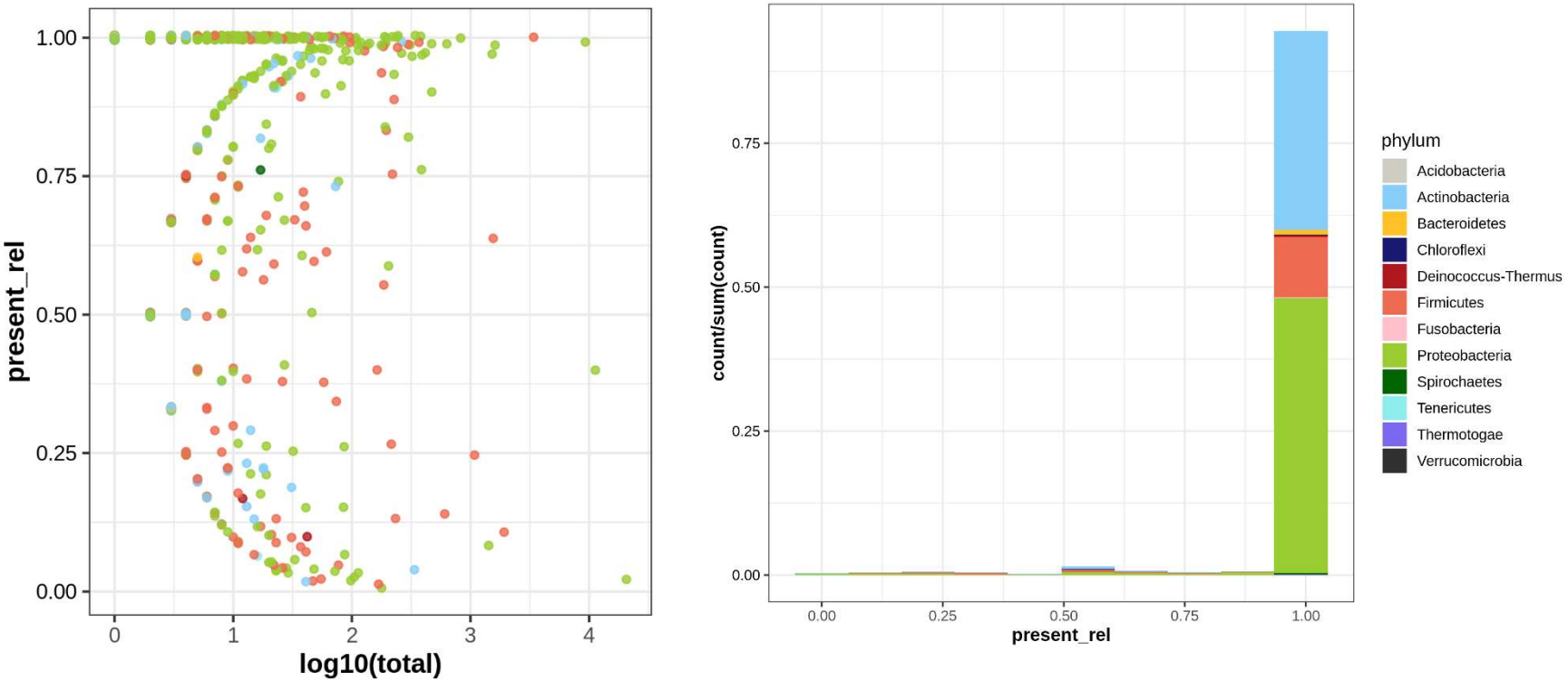

Table S1: Proteins and functions encoded by *iol* gene cluster

Gene	Protein	Function	Literature
iolA	Malonate-semialdehyde dehydrogenase	Conversion of malonic semialdehyde (MSA) to acetyl-CoA + CO_2	[1]
iolB	Isomerase	Isomerisation of 5-deoxy-D-glucuronic acid to 2-deoxy-5-keto-D-gluconic acid (DKG)	[1]
iolC	5-dehydro-2-deoxygluconokinase	Phosphorylation of DKG to DKG 6-phosphate	[1]
iolD	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase	Hydrolysis of 3D-(3,5/4)- Yoshida trihydroxycyclohexane-1,2-dione (THcHDO) to 5-deoxy-D-glucuronic acid	[1]
iolE	Dehydratase	Dehydratation of 2-keto-MI (2KMI) to THcHDO	[2]
iolG1	Inositol-dehydrogenase	Oxidation of of MI to 2KMI	[1]
iolG2	D-chiro-inositol-2-dehydrogenase	Oxidation of D-chiro-inositol to 1-keto-D-chiro-inositol	-
iolH	Isomerase/dehydratase	Unknown	[1]
iolI1	Isomerase	Interconverts 2KMI and 1-keto-D-chiro-inositol	[1]
iolJ	Fructose-1,6-biphosphate aldolase	Cleavage of DKGP into dihydroxyaceton-phosphate and MSA	[1]
iolR	Transcriptional regulator	Repressor of *iol* genes	[3, 4]
iolS	Pyridoxal reductase	Unknown	[1]
iolT1	Permease	Uptake of MI	[5, 6]
iolT2	Permease	Uptake of MI	[5]
iolU	Scyllo-inositol dehydrogenase	Dehydrogenation of scyllo-inositol to 2KMI	[7]
iolW	Scyllo-inositol dehydrogenase	Dehydrogenation of scyllo-inositol to 2KMI	[8]
iolX	Scyllo-inositol dehydrogenase	Dehydrogenation of scyllo-inositol to 2KMI	[8]
reiD	Transcriptional regulator	Activation of P_{iolEG1}	[9]
srfJ	putative lysosomale glykosylceramidase	Unknown, induced by SsrB	[10]

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