

**Supplementary Table 5. Bile salt hydrolases found in genomes of defined community members. Related to Figure 6.**

%ID calculated from amino-acid level alignments by blastp

% deconjugation of TCA: [cholic acid] after treatment / [taurocholic acid] input * 100 (Song et al 2019)			39.89%	101.75%	0.73%	102.05%	95.71%	38.16%	2.89%	39.85%
			Percent amino acid identity by <i>bsh</i> phylotype							
Species	Defined Community	Locus	BSH-T0	BSH-T1	BSH-T2	BSH-T3	BSH-T4	BSH-T5	BSH-T6	BSH-T7
<i>Bacteroides caccae</i>	CR	BACCAC_03140	26.47	24.85	20.75	22.04	22.05	28.4	83.81	23.57
<i>Bacteroides thetaiotamicron</i>	CR	BT_2086	25.49	24.54	20.44	22.36	22.04	28.82	83.86	26.97
		BT_1259	24.17	19.59	23.44	22.18	23.17	26.4	53.89	29.59
<i>Bacteroides uniformis</i>	CR	BACUNI_02933	28.44	27.49	30.03	27.19	29.6	100	30.14	29.21
		BACUNI_00572	26.94	25	22.61	22.44	22.08	30.14	100	30.09
<i>Bacteroides vulgatus</i>	CR,SR	BVU_2699	27.81	29.31	29.13	25.74	30.62	58.15	30.26	50
		BVU_3993	26.56	24.62	21.77	23.47	22.77	28.53	86.26	32.95
		BVU_1032	22.22	45.45	58.33	33.33	29.41	54.55	50	20.65
<i>Bifidobacterium longum</i> subsp. <i>longum</i>	CR	BLLJ_0817	27.68	41.38	36.91	35.44	100	29.6	22.44	36
<i>Blautia obeum</i>	CR,SR	RUMOBE_00028	26.78	76.31	59.69	47.38	39.18	28.08	23.05	24.18
		RUMOBE_03454	27.08	75.62	58.46	50.46	40.13	30.38	25.08	23.57
<i>Blautia torques</i>	CR	ERS852577_00637	28.76	72.24	56.85	46.73	40.31	28.22	22.92	26.61
		ERS852530_03853	27.67	69.14	57.23	49.86	38.99	32.07	24.44	27.04
		ERS852577_05096	27.08	75.31	58.46	50.77	39.38	30.7	25.08	23.57
<i>Collinsella aerofaciens</i>	CR	COLAER_00574	27.37	36.55	33.77	34.67	50.99	28.23	20.07	42.86
		CSV91_00430	27.52	35.97	33.86	35.03	50.95	28.63	20.7	22.06
		CSV91_05910	32.56	25	24	47.06	25.29	38.45	29.17	23.44
<i>Dorea longicatena</i>	CR	DORLON_01571	27.08	75.62	58.46	50.46	40.13	30.38	25.08	23.57
<i>Eubacterium rectale</i>	CR	EUBREC_2835	28.76	72.24	56.85	46.73	40	22.82	22.92	26.61
<i>Faecalibacterium prausnitzii</i>	CR	FAEPRAA2165_00537	25.7	69.52	57.91	48.57	41.5	31.82	22.01	31.58
<i>Enterococcus faecalis</i>	DS	OG1RF_12285	98.87	26.01	26.67	26.28	27.68	27.52	26.26	26.67
<i>Streptococcus infantarius</i>	DS	STRINF_01499	25.98	57.06	100	47.85	36.76	30.03	2.61	27.68
<i>Vibrio cholerae</i>	N/A	VCA0877	25.42	22.63	21.94	22.58	22.74	24.72	45.53	22.58

Root-Mean-Square Distance (RMSD) of spatial variation between predicted structure of RUMOBE\_00028 vs indicated phylotypes

			<b>BSH-T0</b>	<b>BSH-T1</b>	<b>BSH-T2</b>	<b>BSH-T3</b>	<b>BSH-T4</b>	<b>BSH-T5</b>	<b>BSH-T6</b>	<b>BSH-T7</b>
<i>Blautia obeum</i>	CR,SR	RUMOBE_00028	4.051	0.000	0.299	0.294	2.171	3.941	4.862	12.396